GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR

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GAM15 TACATATCTTGAATGTGATC 710 ATAATATTGT 3780 A C ATATA--- - GAGC T AAAA AT

CATTATATATTGAGTCATTA AAATAATGAC G ATGTGATC ATT TTGA GTCATTA CA TA ATTTAAAAT T

GAGCCATTAAAAAATTTAAA ATTA | |||||||| ||| |||| ||||||| || || |||||||||

ATATTTAATTTTAAATAATA T TATATTAG TAA Aatt cagtaat gt at taAATTTTA /

TTGTAAATAATGACATTAAA A C AACCGTTA a aaat t aa-- AT

TTGCCAAAATCGATTATATA

TATTAAATGTA

GAM16 CCGCGCGCGCATGACTACCT 711 CATGACTACC 3781 G Gca g g ga AC G TG

GGGCCAGGTTGAGCGCCACC TGGGCCAGGT CCGC CGC tgactacctg gcca gtt gCGCC CAGGCG T A

AGGCGGTTGAAGGGCGCCTG TGAG |||| ||| |||||||||| |||| ||| ||||| |||||| |

CAGGCGCAGGGCGTGGTGCA GGTG GTG GTTGATGGAC TGGT CGG CGCGG GTCCGC G /

GGTAGTTGAGGGTGGTGG - GGA G G GA AC G GA

GAM17 TCAATAATATACCGCACACT 712 TACCGCACAC 3782 AATAta a ctt tg c tt

TTTATTGCCCCTTTTGTGGC TTTTATTGCC TCAAT ccgc ca ttat c cc T

GTGGTGATTGGCGGAGAGGG CCTT ||||| |||| || |||| | ||

TTGG GGTTG GGCG GT AGTG G GG T

GGAGA- - T-- GT C TG

GAM18 CACTCTGTTACCCCTTTTTA 713 TGTTACCCCT 3783 C tg- ttaactctctaaC TT TATA

ACTCTCTAACATTTTTCTTT TTTTAACTCT CA TC ttacccctttt ATTTTTCT GTTT A

GTTTTATAAGATATAGGCCC CTAA || || |||||||||| |||||||| ||||

AGGAAGATATTCATTTGGAG GT AG AGTGGGGAGG TAGAAGGA CGGA G

GGGTGAACTGAATG A TCA TTTACTTA----- CC TATA

GAM19 TTCTGCACAAGACAGATTGA 714 ACAGATCCTA 3784 CAC C AGCA CC TTT

GCAAGGATCTCCGTTTTACC ACCCAATCTA TTCTG AAGA AGATTG AGGATCT GT A

ACACACAGATCCTAACCCAA TCTT ||||| |||| |||||| ||||||| ||

TCTATCTTACACAGAA AAGAC ttct tctaac tcctaga CA C

ACA a ccaa ca CAC

GAM20 TGTAGCATGTTTAAAAAAGT 715 AAAGTAACAA 3785 CATG- ac caccg tc GTG

AACAAGTCACCGCCTCATCA GTCACCGCCT TGTAG TTTAAAaaagta aagt cctca ACCTGCT T

CCTGCTGTGTTTAAGGTAGG CATC ||||| |||||||||||| |||| ||||| |||||||

TTTTGGGGGCTTACTGCTTT ATATT AAATTTTTTCGT TTCG GGGGT TGGATGG T

TTTAAAAAAATTTATA TAAAA CA ----- TT AAT

GAM21 CGGTGTCGCGCAGGGCGTAG 716 TCGGAGCTGT 3786 G - A - G G G AGC
AGCTTGGGGGCGAGCAGGAC GGGCGTCGCT CG TGTCGC GC GG GC TA AGCTT GGGGCG
A
CGTCTCGGAGCTGTGGGCGT GCGG || |||||| || || || || ||||| ||||||
CGCTGCGGCAGCG GC ACggcg cg ct cg gt tcgag ctCTGC G
G t - g g g g CAG

GAM22 CCACGGGCCCGGTGACTCGG 717 TTCCACGGAA 3787 - CGG-- C --- - GA
AACCTGAAAGAGAGTTCCAC TCAATGTCGG CCACGG GCC TGA TC GGAAC CT A
GGAATCAATGTCGGCATCGT CATC |||||| ||| ||| || ||||| ||
GG GGTGct cgg act ag ccttG GA /
a ctgta a gca A GA

GAM23 TTCATAAACCCTCGCTCACC 718 TAACTTGTTG 3788 C C-- CACCATCTATCAAAA CA
TTC
ATCTATCAAAAAACAAGCAA CCTCAGCTAA TTCATAAA CCT GCT AACAAG AAAGT A
AAGTTTCAGCTCACTTTAAC AGGT |||||||| ||| ||| |||||| |||||
TTGTTGCCTCAGCTAAAGGT AGGTGTTT gga cga ttgttc tTTCA G
TTTGTGGA t aat ctccg---------- aa CTC

GAM24 GTTAAATAAAAATATAAATG 719 TGAAATTATA 3789 A- - G GT
TTATATGTTAAAATGTGAAA TATCATTTGT GTTAAATAAA ATATA AAT TTATAT T
TTATATATCATTTGTTTAAT TTAA |||||||||| ||||| ||| ||||||
Taatttgttt tatat tta agtGTA A
ac a a AA

GAM25 GCAGATCTTATGCTTGTCAG 720 TTAAAGCCCG 3790 CTTATGCT a cc - ttttt
TTAAAGCCCGGAATGTTTTT GAATGTTTTT GCAGAT TGTCAGtta agc ggaat gtt t
TTTTAATTAACAATTCCTGC TTTT |||||| |||||||| ||| ||||| |||
TGTAACTGACACAACAAAAT CGTCTA ACAGTCAAT TCG CCTTA CAA /
CTGC AAACAAC- G T- A TTAAt

GAM26 GTAGCTAGGGTGGTGAGTGG 721 TGGTGAGTGG 3791 A tg t gc gc A
CGCTCGCAGCAGCTAGTGAG CGCTCGCAGC GTAGCT GGG g gagtg gctc agcagct G
CTGCTGAGCAACACTCCCTG AGCT |||||| ||| | ||||| |||| |||||||
CCCCAGCTAC CATCGA CCC C CTCAC CGAG TCGTCGA T
C GT C AA -- G

GAM27 GGGTGTGGTCCGGACCGCTG 722 TCCCAGGCGA 3792 TG GGA TGC- CTCGC C
CGGTAGTTGCCCTCGCAGAT CTACCTCCTG GGG TGGTCC CCGC GGTAGTTGCC AGAT
T
CTGGGTCTCCCAGGCGACTA CGGG ||| |||||| |||| |||||||||| ||||
CCTCCTGCGGGGGGATCATG CCT ACTAGG ggcg ccatcagcgg tCTG G
TCC GT Gg- tcct accc- G

GAM28 GCGCAAAAGACCCCTAGGGA 723 TTTATAGTCT 3793 GC- - CC---- A G- AG T - T T
GAGGAGGTAAGCTAGGTGTG CTAACCAGGA GC AAAA GA CCT GG AGAGG GTAAGC
AGGTG TG GTT A
TGTTTAATAACCATCACCTG TATA || |||| || ||| || ||||| |||||| ||||| || |||
TTTATAGTCTCTAACCAGGA CG TTTT CT gga cc tctct tatttG TCCAC AC CAA A
TATATTCATTTTTAAGC AAT A Tatata - aa ga - T - T

GAM29 TCGTGAATTTTGATTTTTTA 724 TAAAAAGTTT 3794 ------ TTT-- ACCAT
AAACCATTAACTAATTTAAA AATTATTCCA TCGT GAAT GATTTTTTAAA T
AAGTTTAATTATTCCAAATA AATA |||| |||| ||||||||||
ATGA AGTA ctta ttgaaaaatTT A
ataaac ttaat AATCA

GAM30 AGGTGAGCTCCACGTAGGAT 725 AGAGAGCACC 3795 AGCTCCAC G ATACAA A
TTATA
AGCTTAAGATACAATCTCAG TTAAGCTATC AGGTG GTA GATAGCTTAAG TCTC GT C
TTTATACAACACTACAGAGA ATAC ||||| ||| |||||||||| |||| ||
GCACCTTAAGCTATCATACC TCCAC cat ctatcgaattc agag CA A
TAAAACACACCT ACAAAATC a cacg-- a TCACA

GAM31 TTGCTCAACATTTTAATTTT 726 TTTAATTTTA 3796 C- A ttatcttt- t
ATCTTTAATGTTAACATTTT TCTTTAATGT TTGCT AAC Ttttaatt aatg t
AAACTGCAGTTAAAAGTTTT TAAC ||||| ||| |||||||| ||||
AGTAA AATGA TTG AAAATTGA TTAc a
TT - CGTCAAATT a

GAM32 AGAGGGCGTTGGAGAGAAGC 727 TGGAGAGAAG 3797 G Tt-- g tggc g
TTGGCGATGCTGCGGAGCGT CTTGGCGATG AGAGG CG gga agaagct gatgct c
TTGGTTTCTGTCCCGGTCGG CTGC ||||| || ||| ||||||| ||||||
CCTTT TTTCC GC CCT TCTTTGG TTGCGA G
G TGGC G T--- G

GAM33 CCATTAAATAAATTAAAAAA 728 TAAATTAAAA 3798 TTAA aaaa aata - ATCA AA
ATTGGAAATATTGGAATGTA AAATTGGAAA CCA Ataaatta aattgga ttGG AATGTA TTTT T
ATCATTTTAATATAGAAAAA TATT ||| |||||||| ||||||| |||| |||||| ||||
CATACATTACCAAATTCAAT GGT TATTTGAT TTAACTT AACC TTACAT AAAG A
TACTAGTTTATCATTGG TAC- CA-- A--- A ACAA AT

GAM34 GGTGAGAAAGGCTTTTCACG 729 ATGGTGCTCA 3799 AGAAA TTTT ACTT- C -
ATTCCT
CATACTTGCACTGTCAGCAG ACATGCGTGC GGTG GGC CACGCAT GCACTGTCAG
AGTTAT TGT A

TTATTGTATTCCTAACACCA GCCA |||| ||| ||||||| |||||||||| |||||| |||
ACACATAACTACTGATGGTG CCAC ccg gtgcgta cgtggtaGTC TCAATA ACA /
CTCAACATGCGTGCGCCAAA AAa-- c--- caact A C ACCACA
CACC

GAM35 GAAACTTTAAAATTTATATT 730 TTCATGTAAA 3800 AA TAt a a t -- TAA- C CTT
AA
CATGTAAAGTTTTAAGCTTA GTTTTAAGCT ATTTA tc tgtaa gttt aagc ttacaAAAT AT AGGG
CAA A
CAAAATTAAATCAGGGCTTC TACA ||||| || ||||| |||| |||| ||||||||| || |||| |||
AAAAAAGATTGTTTTTCTAG TAAAT AG ACATT CGAA TTTG GATGTTTTG TG TCTT
GTT A
TATATGTTTTGTAGATGTTT -- TTT - - T TA TATA A TTT AG
TAAGCTTACAGATTTTAAAT
TAGGGCTTC
GAM36 TGCAGCAGATGTGCCACGGG 731 AGGTGGGTGC 3801 A A C - CCa gtg gtag----------
- c
CACGTCCCGGTCGGCGTCCA GACCGTAGCC CGGGC CGTCC GGTCG GCGT ggtgg cgacc
ccc g
GGTGGGTGCGACCGTAGCCC CCGC ||||| ||||| ||||| |||| ||||| ||||| |||
CGCAGGGGGCGCAGCAGCGC GTCCG GTAGG CCGGC CGCG CCACC GCTGG
GGG c
CAGGTCGGCCACCACGCGCT C - A T CA- G-- ACCGCGACGACGCGG A
CGGCCAGGATGGCCTGCTGC
ATGCGCTGCA
GAM37 CTGTCACTCATGCCAGTACA 732 TCACTCATGC 3802 - tc a--- GTTTA
CTCGCACCCGTAGTGTTTAT CAGTACACTC CTGtcactcatg ccagtacac gc cCCGTAGT T
ACATAAACTACGGGGGAAGC GCAC |||||||||||| ||||||||| || |||||||
TTGTGTACTGGATATGAGTG GACAGTGAGTAT GGTCATGTG CG GGGCATCA A
ACAG A TT AAGG AATAC

GAM38 CGCGCATGAGCATGCCCTGT 733 TCCATGGGCA 3803 C A - - T - - AG C
ATGCCTCAAGTTTCATAGAG GTGCGCATGC CG GCATG GCA TGCCC TG AT GCCT CA TTT A
TATGTAGGTGATCCATGGGC CG || ||||| ||| ||||| || || |||| || |||
AGTGCGCATGCCG gc cgtac cgt acggg ac tA TGGA GT GAG T
- g g t c G T AT A

GAM39 GTGTCTAGTGACAGACAGGG 734 CACCCGCTCA 3804 - A - G AT CTCCTT
AGTGGATTGCGCTCCTTAAA CTGTCTGTCT GT GTCT GT GACAGACAG GAGTGG TGCG A
CTCCCGCACCCGCTCACTGT ACAG || |||| || ||||||||| |||||| ||||
CTGTCTACAGACTAC CA CAga ca ctgtctgtc ctcgcc acGC /
T - t a c- CCTCAA

GAM40 GTAATAAGTTAAATAAAAAT 735 TAAGTTAAAT 3805 aa a- - g GT
ATAAATGTTATATGTTAAAA AAAAATATAA GTAAt gttaaataaa atata aat tTATAT T
TGTGAAATTATATATCATTT ATGT ||||| |||||||||| ||||| ||| ||||||
GTTTAATAATTAC CATTA TAATTTGTTT TATAT TTA AGTGTA A

A- AC A A AA

GAM41 CTGAGAAGTCATCCAGGTCC 736 TCCAGGAACC 3806 AA G gga - ag gc-- AT TAGG
AGGAACCGGTGGTAGGCGCC GGTGGTAGGC GAG GTCATCCAG tcca acc ggtggt gc ccGTGTTG GGTG A
CGTGTTGATGGTGTAGGAGC GCCC ||| ||||||||| |||| ||| |||||| || |||||||| ||||
AGTTGCCCAGCACGGACCAG CTC CAGTAGGTC GGGT TGG CCACCA TG GGCACGAC CCGT G
TTGACCACCTGGTAGTGGGG -- G GA- T GT ACCA -- TGAC
CTGGATGACCTCGG

GAM42 TGTCTCTTGCTAGGTAGCCT 737 TCTCTTGCTA 3807 tc t c - c t GTC T A
GTACAAAACAGTCCTTTTTT GGTAGCCTGT TG tc tg taggt ag ctg acaaAACA CT TTTTA T
AATGTAAAACAGTGTTTTGT ACAA || || || ||||| || ||| |||||||| || |||||
CCAGACTAGCCTAACACGAA AC AG AC ATCCG TC GAC TGTTTTGT GA AAAAT / CCA CA C A A A C --- C G

GAM43 TCCTGCAGCACCCCCGGTCC 738 TCGCGCAGCA 3808 G G CC G- C --- AC -- T
CGCGCGCTGACCGCGCAGCT CTGCCGGGAC TCCT CA CA CCC GTCCCG GC GCTG CGCG CAGC G
GCTGCTGATCGCGCAGCACT GAGG |||| || || ||| |||||| || |||| |||| ||||
GCCGGGACGAGGGCATGGTG AGGA GT GT Ggg cagggc cg cgac gcgc GTCG C
AAGGA A G AC ag - tca -- tA T

GAM44 TTTTGCAAGTCCCTACCAGG 739 ACCAGGTAGC 3809 A C--- c- ta c- aAAAT
TAGCCGTGCATAAGCTTAAA CGTGCATAAG TTTTGCA GT CCTa cagg gc gtgcataagctt T
ATTAATAAAAAGCTTATGCA CTTA ||||||| || |||| |||| || ||||||||||||
CAAGCCGTCTGATTAGGAAG AAAACGT CA GGAT GTCT CG CACGTATTCGAA A
CACTGCAAAA - CGAA TA GC AA AAATA

GAM45 GTTGGTGTGTGGTAGCGATC 740 TTGGTAGTGA 3810 T G - GAT- TT-- TT
TATCTTTCTTTGTGATCTTG AGCCTGCCAG GTTGG GT TGGTAG C CTATC TC T
GTAGTGAAGCCTGCCAGGCT GCTC ||||| || |||||| | ||||| ||
CCAGC CGACc cg accgtc g gatgg AG / t g c aagt ttCT TG

GAM46 GAGGCCGTTCTGAAAGAGTT 741 TGAAAGAGTT 3811 CG g gt ttt c tT A CGT
GGATTTCAGCACCTTGGGAC GGATTTCAGC GAGGC TTCt aaaga tgga cag acc GGG CGCAC A
GCACCGTAGCTAGTGTGGCT ACCT ||||| |||| ||||| |||| ||| ||| ||| |||||
CTGGTCTGCTTCATTTTTGA CTTCG AAGA TTTTT ACTT GTC TGG CTC GTGTG G
GAAGCTTC -- G -- C-- - T- G ATC

GAM47 GAGTATGTGAGTTTTGTGTT 742 TAGCCTGCTT 3812 TA AGTTT CA- TG GCC
GAGGCAGGCCACTTGCACTT TAACACATAT GAG TGTG TGTGTTGAGGCAGGC CT
CACTTGCATT T
GCATTGCCTTCCAAATGCAG CCCA ||| |||| |||||||||||||| || ||||||||||
GTGAGAGATAGCCTGCTTTA TTT ACac acacaatttcgtccg GA GTGGACGTAA T
ACACATATCCCACAGGTTT GG cctat atA GA ACC

GAM48 GGCGGGGGTGAGCGCGGCCT 743 CGACGCGGAT 3813 C G G- C C G G
CCCTGGCGCCCGAGCGGGCG GCAGGCGCTG GG GGGGGT AGCGC GC TCC TG CGCCC A
ACGCGGATGCAGGCGCTGCC CCCT || |||||| ||||| || ||| || |||||
CTCCC CC Ctcccg tcgcg cg agg gc gcGGG G
- - ga t c a C

GAM49 TGCCAGTCTCCTACCAGAGT 744 ACCAGAGTAC 3814 CA --- cc a a a- tTTTA
ACTTGGCAAAGATCTTTTTA TTGGCAAAGA TGC GTCTC CTa agagt cttggc aag tct G
GTACACAGAGCCTTCGCCAA TCTT ||| ||||| ||| ||||| |||||| ||| |||
GAGCTCTTAGCACGAGATGA ACG TAGAG GAT TCTCG GAACCG TTC AGA /
GCA AG CAC -- A C CG CACAT

GAM50 GGTAAGGCCTGTGAGTAAGC 745 TAATTCAGAG 3815 G- - TGAG-- A CCT
TATCTCCTCCCACAGAAGCT CAGTTATT GGTAA GC CTG TAAGCT TCT C
TAGTAATTCAGAGCAGTTAT ||||| || ||| |||||| |||
T ttatt cg gac ATTCGA AGA C
ga a ttaatG - CAC

GAM51 TCGCGGAGGAGATGAACGTC 746 CACCTGCTGA 3816 A ATGAAC C A T TA
AGCCGGAGCTCCTACATTGG CACTCTACCG TCGCGG GGAG GTCAGC GG GC CC C
GCACCTGCTGACACTCTACC CGA |||||| |||| |||||| || || ||
GCGA agcgcc tctc cagtcg cc cG GG A
a a----- t a - TT

GAM52 AAGTAGTGCGGGTAATGAAG 747 TAGCATAGTA 3817 - AA AGTT AA CTCA - ca t
a tca
AAGTTGCAAGTCTCTCATCT AAAATCAGTT CGGGTAA TG GA GC GTCT TC TGAtag tag
aaaaatc gt g
GATAGCATAGTAAAAATCAG CAGT ||||||| || || || |||| || |||||| ||| ||||||| ||
TTCAGTATACAGATTTTTTC GCTCATT AT CT CG CAGA AG GCTATC ATC TTTTTAG
CA /
TAAACTATCGTGACACAAGA C GA AC-- AA ACAC T AA T A TAt
CAAGCCATCAGTACTTACTC
GCACTTACTT
GAM53 AAATTATTTATAAAATTTGA 1140 TAGAAACTAT 4210 TG----- A A - ac- gaatta T
AAAGAATGTAGAAACTATAA AACTTAGAAT ATTTATAAAATT AAA GA TGtagaaa ctata tta
aaTAT A
CTTAGAATTAAATATTACAA TAAA |||||||||||| ||| || |||||||| ||||| ||| |||||

TATTATATAAATATATAGAT TAAATGTTTTAA TTT CT GTATTTTT GATAT AAT
TTATA C
TTTTATGATCCTTTATAGTA TATGATA C A A ATA ATA--- A
TAATTTTGTAAATAATTT

GAM54 AACACGTGCCCACACTTGGC 1141 TTTGAAACAT 4211 C CCACACTTG A CT C- -
ATTATTTA
AAGTCTCTTGCGGAAAAGCT AGCTTTTCCA GTGC GC AGT CTTG GGAAAAGCTAT
TTTCAAATAC A
ATTTTCAAATACATTATTTA ACAA |||| || ||| |||| |||||||||||| ||||||||||
ATTACAAACGTATTTGAAAC CACG CG TCA Gaac ccttttcgata aaagtttATG /
ATAGCTTTTCCAACAAGCAA C TTTTTAA-- A AC aa c CAAACATT
CTAGCAATTTTTGCACCTGT
T
GAM55 AACCATGCTGATGAATATGA 1142 TGAGGAGTGC 4212 GATGAATA A G -- - A AGA -
A AAAAATA
ACTCAGGAGCTCTCGGAAGG CTTTCTCGAT TGA CTCAG AGCTC TCG GAAGG CACT CC
CAC GG T
ACACTAGACCCACAGGAAAA TGAG ||| ||||| ||||| ||| ||||| |||| || ||| ||
ATATATTACAACCGGTGAGG ACT GAGTC TCgag agc ctttc gtga gg gtG CC /
AGTGCCTTTCTCGATTGAGC AAAAAA-- - A tt t c --- a G AACATTA
TACTGAGTCAAAAAAACGCA
TGGTT
GAM56 GGTTCTCTTGTAGCCCTCCA 1143 TCTCTTGTAG 4213 tc tt a -- a-- -- ---- -- G
ACATTGGAAGCCAGCACTGA CCCTCCAACA GGT tc gt gc cctcc acatt ggA AGCC AGCACT
A
GAAGTGTTTGGGTTAAAGTC TTGG ||| || || || ||||| ||||| ||| |||| ||||||
CCTGATGTAGAGGAGGTCGC CCG AG CA CG GGAGG TGTAG CCT TTGG TTGTGA
G
ACTCGACGGCC GC CT - CT AGA TC GAAA GT A

GAM57 CTCATTTTAAAATAGCTTGT 2188 TAGCTTGTCG 5258 TT AA cgggc attcTTCT
CGGGCTGTGTCTATTCTTCT GGCTGTGTCT CTCAT TAA tagcttgt tgtgtct T
TTATGTCCACAGACACAACA ATTC ||||| ||| |||||||| |||||||
CACAAGCTACCTTACTATGA GAGTA ATT ATCGAACA ACACAGA T
G TC CC CACA- CACCTGTA

GAM58 CCCCTCCTCTTGCAGGTACG 2189 CTTTGGATGG 5259 TGCAGGTA T CG A
TGGCCCCGCCCAGTGGGATG GGGAGGGG CCCCTCCTCT CG GGCCC CCC G
GGCTTTGGATGGGGGAGGGG |||||||||| || ||||| |||
ggggaggggg gt tcGGG GGG /
tag----- t TA T

GAM59 TATGTCATGATCTTAATGTA 2190 TGTCATGATC 5260 c t c c ATT
GCACCTTTATTTGAAAAAAA TTAATGTAGC TAtgt atgatcttaatg ag ac tTT T
GTCCTCCATTAGGATCATCA ACCT ||||| |||||||||||| || || |||
CATA ATACA TACTAGGATTAC TC TG AAA G

C C C A AAA

GAM60 TTGGCCTGGATCTTGAGGTT 2191 AGATGTTGCC 5261 G Gag - cg g c g GG----- A GG
GGAGATGTTGCCGCTCTGGT GCTCTGGTCG CTT AGGTTG atgtt gc ctct gt gcg cGG GTTC TGTTGT A
CGCGGCGGGGGTTCATGTTG CGGC ||| |||||| ||||| || |||| || ||| ||| |||| |||||| |
TGGAGGACGACGAGGACGGC GAG TTCGAC TGCGG CG GGGG CG CGT GCC CAGG GCAGCA /
GTAGCCGGTGCAGCGGGGGA G G-- G AA G A G GATGCGG A GG
AGCGGGCGTGCAGCTTGGAG
GGGAAGGCGTG
GAM61 GCCTTCTACCCTCCTTATAT 2192 TTATATTGAA 5262 TC CC ATAT- T TAT
ATATTATATATTGTTTATTA AAAGGAAGTA GCCT TAC TCCTT ATAT ATA T
TATTGAAAAAGGAAGTACAG CAGG |||| ||| ||||| |||| |||
GT Tgga atg aggaa tata tAT /
c- a- aaagt t TTG

GAM62 TATATCACGCTCTATTGTAT 748 TATTACACGG 3818 A AT TAG TCTAA TT
AGATCGTCTAACGTTGAATC AGCGGATATA TATATC CGCTCT TGTA ATCG CG G
GCTGATATTACACGGAGCGG |||||| |||||| |||| |||| ||
ATATA atatag gcgagg acat tAGT GC A
- c- ta- C---- TA

GAM63 CCGGCTGAGTCATCGCCCGA 749 TGAGTCATCG 3819 Ctga a -- c CACGAC
GGACGCGCCCACGACCAAAA CCCGAGGACG CCGG gtc tcgccc gagga gcgcc C
AAGGTGCCTCCTCGAGGGCG CGCC |||| ||| |||||| ||||| |||||
GGACGTCCGG GGCC CAG GGCGGG CTCCT CGTGG /
TG-- - AG C AAAAAA

GAM64 GTGAGTTTACCACGGCAGCG 750 TCGTAGGCCT 3820 A AG- AA - GT- c- g g atg ACCAT
AAAGCCTTGACGGTCTCGTA TGGTCATGTC C CGGC CGA GCC TTGACG Ct gta gcctt gtc tccgac G
GGCCTTGGTCATGTCCGACA CGAC | |||| ||| ||| |||||| || ||| ||||| ||| ||||||
CCATGCCCCCGTCGGAAAAG G GCCG GCT CGG GGCTGC GG CAT CGGAG CGG AGGCTG /
GCAGAGGCGTACTTGGTAAC C CCA G- T AAT TT G A AAA CCCCC
GTCGGTGGCGTCGACCGCCG
CGGACAC
GAM65 TCCTCACGGGGTGCCTTATC 751 CAGGTCCCCG 3821 - T T C TTT G
TTGTTTTCGAGAGATTCCAG TCGAGGA TCCTC ACGGGG GCCT AT TTG TC A
CATCAGGTCCCCGTCGAGGA ||||| |||||| |||| || ||| ||
aggag tgcccc tgga TA GAC AG G
c - c C CTT A

GAM66 GAGTTGCAAATGCTCCTCCG 752 TGGCGGGAGG 3822 CAA --- - AC- ACT
ACGAGAGGCTCACTCACCAG TTCAGCGTCA GAGTTG ATGCT CCTCC G GAGAGGCTC C
AGCCTCTCTGGCGGGAGGTT CCGG |||||| ||||| ||||| | |||||||||
CAGCGTCACCGGCTC CTCggc tgcga ggagg c CTCTCCGAG A
cac ctt g ggt ACC

GAM67 GGGAGGAGCAGTACGGAATA 753 TATTCCGTAC 3823 GGA GA- GA
G
TCCGGTCAGGAGGGTGGAGT TGCTCCGACC AGCAGTACGGAATATCCGGTCAGGAGGGT
GTT GGGTATCCCATTGGC GC T
TGAGGGTATCCCATTGGCGA |||||||||||||||||||||||||||| ||| |||||||||||||| ||
GCGTAGCGAGCCAATGGGAT tcgtcatgccttatAGGCCAGTCCTCTCA CAA
CCTATAGGGTAACCG CG /
ATCCGTAAACGGAACTCTCC AGG ATG AG A
TGACCGGATATTCCGTACTG
CTCCGACC
GAM68 CGACGCTTTTCTTCCTTCTC 754 ACGCTTTTCT 3824 ttttcttccttctccc C TCC
CCGCAGCCGCTCCCTTCTGC TCCTTCTCCC CGacgc gcagC GC C
GCTGCTCCTTCTCCTCGCGT GCAG |||||| ||||| ||
TG GTTGCG CGTCG CG T
CTCCTCTTCCT----- - TCT

GAM69 GGAGCTGGTCGTAGGCTCCC 755 CGTCAAAGTT 3825 A CCCAGG TATC TA - CG
AGGGACTTTATCTGATACCT AAGCTTGGTC GGAGCTGGTCGT GGCT GACTT TGA CCT
AG A
AGCGAATCCTGAGGCGTCAA ATGA |||||||||||| |||| ||||| ||| ||| ||
AGTTAAGCTTGGTCATGACC CCTCGACCagta ctgg ttgaa act GGA TC A
AGCTCC - ttcgaa ---- gc G CT

GAM70 TGCAGGGGGAATAACCGGAT 756 TGACAAAGAT 3826 C - TAACCGG CC CCT A CC
AG
CCCTGTCCCTAGCATCAAGC ATTTCCCACC TG AGG GGGAA ATC TGTC AGC TCAAG GC
C
CGCAGCCTGCTTTTTGAAGT TCA || ||| ||||| ||| |||| ||| ||||| ||
TGACAAAGATATTTCCCACC ac tcc ccctt tag acag tTG AGTTT CG /
TCA - a ta----- aa --- A TT TC

GAM71 CCGGGTGGGGGGTGGCCCCG 757 CGCTCCGGGG 3827 - C T A C C A ---- A
G
CTGGGCACCGCTGCGCCGCC GCAGCCGGGC GGTGGCCC GC GGGC CCGCTG GC GCCGCC
GGT CCTGGGGC GCCGGG T
GCCAGGTCCTGGGGCAGCCG GGCC |||||||| || |||| |||||| || |||||| ||| |||||||| ||||||
GGGTTCCTGGCGCTCCGGGG TCGCCGGG CG CCTG GGTGGC CG cggcgg ccg
gggcctcg cGGTCC /
GCAGCCGGGCGGCCGCCGGT G T - - - c g acgg - T

GGGTCCGCTGGGCCGCTGCC
CCGCTCCGG
GAM72 GCGCCGGCAAGACCACCTTC 758 TTAAGCTTCA 3828 CG- A CC CTTC A C
GAGATTAAGCCCATGTTTAA CGTCATCTGC GCGC GCA GA AC GAG TTAAGC C
GCTTCACGTCATCTGCAACG AACG |||| ||| || || ||| ||||||
CGC CGCg cgt ct tg ttc aattTG A
caa - ac cac- g T

GAM73 GGTGTCGTCATGACCACCCT 759 ACCCTGTGGG 3829 TC C c g - cccca tCT A C
GTGGGCTCCCCCCAAATGTC CTCCCCCCAA GGTG GTCATGAC ac ct tggg ctcc aatg AGA
CCGGC A
TAGAACCGGCCACGGCCGGT ATGT |||| |||||||| || || |||| |||| |||| ||| |||||
CTCCGTTCTCGGAGACCCGA CCAC TAGTACTG TG GA GCCC GAGG TTGC TCT
GGCCG C
AGTGTCGTCATGATCACC -- C T A A CTC-- C-- - G

GAM74 TTGTGTCCCGCATGCTAGAG 760 TCGCAGAGGA 3830 CGCA AGTA GAG AT - -
-- GA
TATCCTCGAGGAGGATTCTT GCTAGCAGGA TTGTGTCC TGCTAG TCCTC GAGG
TCTTCTA CA GCA CC C
CTACAGCACCGACATGGCCT GGAC |||||||| |||||| ||||| |||| ||||||| || ||| ||
GCATGATGGAGGGTCTCGCA AACAcagg acgatc aggag ctCT GGGAGGT GT CGT GG
/
GAGGAGCTAGCAGGAGGACA agg- g--- acg -- A A CC TA
CAA

GAM75 GTCAGGGCGGCTGACGGTCT 761 CGAGACAAAA 3831 GGCTGACG AA CAAAT
CAAGGGTCCAAATTCCATCG ATGGTCCTGA GTCAGGGC GTCTC GGGTC T
ACCCCGAGACAAAAATGGTC T |||||||| ||||| |||||
CTGAT tagtcctg cagag CCCAG /
gtaaaaa- c- CTACC

GAM76 GAGACGGTCGGGCTTGACGT 763 ACCGAGTTTA 3833 C T ---------- A AG-- CAGCT
C
TGAGGAGCTCCAGCTTGGAC CGACAGCGCA GAGA GG CGGGCT TG CGTTG GAGCTC
TGGA T
TTGTCCACCGAGTTTACGAC AATC |||| || |||||| || ||||| |||||| ||||
AGCGCAAATCTTGTACAGCT TTCT CC GCTCGA ac gcgac tttgag aCCT T
CGTCCTTCTT T T CATGTTctaa - agca cc--- G

GAM77 TCCCTCAGTGTTTGCCAGCT 764 GGGCCTGTGG 3834 - TG C CTTATTT TTT
TATTTCCCCAGTTTTCACGT ACACCTGAGG TCCCTCAG TGTT C AG CCCCAGT C
ACTGGGGCCTGTGGACACCT GA |||||||| |||| | || |||||||
GAGGGA agggagtc acag g tc gggGTCA A
c gt - c------ TGC

GAM78 GCCAGAGTCTGAAAAGTTTG 765 GATCATGGAC 3835 AG GAAA- GTA-- --------- - G
TAGCCTTTATGTCCGCCGCC AAGAGAAAGG GCCAG TCT AGTTT GCCTT TATG
TCCGCC C
CGGCGGATCATGGACAAGAG CCAA ||||| ||| ||||| ||||| |||| ||||||
AAAGGCCAAAAAGACTATGC CGGTT AGA TCAGA cggaa gtac agGCGG C
AAGAGTTGGC G- ACGTA AAaac agagaacag t C

GAM79 GGACCCCAGCCCCGCCGATC 769 CTTGCCTGGT 3839 - CC ------ ATCCCT C
CCTCCCCCAGGGCGTACCCG TCTGGGGCTC GGA CCCCAG CC GCCG CCC C
GCTTGCCTGGTTCTGGGGCT C ||| |||||| || |||| |||
CC cct ggggtc gg cGGC GGG /
c tt tccgtt CCATGC A

GAM80 AGTTTTGCCACAACAAGCCT 775 AAGCCTACTG 3845 AACa ---- --- aa gat
ACTGTCAACACGATGGGAGT TCAACACGAT AGTTTTGCCAC agcct actgt c cac g
GGAGAGCGCAGTGACCGGGC GGGA |||||||||| ||||| ||||| | |||
TGGTGGCAGAGCT TCGAGACGGTG TCGGG TGACG G GTG /
G--- CCAG CGA AG agg

GAM81 GGCTCGTTAAACCCGCCGTG 776 ACCCTGTACG 3846 G AAA GGGCATG a- -- c a
a
GGCATGGACACCCTGTACGG GCACCAGGAA GGCTC TT CCCGCCGT GAC ccct gtacgg
acc gg a
CACCAGGAACGCCAGGTTCG CGCC ||||| || |||||||| ||| |||| |||||| ||| ||
TACCCAGGGACGTCGGACGG TCGAG GA GGGTGGCA CTG GGGA CATGCT TGG
cc c
TGGGGAAAGGGAGCT G AAG GG----- CA CC - A g

GAM82 GAGATTTAATGCTAGTCTAA 777 TATTTTACGC 3847 ATTT C CT- TATATTAA - AT
ATATTTCTATATTAAGATAC TGACATTTTT GAG AATG TAGT AAATATTTC GATA CT C
TATCTTAAGATATCGGTACT ACTC ||| |||| |||| ||||||||| |||| ||
CTGAGATATTTTACGCTGAC ctc ttac gtcg tttatAGAG CTAT GA T
ATTTTTACTC attt a cat TCTCATGG A AT

GAM83 GGCCGCCGCCTCGAGGTGGC 778 CACCATGGCG 3848 CGC - - A A- CCC
TCGCGTCGCCATGGAGACCG ACGCGAGCCC GGCCGC CTCG AGGTGG
CTCGCGTCGCCATGG GACCG GA G
AGACCCGTCAATCAGCGGTC GCCT |||||| |||| |||||| |||||||||||||| ||||| ||
ACCATGGCGACGCGAGCCCG CCGGCG GAGC tccgcc gagcgcagcggtacc cTGGC CT T
CCTCCGAGTCCGCGGCC CCT C c a GA AAC

GAM84 AATTCATTAGAATTGATTTT 762 TTCATTAGAA 3832 at t tt tt-------- A - ATT A
ATTAGAATGAGTTATTTCTT TTGATTTTAT AAttc tagaat ga tta aga TGA GTT TCTTC T

CATCCGAAGATTCAACATCA TAGA ||||| |||||| || ||| ||| ||| ||| |||||
TCTTTTTTTTTCTTAATTTC TTAAG ATCTTA CT AAT TCT ACT CAA AGAAG C
TATTCTAGAATT -- T TT TCTTTTTTTT - A CTT C

GAM85 AGAATCTTCTTCTAATTCAT 766 TTCATTAGAA 3836 TCTTCT- at t tt tt-------- A - ATT A
TAGAATTGATTTTATTAGAA TTGATTTTAT AAttc tagaat ga tta aga TGA GTT TCTTC T
TGAGTTATTTCTTCATCCGA TAGA ||||| |||||| || ||| ||| ||| ||| |||||
AGATTCAACATCATCTTTTT TTAAG ATCTTA CT AAT TCT ACT CAA AGAAG C
TTTTCTTAATTTCTATTCTA ATTTTTT -- T TT TCTTTTTTTT - A CTT C
GAATTTTTTTTATTATTCT

GAM86 ATTTTAGGATCATTAAAATT 767 TAGGATCATT 3837 at---------- tt c
ATTTTTACACTTAAATTTAA AAAATTATTT ATTTtaggatc taaaatta ttta A
TTTTATCAATTTTTTCAGAT TTAC |||||||||| |||||||| ||||
TTTAAAAT TAAAATTTTAG ATTTTAAT AAAT C
ACTTTTTTAACT TT T

GAM87 GAAGTCCACGGTTCCTAAGG 768 TGAAAACGCC 3838 CCA- - TAA C C TG
CCTTTTTACCATGTTTTGAT ACGGAAATCG GAAGT CGGTT CC GGC TTTTTA CA T
GAAAACGCCACGGAAATCGA ATCT ||||| ||||| || ||| |||||| ||
TCTGCTTT TTTCG gctaa gg ccg aaaagt GT /
tcta a ca- c A TT

GAM88 GAAAATAAATGACGGATATG 770 TAAATGACGG 3840 A t g g - - atg
ATGTGAATGATATATCGTCA ATATGATGTG GA AA aaat acg atat gatg tga A
TCGATATACGTGGTTTCTTA AATG || || |||| ||| |||| |||| |||
TC CT TT TTTG TGC TATA CTAC GCT T
A C G A G T ATA

GAM89 GTTATTGGCTCTAATTAGTC 771 TGAAATAGAG 3841 A- A- CATAAAA AACA
ATAAAAGTACAACAATACAG CTAAAAAAC GTT TTGGCTCTA TTAGT GTAC A
TATGCGACCACTGAAATAGA ||| ||||||||| ||||| ||||
GCTAAAAAAC caa aatcgagat agtCA TATG /
aa aa CCAGCG- ACAT

GAM90 GTTTCCGCTTTTCAGCGAGC 772 GAATGCGATG 3842 TT - TTT GA-- GTA T
ATGTACCCTAATGGGAATGC GCTGTTAGTG GT C CGCT CAGC GCAT CCC A
GATGGCTGTTAGTGCGGGAC CGGG || | |||| |||| |||| |||
CA g gtga gtcg cgta gGG A
gg c tt- gtag a-- T

GAM91 AGTACTTGAAATACAGCCCC 773 AAAAACTAAA 3843 AC AAA CCCC AAAAA AAGT
TAGAAAAATCAAAAGTATTT ACCTGTAGAA AGT TTG TACAG TAG TCAA A
CTTGAAAAACTAAAACCTGT CAAA ||| ||| ||||| ||| ||||

AGAACAAAAACT TCA aac atgtc atc aGTT /
Aa aag caaa aaaa- CTTT

GAM92 ATAGAAAAAGATAAGAGGAT 774 CTCTTGGTCA 3844 AA TAAGAG TTA AA A
CGATTAAGCAAAATAAAACT ATTTCGGTTT ATAGAAA GA GATCGA AGCA ATA A
ATGGTGCTCTTGGTCAATTT CTAT ||||||| || |||||| |||| |||
CGGTTTCTAT tatcttt ct ctggtt tcGT TAT A
gg ttaa-- c-- GG C

GAM93 TTGAAATCAATGTTTAAAGT 779 TTTAAAGTTT 3849 -- aa-- a tt t
TTTAAATTGAGTTTTCTCTC TAAATTGAGT TTGAAATCAAT Gttta gtttt aa gag t
TTAAAAACAAGCTAAATAAA TTTC |||||||||||| ||||| ||||| || |||
TTGGTTTTAA AATTTTGGTTA TAAAT CAAAA TT CTc t
AA CGAA A CT t

GAM94 CCGTAATCGTGGTGTTCGTC 780 TTCGAGAATA 3850 AA GG G TCACT A
GTCACTTGTTAACTTTAACG GCGAGCATGG CCGT TCGT TGTTC TCG TGTTA C
TTCGAGAATAGCGAGCATGG |||| |||| ||||| ||| |||||
ggta agcg ataag agc GCAAT T
cg -- - tt--- T

GAM95 TCTGAAATATTTATCTAACA 781 TGAAATATTT 3851 - - acaa--- cC CA
ATGGTCCAATTACAAGTTTA ATCTAACAAT TCtgaa atatt tatcta tggt AATTA A
ATTTTATCACACACAATAGA GGTC |||||| ||||| |||||| |||| |||||
TGTAATATATTCAGA AGACTT TATAA GTAGAT ACTA TTAAT G
A T AACACAC TT TT

GAM96 GAGGTCGTGGAGTACGGTTG 782 TCGTGGAGTA 3852 tc g a g T
ATTTCTTTTTCTTAAAAGAA CGGTTGATTT GAGG gt gagt cggtt atttctttT C
GTAAACTGATTCGATTTCCT CTTT |||| || |||| ||||| |||||||||
T TTCC TA CTTA GTCAA TGAAGAAAA T
TT G - A T

GAM97 CAGTGATCAAGAAACAATAT 783 TATGTAGACG 3853 A AGAAACAA C A GAC A
ACATGATAGGTGACGAAAAT ATGACACTG CAGTG TCA TATA ATGAT GGT GAA A
ATTCATGACTGGTCATATGT ||||| ||| |||| ||||| ||| |||
AGACGATGACACTG gtcac agt atgt tACTG TCA CTT T
- agcag--- a G GTA A

GAM98 AATATTGATTTATATTATGC 784 TATTATGCAA 3854 TTT a a---- a--- a
AACAGTAACAGAACCATTTG CAGTAACAGA AATATTGA Atatt tgc acagta caga c
AAAATACTGTCCTAAGCACA ACCA |||||||| ||||| ||| |||||| ||||
ATGTTTAATGTT TTGTAATT TGTAA ACG TGTCAT GTTT c

--- C AATCC AAAA a

GAM99 ACCCTCCACCCAGCCTCCCA 785 GTCCAGAATA 3855 CC -------- t aata a t ccat-----
TCC
TTGGTCCAGAATAGGGAAGT GGGAAGTCCG T CAT TGg ccag ggg ag ccg
TCCCGGGATC T
CCGCCATTCCCGGGATCTCC CCAT | ||| ||| |||| ||| || ||| ||||||||||
TGATGGTCTCGGGACTCTCC A GTG ACC GGTT CCC TC GGC AGGGCTCTGG
/
TCCCGGCTCCCCATTGGCCA CC CAGTAGAG - A--- C - CCTCCTCTC TAG
GAGATGACGTGCCAGGCATG
GGGCAATCGT
GAM100 GCAATCCTGATATATCGCAA 786 TATCGCAATA 3856 TCC- At gcaatag g
TAGTGGGCCGGGCCCGGTCC GTGGGCCGGG GCAA TGAT atc tgggccg g
AAATAAGGTCAGTCGCCCCT CCCG |||| |||| ||| |||||||
TGC CGTT GCTG TGG ACCTGgc c
CCCC AC AATAA-- c

GAM101 GGGAGATAGTGGACAGCCCC 787 TAGTGGACAG 3857 ag aca cc-- - ca TT
CATTGGGCCATGGGCTTTAT CCCCCATTGG GGGAGAt tgg gcc catt gggc TGGGC T
TGCCCAATGCCCTAATGCAT GCCA ||||||| ||| ||| |||| |||| |||||
AGGTATCAGTCTTCC CCTTCTG ACT TGG GTAA CCCG ACCCG A
-- A-- ATAC T TA TT

GAM102 AACGGGAATGATCGATTGAC 788 GAAAAGGTGA 3858 - GA- A ATGTAAA - ATAA
ACTATGTAAAGAGTTCTTAT CAGTTGAATA AACGGGA AT TCGATTG CACT GAGTT CTT A
AAATTCAAAGCAGCTCGAAA ATCT ||||||| || ||||||| |||| ||||| |||
AGGTGACAGTTGAATAATCT TTGCTCt ta agttgac gtgg CTCGA GAA /
CTCGTT c ata a aaaag-- C ACTT

GAM103 AGCAACCGGGGTCTTTATTG 789 AGTGGGTAGC 3859 TATTG GA -- a ta cccat---------
cC ATA
GCCGAGGGTGCAGTGGGTAG CCCCATTGGG GCC GGGT GC gtggg gcc tgggccg
GGG G
CCCCCATTGGGCCGCCGGGA CCGC ||| |||| || ||||| ||| ||||||| |||
TAGTTACCCAATGGCTCATA CGG TCCG TG TACCC TGG ACTCGGT CCC /
CATAGTCATCATGGTCCCCC TTCAA -- TC A CC TACTACTGATACAT AA ATT
ATAGTCTGCCTGGCAACTTA
AGATCCCATT
GAM104 AACCCTGCCCCCTGACTCCC 790 TCAGTGGGAG 3860 GCCCCCTG TC AA
CATTGGCTAAATGGGTCAGT GTACCCATTA AACCCT AC CCCATTGGCT A
GGGAGGTACCCATTAAGGGT AGGG |||||| || ||||||||||
T TTggga tg gggtgactGG /
attaccca ga GT

GAM105 CGATCAAGTATTCTCAGCCT 791 TGAGTACATC 3861 AA------ - GC TG - AAG -----
AA
GTGATGTCTCACCAAGCCGC GTGGATGACG CGATC GTATTC TCA C TGATGT CTCACC
CC GCCGC T
CGCAATCTGTGGCTTCAAGG AGTA ||||| |||||| ||| | |||||| |||||| || |||||
AGGGTGAGTACATCGTGGAT GCTAG Catgag agt g gctaca gagtGG GG CGGTG /
GACGAGTACCAGAAGAGGAT GAGAAGAC c a- gt t GA- AACTT TC
CG

GAM106 AAGTACATCCTAATTTTAAC 792 CATCCTAATT 3862 c taactctaa--- G
TCTAAAAGGGGTTCCTTGTA TTAACTCTAA AAGTAcatc taattt aagg G
AAATTATTTAAGTTATGGTG AAGG ||||||||| |||||| ||||
TACTT TTCATGTGG ATTGAA TTCC T
T TTTATTAAAATG T

GAM107 GCTAAAGTGAAAGTCCTGGA 793 CCGGAAGTCA 3863 AA AAG T A- TAGCT AC
GGATAGCTTCAAACCTCTTG CTAGAGC GCT AGTGA TCC GG GGA TCAA C
ATTCCGGCCGGAAGTCACTA ||| ||||| ||| || ||| ||||
GAGC cga tcact agg cc CCT AGTT /
ga ga- - GG T---- CT

GAM108 CCCGGGGACGGGGCCACCTA 794 GCCACCTAGC 3864 G ACGG CAC CCA AGC G
GCCAGCCAGCCCGGGGACGG CAGCCAGCCC CCC GGG GGC CTAG GCC CCG G
GGCCACCTAGCCAGCCAGCC GGGG ||| ||| ||| |||| ||| |||
CGGGG ggg ccc ccg gatc cgG GGC G
g ga-- acc cac --- A

GAM109 GCGCTGTGGATTTGTCTTCT 795 TGTGGATTTG 3865 g--- - tct- - a TT
ACGCTAGATTTTTTTTAAGC TCTTCTACGC GCGCt tggatt tg tctac gct ga T
AGTGGATTGTCACAATCTAA TAGA ||||| |||||| || ||||| ||| ||
AGAAGCGC CGCGA ATCTAA AC AGGTG CGA TT T
AGAA C TGTT A A TT

GAM110 CACAGTTTTGCTTTGAAGTG 796 TGAAGTGCCC 3866 T------- Tt ccc a g
CCCAATAGAAGCATTTCCAT AATAGAAGCA CACAGTT TGCT gaagtg aat gaa c
TCACACTTCTAGCATCTTAT TTTC ||||||| |||| |||||| ||| |||
TTGACTGTG GTGTCAG ACGA CTTCAC TTA ctt a
TTTATTCT T- AC- C t

GAM111 GCATCTGGGATGAACTACAC 797 TTCATCATAG 3867 G--- ACACGACTTAC GC
GACTTACGTCTCCGCGAAGG CAGATGC GCATCTG GATGAACT GTCTCC G
AGGCCAGTTCATCATAGCAG ||||||| |||||||| ||||||
ATGC cgtagac ctacttGA CGGAGG /
gata C---------- AA

GAM112 AGGCGCGTATTTTACATGTG 798 CACCCTGCCA 3868 C ATT AT TA A -------- TT
GTACAGGGTAGAAAACCTTG CGTAAACCCG AGGCG GT TTAC GTGG CAGGGT GA
AAACC G
TAGGTTTCAGTTGAGTCACC CCT ||||| || |||| |||| |||||| || |||||
CTGCCACGTAAACCCGCCT tccgc ca aatg cacc gtccca cT TTTGG /
c --- -- -- - GAGTTGAC AT

GAM113 CACTTAAGCTATGATTCCTG 799 TATGATTCCT 3869 Ct attcct t tttcc
TAGTGCTCTTTCCTAAGCTG GTAGTGCTCT CACTTAAG atg gtag gctc T
AGCCTATTTTGCCCATTTTA TTCC |||||||| ||| |||| ||||
AGTG GTGAATTT TAC TATC CGAG /
-- CCGTTT - TCGAA

GAM114 TGTGGAAAACATTAAGAGTT 800 TGGAAAACAT 3870 t ---- taagag tG T
GTTATTGAAAATATTTTTTG TAAGAGTTGT TG gga aaacat ttgttat AAAA A
GTAACAAAACCATGTTTTAG TATT || ||| |||||| ||||||| ||||
GTCCCA AC CCT TTTGTA AACAATG TTTT /
- GGAT CCAA-- GT T

GAM115 ATGCGTTGTTGGCGCACGAT 801 GAGGATTACG 3871 G TG CA--- ------- AAAGTCg a
tg gc ct
CCAACAAAGTCGAGGATTAC TTGGGGCTGC TTGT GCG CGATCCA AC aggatt cgt gg
tg g
GTTGGGGCTGCTGGTACATT TGGT |||| ||| ||||||| || |||||| ||| || ||
CCTGACGAATCCTAAGTGGT GACG CGT GTTGGGT TG TCCTAA GCA CC AC
g
TAAAGAATGGGTTGAGAATT G GT TAAGA AAGAAAT GTGAA-- - GT TT At
GCTGGCAGGGCGT

GAM116 TCTCAGGACATCTCTAGTTA 1698 CATCTCTAGT 4768 Aca- a a- --- tca
CTTCGTGGATCAGATTTTCC TACTTCGTGG TCTCAGG tctct gtt cttcg tgga G
AAATCGAAGCGAACAAGAGA ATCA ||||||| ||||| ||| ||||| ||||
ATAACCTGGGA AGGGTCC AGAGA CAA GAAGC ACCT A
AATA A GC TAA TTT

GAM117 CTAGTTTATTAAATAAAAAA 1699 TAATCCCAGG 4769 TTT A AAAAAA AAAC TTATCTA
TC - A
AAGGGAAAACCTGTTTATCT TACAGTTAAT CTAG ATTA ATAA GGGA CTGT ACCTGG
TT CT T
AACCTGGTCTTCTATTAGGT CCCC |||| |||| |||| |||| |||| |||||| || ||
AATCCCAGGTACAGTTAATC GATC TAAT TATT ccct gaca tggacc aa GG T
CCCTACTATTATATAATCTT TTC A ATCATc aatt ------- ct t A
CTAG

GAM118 GACTTCTTGACTTCCGCCGA 1700 TCGGAACCAC 4770 - - CCGAA ATA- - A GGC
TCAG

AGTGGATAGATTCAAACAGG CCGGAAGATT GACTTCT TGA CTTCCG GTGG GATT C AACA TGCC A
CTGCCTCAGATTTTGGCATC ACAG ||||||| ||| |||||| |||| |||| | |||| ||||
ATGTTGGAAATCGGAACCAC CTGAAga att gaaggc cacc ctAA G TTGT ACGG /
CCGGAAGATTACAGAAGTC c a c---- aagg A G ACT TTTT

GAM119 TAATAGGCCTACGATAAAAT 1701 TTCATTAACA 4771 G TACGATAA- TC T T
GTCAACATATATTTTTTAAT GCCATGGTGT TAATA GCC AATG AACATA ATT T
TTGTGTTTCATTAACAGCCA ATTA ||||| ||| |||| |||||| |||
TGGTGTATTA attat tgg ttac tTGTGT TAA T
g taccgacaa t- T T

GAM120 CCAAACTCAGGAAGGTGACA 1702 ATGGATTGCC 4772 - G AC- T G AT at t c- tc
AATTCAGGAATTCATGGATT GGGTGATTTT CCAAAC TCA GAAGGTG AAA TCA GA TC gga tgc gggtgattt t
GCCGGGTGATTTTCTCCAGA CTCC |||||| ||| ||||||| ||| ||| || || ||| ||| |||||||||
ATTACCCACGCATTCCCGAT GGTTTG AGT CTTCCGC TTT AGT CT AG CCT ACG CCCATTAAG c
CATGATTTTAAACGCCTTCG T G AAA T A -- C- T CA Ac
TGATGTTTGG

GAM121 GCCACCTAGCCAGCCAGCCC 1703 AGCCAGCCCG 4773 CA AG-- G ACGG CAC CCa ag-- g ac -- ca
GGGGACGGGGCCACCTAGCC GGGACGGGGC GCC CCC GGG GGC CTAG gcc ccc ggg gg ggc c
AGCCAGCCCGGGGACGGGGC CACC ||| ||| ||| ||| |||| ||| ||| ||| || |||
CACCTAGCCAGCCAGCCCGG CGG GGG CCC CCG GATC CGG GGG CCC CC CCG c
GGACGGGGCCACCTAGCCAG AC GGCA G GA-- ACC CAC GGCA G GA GA AT
CCAGCCCGGGGACGGGGCCA
CCTAGCCAGC
GAM122 CGAGATTCCTGTACACAGCT 1704 GACCGCATTC 4774 A C CAGCTT AA -- - GC
TGCGAAAGGGGAAGTGGTCA CAACCTGCGT CGAG TTC TGTACA GCG AGG GGAA GTGGTCAC A
CGCACTGGTGACCGCATTCC TGTA |||| ||| |||||| ||| ||| |||| ||||||||
AACCTGCGTTGTACAAGAAA GCTT AAG ACatgt tgc tcc cctt cgccagTG C
TTCG A A ------ g- aa a GT

GAM123 CATGGGATAAGTCAAAGATG 1705 TAAGTCAAAG 4775 Ataagtcaaa - aa tGG TT
TACCAAGCCTTGGGTTTCGC ATGTACCAAG CATGGG gat gtacc gcct G T
AGCAGGCGGTACTATCCCCA CCTT |||||| ||| ||||| |||| |
TG GTACCC CTA CATGG CGGA C /
---------- T -- CGA GC

GAM124 ATGCGTCGCTACTCCCCGCA 1706 TCCCCGCAAG 4776 T TACt - atg- tt
AGGATGGTGGTTTCAACATC GATGGTGGTT ATGCG CGC ccccg caagg gtggt c
ACGTTGCCTTGCCGGGGTAT TCAA ||||| ||| ||||| ||||| |||||
TGCGTCGCGT TGCGC GCG GGGGC GTTCC CACTA a
T TTAT C GTTG Ca

GAM125 GTAAGACTGCCTAACCGTTT 1707 TCAACGGACG 4777 GA AA--- TCAA TG
CAAAGCAGTGGCGTTGCTCA TAAGGCAGAT GTAA CTGCCT CCGTT AGCAG G
ACGGACGTAAGGCAGATTAT TAT |||| |||||| ||||| |||||
tatt gacgga ggcaa tCGTT /
a- atgca c--- GC

GAM126 CGCCGGCCTCCCCCGGCTCC 1708 TCGGTTCGCG 4778 C -- C CC C--- G C - ---
C CC
CGGCCCTCCGCCCCGCCGGC GGGCCGGGGG CGG CTCCCGGCCCT CG CCG
CGGCCCGG C CGCGGC C GC GC C
CCGGGCCCGCGGCCGCCGCC TCCC ||| |||||||||| || ||| |||||||| | |||||| | || ||
CCCGGCCGCCCCCGCGCCGCG Gcc gggggccgggg gc ggc GCCGGGCC G GCGCCG G
CG CG /
CGCCGGGCCGCTTTCGGTTC C ct c tt tTTC - C C CCC C GC
GCGGGGCCGGGGGTCCCGCG
GGGGGCCGGG
GAM127 GTCGAGGGTGTAGCGGCCGG 1709 TAGCGGCCGG 4779 G --- gt ttcaatgt T
TCGTTCAATGTATCCTCCGG TCGTTCAATG GTCGA GGT Gtagcggccg cg atcC C
GATTTTTGGTCGGTCGTTAC TATC ||||| ||| |||||||||| || ||||
GATACCATCGAT TAGCT CCA CATTGCTGGC GT TAGG C
A TAG TG TTT----- G

GAM128 GGGTGCCGCTCCGCCGGGCC 1710 TCCGGCCGAG 4780 C T C ACTC AG
CGGCCGACTCCCGGGAGCGC CCCGGCGGCG GGGTGC GC CCGCCGGGC CGGCCG
CCGGG C
CCCGGTCCGGCCGAGCCCGG CCGC |||||| || ||||||||| |||||| |||||
CGGCGCCGCGCCC CCCGcg cg ggcggcccg gccggc GGCCC /
c c a ct-- CG

GAM129 CTGCTAGTAGGGCTGCTGGG 1711 CTGCTAGTAG 4781 --- T GGG AG C
CTGCTAGTAGGGCTCCTGGG GGCTGCTGGG CTGCTAGTAG GGC GCT CTGCTAGT GGCT C
CTGCTAGTAGGGCTGCTGGG CTGC |||||||||| ||| ||| |||||||| ||||
CTGCTAGTAG GATGATcgtc tcg cgg gatgatcg tcGG T
ggg t --- -- G

GAM130 CTTGCAGTTCACCCACCATG 1712 CACCATGTTC 4782 C ACC t- tttacccg CC GT
TTCGAATTTACCCGCCCCCC GAATTTACCC CTTG AGTTC caccatg tcgaa ccc CC T
CGTTTTGGCAGGGAAACAGC GCCC |||| ||||| ||||||| ||||| ||| ||
TTTCGGCTCATGGTGTAGGA GAAC TTAAG GTGGTAC GGCTT GGG GG /

ATTACAAG A GAT TC TCGACAAA AC TT

GAM131 TGGGAAGACTTGCGCGACCC 1713 ACCCTGAGTA 4783 GA Gac-------- atttaaa tt
TGAGTATTTAAAGGATTTAC TTTAAAGGAT TGG AGACTTGCGC cctgagt ggat a
TATCCGACACTCAGGCAATC TTAC ||| |||||||||| ||||||| ||||
GACAAAGTGCGAGTCTACCA ACC TCTGAGCGTG GGACTCA CCTA /
A- AAACAGCTAAC CAG---- Tc

GAM132 ATAAACCCTATATGAGGAAA 1714 AGGAAATTTT 4784 CCCTA Gag a- c tg
TTTTATTAGTACGTTTGTGT ATTAGTACGT ATAAA TAT gaaattttatt gta gtt t
AACTGCAAAATAAAATTTTA TTGT ||||| ||| |||||||||| ||| |||
AATAAATACTTTAT TATTT ATA TTTTAAAATAA CGT CAA /
CATAA AA- AA - TG

GAM133 GCATATATCCGTTTTCTCCT 1715 TCCTTTGTAT 4785 TATA TT t aacccg - a
TTGTATGAACCCGGTGGGCA GAACCCGGTG GCA TCCGTT Ctcctttg atg gtg ggc A
AGGGCCACATAAAAACATTA GGCA ||| |||||| |||||||| ||| ||| |||
GAGGGGCAACGGGCTGC CGT GGGCAA GGGGAGAT TAC TAC CCG G
C--- C- - AAAAA- A G

GAM134 TTGCGCCACAGCGGACGTAC 1716 CAGCGGACGT 4786 CG ca ac---------- a a attC
ATCAATCAGATTCGTTACTT ACATCAATCA TTG CCA gcgg gt catca tcag G
GACTGATGCACACAAAGAAA GATT ||| ||| |||| || ||||| ||||
ATGCCGCATGGTACAA AAC GGT CGCC CA GTAGT AGTT /
AT A- GTAAAAGAAACA C C CATT

GAM135 TGTAACTTCACGCTACCCTA 1717 TCACGCTACC 4787 tca ctacc- a g aata ACT
AACGTACAATACTGGGACTA CTAAACGTAC TGTAACT cg ctaa c tac CTGGG A
GAACCCAGAGGTAGTTAGAA AATA ||||||| || |||| | ||| |||||
TATACGGTAGTTACA ACATTGA GC GATT G ATG GACCC /
TG- ATATAA - - GA-- AAG

GAM136 GGCCATCTTCCTCATGATGC 1718 TTCCTCATGA 4788 Ctt- tgatgc - gt
CGCGATTTGTCAAGAAATAC TGCCGCGATT GGCCAT cctca cgcg attt c
GCGATTGGGGCTGCATGGCT TGTC |||||| ||||| |||| ||||
TCGGTA GGGGT GCGC TAAA A
CGTC TA---- A GA

GAM137 ACACCCTTACACCGATGATA 1719 TTGGCAGAAT 4789 A CCGA AAGA AGCAGAG
AGACCAACGAGCAGAGAATA CATGAAGGGT ACACCCTT CA TGAT CCAACG A
AACCGCGTTGGCAGAATCAT GT |||||||| || |||| ||||||
GAAGGGTGT tgtgggaa gt acta ggttGC A
- ---- agac GCCAAAT

GAM138 GCTGGGCTGCTAGTAGGGCT 1720 TGGCTTGCTT 4790 TG -- GCT T T- G
GCTGGGCTGCTAGTAGGGCT GCTTGCTTGC GC GGCT GCTAGTAGG GC GGGC
GCTAGTAGG C
GCCTGCTGGCTTGCTTGCTT TAGT || |||| ||||||||| || |||| |||||||||
GCTTGCTAGTGGGGCCGC CG CCGG tgatcgttc cg ttcg cggtCGTCC T
-- GG gtt - tt G

GAM139 TCGACAACTACCTCCGAAAG 1721 TGTTTTGTGG 4791 G --------- --- AAAGT TG T
TGTGTCCTGTTGGATGTTTT ATTAGGTAAA TC ACAACT ACC TCCG G TCC G
GTGGATTAGGTAAAACAGAA ACAG || |||||| ||| |||| | |||
AGTTGTGGA AG TGTTGA tgg aggt t AGG T
G AAgacaaaa att gttt- gt T

GAM140 CTGGAACTGGTGGAACTTGT 3039 GGACGAGGAA 6109 AAC- GAA A- CGCA
CTATGCGCAAATTACAGAGG CACCGTATAC CTGG TGGTG CTTGTCT TG A
ACGAGGAACACCGTATACCA CAG |||| ||||| ||||||| ||
G gacc gccac gagcagg AC /
atat aag AG ATTA

GAM141 GGACGCGGGAATTTCCTTGA 3040 AGGCATCAAG 6110 AC TTT ATT--- A
TGATTACGAGAACTTCGTTT GTTCCTGCCG GG GCGGGAA CCTTGATG ACGAG A
CAGGCATCAAGGTTCCTGCC CC || ||||||| |||||||| |||||
GCC cc cgtcctt ggaactac TGCTT /
gc --- ggaCTT C

GAM142 GAGGTGTCGGTTGACGGAAA 3041 TGACGGAAAG 6111 GGTt - t c- CAACCG
GAGTTTTGGCCAGGGCGGCA AGTTTTGGCC GAGGTGTC gacgg aaagagtt tggc agggCGG T
ACCGTTATAGATTCGTCTTT AGGG |||||||| ||||| |||||||| |||| |||||||
CGCTATGACTCTTTGCTGTC TTCCACAG CTGTC TTTCTCAG ATCG TTCTGCT T
GACACCTT ---- G T CT TAGATA

GAM143 GTCCGATTCGATACAAGAAC 3042 TTGAAGCCTG 6112 GA - AAGAAC- TG- T A
GCCGA T
CCTGTCATGTCTCACCAGGC GGGAGTATGA GTCC TTC GATAC CC TCATG CTC
CCAGGCT AATC G
TGCCGAAATCTGTGGATTGA AGTG |||| ||| ||||| || ||||| ||| ||||||| ||||
AGCCTGGGGAGTATGAAGTG TAGG AGG CTATG Gg agtat gag ggtccga ttAG T
GATGATAGGTATCAGGAAAG AA A GATAGTA tga - g ag--- G
GAT

GAM144 TCATTGACAACTTCAAGATT 3043 ATGGATCTAT 6113 T ----- - GC CGT
TGCTTCCCCGTAAACGGGAA GGTCAAGGGT TCAT GACAACT TCA AGATTT TTCCC A
ATGGATCTATGGTCAAGGGT TGTC |||| ||||||| ||| |||||| |||||

TGTCATGG GGTA ctgttgg ggt tctagg AAGGG /
- gaact a ta CAA

GAM145 AGAGCTTTTCAGACTAAAAA 3044 TACAATATTT 6114 T TC -- A GT- a ga-- -- - TT
TGTGTTACAATATTTATAGA ATAGACTAAG C TT AGA CTA AAATGT tacaat tttata ct aaggata AGA A
CTAAGGATAAGATTATCTCT GATA | || ||| ||| |||||| |||||| |||||| || ||||||| |||
ATATTCTTTCAGAAGATATG G AA TCT GAT TTTACA ATGTTA AGGTAT GA TTCTTAT TCT /
GAGATTGTACCAACATTTAT C CC CA A ACC G AGAA CT A CT
AGACTCTCCAACGCTCT

GAM146 ATCTCGTCCCCATGGAAGAG 3045 CGTTCAACTT 6115 G C AAGA- A-- A C AG
GCGAAAGAGGCACCTAGGCA TCGTCGATAA ATCTC TCC CATGG GGCGAAAG GGC CCTAGG AGC C
GCAGCTTGTTCCTAGGCGTT CCAT ||||| ||| ||||| |||||||| ||| |||||| |||
CAACTTTCGTCGATAACCAT TGGAG AGG Gtacc ctgctttc ttg GGATCC TTG /
GAGGAGGAGGT G A aatag aac c - TT

GAM147 GCCTCAGGGTTCCAGACACG 3046 TCCCTGAGCC 6116 A- T ACACGTTCC - A G C
TTCCGCCGGAGGACTTTGCG TGGACCTGAG GCCTC GGGT CCAG GC CGG GGACTTTGC GC A
GCCAGGGTGGCAGAGTCCCT AGGT ||||| |||| |||| || ||| |||||||| ||
GAGCCTGGACCTGAGAGGT tggag tcca ggtc cg gtc cctGAGACG TG G
ag - --------- a - G G

GAM148 GGTTCTTCGCCAACATGGCG 3047 AAACTGCAGA 6117 ----- A- ATG CTC GTG CC
GTCCTCGCAGGTGTCAAGAC CTGCGACGTA GGTTCT TCGCC AC GCGGTC GCAG TCAAGA C
CCATCTCTTGAAACTGCAGA CGGC |||||| ||||| || |||||| |||| ||||||
CTGCGACGTACGGCGATTTG CCAAGA AGcgg tg cgtcag cgtc aGTTCT A
GAGAACC GGTTT ca cag a-- aa- CT

GAM149 GTGTGTGTGTGTGCGCTCAC 3048 TCACACGGAA 6118 T TG T GGAACGAGAACAA T TG T GA GAG
ACGGAACGAGAACAAGTGTG CGAGAACAAG GTGTG CGC CACAC GTGTG GTG CGC CACACG AC A
TGTGTGCGCTCACACGGAAC TGTG ||||| ||| ||||| ||||| ||| ||| |||||| ||
GAGAACAAGTGTGTGTGTGT CGCGC GTG gtgtg cacac CGC GTG GTGTGT TG A
GTGCGCTCACACGGAACGAG T GT T aacaagagcaagg t GT T G- AAC
AACAAGTGTGTGTGCGCG
CTCACAC
GAM150 TGACGAAATGCCACACATTA 3049 TGAGGAACAC 6119 C A- T - c atcca TAC AT- TT

GGAGTGTGAGGAACACGGGC GGGCATCCAT CACA ATT GGAG Gtga ggaa acgggc tgggc CTGGGG TTC G

ATCCATGGGCTACCTGGGGA GGGC |||| ||| |||| |||| |||| |||||| ||||| |||||| |||

TTTCTTGTCGAATTACCCTA GTGT TAG CCTC CGCT CTTT TGTCCG ATCCG GATCCC AAG /

GACTGCCTACGCCTGTATTT T CG - A A C---- TCA ATT CT

CATCGCCTCCGCGATTTGTG

GGATGATGTCA

GAM151 CGGTGCTGAGGGGTTACAAA 3050 CATGCCGAAC 6120 GG T A CC ACTCC A

GCCGCGTTCACTCCGCATGT GCAACTTCGT CGGTGCTGAG GT AC AAG GCGTTC GCATGTCG G

CGAGCTTGACATGCCGAACG ACAA |||||||||| || || ||| |||||| ||||||||

CAACTTCGTACAACTTAGCA GCCACGATTC ca tg ttc cgcaag cgtacAGT C

CCG aa - c aa c---- T

GAM152 GATCCAGCTGTGGTGCCTAA 3051 TGTGGTGCCT 6121 CAGC - taa- c aCAA

GGACATCAGGGACAAGTACC AAGGACATCA GATC tgtggt gcc gga atcaggg G

CCCTGGTTCCGAACGGTGAC GGGA |||| |||||| ||| ||| |||||||

CACAACGAGATC CTAG ACACCA TGG CCT TGGTCCC /

AGCA G CAAG - CCAT

GAM153 GTATATACTTAGATGAGTCA 911 TTAGTTCTTT 3981 TAC T TCAT TGTC

TTTAAAACTTGTCTATTTAG CTCTAACTTA GTATA TTAGA GAG TTAAAACT T

TTTTAGTTCTTTCTCTAACT TAC ||||| ||||| ||| |||||||| TATAC catat aatct ctt gattTTGA /

tc- - tctt TTTA

GAM154 CCGCATCACCGACCAGGCGG 912 TTCGCGCGTG 3982 CA GA G G GG G G TC

GCGCGGGGAGCGGGCTCTGC TATGGGGAGT CCGCAT CC CCA GCG GCGCG GA CG GC T

TGCGTGTTTTCGCGCGTGTA GCGG |||||| || ||| ||| ||||| || || ||

TGGGGAGTGCGG ggcgtg gg ggt tgt cgcgc TT GT CG G

a- -- a g tt - G TC

GAM155 CACCCGCGCGCGCCGGCCAA 913 CGTGGCGGTG 3983 A G G AA TGC

CACGGCCTGCCTTACGGCCG GGCGGCGCGG C CCCGCGC CGCC GCC CACGGCC C

TGGCGGTGGGCGGCGCGGGG GGG | ||||||| |||| ||| ||||||| G g gggcgcg gcgg tgg gtgcCGG T

g - g cg CAT

GAM156 ACGAGATTGTGAACCTGCGC 914 GCGGACTTTG 3984 ATT TG CCT G A GA - C

CTGGAGATCGAGCGCGCCCG GGGCGTTTTG ACGAG G AA GCGCCT GAG TC GCG CG C

CGACGCGGACTTTGGGGCGT CCGC ||||| | || |||||| ||| || ||| || TTTGCCGCTTCGT TGCTT c tt tgcggg ttt ag cgC GC C

cgc gt --- g c g- A G

GAM157 GCGGCTCGCGCGGCGGGTAA 915 CCCCGTGGAC 3985 CGC - AA ACGA G
GCGGACGAGCCTGCCGCGGC GCCGCCCTCG GCGGCTCG GGCGG GT GCGG
GCCTGCCGC G
GGCGGCGGGCCCCGTGGACG AGCC |||||||| ||||| || |||| |||||||||
CCGCCCTCGAGCCGC CGccgagc ccgcc ca tgcc cGGGCGGCG C
tc- g gg c--- G

GAM158 CGATGAATACTTTAATGACG 916 TATAATGTCT 3986 A TT-- T CC T ATA-- TT
TTATACCTCTACATAATGCT TATCTCGTAT CGATG ATAC TAA GACGTTATA TC AC ATGC A
TATAGCGTGCAACGTTGATA ATAT ||||| |||| ||| |||||||||| || || ||||
TAATGTCTTATCTCGTATAT GTtat tatg att ctgtaatat AG TG TGCG /
ATTG a ctct - -- T CAACG AT

GAM159 TGAGTTTGTCCACAAGTTTG 917 TCCACAAGTT 3987 Gtc -- - - aa
AGGGCAAGAACCTGTTTGCC TGAGGGCAAG TGAGTTT caca agtttg ag ggcaag c
TCTGTAGACTACTGTGTAAA AACC ||||||| |||| |||||| || ||||||
GACTCA ACTCAGA GTGT TCAGAT TC CCGTTT c
AAT CA G T GT

GAM160 GCCGAGTGGCGGTCAACAGC 918 GCCCGGTGCC 3988 GTCAACA A
CTCGCGCCGGGAGAGCCCGG GCTTGGC GCCGAGTGGCG GCCTCGCGCCGGG G
TGCGAGGCGCCCGGTGCCGC |||||||||| ||||||||||||
TTGGC cggttcgccgt CGGAGCGTGGCCC A
ggcccg- G

GAM161 TTGCGACTGGTGCAACAATG 919 TGGCGTGAGA 3989 C GCA---- ATG- TGAAG T
GTTTCGCTGAAGGTTTGAGA CATGGTGTGA TTGCGA TGGT ACA GTTTCGC GTT G
CATGGCGTGAGACATGGTGT CCTA |||||| |||| ||| ||||||| |||
GACCTAAACCATTCGCAA AACGCT ACCA tgt cagagtg CAG /
T Aatccag ggta cggtA A

GAM162 GTCCCAGCGCGCGAATTCGT 920 CAGCCGCGGC 3990 - -- AT---- AC G
GGACGCCGTCTGGCAGCCGC GGACGTCGCT GTC CCAGCGC GCGA TCGTGG GCC T
GGCGGACGTCGCTGGCGCTG GGCG ||| ||||||| |||| |||||| |||
GTGAT TAG GGTCgcg cgct ggcgcc cGG C
T gt gcaggc ga T

GAM163 GCTGCTCTTGCTGCTCTTGC 921 TCTTGCTGCT 3991 T TCTT T TCTT T TCTT T TCTT T T
TGCTCTTGCTGCTCTTGCTG CTTGCTGCTC GC GC GC GC GC GC GC GC C
CTCTTGCTGCTCTTGCTGCT TTGC || || || || || || || || || ||
CTTGCTGCTCTTGCTGCTCT CG CG CG cg cg cg cg CG CG T
TGCTGC T TTCT T ttct t ttct t ttct T T

GAM164 CTGGCCGACCGCGGCGGCGG 922 GGTTGCGCCG 3992 A G AGC T GG
CGAGCGCTTCCGCGTGGCGA CTGCAGCGGC CTGGCCG CCGC GCGGCGGCG GCT CCGCGT
C
GCGCGGCGGTTGCGCCGCTG TGGC ||||||| |||| ||||||||| ||| ||||||
CAGCGGCTGGCCGG GGCcggt ggcg cgtcgccgc tgg GGCGCG /
c a gt- C AG

GAM165 GATCTCAAAGACCGATATGG 923 TCAAAGACCG 3993 caaa cga aaactcaaA- T
AAACTCAAACCGTTATCGGG ATATGGAAAC GATCt gac tatgg CCG T
TACAATAAACCATGACTGTC TCAA ||||| ||| ||||| |||
CAGATT TTAGA CTG GTACC GGC A
C--- TCA AAATAACATG T

GAM166 CAGTCCCGTTGCCCATGAGC 924 TGCCCATGAG 3994 C GTtg -- cag c----- TT G
AGGTACACTTTGGTTCAGGA CAGGTACACT CAGT CC cccat gag gtaca tttgg CAG A
AACTGCCCAAGACATCATGT TTGG |||| || ||||| ||| ||||| ||||| |||
ACACTCCGATGGGAAAGGAA GTCA GG GGGTA CTC CATGT GAACC GTC A
CTG A AAA- GC A-- ACTACA C- A

GAM167 GCGCAGAGCTGTACCAGCGC 925 TACCAGCGCC 3995 G a - ac - T G AGG
CTGGACGCGCTGTTGCTGCC TGGACGCGCT GCGCA AGCTGt ccagcgc ctgg gcgctgt tgC GCC
CTGC G
GCTGCAGGGCTTCGCGGGGC GTTG ||||| |||||| ||||||| |||| ||||||| ||| ||| ||||
TGCGCGCGGCGCCCGGCGCG CGCGT TCGGCG GGTCGCG GGCC CGCGGCG GCG
CGG GGCG C
CTGGAGCGGCTGTGCGC G A C -- C T - CTT

GAM168 GGGCCATGGTCAAGGCGTCT 926 CAGCCGCCGT 3996 CC CAA T GAAAC TCC
GGAAACTGGCCATCCACTTT CGCCATCCC GGG ATGGT GGCG CTG TGGCCA A
GGCCACAGCCGCCGTCGCCA ||| ||||| |||| ||| ||||||
TCCC ccc taccg ccgc gac ACCGGT /
-- ctg c ----- TTC

GAM169 AAGTGGACCGGGAGGACCGA 927 GATCTGGGCC 3997 T C A A G AAG TT A ----
ATG
GGAAGAGTCTTTCCTGATCT CCCGTCCTCT AAG GGAC GGG GG CC AGG AGTCT CCTG TC
TCTGAC A
CTGACATGATGGGTCAGATC T ||| |||| ||| || || ||| ||||| |||| || ||||||
AAGACAGGTTGGATTAGATC ttc cctg ccc cc gg tct TTAGG GGAC AG AGACTG /
TGGGCCCCCGTCCTCTT t - - - g agA TT - AACT GGT

GAM170 TTCACAAGTATTATTAAAAA 928 CACAAGTATT 3998 agtattattaaaaa C A TACAT
TGAGTATCGATAGTTACATT ATTAAAAATG TTcaca tgagtaT GAT GT T

ACCATATCATCCATGCTCAT AGTA |||||| ||||||| ||| ||
GTGGA AGGTGT ACTCGTA CTA TA /
---------- C C TACCA

GAM171 GAGGGTCTGGATGGTGAGCT 929 TGGATGGTGA 3999 T -- ga tt - c TTCG
TGGAGAGAGCGTCTTCGTCA GCTTGGAGAG GAGGG Ctggat ggt gc ggagag ag gTC T
ATGACCTGCTCTCCTGTAGC AGCG ||||| |||||| ||| || |||||| || |||
CTTGTCCAGCTTTC CTTTC GACCTG CCG TG CCTCTC TC CAG /
- TT A- T- G - TAAC

GAM172 GAAGATCGATGTCCCGCCGC 930 CATCGCGTGG 4000 T A - C G AG
CGCTGGCGCAGCTGCGCGGC TGGGACGCGT GAAGA CG TGTCCCGCCGC CG TG CGC C
ATCGCGTGGTGGGACGCGTT TTTC ||||| || |||||||||| || || |||
TTC ctttt gc gcagggtggtg gc ac GCG T
- - c t G CG

GAM173 CGCTCGTGCGGCAGCCGCCC 935 GACCTCGTCA 4005 T - CCA-- G AC T
AGCGAGGTGCAGACCGTCAA CGTGCGCGCT CGCTCG GCGGCAGC CGC GCGAGGT CAG
CG C
CGCGCTGGACCTCGTCACGT GCTG |||||| |||||||| ||| ||||||| ||| ||
GCGCGCTGCTGCTGGGCG GCGGGT Cgtcgtcg gcg tgctcca GTC GC A
- c tgcac g GC A

GAM174 TTGGTTCCGGCCCCGGTTCC 936 GCCCCGGTTC 4006 TT cc ttc ct cc A
GGCTCCGGCCCCGATTCCGG CGGCTCCGGC TTGG CCGg ccgg cgg ccgg ccg T
CTCCGGCCCCGACTCCGGCT CCCG |||| |||| |||| ||| |||| |||
CCGGCCCCGA AGCC GGCC GGCC GCC GGCC GGC T
CC TC TCA CC TC C

GAM175 GTACTATCCCCTGAGGGGAT 943 ACGCCATGAG 4013 A CCCCT- T TTT A c- a-
aag- a
GGTGTTTTCGGAAGACGCCA AAAGCTCTAC GT CTAT GAGGGGA GGTG TCGGA Gacg catg
ga ctct c
TGAGAAAGCTCTACAAGGGG AAGG || |||| ||||||| |||| ||||| |||| |||| || ||||
ACCATCGACATGTTTGTCTC CA GATG CTCCCTT CTAC AGCCT CTGT GTAC CT
GGgg a
CGACCCATCTTCCCTCCTGA - CAAGTC - CC- - TT AG ACCA a
ACGTAGAC

GAM176 CGGGCGCTGGAGGCGAGCGC 944 CATCGAGGCC 4014 -------- G - AG -- GAC
GCAGCGGGCGACGGCAGCCA GTGCTCGCGT CGGGCGC TGGA GCGAGCGCG C CG
GGC G
TCGAGGCCGTGCTCGCGTTC TCAA ||||||| |||| ||||||||| | || |||
AACCCGCACGCGCCCG GCCCGCG actt cgctcgtgc g gc cCG /
CACGCCCa g c ga ta ACG

GAM177 CGCCCGCTCCGGCGCCGGCG 931 CTGGCGCGGG 4001 TCC CG G G TC C -- G - A

AGGGGGTGGTGTCGCGCGGC CGGCCGTGCC CCGC GGCGC GCGA GG GTGGTG GCGCGGC CGG GCC GT TCGGCCG C

CCGGGCCGGTTCGGCCGACT GCGT |||| ||||| |||| || |||||| ||||||| ||| ||| || |||||||

CGGCTGGCGCGGGCGGCCGT GGCG TCGCG CGCT CC CGCCAC tgcgccg gcc cgg cg ggtcGGC /

GCCGCGTCCCACCGCGCCGT TC- -- G G CC t gg g c T

CGCGCGCTCTGCGGCCG

GAM178 GTGCCGCGCCGCCTGGAGTC 932 TCTCGCGGCC 4002 C------ CT T - T CC

GCGGTTCGGCCGGACCGTGC CTTCAACGGC GTGCCG GCCGC GGAG CGCG GT CGG G

ACGCGCTCTCGCGGCCCTTC AC |||||| ||||| |||| |||| || |||

AACGGCAC cacggc cggcg tctC GCGC CG GCC /

aacttcc c- - A T AG

GAM179 TCGCCCTTCCGGAGTGACGC 933 TTCCAAAGCG 4003 CT A G C - T C-- C TCT

ACATAGCTCGCCGGGGCCCG GCGTGTCTGA TCGCC TCCGG GTGAC CA ATA GC CGC GGGGCC GCCT G

CCTTCTGTCCAGGCCGGTTC GTCA ||||| ||||| ||||| || ||| || ||| |||||| ||||

CAAAGCGGCGTGTCTGAGTC AGCGG AGGCC Cactg gt tgt cg gcg ccttGG CGGA /

ACCCGGAGGCGA -- - a c g - aaa C CCT

GAM180 GCAGCCGCAGGATCGACACG 934 TGGAGTAGGC 4004 A AG--- A A AA - T - GG--- GG

AGGAACGGGGTCAGCACGCG GATGTTGTCC GC GCCGC GATCGAC CG GG CGG GG CAGCA CGC TCGAT T

GTCGATGGTGTAGTTGGAGT TCCG || ||||| ||||||| || || ||| || ||||| ||| |||||

AGGCGATGTTGTCCTCCGCG CG CGGCG CTGGTTG GT CC gcc cc gttgt gcg ggtTG G

CCCTGGTTGGTCACCTGGCG - GTCCA - C GC t t a gatga AT

GCGC

GAM181 TGCGTCTGCAACGGCATCAT 937 CATCATGTTC 4007 C -- a- at tacac tgc

GTTCCTACACGCCTTGCACC CTACACGCCT TG GTCTGCA ACGGc tc gttcc gcct a

TGGGTGGAACGAGCGCCGTC TGCA || ||||||| ||||| || ||||| ||||

CTGCAGACCG GC CAGACGT TGCCG AG CAAGG TGGG /

- CC CG -- ----- TCC

GAM182 TCTGCGACTGCACCTGCTCC 938 CTTGCGGAAC 4008 CTGCA C TC TTTG

TCCAGGCATTTGATCATCTG AGGTCGCGGA TCTGCGA CCTG TCC CAGGCA A

CTTGCGGAACAGGTCGCGGA ||||||| |||| ||| ||||||

aggcgct ggac agg gttcGT T

----- a c- CTAC

GAM183 GATCCGGGACCGCCGTAGCG 939 CGCCGTAGCG 4009 Cc c --- g tttt- tT
GGGTGTTTTTTAATTTATTT GGGTGTTTTT GATCCGGGA gc gtag cg ggtgt taa T
TATATATACGCTATGTATCT TAAT |||||||||| || |||| || ||||| |||
ACTGTTTTTCCGGGTC CTGGGCCTT TG CATC GT TCGCA ATT A
TT T TAT A TATAT TT

GAM184 GCGCCTGGACGTTGCACGCG 940 CGTTGCACGC 4010 - A a gcg ta a
GCGGGTACCGAAAGCGGCGC GGCGGGTACC GCGCC TGG cgttgc cgcg gg ccg a
TAACGCGGCAACGGCCACGG GAAA ||||| ||| |||||| |||| || |||
CGC CGCGG ACC GCAACG GCGC TC GGC a
C G - AA- GC G

GAM185 GCCTGCGTCGCCTATGCTTC 941 TCGCCTATGC 4011 c------- - tcgc - GA CCT
GCGCGTCACCACGACACCTT TTCGCGCGTC GCCTGCGt gcc tatgct gcgtc accaC CA T
CCTTGAAGTGGTAGACGTCT ACCA |||||||| ||| |||||| ||||| ||||| ||
TCGGCATGCGGCAAATCGTC CGGACGCA CGG GTACGG TGCAG TGGTG GT /
ACGCAGGC CTGCTAAA C CTTC A AA TCC

GAM186 GATGTTCAGCAGGAAGCGCA 942 TCCATGAGCT 4012 T GA C GA C T C T - TC
TGATGGACTTCTTGGCGTCG CCACGATCCG GA GTTCAGCAG AGCG AT TGGA TTC TGG G
CGGT CG T
GTCGTCTTGTCGTGCCGCTC CTGG || ||||||||| |||| || |||| ||| ||| | |||| ||
CATGAGCTCCACGATCCGCT CT CGAGTTGTC tcgc ta acct gag acc C GCCG GC T
GGCTGTTGAGCTC - gg c gc c t t - T TG

GAM187 AGGAGATTGCTATTAGTAAG 945 TACAATTTCT 4015 - TT TAAG GG TTT
TGGGGCCATTTTTATATTAA TTAGCACATT AGGAGAT TGCTA AG TG GCCATT A
TGGTTACAATTTCTTTAGCA TCCT ||||||| ||||| || || ||||||
CATTTCCT tccttta acgat tc ac TGGTAA T
c t- ttta at TTA

GAM188 CAGCTGGGTGGCCAGGCCGG 946 CAGCAGCTTC 4016 TG CAG CGG - - C
AGAGGCTCTGGCCCGGGTCC TGCATGTTGC CAGCTGGG GC GC AGAGGCT CTGG C C
AGCAGCTTCTGCATGTTGCC CCAG |||||||| || || ||||||| |||| |
CAGCTG GTCgaccc tg cg tcttcga gacC G G
gt ta- --- c T G

GAM189 GTCGAAGAGGCTGGCGTGCG 947 TGGCGTGCGC 4017 CG G - t - c tcca g
CGTTCCACTCGTCCGAGACC GTTCCACTCG GT AA AG GC ggcg tgcg gt ctc t
TGCCGCACCGTCGCACTGTT TCCG || || || || |||| |||| || |||
AAAC CA TT TC CG CTGC ACGC CG GAg c
AA G A - C - TCCA c

GAM190 GCGCGGCACAGTGCCAACGC 948 ACGCGAAGCG 4018 G - TG A gaag - cgt
GAAGCGCGCATGCGCACGTT CGCATGCGCA GC CGGCA CAG CC acgc cg cgcatgcgca t
GAACTGCGCATGCGTCGGCG CGTT || ||||| ||| || |||| || ||||||||||
TCGGTGTTGTTGCCGGGC CG GCCGT GTT GG TGCG GC GCGTACGCGT G
G T GT C ---- T CAA

GAM191 TCCCGTAATACTCCGCGATC 949 TGGAAGCGGT 4019 ATAC- CA TA CGA - - C
AGTTACCGTGGCGACGTTTC ACCGCGGGCG TCCCGTA TCCGCGAT GT CCGTGG
CGTTTC AG GGCG A
AGGGCGCATGCGCCTCTGGA CGTC ||||||| |||||||| || |||||| |||||| || ||||
AGCGGTACCGCGGGCGCGTC GGGGCAT GGGTGctg cg ggcgcc gcgaag tC CCGC T
GTGGGCACAGTACGGGG GACAC -- cg atg g T G

GAM192 AACAGCCGTTATTAGTTAAT 950 TTGCTTATGG 4020 -- TAGTTA c t - --- tt-- A C
TGCTTATGGCCAGTCCCTAG CCAGTCCCTA CAGC CGTTAT Attg tta ggccagt ccct agc TG
AGAAG A
CTTTGAAGAAGCAGCTTCTA GCTT |||| |||||| |||| ||| ||||||| |||| ||| || |||||
CATTTTGTTTTGAGGGTGCT GTCG GTAATG TAAC AGT TCGGTCG GGGA TTG AC
TCTTC /
GGCTTTGATCAATGTAATGG TG ------ T T T GTT TTTT A G
TGCTGTT

GAM193 GCTCTGTTCCCGCATAGCTG 951 GGAGAAAGCG 4021 GTTC CATA GA - ATAAA
ATCCCGTATAAATATAATAA TAACGGAGAG GCTCT CCG GCT TC CCGT T
CGGAGAAAGCGTAACGGAGA C ||||| ||| ||| || ||||
GC cgaga ggc cga ag ggCA A
---- aatg a- a ATAAT

GAM194 GCGCATGCGCCTGGGGGCTT 952 CAGCTCGCGG 4022 G TTCTAT A
TCTATGCGCGCATACGCGCG GTGTATGCGT GCGCATGCGCCTG GGGCT GCGCGC T
CAGCTCGCGGGTGTATGCGT |||||||||||| ||||| ||||||
tgcgtatgtgggc ctcga cGCGCG A
g ------ C

GAM195 GGGGGTCGGGGGGGTGCGCAG 953 TGCCCTGGCC 4023 T G G GGTCGGA C T
GC C- T
GGCGGTGCCCCGGGTCGGAA TCCCCTCCCC GC CAGGGCG TGCCCCG ACCCCCGGGTG
GGT CGG GG GGGGCT C
CCCCCGGGTGCGGTTCGGGC C || ||||||| ||||||| |||||||||| ||| ||| || ||||||
GGCGGGGCTTCCCGGCTCCT cg gtcccgt GCGGGGC TGGGGGCCCGC TCG GCC CC
CCTCGG C
TCCACCGGCTCGCCCGGGGG - - A ------- - - A- TT C
TCGGGGCGATGCCCTGGCCT
CCCCTCCCCC
GAM196 CTGACAGTAGCGGGTAATAA 954 ATCACTTTCA 4024 --- C TAATAAAAACAAT TT-
TTTTT--- ACA

AAACAATAGGATTTTTATCG CGGTGATTTA CAGT AG GGG AGGAT TTATCGT TATGTT A
TTTTTTTATGTTACAAAACA TTCT |||| || ||| ||||| ||||||| ||||||
ACGTATCACTTTCACGGTGA GTCG TC CCC tctta agtggca aTGCAA /
TTTATTCTTGCTATTCCTTT GGT - TTTTCCTTATCGT ttt ctttcact CAA
TCCCCTTGGGCTGTCAG

GAM197 CTACGTGGAAAGCAAGCCCA 955 TAACGAACTG 4025 T AAA A CCACta - tc- act A TT AA
CTAACGAACTGTCTCAACGA TCTCAACGAC CTACG GG GCA GC acgaa ctgtc aacg gca CG TCGT C
CTGCAACGTTTCGTAACCAA TGCA ||||| || ||| || ||||| ||||| |||| ||| || ||||
GCGACCGATGCCCGTTAGCG GATGC CC CGT CG TGCTT GACAG TTGC CGT GC AGCG C
ACAGCTTCGTCTGCCTGCGA - AG- C TC---- C CGA C-- A C- AA
CCCGTAG

GAM198 CATGCGCAACAGGTCCAGCT 956 CATTAAACAG 4026 ACAG ---- A C
TAAAGGCGCACTTGTCATTA GCTGGACATG CATGCGCA GTCCAGCT TAA GGCG A
AACAGGCTGGACATGCGCGT CGCG |||||||| |||||||| ||| ||||
G GTgcgcgt caggtcgg att cTGT C
a--- acaa a T

GAM199 ATTTGACCCCCAGAACTATG 957 CAGAACTATG 4027 CCCC--- t at ct
TATCAGCCTAGAGTTGCAAC TATCAGCCTA ATTTGA cagaacta gt cagc a
TAGTTCTGACTTTGTTCAAA GAGT |||||| |||||||| || ||||
T TAAACT GTCTTGAT CA GTtg /
TGTTTCA - AC ag

GAM200 CTGTAGAACTTGCCATTCTC 958 TAGAACTTGC 4028 a actt tc- aACATTAA
ATTGACAACATTAACAATAC CATTCTCATT CTGt ga gccattc attgac C
ATTAGTCAATCTTGAATGGC GACA |||| || ||||||| ||||||
TCAATAG GATA CT CGGTAAG TAACTG A
A ---- TTC ATTACATA

GAM201 GATCGTCTGCCCGCGGCCGC 959 TTCGAGCGTC 4029 T - --- G C ACG---------- GT
TCACGTTCACGCCGTGGAGG AGCGGCGTGG GA CGT CTG CCCGCG CCGCT ACGTTC CC G
ATCTGGAAGAATTCGAGCGT GGAA || ||| ||| |||||| ||||| |||||| ||
CAGCGGCGTGGGGAACAGCA CT GCA GAC gggtgc ggcga tgcgag GG /
CGTC - C aag - c cttAAGAAGGTCTA AG

GAM202 GCTGCGTGGAGAGACGGCGG 960 ATGCGGTTCG 4030 ATGA T GA GTGGTTT G A-- G
GGAATGATCGTCTCCGATGC GGGACCCGCG ACGGCGGGGA TCG CTCC TGCGGGTT CCCGAGCCG ATC GA C

GGGTTGTGGTTTCCCGAGCC GGGA |||||||||| ||| |||| |||||||| ||||||||| ||| ||
GGATCAGAGCCCTCACGGAT TGTCGCCTCT AGC Gagg gcgcccag gggcttggc taG
CT C
GCGGTTCGGGGACCCGCGGG ---- - g- ------- g GCA C
GAGCGATCTCCGCTGTCGTC
TCCCGCGGC
GAM203 GTAAAATGGCCTTGGTATGT 961 TGGTATGTGT 4031 CT--- tg----- ta
GTGGCTACTAATAGGCTTAG GGCTACTAAT GTAAAATGGC tggtatgtg gctactaa g
TAGTAATATTTTGCATACCA AGGC |||||||||| ||||||||| ||||||||
TTACTGCTATTTTGC CGTTTTATCG ACCATACGT TGATGATT /
TCATT TTTATAA cg

GAM204 TAGACAATGGACTGTCTTTG 962 TATCTTAAGA 4032 --- TCTT-- AAAA - GAT
TCTTGAAAAAGTATCTTACG TATTTCTTTA TAGACA ATGGACTG TGTCTTGA GTATCTT AC
A
ATAGTAGTAAAGATATCTTA GTCT |||||| |||||||| |||||||| ||||||| ||
AGATATTTCTTTAGTCTATA GTTTGT TAtctgat atagaatt tatAGAA TG /
ACTGTTTG CAA ttcttt c--- A ATG

GAM205 GCTAAAAGAGGGTTACGTGC 963 AAGAGGGTTA 4033 - - ta ccc---- g
CCGGGACGGTGTCCCACAAC CGTGCCCGGG GCTAAaa g agggt cgtg gggac g
CACATGATGCCCTACTTTTT ACGG ||||||| | ||||| |||| |||||
AGC CGATTTT C TCCCG GTAC CCCTG /
T A TA ACCAACA T

GAM206 CTGTTTCTGATTCAGATTCC 2958 TTAATAGTGG 6028 TC - ATTCC G AA C
CCTTGGCTAAAAGTTGCATC AGGTTGCCCT CTGTT TGATT CAG CCTT GCTA AGTTG A
AATTAATAGTGGAGGTTGCC GTAG ||||| ||||| ||| |||| |||| |||||
CTGTAGTCACGGACAG GACAG ACTga gtc ggag tgat ttAAC /
GC t ccgtt g aa T

GAM207 CGGCCGTGTGCGCAGGTTAC 2959 GTACTCCAAA 6029 T C TACG G C TC
TACGTGGGGGACTCACTCTT CGTGACCTCG CGGCCG GTGCG AGGTTAC TGGGG ACT AC T
TGTTGGTACTCCAAACGTGA TACT |||||| ||||| ||||||| ||||| ||| ||
CCTCGTACTGGTTG GTTGGt catgc tccagtg acctc tgG TG /
- - caa- a T TT

GAM208 GGGCGCTAAACCTCTGAGAC 2960 TGATTTGGCT 6030 CTAA-- TCT C Ttg cta c c
CCGTTGATTTGGCTATCACC ATCACCCCTT GGGCG ACC GAGAC CG atttgg tca cc t
CCTTGGGATGACCCCAAATG GGGA ||||| ||| ||||| || |||||| ||| ||
TGAGTTTCTGGTGACACACG TCCGC TGG CTTTG GT TAAACC AGT gg t
CCT ACACAG T-- A G-- CC- a g

GAM209 AGATATCATGGGAGGCGCTG 2961 TCCCAGAAAG 6031 ATCA G-- AAG TC

GGAGAAAGTCTCCCAGAAAG TCTCCCAGAA AGAT TGGGAGGC CTGGGAGA TC C
TCTCCCAGAAAGTCTCCCAG AGTC |||| |||||||| |||||||| ||
AAAGTCT Tctg accctctg gaccctCT AG /
aaag aaa GAA AC

GAM210 ATGTGCTACCTGCCGACAGT 2963 TCTGTACGGT 6033 C CT GA TCA T CAA ---
C CA
GTTGTCAAGGTTGGTGTCAG AACTGATATC TG TAC GCC CAGTGTTG AGGT GGTGTCAG
GCC TGGGGT GCT C
CAAGCCTGGGGTCGCTCACA TACC || ||| ||| |||||||| |||| |||||||| ||| |||||| |||
AAGCACTCTGTACGGTAACT AC ATG CGG GTCGTAGC Tcca ctatagtc tgg gtctCA CGA
/
GATATCTACCTCCCGATGCT - TT -- CC- t aa- cat - AA
GGGCTTGTACACAT

GAM211 CTTTTTTACGACTCCATCAG 2962 CATCAGAAAG 6032 A CTCca g g t a G GACCA -
AAAG
AAAGAGGTTTAATATTTTTG AGGTTTAATA TT CGA tca aaaga gtt aat ttttT TGA TCG
AAGAGAG A
TGAGACCATCGAAGAGAGAA TTTT || ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||
AGATAAAACTTTTTTACGAC AA GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTC T
TCCATCAGAAAGAGGTTTAA - ACCAG G A T G G ACCTC A AAAA
TATTTTTGTGAGACCATCGA
AGAGAG
GAM212 TAAAATTAAATTAATTATAA 2964 TAAGTTAGTA 6034 - - TA-- - A-- - T
AATTATGTATATGATTTACT ATACATAAAT TAAAAT TAA ATTAAT TAAAATT ATGTAT
TGATTTA CTAAC T
AACTTTAGTTAGATAAGTTA TTTA ||||||| ||| |||||| ||||||| |||||| ||||||| |||||
GTAATACATAAATTTTAGTA ATTTTA ATT TAATTA attttaa tacata attgaat GATTG T
TATTAATATTATATTTTA T A TATG a atg A A

GAM213 TTACCTGCAGCCTAACCCTA 2965 TGTGTTGGTG 6035 C-- AACC CCTA - T T
GCCCTAACCCTAGCTCATGC ACAGTCCTTG TTACCTGCAG CT CTAGC AC CC AGC C
TTGGAGTGTGTTGGTGACAG CAGG |||||||||| || ||||| || || |||
TCCTTGCAGGTGA AGTggacgtt ga ggttg tG GG TCG A
cct cagt tg-- A T T

GAM214 GGAAATAGCCTTTGGATTAT 2966 CAAGATCAAT 6036 T TA CC A GCC
GCCTTTGATAGTGCCTCAGG CCAACGGTTG GGAAATAGCC TTGGAT TG TTTG TAGT T
CTACAAGATCAATCCAACGG TTTC |||||||||| |||||| || |||| ||||
TTGTTTCC Cctttgttgg aaccta ac gaac ATCG /
c -- ta - GAC

GAM215 ATGGATTTTACTAGATCATT 2967 TACTAGATCA 6037 - TTt - attt- acc
TATATACCAAAAAATATTAT TTTATATACC ATG GAT ac tagatc atat a

ACGATCTACGTTTTATTATA AAAA ||| ||| || |||||| ||||
T TAT TTA TG ATCTAG TATA a
A TTT C CATAT Aaa

GAM216 CTTTTTTACGACTCCATCAG 2968 CATCAGAAAG 6038 A CTCca g g t a G GACCA - AAAGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA T CGA tca aaaga gtt aat ttttT TGA TCG AAGAGAG G
TGAGACCATCGAAGAGAGAA TTTT | ||| ||| ||||| ||| ||| ||||| ||| ||| |||||||
AGAGATAAAACTTTTTTACG A GCT AGT TTTTT TAA TTG AGAAA ACT AGC TTTTTTC A
ACTCCATCAGAAAGAGGTTT - ACCAG G A T G G ACCTC A AAAAT
AATATTTTTGTGAGACCATC
GAAGAGAG
GAM217 CCACCTGCCCGCCCGCCCGC 2969 AGGGAGCGAG 6039 - CG- C-------- C CCA G CGC
CCACCTGACCCGCGCAGAGG CTGTTGAGTT CCAC CTGCC CC GC CGC CCT ACC G
TAAGGGAGCGAGCTGTTGAG GGAT |||| ||||| || || ||| ||| |||
TTGGATTGGCAGAGTGG GGTG GACGG gg cg gcg gga TGG C
A Tta ttgagttgt a ag- A AGA

GAM218 ATAAAAATATTTTTGTAAAA 2970 AATATTTTTG 6040 aaaa a-- GA
CTTTTTTTATGAGACCATCA TAAAACTTTT ATAAAaatatttttgt ctttttt TGA C
AAGAGAGAAAGAGAATAAAA TTTA |||||||||||||||| |||||||| |||
ATATTTTTGT TGTTTTTATAAAAATA GAAAGAGA ACT /
AGA- GAA AC

GAM219 GTGGAGGAGAGAGAGAAATA 2971 GAGGAGAGAG 6041 - - - aataag - T
AGCACCTTTACCTTTTTTGG AGAAATAAGC GTG gag gagag agaga cacctTTA CCTT T
GGATAAAGGTGAATCTCTAC ACCT ||| ||| ||||| ||||| |||||||| ||||
TCTCGCTCTCAC CAC CTC CTCTC TCTCT GTGGAAAT GGGG T
T G A AA---- A T

GAM220 CCCCCGACTCCAACCTCATT 2972 TCCCAGAACT 6042 AACCTCA-- TC -- T CGTA -- - GG GA
CAAAATCCCGCTTGAGTTCC CTAGACCGGT TTCAAAA CCG CT GAGTTC GGGGAAGTGA GTCT C T
GTAGGGGAAGTGAGTCTGGC GTTT ||||||| ||| || |||||| |||||||||| |||| |
GATTTGAGAGACCCCTCGCT AAGTttt ggc ga ctcaag cctCTTCGCT CAGA G /
TCTCCCAGAACTCTAGACCG GCTTCTAAG gt ca t ac-- CCC GA TT
GTGTTTTGAAGAATCTTCGA
GAGTCTGGGGG
GAM221 GATGGTCTCATAAAAAAAGT 2973 ATAAAAAAAG 6043 G TCATAAAA TTTTAC ATTCT- CTCTCTT TG
TTTACAAAAATATTTTTATT TTTTACAAAA AT GTC AAAG AAAAATATTTTT CTTT TGA G
CTCTTTCTCTCTTTGATGGT ATAT || ||| |||| |||||||||||| |||| |||

CTCATAAAAAAAGTTTTACA TG TAG TTTC TTTTtataaaaa gaaa aCT /
AAAATATTTTTATTCTCTTT G TTTCTCTC TCTTA- catttt aaaat-- CT
CTCTCTTTGATGGTC

GAM222 CGCGTTAGTGGTCCGTGGGA 2974 TTAGTGGTCC 6044 -- c g a agtT CCAT G
AGCTAAGTTGGCCATTGGAG GTGGGAAGCT CGCGt tagtggtc gtg ga gcta GG TG A
ACACCTAGCTTGCACAGACC AAGT ||||| |||||||| ||| || |||| || ||
ACTACCACGCG GCGCA ATCACCAG CAC TT CGAT CC AC G
CC A G - ---- ---- A

GAM223 GAAATGCCGCGTGATATCCC 3030 TATCCCTATG 6100 C A- a ttc gtTATG
TATGGTTCAGTTGGTTGTTA GTTCAGTTGG GAAATGCCG GTG tatccct tgg agttggtt T
TGTAAAAGAGACCAGCTTTC TTGT ||||||||| ||| ||||||| ||| ||||||||
CAGGGGATACACACACGGCG TTTTGCGGC CAC ATAGGGG ACC TCGACCAG /
TTTT A AC - TT- AGAAAA

GAM224 GATGCTGTGGGACAGCGCAT 3031 CACTCTATGC 6101 GA C - - GGTA
AGAGTGTCTGAGTTCTGGTA ACTGCTTCGC GATGCTGTGG CAG GCATAGAGTGTCTG AG
TTCT A
ATGGAGGGATCTCCAGGCAC AGCG |||||||||| ||| |||||||||||||| || ||||
TCTATGCACTGCTTCGCAGC CTgcgacgct gtc cgtatctcacGGAC TC AGGG /
GTC tc a C T AGGT

GAM225 GCAAGATCCCGCATGAGTCC 3032 TAGCTTAGAG 6102 A TC CAT TCC CGT - T
CTCTGAGCCGTTAGTTGTGA AGTCTCTCAC GCA GA CCG GAG CTCTGAGC TAGTT
GTGATA A
TATACTTATCACTAACTAGC GGTG ||| || ||| ||| |||||||| ||||| ||||||
TTAGAGAGTCTCTCACGGTG CGT CT ggc ctc gagattcg atCAA CACTAT C
TCTGC - gt act tga --- T T

GAM226 GCGCGTCGTGTACTGTAACA 3033 ACTACATCAA 6103 GT-- T AACAT-- AAATTA
TGTCCAAATTACAGGAAAAG CGTACGAAAG GCGCGTC GTAC GT GTCC C
GACTACATCAACGTACGAAA ATGT ||||||| |||| || ||||
GATGTGC CGtgtag catg ca caGG A
aaag - actacat AAAAGG

GAM227 CCACGCCGAAAAGATGTCCA 3034 TCTCTCACAA 6104 C AA--- T A TCGTCAAGAT ACC
GGCTCGTCAAGATGGGACCC TCTGCGTGG CCACGC GA AGA GTCC GGC GGG C
TTTTCCGCCGGATCTCTCAC |||||| || ||| |||| ||| ||| |||
AATCTGCGTGG ggtgcg ct tct tAGG CCG CCT /
t aacac c - ---------- TTT

GAM228 CTGCCCGACCTAAAGTCCTT 3035 TCATGGGGGA 6105 AC AAA- A- A- - AA
CAAGGCCAAGTGCAATGTGA CCCAGAGTGC CTGCCCG CT GTCCTTCA GGCC AGTG C T

CGCTGAGGCTCATGGGGGAC GGGC ||||||| || |||||||| |||| |||| |
CCAGAGTGCGGGCAG GAcgggc ga cagggggt tCGG TCGC G /
gt gacc ac AG A TG

GAM229 GTGTGTGCTGGATTTCTGCA 3036 AGGGGCAGAT 6106 GT- T- TT- AA- GGCC
ATGTGGCCATGGAACAGGGG CCTCCCCGCC GTGT GC GGA TCTGC TGT A
CAGATCCTCCCCGCCGAACA GAAC |||| || ||| ||||| |||
C CAca cg cct agacg aCA /
agc cc cct ggg AGGT

GAM230 GGACGCGTCTAGTATCTACG 3037 TCTAGTATCT 6107 CG --- cta- acct g
TCTCACCTCTGAATAGTCTA ACGTCTCACC GGA CGtct agtat cgtctc ct A
GAGACGCCAAATACTTTAAG TCTG ||| ||||| ||||| |||||| ||
ACGGATCC CCT GCAGA TCATA GCAGAG GA A
AG ATT AACC ATCT T

GAM231 GCGGGAGCTGGGATCCTGGA 3038 TGGGATCCTG 6108 - gg - - aga ag
GGACAGAGCCAGGTCAGGCG GAGGACAGAG GCGGGAG Ct gatc ctg gaggac gcc G
TCCTCTTGGCGGTCAGGTCT CCAG ||||||| || |||| ||| |||||| |||
CCCGT TGCCCTC GG CTGG GGT CTCCTG CGG T
T A- C T --- AC

GAM232 TTTTTGAACAATACGCACTG 3058 TATAATAAAT 6128 ACA TG--- A GTGA -- G
GTAATATCCGTGATCCCGTG CGTGTGTATC TTTTTGA ATACGCAC GT ATATCC TC CC T
TGGAAGAGAGAGGATATAAT TCAA ||||||| |||||||| || |||||| || ||
AAATCGTGTGTATCTCAAAA AAAaact tatgtgtg ta tatAGG AG GG G
A c-- ctaaa a AGAG AA T

GAM233 GGCTCTCTGCGGCTCGCGTT 3059 TCTCTGCGGC 6129 tc ctcgc t ttcCC G
CGCGTTCCCCGGTGACGAAA TCGCGTTCGC GGC tctgcgg gt cgcg CG T
CCCGCGCACACCGCAGAACG GTTC ||| ||||||| || |||| ||
CC CCG AGACGCC CA GCGC GC G
CA A---- C CCAAA A

GAM234 AAGAATATATCTTAAGATAG 3060 TATCTTAAGA 6130 AT- t ctt gAAAGAGAT
TAGCTTTTCTGAAAGAGATA TAGTAGCTTT AAGA Atatc taagatagtag ttct A
TATATATTAAGAGTACTACT TCTG |||| ||||| |||||||||| ||||
ATCTTGCGATATTAGTCTT TTCT TATAG GTTCTATCATC GAGA /
GAT C AT- ATTATATAT

GAM235 TGTCCTCTATGGGTCTCAGA 3061 TATGGGTCTC 6131 TCt t - -- - TG CGT
TGCCTGGCGGCCCTGCCGTA AGATGCCTGG TGTCC atgggtc cagatg cct ggcggcC C C A
CACGTGGAGGTTGCCCGGGG CGGC ||||| ||||||| |||||| ||| ||||||| | |

TTATCTGCGACCCGTGGACA ACAGG TGCCCAG GTCTAT GGG CCGTTGG G G /
--- C T GC A GT CAC

GAM236 AAATTTTAAACTGCAATGTC 3062 TAAGAGTTTT 6132 AACTGCAAT CCTCTG GA TT
TCCTCTGAAAACTCTGATAG ATCTAAAGAT AAATTTTA GTCT AAAACTCT TAGA A
ATTATCTCTAAGAGTTTTAT TTTT |||||||| |||| |||||||| ||||
CTAAAGATTTTTTTTCCTAA TTTAGAAT taga ttttgaga atCT /
GATTT CCTTTtttt aatcta -- CT

GAM237 GATGCGGGAGATAAGCCAAA 3063 GTCAAGTACC 6133 C GG AAG A-- TATAAA C
CTTTATAAAGACCATGGTCG TGGACGTCTT GATG G AGAT CCA ACTT GAC A
TCAAGTACCTGGACGTCTTT TCTG |||| | |||| ||| |||| |||
CTGTC CTgt c tctg ggt tgaa CTG T
- tt ca- cca ctg--- G

GAM238 TATTATCGAAATTGTATTAG 3064 TATTAGGAGA 6134 A ta a aaatt ca
GAGAAATTATAAGACAATTT AATTATAAGA TATTATCGAA TTG tt ggag ataaga a
TTTTATCACCATTCCAGAAT CAAT |||||||||| ||| || |||| ||||||
TAAGTTTGATAATA ATAATAGTTT AAT AG CCTT TATTTT t
G TA A ACCAC TT

GAM239 ACGTCCAGCCTCTCGGCCGA 3065 TGCACAGTCT 6135 AG TC - GA GC--------- GG
GGACGCCGTGGTAGACGAGT CGGGCCTGAA ACGTCC CC TC GGCC GGAC CGT T
GGTGCACAGTCTCGGGCCTG GGGA |||||| || || |||| |||| |||
AAGGGAAGGACGT TGCAGG gg ag ccgg tctg GCA /
Aa ga t gc acacgtGGTGA GA

GAM240 GATGCCTGACCGCCTCACTG 1 AAGGACCAAA 3071 G ----- C CT --------- AAAC- AA
CTGTCCTAAACAGGTACAAG AGTTTAGCCT GAT CCTGA CCGC TCA GCT GTCCT
AGGTAC G
ATGTACTTTCTCAAGGACCA GAGC ||| ||||| |||| ||| ||| ||||| ||||||
AAAGTTTAGCCTGAGCGGGA CTA GGACT GGcg agt cga cagga TTCATG /
CAATCAGGATC - AACAG - c- tttgaaaac aCTCT TA

GAM241 GAGATTCTTGCAGCGGATAT 2 TGAGTAGAGT 3072 GA T GCGGATA A AT
TTATACGGGATTAGTTTGAG ACACATGCGG GA TTCT GCA TTTAT CGGG T
TAGAGTACACATGCGGAGCA AGCA || |||| ||| ||||| ||||
TC CT gagg cgt agatg gtTT /
ac - acacatg a GA

GAM242 AGGGGAACTTATGACTGTTA 3 TGTTATAAAA 3073 TAT Ct t ataa a
TAAAAAATAAGAATAAGATT AATAAGAATA AGGGGAACT GA gt ataaaaa gaat a
CCATTTTTATTATTATCTGG AGAT ||||||||| || || ||||||| ||||

TTCTCCT TCCTCTTGG CT TA TATTTTT CTta /
T-- AT T AC-- g

GAM243 ACATGTCCTCCCTGCTCACC 4 TCGCGGAGGA 3074 T - T- - AAGAAC
ATGAAGAACCTCATGCACGT GGGCCTGT ACA GTCCTCC CTGC CA CCATG C
GGTTGTCGCGGAGGAGGGCC ||| ||||||| |||| || |||||
TGT tgt cgggagg ggcg GT GGTGC T
c a ct T ACGTAC

GAM244 CACCTGCTGAACGCGGGCTT 5 CAGCCACGGC 3075 - TGAAC TC T-- CAC CC
CGCCTGCCACGGCCCCCCGG CAGCTCGCCA CACCT GC GCGGGCT GCC GC GGCC C
GCCTCAGCCACGGCCAGCTC CCTG ||||| || ||||||| ||| || ||||
GCCACCTGCGAGGTG GTGGA Cg cgctcga cgg cg CCGG /
G tccac c- cac acT GC

GAM245 GCTCTCCGACGTCAGCCGCG 3066 ACTGGTCGGG 6136 G A G -- G ACG
CAGGGCACGTACCAGCACTG GTAGGCGTGG GCTCTCC ACGTC GCC CG CAG GC T
GTCGGGGTAGGCGTGGAGAG AGAG ||||||| ||||| ||| || ||| ||
T Tgagagg tgcgg tgg gc gtc CG A
- a g tg a ACC

GAM246 TCTGGGGTCCAGGACACAAT 3067 TCCAGGACAC 6137 TG tc c aa tagag
CTCTGCTAGAGCGCAACCGC AATCTCTGCT TC GGG cagga ac tctctgc C
GGGGAGGGTTCCTGAGCTCT AGAG || ||| ||||| || |||||||
GGA AG CTC GTCCT TG AGGGGCG G
GT GA - GG CCAAC

GAM247 TGGGTGGTTAACAAGAACAA 3068 CTGCGCCCTC 6138 TAACA ACAACAC CT- TT- A
CACCCTGCTGCGCTTTGACT AGGTCCCTCT TGGGTGGT AGA CCTG GCGC TG C
ACACCTGCGCCCTCAGGTCC GCCA |||||||| ||| |||| |||| ||
CTCTGCCACCCA ACCCaccg tct ggac cgcg AC T
----- ccct--- tcc tcC A

GAM248 CCCCTGTTTGACTTTTACGC 3069 TCCCCCAGTC 6139 --- G CGC C CA - G AGG
A C
GGTGGGCGCGCCGGGCGCCA CCTGGCCCCC ACTTTT AC CGGTGGG GCCGGG GC GGGG
TGT GCCTAC GCC CC A
GGGGTGTGGCCTACAGGGCC GCCG |||||| || ||||||| |||||| || |||| ||| |||||| ||| ||
ACCCACAGGGGCATGGTGGG TGAGGA TG gccgccc cggtcc tg cccc ACA CGGGTG
CGG GG C
CAACATCCCCCAGTCCCTGG CTT G c-- c ac t A GTA - A
CCCCCGCCGGGTTTCAGGAG
TGCAGGGG
GAM249 GGGGCCCGCCAGCTACGCGA 3070 GCGGGCCATG 6140 - --- ACGT AG G AACC
GA G CA

GCTACGTGGTCAGGGGGGAC GTCGCCTTCG CCGCCAGCT ACGCGAGCT GGTC GGG
GAC TGGT CG CCGT G
AACCTGGTGACGGCCGTCAG ACCA |||||||||| |||||||||| |||| ||| ||| |||| || ||||
CTACGGGCGGGCCATGGTCG GGTGGTCGG TGTGTTTGa ccag tcc ctg accg gc
GGCA /
CCTTCGACCAGTTTGTGTCC A ACC ---- ct g gt-- g- g TC
AGGCTGGTGGACAACCCC

GAM250 GCGTCTAAATTTAAAAAAGT 6 TCTAAATTTA 3076 a ----- ag - A CC
TTATATATTAGTACCAAATA AAAAAGTTTA GCGtcta at ttaaaaa ttta tataTT GTA A
TAAATATACTAAAGATTTTT TATA ||||||| || ||||||| |||| |||||| |||
AATTATAGTATGGACGT TGCAGGT TG AATTTTT AAAT ATATAA TAT /
A ATATT AG C A AA

GAM251 TGTTTACAATAGTAACTAGT 7 TTAGAAGATT 3077 T - CTAGTAA AG
AAAATGAAGTCATCATTAGA TATTATCTGT TGT TACA ATAGTAA AATGA T
AGATTTATTATCTGTATACA ATAC ||| |||| ||||||| |||||
Aca atgt tattatt ttACT /
t c tagaaga AC

GAM252 GGTTAGAAACATTTGGTTTA 8 TATGACAATT 3078 AGAAACAT GTT c ccggatacc- T
AA
TGACAATTCCGGATACCTTT CCGGATACCT GGTT TTG tatga aatt ttttcTCAG AT T
TCTCAGTATAATCAAATCTT TTTC |||| ||| ||||| |||| |||||||| ||
GGGAAGATCAATAAGAAAGT CCAA AAT ATACT TTGA AGAAGGGTT TA C
TTTCATATAATAATATAACA GACAATAT AAT T AAGAATAACT C AA
GAACC

GAM253 GGCTGCCTAATCTTACAGGG 9 TGCTATCGGG 3079 T A- ACA GG AAGACA
AGCAGAAAGACACACAGACT AGATCAAGGT GGC GCCT ATCTT G AGCAGA C
CTGCTATCGGGAGATCAAGG GCC ||| |||| ||||| | ||||||
TGCC ccg tgga tagag c tcgtCT /
- ac gg- ta CAGACA

GAM254 ATAAGTTTATATATATATTA 10 TATATTATTG 3080 a cccga C GACCCGC --
ACC
TTGGCCCGAGTGCGAGCCCT GCCCGAGTGC TATAtat ttattgg gtgcgagc CTGG GCCAGC
TCTCACG G
GGGACCCGCGCCAGCTCTCA GAGC ||||||| ||||||| |||||||| |||| |||||| |||||||
CGACCGTGCCCGTGAGAACG ATATATG AATAACT CACGCTTG GACC CGGTCG
AGAGTGC T
CTGGCAGAATGCCAGCGTTC - CAAAA C GTAAGA- CA CCG
GCACAAAACTCAATAAGTAT
ATATATATTAT
GAM255 GGCGAGGGTCCTGGCAGAAG 11 TGGCAGAAGG 3081 TCCt CT--- TAG C
GCCGGCCGGTCGGAGCTGGC CCGGCCGGTC GGCGAGGG ggcagaaggccggccggtcggag
GGC CCGGC G

TAGCCGGCCGCGGCTGGATG GGAG |||||||| |||||||||||||||||||||| ||| |||||
TCTGTCTCTCTGGCTGGCCG CTGCTTCC TCGTCTTTCGGCCGGTCGGTCTC CTG
GGTCG C
GCTTTCTGCTCCTTCGTC ---- TCTGT TA- G

GAM256 TCCCTGCTTGCTCACGGCCG 12 GAGGACCCCG 3082 G CC-- A - TC CCT
CCCCTCACCCTTCTCCCTTT GCGGTGAGCA TCCCTGCTTGCTCAC GCCG CCTC CC CT TC
T
CGCGATTGGCGGGAGGACCC AGCA |||||||||||||| |||| |||| || || ||
CGGCGGTGAGCAAGCAGGGA AGGGacgaacgagtg cggc ggag GG GG AG T
g ccca - C TT CGC

GAM257 CCCGCCAAGTGAGCTCCGCC 13 AGACGGGGGT 3083 CCA A CGG G
CACCCAGCCCCCACCCTCAT GGGGGCTGGG CCCG
AGTGAGCTCCGCCCACCCAGCCCCCACCCTC TCT GCCCG G
CTCGGGCCCGGGGGCGGGCA TGGG |||| |||||||||||||||||||||||||||||| ||| |||||
GACGGGGGTGGGGGCTGGGT GGGC TCACTCGAGGCgggtgggtcgggggtggggg aga
CGGGC G
GGGCGGAGCTCACTCGGG --- c --- G

GAM258 GGCGTGTCGCGCTCGCTCGC 14 AGGCAGCCGC 3084 T - C C--- CG TT
CCGGGCGGTTCATCCGCTTC GGCCGCC GGCG GTCGCG CT GCT GCC GGCGG C
GGCTTTAGGCAGCCGCGGCC |||| |||||| || ||| ||| |||||
GCC ccgc cggcgc ga cgg CGG TCGCC /
- c - aTTT CT TA

GAM259 GGCCACATGTGCGGTATGGG 15 TGACGCTGAC 3085 ACA --- ATG G TATC
GGTCGACTATCAAAACGTGG TTACAACGGC GGCC TGTG CGGT GGGGTC AC A
CCCTGACGCTGACTTACAAC C |||| |||| |||| |||||| ||
GGCC ccgg acat gtcg tCCCGG TG /
ca- tca cag - CAAA

GAM260 CCTCCAGTACGTCGTGGTCA 16 TCCAGTACGT 3086 c cgtc t c--- a CG
ACGGTACAGACGTGTTTTTG CGTGGTCAAC CCt cagta gtgg caa ggt CAGA T
GACCAGCCTTGCCATATGCT GGTA ||| ||||| |||| ||| ||| ||||
GCAGG GGA GTCGT TACC GTT CCA GTTT G
C A--- - CCGA G TT

GAM261 GCTTGCTTTGGCCCGCCTTG 17 TAGCCCCCTG 3087 - TTT C---- CT CTT C TT TCG
CGCTTTTGCATTTGGCTCGC GCCCGCAGTG GC TTGC GGCC GC TGCG TTG AT GGC C
CCCTGCCCGGTTTAATTTGC C || |||| |||| || |||| ||| || |||
ATAGCCCCCTGGCCCGCAGT cg gacg ccgg cg ACGT AAT TG CCG C
GC t c-- tcccc at TT- T GC TCC

GAM262 TCCCTGCTTGCTCACCGCCG 18 GCTTGCTCAC 3088 c gggt c AA GCGA
GGGTCCTCCCGCCAATCGCG CGCCGGGGTC TCCCTgcttgctcac gccg cctc CGCC TC A
AAAGGGAGAAGGGTGAGGGG CTCC |||||||||||||| |||| |||| |||| ||
CGGCCGTGAGCAAGCAGGGA AGGGACGAACGAGTG CGGC GGGG GTGG AG A
C ---- A GA AGGG

GAM263 GGGAAAGAGAAGGAGGGGAA 19 AGGGGAAGGA 3089 AAGA A AG Aa aa agaa cc
GGGGAAGGAGAAGGCGCCGC GAAGGCGCCG GGGA GA GG GGG gggg gg ggcg g
ACTGCCGCCCGCTCCCGGCC CACT |||| || || ||| |||| || ||||
CGCCGTCCGTCCC CCCT CT CC CCC CCCT CC CCGt c
GC-- G G- GG CG CG-- ca

GAM264 CGCATAAGGCACCGCGGCTG 22 TAAGGCACCG 3092 taag a-- gg - tc ACAG
GGCCCTTCACACAGGCAAAA CGGCTGGGCC CGCA gc ccgcggct gcc ct AC G
GTAGGGAGGCAGGGCCGCGG CTTC |||| || |||||||| ||| || ||
CGAGTAATTTGCG GCGT TG GGCGCCGG CGG GG TG C
TTAA AGC GA A GA AAAA

GAM265 CCGAGTGAGCTCCGCCCACC 23 CGAGATGAGG 3093 C --- GC
CAGCCCCCACCCCCGTCTGC GTGGGGGCTG CCGAGTGAGCTCCGCCCACCCAGCCCCCACCC
CGTCT GCCC C
CCGCCCCCGGGCCCGAGATG GGTG |||||||||||||||||||||||||||||| |||||| ||||
AGGGTGGGGGCTGGGTGGGC GGTTCACTCGAGGCGGgtgggtcgggggtggg gtaga CGGG
C
GGAGCTCACTTGG a gcC CC

GAM266 GGGGGAAAGGGGAAGGAGGG 24 CCGCCGCCCA 3094 G AAAG- AA G A TAGAA A C
GAGGCTAGAAGCAGCGGGCG TCCGCCTAGC GG GG GGG GGA GGG GGC GC GCGGG G
GGCCCGTCGTCCGCCGCCCA GGCT || || ||| ||| ||| ||| || |||||
TCCGCCTAGCGGCTGCC CC tc tcc cct ccc ccg TG TGCCC G
G ggcga g- a g cc--- C G

GAM267 GGACAGGCCCCCCCGCTGGC 25 CATTGGATTT 3095 G- C T C TA- A TCTCG
GCAAAAATACAATAGCTCTC TTTGCCCGCG GGACA GCCCCC CGC GG GCAAAAA CAAT GC
A
GATTATCCGCCATTGGATTT CGGG ||||| |||||| ||| || ||||||| |||| ||
TTTGCCCGCGCGGGGGCGAT CCTGT CGGggg gcg cc cgttttt gtta CG T
GTCC AG c - - tag c CCTAT

GAM268 GCCGCAGCCCCAGCTGCCCC 26 CAGCTGCCCC 3096 - A CC t - - g- g
CCCGGCGCGCGCGATAGCGA CCCGGCGCGC GCCG C GC cagc gccccccg gcg c cgc a
GGTTGCTCGGGGGGGCGCTG GCGA |||| | || |||| ||||||||| ||| | |||
TTGCCGCCGGC CGGC G CG GTCG CGGGGGGGC CGT G GCG T

C C TT - T T GA A

GAM269 CCATAAAGACCATTACCTCG 20 TGCCTTAGAG 3090 AAA ATTA --- - GTT
GGGCTCCAGTTTGGTGTGGA AGGGGGTTAG CCAT GACC CCTC GGGGC TCCA T
TGCCTTAGAGAGGGGGTTAG TGG |||| |||| |||| ||||| ||||
TGG ggtg ttgg ggag ttccg AGGT G
a-- g--- aga t GTG

GAM270 TGGATTATTTCTCCCAACAC 21 TATTTCTCCC 3091 Ttattt ca ag CA AAC
CCCAGTATTCAACAACATCA AACACCCCAG TGGA ctcc acacccc tatt AC A
GTGATAAGGGGTGTGGAGTC TATT |||| |||| ||||||| |||| ||
TCCA ACCT GAGG TGTGGGG ATAG TG /
CT---- -- A- -- ACT

GAM271 CCACCCAGAGCCACATGAGG 27 ACGGACCCAC 3097 AGA A- A A CG G
ATCCCGTCGCGGGAACGGAC ATGGCGGCGG CCACCC GCC CATG GG TCC TC C
CCACATGGCGGCGGAGGGTG AGGG |||||| ||| |||| || ||| ||
G GGTggg cgg gtac cc agg AG G
agg cg a c ca G

GAM272 CCATGTCAGAGGTCCAGTAC 28 TCAATGGGTT 3098 T - T GATAC TC- AA
CCATGATACTGGCATCACTG TGTGGCCTTT CCATG CAGAGGTC CAG ACCCAT TGGCA
ACTGTT A
TTAAACAGACAGTTCTTGTC GCCA ||||| |||||||| ||| |||||| ||||| ||||||
AATGGGTTTGTGGCCTTTGC GGTac gtttccgg gtt tgggta actGT TGACAG /
CATGG c t - ----- TCT AC

GAM273 GAGAACAGATGAGGTCGTCG 29 TATAATGGAA 3099 A - G --------- AAA
CAGAAAATCTCCTGTATAAT GGGGATCATC GAGA CAGATGA GGTC TC GCAG A
GGAAGGGGATCATCATCTGT ATCT |||| ||||||| |||| || ||||
CTT TTCT Gtctact ctag gg tGTC T
- a g aaggtaata CTC

GAM274 TATCCAATATGTTGTTGTGA 30 TCCAATATGT 3100 a g a - ATTTC ACA -
GTCAGT
ATGGCACAGATGTATTTCTG TGTTGTGAAT TAtcca tatgtt ttgtga tggcaCAGAT GT TGGA GCC
CT T
GAACAGCCCTGTCAGTTTTT GGCA |||||| |||||| |||||| |||||||||| || |||| ||| ||
CCAAGAGGCCTATCCAACAA GTAGGT GTACGA GACACT ACCGTGTTTA CA ACCT
CGG GA /
TTTGTGCCAGTCACAGGAGC C G G A ----- ATC A ACCTTT
ATGCTGGATG

GAM275 ATCACTCAATTCCAGACCCT 36 CATCACAGGT 3106 TTCCA TG AC - A AGCACT

GCCTACGAGTATAGGAGCAC GGGGTCCTTG ATCACTCAA GACCC CCT GA GT TAGG A
TATCAATCCCTGGGCATCAC GGTG |||||||||| ||||| ||| || || ||||
AGGTGGGGTCCTTGGGTGAT TAgtgggtt ctggg gga ct cG GTCC /
c---- gt ca a G CTAACT

GAM276 GGCCGCCGCGCGCCCCCGCC 31 CCGCCGCGCG 3101 C C CCCC C C C CCCC C C C GC
CGGCCGCCGCGCGCCCCCGC CCCCCGCCCG GGC GCCG GCG CGC CGGC GCCG GCG CGC CGGC GCCG GC C
CCGGCCGCCGCGCGCCCCCG GCCG ||| |||| ||| ||| |||| |||| ||| ||| |||| |||| ||
CCCGGCCGCCGCGCGCCCCC CCG CGGC CGC GCG GCCg cggc cgc gcg gccg cGGC CG C
GCCCGGCCGCCGCGCGCCCC C C CCCC C c c cccc c c C CC
CGCCCGGCCGCC

GAM277 AGGGACTCCGGAGAAGGAAG 32 GCGCGCCCTT 3102 CTCC A- C T CG
GCTGCTCCGCGCACCGGCGC CTCCTCTCCC AGGGA GGAGA GGAAGG TGC CCG C
GCCCTTCTCCTCTCCCCTCC CTCC ||||| ||||| |||||| ||| |||
CT TCcct cctct tcttcc gcg gGC /
cc-- cc c c CA

GAM278 GGGGCTTGGCCGCCGAGGTG 33 CACCTCGGCG 3103 TT ---- GGC
CGCCCCGGCCGGAGGGGCCC GCCGCCCC GGGGC GGCCGCCGAGGTGC GCCCC C
CCGCACCTCGGCGGCCGCCC ||||| |||||||||||||| |||||
C ccccg ccggcggctccacG CGGGG /
-- CCCC AGG

GAM279 AGAAACACGAGGCGGGGGTC 34 AACCCGTATC 3104 C TC - --- CAG A CA - ACC
CCAGAAAGGGCAGGCAGGTC CTTTTTTTCT AGAAACA GAGGCGGGGG CC AGAAA GGG GC GGT GC CGC G
AGCCGCACCGCCCGCGAGCC AGGT ||||||| |||||||||| || ||||| ||| || ||| || |||
AACCCGTATCCTTTTTTTCT TCTTTGT TTTTGTTTTT gg tcttt tcc tg cca CG GCG /
AGGTGTTTTTGTTTTTGTTT - Gt a ttt ta- c aC A CCC
CT

GAM280 GGAAAGCGGAAAAACGGAGG 37 AAGCGGAAAA 3107 aa- aaaa G - AA - TCCCG
ATGGAAGGGCAGAAGATGGG ACGGAGGATG GGA gcgga cggaggatggaagG C AG GATG GGGAG A
GAGTCCCGATCCTCCTCCTG GAAG ||| ||||| |||||||||||||| | || |||| |||||
CATCCCCTCGCCTTCCATTC CCT CGCCT GCCTCTTACCTTCC G TC CTAC TCCTC /
TCCGGCCCTCCGCGAGTCC GAG CCCG - C CC G CTCCT

GAM281 GGGCCGCGGGCCAGCAGACG 38 CCCACGCCTC 3108 ------- CCA AGAC GGC

GGCCGCGGCGCCAGCGGCCC CCGCCGCATT GGGCC GCGGG GC GGGCCGC G
ACGCCTCCCGCCGCATTAGG AGGC ||||| ||||| || |||||||
CCC CCcgg cgccc cg cccGGCG /
attacgc tc- ca-- ACC

GAM282 GAAAATTTGTGAGTATATCA 35 TGAGTATATC 3105 A ---- tatcag atta
GATCATATTATAAAGATGAT AGATCATATT GAAA TTTGt gagta atcat t
ATAAGTTACTTTGAAACAGG ATAA |||| ||||| ||||| |||||
ATTTC CTTT GGACA TTCAT TAGTA /
A AAGT TGAATA GAaa

GAM283 GCAATGTTAAAGTGACTCCT 39 TTAAAGGTAA 3109 - TAAA CT- AGAT- AC T
CCAGATTACTCACCTATAAT GAGTTATGAC GC AATGT GTGACTC CC TACTC CTA A
AGCGAGTATTAAAGGTAAGA GCAT || ||||| ||||||| || ||||| |||
GTTATGACGCATTAGC CG Ttacg tattgag gg ATGAG GAT /
A cag- aat aaatt C- A

GAM284 TATCAAGATGTGTATATTTG 40 CAGCACAAAT 3110 - ---------- CGAAAA G
CGAAAATTGTGGAGACATAG CAAAAGTATT TATC AAGATGTGTAT ATTTG TTGTG A
CAGCACAAATCAAAAGTATT AATA |||| |||||||||| ||||| |||||
AATACATGTCTTAGATG GTAG TTCTGTACata taaac GATAC G
A attatgaaaac acgac- A

GAM285 GCCGAGGACTTACTTGACGA 41 ACGAATCTCC 3111 A AC TTG t t
ATCTCCTGTGGACTTGGTTC TGTGGACTTG GCCG GG TTAC acgaatc cctgtggac t
GCAGGGGTTTGTGTGACCCG GTTC |||| || |||| ||||||| |||||||||
GT TGGC CC AGTG TGTTTGG GGACGcttg /
- -- --- - g

GAM286 GGGCTGATGTAGAGATGAGA 42 AAGCCGCCCA 3112 ----- T G - G TA
ATTGTTCTGGGGGGCTTTGG GAATAGGTTT GGGCTGA TG AGA ATGAGAAT TGTTCTGGG
GGCTTTGGCCA A
CCATAAACTGGCTAAAGCCG TCGT ||||||| || ||| |||||||| ||||||||| ||||||||||
CCCAGAATAGGTTTTCGTGT TCTGACT AC TTT tgcttttg ataagaccc ccgaaATCGGT /
TTCATGAACTCAGTCT CAAGT - G g g CA

GAM287 GTCTGGACCGCACAGTGTGT 43 CCGCACAGTG 3113 GAcc c g ag A
GTGGCAAAGGCATCGGCGTT TGTGTGGCAA GTCTG gca agtgtgtgt gcaa gc T
GCGACGCGCGCTTTGTTCAG AGGC ||||| ||| ||||||||| |||| ||
CAGGC CGGAC TGT TCGCGCGCA CGTT CG C
GACT T G G- G

GAM288 GTGTCTATGCCACGTTGCTC 44 TATGCCACGT 3114 Cta ccac ctc ac C

GCACATGCGTATCACAGTAC TGCTCGCACA GTGT tg gttg gc atgcgTAT A
GCGTAGCCATAACCTTACAC TGCG |||| || |||| || ||||||||
TCACGC CGCA AC CAAT CG TGCGCATG C
CTC ATTC AC- A- A

GAM289 CGGCTGTTTGTTAAGCAGGA 48 AAGCAGGAGC 3118 C TT a -- acgc - g
GCCCCACGCCTCCCGAAAGG CCCACGCCTC CGG TG TGTTaagc ggagc ccc ctc cc a
TGAGAGAGGGCCGCTTCCGC CCGA ||| || |||||||| ||||| ||| ||| ||
TTGATATCATCTG GTC AC ATAGTTCG CTTCG GGG GAG GG A
T T- C CC AGA- T A

GAM290 CAACCATTTCCGGTCGCTTA 49 TAAGGGAAGA 3119 TTTC G--- C--- - A
TACGAGGTAGAGTTCTGCTC TCGATGTTGG CAACCA CGGTC CTTATA GAG GTAG G
TCACGTTATAAGGGAAGATC TTG |||||| ||||| |||||| ||| ||||
GATGTTGGTTG gttggt gctag gaatAT CTC CGTC T
tgta aagg TGCA T T

GAM291 TCTCCACTCTCTCGGTGTTC 50 TCGGTGTTCC 3120 - Ct - a gtcctcAAT ATACTCA GTTA
CAGAGGCATGTCCTCAATGC AGAGGCATGT CACTCT cgg tgttccag ggcat GCTGGT ATGGC T
TGGTATACTCAATGGCGTTA CCTC |||||| ||| |||||||| ||||| |||||| |||||
TCAAAGCCGTGGGCCAGCGT GTGGGA GTT ACAGGGTC CTGTG CGACCG TGCCG /
GTCCTGGGACAGTTGCAAGG T AC G - --------- GG----- AAAC
GTGTGATGA

GAM292 GTCAGGACCCCTTTGGTCCA 51 ACCCCTTTGG 3121 a tg t-- a --- g T
TGTCGCGCGGGTCCTCCGGT TCCATGTCGC GTCAGG cccctt g cc tgtc gc cggG C
TCAGGCAGGCGTCTGAAGGG GCGG |||||| |||||| | || |||| || ||||
GCTTGAC CAGTTC GGGGAA C GG ACGG TG GCCT /
- GT TGC - ACT - C

GAM293 TTCCCGGGGAGGAGGGCACC 45 TTCCCGGGGA 3115 GGA - A AGG GGA - A AGG --- AG
AGGTTCCCGGGGAGGAGGGC GGAGGGCACC GGA GG GC CC TTCCCGGGGA GG GC CC TTCCCGGGGA GG G
ACCAGGTTCCCGGGGAGGAG AGGT ||| || || || |||||||||| || || || |||||||||| ||
GGCACCAGGTTCCCGGGGAG CTT CC CG GG AGGGGCCCTt cc cg gg aggggccctt CC G
GAGGGCACCAGGTTCCCGGG GGA A - AGG gga a - agg GGA AC
GAGGAGGGCACCAGGTTCCC
GGGGA
GAM294 CACCTCTCCATAGTTGCAAA 46 TAAAATGTTG 3116 CATAGTT AAA T AAAT CAAG GACT C
TACGCTACGAAATGCCCAAG GCCGCGTGTG CACCTCTC GC TACGC ACG GCC GACATT AAA G

GACATTGACTAAACGTGTTT TAGG |||||||| || ||||| ||| ||| |||||| |||
CTAAAATGTTGGCCGCGTGT GTGGAGGG TG atgtg tgc cgg ttgtaa TTT T
GTAGGGTTTTCAGAGGGAGG AGACTTT gg- - gc-- ---- aatC G
TG

GAM295 TACCCAGCCGGGTTTACGCA 47 ACGCAGCTGC 3117 C g t a T
GCTGCGTATACCCAGCTGTG GTATACCCAG TACCCAGC GGGTTTac cagctgcgta accc gctgtG T
TTTACGCAGCGGGGTTTACG CTGT |||||||| |||||||| |||||||||| |||| ||||||
CAGCTGGGTAGACCCAGCTG ATGGGTCG CCCAGATG GTCGACGCAT TGGG CGACGC
T
GGTA A G T G A

GAM296 GAAGGAGGGTTGAATACAGT 52 TGGTATTCCC 3122 G GT A TG G CGC c agct -
- tT
TGGGGGTAGTCCGCTGGTAT AGCTGAGGTT GAGG TGAAT CAGT GGGGTA TC tggtatt cc
gaggt tgcc A
TCCCAGCTGAGGTTGCCTTA GCCT |||| ||||| |||| |||||| || ||||||| || ||||| ||||
TTTGGTAATGCTTCCGGAAA TTCC ATTTG GTTA CCCCAT AG ACCATAA GG CTTCG
ATGG T
TACCACCTGAGTACCCCATT G AT - -- G TCC A C--- TA TT
GGTTTATACCTTGTTT

GAM297 GTGGGCGCCGCGCGCGTGCT 53 GAGTGCGCGC 3123 G C TG GTC A GCT- CA
CTCTCAGTCGCGCCTAGCTG GCTGCGCTGA GT GGCGC GCGCGCG CTCTCTCA GCGCCT
GCT TC A
CTTCCAACAGACAAAAGCGG C || ||||| ||||||| |||||||| |||||| ||| ||
GGCGTTAGTGAGGGAGTGCG ca tcgcg cgcgcgc gagGGAGT TGCGGG CGA AG /
CGCGCTGCGCTGAC g t gt GAT G AAAC AC

GAM298 AAAGACTCGCTCAACAGCCC 54 TGGATTAGGT 3124 CGC A - GAAAA A CC
GAAAACCATCAGCCCGACCG GCTGCTGGAC AAAGACT TCA CAGC CC CCATC GC G
CCGATGGATTAGGTGCTGCT AAGT ||||||| ||| |||| || ||||| ||
GGACAAGTCTTT TTTCtga ggt gtcg gg ggtAG CG A
aca c t atta- C CC

GAM299 GCTCTGAATTTTTCTGCGCA 1590 TTAGTCAGAT 4660 AATTTT - ------ GAC
CATCTACATAA G
TGCGCGACTCCTCATCTACA AGCAGGGC GCTCTG TCTG C GCATGCGC TCCT
TTTAT C
TAATTTATGCACATAAAAGG |||||| |||| | |||||||| |||| |||||
ATTAGCGCATGCAAATTAGT cgggac agac g CGTACGCG AGGA AAATA A
CAGATAGCAGGGC gat--- t attAAA ATT ---------- C

GAM300 TTGACCGGCAAGTTCCAGGC 1598 CACCAGGGAC 4668 -- CA A CA TG- TG
ATCCTAAGTGCTTGATGTAG TACCTAGGTC TTGACC GG AGTTCC GG TCCTAAG CT A
ACCCTTAGGGCACCAGGGAC AA |||||| || |||||| || ||||||| ||

TACCTAGGTCAA aactgg cc tcaggg cc GGGATTC GA T
at a- a ac CCA TG

GAM301 CTGCTGGACGGAGGTAGTAT 1599 AGGTAGTATA 4669 C CGGa c t T- ACAA
AATCAGCTAGGCCTCAGTAT ATCAGCTAGG CTG TGGA ggtagtataat agctaggcc cAGTATTCTA
GTA A
TCTATGTAACAAATGAATGC CCTC ||| |||| |||||||||| ||||||||| |||||||||| |||
CCTAGAGTACTGCGGTTTAG GAC ACCT CCGTCATATTG TCGATTTGG GTCATGAGAT
CGT /
CTAGTTATACTGCCCGGTTC C TGGC A C CC AAGT
CACCAG

GAM302 CCTGGAGGGGTGTCACATTC 1600 TGTGATAGCC 4670 - - G T- C--- - ACG
TGTGACCGCGACGTTGACGT CATCACAGG CCTG GA GGG TGTCACATTCTG GAC
GCGACGT TG T
TAGACACACGTCGCTGCCGT |||| || ||| |||||||||||| ||| ||||||| ||
CCTCAGAATGTGATAGCCCA ggac ct ccc atagtgtAAGAC CTG CGCTGCA AC T
TCACAGG a a g TC CCGT C AGA

GAM303 GCTGTTGCGTTGGTTGGGAG 1601 TGTTGCGTTG 4671 t t-------- g
TTTGGGGACCAAATTTCTAT GTTGGGAGTT GCtgttgcg tgg tgggagtttgg G
AATTGGTGTCACCGCGGCAG TGGG ||||||||| ||| ||||||||||
C CGACGGCGC ACT ATCTTTAAACC /
C GTGGTTAAT A

GAM304 GTGGCTCGCGACCACCCACC 1591 TTGGACCCGT 4661 C - ---- ---- T ATT
TGGATTTTGGACCTGGCTTT GGCTCGCGAC GTGG TCGCGA CCAC CCA CC GG T
TGGACCCGTGGCTCGCGACC CAC |||| |||||| |||| ||| || ||
AC cacc agcgct ggtg ggt GG CC T
- c ccca tTTC T AGG

GAM305 GGCTGACCCAAAATTTTAAA 1592 AGAGGGCCAG 4662 A A A G AT- GTA TA
AATTGGGGTTAGCCATCCTG GCTGACCCAA GGCTGACCC AA TTTTAAAA TT GGGTTAGCC
CCT CAAAAA T
TACAAAAATATTACTTTTTG AATT ||||||||| || |||||||| || ||||||||| ||| ||||||
AGAGGGCCAGGCTGACCCAA CCGATTGGG TT AAAATTtt aa cccagtcgg ggg GTTTTT T
AATTTTAAAAATTGGGGTTA G A a a acc aga CA
GCC

GAM306 CCGGCATGCTTCTCGCCCGA 1602 CGGGCAGATC 4672 AT T CC CC AT TC
TCCCCCCGATCTCACCCGGC CTGTGAGATG CCGGC GC TCTCGC GATC CCCG C A
CGGGCAGATCCTGTGAGATG CGCC ||||| || |||||| |||| |||| |
CGCCGG GGccg cg agagtg ctag gggc G C
-- t tc ac CG CC

GAM307 GCGCGCATAATGGCGGACCT 1603 GTCTATGGTT 4673 - TAATG G - AAAA C
AGGCCTAAAACCCCCAGGAA GGCTGCGCTG GC GCGCA GC GACC TAGGCCT CC C
GCGGGTCTATGGTTGGCTGC C || ||||| || |||| ||||||| ||
GCTGC cg cgcgt cg ttgg atctgGG GG C
t ----- g t CGAA A

GAM308 AGCCCTCAGACCGCGTCCGC 1604 TCTGTGGAGT 4674 AGAC CG G CC G ---- T GT A G TG
GCCCCGGGCCAGCCTAGCGT TTGGTTTCGA AGCCCTC CG TCC CGC CGG CC AGCC AGC CGCA AC TC G
CGCAAACGTCTGGAAGAGTC GGGC ||||||| || ||| ||| ||| || |||| ||| |||| || ||
TGTGGAGTTTGGTTTCGAGG TCGGGAG GC AGG GCG GCc gg ttgg ttg gtgt tG AG /
GCCGTGCGGGGAAACGCAGA AC-- AA G T- g agct t ag c - AA
GGGCT

GAM309 CGTTAAGGTGTACGTGCGTG 1605 TAAGGTGTAC 4675 aagg tg gtgt GT
TACGAGACCGCGTGCGAGCG GTGCGTGTAC CGTt tgtacg c acgagaCCGC G
GTCTCGTCGTAGTGCGTATG GAGA |||| |||||| | ||||||||||
AACG GCAA GTATGC G TGCTCTGGCG C
---- GT ATGC AG

GAM310 GAATATTTTTAAAGACTTTT 1606 TTAAAGACTT 4676 t ctttttc t
TTCCCCAACCTCTGGGTTGG TTTTCCCCAA GAATATTTt aaaga cccaacc c
GTTTTTTCTCTTTAAAATAT CCTC ||||||||| ||||| |||||||
TC CTTATAAAA TTTCT GGGTTGG T
- CTTTTTT- G

GAM311 CCCGGGGAGATAGGCGCTCG 1607 CACGTCTTTG 4677 C- TC ----- - T- AA- - G- - C
CGGAGAGGGGGTTGGGCGAA CCCCTTGCTC G GC GC GGAG AGGGGGT GGGCG GGA CGGG GGGGTG GTGC T
GGACGGGGGGGGTGGTGCCT CAGT | || || |||| ||||||| ||||| ||| |||| |||||| ||||
GGCGCGCGCCCCAGCCCGTT C TG CG cctc ttccccg tctgc CCT GCCC CCCCGC CGCG /
CCGCACGTCTTTGCCCCTTG CT GA TTtga g tt acG T GA G G
CTCCAGTTTGCAGGTTCCCT
CTTTCTCCAGG
GAM312 TCCCCCAAAGACACTCTCGG 1611 CGGTTGGGCG 4681 C AAGACACTCT G AGG
CCGACCGCAGAGGGATAACT CGTGGGCGA TC CCCA CG CCGACCGCAG G
GCGGTTGGGCGCGTGGGCGA || |||| || ||||||||||
ag gggt gc ggttggcGTC A
c gc-------- g AAT

GAM313 GAGAGTGACCACACAAGAAG 1612 TTAAATTTTT 4682 G CAC GAAA G
AGAAAAAAAGTCATTTTAAA TTATTGGTTA GAGA TGACCA AAGAAGA AAAA T
TTTTTTTATTGGTTAATTTC ATTT |||| |||||| ||||||| ||||

Cttt attggt ttttttt ttTT C
a ta- aaa- A

GAM314 AGCAGACAGGTTAGAGCACT 1593 TGTTGTGTGA 4663 AG AG GAGC - a ag a
GTTGTGTGATGTGAGAGGAG TGTGAGAGGA AGC AC GTTA ACtgttgtgtgatg tg gagg t a
TAAGTGTGTCTCCACCATCG GTAA ||| || |||| ||||||||||||||| || |||| |
CATAACAGTTGATAGGTGGG TCG TG TAGT TGACAATACGCTAC AC CTCT G G
CT GG GA ---- C - GT T

GAM315 CGATGTGTTTGACAATGTAC 1594 TAGAAAGCTC 4664 - CAATGTAC TTT A---- TG GG GA CT A
TCTTTGCTTTCAACTGCAGG TGATCAAACT GTTTGA TC GCTTTC AC CAG TGTTTTA ATGG TC A
GTGTTTTAGAATGGCTTCAA TCAT |||||| || |||||| || ||| ||||||| |||| ||
CAGATTCATTAAAATGTTCT caaact ag cgaaag TG GTC GTAAAAT TACT AG C
GTGGTCCATAGAAAGCTCTG t -------- tct atACC GT TT -- T- A
ATCAAACTTCATTG

GAM316 TCTGGATCTTGGTAGGCGGC 1595 CTTGTGCTGT 4665 TG A TT ----- C ACT
CGCGAGGGACTGTTGCTTCT GAATTCTATC TC G TC GGTAG GCGGC GCGAGGG G
TGTGCTGTGAATTCTATCTT TTGA || | || ||||| ||||| |||||||
GACTGGA AG C ag ctatc tgtcg tgttcTT T
GT - tt ttaag - CGT

GAM317 AATGCTATGGAATTAGTAGT 1613 TATGGAATTA 4683 gaatt ta g C GT
GGGACCCGGGCGTGGTCCAG GTAGTGGGAC AATGCtatg ag gt ggacccggG GTG C
TATCCTGGGTCTGGCCGCTT CCGG |||||||||| || || ||||||||| |||
GTAGCATT TTACGATGT TC CG TCTGGGTCC TAT C
----- GC G - GA

GAM318 CCCAATGTGCAAATGTGGTT 1596 GAAGTGGAAA 4666 AAT CAAA T- G GG CT- CCT
TGTATGGCTACTTTGTGTTC CCCTCAGTCA CCC GTG TG GGTTT TAT CTA TTGTGTT A
CTAAAAAATGCAACAATAGA CGGG ||| ||| || ||||| ||| ||| |||||||
AGTGGAAACCCTCAGTCACG ggg cac ac ccaaa gtg gAT AACGTAA /
GG --- tg-- tc g aa AAC AAA

GAM319 GCGACCTCGTGAATATGAGG 1597 TGAGGACCAA 4667 C-- C ATAt ca----- accc GC
ACCAACAACCCTGTGCTTGG CAACCCTGTG GCGA CT GTGA gaggac aca tgtgcttg G
CGCTCAGGCGCAAGTGTGTG CTTG |||| || |||| |||||| ||| ||||||||
TAATTTGTCCTCCAGATCGC CGCT GA CGCT CTCCTG TGT ACGCGGAC /
AGCAATCGC AAC - AGAC TTTAATG GTGA TC

GAM320 ACTAACCCTAATTCGATAGC 1608 ACCCTAATTC 4678 ctt G
ATATGCTTCCCGTTGGGTAA GATAGCATAT ACTAaccctaattcgatagcatatg CCC T

CATATGCTATTGAATTAGGG GCTT |||||||||||||||||||||||| |||
TTAGT TGATTGGGATTAAGTTATCGTATAC GGG /
AAT T

GAM321 TATCGCAGCGTTGCGACATC 1614 TCGCAGCGTT 4684 c cg-- ccTA C -
ATAAGCCTAAGA TG
GTCTCCTACATTCTCGTTGA GCGACATCGT tg gacat tct CATT TCGTT GAATA
AATTTTGCA C
ATAATAAGCCTAAGAAATTT CTCC || ||||| ||| |||| ||||| ||||| |||||||||
TGCATGCATTGCGAGATTGT AC TTGTA AGA GTGA AGCGA CTTAT
TTAGAGCGT /
AATATTCAAGCGAAGTGAAG - TTTA A--- - A AATG-------- TA
AATTTATGTTCAGCCTTGCG
GTA
GAM322 AGCGGGGTCTCGGAGCTCCT 1615 TGGCGTGTTT 4685 ---- CTCC G GA GAA-- T
AGGTCAGACCACGAAAGGTC TCTGAGGTTA AGCGGGGG TCTCGGAG TA GTCA CCAC
AGG C
AGCCTGCAAGGTGGATGGCG TCCC ||||||| |||||||| || |||| |||| |||
TGTTTTCTGAGGTTATCCCC TCGCccc ggagtctt gt cggt GGTG TCC A
GCT tatt tt-- g A- GAACG G

GAM323 GACATTAATTCTTACGCTCA 1616 TCTTACGCTC 4686 TAATtctt tcat tact g
TGGGTACTTCGGTGACGACC ATGGGTACTT GACAT acgc ggg tcg t
CTTATGCGTTAAAATGTGTT CGGT ||||| |||| ||| |||
TTGTG TGCG CCC AGC G
TAAAAT-- TATT ---- A

GAM324 CTCCCGGGTACTTACTCGCT 1609 CGTCCATGTT 4679 TACTC AACT- T CG- TC A TT-
G A- TT
AACTCTCGCTGCTCGGGCTC GATCAGGTCA ACT GCT CTCGC GCT GGC GGT AAC
GACGC CTT GT C
GGTAAACTTGACGCGCTTAG TCGG ||| ||| ||||| ||| ||| ||| ||| ||||| ||| ||
TTTCGTCACAGAAGGCGTCC TGG TGA GGGTG Cgg ctg cta ttg ctgcG GAA CA G
ATGTTGATCAGGTCATCGGC TAC-- AACTT C cta ga g tac - GA CT
CGTGGGTTCAAAGTCATGGT
TCCCGGGG
GAM325 GGAAAACGTAAAGGTGGGCC 1617 TGCCTAACCT 4687 AA AA GC --- CT-- A C AG
CGGTCAGCTGGACGTCCGAG GATACCTGGA GGA ACGT AGGTGG CCGG TCAG GG
CGTC G T
TCTCCGATGCCTAACCTGAT TCTA ||| |||| |||||| |||| |||| || |||| |
ACCTGGATCTACCTATGTTC CCT TGTA TCCatc ggtc agtc cc gtAG C /
C -- -- ta cat caat - C TC

GAM326 TGTATTTATGTTTATTTTTT 1610 TTTATGTTTA 4680 ttt tt tttatt T-- T TA T
TATTATTTATTAATATATTT TTTTTTTATT TGTA atgt atttt atttATTAA ATATT GTGT AAA T
GTGTTAAAATTATTTTCTAC ATTT |||| |||| ||||| ||||||||| ||||| |||| |||

ATTAATATTATTTAATAAAT ACAT TATA TGGAA TAAATAATT TATAA TACA TTT A
TAAAATAAGGTTTATATTTT TT- TT TAAAAT TAT T TC T
ACA

GAM327 TTGTAATAACATTATTTACA 1618 ATTAAATTTA 4688 TTAT-- t tat--- tat
TTAAATTTATCATTTAATAT TCATTTAATA TTGTAATAACA TTACat aaatt catttaa t
TTTTCTTAAATGTATTTCAG TTTT |||||||||||| |||||| ||||| |||||||
TTTCATGTGGTTTATTTGTT AATATTATTGT GGTGTA TTTGA GTAAATT t
ATTATAA TTATTT C CTTTAT CTt

GAM328 CGCCGGTGGCGCGTCCGCGC 1619 TCGGCGCGAC 4689 G G - G T AAAA
GGCGGGTGAGGAAAACCGTC GGACGCGTAG CGCCG TG CGCGTCCG CGCG CGGG GAGG
C
CCTCCTCGGCGCGACGGACG CGGC ||||| || |||||||| |||| |||| ||||
CGTAGCGGCG Gcggc at gcgcaggc gcgc gctC CTCC /
g - a g - CTGC

GAM329 GTAGAAGTCTCAGGCTAGCC 1620 AGTCTCAGGC 4690 ag g - cc - - AAAATAAAC GT
CT
GGCAGCCCCAAAATAAACGT TAGCCGGCAG GTAGA tctca gc tag ggca gc ccc GT CGT C
GTCGTCTCGAACGGAACTAA CCCC ||||| ||||| || ||| |||| || ||| || |||
ATACCGGGTGTGTGTCTCTG CGTCT GGAGT TG GTC CTGT TG GGG CA GCA /
TGTGTGAGGTCTCTGC CT G T T- G T CCATAAAT- AG AG

GAM330 GGCGCGTCGGCGGCCGTGAC 1625 TTCGATGAGC 4695 - ------ - TGAC GAG
TCGAGCGGCGAGCGCCGGCC CGCCCGAAGG GGCGC GTC GGCGGC CG TCGAGCGGC
C
GTTCGATGAGCCGCCCGAAG GACA ||||| ||| |||||| || |||||||||
GGACAGCGCC CCGCG cag ccgccg gt agcttGCCG G
a ggaagc a ---- GCC

GAM331 GTGTTTATATAATTGTTTAG 1621 AGATTACAGT 4691 TT A---------- TTAGG C
GGGCAAGTCAGATTACAGTA AGATTTTAAA GTGT ATAT ATTGT GG A
GATTTTAAAAATATTTACAC AATA |||| |||| ||||| ||
CACA Tata tgaca CT A
TT aaaattttaga ttaga G

GAM332 TTTTTTGGTTATTGGAAATG 1626 ATCTCCTTGA 4696 TTAT --------- C
AGATTTCTGAAAATCTCCTT TAAGATTTCC TTTTTTGG TGGAAAT GAGATTT T
GATAAGATTTCCATTTCAAA ATTT |||||||| ||||||| |||||||
AGA AGAAAACt accttta ctctHAA G
tt-- gaatagttc A

GAM333 TATTATGTATTTTTATTCCG 1622 TATGTATTTT 4692 t g t gctagaa--- GAT

CTAGAACTATAGATGCTAAT TATTCCGCTA TAT at tattttta tcc cTATA G
GTAGAAACAAAGAAGGATTA GAAC ||| || |||||||| ||| |||||
AAAATAGATTGTA ATG TA ATAAAAAT AGG GATGT C
T G T AAGAAACAAA AAT

GAM334 GGAGCTAATAAATACACGGG 1623 TAAGTGTATT 4693 AATA GG AG GA GA
TAAGCGGACGGATATACGGC GGAAGCTCT GGAGCT AATACAC GTA CG CG T
GATATAAGTGTATTGGAAGC |||||| ||||||| ||| || ||
TCT tctcga ttatgtg tAT GC GC A
agg- aa A- G- AT

GAM335 GTTCTGATCTTTCTTGTACA 1624 TTCAAGTTTT 4694 T -- c-- tt --- c taa- C AG GA
TTCA
TGTTCAAGTTTTCGGCGGTT CGGCGGTTAA CT GTACA TGtt aagt tc gg ggt gatg TTT A
TAG A
AAGATGCTTTAGAGATAGTT GATG || ||||| |||| |||| || || ||| |||| ||| | |||
CAAGATTTTAGATTCAAAAC GA CATGT ACGA TTTA AG CC CTA CTAC AAA T ATT
/
ATCACTTATCTCCACAGATC - TA ACC CT ACA T TTCA A CT AG TTAG
ATTTCCAAGCAATTGTACAG
AAAGATAGAAT
GAM336 GGATATCCTGTAGTTTTTGA 1627 ATCCTGTAGT 4697 at t gt ggtttttT G
TGGTTTTTTGGTTGATGACT TTTTGATGGT GGAT cc gta ttttgat GGTT A
TACACAAGATCAAAAGTTAC TTTT |||| || ||| ||||||| ||||
TGGTAATCC CCTA GG CAT AAAACTA TCAG /
AT T TG GAACACAT T

GAM337 TCATAGATATGATACAACAC 1632 TGAGTTAAAA 4702 TGATACAACAC CAA---
aaaaata aa
AACACTACAAATTATATGAG AATATAGAAT TCATAGATA AACACTA ATTATAtgagtta
tag t
TTAAAAAATATAGAATATCT ATCT ||||||||| ||||||| |||||||||||| |||
AATAAATAATTTATGTAATA AGTATTTAT TTGTGAT TAATGTATTTAAT Atc /
CTAGCTAGTGTTTATTTATG ---------- CGATCA AAATA-- ta
A

GAM338 GTCTGAGGGATGGCTCGTCC 1628 TGAGGGATGG 4698 t tc cca aa ACAC
AACAAACCACACATCGAGGA CTCGTCCAAC GTCtgaggga ggc gt aca cC A
ATGTAATACCTGTCCTCTCT AAAC |||||||||| ||| || ||| ||
CAGAT TAGACTCTCT CTG CA TGT GG /
C TC TAA AA AGCT

GAM339 TACAGTTTGCCCAATGTAAA 1629 TAAACGATAA 4699 CCCA- t c caa- - AA
CGATAAGCAATAAAGGTCAT GCAATAAAGG TACAGTTTG ATG aaa gataag taaaggt cat A
AAACAGATGAACTTTTAAGA TCAT ||||||||| ||| ||| |||||| ||||||| |||
TTTTATTTTTCATACACTCG ATGTCGAGC TAC TTT TTATTT ATTTTCA GTA C

AGCTGTA TCACA - - TAGA A GA

GAM340 GGATTATGGGGCTAGCTCAG 1633 TAGCTCAGCT 4703 Cta -- ctcgct at
CTCGCTAATGCATAATAGCA CGCTAATGCA GGATTATGGGG gc tcag aatgc a
TTCAACTGACAGCAACCCCA TAAT |||||||||| || |||| |||||
TAGTCT TCTGATACCCC CG AGTC TTACG a
AA- AC AAC--- At

GAM341 GGAGCCGGGAGGATAGCTCA 1634 TTATGTATAT 4704 C TA-- TC GTTAAG
ACCTGTTAAGAACTCAGAAG TCTTCCTTGC GGAGC GGGAGGA GC AACCT A
GTTATGTATATTCTTCCTTG TCC ||||| ||||||| || |||||
CTCC cctcg tccttct tg ttGGA A
t tata ta AGACTC

GAM342 TAAAATATAAATAAGATCAG 1638 TGAGTCGAGC 4708 AATAAGA A GAG A- - ATA
CT
ATTGTGAGGGCCACTCACTC AGGCCACAGA TAAAATATA TCAG TTGT GGCC CTC
ACTCAC TTCGG G
ACATATTCGGCTGCGTCCGG CTGG ||||||||| |||| |||| |||| ||| |||||| |||||
AGTGAGTCGAGCAGGCCACA ATTTTATAT ggtc gaca ccgg gag tgagtG AGGCC C
GACTGGGTAAGAATATATTT AAGAATG a --- ac c --- TG
TA

GAM343 TGGACCGCATGGTGACCGAC 1630 CCAGCGCGAG 4700 - A- T ACG GA C
GTGCGCGAGGCCGTGGCCCA CGGTTCCACC TGGAC CGC TGG GACCG TGCGC GGC G
GCGCGAGCGGTTCCACCGCG GCGA ||||| ||| ||| ||||| ||||| |||
AGTCCA ACCTG gcg acc ttggc gcgcg cCG T
a cc - ga- ac G

GAM344 GCCATCCTGAATCCCCACTG 1631 ACCCCAATGA 4701 CA TGA -- T CT C CC
TCTACA A TA
GCTCCCGCCGCCGGGGTTCT CGGGTTCCTG GC TCC ATC CCCAC GG CCCG CG GGGGT
CGGGCG G C
ACACGGGCGAGTACGACATG TGGG || ||| ||| ||||| || |||| || ||||| |||||| |
CCCGACCCCAATGACGGGTT CG AGG TAG gggtg cc gggc gt cccca GCCCGT C /
CCTGTGGGACGATGTGGACA AC TG- CA t tt a aa ------ A AG
GC

GAM345 GCGTATCCCACCTTTGAAAG 964 CACCTTTGAA 4034 Cca----- aaagc -- cgAAA
CACCTCCTAACGAAAGACCT AGCACCTCCT GCGTATC cctttg acc tcctaa G
AATTGGGAAAGGTTAAACGA AACG ||||||| |||||| ||| ||||||
AGGACAAAGACGATACGC CGCATAG GGAAGC TGG AGGGTT A
CAGAAACA AAAT- AA AATCC

GAM346 TATTTCAGAACAACAATCTG 965 AGACGATAGT 4035 AGAACAACAA CT-- - ------- -
AACATC GTT

CTCCCACTGCTCCTATCGAA GACGACGAAG TTTC TCTG CCCAC TGC TC CTATCG
CG A
CATCCGGTTAATAACGCAGA TAGG |||| |||| ||||| ||| || |||||| ||
CGATAGTGACGACGAAGTAG GAAG AGAT GGGTg atg ag gatagc GC A
GTGGGCCTATAGAAGTACAA CCGAACATGA ATCC g aagcagc t agaC-- AAT
GCCGAAGTA

GAM347 ATTTCACGTGGCTTAGAATC 966 TGACTACACC 4036 C ---- CT AATC TTGG
GAATACTTGGACTGACGTAT TTTAGCTGAA ATTTCA GT GG TAG GAATAC A
TTATGACTACACCTTTAGCT AT |||||| || || ||| ||||||
GAAAT taaagt cg cc atc TTTATG C
- attt ac agtA CAGT

GAM348 TGCTAAACTAATGATGAAGA 1635 ATGAAGATTA 4705 CTAAT tta ----- a AA AC
TTAATGCGGAGGTCTGATAA ATGCGGAGGT TGCTAAA Gatgaaga atgc gg ggtctgaT
GAATAA C
GAATAAACCTTATTATTCAG CTGA ||||||| |||||||| |||| || |||||||| ||||||
ATTAGGCCCCAAGAGGCATT ACGATTT CTACTTCT TACG CC CCGGATTA CTTATT
T
CTTCATCTCCTTTTAGCA TCCT- --- GAGAA - GA AT

GAM349 ACAAGTATACCTTCTACTTC 1636 TACCTTCTAC 4706 tac acttc- ta T
TATTGATAATCAGTTTACTG TTCTATTGAT ACAAGTA cttct tattga atcAG T
ATACTCAATGTTATTGGGAA AATC ||||||| ||||| |||||| |||||
GTTATTTGT TGTTTAT GAAGG GTAACT TAGTC T
T-- GTTATT CA A

GAM350 GCTGCGTTTATGGGTGGAGG 967 TTTATGGGTG 4037 GC t ga GG
TCTCCTGTCTGGATTAGGAC GAGGTCTCCT GCT Gt tatgggtg ggtctcctgtct A
AGGGGATTGGCGCTTATGCA GTCT ||| || |||||||| ||||||||||||
CAAGGC CGG CA GTATTCGC TTAGGGGACAGG T
AA C GG AT

GAM351 CTATTATTCTAAACTAAAAT 1637 ACTAAAATAA 4707 TCTAAac ccatt tttATTC
AACCATTTATACTTTTATTC CCATTTATAC CTATTAT taaaataa tatact C
CATAACGTAGTATATAGATT TTTT ||||||| |||||||| ||||||
TATTTTATTCTTTTATAATG GGTAATA ATTTTATT ATATGA /
G TTTTCTT TAGAT TGCAATA

GAM352 GAGCTCTCGATAAAAAAGTT 968 GATAAAAAAG 4038 -- - C AACTC TCg-- - --
a
TTTCTATAACTCGAGCTCTC TTTTTCGAAA ATA AAAAAGTTTTT TAT GAGCTC ata
aaaaagtttt tcga a
GATAAAAAAGTTTTTCGAAA TCTC ||| |||||||||| ||| |||||| ||| |||||||||| ||||
TCTCGATAAAAACTTTTTCT TAT TTTTTCAAAAA ATA CTCGAG TAT TTTTTCAAAA
AGct t

ATAACTCGAGCTCTCGATAA AA C - GCT-- CTCAA C AT c
AAAACTTTTTCTATAACTCG
AGCTC
GAM353 AAAAGCTTTTCGAAATCTCG 972 AAGCTTTTCG 4042 aat t------ C TAAC CT
TAAAAA TT
ATAAAAACTTTTTCTATAAC AAATCTCGAT cga ctcga aaaaACTTTTT TA TCGAG CTCGA
AG T
TCGAGCTCTCGATAAAAAAG AAAA ||| ||||| |||||||||| || ||||| ||||| ||
TTTTTCTAACATTCGAGCTC GCT GAGCT TTTTTGAAAAA AT AGCTC GAGCT
TC /
TCGATAAAAAAGTTTTTCTA CTC CAATATC - ---- TC TACAA- TT
TAACTCGAGCTCTCGATAAA
AAAGTTTTT
GAM354 GAGCTCTCGATAAAAAAGTT 973 GATAAAAAAG 4043 -- A GT C AACTC TCg-- a ---
- a
TTTCTATAACTCGAGCTCTC CTTTTCGAAA ATA AAAA TTTT TAT GAGCTC ata aaaagcttt
tcga a
GATAAAAAAGCTTTTCGAAA TCTC ||| |||| |||| ||| |||||| ||| |||||||||| ||||
TCTCGATAAAAAAGTTTTTC TAT TTTT AAAA ATA CTCGAG TAT TTTTTGAAA
AGct t
TATAACTCGAGCTCTCGATA AA C TG A GCT-- CTCAA C AAAT c
AAAAAGTTTTTCTATAACTC
GAGCTC
GAM355 AGTTTTTCTATAACTCGAGC 978 TAACTCGAGC 4048 AACTC TCG-- A CGAAATC CT
TAAAA TT
TCTCGATAAAAAAGCTTTTC TCTCGATAAA GAGCTC ATA AAAAGCTTTT TCGAG
CTCGA AG T
GAAATCTCGAGCTCTCGATA AAAG |||||| ||| |||||||||| ||||| ||||| ||
AAAAGTTTTTCTATAACTCG CTCGAG TAT TTTTTgaaaa agctc gagct TC /
AGCTCTCGATAAAAAAGTTT GCT-- CTCAA C aat---- tc caatA TT
TTCTATAACTCGAGCTCTCG
ATAAAAAAGCT
GAM356 GTTTTTCTATAACTCGAGCT 1639 TAACTCGAGC 4709 ACTC TCG-- A GT C TAAC CT
TAAAAA TT
CTCGATAAAAAAGTTTTTCT TCTCGATAAA GAGCTC ATA AAAA TTTT TA TCGAG
CTCGA AG T
ATAACTCGAGCTCTCGATAA AAAG |||||| ||| |||| |||| || ||||| ||||| ||
AAAAGTTTTTCTATAACTCG CTCGAG TAT TTTT aaaa at agctc gagct TC /
AGCTCTCGATAAAAAAGTTT CT-- CTCAA C Tg a ---- tc caatA- TT
TTCTATAACTCGAGCTCTCG
ATAAAAAAGC
GAM357 GTTTCGGGGATTGTGAACCG 969 GGGGATTGTG 4039 -- tg aa---------- g- tga
TGGCTGAGGGTGTAGATGGG AACCGTGGCT GTTTCgg ggat tg ccgt gc g
ACAGGAAAAAGCGTGTGATC GAGG ||||||| |||| || |||| ||
TGACCGAGGC CGGAGCC TCTA GT GGTA TG /
AG GT GCGAAAAAGGACAG GA TGg

GAM358 TAGTAATAATTTTAATCTTT 970 TCTTTGACGC 4040 T tct acgc a a taAT-- T T
TAACGC A

GACGCCTACAGCAGTAGTAA CTACAGCAGT AT TTAA ttg ctac gc gtag AAT TTAA GTT
CTAC A
TAATTTTAATGTTTAACGCC AGTA || |||| ||| |||| || |||| ||| |||| ||| ||||
TACAACAGTAGTAATAATTT TG AATT AAT GATG CG CATC TTG AATT TAA
GATG C
TAATGTTTAACGCCTACAGC T TT- AAT- A A CGCAAT T T TAAT-- A
AGTAGTAATAATTTTAATGT
TTAACGCCTA
GAM359 GTAGTAATAATTTTAATGTT 971 TTAATGTTTA 4041 TAAT-- T t taacgc a
TAACGCCTACAACAGTAGTA ACGCCTACAA GTAG AAT ttaa gtt ctac a
ATAATTTTAATGTTTAACGC CAGT |||| ||| |||| ||| ||||
CTAC CATC TTG AATT TAA GAtg c
CGCAAT T T TAAT-- a

GAM360 GGGGTGATCCGGATGCGTGG 974 TCCCGCGGAT 4044 GG A GA T CA CGA
CAAGAGGCCTCGAGCTTGGG GGACGTTCT GG TG TCCG TGCG GG AGAGGCCT G
CTTCTCCCGCGGATGGACGT || || |||| |||| || ||||||||
TCT tc gc aggt gcgc cc tCTTCGGG /
tt - ag - -- TTC

GAM361 CTACAGCAGTAGTAATAATT 975 CAGCAGTAGT 4045 a a taat-- t t TAACGC A
TTAATGTTTAACGCCTACAA AATAATTTTA CTAc gc gtag aat ttaa gtT CTAC A
CAGTAGTAATAATTTTAATG ATGT |||| || |||| ||| |||| ||| ||||
TTTAACGCCTACAGCAGTAG GATG CG CATC TTG AATT TAA GATG C
A A CGCAAT T T TAAT-- A

GAM362 AAACATTAAAATTTAGCTAC 979 CAGCAGTAGT 4049 TA- - CTACA AG TA
GCCTACAGCAGTAATAATGT AATAATTTTA AAACATTAAAATT GCTAC GC GC TAA A
TTAACGCCTACAGCAGTAGT ATGT |||||||||||| ||||| || || |||
AATAATTTTAATGTTT TTtgtaattttaa tgatg cg CG ATT T
taa a acATC CA TG

GAM363 GGCGAAAAAATAATTATTCC 986 AAAATGCTTT 4056 AAAA CCGGCC AAATTCT C
A
GGCCCGCCAAATTCTGCATC CCGGCGAAAA GGCG AATAATTATT CGCC GCAT TTGTG
A
TTGTGAAACTACAAAATGCT AATA |||| |||||||||| |||| |||| |||||
TTCCGGCGAAAAAATAATTA CCGC TTATTAataa gcgg cgta aaCAT A
TTCCGCC C--- aaaa-- ccttt-- a C

GAM364 CTTTAGATAAAGTAGTTTTT 980 AAGTAGTTTT 4050 Aaa- tttt- c gT
TGATATCGAATGGTAAAGTA TTGATATCGA CTTTAGAT gtagt tgatat gaatg A
TTTATATCATCTATACTATA ATGG |||||||| ||||| |||||| |||||
ATCATCTAGAG GAGATCTA TATCA ACTATA TTTAT A
CTAA TATCT - GA

GAM365 TGTATCGTTAAAATCTGAAT 981 TACGTTAACA 4051 A TTA AATAAAC - A
AAACCGTAGCTAATAGGTAT GGTTTCGAAA TGT TCG AAATCTG CGTA GCT A
ACGTTAACAGGTTTCGAAAC CA ||| ||| ||||||| |||| |||
A aca agc tttggac gcat TGG T
a --- aatt--- A A

GAM366 TTAAAAGGGCATATAAGTTT 987 TATAAGTTTT 4057 CAta- - aa t TTT- GT T
TCAAGAAGAATACCTTTTAT CAAGAAGAAT TTAAAAGGG taagtt ttc gaagaa acct ATGTA TGATAGA T
GTAGTTGATAGATTTATCTG ACCT ||||||||| |||||| ||| |||||| |||| ||||| ||||||| TCATACGTTTATAGGTTTCT GGTTTTCCC ATTTAA AAG CTTCTT TGGA TGCAT ACTGTCT T
TCAAGAATAATTTAGATACC CATAG T AA - TATT -- A
CCTTTTGG

GAM367 TTGTATTTGGCGCGAGTAAG 988 TATTTGGCGC 4058 - c-- a aa- -- gaAAAA-- --- TA
CCTATGAAAAACTTCCTTCT GAGTAAGCCT TTGtatt tgg gcg gt gc ctat CTTCCT TCTATGC T
ATGCTATATGTGTAGAAATA ATGA ||||||| ||| ||| || || |||| |||||| ||||||| GGAAGCAGAAGTAGTAGCAG AACATAA GCC CGC CA CG GATG GAAGGA AGATGTG /
CGAGACCGCCATCCGTAATA T TAC - GAG AC ATGAAGAC TAA TA
CAA

GAM368 GTTGCTATGGCTGCTGTTCA 976 TGGCTGCTGT 4046 At---- t t tcaa a - cTC
ACGGACCCGCCTCTTTTTGT TCAACGGACC GTTGCT ggc gc gt cgg cccg c T
CGGGCCGACTGTTGCCTGTA CGCC |||||| ||| || || ||| |||| |
CAAGCAGC CGACGA CCG TG CA GCC GGGC G T
ACATGT T T ---- - T TTT

GAM369 CTGCTTACGTTTTACTTTAA 977 TAACAGGAAA 4047 ---- A TTAATAAA TTT
TAAAGTTAAGTTTTAAGTTT TGCTCTTAGG CTGCTTA CGTTTT CT GTTAAG T
TAACAGGAAATGCTCTTAGG CAG ||||||| |||||| || ||||||
CAG gacggat gtaaag ga caatTT A
tctc - -------- TGA

GAM370 GACACGCTCTGGGCCGCGCC 982 GCGCGGCGCG 4052 GCTCT - TCCTCGTCT GA
GCTCCTCGTCTGCCGTGATC GACCTTTCAA GACAC GGG CCGCGCCGC GCCGT T
AAGCGGCGCGGCGCGGACCT GTGT ||||| ||| ||||||||| |||||
TTCAAGTGTT Ttgtg tcc ggcgcggcg cgGCG C
aactt a --------- AA

GAM371 GTGGATCCTTTACCGCTCAT 983 TCCTTTACCG 4053 A --- ------ -- - - GTTTTAC TCG

ATGGCTTCTGTTTTACGGTT CTCATATGGC G tcctt tacc gc tcatat ggc ttct GGTTCCCGG
T
CCCGGTCGTTCTGTCGGGAA TTCT | ||||| |||| || |||||| ||| |||| |||||||||
CCAGAGTGCCTATATGAACG C AGGGA ATGG CG AGTATA CCG GAGA
CCAAGGGCT T
CAATTTTGGTATGAAGGGAC C AGT TTTTAA CA T T ------- GTC
CCAT

GAM372 GAGTTCGGCGTCGCGCGCGC 984 GTCGCGCAGT 4054 - ---- CAT TCC C- -- TA
-- G
CCAGGCTCATGGAGTCCTCG TCGCGCACGC C GCGCGCGC CCAGGCT GGAG TCGCG
CGCGAG GCG GC GC T
CGCCGCGAGGCGTAGCGCGT GATT | |||||||| ||||||| |||| ||||| |||||| ||| || ||
GAGCAGGTCGCGCAGTTCGC G CGCGTGCG GGTCTGG CCTC agcgc gcgctt cgc tg
CG G
GCACGCGATTCTCCCAGGTC A AATT AC- tt- ac ga gc GA A
TGGTTAAGCGTGCGCAGGTC
CTGGATCTC
GAM373 GCGTGGTGAACAGCAGCTTG 985 TGAACAGCAG 4055 tg -- gca - c---------- c
TCGCGCTCATAAGCCAGCGG CTTGTCGCGC GCGTGG a aca gcttgt cg gct a
TTCGGCCGCCACGTACAAGC TCAT |||||| | ||| |||||| || |||
GGATGTGCTTGCCGCGC CGCGCC T TGT CGAACA GC CGA t
GT CG AGG T ACCGCCGGCTTGGCGAC A

GAM374 TTCCTCGAATTCACAGGGTG 989 GTGCCTTGTT 4059 CG ATTCACA t c - gtat
CCTTGTTTTATCTGCCGTAT TTATCTGCCG TTCCT A GGgtgcct gttttat tg cc g
GGACAGGACGAATGGAATTG TATG ||||| | |||||||| ||||||| || ||
GGCGCTCACGTTAAGGAA AAGGA T CTCGCGGG TAAGGTA GC GG /
AT GCA---- T A A ACAG

GAM375 TGCGCCTCCAGCCGCTCCGA 994 ACGCGTACCT 4064 CT-- - T --- AC C
GCGCACCTTCTTGAAGACGC CGGGCGCGTT TGCGC CCAGC CGC CCGAG CGC CTT T
GTACCTCGGGCGCGTTGGCT GGCT ||||| ||||| ||| ||||| ||| |||
ACGCGCA ACGCG ggttg gcg ggctc gcg GAA T
CAtc c - cat ca G

GAM376 CGCTCGGCTTGGTCTTCACG 1003 TACGCACCAA 4073 CT - TC CCA----- -- ACCA
TCCAGCAGCGGTACCAGTCC TCCACGTAGA CG CGGCT TGGTCT ACGT GC AGCGGT
G
CACCGTTACGCACCAATCCA GACC || ||||| |||||| |||| || ||||||
CGTAGAGACCATAGTCGTCG GC GCTGA Accaga tgca cg tTGCCA /
T- T ga cctaacca ca CCCT

GAM377 TCCTCAACAGCAGGGACCAC 990 GGCCAGGAGG 4060 AACAGCA CCA A AAA G GA
CACCAAACCGAGGGCCTGAT CAATCCCAGA TCCTC GGGA CC CC CCGAGG CCT T
CAAGGACCTCGGCCAGGAGG GGAG ||||| |||| || || |||||| |||

CAATCCCAGAGGAGGAGGA AGGAG ccct gg gg ggCTCC GGA /
gaggaga aac a acc A AC

GAM378 GCGTGTCCGGTGCTCCCCGA 995 TCTAAGGGTC 4065 G --- -- GA TT A GA T T
TGGAGATTTGAAGGAGGTGA GAGCAGAGCT GCGT TCCGGT GCTC CCC TGGAGA TGA G
GG GAGC T
GCTTTTGCTCCCATCTCATC GGAG |||| |||||| |||| ||| |||||| ||| | || ||||
TCTAAGGGTCGAGCAGAGCT TGCA aggtcg cgag ggg atctCT ACT C CC CTCG T
GGAGACGT g aga ct a- -- - TA - T

GAM379 ACCCGGGATGGGTCTGTCGA 1004 TCGAAAGCTA 4074 A -- aaa ta gcg gT
AAGCTAGCCAAGTCGCGCTG GCCAAGTCGC ACCCGGG TGGGTCTG tcg gc gccaagtc ct T
TTATGGGAGGATTTGGCGCG GCTG ||||||| |||||||| ||| || |||||||| ||
TACGAACCAGACCCACCCGG TGGGCCC ACCCAGAC AGC CG CGGTTTAG GG A
GT - CA ATG -- GA- GT

GAM380 CGTTGATGGCGAAGGCAGCT 1005 GCGAAGGCAG 4075 Ggc c ta- -- tt
ATATCGCGGTTTTACTGCTT CTATATCGCG CGTTGAT gaagg agc tatc gcgg t
GATGAATGCTACCTTCCAAT GTTT ||||||| ||||| ||| |||| ||||
TAACG GCAATTA CTTCC TCG GTAG CGTC /
AC- A TAA TT AT

GAM381 CCTCCAGCTCCAACTCCCGC 1006 CTCGCCTTGG 4076 -- CTC A CATT C - TAT T C
ATTCGCTGCCTTATGGCTGA TGTATCGCAA CCTC CAG CA CTCCCG CG TGC CT GGC
GAGCT A
GCTCATCGGCTCGCCTTGGT TGGG |||| ||| || |||||| || ||| || ||| |||||
GTATCGCAATGGGAGATGAT GGAG GTC GT GAgggt gc atg gg ccg ctcGG T
TCTGTTGAGG TT TTA A aac- t t tt- - C

GAM382 GCCCTAGTAACCAATGCTCA 1007 TCCCCAGGGT 4077 ACCAAT- CACAATT---------- AAT
GATATACAA
GTCACAATTTGACCTAATGG CATTAACAAT GCTCAGT TGACCT GGGAGAT
C
GAGATGATATACAACGAGCA CTAT ||||||| |||||| |||||||
GAAAATTTCCCCAGGGTCAT TGGGTCG actggg ccctTTA /
TAACAATCTATACACTATGC ATAACTC TATCACAtatctaacaatt ac- AAAGACGAG
TGGGTCTCAATATACATGGG
C
GAM383 GGCGGCCGGGGGCCCGCGGC 991 TCCGCGGTCC 4061 CCG- - C --- C A A
GCGTCAGGCGCCATAGGTGC ACCATACCCG GGCGG GG GG CCGCGG CG GTC GGCGCC
T
CGACCGAGTCCGCGGTCCAC CC ||||| || || |||||| || ||| ||||||
CATACCCGCC ccgcc cc cc ggcgcc GC CAG CCGTGG /
cata a t tGA - - A

GAM384 CGGTGCGTCCCGGCGGACAT 992 ACATGCTGGG 4062 CGT- aca g t gga T CG
GCTGGGCCTACCGTGGACTC CCTACCGTGG CGGTG CCCGGCGG tgct ggcc accgt ctcCAT
TC A
CATTTCCGAGACGACGTGGG ACTC ||||| |||||||| |||| |||| ||||| |||||| ||
GGGAGCGGTGGTTGAGCGCG GTCGC GGGCCGCC GCGA TTGG TGGCG GGGGTG
AG G
CCGCCGGGTGAACGCTG AAGT GC- G - AGG C CA

GAM385 GGCCTTATAGATCTCCGGAT 996 TAGATCTCCG 4066 TTAta - g a gga
CGATGCGGACGGGGGTAATG GATCGATGCG GGCC gatc tcc gatcg tgc c
ATCAGGGCGATCGGAACGGC GACG |||| |||| ||| ||||| |||
C CCGG CTAG GGG CTAGT ATG g
CAAGG C A A GGG

GAM386 GGGGCAGTCGGGGAAGTGGC 1008 TGACGGGGGT 4078 G AG - -- A AG-------- - AA
T GC
TGTCGAGCACGTAGCCCTGC TCGCGAAGAC TCGGGGA TGG CTGT CGAGC CGT
CCCTG CACC GA CT T
ACCAAGATCTGCTTAAAGTT GGGC ||||||| ||| |||| ||||| ||| ||||| |||| || ||
CGGGTGACGGGGGTTCGCGA GGCCCCT ACC GGCG GCTcg gca ggggc gtGG CT
GA T
AGACGGGCTCGCGGCGGACC - AG A GC g gaagcgcttg a G- T AA
AGATCCCCGGAGCTCC

GAM387 TTTTTACCTTTTGAAGAGCA 1009 TACCTTTTGA 4079 -- ag --- c aa
GCGCTTAAAGCGGGCACTAG AGAGCAGCGC TTTTtac cttttga agc ag gctt A
AGCTGTTAGAAGAAGTAGAA TTAA ||||||| ||||||| ||| || ||||
A AAAGATG GAAGATT TCG TC CGGG /
AA G- AGA A CG

GAM388 ATATAAGGGCACTTCTACTG 993 AAGGGCACTT 4063 a - ttcta a AAA TCA- A
ATGATAGGCAAAATGTATCA CTACTGATGA ATATa gg gcac ctg tgataggCA TGTA TTTG C
TTTGACCCTAAACAGCTACA TAGG ||||| || |||| ||| ||||||||| |||| ||||
AATGTTTATTATAGGCTGTG TATGT CC CGTG GAT ATTATTTGT ACAT AAAT C
CTCCCTGTAT C T TCG-- - AA- CGAC C

GAM389 GCGCGCACAAGGTCATAACA 997 TTTGTCACAG 4067 CACAAG - A AA TAT- T
ATGGCATATGCTGGTTTAAT TAGTAGACAA GCGCG GTC AT AC TGGCA GCTGGT T
CAGCTATTTGTCACAGTAGT CACG ||||| ||| || || ||||| ||||||
AGACAACACGCGT TGCgc cag tg tg actgt CGACTA /
acaa-- a a ac ttAT A

GAM390 ACTTGTAAATATCCAGATTT 1010 CGAGAGCAAT 4080 A- - TTTCTTAAAGAT T G TG
TCC T AT

CTTAAAGATGCAAAATGATG GTTATGCTAG TCCA GA GCAAAA GATGT TA GTGAT
TGCTTTT TT G
TGTATGGTGATTCCTGCTTT ACAT |||| || |||||| ||||| || ||||| ||||||| ||
TTTTATGCAAGGCGAGAGCA AGGT CT TGTTTT Ttaca at tattg acgagag GG C
ATGTTATGCTAGACATTTTT GG G ---------- T g cg ta- c AA
TTGTTCGTGGAGGCAAGACA
GGT
GAM391 GGAAGAACAAGGATTATATG 998 TATGGAACAC 4068 ACAA TTA t acga- a
GAACACGATTATTATAAAAT GATTATTATA GGAAGA GGA ta ggaac ttatt t
AACAATAGTTCCTGGTTCCT AAAT |||||| ||| || ||||| |||||
CTTCC CCTTCT CCT GT CCTTG AAtaa a
---- TG- - ATAAC a

GAM392 AGACCAAGAACAAGATCGTG 1011 TCGGTTGGCG 4081 GAACAAGAT G A AT
AACACGATGATATAGAATCA TGATTGGTTT AGACCAA CGT AAC CGATGAT A
TCGGTTGGCGTGATTGGTTT ||||||| ||| ||| |||||||
tttggtt gcg ttg gctACTA /
agt------ g - AG

GAM393 TCTTGATTGCAGACATGAGG 999 TGAAATATCC 4069 TTGA A GGAA C tat ttc ta
AATGCTGAAATATCCGATTC GATTCATCTC TC TTGC GACATGA TG tgaaa ccga atctc g
ATCTCTAGATGAGGTAGCTC TAGA || |||| ||||||| || ||||| |||| |||||
GGTCTTTCAACAATTATGTC AG AGCG CTGTATT AC ACTTT GGCT TGGAG /
GGCGAGATTGA TTAG G A--- A CT- CGA Ta

GAM394 TCTGGCACTTCAACGGCTTC 1000 CTAGAAGGTG 4070 ACTT- A G GG
TGGGGTGGGTTTCATCCTAG ATGTTTTGGC TCTGGC CA CG CTTCTGGGGTG T
AAGGTGATGTTTTGGCCGGA CGGA |||||| || || ||||||||||
aggccg gt gt gaagatcCTAC /
gtttt a g TT

GAM395 ACCGCCCTTTACCCAGTCTG 1001 TTCCAGATCA 4071 ACCCAGTC AT A G CCCA
ATCTGATGCAACAGACCCCA AAGAGGGTGG ACCGCCCTTT TGATCTG GCA CA AC A
AAGACGTGTGTGTTCCAGAT T |||||||||| ||||||| ||| || ||
CAAAGAGGGTGGT tggtgggaga actagac tGT GT TG /
a------- ct - G CAGA

GAM396 GGTCGGAACTCTCCCTGGGG 1002 TCGGAACTCT 4072 --- g - - c cttttTGCC
GCTTTTTGCCACCTCCACTC CCCTGGGGGC GGtc g aact c tcc tggggg A
CCCCCAAGGATGAAGTTGCG TTTT |||| | |||| | ||| ||||||
TTGACC CCAG C TTGA G AGG ACCCCC /
TTG G A T A CTCACCTCC

GAM397 GCGGCGTCGGCGTAGAACCG 1012 TCAGCCTTTT 4082 TAG T AC--- A

TTAAAGGCACGGGAAATCCC GCGGTTACCG GCGGCGTCGGCG AACCGT AAAGGC GGG A
AATCAGCCTTTTGCGGTTAC CTGG |||||||||||| |||||| |||||| |||
CGCTGGCGCCGC CGCCGCggtcgc ttggcg tttccg CCC A
ca- t actAA T

GAM398 TGCCTTTTCTGAGAGGTTTC 1013 TGAGAGGTTT 4083 TTTTCt- t c gttt- CT
AAACGATTGTTTACCTTTTG CAAACGATTG TGCC gagaggtt caaa gatt aC T
TTTCCAAATTTTTGCAACTT TTTA |||| |||||||| |||| |||| ||
TTCTCACTACGGCA ACGG CTTTTCAA GTTT TTAA TG /
CATCACT C - ACCTT TT

GAM399 TGTTTTGAACGGGTGGGATG 1014 TCCCCTGGTT 4084 T TG G T C- TC AT- T----
TTT
ACAGGTTCGCGTATGATTTC TGACATA TGT T AAC GG GGGATGA AGGT GCGT GA
TTCGCGTTTGG C
GCGTTTGGTTTCGATTTTAG ||| | ||| || ||||||| |||| |||| || ||||||||||
GCGTGAATAGTTTCTTCACG ata a ttg tc ccctATT TCTA TGCA CT AAGTGCGGATT G
TATATCTTTTTATCCCCTGG c gt g - TT TA CTT TTGAT TTA
TTTGACATA

GAM400 CGGGATTTTCTTTCCAGTTG 1015 TTCCAGTTGG 4085 TT tc tt - ataac a
GCCCGATAACGTACTTACCC CCCGATAACG CGGGA TTCTt cag ggcc cg gt c
CCACGCGGTCCTGTAAGAAT TACT ||||| ||||| ||| |||| || ||
CTCTCG GCTCT AAGAA GTC CTGG GC CA t
CT T- -- C ACCCC T

GAM401 TCCATTTTTATCCTCGCACT 1016 TGAAATGAAA 4086 -- CG C TTC CTC C
TCTTCGCTCTCAAAGCCGCC GGATGGAAAC TCCAT TTTTATCCT CA TTC GCT AAAG C
TTTAAAGTTGAAATGAAAGG ATGG ||||| ||||||||| || ||| ||| ||||
ATGGAAACATGGA Aggta aaggtagga gt aag TGA TTTC G
ca aa a t-- AA- C

GAM402 GACTTCACAGAAGAGGGCAA 1017 TACCATAGTC 4087 C-- G C C - C T GTT
ACA
AACAAAAACATTGTGTGTAG TTATTTTTTT GACTT ACAGAA AGGG AAAA AAA AA ATTGTG
GTAGT AGATA G
TGTTAGATAACAGTCATATT TTCT ||||| |||||| |||| |||| ||| || |||||| ||||| |||||
TTAGCTACCATAGTCTTATT CTGAA TGTTTT TCtc tttt ttt tt tgatac catCG TTTAT /
TTTTTTTCTCTGTTTTGTTT TTT G t t a c - AT- ACT
TAAGTC

GAM403 CAGATATATCGATATCCAAT 1018 TATCCAATTA 4088 TATCG c - --- a t T
TAGGCAAGTGAAACTTCAAT GGCAAGTGAA CAGATA Atatc aattaggc aagt ga act CAATA G
ATGTTTATTGCAGTCTCCAA ACTT |||||| ||||| |||||||| |||| || ||| |||||
ATTTAGTTTAGTTTGATATG GTCTGT TATAG TTGATTTG TTTA CT TGA GTTAT T
TTGTCTG TG--- T A AAC C C T

GAM404 CCTGCCGAGGAACGTCACCA 1019 TGTCGAGGAC 4089 AG- G C- GC- T ----------
GG
GGTGCGGTTGCAGGGGGCAG GTATCCCTGC CCTGCCG GAAC TCA CAGGT GGT GCAGGG
GGCAGTCG A
TCGGGAAAGTGGCTGTCGAG ACCA ||||||| |||| ||| ||||| ||| |||||| ||||||||
GACGTATCCCTGCACCAAGA GGGCGGT CTTG AGT GTCTA cca cgtccc ctgtCGGT
A
TCTGTTTGAAGTTCGGGTGG GGG A TT GAa - tatgcaggag GA
CGGG

GAM405 GATGAAGATTAATTGCGGAG 1026 TTCCTTAAGG 4096 AATT G AATC- CAA
GAATCAGGAATTCAACTTTA CCTCGTCCGA GATGAAGATT GCG AGG AGGAATT C
GTTCCTTAAGGCCTCGTCCG ATCT |||||||||| ||| ||| |||||||
AATCTTCATC CTACTtctaa tgc tcc tccttGA /
gcc- - ggaat TTT

GAM406 TTAGCTTCTAAGGTGATTAT 1027 TAAGGTGATT 4097 t-- a a t A T GCTAATT GC
ATTTTAGTATTAAATTTTGC ATATTTTAGT TTAGCTTC aaggtg tt tattt agtatta AT TT GCTT T
TAATTGCTTGCTATAAAGTT ATTA |||||||| |||||| || ||||| ||||||| || || ||||
GAAATGTCTAATGCTTAAAT AGTCGAAG TTTCAC AA GTAAA TCGTAAT TG AA TGAA
A
GAACACTTTTTTGAAGCTGA TTT - - T C T AGT---- AT

GAM407 GTCTACTAGAGCCTTGCTGT 1020 CACCCGTAGA 4090 ACTAGA C A TAT A
TAACGGTATCTGATACAGCA CAACGAGGCG GTCT GCCTTG TGTT ACGG CTG T
CCCGTAGACAACGAGGCGGG GGAC |||| |||||| |||| |||| |||
AC cagg cggagc acag tgcc GAC /
g----- a a cac A

GAM408 GACGTATCAGATTTTTACAC 1021 TATCAGATTT 4091 a atttttaca aaaccaACT--------- G
CCAAACCAACTGCGTGCGCA TTACACCCAA GACGt tcag ccc GC T
GCGTTTATTAAGGACGCGGG ACCA ||||| |||| ||| ||
ACTGCTACTGAGGCGTC CTGCG AGTC GGG CG G
G ATCGTCA-- CGCAGGAATTATTTGCGA C

GAM409 GGGGAACTTGGGCATGGGGG 1031 GGGCATGGGG 4101 ACTTg gg g a TTG
CTACGGTCACGTTGTTGAGG GCTACGGTCA GGGGA ggcat gggctacg tc cgttG A
ATCAGCGGGGCGTAGTCTGT CGTT ||||| ||||| |||||||| || |||||
GCTATTGTCCCT TCCCT TCGTG TCTGATGC GG GCGAC G
GTTA- -- G - TAG

GAM410 CTCCACCTCTGGAATTCAGG 1022 TCAGGACCTG 4092 AC AA-- a t ga tg
ACCTGCAGACTCTGAGTGAG CAGACTCTGA CTCC CTCTGG Ttcagg cc gca ctc a

CTTGTTGGCCCTGAAAATGC GTGA |||| |||||| ||||||| || ||| |||
CGGAGAGGGAG GAGG GAGGCC AAGTCC GG TGT Gag /
GA GTAA C T TC tg

GAM411 ATTTCAGTCTAAATGCTAAA 1023 TGTAAATGGA 4093 TC AA CA C
TCAACAGAATCAAGTTCTGT GTATTTATCT ATTTCAG TAAATGCT AT ACAGAAT A
AAATGGAGTATTTATCTGAG GAGA ||||||| |||||||| || |||||||
AT Tagagtc atttatga ta tgtCTTG /
t- gg aa A

GAM412 CAGCCACTTATGAATTAATT 1024 TGAATTAATT 4094 CC A-- attcttctg---- ca
CTTCTGATAGCTCATTTCGG CTTCTGATAG CAG ACTT tgaatta atagct T
TTATAATATCCAATTAATAA CTCA ||| |||| ||||||| ||||||
TTCAAAAAAGTCTCTG GTC TGAA ACTTAAT TATTGG T
TC AAA AATTAACCTATAA CT

GAM413 CATTCAGTTTTATAAGAATT 1025 TATAAGAATT 4095 T T - tat-- --- actT G
ATCAGATTCTAACTTGCTGT ATCAGATTCT CAT CAGT Ttat aagaat cagat tcta GCT T
CAGGCTGTAGACCCATTTGC AACT ||| |||| |||| |||||| ||||| |||| |||
TAATATTTTTCATGGTACTG GTA GTCA GGTA TTTTTA GTTTA AGAT CGG C
ATG - T C TAATC CCC GT-- A

GAM414 GTGTGTCTTATCATGCATAT 1028 TCAACATATT 4098 ---- T A TATAAAGAAA CA
AAAGAAATTGAGGACAAACA AAACTGCAGG GTGTG TCT ATC TGCA TTGAGGA A
TCCTCAACATATTAAACTGC ATTG ||||| ||| ||| |||| |||||||
AGGATTGGATCCCCACAC CACAC AGg tag acgt aactCCT A
CCCT t g caaattatac AC

GAM415 AAGTTAAAACTGTTGCTAGA 1029 TGCTAGATCT 4099 AA Ttg tctttt gata
TCTTTTAATGAGATATTATA TTTAATGAGA AAGTT AACTG ctaga aatga t
ATCATTTCTAGGTAGTTCCA TATT ||||| ||||| ||||| |||||
ATTT TTTAA TTGAT GATCT TTACT t
CC G-- ------ AATA

GAM416 CCCATTAGAGTTCTGACAAA 1032 TTAGAGTTCT 4102 t ctgaca aa TG
TCAAACCATGTATTTGGGTG GACAAATCAA CCCAt agagtt aatca cca T
GTTCGCCTGACTTTCATGGG ACCA ||||| |||||| ||||| |||
GGGTA TTTCAG TTGGT GGT A
C TCCGC- G- TT

GAM417 GCCGCCTCCCCCGAGTCTTC 1033 CAAGAACTGT 4103 C CC A C ATG---- G
GGAATGTCTTGGCGGCCGTC TATCCCGAGG GCCGC TC CCG GTCTT GGA TCTTGGC G
AAGAACTGTTATCCCGAGGC CACG ||||| || ||| ||||| ||| |||||||

ACGGATGAGCGGC CGGCG AG Ggc cggag cct agaacTG C
- TA a c attgtca C

GAM418 CTACATCTGCCTGTGTTACT 1037 TACCTCAGTT 4107 C C--- T- TACTTAC T CC
TACCCTTATGCCATATTATT AATAGATATA CTA ATCTG CTG GT CCT ATG A
AGGATTACCTCAGTTAATAG G ||| ||||| ||| || ||| |||
ATATAG gat tagat gac ca GGA TAT T
a aatt tc tTA---- T TA

GAM419 GAGGCCACACCCACATGGAG 1030 AGGCCACACC 4100 A--- ACAC CA A--- ACAC CA A--- ACAC A
GCCACACCCACATGGAGGCC CACATGGAGG TGG GGCC CCA TGG GGCC CCA TGG GGCC CC C
ACACCCACATGGAGGCCACA CCAC ||| |||| ||| ||| |||| ||| ||| |||| ||
CCCACATGGAGGCCACACCC ACC CCGG GGT ACC ccgg ggt acc ccgg GG A
ACATGGAGGCCACACCCACA CACA A--- AC CAca a--- ac caca a--- T
TGGAGGCCACACCCACATGG
AGGCCACACC
GAM420 AGTGCGGGTTACACAGTGCG 1034 TACACAATTG 4104 -- TAC- GC - ACA
TGTTACACACCGGGTATACA TTCCTGCTCG AGT GCGGGT ACAGT GTGT TAC C
CAATTGTTCCTGCTCGTTAA TTAA ||| |||||| ||||| |||| |||
CT TCa tgctcg tgtta caca ATG /
at tcct a- t GGC

GAM421 TAAGCTTTTCCTTTGGAGCT 1035 TTGGAGCTCC 4105 TTTTCCTtt tcctcc - c
CCTCCCTAAATGCCTTGGCT TCCCTAAATG TAAGC ggagc ctaaat gc t
ATTTAGCCTTCCGCTCCTGT CCTT ||||| ||||| |||||| ||
CTGCTTA ATTCG CCTCG GATTTA CG t
TCTGT---- CCTTCC T G

GAM422 GCAGGAACTTCATGATGGAC 1036 TGATGGACTT 4106 CTTC------ cttcttg - t
TTCTTGGCGTCGCTACCGCG CTTGGCGTCG GCAGGAA Atgatgga gcg tcgc a
GTCGTGCTTCTCCATCATCT CTAC ||||||| |||||||| ||| ||||
CCACCATCTTCTTGC CGTTCTT TACTACCT TGC GGCG c
CTACCACCTC CTTCG-- T C

GAM423 AGCTGTTGGCCACCAGCCGG 1038 AGCCGGTTGT 4108 TG a t t tcca --- c AAC G
TTGTCCTCCACGGGCAGCGC CCTCCACGGG AGCTGT GCCACC gccggt g cc cgg gcag GCGCGG GGC T
GCGGAACGGCGTCGCCTCCT CAGC |||||| |||||| |||||| | || ||| |||| |||||| |||
GCGCCTTGCGCACCGCCTCG TCGACA TGGTGG CGGCCA C GG GCC CGTT CGCGTC CCG /
GTCACCGGCAGGTGGTACAG -- A - T CTCC ACG C CT- C
CT

GAM424 AGCTCGCAGCTTGTTTGGCG 1039 TCTCGTTGCC 4109 CG TT TT TT TA
ACTTGAGAGTTAAACACTCT CTGCTGCTGA AGCT CAGC GT GGCGAC GAGAGT A
CGTTGCCCTGCTGCTGAGGC GGCT |||| |||| || |||||| ||||||
T tcgg gtcg cg ccgttg ctctCA /
a- t- tc -- CA

GAM425 ATTGATTGAGCAACTGCAGC 1040 TACTGCACCT 4110 A CAAC ------ AATA
CGGGAATAATGAAGTCTGGA CCTCAACCAA ATTG TTGAG TGCAG CCGGG A
TCTTACTGCACCTCCTCAAC T |||| ||||| ||||| |||||
CAAT taac aactc acgtc GGTCT T
c ctcc atTCTA GAAG

GAM426 GCCACGACTCCTGAAGGCGA 1044 CACACGTTAT 4114 -- T AA GA T-- AG A TT
CCTATACGAGGTAGAGTTCT TAGGGCTAAC GCCA CGAC CCTG GGC CCTA ACG GT GAG
C
GCTCACACGTTATTAGGGCT AGGT |||| |||| |||| ||| |||| ||| || |||
AACAGGTGTTGGTTGGC CGGT GTTG ggac tcg ggat tgc ca cTC /
TG t aa -- tat a- - GT

GAM427 GCCAGGTGGCTAGAATCCCG 1041 CACCGGAGAA 4111 --- - GAA - CG CAA AACG
CGGACAACGTAGCTGCTAAC AATACGCCCA GCCAGGT GGC TA TC CCG GA
CGTAGCTGCT A
GACTACAGGCAGCTACGCTC AGCC ||||||| ||| || || ||| || ||||||||||
ACCGGAGAAAATACGCCCAA CGGTccg ccg at ag ggc cT GCATCGACGG C
GCCTGGC aac c aaa a ca C-- ACAT

GAM428 TACGATTTAAATATTATGTA 1042 TAGTACATAC 4112 TTT ATTATGTAAC T C CACT
ACTCTGTATTTATTCGACAC AGAATTTCTT TACGA AAAT TCTGTAT TATT GA A
TATTAATCTAGTACATACAG TCGT ||||| |||| ||||||| |||| ||
AATTTCTTTCGTA Atgct ttta agacata atga CT /
ttc ---------- c t AATT

GAM429 CTCGCCCTCTTGGTCGGCGT 1043 TCTTGGTCGG 4113 CCtct - c c----- c G CTCG T
CTCATTGCCGGGTACTCGAA CGTCTCATTG CTCGC tg gt ggcgt tcattg cgg TA AATCC G
TCCTGCGGATTACATAGCTG CCGG ||||| || || ||||| |||||| ||| || |||||
TTAATGAATACACACGCCTA GAGCG AC CA CCGCA AGTAAT GTC AT TTAGG /
CGCACCCCGCGAG CCCC- G T CACATA T G ACA- C

GAM430 TGGGTGCCTACGACCTCATG 1045 CACACCTCGG 4115 CC GAC C G T C-- AAC
GACGGCCTAGCTGTTAACGA CGGTCCATAA TGGGTG TAC CT ATGGAC GCC AG TGTT G
ATAGACACACCTCGGCGGTC GAAA |||||| ||| || |||||| ||| || ||||
CATAAGAAAGTATGCCCA ACCCGT ATG ga tacctg cgg tc acAG A
-- aaa a g c cac ATA

GAM431 GATTAGATATCTCTTAACCC 1046 AATGAAATTA 4116 CT CCAA C -- TTCa----- a
atagcta at
CAATACTCATCTCCTTCAAT TAGCTACGTC TCT TAACC TACT ATC TCC atg aatt cgtct
c
GAAATTATAGCTACGTCTAT TATC ||| ||||| |||| ||| ||| ||| |||| |||||
CTACAGACGCACGAATTACA AGA ATTGG GTGA TAG AGG TAC TTAA GCAGA
T
TAACTTAAACGGAAAGATAG TC C--- - AA CAAATTCAA A GCAC--- CA
TGCGGTTACTAGATATCCCC
ATC
GAM432 GCCCGCCCGTCGTTACCTCA 1052 TCACGCGCCA 4122 C- ---- T T CAATG TATTTCC
ATGTGATATTTCCAGACTTC AGGTTCGGC GCC GCC CG CGT ACCT TGA A
TTCAAGCTAGGTCACGCGCC ||| ||| || ||| |||| |||
AAGGTTCGGC cgg tgg gc gca tGGA ACT /
ct aacc - c TCGA- TCTTCAG

GAM433 GAACAAGAGCCTGCTGTCCC 1047 TACCAGCAGG 4117 AA CC T - A TTC ACC
TGATGTTCGGACCAATGACC TGACGCACCT GAAC GAG TGC GTC CCTG TG GG A
TACCAGCAGGTGACGCACCT CAGG |||| ||| ||| ||| |||| || ||
CAGGTTC CTTg ctc acg cag ggac ac CC A
ga c- - t g cat AGT

GAM434 CGGGCATGGATCTCTCGCGG 1048 CATGGATCTC 4118 ca-- t c gg G G GTAT
GGTGCGTAGGCGTGTGTATT TCGCGGGGTG CGGG tggatc ct gcgg tgcgtaG C TGT T
CATTAACAGCTATGTAATCC CGTA |||| |||||| || |||| ||||||| | |||
GCAGGATTCGAGTACCCG GCCC GCTTAG GA CGCC ATGTATC G ACA C
ATGA - - TA - - ATTA

GAM435 GGGGCATACTTTCTCATGGA 1049 TGAGGTCGTA 4119 - A TT CC G GTCTA
CCCCCGAGTTGTGTCTATTC GGCACCC GGG GC TAC TCTCATGGAC CC AGTTGT T
GTTAACAGCTAGGCCGTCCA ||| || ||| |||||||||| || ||||||
TGAGGTCGTAGGCACCC ccc cg atg ggagtACCTG GG TCGACA T
a g ct CC A ATTGC

GAM436 GCCCCAACTCCTCGCCCTAC 1053 TGGGAGGGCG 4123 CCAAC A T AG ATG- GC
ACC TA
CTCAAGATCTATGTGGCCAC AGGGCGGC GCC TCCTCGCCCT CC CA ATCT TG CACG
GC T
GACCGCTATCTCGCCCGTGT ||| |||||||||| || || |||| || |||| ||
TCAAGCCAGATGTGGGAGGG cgg gggagcggga gg gt TAGA AC GTGC CG C
CGAGGGCGGC c---- - - G- CCGA TT C-- CT

GAM437 AGGATCCAGGACATTATCTC 1054 TGTCAGGGAC 4124 A ACA TA A GAGA G

TGGCGTCACGGAGACGGGGG GGCACCTGGA AGG TCCAGG T TCTCTGGCGTC CG CGG G
ACCGAGTGGATGTCAGGGAC ACCT ||| |||||| | |||||||||| || |||
GGCACCTGGAACCT tcc aggtcc g agggactgtAG GT GCC G
a ac- gc - GA-- A

GAM438 CAGTTTGGGCATACTTTCTT 1055 TGAGGTCGTA 4125 GT- CA-- TT C G G GTCTA
ATGGACCGCCGAGGTGTGTC GGCACCCAGT CA TTGGG TAC TCTTATGGAC GCC AG TGT
T
TATTCGTTAACAGCTAGGCC AATG || ||||| ||| |||||||||| ||| || |||
GTCCATGAGGTCGTAGGCAC gt gaccc atg ggagtACCTG CGG TC ACA T
CCAGTAATG aat acgg ct C A G ATTGC

GAM439 GCCAGGCTTGGGCGTATTTT 1056 TACGTTGTCC 4126 CTTG GTATTT - TG C TAG
CTCCGGTGAGCGTAGCTGCC GCGGGATTCT GCCAGG GGC TCTC CGG AGCGTAGCTGC
TG T
TGTAGTCGTTAGCAGCTACG AGCC |||||| ||| |||| ||| |||||||||| ||
TTGTCCGCGGGATTCTAGCC CGGTCC ccg aggg gcc ttgcatCGACG AT /
ACCTGGC A--- atctt- c tg - TGC

GAM440 TAGTGGAATTGTACTCCCAG 1050 TTCAACTTGC 4120 GA T CTCCC GCCTT- A
TGCCTTTAGCAAATGCTATA TGTCTCACTG TAGTG AT GTA AGT TAGC A
TTCAACTTGCTGTCTCACTG ||||| || ||| ||| ||||
gtcac tg cgt tca ATCG A
tc t ----- acttAT T

GAM441 AATGAATCTGGAATAGTATC 1051 TCTGGAATAG 4121 TG c tatctacaacatt - CATTT
TACAACATTAGCAGCATTTA TATCTACAAC AA AAt tggaatag aG CAG A
TAAAACTGTCTTTTCCTACT ATTA || ||| |||||||| || |||
ATATCTATTCCAAATTTGTT TT TTA ACCTTATC TC GTC /
GT A TATATCATCCTTT T AAAAT

GAM442 ATAGAACTTGATTTATTTGT 1057 TAAATTGGAT 4127 TT - TGAT A- CCA
TGATTTGCAGTTCCAATAAA CTTGTTCTGT ATAGAAC GATTTA TTTGT TTGC GTT A
GCCCGCGATATAAATTGGAT ||||||| |||||| ||||| |||| |||
CTTGTTCTGT tgtcttg ctaggt aaatA AGCG CGA /
tt t T--- CC AAT

GAM443 ATAATTCATATAATAAATAT 1058 TAATGTATAT 4128 TAATA ta a- gt----- ca
AATGTATATAGTTTGTTCTC AGTTTGTTCT ATAATTCATA AATA atgtat tagttt tct t
ATTTAGATCATTTAAAATTA CATT |||||||||| |||| |||||| |||||| |||
AAATATGTCTTATTGTTTAT TATTAAGTAT TTAT TGTATA ATTAAA AGA /
GAATTAT TTG-- TC AA ATTTACT Tt

GAM444 ATTGTTACCTGCTGCAAGTG 1059 CAGCCCTAGA 4129 C GCTGCA TG Cc ccc a t-
cCT- TC TTC
TGACGCCAGCCCTAGAAAGC AAGCTTGTTT TA CT AGTG ACG ag tagaa gc tgttttca AC
AC C
TTGTTTTCACCTACTCACTT TCAC || || |||| ||| || ||||| || |||||||| || ||
CCCTTGTATGTCTGATGAAA AT GA TCGC TGT TC ATCTT CG ACGAAAGT TG TG
/
GCATTGCTTCTACTTCTCAT A ------ CT AC TTC - TT AGTC TA TTC
GTTCCGCTAGATAACAAT

GAM445 TGGGCTAGCTAAAAGTGAAG 1060 AAAGTGAAGA 4130 T C aaag- aat- a- ta
AAATTGAAGTATAAGTTACA AATTGAAGTA TGGGC AG TA tgaaga tga gta a
CTCATATATTTTTAATAAGT TAAG ||||| || || |||||| ||| |||
AACTGCCCA ACCCG TC AT ATTTTT ACT CAT /
- A GAATA ATAT CA Tg

GAM446 CAAGGCGGCCAAGAGGCAGA 1061 AGAGGCAGAC 4131 CCAa - gaccta t aaaA
CCTAAGGGCTCTAAAACTAA CTAAGGGCTC CAAGGCGG gag gca agggc ct C
AAAGCGCCCTACATGCTCTC TAAA |||||||| ||| ||| ||||| ||
CTGCTTTG GTTTCGTC CTC CGT TCCCG GA T
---- T ACA--- C AAAA

GAM447 GTGTTGCTAATAGAATTTCA 1062 TGACTGAATG 4132 TT TAATAG CG -- t tgt ga-
AA
TCGAATGACTGAATGTTGTG TTGTGTCCGA GTG GC AATTTCAT AAtga ctgaa gttg ccgat
tGTA A
TCCGATGATGTAAAATTCTA TGAT ||| || |||||||| ||||| ||||| |||| ||||| ||||
TGAAAATTGGTTTAACTTTC CAC TG TTGGAGTA TTACT GACTT CAAT GGTTA
GTAT T
AGACTCATTATGAGGTTAGT T- TATGA- -- CA T TT- AAA CT
ATGTTCAC

GAM448 GATAAGGAAGAGTTTTTTTG 1063 TAAGGAAGAG 4133 - gttttttgtgttt- CT T
TGTTTTCATTTTCTCCTATA TTTTTTTGTG GAta aggaaga tCATTTT CC A
GGTTGAAATGGTATAGTTTC TTTT |||| ||||||| ||||||| ||
CCAGAATTTTCTTGTGTC CTGT TTCTTTT GGTAAAG GG T
G AAGACCCTTTGATAT TT A

GAM449 ATTTCTCGGTTTTCTGGTGT 1067 TGAGTGCAAA 4137 T TTA TG GA ATC t gcaaa
t tt
TAAAATTAATTTTGTGAAGT TAGGATGTTA TTTCTGG GTTAAAA ATTT T AGTA TG gagt
tagga gtta t
AATCTGTGAGTGCAAATAGG TTTC ||||||| ||||||| |||| | |||| || |||| ||||| ||||
ATGTTATTTCTTAATTTTCT AAAGATT CAATTTT TGAA A TCAT GC CTCA GTCTT
TAAT /
GAACTCCGTACTAATGAAGT T --- GT A- --- - A---- T Tc
TTTTAACTTTAGAAAACCAG

AAGT
GAM450 GACACATGGTGGAGTTTATG 1064 TATGGAGTGG 4134 A TGG TTt gagt a a tg--- -----
TAAAAC
GAGTGGTCTCAGGAGCTGTC TCTCAGGAGC C CA TGGAG atg ggtctc gg gc tcG AGCAG
C
GAGCAGTAAAACCCTGTGTC TGTC | || ||||| ||| |||||| || || ||| |||||
TGCTTTTACCGAAAATTGCC G GT GCCTC TGC CCAGAG CC CG AGC TCGTC
/
CGAGACCTCAACGTCCCTCC - T-- CC- AACT - - TTAAA CATTT TGTGTC
GTTGGTC

GAM451 GTTGTCACTTATCGATACGT 1068 TATCGATACG 4138 CACTtat c caac at
TCGTCAACGTGATACCCGCC TTCGTCAACG GTTGT cgata gttcgt gtg A
ACGAACATATCGTCCCTCGC TGAT ||||| ||||| |||||| |||
GAC CAGCG GCTAT CAAGCA CGC /
CTCCCT- A C--- CC

GAM452 TAAACCAATGGATGTAGTTC 1069 TGGAAGTTTC 4139 G------- - TCA CACGATT aa tcg
-- g
AGATAACACGATTGTGGAAG GCCTTATACG AT GATGTA GT GATAA Gtgg gtt ccttat
acg a
TTTCGCCTTATACGGACGCG GACG || |||||| || ||||| |||| ||| |||||| |||
TGCATAGGGACAACACCACT TA CTGCAT CA CTATT CACC CAA GGGATA
TGC c
AACTTATCCGTACATACGTC ATCACAAA A TGC CAAT--- A- CA- CG g
AAACACTAATTGGTTTA

GAM453 GAGGAGTTAATTTTTCTACG 1070 TCTACGGTGG 4140 GT---- tc tg c taa gc
GTGGCGTGTTTAAACTGCTC CGTGTTTAAA GAGGA TAATTTT tacgg g gtgtt act T
AAAGTATAACATCTTTCCGT CTGC ||||| ||||||| ||||| | ||||| |||
AAGAAAATTGTTTATATCCT CTCCT GTTAAAA ATGCC T TACAA TGA C
C ATATTT GA TT C TA- AA

GAM454 CTTTTTTTACCAAACACAAT 1071 TTTAACAGTA 4141 ACCAAACAC TTTAAAA--- TTAC-
TT AA
TTTATTTTTAAAATGTTTTA TATCTTCAAT CTTTTTTT AATTTTATT TGTT GGG TT A
CGGGTTTTAAAACAGATTCC AGAA |||||||| ||||||||| |||| ||| ||
CTATTTAACAGTATATCTTC GAAAAAAG TTaagataa acaa CCC AG A
AATAGAATTTCCACTTACGA CATTCACCT cttctatatg tttAT TT AC
AAAAAG

GAM455 GCACGGACTCTCGTCGTAGC 1065 ACTCTCGTCG 4135 ctctc gt cgttcaaatC A
ACGTTCAAATCGGTTTATTA TAGCACGTTC GCACGGa gtc agca GGTTT T
AAGCCCTCATGCTCAGACTC AAAT ||||||| ||| |||| |||||
CGTGT TGTGCCT CAG TCGT CCGAA T
----- AC ACTC------ A

GAM456 CTGTACCCCACCCCCCTTCT 1072 TTTGTCCCAG 4142 CCCC C AA- - - TC T
AAATAAATTTCCGATCCCTG GAGCGGGGTC CTGTA ACCCC CTTCT ATAAAT TTCCG A CC
G
GAGGTTTCCGGAGTATTTGT CTAT ||||| ||||| ||||| |||||| ||||| | ||
CCCAGGAGCGGGGTCCTATG GACGt tgggg gagga tgtttA GAGGC T GG G
CAG atcc c ccc T C TT A

GAM457 TTCGTGAGCTCTTTTTACGA 1073 CCCGGTAGTT 4143 GC--- TTTTAC G A
CTACGGGGCTATGGAGCCCG ACTTGGACAA TTCGTGA TCT GACTAC GGGCT T
GTAGTTACTTGGACAATATC TATC ||||||| ||| |||||| |||||
ATGAG GAGTAct agg ttgatg cccGA G
ataac ttca-- g G

GAM458 ATTGTCACCGTCGATGTGTT 1074 TAGCACATCG 4144 CCGT- - GGTGTC- -- AAC
GCTGGTGTCGACGGTCGTGA TTTATTGACA ATTGTCA CGATGTGTTG CT GACGGTC
GTG T
ACTTGACACCGGGCCGTTTT GT ||||||| |||||||||| || ||||||| |||
ATTAAAGATAGCACATCGTT tgacagt gctacacgat GA TTGCCGG CAC /
TATTGACAGT tattt A AATTATT GC AGT

GAM459 TCGATGATTCTTTGTTCGCA 1075 CACCAGGTCC 4145 T TT - a gt--- ag - ctt
CCAGGTCCTCAGCGCCGCTT TCAGCGCCGC TCGA GATTC TGTT CGc ccag cctc cg ccg a
AAATTCGGCCGAGGAGGCTC TTAA |||| ||||| |||| ||| |||| |||| || |||
AATTGGAGCGTGACATCGAA AGTT CTAAG ACAG GCG GGTT GGAG GC GGC a
TCTTTGA T CT T A AACTC GA C TTA

GAM460 CCCCCCGATTCCCACATGCG 1076 TAGCCGTTCT 4146 AT CATGC cc -- c-- c
TAGCCGTTCTAGCTCCGTCG AGCTCCGTCG CCCCCCG TCCCA Gtag gttc tagctc gtcg t
CTAGCGATCTTGGGCTATTG CTAG ||||||| ||||| |||| |||| |||||| ||||
AACCTATCTGGGACGGGGGG GGGGGGC AGGGT TATC CAAG ATCGGG TAGC a
-- C---- -- TT TTC g

GAM461 AGGTAACCCAGAACTGAAAA 1066 TGAAAAAAAG 4136 ACC--- AC- aaa-- a ga
AAAGATATAGTGAAGGACTA ATATAGTGAA AGGTA CAGA tgaaa agat tagt a
GATTTAGCAATTTCAATGTC GGAC ||||| |||| ||||| |||| ||||
TGAAAATATACCT TCCAT GTCT ACTTT TTTA ATca /
ATAAAA GTA AACGA G gg

GAM462 CGTAATATAGATGTTTGTCT 1077 TAGATGTTTG 4147 T a tt ctaatttag TC A AA
AATTTAGTAAAATCAAGAGA TCTAATTTAG CG AATAt gatgt gt taaaA AAGAG AT A
ATAAATTAATCCTTTTCTTT TAAA || ||||| ||||| || ||||| ||||| ||
TTAATACCCACATCATATTC GC TTATA CTACA CA ATTTT TTTTC TA T
G - - CC TA------- TC C AT

GAM463 AAAGCTAGAAACCGTGCCTC 1078 TACAGAAGAA 4148 AAA GCC CA TAG
CATATTTAGTATATGATACA TGGAAATTAG AAAGCTAG CCGT TC TATT T
GAAGAATGGAAATTAGCTTT CTTT |||||||| |||| || ||||
tttcgatt ggta ag atAG A
aaa aga ac TAT

GAM464 ACAGAATAAAAGAAGCAGTC 1079 TTTACCGGTT 4149 TAAA--- A-- GT AG AG
GAGGAGTTAAAGCAAATTGA GCCCATCTGT ACAGAA AGA GCA CG GAGTTAA C
TTTACCGGTTGCCCATCTGT CTAA |||||| ||| ||| || |||||||
CTAATTTCTGT TGTCTT tct cgt gc tttAGTT A
Taatctg acc tg ca AA

GAM465 TTTCATTTCTAAAATAATAT 1080 TCTAAAATAA 4150 - - at tttctaa
TCGTTTTCTAATTCTTTTAT TATTCGTTTT TTTC ATTtctaaaat aat tcgt T
ATGGTCATTAATTTTAGAAA CTAA |||| |||||||||| ||| ||||
TCGAAA AAAG TAAAGATTTTA TTA GGTA T
C A CT TATTTTC

GAM466 TTGTAATATAGACATATAAA 1081 TGATTGTAAC 4151 CA- A---- T C
TCTCTTCATTAAGTGATTGT ATAGTATCTA TTGTAATATAGA TAT AATC CTT A
AACATAGTATCTATATTATA TATT |||||||||||| ||| |||| |||
A AATAttatatct ata ttag GAA T
atg caatg t T

GAM467 AATCTATTAGATGATATATT 1082 TATTAGATGA 4152 -- at-- ataaA
TCGTATAAACACATAATGGA TATATTTCGT AATCtat tagatgatat ttcgt C
TAAAATATTATCTAATGTAG ATAA ||||||| |||||||||| |||||
ATT TTAGATG ATCTATTATA AGGTA /
TA AAAT ATACA

GAM468 GTAGGTGCTTTTCAGACATC 1083 TGGAATGGGA 4153 TG------ TT GA- CGG-- GA
CGGTGCAGATTATGCAGAAA AGATAAGAAT GTAGG CTT CA CATC TGCA T
TGATGGAATGGGAAGATAAG CCTA ||||| ||| || |||| ||||
AATCCTAC Catcc gaa gt gtAG ACGT /
taagaata gg aag TAAAG AT

GAM469 TATCGTTGTTTTTATATATA 2975 TCGTTGTTTT 6045 c t ata- T - AA
AATATAATTATGAAAAAATA TATATATAAA TAt gttgtttt atatataa taA TAT GAAA A
TTTCAATATTTAAAAGTTAT TATA ||| |||||||| |||||||| ||| ||| ||||
ATGTTGAAATAACAGTA ATG CAATAAAG TGTATATT ATT ATA CTTT /
A T GAAA T A AT

GAM470 TATGTTTATAATAAATATTA 2976 TAATAAATAT 6046 Ata a tt g A
ATTAAAATGATAAAATTATA TAATTAAAAT TATGTTT ataa tattaa aaaat ata A
ATTTTTTAATAATTGTAAGA GATA |||||||| |||| |||||| ||||| |||
GACATA ATACAGA TGTT ATAATT TTTTA TAT A
GAA A -- A T

GAM471 ATTGTATTTGATGTATTTTA 2977 TATTTGATGT 6047 t t GCTATAAT T T TTT
GATATAATGCTATAATAATT ATTTTAGATA ATTGtatttga gtat ttagatataat AA TATATT GATGCA
T
ATATTTGATGCATTTTAAAT TAAT |||||||||||| |||| |||||||||||| || |||||| ||||||
TGTATTTGATGTATTTTAAA TAATATAGATT TATG AGTTTATGTTA TT ATGTAG
TTATGT A
TTGTATTTGATGTATTTTAG T T AAT----- T T TAA
ATATAAT

GAM472 ATTATATGATTATAGTTTCT 2978 TATATGATTA 6048 tta ttctatttttAC CCT-- G
ATTTTTACAGTACCTTGACT TAGTTTCTAT ATtatatga tagt AGTA TGACTAAA T
AAAGTCTTTAGTCACACAAT TTTT ||||||||| |||| |||| ||||||||
ACTACCAACCTACACTATTA TAGTATATT ATCA TCAT ACTGATTT /
TATGAT --- CATCCAACCA-- AACAC C

GAM473 GGATAAAAATTTTTTAGAAA 2979 TACTTCATCG 6049 TTTTT ATATAAAA t tc gg a taaaC-
AT A
GATATAAAAATACTTCATCG GGGTAAATAG AGAAAG Atact ca gg ta atag ATAAAA
ATA A
GGGTAAATAGTAAACATAAA TAAA |||||| ||||| || || || |||| |||||| |||
AATATAAAATATTCTTTTAT TTTTTC TATGA GT CC GT TGTT TATTTT TAT /
CTATTTTTGTATGTTCCATT ----- CTAATTA- - TA TT A TTTATC CT A
GAGTATATTAATCCTTTTTT
TTTTAATTCC
GAM474 GTTTCATAATCTATTAGATG 2981 ATAGAAATTA 6051 CATA A AC- AA AC
ATACGTTTCAAATAAACACA CGTTACTAAT GTTT ATCTATTAG TGAT GTTTC ATAA A
TTATAGAAATTACGTTACTA AGAT |||| |||||||||| |||| ||||| ||||
ATAGATAAAC CAAA tagataatc attg taaag taTT /
---- - cat a- AC

GAM475 ATTTTAAAATCTGCCGTGTC 2986 TTTAAAATCT 6056 a -- c tct tC T
TAGTCTCGTTATTACAGGAT GCCGTGTCTA ATtttaaa tct gc gtg agtc GT A
TCCTCGCAGTTTAGAATTTA GTCT |||||||| ||| || ||| |||| ||
AAAT TAAAATTT AGA TG CGC TTAG CA T
A TT A TCC GA T

GAM476 GTCACAAAGTGAAAGAACCG 2987 TGAAAGAACC 6057 ACAAA c t a tt A ATTTTAA
A
TATAGTTTGGAACATTGTTA GTATAGTTTG GTC Gtgaaagaa cg at gt ggaac TTGTTAA AGT
G

AATTTTAAAGTAGAAACTCC GAAC ||| ||||||||| || || || ||||| ||||||| |||
ATTAATAAAGTTTTCATAAT CAG CATTTTCTT GC TA TA TTTTG AATAATT TCA A
CCGATTCTTTTACAAAGGAC GAAA- A C A C- A ACC---- A

GAM477 GCCTTCCAAACTGGTGAGAT 2980 TCCAAACTGG 6050 c-- tgagataatta - GT
AATTAGGAAGAAGTGGGATT TGAGATAATT GCCTt caaactgg ggaA GAA G
CATTCCGAAATCCAGTTTGT AGGA ||||| |||||||| |||| |||
GTAGGGC CGGGA GTTTGACC CCTT CTT G
TGT TAAAG------ A AG

GAM478 TGCCAGTGTTTGGCAGTTTT 2982 ATACTAAAGT 6052 A - TTTTACCG TG G- A GA
TACCGTTGGTTGTGTAGAAT GACCGAGCAT TGCC GTGTTTG GCAGT TTGGT T TAG
ATTGG A
TGGGAAAGCTAATACTAAAG CCAC |||| ||||||| ||||| ||||| | ||| |||||
TGACCGAGCATCCACTGTAC ACGG CGTAAAC TGTca agcca g atc taATC /
AAATGCGGCA - A cctacg-- gt aa a GA

GAM479 GCTTGGCGTTTGGATTGTCT 2988 TATGACAATC 6058 CG -- TA------- AA
ATTCCAATGCAAATAGCATT TTAAGAGACC GCTTGG TTT GGATTGTC TTCCAATGC A
GGAGGGTATATATGACAATC AGGT |||||| ||| |||||||| |||||||||
TTAAGAGACCAGGT tggacc aga tctaacag GAGGTTACG /
ag at tatATATGG AT

GAM480 AGCTGGGTACTATAAAAATC 2983 TAATTCTGAA 6053 T TA AAAAA AACCACAG GT
AAACCACAGATAGGTTATAC TGGGGCCCGC AGC GGG CTAT TCA ATAG T
TATAATTCTGAATGGGGCCC T ||| ||| |||| ||| ||||
GCT tcg ccc ggta agt tATC A
- gg ----- cttaa--- AT

GAM481 CTCGTAAATAAAGACGCACA 2984 TGGCGTGTAC 6054 A-- AC AGA T CATATAGT
GACCTCACGCATATAGTACC TTTATTACAA CTCGT AATAAAG GCAC CC CACG A
ATCACACCGTGTGGCGTGTA CGAG ||||| ||||||| |||| || ||||
CTTTATTACAACGAG gagca ttatttc tgtg gg GTGC C
aca a- c-- t CACACTAC

GAM482 TGCAGATCTTTTTTGTGAAA 2985 TCTTTTTTGT 6055 tct- a TTTG
AAAAAATAATTATTTTTTTG GAAAAAAAAA TGCAGA tttttgtg aaaaaaaataatTATTTT C
CGCGCCGGAATAATTATTTT TAAT |||||| |||||||| ||||||||||||||||
TTTTGCGCGGAAATATTTTT ACGTTT AAAGGCGC TTTTTTTTATTAATAAGG G
GCA TTAT G CCGC

GAM483 TTAAACTTATTACTACTGCT 2989 TTGTAGGCGT 6059 A ATT TA T GC TAAACATT
ATAGGCGTTAAACATTAAAA CAAAGATTAA TTAA CTT AC CTGC ATAG GT A

TTATTACTACTGTTGTAGGC |||| ||| || |||| |||| ||
GTCAAAGATTAA aatt gaa tg gatg tGTC CA /
a ac- cg t AT TTATTAAA

GAM484 GCGTTAAACATTAAAATTAT 2991 ACTGCTGTAG 6061 TT- ATTA t gta t ac
TACTACTGCTGTAGGCGTTA GCGTTAAACA GCG AAACATTAAAATT CTac gct ggcg taa a
AACATTATTACTGCTGTAGG TTAT ||| |||||||||||| |||| ||| |||| |||
CGTAGCTAAATTTTAATGTT TGC TTTGTAATTTTAA GATG CGG TCGT ATt t
TTTTCGT TTT ATC- - ATG C at

GAM485 GGCATTCCTGATATTCATGT 2992 TAAAGTGCTA 6062 A AT- TC- - t a t cc
TAAAGTGCTATACTATAACC TACTATAACC GGC TTCCTG AT ATGT taaag gct tac ataa a
ATCTTATGTGGGCTCTTTAT ATCT ||| |||||| || |||| ||||| ||| ||| ||||
ACATCTTATTGGCAGGAGGC CCG GAGGAC TA TACA ATTTC CGG GTG TATt /
C - GGT TTC T T - - ct

GAM486 TCCCTGGTAGCTACTGAGCA 2990 TGGCACAACG 6060 C AG AGC TAAC CTT - TG
AGAT---------- C
GCAGCTGTTTAACAGGCCCT AGGCCTTTGT TG CAGC TGTT AGGCC TTG GC CAG
C C
TTTGGCTGCAGAGATCCCAG AACA || |||| |||| ||||| ||| || ||| |
GGCCATAACAATGGCATACT AC GTTG acaa tccgg aac cg GTC G A
GTGGCACAACGAGGCCTTTG - A- GTT tgtt agc a gt ATACGGTAACAATACCG G
TAACATTGGTTGACACTACC
AGGGG
GAM487 CGAATTGCTGGTATTGTGGT 2993 TACACCACTC 6063 T CT-- T TG CG GT C GGT T
TCATC
GCGGTGTCCTCGACGGTCCA CATTATCTAT CGAA TG GGTA TG GTG GT CCT GAC CCA
GTG T
TGTGTCATCTTATAATCACT TTAC |||| || |||| || ||| || ||| ||| ||| |||
TGGTCAGTCCAGGGTACACC GCTT at ctat ac cac ca GGA CTG GGT CAC T
ACTCCATTATCTATTTACTT c ttat t ct ca tG C ACT T TAATA
CG

GAM488 GCCGTCACCGTGTCGCAGCT 2994 TCGCAGCTCT 6064 TCAC tcgca cccc-- tcct
CTTCCCCGGCCTCCTCCTGC TCCCCGGCCT GCCG CGTG gctctt ggcc c
TGGCCTACTGCGAGAGCCAC CCTC |||| |||| |||||| ||||
CGCGCCGGC CGGC GCGC CGAGAG CCGG C
C--- CAC-- CGTCAT TCGT

GAM489 GCGTCTCCGGTCCCGATCGA 1084 GCGAGCGTGC 4154 T --- AT AC G - CAT
CCGGTCGCCCCGTCGCATTG GCGGGATCCC GCGTC CCGG TCCCG CG CG TCGCCC
CGTCG T
TTCGACGCGGGCGAGCGTGC CGGC ||||| |||| ||||| || || |||||| |||||
GCGGGATCCCCGGCGACGC CGCAG ggcc agggc gc gc agcgGG GCAGC /
c cct -- gt g C TTG

GAM490 TCCCGGGCGCTGACGCCGCC 1085 GTCGTTCTTT 4155 G- GACGCCG CATCA G A
GACGACATCAGACGAGCGGA CGTCGGGAGA TCCCGG CGCT CCGACGA GACGA CGG T
TCTCCGGTCGTTCTTTCGTC AGAA |||||| |||| ||||||| ||||| |||
GGGAGAAGAAGCGAGCCGGG AGGGCC GCGa ggctgct ttgct GCC C
A GA agaagag ttc-- g T

GAM491 CGGAGGAGGCAGACAGACGG 1086 AGGCAGACAG 4156 c cagac cag CCG
CAGGCGGCCGGCCGGGCACC ACGGCAGGCG CGGAGGagg aga gg gcggccgG G
GGCTGCAACCCTCTCCTCTT GCCG |||||||||| ||| || ||||||||
CTG GTCTTCTCC TCT CC CGTCGGCC /
- ----- CAA ACG

GAM492 TCGCGGGCCGCTCGCTATGC 1087 TATGCCGACT 4157 C C-- ta c t tga aT
CGACTGACGTTGACGTTAAT GACGTTGACG TCG GGGC GCTCGC tg cgac gacgt cgtta A
ATATAACGACGTCGTCGACG TTAA ||| |||| |||||| || |||| ||||| |||||
ACGCGGGTTCTGCTCCCGA AGC CTCG TGGGCG GC GCTG CTGCA GCAAT /
C TCT CA A - --- AT

GAM493 CGGCTCCTCCGCCTCGGGCG 1088 TGTGTCTGAC 4158 T --- C C C ---------- T AG
ACGGGGGCTCGGAGATGACC ACTCCTCCCC CGGC CCT CCGCCT GGG GA GGGG
GC CGG A
GGCTGTGTCTGACACTCCTC TTCC |||| ||| |||||| ||| || |||| || |||
CCCTTCCTCAGGCGGCCCGG GCCG GGG GGCGGA CTc ct cccc CG GCC T
GCGCCG C CCC - - t tcctcacagtctgtgt - AG

GAM494 GGGGGTGGTCAACGCCCTAG 1092 ACCCGGCCTA 4162 A C A A CTacc ------ act t t
GA
AGAGCGTGACCGTCTACCCG CGACTGCGTG CG CCTAGAG GCGTG CCGT cggcc tacg
gcg gc ctCC T
GCCTACGACTGCGTGCTCTC CTCT || ||||||| ||||| |||| ||||| |||| ||| || ||||
CGATCTGGAGGCCGCCATGT GC GGGTCTC CGCAC GGCA GCCGG GTGT CGC
CG GAGG /
GCCTGCTGGCCGCCTACGGG G A G G TCC-- TCGTCC AC- - - TC
CACGCGCTCTGGGACGGCCG
CGACCCCC
GAM495 GGCCTCGGGGGCAACGGGGG 1093 CAGCCGCGTC 4163 T GCAACG G GCT- T
CGGCGCTCTGCTCATGCAGC AACCCCGTGG GGCC CGGGG GG GCGGC CTGC C
TCAGCCGCGTCAACCCCGTG CC |||| ||||| || ||||| ||||
GCC ccgg gcccc ct cgccg GACG A
t aa---- g acTC T

GAM496 GCGCGTTTGCGCACGTTCAC 2995 TCGCGAGTGA 6065 T C TT Ctc gag gtt gG
CTCGCGAGTGACGTTGTGGA CGTTGTGGAT GCGCG TTGCG ACG CAC gc tgac gtggatgcg
A

TGCGGGAGCGCGCGTCCACC GCGG ||||| ||||| ||| ||| || |||| |||||||||
AAGTCGAGAGCCTCGTGTTC CGCGT GACGC TGC GTG CG GCTG CACCTGCGC G
GTCGCAGTTGCGC T - TT CTC AGA AAC GC

GAM497 TTAAAAATATGGTTTCAGAT 1089 TTTCTGGCTT 4159 T TTTC T C ttt ct ta a --- CT
TGTCTATTTCTGGCTTTTAA TTAAAAATAA TTAAAAA ATGG AGA TGT TA ctgg tt aaa taaa
aac T
AAATAAAAACCTTTCGTTTC AAAC ||||||| |||| ||| ||| || |||| || ||| |||| |||
CTTTACTTTCGAACCAGTTT AATTTTT TACC TTT ACG AT GACC AA TTT ATTT TTG
/
ATGCACTTTATTTCCATTTT - TTTA C T TT- -- GC C CCT CT
TTAA

GAM498 GTGGCGAGTCTTTTAAAGTA 1099 AAGTATACTT 4169 TCTT- -- ctt- aaatattcgtTCA
TTTAATTT
TACTTCGTAAAATATTCGTT CGTAAAATAT GGCGAG TTA aagtata cgta GTAGAT
A
CAGTAGATTTTAATTTAAAA TCGT |||||| ||| ||||||| |||| ||||||
CTCCTATCTATAATTCTTTC CCGTTT AAT TTTATAT GCAT TATCTA /
ATACGTTTTTATATTTACTA TTTTT CA TTTT ACTTTCTTAA--- TCCTCAAA
ATTTTTTTTGCCAT

GAM499 ATGATAAAATTTCAACACAT 1107 CAAAAGCCTT 4177 - TT- C TA- GTA ACA TCC
ACTTGTACAGATGACATATT GTTTTGTATA ATGATAA AAT CAA ACA CTT CAGATG TATT A
TCCACCTGATAACATTTGCA TTCT ||||||| ||| ||| ||| ||| |||||| ||||
AAAGCCTTGTTTTGTATATT TACTATt tta gtt tgt gaa GTTTAC ATAG /
CTTATCAT c tat t tcc aac A-- TCC

GAM500 AAATGGATTTATAGGTTTTG 1108 ATGGATTTAT 4178 tat ttt---------- gct
TAGCTAATAATACTTTTCCA AGGTTTTGTA AAatggatt aggt gta a
TTTTCTACCTTTGATCCATT GCTA ||||||||| |||| |||
T TTTACCTAG TCCA CAT A
TT- TCTTTTACCTTTT AAT

GAM501 ATTTTCTCATCTAATAATAA 1109 TGGCAATATA 4179 AAT TTT ---- TC A CTA CTGT
AAC
GTTTAATAGAGGTCCTTTTA TAAGTAAAAG AATAAG AATAGA GG CTTTTATT ATGTA GCT
ATTCA A
TTAATGTACTAGCTCTGTAT CTCC |||||| |||||| || |||||||| ||||| ||| |||||
TCAAACACCATGGATTGTGG TTGTTT TTATCT cc gaaaatga tatat cgg TAGGT /
CAATATATAAGTAAAAGCTC T-- --- ACGA tc a aa- tGT- ACC
CAGCATCTATTTTTGTTTCA
ATTCCGTAGT
GAM502 GTAGCGAGTCTTTTAAAGTA 1090 TAGATTTTAA 4160 C CTT--- A TCGTAAAA
TACTTCGTAAAATATTCTTT TTTAAAACTC GTAG GAGT TTAAAGT TACT T
CAGTAGATTTTAATTTAAAA CTAT |||| |||| ||||||| ||||
CTCCTAT tatc ctca aatttta atGA /

- aaattt g CTTTCTTA

GAM503 AGACGTATTAGCGGATCTAA 1091 TAAGAATATA 4161 CTA CCA- A A
CTTTTGAAAATATAC TG TCC
TGGAATCCAATTGATTGACT GCAACAATGA GAT ATGGAAT ATTG TTG CTAT
ATTTTTA A G
ATCTTTTGAAAATATACATT TAAT ||| ||||||| |||| ||| |||| ||||||| |
TTTATGATCCGATACTTGTA CTA TACCTta taac aac gata taagaat T A
AGAATATAGCAACAATGATA C-- atag - - ---------- GT CAT
ATTCCATCATCGTGTTTTTT
TGCCTCT
GAM504 GAAATATACCGTAAATCAAA 1094 CAAAAGCTTT 4164 A AAATC TTCCATT
ACCACATAATC G
GTTGTTTCCATTAAAAGTTA TTTGCGACTT GAAAT TACCGT AAAGTTGT AAAAGTT
GAAT T
CCACATAATCGAATGTCAAT TTAG ||||| |||||| |||||||| ||||||| ||||
TCCAAAAGCTTTTTTGCGAC CTTTA ATGGTA tttcagcg ttttcga CTTA C
TTTTAGCATGGTAATTTC - Cgat- tt----- aaac------- A

GAM505 CCGCCCGCGCGGCATCTCAT 1100 CATCTCATTA 4170 - - ca gcccgg CTTC
TAGCGCCCGGCGCGGGCGGC GCGCCCGGCG CCGCCCGCG CG G tctcattagc cgcgggCGG
C
TTCCGCTTCCGCCCGCGATG CGGG ||||||||| || | |||||||||| |||||||||
CTAATGAGACCCTCGTCGCG GGCGGGCGC GC C AGAGTAATCG GCGCCCGCC /
GGCGG T T CC TA---- TTCG

GAM506 GTTTCTATATTAATAGGAGA 1101 TCTATATTAA 4171 tattaatagga AG AGT
TAGTTGTTGAGTCATAGTAA TAGGAGATAG GTTtcta gatagttgtTG TCAT A
AAATGAAATGATAACTGTTT TTGT ||||||| |||||||||| ||||
AGAAAT TAAAGAT TTGTCAATAGT AGTA /
---------- AA AAA

GAM507 TTCTTGTTTGTTTATTTCTG 1110 AATACAGATA 4180 -- T CT-- CTA AT----------
C
CTTCTAATCTATTATTTGCA CTAATGTTTC CT TGT TGTTTATTT GCTT ATCT
TATTTG A
ACAAATACAGATACTAATGT AGGG || ||| ||||||||| |||| |||| ||||||
TTCAGGGGATAAGTTTCCGA GA ACA ACAAATAAG TGAA TAGg ataaAC /
ATAAACATACATTAGGG TT T CCTT --- ggactttgtaatcatagac A

GAM508 GTGCGCTTTGTACTCAGCTT 1095 TTGGTTGACT 4165 C T C TGTCTTCGA TCT
GTCTTCGAAACGATTCTCCG GCGCAGCTCA GTG GCT TGTA TCAGCT AACGAT C
ATGTTGTTGGTTGACTGCGC C ||| ||| |||| |||||| ||||||
AGCTCAC cac cga gcgt agttgg ttGTTG C
t c c --------- TAG

GAM509 CTTGTAAACTTCATCGTTTA 1096 TTAGAAAATA 4166 A TTCAT ---------- ATAA C T AT

TTGTTATATAATTTCCTGTA GCAATGATTT CTTGT AAC CGT TTATTGTTAT TTTC TG AG A

GATAAAACTTTAGAAAATAG TCCC ||||| ||| ||| |||||||||| |||| || ||

CAATGATTTTCCCTTTACGT GAGCA TTG GCA agtaacgata aaag at TC A

CCGTTAACGAG A CCT-- TTTccctttt ---- - t AA

GAM510 ACGTTAAAGCTAAATTGCTT 1102 TTAAAGCTAA 4172 taa taa cttat tg T

ATGGTGGGTGGGTCTTCTTA ATTGCTTATG ACGt agc attg gg gGTGGG C

CTTGCCCGGTCTGCTGTCAC GTGG |||| ||| |||| || ||||||

GT TGCA TCG TGGC CC TCATTC T

CTG TC- ----- GT T

GAM511 TATCTTTGTTAATTAGCGTA 1111 TCTTTGTTAA 4181 - atta----- tAACTCT

AATTTTAACTCTTTTCCAAA TTAGCGTAAA TAtctt tgtta gcgtaaattt T

TAAGTTTATGTAACAACAAC TTTT |||||| ||||| ||||||||||

TAACATGAGATA ATAGAG ACAAT TGTATTTGAA T

T CAACAACAA TAAACCT

GAM512 GCACCGGTGTTATCTGTTCA 1114 TATCTGTTCA 4184 C T tat tg tccct - aCAA---------- T

GTCCCTGCCAACTACAATTG GTCCCTGCCA GCAC GG GT c ttcag gc caact TTG T

TTTGCAAAGGTCTTTTACCG ACTA |||| || || | ||||| || ||||| |||

AAAGTTGTGTCAATCTGAGT TGTG CC CA G GAGTC TG GTTGA AAC T

GGCTACCCCTGTGT T C TC- GT TAAC- T AAGCCATTTTCTGGA G

GAM513 CGTTGTGGATTGTCTGACCT 1097 TTGAAAAAAT 4167 TT TG TGTC CT--- aaaattttt ccg

TTGAAAAAATTTTTGTGTCC TTTTGTGTCC CG G GAT TGAC ttgaa gtgt t

GTGTAGCATTTCAATAAAAG GTGT || | ||| |||| ||||| ||||

TCATTATCTGCTCCG GC C CTA ACTG AACTT TACG /

CT GT TT-- AAAAT --------- Atg

GAM514 CACTATGTCGTGGATTAGTT 1112 TTCTCATGAA 4182 G TAGTT GACAC -- A ATAA -- - TA

TAGATGACACTTGTTGTAGG CGGAACGATT GAT TAGAT TTGT TGTAGGAG TTGT GTTC GGGGCCG T

AGATTGTATAAGTTCGGGGC CCTA ||| ||||| |||| |||||||| |||| |||| |||||||

CGTATGGGTGGTTCTCATGA CTA ATCTG GACA ACatcctt agca caag tcttGGT G

ACGGAACGATTCCTACAGTA T TAC-- ACCTA TG - agg- tac GG

CAGATCCAGTCTACATATCT

GTTATAGTG

GAM515 CCACGTCGTTGGTTTCTTTT 1115 CGTTCCGTTA 4185 C C ----- TTTATCAT- TTG

ATCATCTTCTTGTACTTGAG GAAACGTTTT CCA GT GTTG GTTTCT CTTC T

GCGTTCCGTTAGAAACGTTT CAAC ||| || |||| |||||| ||||
TCAACAACTTGG GGT CA caac caaaga GGAG A
T A ttttg ttgccttgc TTC

GAM516 CGAAGAATGTCGTGCCGTTG 1116 TACCCCGCCG 4186 AAT T CGT- TTGT TG
TTGTTGTTTACGTGATACGT ACTCCTTTG CGAAG GTCG GC TGTTG TTACG A
GGTGTTCGATACCCCGCCGA ||||| |||| || ||||| |||||
CTCCTTTG gtttc cagc cg atAGC GGTGC /
ct- - cccc TTGT AT

GAM517 GGGCTCTCTGCCGTGCGAGG 1098 CCGCGCAGCA 4168 C C AG C CACAGACAC
CTCCTCACAGACACACAGCA GATAGCCC GGGCT TCTGC GTGCG GCT CT A
AGAAAGAAGCGCCGCGCAGC ||||| ||||| ||||| ||| ||
AGATAGCCC cccga agacg cgcgc CGA GA /
t a cG A AAGAACGAC

GAM518 GTGCAGAGACCGCCTGGGTG 1103 AAACACCCGT 4173 C GA TTTTAG AA
TGACTGTTTTTAGGCCTAAC GCGGTCTCTG GTGCAGAGACCGC TGGGTGT CTGT GCCT C
AAAGGCACAGAAACACCCGT TAT |||||||||||| ||||||| |||| ||||
GCGGTCTCTGTAT tatgtctctggcg gcccaca GACA CGGA /
t aa ------ AA

GAM519 GAGACAAGCTTTCAATATCT 1104 TTCAATATCT 4174 A T a--------- --- gtaaa
GAATCTAAAGTAAAGTCATG GAATCTAAAG GAGACA GC ttca tatctgaa tctaaa G
TTTAGAAGTTTCGGATAAAT TAAA |||||| || |||| |||||||| ||||||
TTATTAATGAATGCATGTCT TTCTGT CG AAGT ATAGGCTT AGATTT /
T A T AATTATTTAA TGA GTACT

GAM520 TATTTTCAAATAGCCGATTT 1105 TTGAATCTGT 4175 T C ------ GTTTT--- TGT T
TC
GCAGTTTTCAGTGTTTCGAT TCCTCCATGC TATTTTCAAA AGC GATT TGCA CAG
TTCGATT CG C
TTCGTCCAGTTGTGATTGAA ATTT |||||||||| ||| |||| |||| ||| ||||||| ||
TCTGTTCCTCCATGCATTTT ATAGAAGTTT TTG TTAG acgt gtc aagttAG GT A
ATGATTTGTTTTTTGAAGAT T T TATttt acctcctt t-- T TG
A

GAM521 GTATTCAGCAATTGACACAT 1106 TTCGTGTTTA 4176 C CACATTT T- G
TTTACGGTGCCTGTGTAGGT TTCAATTCTG GTATTCAG AATTGA TACGG GCCT T
TTTCGTGTTTATTCAATTCT AGTA |||||||| |||||| ||||| ||||
GAGTAT Tatgagtc ttaact gtgct TGGA G
- tattt-- tT T

GAM522 GAACGTCTCTCTCTCCTGTG 1113 TTCAGCATAA 4183 C T C TC- CA-- GTTTTCG
T

TCGATCGCAGAGCGTTTTCG GTTTATTTTG GAA GTC CTCTCTC TGTG GATCG GAGC GAACTG C
GAACTGTCCTCGGTTCAGCA GTCT ||| ||| ||||||| |||| ||||| |||| ||||||
TAAGTTTATTTTGGTCTATT CTT TAG GGGGGAG ATAT ctggt tttg cttGGC C
ATAGAGGGGGTGATTTC - T - TAt ttta aatacga T

GAM523 GAAAGGCATGTGGGTTAATG 1117 TACCACAGGT 4187 C G - TA AAA-- TAC- A- TT
ATTAAATCAGGTACTATGCC ACCTTTT GAAAGG AT TG GGT ATGATT TCAGG TATGCC TC T
ATCTTTAGTGAAAGGCATGT |||||| || || ||| |||||| ||||| |||||| ||
TTTCTTGGGCATAAATCATA ttttcc tg ac cca tACTAA GGTTC GTACGG AG A
CCACAGGTACCTTTT a g a -- ATACG TTTT AA TG

GAM524 AGTTTAGATGACACTTGTTG 1118 TAGAAGATTG 4188 TG C TG a - taagt-- ggg G CAT
TAGAAGATTGTATAAGTTCG TATAAGTTCG A ACA T TTGtag agat tgta tc gcCGTAGGGGT GTTCT G
GGGCCGTAGGGGTGGTTCTC GGGC | ||| | |||||| |||| |||| || ||||||||||| |||||
ATGAACGGAACGATTCCTAC T TGT A GATATT TCTA ACAT AG TGGCATCCTTA CAAGG /
GGTACAGATCCAGTCTACAT GT C GT G T CTGACCT ACA G CAA
ATCTGTTATAGTGACTGTTG
TCTATGCT
GAM525 AGGACAATTTTTGAGTTCTA 1122 CAATTTTTGA 4192 --------- tctatttc- C
TTTCAATGTCATCACATTTT GTTCTATTTC AGGAcaat ttttgagt aatgT A
CGACAATATTCAAAATCATC AATG |||||||| |||||||| |||||
GCTTATTGTTTT TTTTGTTA AAAACTTA TTACA T
TTCGCTACT TAACAGCTT C

GAM526 GGTTGTATTAAAGGCTTAAT 1123 TAATGCTGTA 4193 GGCTTAATTT T AATACC TGT
TTCAGCTTTATCAATACCTA TTTAATACAA GGTTGTATTAAA CAGC TTATC TAG A
GTGTAAATCTAACAGATAAT CT |||||||||||| |||| ||||| |||
GCTGTATTTAATACAACT tcaacataattt gtcg aatAG ATC /
at-------- t ACA--- TAA

GAM527 TGCTTATACTCTAAGAGTAT 1119 TAAGAGTATC 4189 T---------- C G
CGCCACCGACGACGACGACG GCCACCGACG gagtatcgccaccgacgacgaCGACGGCAGTCGC GC CGGC A
GCAGTCGCTGCCCGGCGAAG ACGA |||||||||||||||||||||||||||||||| || ||||
CCGAGCCGCCGCGAAGCGGC CTCATAGCGGTGGCTGCTGCTGCTGCCGTCAGCG CG GCCG /
GAGCGACTGCCGTCGTCGTC AGCGGCGAAGCGCCGC A A
GTCGGTGGCGATACTCTTAG
AGTATAAGCA
GAM528 ATTCATAGTTTTTAAAATTT 1120 CAAATGGAAA 4190 A TTTTTA- A AAA
TTACATTTGAGAAATCATAT ATTTGTTTTA ATTC TAG AAATTTTT CATTTGAG T

TCAAATGGAAAATTTGTTTT TCTA |||| ||| |||||||| ||||||||
ATCTAAGAAT TAAG atc tttaaaag gtaaacTT C
A tattttg - ATA

GAM529 TACCAGAGTTTCGTGATGAT 1121 TGATTTGTTA 4191 - G A ga t ctaaa
GATTTGTTATGTGATCCTAA TGTGATCCTA TACCAGAGTT TCGT ATG t tttgt atgtgatc a
AAATCGCGATTACATACAAG AAAA |||||||||| |||| ||| | ||||| ||||||||
CTGCATGCGATGACTTTGGT ATGGTTTCAG AGCG TAC G GAACA TACATTAG /
A T - - TC - CGCTa

GAM530 ACCTTCTGAGCTGATGGTCT 1129 TCCGAAGACC 4199 TG GAT- ACT - GATG
ACTGACCTGATGATGAAGAG TTGGAGCTGA ACCTTC AGCT GGTCT GA CCT A
GATCCGAAGACCTTGGAGCT AGGT |||||| |||| ||||| || |||
GAAGGT tggaag tcga ccaga ct GGA T
-- ggtt agc A GAAG

GAM531 GGTACTTTCTTTGCCAAAAA 1133 AGAAAGTTTT 4203 TTT - - AAA- G GA AG TT A
AAAAGTTGATTGAAGTCATT TAGCGTGTGT GGTAC CTTTG C CA AAAAA TT TTGA TCA
TTC C
TTCACAAGAATTGATCAGAA CAAA ||||| ||||| | || ||||| || |||| ||| |||
AGTTTTTAGCGTGTGTCAAA CCGTG Gaaac g gt ttttt aa gaCT AGT AAG A
GTGTGCC T-- t t gcga g a- -- T- A

GAM532 TTGATAACAGTTGAAAGCCA 1134 TTGAAAGCCA 4204 A t gc attt aa
AATATTTGCCAAAATCGGTT AATATTTGCC TTG TAACAGt gaaa caaat gcc a
TCAATTTGCGTTTCGCTGTT AAAA ||| ||||||| |||| ||||| |||
GCCAA AAC GTTGTCG CTTT GTTTA TGG a
C - GC ACTT CT

GAM533 ACTTTCATCCTGATCACCTG 1124 TAACGAGATT 4194 CCTGA A -------- C C A G
G
TATCCTCTCTCTACTCTACG GAAGAGACAG ACTTTCAT TCACCTGT TCC TCTCT TA TCT
CGT ATCG T
TGATCGGTGACGGTAACGAG ACAA |||||||| |||||||| ||| ||||| || ||| ||| ||||
ATTGAAGAGACAGACAACGG TGGAAGTA AGTGGACA GGG agaga gt aga gca
tGGC G
GACAGGTGAGACAATGAAGG ACAG- - Caacagac a t - a A
T

GAM534 GAGAGGTGTAAAAGATATAT 1125 TACACCGCCA 4195 AAAAGATATA TCG-- A
GGCTCGATCAGCTGATACAC CCGTAAAACC GAGAGGTGT TGGC ATC G
CGCCACCGTAAAACCACGCC ACGC ||||||||| |||| |||
TCTC CTCTCcgca accg tAG C
ccaaaatgcc ccaca T

GAM535 CCGCCATTTTAAGTAGCTGA 1126 AAGTAGCTGA 4196 aa ga a t GTAAAG
CGTCAAGGATTGACGTAAAG CGTCAAGGAT CCGCCATTTT gtagct cgtc aggat gac G
GTTAAAGGTCATCCTCGGCG TGAC |||||||||| |||||| |||| ||||| |||
GAAGCTACACAAAATGGTGG GGTGGTAAAA CATCGA GCGG TCCTA CTG /
CA AG C - GAAATT

GAM536 GTGCGTACGTCACAAGTCAC 1127 TAGGCCCCGT 4197 CAC GA A CG GTAA
GTGGAGGGGACCCGCTGTAA CACGTGACTT GTGCGTACGT AAGTCACGTG GGGG CC CT
C
CCCGGAAGTAGGCCCCGTCA ACCA |||||||||| |||||||||| |||| || ||
CGTGACTTACCACGTGTGTA CATGTGTGCa ttcagtgcac cccc gg GA C
C cca tg - at AGGC

GAM537 CCGGCGGACGCACCTCGAGA 1130 GACCGGGCCG 4200 - C - GA -- GC -- G - ACGA
A CAG
GGGCCCCGGGCCCGACGGCC CCCGATCGAA CA CT CGA GGGC CCCGG CCGA CG CC
GCGGCG TG GGTCG A
GCGGCGACGATGAGGTCGCA GATG || || ||| |||| ||||| |||| || || |||||| || |||||
GATCTCGACCCCGGAGGCGC gt ga gct cccg gggcc gGCT GC GG TGCCGC GC
CCAGC /
CGTAGGGCGACTCGGACCGG C a a ag cc a- CA G A GGAG C TCT
GCCGCCCGATCGAAGATGCC
GTTCCTCCCGG
GAM538 GCAGCATATGGATATGTAGA 1135 CAGGAGACCA 4205 GCA GA AGAA--- AA
ATTTTGTGCAAAAAGTACAG AAACATACAC GCA TATG TATGT TTTTGTGC A
GAGACCAAAACATACACATG ATGA ||| |||| ||||| ||||||||
AATGC CGT gtac ataca aggacATG /
Aa- ac aaaccag AA

GAM539 TTGGATCTTGTTCTGTTAGT 1128 TGGAAAAATC 4198 CT - TAG - TTG-- TACGTA
ACTGGTTGTCCAGATACGTA CAGCTAATGC TTGGAT TGT TCTGT TA CTGG TCCAGA A
AACTTCTTTCTGGAAAAATC AGAT |||||| ||| ||||| || |||| ||||||
CAGCTAATGCAGATATATTA GGCTTA ATA agacg at gacc aggtCT A
TTCGG TT t ta- c taaaa TTCTTC

GAM540 CCCGGGCTCCCCGTTCCCCG 1131 CTCCCCGTTC 4201 TTCCC A T- CT - TTCCC A T-
CT - TT
AGGGTCCCGGGCTCCCCGTT CCCGAGGGTC CG CG GGG CCCGGG CCC CG CG GGG
CCCGGG CCC CG C
CCCCGAGGGTCCCGGGCTCC CCGG || || ||| |||||| ||| || || ||| |||||| ||| ||
CCGTTCCCCGAGGGTCCCGG GC GC CCC Gggccc ggg gc gc ccc GGGCCC GGG
GC /
GCTCCCCGTTCCCCGAGGGT CCCTT - TC t- a ccctt - tc T- A CC
CCCGGGCTCCCCGTTCCCCG
AGGGTCCCGGG

GAM541 GGCCTAGAGAAGGAGAGGGA 1132 CCGCTCCATG 4202 AG AAG G----- TCT AA
GCTCTATCTAAAGAAGATCC GAGTCTCAGC GGCCT AG GAGA GGAGC ATCT A
GCTCCATGGAGTCTCAGCTG TGCA ||||| || |||| ||||| ||||
CAGGCC CCGGa tc ctct cctcg TAGA /
cg ga- gaggta cc- AG

GAM542 GTTGGAAACTTACTCGCCAC 1136 TGGAAACTTA 4206 a tactc - cccaCCC- GA
CCCCCACCCGCTGGGAAAGC CTCGCCACCC GTtggaa ct gcc accc GCTGG A
CGGCATCATCGAGGGTGGGC CCCA ||||||| || ||| |||| |||||
ACAATAGTTCTAGC CGATCTT GA CGG TGGG CGGCC /
- TAACA G AGCTACTA GA

GAM543 CCGGTGGAACTCGTGACAGA 1137 CATCGTGGAG 4207 A - CA G --- AC
TGTCTACGCCACCCTAGGCA ATCATCGACG CCGGTGGA CTCGT GA GAT TCTAC GCC C
TCGTGGAGATCATCGACGAG AGCT |||||||| ||||| || ||| ||||| |||
CTCTACCGG GGCCATCt gagca ct cta aggtg cGG C
c g a- g cta AT

GAM544 AGTTTGCCATGCTACAGTTT 1138 GCTACAGTTT 4208 T C g -- ttg- -- atcacat
GCATACGATCACATCCAATC GCATACGATC AGTT GC AT ctac agt cat acg C
CCACGTCAATGAAATGCTAA ACAT |||| || || |||| ||| ||| |||
GTAGAATAGCAACT TCAA CG TA GATG TCG GTA TGC C
- A A AA TAAA AC ACCCTAA

GAM545 GCGCAAGCTGATCGAGCCGT 1139 AGAGTACGTT 4209 AA- T T C CGCC- AATCAG C
AA TT
GCGCCCTCAATCAGAAGCGC TACTACGAGA GCGC GC GA CGAGC GTG CTC AAGCG
TACTTT G T
TACTTTAAGTTTGGCAAAGA ACTA |||| || || ||||| ||| ||| ||||| |||||| |
GTACGTTTACTACGAGAACT CGTG CG CT GCTTG CAC gag tttgc atgaga C /
ACACGTTCGTCCGCAAAGTG AAA C - - atcaa catca- - AA GG
C

GAM546 CATGTGCAGCACTGGAAGTG 3052 TTTACGCATA 6122 T A- GAA- - ---- aa------ - tt
TTTACGCATAGAAGCAGCCT GAAGCAGCCT CA GTGC GCACTG GTGtt tac gcatag gc
agcctta A
TATTATTTAAGGCTCGTGAA TATT || |||| |||||| ||||| ||| |||||| || |||||||
ATGGGCTATGCACAAGTAGG GT CACG CGTGAT TACAG ATG CGTATC TG
TCGGAAT /
ACATCAAATAGTGCCAGCAC - AC AAAC G AACA GGGTAAAG C TT
TG

GAM547 TGCTGCTGTGGTTTTTAGCC 3054 TGTGGTTTTT 6124 - t tt c t TT
ACAGTGTTTATTTGTATATT AGCCACAGTG TG CTGC gtggtt tagc acagtgtt aT G
AGTACTGTTGTTAAACTACT TTTA || |||| |||||| |||| |||||||| ||
GCAGACA AC GACG CATCAA ATTG TGTCATGA TA T

A T -- T T TA

GAM548 GATGTAATGTCCGTATTCTT 3053 TGTAATGTCC 6123 g tcc- ttca a TG
CAGGTATCTGTCGGAACCAG GTATTCTTCA GAt taatg gtattc ggt TC T
TCGAGTATAGTTCGTTGAAT GGTA ||| ||||| |||||| ||| ||
C CTA GTTGC TATGAG CCA AG /
A TTGA CTGA - GC

GAM549 GTTGCTGTTCGTGTCGCGAA 3055 TTGAGTCGTA 6125 G G---------- C
GCTAGTTTTGAGTCGTAATT ATTGCAGCAG GTTGCTGTTC TGTC CGAAG T
GCAGCAGGCAGAGCAGCAGC GCAG |||||||||| |||| ||||| CGACGACGAg acgg gttTT A
- acgacgttaatgctga G

GAM550 GCGGGTCGTCGCGGGGACTG 3056 ACTGGTTTGG 6126 T C ct t- t ta ta-- T
GTTTGGCGTGCGTACGTACG CGTGCGTACG GCGGG CGT GCGGGGa ggtt ggcg gcg cg cgTGT T
TGTTTCTGCACGGCTCCGGC TACG ||||| ||| ||||||| |||| |||| ||| || ||||| CGCCGCTTCGGCCTCCCTGC CGCCC GCA CGTCCCT CCGG TCGC CGC GC GCACG C
ACGCCCGC - - -- CT - CG CTCG T

GAM551 GTGGTGGAATATATGTTGAC 3057 TGGAATATAT 6127 tatgttgac ----- A - AGA GAT
GCAGTCGGCGACTCGGCAGA GTTGACGCAG GTGGtggaata gcagtcg gCG CTCG GC GC C
GCGATCTGGAGCGGCTCGAG TCGG |||||||||| ||||||| ||| |||| || || GCGCACGATCGGCTGCTGTT CATTACTTTGT CGTCGGC CGC GAGC CG CG T
TCATTAC --------- TAGCA G T G-- AGG

GAM552 GGCCCCCTCCCGAGCTGGGG 471 CGGCCCCCTC 3541 -- CC CT C ATCCC
CCCGGATCCCCGACCTCCCC CCGAGCTGGG GGCCCC CTC GAG GGGGCC GG C
GGCCCCCTCCCGAGCTGGGG GCC |||||| ||| ||| |||||| || CC ccgggg gag ctc ccccgg CC G
tc cc -- c CTCCA

GAM553 GCCCGTCTTCAACCTGGTGC 472 CCCCTGAAAA 3542 - TC AC T --------- CTT
TGGACTTTGACCTCCCCCTG AGCCCGGCCT GC CCG TTCA CTGG GCT GGA T
AAAAAGCCCGGCCTGAGCCT GAGC || ||| |||| |||| ||| |||
GGAGC CG GGT gagt ggcc cga cCT G
A Cc cc - aaaagtccc CCA

GAM554 CCCGGCCCCCTCCCGAGCTG 479 CCCGAGCTGG 3549 C -- CC CT C ATCCC
GGGCCCGGATCCCCGACCTC GGCCCGG CC GGCCCC CTC GAG GGGGCC GG C

CCCGGCCCCCTCCCGAGCTG || |||||| ||| ||| |||||| ||
GGGCCCGG gg ccgggg gag cTC CCCCGG CC G
c tc cc -- C CTCCA

GAM555 CGACCTTCCCGGCCCCCTCC 480 TGGGGCCCGG 3550 ACCT- C -- CC Ct c tccccc tt
CGAGCTGGGGCCCGGATCCC ATCCCCCCGG CG TCC GGCCCC CTC GAG ggggcc gga
cgg c
CCCGGTTCCCCCGACCTTCC TTCC || ||| |||||| ||| ||| |||||| ||| |||
CGGCCCCCTCCCGAGCTGGG GC AGG CCGGGG GAG CTC CCCCGG CCT GCC /
GCCCGGATCCCCCG CCCCT C TC CC -- C TCCA-- Cc

GAM556 CGAGCTGGGGCCCGGATCCC 485 TCCCCGGCCC 3555 C TCCCCCGACCtc c -- cc ct
C TTCCCC
CCGACCTCCCCGGCCCCCTC CCTCCCGAGC GGGGCC GGA cc ggcccc ctc gag gggGCC
GG C
CCGAGCTGGGGCCCGGTTCC TGGG |||||| ||| || |||||| ||| ||| |||||| ||
CCCGACCTCCCCGGCCCCCT TCCCGG CCT GG CCGGGG GAG CTC CCCCGG
CC /
CCCGAGCTGGGGCCCGGTTC C TCCACCCCCTT- C TC CC -- C CTCCAG
CCCCACCTTCCCGGCCCTCG
CCCG
GAM557 TCAAAGGTCAAGCCGGTAGC 473 AAGGTCAAGC 3543 aa aag ------- tc
GGCGTTCCCTACGCTGCTTT CGGTAGCGGC TCA ggtc ccggt agcggcgt C
CTCAGGCCGGAAGACCAATG GTTC ||| |||| ||||| |||||||
A AGT CCAG GGCCG TCGTCGCA /
AA AA- GACTCTT TC

GAM558 TGTGGCCAGGATGCTCTTCC 474 GGAGCTCCTC 3544 --------- T CGAGACC
GAGACCAAAATGAAGAGGAG CAACACATGG TGTGGCCA GGA GCTCTTC A
CTCCTCCAACACATGGCCAT CCAT |||||||| ||| |||||||
A Ataccggt cct cgaggAG /
acacaacct - AAGTAAA

GAM559 GCGTCTGTATTAAATATTTC 481 TCTAAATTTT 3551 GTATTAA tc tt t a TTTTTA-
ACT
TAAATTTTTAGGTAATAATA TAGGTAATAA CGTCT ATATT taaattt agg aat atataT ATTGTA
T
TATTTTTTAATTGTAACTTA TATA ||||| ||||| ||||||| ||| ||| |||||| ||||||
TCTATAATACTATTTATATG GTAGA TATAA ATTTAAA TTC TTA TGTATA TAATAT
/
TAATTCTTTTAAATTTACTA AATTTC- TC TT - A TTTATCA CTA
ATATCTTTAAAGATGT

GAM560 ACCTCTCCAGGTATACAGAA 482 CCTCAACGAA 3552 - AG TATACAGAA C A T
GAGCGGGAGTTTTAACACCT CTCTCGGATG ACCTC TCC G GAG GGG GT T
CCTCAACGAACTCTCGGATG AGGT ||||| ||| | ||| ||| ||

AGGT tggag agg c ctc TCC CA T
t ct tcaagcaa- c A A

GAM561 TGGGGGTTGAGTACTTGGGA 483 TAAGGAAAAC 3553 TTGA A ACCC CA G
CCCTCCTTATCCAAGTGAAA CCAAGACCCT TGGGGGG GT CTTGGG TCCTTATC AGT A
ATTAGATAAGGAAAACCCAA CCA |||||| || |||||| |||||||| |||
GACCCTCCA acctcc ca gaaccc aggaatAG TTA A
---- - aaa- A- A

GAM562 CCCGGTGATTCAGGACTGCC 486 TCGTCGCAGT 3556 GATTCA CCCTATT GAA
CCTATTTGACATGAAGATGA CCACCGGG CCCGGT GGACTGC TGACAT G
ATGTCGTCGCAGTCCACCGG |||||| ||||||| ||||||
G gggcca cctgacg gctGTA A
------ ct----- AGT

GAM563 TATAGATATTTACGGAGTAT 475 TATTTGGTAC 3545 G ---- TGAA TAC
ATGAACTGTATACCGATTTA GTAAGTATGT TATA ATATTTACG GAGTATA CTGTA C
CAGAATTTGTATTTGGTACG ATA |||| ||||||||| ||||||| |||||
TAAGTATGTATA atat tatgaatgc tttatGT GACAT G
g atgg TTAA TTA

GAM564 GTGATATTGTGGGGTCGTGA 476 TTGTGGGGTC 3546 tt--- tc t - tg TG
TGATATTGACTGTCTGTTGG GTGATGATAT GTGATA gtgggg gtga gat at ac T
TGATTCTCACCCTCATTGGC TGAC |||||| |||||| |||| ||| || ||
TTATTAT TATTAT TACTCC CACT TTA TG TG /
TCGGT -- C G GT TC

GAM565 GAGGAGCTGCCGGTTGCCAT 477 CAGCAGGCCT 3547 ------ G TTCAAGCT
TTTTCAAGCTGCTAAACCAC AAGAAGCTCC GAGGAGCT GCC GTTGCCATTT G
GAGTGGCAGCAGGCCTAAGA TC |||||||| ||| ||||||||||
AGCTCCTC ctcctcga cgg cgacGGTGAG C
agaatc a CACCAAAT

GAM566 TGTTAGCCAACAACGACATC 478 TAGCCAACAA 3548 a caaca c---- t acC A
CGTGTACCAGAAATCTTAGC CGACATCCGT TGTt gc acga atccg gt AG A
TTGGATAATCATCGTAGCAG GTAC |||| || |||| ||||| || ||
ACA ACAG CG TGCT TAGGT CG TC A
A A---- ACTAA T AT- T

GAM567 TCTCTTCGAAGAACCCAGAA 484 TCGAAGAACC 3554 T accca-- tca aaaTA
TCAGTCAAATAACAGTGGAC CAGAATCAGT TC CTtcgaaga gaa gtc A
GACTTCAAACTCCTTTTCGA CAAA || |||||||| ||| |||
AGGA AG GAAGCTTTT CTT CAG /

- CCTCAAA CAG GTGAC

GAM568 CCCGTGGGGGGTCTTAGTGG 487 TAGCACCGCT 3557 T G TCT - AC A A
AAGTGACGTGCTGTGAATAC ATCCACTATG CCCG GG GGG TAGTGGA AGTG GTGCTGTG AT
C
AGGTCCATAGCACCGCTATC TCTC |||| || ||| ||||||| |||| |||||||| ||
CACTATGTCTCGCCCGGG GGGC CC ctc atcacct tcgc cacgatAC TG A
- G tgt a -- C G

GAM569 GTGTGGAGTCTGTTGAGAAT 488 GAGAATGCCA 3558 GT- T a-- - t tagtc A A
GCCATGCTATAGTCATAGGA TGCTATAGTC GTGTGGA CTGT gaga tgc ca gcta atagG TTCA
A
TTCAAAATTGAACTTGTTTG ATAG ||||||| |||| |||| ||| || |||| ||||| ||||
TTAGTTGTGTAAAATCTTTA CATACTT GATA TTCT ATG GT TGAT TGTTC AAGT A
TAGTTATTCATAC ATT T AAA T - TGTT- - T

GAM570 TGTGCCGCTTGGAGGGAAAC 489 TCAGTGGTTT 3559 CCG TGG T C AG TT
ATGACCACCTGAAGTCTGTT TGTTTCCTTG TGTG CT AGGGAAACA GACCAC TGA TCTG A
AACCAGGTCAGTGGTTTTGT ATAG |||| || ||||||||| |||||| ||| ||||
TTCCTTGATAGAGACACA ACAC ga ttcctttgt ttggtg act GGAC /
AGA tag t - -- CA

GAM571 TTTGATCGGTGTAGATTTTG 493 GATTTTGTTG 3563 -- G tg-- t t GTG
TTGTATTTGGTTGAATTCTG TATTTGGTTG TTTGA TCG TGTAgattttgt tat tgg tgaattCTG T
GTGTCGAATAGAATTTATCT AATT ||||| ||| |||||||||||| ||| ||| |||||||||
GTATGGTCCGCAAAGTCTAT GGACT GGC GTATCTGAAACG GTA GTC ATTTAAGAT C
GGCGGGTTCAGG TG G CCTG T T AAG

GAM572 CTTTAGTGGGAACTAGTGGG 501 TACCCCTATC 3571 TA A A GTGCT T
AGTGCTGTGCCTCGGGTACC CTATAGGTCC CTT GTGGGA CT GTGGGA GTGCC C
CCTATCCTATAGGTCCTACC TACC ||| |||||| || |||||| |||||
GGAG GAG catcct gg tatcct catGG /
Gc - a atccc G

GAM573 AGGCATTGTTAACCTTTGGT 502 AACCTTTGGT 3572 TT Taa ga a - T TAAAT
GGAACCTAGTGTTAGTGTTG GGAACCTAGT AGGCA GT cctttggtg acct gtg ttaGTG TGTGCTG
A
TGCTGTAAATAAGTGTCCAG GTTA ||||| || ||||||||| |||| ||| |||||| |||||||
CGCACCACTAGTCACCAGGT TCCGT CA GGAGGCCAC TGGA CAC GATCAC
ACGCGAC A
GTCACCGGAGGCTACTTGCC T- TC- TG C T C CTGTG
T

GAM574 GGGGCTCTGTAACATTTGGT 503 ATGCTGCTGG 3573 TCT ACA G a - - -- aa

GGGACCTGATGCTGCTGGTG TGTGCTGTAA GGGGC GTA TTTGGTGG ACCTG tgc tgc tggtgtgct gta t

TGCTGTAAATAAGTGCCTAG ATAA ||||| ||| |||||||| ||||| ||| ||| ||||||||| |||

CACATCACGTAGGCACCAGG CTCCG CAT GGACCACT TGGAC ACG ATG ACTACACGA CGT a

TGTCACCAGGGCTACTTGCC TT- CG- G C G C TC Ga TC

GAM575 GGCAGGTGGAGTGGGACACA 504 CTGGTCCCTA 3574 A T-- ACAGT A A

GTTAGAGAACATTAGTCCTC TCTCCACCCG GGC GGTGGAG GGGAC TAGAG AC T

TGGTCCCTATCTCCACCCGC CC ||| ||||||| ||||| ||||| ||

C ccg ccacctc ccctg gtcTC TG T

c tat ----- C A

GAM576 CAAGCCTGCTGCTCAATTGT 490 TGTATATATT 3560 AGCC TCAATt c c tg tg

ATATATTCCTCTTGTGTTGT CCTCTTGTGT CA TGCTGC gtatatatt ct ttg t t

AGTGTGCAATAGTAGTATGT TGTA || |||||| ||||||||| || ||| |

ATCCTGTTGTAGTACGTG GT ATGATG TATGTATGA GA AAC G a

GC-- TTGTCC T T GT TG

GAM577 GTCGTGCAGTCCCAGCGAGC 491 TCACAAAACG 3561 - AGT A A CA T CAG-- A G

GCAGCGGTACCAGGTAACGC TCTGCACCGC GT CGTGC CCC GCG GCG GCGG AC GT ACGCG A

GGACACGTGTCACAAAACGT CTGT || ||||| ||| ||| ||| |||| || || |||||

CTGCACCGCCTGTCGGGCCA CA GCACG GGG tgt cgc cgtc tg ca tGTGC C

GCACGTAC T ACC C c ca - caaaa c A

GAM578 GGTAAGTTAACAGAGTTTTT 492 TAAGTTAACA 3562 a g ttt aa TG

TATAAAAATCTGGTATGATT GAGTTTTTTA GGt agttaaca agt ttata AATC G

CTATAAGCTTGTTAACTAGC TAAA ||| |||||||| ||| ||||| ||||

T TCG TCAATTGT TCG AATAT TTAG T

A - --- C- TA

GAM579 ATTTAGTTTCACACTCCACT 494 TGGGGTCGAA 3564 CAC C AAGTG

AGCCAAGTGAGTTCCGGGTT GACTAGAT ATTTAGTTT ACTCCA TAGCC A

GTTGGGGTCGAAGACTAGAT ||||||||| |||||| |||||

tagatcaga tggggt GTTGG G

agc T GCCTT

GAM580 GCCGCAGGGCACCTGGCCGG 495 TATCAGGGCC 3565 ----- A CC T GCC

CGTGCCGCCGAAGGGCCGCT TCGAGCTGCG GCCGCAG GGC CCTGG GGCG GCC G

ATCAGGGCCTCGAGCTGCGG GC ||||||| ||| ||||| |||| |||

C cggcgtc ccg ggact tCGC CGG /

gagct - a- - GAA

GAM581 GCTGCGGCTGGTGCTGCAGC 496 CTGCAGCTGC 3566 TG c------ aaa cga CT -
AAG
TGCTGCTGGAAAACCGACGG TGCTGGAAAA CGGC GTGctgcagctg tgctgg ac CGGCGT
GCGCCG C C
CGTCTGCGCCGCAAGCTGCG CCGA |||| |||||||||||| |||||| || |||||| |||||| |
TCGGCGCCTGCGCCGGATGT GCCG CGCGACGTCGAC ACGGCC TG GCCGCG
CGCGGC G /
ACCGGCACTTCGTCCAGCTG -- CTGCTTC A-- TAG TC T CGT
CAGCGCGCCGCGGC

GAM582 TTCTAAGTGTGCAGGTGTGA 497 CACACTTTTG 3567 A- C AA------- G
GTAACTTTGAAAAAAGACCC CATTGGGGAA TTCT AGTGTG AGGTGTGAGT CTTT A
GCAAAACTCACACTTTTGCA |||| |||||| |||||||||| ||||
TTGGGGAA aagg ttacgt ttcacacTCA GAAA A
gg t AAACGCCCA A

GAM583 GTAAATATATGTAAACTGTG 505 TACAGTGTGG 3575 TAT AA---- GT AC A
TACAGTGCGGAACGTTAAGG AGACCTTTAT GTAAATA GT ACTGTGTACA GCGGA GTT A
GACATCTGTTGTATACAGTG TTGC ||||||| || |||||||||| ||||| |||
TGGAGACCTTTATTTGC cgtttat ca tgacatATGT TGTCT CAG G
ttc gaggtg -- A- G

GAM584 GCGGCCGTCGAGATGACGCT 506 CCAGAGCGGC 3576 -- GA A GCA-- AGG
CGCACTTGAGGCGACACAGG AGGTCGATGA GCGGC CGTCGA TG CGCTC CTTG C
CACCAGAGCGGCAGGTCGAT CGCT ||||| |||||| || ||||| ||||
GACGCTGC CGtcg gtagct ac gcgag GGAC G
ca gg g accAC ACA

GAM585 TACCTTACCCATTGTACCTA 507 ACCCATTGTA 3577 T--- ---- ac A
TATGTATTGTATACACAGTG CCTATATGTA TACCT acccat tgt ctatatgtattgt T
TATGTAGACACATGTAGTGG TTGT ||||| |||||| ||| ||||||||||||
GTTTGTGGGTG GTGGG TGGGTG ACA GATGTATGTGACA A
TGTT ATGT CA C

GAM586 GGAGTATACGTAGGCTAGGA 508 TATACGTAGG 3578 A a c a ag- a a TA
AGACAAAGTAAGGCTTGGTC CTAGGAAGAC GG Gt ta gt ggct ga gac aag A
ATCACCAGCCGCTTAAACAC AAAG || || || || |||| || ||| |||
C CC CA AT CG CCGA CT CTG TTC /
A A T - CCA A G GG

GAM587 GGCGGTGGGTCTCGGGCCAA 498 GCGCTCCGAA 3568 G- C-- CCAAAC - T
ACGCCGTCGTAGACGACGCG AAACGACGCC GGCGGTG GT TCGGG GC CGTCG A
CTCCGAAAAACGACGCCGCC GCC ||||||| || ||||| || |||||
ccgccgc ca agcct cg gCAGC G

ag aaa ------ c A

GAM588 GCACACCAGGCTCTTGGCCC 509 TTTGCTGAAC 3579 C CTCT CAC - TG
ACCAGAGACACTGTCACGTG GGCCACTCTA GCACAC AGG TGGCC CAG AGACAC T
TTTGCTGAACGGCCACTCTA GTGT |||||| ||| ||||| ||| ||||||
GTGTGT TGtgtg tct accgg gtc tttGTG C
a c--- caa g CA

GAM589 GCCCGTACCACTGCCATCGC 510 CGATGTGTGT 3580 - AC CCA GCC ATACATGCGC
G TAC
CCTTTGGATACATGCGCACA AAAACACCGG GCCCGT ACC TG TC CTTTGG
ACACACAT GCA C
CACATGGCATACCCATTGCG AGAC |||||| ||| || || |||||| |||||||| |||
ATGTGTGTAAAACACCGGAG CGGGCG TGG AC AG gaggcc tgtgtgta cGT /
ACAGAACCATGGGTAGCGGG A GT CA- Aca acaaaa---- g TAC
C

GAM590 GGTAGCGGGCAGTCCGACGA 511 AGACAAGGGT 3581 ------ G GACGACAC CA
CACGGCCACCAGCCAGACAA GCCATTCTGC GGTAGCG GGCA TCC GGC C
GGGTGCCATTCTGCGTTGCC GTTG ||||||| |||| ||| |||
CCgttgc ccgt ggg CCG /
gtctta - aacaga-- AC

GAM591 TGCCTGTCTCTCCATGTTAA 512 AAGAGCCTTG 3582 TCTCT-- ------- G CGC
GGTTGTTGACGCTGGCTTCA ATACGATCTG TGCCTG CCAT GTTAAGGTT TTGA T
AGAGCCTTGATACGATCTGT TGGC |||||| |||| ||||||||| ||||
GGCCCTCTTCAGGCA ACGGAC ggtg tagttccga aaCT G
TTCTCCc tctagca g TCG

GAM592 CGGCAGTTACCTGTTGTATC 513 TACCTGTTGT 3583 A- - tc a -- ---------- CT
GCAAGGCTCACGTGGAGCTG ATCGCAAGGC C GT tacctgttgta gca ggct cacGTG
GAG G
TCACTCTCCAGCAACAAGGT TCAC | || |||||||||| ||| |||| |||||| |||
GCAACACGTGGAAGCCGTGC G CA GTGGACAGCGT CGT CCGA GTGCAC
CTC T
TGCGACAGGTGTACACGCCG CA T -- G AG AACGTGGAACAACGACCT AC

GAM593 GCCACACGTCCAACTGCTTC 499 ACGGACAAAA 3569 A --- CTTCCCGAA T TTA
CCGAACGTCTCGTTATATAG CCAGTTCCCG GCC CACGTCC AACTG CGTC CG T
TGCGACGGACAAAACCAGTT GACG ||| ||||||| ||||| |||| ||
CCCGGACGTGGGC CGG GTgcagg ttgac gcaG GT A
- ccc caaaacag- C GAT

GAM594 GTTTGAGTGTGGTAGCGCTG 500 TGAGTGTGGT 3570 Tt - g - t gag G AACCCC G

TGTGAGTTGGCGGTGGAACC AGCGCTGTGT GT gag tgt gtag cgctg gt tTGGC GTGG CTCGTG T
CCCTCGTGGTGACACGAGCC GAGT || ||| ||| |||| ||||| || ||||| |||| ||||||
CCCGTGGCCAAAAGCCCAGT CA CTC ACG CATT GTGAC CG AACCG TGCC GAGCAC G
GTTTACAGCACCTCTCAC CT C A T C AA- G CCC--- A

GAM595 AAGAAGATTACTCTTGATGC 514 AGACCCGATT 3584 T C TG TG---------- TCA - CAC A
TTGGCTCTCAGAAAGAATGG CTTTTGAGTC TA TCT A CTTGGCTC GAAAGAAT GG CTCAA G
CACCTCAAAGTTTTGAGACC GAGA || ||| | |||||||| |||||||| || |||||
CGATTCTTTTGAGTCGAGAA GT AGA T gagctgag ttttctta cc gaGTT T
CCTTACCCCCAACCCTTGAG C T GT CCCAACCCCCATTCCAa --- g ca- T
ATTGCTTTTCTT

GAM596 CGGGAGGACCGCCGACGCCG 515 TACCGTAGCA 3585 ACG G C- AA- CTC CAGA- G TG A AGC
TGTCCGGAAGCCTCGTCGGA GGAGCGGCGC GCCG CC TGT CGG GC GTCGGAG GG CCAGG TTT TAT A
GCAGAGGGCCAGGTGTTTAT CTCC |||| || ||| ||| || ||||||| || ||||| ||| |||
ATAGCAGCAGATAGAGATCC cggc gg acg gcc CG CAGCTTC CC GGTTC AGA ATA G
TTGGACCGAAACCTTCGACC ga- - at atG CC- CAAAG A CT G GAC
CGCGTACCGTAGCAGGAGCG
GCGCCTCCCG
GAM597 TCGCTGAACAAATTGTATCC 516 CAGGACCCCG 3586 C A- TA C- - CC --- - G
TCTCAGGGCCTCCTCCGCGT CTGAGGAAGA TCGCTGAA AA TTG TC TCTCAG GG TCCT CC GCGTC T
CGTTGATGTAGGCACAGGAC CGCG |||||||| || ||| || |||||| || |||| || |||||
CCCGCTGAGGAAGACGCGAG AGCGATTT TT Agc ag ggagtc cc agga GG TGTAG /
GTTCTTTAGCGA C GG gc aa g cc cAC A T

GAM598 GCGAGGCACGTCTCACGGTG 517 CCCGAGCTTT 3587 C-- ---------- AC TT
TTTTTCACCCCGAGCTTTAA AATATATATA GCGAGG ACGT CTC GGTG T
TATATATAGAAACACGTTTA GAAA |||||| |||| ||| ||||
TTTCGC CGCTTT TGCA gag cCAC /
ATT Caaagatatatataatttc cc TT

GAM599 AGTGGAATGTTCTACCACAA 518 CCACCCAGAA 3588 GAATG CCACAAGGA AT CC CCA
GGATGGGTATGTAGCCCTGC GATTATAGAA AGTG TTCTA TGGGT GTAG CTG T
CATTTATCAGACTACCACCC AACA |||| ||||| ||||| |||| |||
AGAAGATTATAGAAAACATT TTac aagat accca cATC GAC T
aa--- attagaag- c- A- TAT

GAM600 CTGCAGCAGTATATTGGTGT 519 TTTCCAGGAA 3589 AGCA AT GTGAA G AAG
GAAGGAAGGACTAAGTCAAA CCAATCAACA CTGC GT ATTGGT GGAAG ACT T
GGTATTTCCAGGAACCAATC GGCG |||| || |||||| ||||| |||
AACAGGCGG Ggcg ca taacca ccttt TGG C
ga-- ac agga- A AAA

GAM601 TCTATGCATATGCATGAGAG 525 TTCATGAGCC 3595 A TT A T CC
TCATAAA
ATTCATGCATATGAATGAGA TCTCATGCAT TATGCATATGCATG GAGA CATGCATATG
ATGAGAG CTCAT ATAT C
GTCTCATCCATATTCATAAA ATGC |||||||||||||| |||| |||||||||| ||||||| ||||| ||||
CCTCATCCATATTCATGAGC GTACGTATACGTAC TTTT GTAcgtatac tactctc gagta tATA
/
CTCTCATGCATATGCATGTT A T- g c ct CCTACTC
TTTACATGCATATGCATGGA

GAM602 ACTTACATAGTGACAACGGG 1640 TACATAGTGA 4710 tgacaacggg --- tT
CCGTGCTTTACTGCACACAG CAACGGGCCG ACTtacatag cc gtgc T
GATAGAAAATCTATGTAAGT TGCT |||||||||| || ||||
TGAATGTATC GG CACG A
TAAAAGATA- ACA TC

GAM603 CATTCGGATAGGTTAATGGT 520 TAGGTTAATG 3590 -------- aatg g gc
TGGGTCGCGCAGACCGGATA GTTGGGTCGC CATTCGGA taggtt gtt ggtc g
AAGCCTGCAACGTATTCTGA GCAG |||||||| |||||| ||| ||||
GTG GTGAGTCT GTCCGA TAG CCAg /
TATGCAAC AA-- G ac

GAM604 CAACTGCGTTTCAATGCATT 521 TCAATGCATT 3591 C c at-- ttcttt T C C TTC---
CAA
GAATCTTCTTTACGTAGTCG GAATCTTCTT CTG GTTt aatgc tgaatc acg AGT GT TCG
TTTCT G
TCTCGTTCTTTCTCAAGGTT TACG ||| |||| ||||| |||||| ||| ||| || ||| |||||
AGAAATTGTATCGAACTGCT GGC CAAG TTACG GCTTGG TGC TCG CA AGC
AAAGA /
CGTTGATCTGGTTCGTCAGG A T GACT TCTAGT - T - TATGTT TTG
CATTTGAACACGGTATTTG

GAM605 TCCTCAACAACGTCTGTTAT 522 TCCGCGAGCT 3592 C AAC T TTAT- - TC--- TG
GCCGCTCACTGTTTTGTTCT TTATCAGCAA TCCT AAC G CTG GC CGC AC T
CCGCGAGCTTTATCAGCAAG GTTT |||| ||| | ||| || ||| ||
TTTAGGA AGGA ttg c gac cg gcg TG T
t aa- - tattt a cctCT TT

GAM606 GCACGTGCTACCGACCAGCG 523 TATTTAGTAA 3593 ---------- CCG A T
CTTTTAGAGGCGCGGTATTT CTGACATAAC GCACGT GCTA ACC GCGCTT T

AGTAACTGACATAACTTTGC TTTG |||||| |||| ||| ||||||
GTGC CGTGCg tgat tGG CGCGGA A
tttcaatacagtcaa tta - G

GAM607 GCACCGCAAGCCACGTACAT 524 GCCACGTACA 3594 - A---- -- a t a a
TGTACCTCAAAAGAGGAATA TTGTACCTCA GCACC GCA gcca cgt cat gt cctc a
TGACGAATGGCCGAGATGCT AAAG ||||| ||| |||| ||| ||| || ||||
GGTGC CGTGG CGT CGGT GCA GTA TA GGAg a
T AGAGC AA - - A a

GAM608 GGCAACCTTGAAGTTCTGAC 526 TTGAAGTTCT 3596 Ctt a - - aact tg CTCA
GAACTATCTTGCAGCTTGTT GACGAACTAT GGCAAC ga gttct ga cg atct CAGCTTGTTT A
TCTCAATTTTAAACGAGCTG CTTG |||||| || ||||| || || |||| ||||||||||
AGATCCGATCAAGAACTCGT CCGTTG CT CAAGA CT GC TAGA GTCGAGCAAA /
TGCC --- - A A C--- -- TTTT

GAM609 GTTCACATGATTCCGGCATC 1641 TCCGGCATCG 4711 ATGAT tc ------- aaaa
GAGTGTTGCAAAATCGAAAG AGTGTTGCAA GTTCAC tccggca gagt gttgc t
CAACTTTCTTTGCTCTGTCG AATC |||||| ||||||| |||| |||||
GATGGTGAAT TAAGTG AGGCTGT CTCG CAACG c
GT--- -- TTTCTTT AAAG

GAM610 CGAGAGGAAACAAACTGTCT 1642 GAGGAAACAA 4712 - caa tt---------- c
TGGAACAATTTCCTTGAAGA ACTGTCTTGG CGAgag gaaa actgtc ggaa a
TTTTAAAACGGCAGTTTTCT AACA |||||| |||| |||||| ||||
CTCTCG GCTCTC CTTT TGACGG CCTT A
T --- CAAAATTTTAGAAGTT T

GAM611 GAGTGGCAGCTACAACACCT 1643 TACAACACCT 4713 C- ta- a c ctcg a
CCTCGTCTAACTCTAGAATT CCTCGTCTAA GAGTGG AGC ca cac tc tcta c
CGAGTGATGGCCGCTTACCA CTCT |||||| ||| || ||| || ||||
CTC CTCACC TCG GT GTG AG AGAt t
AT CCG A - CTTA c

GAM612 GGTGAGCTCCCCAAGTTTTA 1647 CCCCAAGTTT 4717 ----- gttttact t aaa
CTTCTCTAAACAAAAAGGAT TACTTCTCTA GGTGAGCT ccccaa tc ct c
GCTCGGATTGGGGCACGAAG AACA |||||||| |||||| || ||
CTCACC CCACTCGA GGGGTT AG GA a
AGCAC AGGCTCGT - AAA

GAM613 CAGGCTAAAACAAAGGAGGC 527 TGTGAAGGCA 3597 A- AAA--- G GATTT - A GG - AG TCG
GATTTGGGAGGGATAACGGT AAGGTCATCT AC GGA GC GGGAGG GAT AC TTGTTTTC CACC GGGG A

TGTTTTCCACCAGGGGGTCG TCTT || ||| || ||||||| ||| || |||||||| |||| ||||
ACCTTTTCTAGGGTGTGAAG TG CCT CG TCttct cta tg aacggaag gtGG TCTT C
GCAAAGGTCATCTTCTTCTG AA GAAATA A ----- t c ga t GA TTC
CATCCATAAAGGTAATTGGT
TTG

GAM614 TGCCTGAGAGTAAACATTGA 528 TGAGAGTAAA 3598 - -- aaacat a ataaaAC
CGGATAAAACAAAAATGCCC CATTGACGGA TGCC tga gagt tg cgg A
CGCATAACTCTATCATGGCA TAAA |||| ||| |||| || |||
ACGG ACT CTCA AC GCC A
T AT AT---- - CCGTAAA

GAM615 TCTTAACCAAATGTTGGAAG 529 TGGAAGATCA 3599 T- A AAA tg aa t ta- gct
ATCATTTTTTTACCTGCTTT TTTTTTTACC TC TA CC TGT g ga cattttt cct T
AAAGGCCTGAAGGGTGTCGG TGCT || || || ||| | || |||||||| |||
TTGGCAAGGCTATTGA AG AT GG ACG T CT GTGGGAAG GGA /
TT C A-- GT GG - TCC AAT

GAM616 GCAAGCCCATTCTGCCAGTT 530 TGCCAGTTGG 3600 C ag tg ggat gctag
GGGGATTGGCGGCTAGAAAA GGATTGGCGG GCAAGCCCATT tgcc t g tggcg A
CCGCGCCATAGCTGGAGGGC CTAG |||||||||| |||| | | |||||
AAAATGGGCTTGC CGTTCGGGTAA ACGG G C ACCGC A
A GA GT GAT- GCCAA

GAM617 GGCTCCCATCCACGTGTAGG 531 CACGTGTAGG 3601 C a ag--- gac t
TTTCGACGTCGTAGGTGACA TTTCGACGTC GGCTC CATCc cgtgt gtttc gtcg a
AAGAGGCGTTCGACGCGAGG GTAG ||||| ||||| ||||| ||||| ||||
ATGAGAGCC CCGAG GTAGG GCGCA CGGAG CAGT g
A A GCTTG AAA G

GAM618 TTGACTTGCAGGAGACGGGT 532 CAGGAGACGG 3602 TG TG a--- - aagg-- atg
AAGGGCCGATGCCAGGCGGC GTAAGGGCCG T ACT c ggaga cgggt gccg c
GATGAAACTTGATTTCCATT ATGC | ||| | ||||| ||||| ||||
GGTGAGTTGG G TGA G CCTTT GTTCA CGGC C
GT GT GTTA A AAGTAG GGA

GAM619 TTCTAACTCTTAACATTTTT 1644 TCGAATAGCA 4714 A- TTAA TT - AAAAT - TATT
TTT
ATTTATTTAAAATGATACCT TAAGTTTGAA TTCT ACTC CA TTTAT TTATTT GATACC TTTGT
TA T
TTGTTATTTATTTTATTCTA ACGA |||| |||| || ||||| |||||| |||||| ||||| ||
TTTTGCGAACGGTATCGAAT AAGA TGag gt gaata gataag ctATGG AAGCG AT A
AGCATAAGTTTGAAACGAGT AG caaa tt c ----- C TTTT CTT
GAAGAA

GAM620 GAAGAAGTTATAGACAAATT 1645 TGATACGATA 4715 GT-- ACAAATTAT AAAACT

ATTCATTCTAAAACTATAAA CTATATGTAT GAAGAA TATAG TCATTCT A
AACAGAATGATACGATACTA TCTT |||||| ||||| |||||||
TATGTATTCTTC Cttctt atatc agtAAGA T
atgt atagcat-- CAAAAA

GAM621 CTATCGTATGGATAAATATA 1646 TCTAGAATAC 4716 -------- AAA--- tc tacaaaaatatg---
ATCT
TTCTAGAATACAAAAATATG AAAAATATGG GT ATGGAT TATAT tagaa gtcta C
GTCTAATCTCGCTACTGGAT TCTA || |||||| ||||| ||||| |||||
AAATCGAAAAATACTTTTTA TA TATCTG ATATA ATTTT TAGGT G
TTATATACATATAGTCTATT AAACAAAT ATATAC TT TCATAAAAAGCTAAA
CATC
AAACAAAATGATAG

GAM622 GTCACTAGAGACAGCTTGGC 1655 ATGGATGGAC 4725 A- CA GC - GCCA TA TT
GAAGGGGCCAGCCACCATTT TCTTTCACAA GTCACTAG GA GCTTG GAAGGGG CCA
CCATT CAC T
ACACTTTTGGTGATAATGGA GCCT |||||||| || ||||| ||||||| ||| ||||| |||
TGGACTCTTTCACAAGCCTC CGGTGATT Ct cgaac ctttctc ggt ggtaA GTG /
GATTAGTGGC AG c- a- a a--- TA GT

GAM623 GTTTAACAATGGGATATAGA 1656 TAGATGACAC 4726 AATG TA cactaaaga t GA
TGACACTAAAGAATACTATT TAAAGAATAC GTTTAAC GGA tagatga atactat GT A
GTGAACAACATGGTATGAAT TATT ||||||| ||| ||||||| ||||||| ||
TATCTAACTCCGTTAGAC CAGATTG CCT ATCTATT TATGGTA CA /
---- CA AAG------ - AC

GAM624 GGCGCCGGCGGCCGGCACCG 1657 GGCCGGCACC 4727 - - g a ga--- aa-- ttt
GAAGCAAGCATTTCTAACTG GGAAGCAAGC GGCGCC G GC gccggc ccg agc gca C
CGCGAGCTGGTAGCGGCGCC ATTT |||||| | || |||||| ||| ||| |||
GGCGGCACGGGCGCC CCGCGG C CG CGGCCG GGC TCG CGT T
G A G C GATGG AGCG CAA

GAM625 GCCCGACCCCCGGGCGCCCC 1648 TGTCCAGGGG 4718 CG C C CAA - G
CAAACTTTGTCCAGATGTCC TCCCCGAGGG GCC ACCC CGGG GCCCC AC TTT T
AGGGGTCCCCGAGGGTGAGG TGAG ||| |||| |||| ||||| || |||
C CGg tggg gccc tgggg tg AGA C
ag a c acc t C

GAM626 ATGGACATTGTTATGTTATA 1649 TATGTTATAG 4719 Tta--- tag ttaat a- tA
GCTTTTAATGGAAATAAAGT CTTTTAATGG ATGGACATTG tgtta ctt gg aa A
TTGGCCTTCACAAGATTTAA AAAT |||||||||| ||||| ||| || ||
TACAAGATCAATGTCCAT TACCTGTAAC ATAAT GAA CC TT A
TAGAAC TTA CACTT GG TG

GAM627 TCCTTTGCTCAAGCATATAT 1650 AAAGGTACTT 4720 CTC A AACa- acttatgaaa aaaa
AACAAAGGTACTTATGAAAA ATGAAAAGGA TCCTTTG AAGC TATAT aaggt agg a
GGAAAAAGCAACCTACTTTA AAAA ||||||| |||| ||||| ||||| |||
CGAGATATAGCTTTTCCAAA AGGAAAC TTCG ATATA TTTCA TCC /
GGA CTT - GAGCA ---------- AACG

GAM628 CGCTGTCGCAGCTCTTTCCC 1651 TCGCAGCTCT 4721 t - -- c tggc
GGCCTGGCTCTGTTGGCCGT TTCCCGGCCT CGCTG cgca gctctt tc cggcc t
GACCGAGAGCGTGCGCAGCG GGCT ||||| |||| |||||| || |||||
GCGAC GCGT CGAGAG AG GCCGG C
- G CC T TTGT

GAM629 CTGAGAATACTGAGGATTGG 1652 TGAGGATTGG 4722 GAG tga t ct--- - ta
GGATGGCTGGCATATACTGA GGATGGCTGG CT AATAC ggat ggggatgg gg ca T
CTCTTTTCCATCCCCCATCT CATA || ||||| |||| |||||||| || ||
GTATTGAAG GA TTATG TCTA CCCCTACC TC GT /
AG- --- C TTTTC A CA

GAM630 ATCTGGAAGAAAAATTATAC 1653 TCTGTCATCT 4723 AAGAAAAATT ctg gcaga- T
AAA
TCTGTCATCTGTATTAGCAG GTATTAGCAG ATCTGG ATACt tcatctgtatta atg GT T
AATGTGTAAATCAAGCCATG AATG |||||| ||||| |||||||||||| ||| ||
GAATATGGTATAGATGAAGT TAGATC TATGA AGTAGATATGGT TAC CG /
ATTATCCAAACTAGAT AAACCTAT-- --- ATAAGG - AAC

GAM631 TTACAATGTCAAACAAACTA 1654 TACCACTATA 4724 CAA A A AA C CTGCA GGAA
TTATATT--- GA
GGAATCTAAATACTTCCACT TATACACAGA ACT GGA TCT ATA TTCCA TG ATATAT
ATGA T
GCATGGGAAATATATTTATA ATTG ||| ||| ||| ||| ||||| || |||||| ||||
TTATGAGATCATCATTCCTA TGG TCT AGA TAT AAGgt ac tatata TACT /
CCACTATATATACACAGAAT --- A A AA - taag- aca- tcaccatCCT AC
TGGAATATAAAGAATCTAGG
TCACCTTGTAA
GAM632 ACAGATGAATACTTGGAAAT 1663 AGTTATTTGG 4733 A- AA- -- TG --- - TAA
TGAACCCCTAAAGAATGGGA TTTTATCAAG ACAG TG TACTTG GAAAT A AC CCC A
GTTATTTGGTTTTATCAAGT TACT |||| || |||||| ||||| | || |||
ACTACAGACTGT TGTC AC atgaac ttttg t tg GGG G
AG Atc ta gt tat a TAA

GAM633 AGTCGCAAGGGCCAAGGCAG 1664 TCGCAAGGGC 4734 c aaggg c a- tt GC ------ C
AGCTTCTACGCTTGGACCTT CAAGGCAGAG AGt gc ccaagg ag gc cTAC TTGGA CCTT A
CACGAAGGAGACTATCCAGA CTTC ||| || |||||| || || |||| ||||| |||
GTGGCTGCAGCTCCTTGGAG TCA CG GGTTCC TC CG GGTG GACCT GGAA C

AAGCAACT A AAGA- - GA TC A- ATCAGA G

GAM634 AGGTAATTTCATAAAGGACA 1665 AAGGACACTG 4735 AATTT aa-- cact t t
CTGCTGGAGGTATTTTTGGA CTGGAGGTAT AGGT CATA gga gctggaggta tt t
ACTGCCTTTAGTTTTCTGGG TTTT |||| |||| ||| |||||||||| ||
ATATGTAAAACCT TCCA GTAT TCT TGATTTCCGT AA G
AAAT- AGGG TT-- C G

GAM635 ATACAGCAAGACAAATGGGC 1658 TGCCAAGTTT 4728 GCA AAATG AACG G
ATTAAACGTCTGGGCCACCA AGATGTGT ATACA AGAC GGCATTA TCTGG C
GGTGGTGCCAAGTTTAGATG ||||| |||| ||||||| |||||
TGT tgtgt tttg ccgtGGT GGACC C
aga aa--- ---- A

GAM636 GTGGTATTCAATGATTTGAA 1659 TCAATGATTT 4729 -------- agtgAAAGTT T- G
TTGGGAATA
TTTCAGAAGTGAAAGTTACC GAATTTCAGA tt gaatttcaga ACCCAG GA TGTCAGGG
T
CAGTGAGTGTCAGGGTTGGG AGTG || |||||||||| |||||| || ||||||||
AATATGTGCAGGTTCTTTGA AG TTTAGAGTCT TGGGTT TT ACAGTTTC /
CAGTTTTTTGGGTTCTGAGA TAAGAACT ---------- TT G TTGGACGTG
TTTTCAAGAATGAATCAAAT
GTCTAC
GAM637 GCCTCTGATCTCATGATACA 1666 ATCATGCCTG 4736 G ATGATA TG A- G C
TTGGAATGAGTTTGCATTCA ATGACATTGG GCCTCT ATCTC CAT G ATGA TTTG A
AGATCATGCCTGATGACATT GGAT |||||| ||||| ||| | |||| ||||
GGGGATGGAGGC CGGAGG taggg gta c tact GAAC T
- gttaca gt cg a T

GAM638 CTGCCAATTATGTTCACTGG 1667 TGCCCTTTTC 4737 CAATTATGTTCACT TTT A
GGGGCTTTATCAATATCAAT AAAAAGCAG CTGC GGGGGGC ATCAAT T
TGATGCCCTTTTCAAAAAGC |||| ||||||| ||||||
AG gacg tttcccg tAGTTA C
aaaaact------- --- A

GAM639 TGGACAACTACTTTTTAGCA 1660 TAGCACAAAT 4730 CAAC TTta acaa--- ata tct
CAAATCCAGATATATCTTCC CCAGATATAT TGGA TACTT gc atccag ta t
TTTAAATTGGGTACCGAAGG CTTC |||| ||||| || |||||| ||
CGCTGAGTATTTCCA ACCT ATGAG CG TGGGTT AT c
TT-- TCG- GAAGCCA AA- TTC

GAM640 TGCCAAGAGGACAGATACCA 1661 AAGGGGAAAG 4731 TAC ATG----- a ag -
ccaaataAA TTTG
GATGCCATAAAGGGGAAAGA AGTTCCACCA GA CAG CCATA aggggaa agtt cca
TCCGTT T

GTTCCACCAAATAAATCCGT AATA || ||| ||||| ||||||| |||| ||| ||||||
TTTTGTGGTTTGACGGAGGG CT GTC GGTGT TCTCCTT TCAA GGT AGGCAG
G
GCGTTTTGGCAACTGTTCCT C-- GTATTTTA C G- C TTTGCGGGG TTTG
CTCTGTGGATTTTATGCTGC
TCTGTCCCGCA
GAM641 GGCTTAAATATTTAATGCAA 1662 TTTAATGCAA 4732 TTAAATAtt atg ag tg
TGTAAAAGCTTATGCTTTTA TGTAAAAGCT GGC taatgca taaa ctta C
AGTCTTTAAGCTGCATTATC TATG ||| ||||||| |||| ||||
TTCCATTGCC CCG ATTACGT ATTT GAAT T
TTACCTTCT CGA CT TT

GAM642 AAACAAGGAATGCATATGGT 1668 AGGAATGCAT 4738 Aa- a - ac---- GG -- T
TGCGACACCCGGGTACGTCC ATGGTTGCGA AAAC ggaatgc ta tggttgcg accCG T ACG C
GCGTTTGTTCGGGTATACAC CACC |||| ||||||| || |||||||| ||||| | |||
CGCGACCACTGCGCATTCTG TTTG TCTTACG GT ACCAGCGC TGGGC G TGC C
CCGTTT CCG C C CACATA TT TT G

GAM643 GTTTTGGTACCCTTTCTAAT 1669 TACCCTTTCT 4739 TT cc aa ccga- ---- TT AT
GCGCCGAGGAGCGTTCCGAT AATGCGCCGA GTT GGtac tttct tgcg gg agCG CCG A
ACCCGGGCCGTTGAACCCAC GGAG ||| ||||| ||||| |||| || |||| |||
ATCCGCGAGAAACCGTGCCC CGG CCGTG AAAGA GCGC CC TTGC GGC /
GGGC GC CC -- CTACA CAAG CG CC

GAM644 TCCCGTGTACCAGTGTACCT 1670 TTAAGGGTAA 4740 CC A AGTG-- CT AT
TTCTACTATTTAGGTTAAGG ATAAAGGCAC T CGTGT CC TACCTTT ACT T
GTAAATAAAGGCACATGTAA ATGT | ||||| || ||||||| |||
A gtaca gg atgggaa tGG /
At c aaataa t- AT

GAM645 CCAGGTTTACAGTTTCTAAG 1671 TACAGTTTCT 4741 GTTta c----- - tt
CGTGTTTTGTCATCGTTTAT AAGCGTGTTT CCAG cagttt taagcg tg t
TTTTTAAACTGACCAACTGG TGTC |||| |||||| |||||| ||
GGTC GTCAAA ATTTGC Ac t
AACCA TTTTTT T tg

GAM646 GACAATTACATCTTCTTCTC 1672 GGGCTCGAGA 4742 AA C -- T- AGATA GACT
TGCAGATACCGACTACTCAG AACGGAGATT GAC TTA ATCTTC TTCTC GC CC A
GGGGCTCGAGAAACGGAGAT TAAC ||| ||| |||||| ||||| || ||
TTAACGGTC CTG aat tagagg aagag cg GG /
Gc t ca ct gg--- ACTC

GAM647 CCGCTCCTGACGCGATTGAC 1673 TGTCCCAGGT 4743 CTGA GA TGG TT
CTGGAACCGTTTACAGAAGA TGATTTCCAG CCGCTC CGC TTGACC AACCG T

TGTCCCAGGTTGATTTCCAG |||||| ||| |||||| |||||
gacctt gtt accctg GAAGA /
ta-- gg tA- CA

GAM648 ACGCCCAAACTCATCCTGGA 1674 CGAGTTCATC 4744 -- TCCTGGAGT AAT GGA
GTGCAAAAATCTGGATCTTA CAATTCCA ACG CCCAAACTCA GCAAA CT T
CAACACGAGTTCATCCAATT ||| |||||||||| ||||| ||
CCA acc aacctacttg agcAC CA /
tt --------- AA- TTC

GAM649 AGCCCGGGTTTTGTTTCAAG 1680 GTTTTGTTTC 4750 ttgtttcaagcacaaaaca G T
CACAAAACAAAAGAGAGATA AAGCACAAAA AGCCCGGgtt aaA AGAGATAGC T
GCTTTGTGGAGAGCTATCCC CAAA |||||||||| ||| |||||||||
TTCAAAGCC CCGAAACTTC CCT TCGAGAGGT T
---------- A G

GAM650 TACATTTTTCTATGTTACTT 1675 TCTATGTTAC 4745 Tt t ct tag a----- ATTATATT
TTAGTTCGTATCAGATTATA TTTTAGTTCG TACATTT cta gtta tt ttcgt tcAG C
TTCTAGAGCTTCCTGACTAC TATC ||||||| ||| |||| || ||||| ||||
TAACGAAATTAATATGATTT ATGTAAA GGT TAGT AA AAGCA AGTC T
GGCCAAATGTA CC T AT TTA ATCATC CTTCGAGA

GAM651 GCTGGGCCTAATTACGCTGT 1676 ACGCTGTCCG 4746 CCTAATTacg c ------- cgc
G
CCGCCTGTTCCACGCGCGTG CCTGTTCCAC GCTGGG ctgtc gc ctgttcca gcGTGTCG C
TCGGCTACGACACGCTGGAG GCGC |||||| ||||| || ||||||| |||||||
CAGCTTCCACGCGACAGATC CGACTC GACAG CG GACGAGGT CGCACAGC T
CGTCTCTCAGC TCTGCCTA-- - CACCTTC --- A

GAM652 GGCTGACAGGATCGTCCCCT 1677 TGACAGGATC 4747 t- - g tg g AT
TGGCTCGTGATCCTACAAGG GTCCCCTTGG GGC gacag gatc tcccct gctc TG C
GCAGGGGGGGTCTCTGTTCT CTCG ||| ||||| |||| |||||| |||| ||
GCC CCG TTGTC CTGG GGGGGA CGGG AC C
TC T - -- A AT

GAM653 CGTGCCGGGACCCCGACAAG 1678 CGAGAAGCGC 4748 T A C ACAA - ACA
GCCTTCTTGCCGACATTACT CCGACGCGGC CG GCCGGG CC CG GGC CTTCTTGCCG T
GGCGAGAAGCGCCCGACGCG CTGG || |||||| || || ||| ||||||||||
GCCTGGCCG GC Cggtcc gg gc ccg gaagagcGGT /
- - c agc- c CAT

GAM654 CTGCATCTGGGATCGCGCTC 1679 TGGGATCGCG 4749 G - --- c gga C GT
GGAGCTCTCCCACCCCGTGT CTCGGAGCTC CT CA TCtg ggatcg gctc gctctcccAC CC G

TGGAGTGGGAGAGCACAGAG TCCC || || |||| |||||| |||| |||||||||| ||
CTGGTCCTGACGGACTGGAG GA GT AGGC CCTGGT CGAG CGAGAGGGTG GG /
G C AGT - ACA A TT

GAM655 GCGGGGGGGCGACGCAGACG 1681 CGACATGATT 4751 - -- AC ACGG- A
TACGGCGGCAGAGGCCGACA CCTGCCCGTC GCGGGGGGG CGAC GCAG GT CGGC G
TGATTCCTGCCCGTCGATCC GATC ||||||||| |||| |||| || ||||
CCCTGT TGTCCCCct gctg cgtc ta gcCG A
a cc ct gtaca G

GAM656 CCTCTGCCACCGATGACGCC 1682 TCCGTCCGCC 4752 C-- GAT-- C--- C - A
CGTCGACGACGAGCCGTCCG CTCGGTGTCC CCTCTGC ACC GACGCC GT GACG ACG G
TCCGCCCTCGGTGTCCGCCA GCCA ||||||| ||| |||||| || |||| |||
GGTCCCGCGGAGG GGAGGCG TGG ctgtgg cg ctgc tGC /
CCC accgc ctcc c c C

GAM657 CGACATCTGAGGCTCATACT 1683 TGAAAGATTA 4753 C ----- CTCATACT A G
TAATCTATCAGACGGTGTTG TTACCTCTGA CGA ATCT GAGG TAATCT TCAGACG T
TCTGAAAGATTATTACCTCT GAGG ||| |||| |||| |||||| |||||||
GAGAGGATATCG GCT TAgg ctcc attaga agtCTGT G
A agagt att----- a T

GAM658 GGATAGCAACATTTATAGGT 1684 TATTATCTTA 4754 TTTATAGGTTCTCTC A TT A
AAAATAT A TA
TCTCTCTGAAAGAGGTTTAA ATATATAGTC TGA AGAGG TAAGGAT GTA
GGATAGTA TCT A
GGATAGTAAAAATATGGATA TTTA ||| ||||| ||||||| ||| |||||||| |||
GTAATCTTAAGATAGATATT ACT TCTCC atttctg tat tctattat AGA G
ATCTTAATATATAGTCTTTA ---------- C C- a ataat-- - TA
CCCTCTCTCATGCTCTCT

GAM659 TGCGCATGAAAATATCATTA 1685 TGAAAATATC 4755 GC tg atca t- AC
AATTGTTTTAAACATTCTTA ATTAAATTGT TGC A aaaat ttaaattg tttaA A
AATTCAATTTAAAATAATTT TTTA ||| | ||||| |||||||| |||||
TTGTAGCA ACG T TTTTA AATTTAAC AAATT T
A- GT ATAA TT CT

GAM660 TCTCGTTAGCCTGGGTAGGA 1691 AGGAATTGCG 4761 C CC TA AGACCCA A
CACTGA TAAC
AAGACCCAACCGCGATACCC GTTTCCCCCA TCT GTTAG TGGG GGAA ACCGCGAT CC
TCTT T
ACTGATCTTTAACTTTATGA TTAG ||| ||||| |||| |||| |||||||| || ||||
GAAAAACAGGAATTGCGGTT AGA Cgatt accc cctt tggcgtta gg AGAG /
TCCCCCATTAGCAGA - -- -- ------- a aCAAAA TATT

GAM661 GGCGGTATCGGTACATATAC 1686 TATCGGTACA 4756 GG---- tacatata attcacC
GTAATTCACCTTCACAAAAT TATACGTAAT GGC tatcgg cgta T
ACGGAGTCTTCGATAATAAT TCAC ||| |||||| ||||
AGCC CCG ATAGCT GCAT T
ATAATA TCTGAG-- AAAACAC

GAM662 GTCGCTGAGGAAATCACGAA 1687 TCTACAATGA 4757 -- G- CGA- ATT
GACCATTCAGTCGGTCTACA TTTCCTGAAG GTC GCT AGGAAATCA AGACC C
ATGATTTCCTGAAGCTTGAC CTTG ||| ||| ||||||||| |||||
CAg cga tcctttagt tctGG A
tt ag aaca CTG

GAM663 GGGTCGCGGCCCGAAGGCGG 1688 TACCCATCCC 4758 - CC--- C GA-- CTC CAGT
AGATGCCGAGCTCGGCCAGT CCTTCCACCC GGGTCGC GGC GAAGG GGA TGCCGAG
GGC T
TCGATGCCCTCGGTACCCAT GTCG ||||||| ||| ||||| ||| ||||||| |||
CCCCCTTCCACCCGTCGGCG CCCAGCG ctg cttcc cct atGGCTC CCG /
ACCC g cccac c accc --- TAGC

GAM664 GTTCTCCCGTTGCTATTGCA 1689 TGGGATGTCT 4759 CC TG TA- A--- C---- C
ACATCCCCGGACACAAGTGT CAGCAAGACG GTTCT CGT C TTGC ACATCCC GGACA A
CCCTTCTGGGATGTCTCAGC TGAT ||||| ||| | |||| ||||||| |||||
AAGACGTGATGCAGAAC CAAGA Gta g aacg tgtaggg CCTGT A
C- gt cag actc tCTTC G

GAM665 GATCGATCGCACCGTGCAAG 1690 TACCACGGTG 4760 GATC-- CAAGC -------- A
CGTACAGCAATTGCAAAACT CACACGAGAT GATC GCACCGTG GTACA GC A
AATGTACCACGGTGCACACG C |||| |||||||| ||||| ||
AGATC ctag cgtggcac catGT CG T
agcaca ----- AATCAAAA T

GAM666 TCGGATTATCCACCGAGGAC 1692 ACCGAGGACC 4762 AT- ac caa c aag
CAAGTCGAAAGTTTTATCAA AAGTCGAAAG TCGG TATCC cgaggac gt ga t
TGTCCTCGCGGATACCGCTG TTTT |||| ||||| ||||||| || ||
G GGTC ATAGG GCTCCTG TA CT t
GCC C- --- A Att

GAM667 AGCCCGGGGTCCAAAAGAGT 1693 TCCAAAAGAG 4763 G aaa ggg caaca
GGGTCGTACAACACGTCATC TGGGTCGTAC AGCCCGGG tcc agagt tcgta C
TACGAACTCTAGGATCCGGG AACA |||||||| ||| ||||| |||||
TT TTGGGCCT AGG TCTCA AGCAT G
- A-- --- CTACT

GAM668 TGCCCTCGAAGCGCCAGATA 1694 TCGAAGCGCC 4764 --- ------ g acag-- g
CAGATTTGAGCAAGTATAAA AGATACAGAT TGC CCtcga agc ccagat attt a
GATCTGGGCTTCAAAGTCGA TTGA ||| |||||| ||| |||||| ||||
GGTTAGCA ACG GGAGCT TCG GGTCTA TGAA G
ATT GAAACT - GAAATA C

GAM669 AAGCGTTATCACACTGCGAC 1987 TATCACACTG 5057 Ttat t cgt tg aaAA
GTGCTGACAAAACCCACGTT CGACGTGCTG AAGCG cacac gcga gc ac C
GGTTTTGCCGTGTGCATTCG ACAA ||||| ||||| |||| || ||
CTT TTCGC GTGTG CGTT TG TG /
TTAC C T-- GT CACC

GAM670 GTGGTAGCGCTGTGTGAGTT 1695 GGTGGATCCC 4765 G - T GAG g atcccc g
GGCGGTGGATCCCCCTCGTG CCTCGTGGTA GT GTAG CGCTG GT TTGGC gtgg ctcgtg t
GTAACACGAGCCCCCGTGGC ACAC || |||| ||||| || ||||| |||| ||||||
CAAAAGCCCAGTGTTTACAG CG CATT GTGAC CG AACCG TGCC GAGcac a
C A T C AA- G CCC--- a

GAM671 TAGCGACCAAATGCAACATA 1988 AGACAAAATT 5058 CCAAAT- C TA CTTAG-
CTATTTATC ATGA
AACTTAGACAATCTATTTAT GTAACCACTT TAGCGA GCAA A AA ACAAT TCC C
CTCCATGACTATCGGAACAG CGTT |||||| |||| | || ||||| |||
ACAAAATTGTAACCACTTCG ATCGCT CGTT t tt tgtta AGG /
TTTTGCTCCTTCATCGCTA ACTTCCT t gc caccaa aaacagaCA CTAT

GAM672 GGCGACACATTTCTAGACAG 1995 TTTACATATT 5065 CACA CT CA CT - - A
GCTGTTGAAAATGGACTACT ACCCTTCTTC GGCGA TTT AGA GG GT TG AAAATGG C
GTTTTACATATTACCCTTCT AAAT ||||| ||| ||| || || || |||||||
TCAAATCGCC CCGCt aaa tct cc ta ac tttTGTC T
---- ct tc at t a A

GAM673 GGTATATCCCTCTAAATCTG 1696 TCTAAATCTG 4766 ---- C-- - tgatg A A- AT
ATGTTTTTGCATGGACGAGG ATGTTTTTGC GGTATA TCC tcta aatc tttttgcatgg CG GGT T
TATTGTGCCCCCGACCATGT ATGG |||||| ||| |||| |||| |||||||||| || |||
AAAAGTTGTGATTGTAGGTC CCGTAT AGG GGAT TTAG GAAAATGTACC GC CCG
/
AGGATCCATATGCC ACCT ACT G TGTT- A CC TG

GAM674 GTCGCTGTCCCCGGCCGTGA 1697 TCCCCGGCCG 4767 ---------- ga ggag gCT
GCGGAGCCGTGCTCTGGGAC TGAGCGGAGC GTCGCT Gtccccggccgt gc ccgt C
GGGGAGGCGGCGGCCGGGGA CGTG |||||| |||||||||||| || ||||
CGAAGAAGAGAAGGAGCGGC CGGCGA CAGGGGCCGGCG CG GGCA T
GGAAGAGAAGAAG G- GAGG GGG

GAM675 GCTTCGCCGCGGCCCGCGAC 1989 GACACGGTGG 5059 GC G G G G ---- G GG
CGCGCGCTGCGCGCGGTGCC CGGGCGCGGT GCTTCGCCGCG CCGC ACCGCGC CTGC CGC GTG CCGT GC C
GTGGCGGCCGGCGATGGTGG GGCG |||||||||| |||| ||||||| |||| ||| ||| |||| ||
ACACGGTGGCGGGCGCGGTG CGAGGTGGCGC Ggcg tggcgcg ggcg gtg cac GGTA CG /
GCGGACGCGGTGGAGC A- g - - g agGT G GC

GAM676 TTCGTGGCGGGCGGCCTGAT 2002 TCGGGCCCGG 5072 - G GA - G T GG T GGCT - C
CCTGCTGGGCGCGTGCGGGC CGCGGAGAAG GGGC GCCT TCC TGCTGGGC CG GC GCTGACGG GT GTGCC GCCG G
TGACGGTGTGGCTGTGCCGC GCGG |||| |||| ||| |||||||| || || |||||||| || ||||| ||||
CGCGCGCGGCGGGCGCTCGA CCCg cgga agg gcggcccg gc CG CGGCTGCC CA CGCGG CGGC C
CCCGTCGGCGCTCGGGCCCG T g ag c g t -- - GCT- G G
GCGCGGAGAAGGCGGCCCTG
CTCGAG
GAM677 ACATTATATACATTATATAC 1990 TACATTATAT 5060 CAT CAT CAT CAT CAT CAT C
ATTATATACATTATATACAT ACATTATATA ATA TATATA TATATA TATATA TATATA TATATA TATATA A
TATATACATTATATACATTA CATT ||| |||||| |||||| |||||| |||||| |||||| ||||||
TATACATTATATACATTATA TAT ATATAT ATATAT ATATAt atatat atatat atATAT /
TACATTATATACATTATATA TAC TAC TAC tac tac tac T
CATTATATACATTATATACA
TTATATACATT
GAM678 ACCCCGCTCCTGGGACAAAT 2003 TAGAAGGGGG 5073 GGGAC C--- AAA T
ACTCCGGAAACCTCCAGGGA GTGGGGT ACCCCGCTCCT AAATA TCCGG CC C
TCGGAAATTTATTTAGAAGG |||||||||| ||||| ||||| ||
GGGGTGGGGT tggggtggggg tTTAT AGGCT GG C
gaaga TTAA AG- A

GAM679 CTGTGACCAAGATAGAGAGC 1991 ACCAAGATAG 5061 acca gctcc-- tGAAT T CTA AGTTT
TCCTTTGGTGAATCCATCTC AGAGCTCCTT CTGTG agatagaga tttgg CCA CT TGTTTC A
TATGTTTCAGTTTAACCAAG TGGT ||||| ||||||||| ||||| ||| || ||||||
AAACAGTCAGCTGGTCTAAA GACAT TCTATCTCT AAATC GGT GA ACAAAG /
ATTTCCATCTCTATCTAATA AA-- ACCTTTA T---- C CTG AACCA
CAG

GAM680 AGAAAACCAGGCAGCGTTTG 1992 TACACAGCGT 5062 AC GCA - A TT T
TAACGCTTTGGTATACCAGC ACTGAATTTC AGAAA CAG GCGTT TGTA CGCT GG A
GATACACAGCGTACTGAATT T ||||| ||| ||||| |||| |||| ||

TCT tcttt gtc tgcga acat GCGA CC T
aa a-- c A -- A

GAM681 TGTAGTCCTACAATCAAGCG 1993 CACCTCTAAG 5063 A T ATCAA- --- T A- AC
AGGTTGTAGACGTTACCTAC CATAACCTGT TGT GTCC ACA GC GAGGT GTAG CGTT C
AATGAACTACACCTCTAAGC CGGG ||| |||| ||| || ||||| |||| ||||
ATAACCTGTCGGGCACA ACA Cggg tgt cg ctcca cATC GTAA T
- c ccaata aat - AA CA

GAM682 TTACTATTGGACTGTTTATA 1994 TGGACTGTTT 5064 ATt c atactta--- aaA CAC
CTTATCTTCAAATGTTCACT ATACTTATCT TTACT gga tgttt tcttc TGTT T
CACAGCAGCGAAGGGGACAC TCAA ||||| ||| ||||| ||||| ||||
TAGAAAACACTCCCAAGTAG GATGA CCT ACAAA GGAAG ACGA /
AC- C AGATCACAGG CG- CAC

GAM683 TAACCTTAGCTCTAACTCTG 1996 TCTAACTCTG 5066 C Ct actctgaccc c a
ACCCTAGGCCTAACCCTAAG ACCCTAGGCC TAA CTTAG cta taggc ta c
CCTAACCCTAACCGTAGCTC TAAC ||| ||||| ||| ||||| ||
TAAGTTTA ATT GAATC GAT ATCCG AT C
T TC GCCAATCCCA A C

GAM684 GCAGCGCGGCGCACAGAGCG 2004 AGACTGTTTG 5074 ---- -- C AGC A
AAGGCAGCGGCTTTCAGACT CCAAGCGCAG GCA GCGC GGCG ACAG GAAGGC G
GTTTGCCAAGCGCAGTCTGC TCTG ||| |||| |||| |||| ||||||
Cgt cgcg ccgt tgtc CTTTCG C
ctga aa t aga G

GAM685 GCGCGCCTCGTCGACCGGGC 1997 GCCCGGGTCT 5067 CCTCGT CGA A C
GACCGGACCCCGCGGGCCCG CGGTCGTTCA GCGCG CGACCGGG CCGG CCC G
GGTCTCGGTCGTTCACGCGC CGCG ||||| |||||||| |||| |||
Cgcgc gctggctc ggcc JGG /
actt-- tg- c C

GAM686 GTCCGAGGTCCTGGTCGCAT 1998 TCGTGGGTGT 5068 G CATTAtc gtgttc tcca AT
TATCGTGGGTGTGTTCTTCG GTTCTTCGTC GTCCGAGGTCCT GTCG gtgggt ttcg gc C
TCCAGCATCCAGGCCGCTCG CAGC |||||||||||| |||| |||||| |||| ||
AGACCCGCTGGCGAGGGCCT TAGGCTCCGGGA CGGT CGCCCA GAGC CG C
CGGAT G ------- ------ TCGC GA

GAM687 TTCAGTACGTAGTAGCTTCT 1999 TGAGCCAGTT 5069 G - TAG - C C C T
CGAACAGATTCGTTCGTTTA TTTTCAGATG TTCA TAC GTAG CT TCT GAA AGATT GTTCGTT A
CAATGAGCCAGTTTTTTCAG GATT |||| ||| |||| || ||| ||| ||||| |||||||
ATGGATTTTACTGTGGTGAA AAGT GTG CATT gg aga ctt tttga cgagtAA /

G T tta t - t c C

GAM688 GTCCTTCTCTGCTTCTTTTC 2000 TCTCTGCTTC 5070 - t tcttt ttctcTT
TGTGTTCTCTTGCCTTTTTT TTTTCTGTGT GTCCTtct c gct tctgtg G
CACGGGGGCTGAAGAAGGAC TCTC |||||||| | ||| ||||||
CAGGAAGA G CGG GGGCAC C
A T ----- TTTTTTC

GAM689 GGGAGGTTCTTATATTCCAG 2009 TCCCCTGGGT 5079 TTCTTATAT CTC- GTA
GGCTCTGACAGGTATCTCAC TTTCTCCT GGGAGG TCCAGGG TGACAG T
TGTTATCTCCCCTGGGTTTT |||||| ||||||| ||||||
CTCCT tcctct gggtccc ATTGTC C
ttt------ ctCT ACT

GAM690 ATATACCCCCAATTAGCCCC 2001 TTCACATAAA 5071 ATTA-------- A AC--- GT -
TGGC T
CAATTGGCACATGGTAATAT CAGCCAGCTG A GCCCCCA TTGGC ATG AATAT
ACCGCCA GCCG G
ACCGCCATGGCGCCGTGCTT GGGG | ||||||| ||||| ||| ||||| ||||||| ||||
GGTATTGGTGGTGATGTTCA T Tgggggt gaccg tac ttGTA TGGTGGT TGGT C
CATAAACAGCCAGCTGGGGG GGATTTGTTTTG c acaaa ac G TA-- T
TGTTTTGTTTAGGTGGGCTT
TTGTGGTATAT
GAM691 AGATCTCCCCCATGCAAATG 2005 TGGAATAGGT 5075 TCT T AAA---- GG GG
TTTTAGGGTAGGCTGTACAT AAACGCTTGG AGA CCCCCA GC TGTTTTA GTA C
GGAATAGGTAAACGCTTGGG GGGT ||| |||||| || ||||||| |||
GGTCTTCT TCT gggggt cg ataaggt CAT /
TCt t caaatgg A- GT

GAM692 GTTTGGGAAAAGGAGATTTC 2006 TATCTTGCAG 5076 A G C G ---- TT C
TGCAGGTGCAGTGGTTCCCC CTTTAGAAAT GTTTGGGAAA G AGATTTCTG AG TGCA GTGG
CC C
CGGGCCTTATATCTTGCAGC CTGC |||||||||| | ||||||||| || |||| |||| ||
TTTAGAAATCTGCTTTCTCA CAAACTCTTT c tctaaagat tc acgt tATT GG C
AAC - g t g tcta CC G

GAM693 GTCCAACAACATATACTCAT 2007 AACAACATAT 5077 Caa atatact-- agcttaTC
AGAGCTTATCAAACATCCCC ACTCATAGAG GTC caac catag A
TGTGCCCATCTAGGTTGCCA CTTA ||| |||| |||||
GAC CAG GTTG GTGTC /
ACC GATCTACCC CCCTACAA

GAM694 GGTTTAATATTTTCTTAGTA 2008 TATTTTCTTA 5078 Ata-- a- g- at-- AAAA TG
AG

CAAAAGTCAATGTTTTAAAA GTACAAAAGT TTTA ttttctt gtacaaaa tca GTTTT TATATGGA
AG A
TATATGGATGAGAGAATATT CAAT |||| ||||||| |||||||| ||| ||||| |||||||| ||
TGTCTGTATAAAAACTGTGT GAGT AAAAGAA CATGTTTT AGT CAAAA ATATGTCT
TT A
GAAATTTTGTACCAAAGAAA GCAAA AC AA GTGT ---- GT AT
AAAACGTGAGCC

GAM695 CCATCAGAAAGAGAATAAAA 2010 TCAGAAAGAG 5080 AGA- AAAA T A CCA -
AAAGA
ATATTTTTGTAAAACTTTTT AATAAAAATA AG ATAAAAATATTTTTGT CTTTTT ATG GA TCG
AAGAGAG G
TATGAGACCATCGAAGAGAG TTTT || |||||||||||||| |||||| ||| || ||| |||||||
AAAGAGATAAAACTTTTTTA TC TGTttttataaaaata gaaaga tAC CT AGC TTTTTTC A
CGACTCCATCAGAAAGAGAA AAAA aga- c - C-- A AAAAT
TAAAAATATTTTTGTAAAAC
TTTTTTATGAG
GAM696 TATTAAATGTTGTATTTTTA 2014 TTAAATGTTG 5084 - gttgt cta CA TA
CTAGGTTCAGGTATATTCTC TATTTTTACT TAtt aaat attttta ggtT GG T
AAACCCATAAAAATTTTTAA AGGT |||| |||| ||||||| |||| ||
TTTCAATA ATAA TTTA TAAAAAT CCAA TC A
C ATTTT AC- AC TT

GAM697 CATCGTTAAAATTTTTAGCA 2011 TAGCATATCC 5081 TT c ccatcattt t AAA C--- TT
TAAA
TATCCATCATTTTTTAAATT ATCATTTTTT tag atat tttaaa TTTC TGATTCT TAGA TCCA
T
TTCAAATGATTCTCTAGATT AAAT ||| |||| |||||| |||| ||||||| |||| ||||
TCCATAAATATCCTGGATCT ATC TATA AAATTT AAAG ACTAAGA ATCT AGGT
/
AAATTAGAATCAGAAACTTT AT T TTT------ C --- TTAA -- CCTA
AAATTTATATTCTATAGTTT
TTAATGATG
GAM698 GACGGTGGAGGGGCGGGCGC 2012 GCGCTTGGCC 5082 GGA- G CGGG G
CACGGGCTCGGGGGAGGATG TGCAGACCGT GACGGT GGG CGGGCGCCA CTC G
GCGCTTGGCCTGCAGACCGT C |||||| ||| |||||||||| |||
C ctgcca tcc gttcgcgGT GAG G
gacg g AG-- G

GAM699 GTTGCCGGCGCGGGCCCAGA 2018 GTAGAGCGTC 5088 G G - GA-- C GAA GA
A
CGCTCGGGGCGAAGCTCTGG TCGACGGAGG GTTGCC GC CGGG CCCA CG TCGGGGC
GCTCTG GGTCC G
AGGTCCAGCGGGCCGTAGAG TGGG |||||| || |||| |||| || ||||||| |||||| |||||
CGTCTCGACGGAGGTGGGTC TAATGG CG GCCC gggt gc agctctg cgagat CCGGG /
CCGGCGGGTAAT G - T ggag - --- g- C

GAM700 GTATGGGAAAACAAATAGGT 2019 TTCACACGTT 5089 - A A --- GTTA
GGACTGTTATTGTGGGTTCA ATATGTTCTC GTA TGGGA AACA ATAG GTGGACT T
CACGTTATATGTTCTCCTAG CTAG ||| ||||| |||| |||| |||||||
TAC CAT atcct ttgt tatt cacttGG /
g c a gca GTGT

GAM701 CCATGATGAAGGTCCTCAAT 2013 ATGAAGGTCC 5083 A - - ctcaa a ag T T-- GA
GCCATCAAGGAGTCTGGTAA TCAATGCCAT CC TGatga ag gtc tgcc tca GAG CTGG AAG C
GGACTACTTCATCCAGCTCG CAAG || |||||| || ||| |||| ||| ||| |||| |||
ATGAGGCAGACTCTGTCATC GG ACTACT TC CAG ACGG AGT CTC GACC TTC /
AGG - G T ----- - AG - TAC AT

GAM702 GTAGACGTAATCGACTTAGA 2020 TGACGTGATT 5090 G ------ AC A ATTA
AGCGGATTATAAAACCGTAT TATTACATGT GTA ACGT AATCG TTAGA GCGG T
TTGACGTGATTTATTACATG ATAC ||| |||| ||||| ||||| ||||
TATAC cat tgta ttagt agtTT TGCC /
a cattat gc A AAAA

GAM703 AACTACCTCTTAAGCTTTTG 2025 TTGCACAGTT 5095 CC - TT GA TT TA--- T--
AATT
TGGATGGTTTCAATATGTGC TTTTGTATTA ACTA TCT TAAGCTT GTG TGGT CAA TGTGCG
AGAGGTT T
GTAGAGGTTAATTTAAAGAG CTTA |||| ||| ||||||| ||| |||| ||| |||||| |||||||
ATTTCTTGTTGCACAGTTTT TGAT AGA GTTCGGG Cat atta gtt acacgt TCTTTAG A
TTGTATTACTTACTTGGGCT AC A TT tc t- ttttg tGT AGAA
TGAAGACATAGTT

GAM704 CGTAATTGTATCAGCGAATG 2015 TGTATCAGCG 5085 tg at aa t at- T T
TACATGAATCATTTATCCTA AATGTACATG CGTAAT t cagcg tgtaca ga cA TTA C
ACTGCAATCTGTGCACACGC AATC |||||| | ||||| |||||| || || |||
TGTAGTGATTGCG GCGTTA G GTCGC ACGTGT CT GT AAT /
GT AT AC - AAC C C

GAM705 GTAACGGTAAAATAATATAA 2016 AAGTAGATCT 5086 AAAA ATAAAC G AC
ACTTAGTTTAACTCCTAAAG GATTAATTGT GTAACGGT TAAT TTA TTTA T
TAGATCTGATTAATTGTTAC TAC |||||||| |||| ||| ||||
cattgtta atta gat aaAT /
---- gtcta- g CC

GAM706 GCGACAAACTTGAGGACCAA 2017 TAGAGCAAGC 5087 - AG-- AAATAAT TG C
ATAATGCATTGGCAATTGAT TTTGTTGT GCGACAAA CTTG GACC GCAT G A
GCGGTTAGAGCAAGCTTTGT |||||||| |||| |||| |||| |
TGT tgttgttt gaac tTGG CGTA T /
c gaga ------- GT A

GAM707 TATGTATCCTCTGGTACTCA 2026 TGGTACTCAC 5096 C--- tg ta - caat CC
CAGACAACAATGGCGACCAT AGACAACAAT TATGTAT CTC g ctca cagacaa ggcgA A
CTTGTCTTGTTTGTTGAGCC GGCG ||||||| ||| | |||| ||||||| |||||
TGGAGACGTGTACATA ATACATG GAG C GAGT GTTTGTT CTGTT /
TGCA GT C- T ---- CT

GAM708 GGATACTCCTATTACGTCGA 2032 TATTACGTCG 5102 TACTCC c c tca tataGA
AGTCAGAGGTATAGAACTTT AAGTCAGAGG GGA tatta gt gaag gagg A
CCCCTCCTTTTTCTACATGA TATA ||| ||||| || |||| ||||
TATCCCGTTCC CCT ATAGT CA CTTT CTCC /
TGCCCT A T TTC CCTTTC

GAM709 ACCACTATAATCCCCGCTTC 2033 TATAATCCCC 5103 a ccccgctt aatctCTACTT GA
CTATAATCTCTACTTCCTAT GCTTCCTATA ACCACt taat cctat CCTAT T
GATTAAATGGGTAATTAAAT ATCT |||||| |||| ||||| |||||
GATGGGTAATTAAGTGGT TGGTGA ATTA GGGTA GGGTA T
- AT------ GTAAATTAAT- AA

GAM710 GAGGATGTCATCGTGCGTAG 2037 CATCGTGCGT 5107 cat c ----- agttg CG
TCTTCCCAGTTGTCCCGCGC AGTCTTCCCA GAGGATGT cgtg gtagtcttc cc TCCCG C
TTATGGGAATGGGGTCTTTG GTTG |||||||| |||| ||||||||| || |||||
AAGACTATCCACGTCACGTT TTTTTGCA GCAC TATCAGAAG GG AGGGT T
TTT CT- C TTTCT GGTA- AT

GAM711 TTCATCAATTAATGCCTATT 2021 TTAATGCCTA 5091 --- tta tta a t
ATGATGTAGTCTCTGCGCAT TTATGATGTA TTCA TCAA atgccta tg tgtag c
AGGTATGATTTGAAGTTGAG GTCT |||| |||| ||||||| || |||||
GAGT AGTT TATGGAT AC GCGTC /
TGA TAG --- - t

GAM712 CTCGCCGGGGCTCTAGAATA 2022 TAGAATACAA 5092 CCGG Cta c -------- a
CAAAATGCGCACGGACGCTC AATGCGCACG CTCG GGCT gaata aaaatgcgc acgg c
GTATAAACTCGCGCATTTTT GACG |||| |||| ||||| ||||||||| |||||
ATTTGAAGTTAAATCGAG GAGC TTGA TTTAT TTTTACGCG TGCT g
TAAA AG- - CTCAAATA C

GAM713 AATCGCGCCGTAGAGACACG 2023 CACAGCTACG 5093 G AGACAC A T A- AA CA
TACGCGTTGTATTAACACAT GCGGGATT AATC CGCCGTAG GT CGCG TGT TT CA T
ACTGGAAAGAACATCGCGCA |||| |||||||| || |||| ||| || ||
CAGCTACGGCGGGATT ttag gcggcatc ca GCGC ACA AA GT /
g ga---- c T AG AG CA

GAM714 AGGCCCTGTTTTATTAACAA 2024 GCCCTGTTTT 5094 c t tt-- t - TT AGGAAA TT
CATTAAAGCATTCTCAGAGG ATTAACAACA AGg cctgt tta aacaacat aaAG CA CTCAG GG T
AAAGGTTTAACCACAGCTGA TTAA ||| ||||| ||| |||||||| |||| || ||||| ||
GTGCCTTTTATGTTGTTTGC TCC GGATA AAT TTGTTGTA TTTC GT GAGTC CC /
TTAATATAGGCCCT C T TCGT T C -- GACA-- AA

GAM715 TCCTTTTTGTGCTATGTCGG 2027 TTTGTGCTAT 5097 - ct c gtta C TCCA
AGTTACAAACAAATCCACAA GTCGGAGTTA TCCTT tttgtg atgt gga caaa AAA C
ATTTTATTTGCCCATCCTAC CAAA ||||| |||||| |||| ||| |||| |||
ATTTACAAACAAGGA AGGAA AAACAT TACA CCT GTTT TTT /
C T- T ACCC A TAAA

GAM716 GCCGCAGACACTGTGGCGGA 2028 TATCACGTCC 5098 G CACTG C - - GA
CGTGAACCCGACTGGGAGTA ACCGACTCTG GCC CAGA TGG GGACGTGA AC CC C
TCACGTCCACCGACTCTGGG GGC ||| |||| ||| |||||||| || ||
C cgg gtct gcc cctgcact tG GG /
- ca--- a a A GT

GAM717 GCCGGTTAGTATGACTTACT 2038 TAAGACACAG 5108 T-- GA TA-- A---------- TA
TGTATAATAAGTATAGTTTT AAATACTGTA GCCGG TAGTAT CT CTTGTATA TAAG
T
AAACTGATTTTAGCAGAATA TCCG ||||| |||||| || |||||||| ||||
TATAAGACACAGAAATACTG CGgcc gtcata ga gaatATAT ATTT A
TATCCGGC tat aa caca AAGACGATTTTAGTCAA TG

GAM718 CTCATATGGTGCTCATTACG 2029 TAGCCTTGAA 5099 TG T TAC -- AAG
TTCAAGTGTTGAAGGATCCA CTGTGGTGCC CTCATATGG C CAT GTTCAAG TGTTG G
ATAGCCTTGAACTGTGGTGC ATGT |||||||||| | ||| ||||||| |||||
CATGTGAG GAGtgtacc g gtg caagttc atAAC /
gt - t-- cg CTA

GAM719 ATCCACGTTATCTCTGATTG 2030 TAGGAGACGA 5100 TATCTCTG AAAA C
TCAAAATAGACTAGTCTAGG TAAATCCTAT ATCCACGT ATTGTC TAGA T
AGACGATAAATCCTATGTGG GTGG |||||||| |||||| ||||
GT TGggtgta tagcag atCT A
tcctaaa- agg- G

GAM720 GCGTTGAGGGATAAGAGTAG 2031 TGTCGTGTTT 5101 T A TAAGA TA A TT
CATGTTCCTACTTAAGGAAG TCCACACGT GCGT G GGGA G GCATGTTCCT C A
GAATATGTCGTGTTTTCCAC |||| | |||| | ||||||||||
ACGT tgca c cctt t tgtATAAGGA G /
- a ttg-- gc A GA

GAM721 ACTTGTGTACTTTCTAGGGG 2043 CAATACCTAG 5113 GTACTTT GGCTC-- CCT
CTCCCGGCCTTCCTTCCGGT TGAAGCAAGT ACTTGT CTAGG CCGG T
ACAATACCTAGTGAAGCAAG |||||| ||||| ||||
T tgaacg gatcc GGCC C
aagt--- ataacAT TTC

GAM722 ATCGTTAGCACACCTTAAAG 2034 TAGCACACCT 5104 GT- a aaaga a aAATACAG- T
A
ATTAGAAGAAATACAGGTTA TAAAGATTAG ATC tagcac cctt tt gaag GTTAG GTAATAATA
C
GTGTAATAATAACGTATTAT AAGA ||| |||||| |||| || |||| ||||| |||||||||
TATCTAGCACAAAAATGTTT TAG ATTGTG GGGA AA CTTT CGATC TATTATTAT /
CAAAGGGCGTGTTATTAGAT ATT C ----- - GTAAAAACA - G

GAM723 GTTAAATTACGTGATTATAT 2035 CGTGATTATA 5105 AAT cg at - tctgC
TATAAGTTATCTGCTTACTT TTATAAGTTA GTTA TA tgattat tataa gtta T
TAACATTATATAGTAATTAT TCTG |||| || ||||||| ||||| ||||
ATACTAAC CAAT AT ATTAATG ATATT CAAT /
C-- AT AT A TTCAT

GAM724 CTGTATTTCTTCTAATCTTT 2039 TATCACGGGA 5109 TATT C TAA CTA
AAGGTGTGCTAACGATATAT TTAAAAGGTT CTG TCTT TAATCTT GGTGTG A
CACGGGATTAAAAGGTTATT ATTA ||| |||| ||||||| ||||||
AG Gat ggaa attaggg ctatAT /
tatt a ca- AGC

GAM725 TGTCATCAGTGTTGTCAGGG 2036 GGCCATTGTC 5106 T T - TGT a t t g t t - TGA-
AG
TCCTGTGGGCCATTGTCATC ATCAGTGTTG TG TG CAG GGTCC Gggcc ttg ca ca tg tg cag
GGTCC GGC C
AGTGTTGTCAGGGTCCTGAG TCAG || || ||| ||||| ||||| ||| || || || || ||| ||||| |||
GCAGCGGGTCATGTGGGCCA AC AC GTT CCGGG CCTGG GAC GT GT AC AC GTT
CCGGG CTG /
TTGTCATCAGTGTTGTCAGG T T A TGT - T T G T T A TGTA GG
GTCCTGTGGGCCATTGTCAT
CAGTGTTGTCA
GAM726 GCGGAGTCTGGCAACGCCCG 2040 TGTGTTAAGG 5110 - C - ----- G - - TG
GGTCCTTGCTACCTGTGTGG GCTGGGTAAA GCG GAGT TGGCA ACGCC C GGTCCTTG C
TACC T
TGTGTTAAGGGCTGGGTAAA GGTG ||| |||| ||||| ||||| | |||||||| | ||||
GGTGTCTGCCAATTCTCGC CGC CTTA ACCGT Tgtgg g tcgggaat g gtGG /
T - C aaatg g t t TG

GAM727 GCATCTCCAATAAGTAGATC 2041 TCTCCAATAA 5111 ataagtaga gata G GCG G
CAGATACCTAAGACTGCGTT GTAGATCCAG GCAtctcca tcca cCTAA ACT TT A

GAAAAAAGAGTGTTAGGGTT ATAC ||||||||| |||| ||||| ||| ||
GGAAAAGTGGGGGTGT TGTGGGGGT AGGT GGATT TGA AA A
GAAA----- TG-- G GA- A

GAM728 TTTGACTATTTCGAAAGAGT 2042 TATTTCGAAA 5112 t aaa-- tattaacagt AA- GT
TATTAACAGTTACCGTCAAT GAGTTATTAA TTTGAC atttcg gagt TACCGTC TGC T
GCGTTGGAGCAAGCGACGGT CAGT |||||| |||||| |||| ||||||| |||
GTATCCTATATTCGGAAGTG AGACTG TAGAGT CTTA GTGGCAG ACG G
AGATGTCAGA - GAAGG TATCCTAT-- CGA AG

GAM729 GACCCCTTTATAAGATTTAC 2046 TATAAGATTT 5116 CTTta - gac tt- gAG TGATC
AGACGATTTTAGAGGAGAAA ACAGACGATT GACCC taagattt aca ga tta GAGAAA A
TGATCAATACTTTTTTCAAT TTAG ||||| |||||||| ||| || ||| ||||||
AATGCTCAGATGTGGAATTT CTGGG ATTTTAAG TGT CT AAT CTTTTT /
TACGTTCGGGTC CTTGC G AGA CGT AA- TCATA

GAM730 GCGATGGTAGGTCAGTGGTA 2047 AGTGGTAATA 5117 - AG Ca - --- cagccg- T TC
GCTCC
ATATGACCAGCCGTGTTGAT TGACCAGCCG TGGT GT gtggta atat gac tgttGAT GT
CATTGG A
TGTTCCATTGGGCTCCACTT TGTT |||| || |||||| |||| ||| ||||||| || ||||||
TACCGATGATGCTGTCAGCA GTCA TA CACCGT TATA CTG ACGACTG CG
GTAGCC /
AACATTTGTCTAAATATGTG T CT A- G AAT TTTACAA T TA ATTTC
CCACAATTCACTGTTCGC

GAM731 AAGCGCAAGAGTCCCAACAT 2044 TATGGGGGTT 5114 C AA C ---- ACT
TCCTCATACAGAGACTGTAG TAATGTTGAG AAG GC GAGTC CAACAT TCCTCATACAGAG G
ACTTTGTATGGGGGTTTAAT ACTC ||| || ||||| |||||| ||||||||||||
GTTGAGACTCGCCTT TTC CG ctcag gttgta gggggtatGTTTC T
- -- a attt AGA

GAM732 GACTATTTCAAAAGAGTTAC 2045 TATTTCAAAA 5115 t aaa-- tac cagt AA- GT
TAGCAGTTACCGTCAATGCG GAGTTACTAG GAC atttca gagt tag TACCGTC TGC T
TTGGAGCAAGCGACGGTGTA CAGT ||| |||||| |||| ||| ||||||| |||
TCCTATATTCGGAAGTGAAA CTG TAAAGT CTTA ATC GTGGCAG ACG G
TGTC - GAAGG T-- CTAT CGA AG

GAM733 CCAGTGTGCTCTGGGCGCCG 2048 CGGTCCGCGC 5118 ---- C-- C G GATC A T
- A
GACGTGGAGATCAGCACGGT TTTCGCGTCG CCA GTGTG TCTGGG GCCG ACGTGGA
AGC CGG CCGCCG GC C
CCGCCGGCACAGCGCGGCGG GCTC ||| ||||| |||||| |||| ||||||| ||| ||| |||||| ||
TCCGCGCTTTCGCGTCGGCT GGT TACAT GGACTc cggc tgcgctt tcg gcc ggcGGC CG /
CTCAGGAACTACATGTTTTG TTTG CAA t - ---- c t G A

G

GAM734 GTCTTCTCTATCTACTGGCA 2059 TGCACGAAAC 5129 C A G G-- C---- A TG- CTAC-
T
GGGCCACTCCGAGTTGGTCT TAGTGGTCGA GTCTTCT TATCT CT GCA GGCCACT CG GT
GT ATCC T
ACATCCTTACGGGTCTCACA ATGT ||||||| ||||| || ||| ||||||| || || || ||||
CACTGCACGAAACTAGTGGT CAGGGGA GTAGA GG tgt ctggtga gc cg CA TGGG A
CGAATGTGGGCAGATGAAGG A C G aag tcaaa a tCA CACTC C
GGAC

GAM735 CGGAATCTATATGATTCGGG 2060 TGATTCGGGT 5130 AAT g tt gg ggga
TCTCGGACGGGAATATGGGT CTCGGACGGG CGG CTATAt a cg tctcggac a
CCGAGGAACGTGGTATGGCC AATA ||| |||||| | || ||||||||
G GCC GGTATG T GC GGAGCCTG t
--- G -- AA GGTa

GAM736 TGCCTGCACAAGTACCAGGA 2061 CAAGTACCAG 5131 C Aca aggagg - ac
GGGGCTGTCGACTATCGAGC GAGGGGCTGT TGC TGC agtacc ggctg tcg T
AGCTGCAATCGGTGCTACAG CGAC ||| ||| |||||| ||||| |||
CAGCA ACG ACG TCGTGG TCGAC AGC /
- ACA CTAACG G TA

GAM737 GACTAAACTTCCTGGGGACT 2053 TAAACTTCCT 5123 -- g c - TG A
AGAGGTGTGGAAACTTTGCT GGGGACTAGA GACtaa acttcctg gga tagaggt g GA A
GCCTCTGCTTCACGGGAAGT GGTG |||||| |||||||| ||| ||||||| | ||
TTTTGGTT TTGGTT TGAAGGGC CTT GTCTCCG C TT /
TT A C T GT C

GAM738 CCTGGAGATGATGCTGACAG 2049 TGATGCTGAC 5119 - tg---- g gta t
TATGATTTTTTACAAAGTAA AGTATGATTT CCTGG AGA at ctgaca tgatt t
CTGTTGTTGATCCCATACTC TTTA ||||| ||| || |||||| |||||
CTCAT CCC TT GTCAAT AAACa t
A TAGTTG - G-- t

GAM739 CATTGTCGGTGTGCTTTCGG 2050 TGCTATAGAA 5120 T- TCGGG GTCATAATCAT
CATG
GATTAGCAGTCATAATCATC GGCTTTACCG CATTGTCGG GTGCTT ATTAGCA CTG T
TGCATGTTCATTTTTGCTTG AC ||||||||| |||||| ||||||| |||
CTGCTATAGAAGGCTTTACC cagccattt gaagat cgtCGTT TTT T
GAC cg at--- CG--------- TTAC

GAM740 CTCCGATCTCGAGCCGCAGC 2051 TTAGCGCCAT 5121 T A T GCCC G T-- TT
CCGGCGGTGTCTCTTTCAGT CATGTGGTTC C CCG TC CGAGCCGCA GGCG TG CTCT C
GGAGCGTTAGCGCCATCATG GTGG | ||| || ||||||||| |||| || ||||

TGGTTCGTGGCGGTG G GGC gg gcttggtgt ccgc at GAGG A
T - t acta g tGC TG

GAM741 GAGGAGGCCGTAAATATGGC 2052 CGTAAATATG 5122 A C a---- gc gg
GCTCGTGGCCTGCGAAGCCG GCGCTCGTGG GAGG GG cgta atatggc tcgt c
TGTCTCCCTACGACCGCTTC CCTG |||| || |||| ||||||| ||||
CTTC CC GCAT TGTGCCG AGCg /
G A CCCTC A- tc

GAM742 GTGCGAAGCCGCTTCTCCGG 2054 TCCCGGACCT 5124 A C- TTC C -- CA
GCGCGAGGTGCCCACCTGGC GCCTGCTCTG GTGCG AGC GC TCCGGG GCGAGGT GCC C
CCGCCTCGTCCCGGACCTGC CGC ||||| ||| || |||||| ||||||| |||
CTGCTCTGCGC cgcgt tcg cg aggccc tGCTCCG CGG /
c tc tcc - CC TC

GAM743 TGAGTATAGACCCAATCCTT 2055 TATAGACCCA 5125 ta-- ccc- aaac TTAA
AAACTGATTTAAAACCCCAT ATCCTTAAAC TGAG taga aatcctt tgat A
CAAGAGGGTTCTCTTCTAAT TGAT |||| |||| ||||||| ||||
TCCTCA ACTC ATCT TTGGGAG ACTA A
CTTA TCTC A--- CCCC

GAM744 TTAGTAGAGTTGGGTAATGT 2056 TGGGTAATGT 5126 a ----- g- a - ------ TATGA
AAA T
TATAGCTAGTCTTGGACCGA TATAGCTAGT ta tg ttata ct gtctt gG ACCGAGT TCAATT
GT G
GTTATGATCAATTAAAGTTG CTTG || || ||||| || ||||| || ||||||| |||||| ||
CAGCAAGGATTGAATTATTT AT AC AATAT GA CAGAA CC TGGTTTA AGTTAG
CG C
GGTAACTAACCAAAGACAAG G TACCA AA A A AATCAA TTA-- GAA A
AATATAAACCATCAGTACCT
GACTTGACTAA
GAM745 GCGACCGCACAGCAGGGAAT 2066 CCGCACAGCA 5136 Acc a c gaat ta cAAAA
TGTAGCACAAAATAATACTG GGGAATTGTA GCG gc cag agg tg gca T
CGCCACCAACCTACTGCGCA GCAC ||| || ||| ||| || |||
TGCGC CGC CG GTC TCC AC CGT /
GTA C A AACC CG CATAA

GAM746 TCTCTGAATTTATTAATTTA 2057 TGTCAAGTCG 5127 TG TAA A AAC - T-----
TT
TCAGCCTTTGAAAAACTACT GTACGTATTC TCTC AATTTAT TTTATCAGCCTTTG AA TAC
TACCG CAGCT A
ACCGTCAGCTTTAACGGCTG CAAA |||| ||||||| |||||||||||||| || ||| ||||| |||||
TCAAGTCGGTACGTATTCCA AGAG TTGAATA AAATAGTTGGaaac tt atg atggc
gtCGG /
AAGGTTGATAAAATTATAAG CA TTA c --- c tgaact CA

TTACGAGA

GAM747 GTGAGTATCTGTCTTGTAGA 2062 TGTCTTGTAG 5132 A g ga aacgc a - AA
CAAACGCATGAAAAGAGCTA ACAAACGCAT GTGAGT TCt tcttgta ca atga aAGAGCTAA TG G
ATGAAGCAACACTTGGCTCT GAAA |||||| ||| ||||||| || |||| |||||||||| ||
TATCATACATCTGCTTGCAA CACTTA AGA AGAACGT GT TACT TTCTCGGTT AC C
GAAGAGATTCAC G - TC CTACA A C AA

GAM748 GTCGACGACGAAGATGCAGT 2058 ACGAAGATGC 5128 a gc- tt c TTAAC
GGTTGTGCGCGGTTAACGGA AGTGGTTGTG GTCGACG cgaagat agtgg gtg gcgG G
GTTCCGCCTACTTTTACTTC CGCG ||||||| ||||||| ||||| ||| ||||
AATCTTTGCGTCGGC CGGCTGC GTTTCTA TCATT CAT CGCC /
- ACT TT C TTGAG

GAM749 GCGCAGCAGCTGCTCGCGCA 2063 CAGCAGCTGC 5133 a- a-- agagaca TT
GAGACAGTGTTTGCGGCGCG TCGCGCAGAG GCGc gc gctgctcgcgc gTGT G
GGCGCGGGCGGCAGAGCGCG ACAG |||| || |||||||||| ||||
CGC CGCG CG CGGCGGGCGCG CGCG /
CG AGA GG----- GC

GAM750 CAGCGGCACGGCGTTGTTGA 2067 TGTACAGACA 5137 GCG TGATG T GAA
TGGTCTTGGGCTGGAACGAG CGTGCTGTTG CAGCGGCACG TTGT GTC TGGGCTG C
CGGTCCGTGATGTACAGACA |||||||||| |||| ||| |||||||
CGTGCTGTTG gttgtcgtgc gaca tAG GCCTGGC /
aca tg--- T GAG

GAM751 TCTGAGGGATGGCTCGTACA 2064 TAATACCTGT 5134 T TC CA AAACACAC
ACAAAACACACATCGAGGAA CCTCTCTCAG TCTGAGGGA GGC GTA ACA A
TGTAATACCTGTCCTCTCTC A ||||||||| ||| ||| |||
AGA agactctct ctg cat tGT /
c tc aa AAGGAGCT

GAM752 ATCTCCTTAAAGGAAATAAA 2065 TCATACTTAA 5135 GAAATA - - AC-- A-- TT
TACCTGGGCTACTTAAGAGA TATAGGCCTT ATCTCCTTAAAG AATAC CTG GGCT TTAAG
GAGT T
GTTTTATACTCATACTTAAT AGAG |||||||||||| ||||| ||| |||| ||||| ||||
ATAGGCCTTAGAGTATTCCC TAGAGGAATTTT TTATg gat ccgg aattc ctCA /
TATTTTAAGGAGAT ATCCC- a t atat ata TA

GAM753 AATGAAGTAGATCAACACTA 2069 AAGTAGATCA 5139 aa ag ac- tt-- t
TTTGGAATATATTCTATAAT ACACTATTTG AATG gt atca acta tggaa A
TAGTATATGATACATAGCAT GAAT |||| || |||| |||| |||||
T TTAC TA TAGT TGAT ATCTT T
GA CA ATA TAAT A

GAM754 GTGTACAAATGTATATGTAA 2068 TCCCAAGGCG 5138 ACA AAACACA GGAAA
ACACAACAGGAAAATATACA TATACATTCT GTGT AATGTATATGT ACA A
TGTCCCAAGGCGTATACATT AACA |||| |||||||||| |||
CTAACAC Caca ttacatatgcg tGT T
atc gaaccc- ACATA

GAM755 AAATACATTTTCTCTCCGAG 533 AGGCAAAACA 3603 TTTT- C-- GA-- - ACG G AA
GTGAGGTATTATGTACGTGC TAGTTACCAA AAATACA CTCT CGAGGT GGTA TTATGT
TGCC GG T
CGGGAATGGTTCAGGCAAAA TGAC ||||||| |||| |||||| |||| |||||| |||| ||
CATAGTTACCAATGACTTCG TTTGTGT GGGA GCTTca ccat gataca acgg CT G
CCAAGGGTTCGTTGTGTTT TGCTT ACC gtaa t aa- a TG

GAM756 GGATGTCGGGGGTTTGAAAA 2070 ACTCAATTTT 5140 ATG- - AAATATA TC G ca t
agta c
TATAGGAACATCGAGACTCA CCAGTATCCC GG TCGG GGGTTTGA GGAACA GA act attt
cc tcc a
ATTTTCCAGTATCCCAAGGG AAGG || |||| |||||||| |||||| || ||| |||| || |||
AGGGGGTAGATGGTGTCTGT CC AGCC CTCGGGCT CTTTGT CT TGG TAGA GG
AGg a
TTCAAGGTCGGGCTCACCGA GATA A GGAA--- -- G -- T GGG- g
ATAGCC

GAM757 GCCGGCGCTTTCTATCTCAC 2075 TCTCACCGTA 5145 CG T tc-- --- aatgct t
CGTAGAATGCTTCGTCCACG GAATGCTTCG GCCGG CTT CTA tca ccgtag tcg c
ATTACGGGCGTGACAATTAG TCCA ||||| ||| ||| ||| |||||| |||
AAGTACCGGT TGGCC GAA GAT AGT GGCATT AGC c
AT - TAAC GCG ------ a

GAM758 CATTTTTCACACCGGAATCG 2071 CACCGGAATC 5141 TT- c- g cgagtaaaa a
AGTAAAACATAATATGCAAA GAGTAAAACA CATT TCA acc gaat cat a
AAATAGTTCGGGTATTGATA TAAT |||| ||| ||| |||| |||
TAATG GTAA AGT TGG CTTG GTA /
TAT TA G ATAAAAAAC t

GAM759 CGCAATCGAACATTTGTAGC 534 TCGAACATTT 3604 C g t - attt CTCG
ATTTCATATTCTCGTAGAAT GTAGCATTTC CG AAtc aacatt gta gc catatT T
AATGTGTCTGGCATGCAATG ATAT || |||| |||||| ||| || ||||||
TTGATTCG GC TTAG TTGTAA CGT CG GTGTAA A
- - - A GTCT TAAG

GAM760 CGCGTATCGGCGTCCCGGCG 541 TGGCGGTCCC 3611 T G T C G T-- GG
CGGCGAGCGTCTGACGGTCT GCGTCGGGTC CGCG ATC GCG CCCGGCGCGG GA CGTC
GAC T

GTCTCTGGCGGTCCCGCGTC GTGG |||| ||| ||| |||||||||| || |||| |||
GGGTCGTGGATCCGTG GTGC TAg tgc gggctgcgcc ct gcgg CTG /
C g t - g tCT TC

GAM761 ATCGTTTGTGTATAGTGGTA 2072 TGTATAGTGG 5142 t ag---- ta-- at
GGAGCATAGACGCTTCGTTT TAGGAGCATA ATCGTTTG gtat tgg ggagc a
TCAATATTGATACCAAGCGG GACG |||||||| |||| ||| |||||
T TGGCGAAC CATA ACT CTTCg g
- GTTATA TTTG ca

GAM762 ATAATATTGAACATATTTTA 2076 TATTTTATTG 5146 T GA- tgtata t
TTGTATATATTTTAAAAATA TATATATTTT ATAA ATT ACAtattttat tattt a
GCTTTATAAGATATGTGAAA AAAA |||| ||| |||||||||| |||||
GTTTTAT TATT TGA TGTATAGAATA ATAaa /
T AAG TTTCG- a

GAM763 GGTGTAATAGGTTTAAGACT 542 TAATAGGTTT 3612 --- - - ttctacta-------- T ATTTT
TCTACTAAAATATTTAAAAT AAGACTTCTA GGTGtaa tag gtttaag ac aAATAT TAAA T
TTTTATCATGTTTATGTATT CTAA ||||||| ||| ||||||| || |||||| ||||
TGTATTCTTTCTCCATCGTA CCATATT ATC CAAATTC TG TTTATG ATTT A
CTTAAACTCTACAATTATAC AAC T A CTACCTCTTTCTTATG T GTACT
C

GAM764 CCAGAACACTTTGTAACAGT 2073 TAGCATCCCA 5143 AACA ------ A A CC TT
GCACCATTTTTCAGATTTTG TAAGAAAACT CCAG CTT TGT AC GTGCA ATT T
TATCGTAGCATCCCATAAGA GG |||| ||| ||| || ||||| |||
AAACTGG ggtc gaa acg tG TATGT TAG /
aaaa taccct a C TT AC

GAM765 TCCAAAGATCGTTGTACTAC 2074 GATCGTTGTA 5144 -- t gtactacc t T
CTGTTCTAAATTATTACATA CTACCTGTTC TCCA AAga cgtt tgttc aaaTTAT A
ATTTGAATATTCCATAAGCG TAAA |||| |||| |||| ||||| |||||||
TCTTTATGGA AGGT TTCT GCGA ATAAG TTTAATA /
AT - ATACCTT- - C

GAM766 CACCGTCGAGCAGTCCGTCA 549 GAGCAGTCCG 3619 gag tc tc g - ---- G GG
CCCGGTCGCGGCGCCGACGA TCACCCGGTC CACCGTC cag cg accc gtcg cg gC
CCGACGAC C
CGGCCGAGTCGTCGGAGTCT GCGG ||||||| ||| || |||| |||| || || ||||||||
CTCGCCGACGGGGTCGTCTG GTGGCAG GTC GC TGGG CAGC GC TG GGCTGCTG
C
AGACGGTG A-- T- -- G C TCTC A AG

GAM767 CCCGGTGCCTGGCCTCTTTC 550 TGTGATTCAC 3620 G C TTTCTCt ---- --------
cccttgac A

TCTGTGATTCACCCAACGCC CCAACGCCCT G TGCCTGG CTC gtga ttcacc caacg
GG C
CTTGACGGACCTCCATACTC TGAC | ||||||| ||| |||| |||||| ||||| ||
GTTGTCTCTACCGGTGAGGC C ACGGGCC GAG TACT GAGTGG GTTGC
CC C
TTTCATCTATTTCGAGACCG - A CTTTATC TTCG CCATCTCT TCATA--- T
GGCACGGG

GAM768 GTCGCCGCTGCCGTCTCTTC 543 TGACCAGGGG 3613 T - - -- -- CTCGTCCT
AGCCTCGTCCTCCTCCTCCT CTTGGCACGC G CGC CGC TGCC GTCTCT TCAGC C
CGCTGACCAGGGGCTTGGCA GCGC | ||| ||| |||| |||||| |||||
CGCGCGCGC C Gcg gcg acgg cgggga agtCG C
- c c tt cc CTCCTCCT

GAM769 TCCGGGGGTAGCAGGCCTTC 2077 TAGCAGGCCT 5147 - t aa ct
TGGAAAGCCTTGAGCTGCTC TCTGGAAAGC TCCGGGG Gtagcaggccttc gg agc t
GAAGGCCTGCTGCGCCTTGG CTTG ||||||| |||||||||||| || |||
A AGGTTCC CGTCGTCCGGAAG CT TCG /
G - CG Ag

GAM770 AATACTGATGTTGCTTTTCT 535 TGATGTTGCT 3605 C -- tttc aaAC
TGGAAATAAACTATTGGTTT TTTCTTGGAA AATA tgatgt tgct ttggaaat T
TTAATACTAGCATTGCATCA ATAA |||| |||||| |||| ||||||||
TTATT TTAT ACTACG ACGA AATTTTTG /
T TT TCAT GTTA

GAM771 AATTAAATTTGTAAATATAT 536 TATTTAATGG 3606 ---------- ggt- tt-- tt T C TTG
TTAATGGTGGTCTTTGTTGT TGGTCTTTGT AATAtat ttaat ggtc tgttg GA TATTTT AA G
TGATTATTTTCAATTGGTTC TGTT ||||||| ||||| |||| ||||| || |||||| ||
TTTAAAATATTTTTCAACAT TTATATA AATTA TTAG ACAAC TT ATAAAA TT T
TTTGATTTAAAATTAAATTT CTATTCTTTTTA AAAT TTTT TT T - TCT
TTCTTATCATATATTTCATT
ATTAATT
GAM772 GAAAGAAATGTATCGTTAGA 537 TGTGGTCGTC 3607 AA- AT- TTA TGA
CCACACTTTGAGTTCGGGTG CGTAGGCAGA GAAAGA TGT CG GACCACACTT G
TGGTCGTCCGTAGGCAGAGT GTCT |||||| ||| || ||||||||||
CTTTT TTTtct acg gc ctggtgtGGG /
gag gat ctg CTT

GAM773 GGCTGGGTGGACCCCTTGGC 538 ACCCCTTGGC 3608 TG cct aacac ag C
GAACACGTGAGGCCCCGCGG GAACACGTGA GGC GGTGGacc tggcg gtg gcc C
CGCACTGCCACAGGTCCACC GGCC ||| |||||||| ||||| ||| |||
GCC CCG CCACCTGG ACCGT CAC CGG G
-- AC- ----- G- C

GAM774 GATTTCGTGCTCGATTTACC 539 TTGAATATAC 3609 T C GATTTACCTAAA a ta g - a
TAAATTGAATATACACGATA ACGATACAAT GATT CGTG TC ttga ta cac at ac a
CAATGGTGGTGGTGGGTAAT GGTG |||| |||| || |||| || ||| || ||
CAAATCAGACAGTTAGAATA CTGA GCAT AG AACT AT GTG TG tg t
CGTAGTC T A ATTGACAGACTA A GG G g g

GAM775 TCTATCTCAACACGTTGATT 540 TAGCAGCGGA 3610 T- TT TT TT- ca- a ga - TT
TACGTTTAGCAGCGGACAAT CAATCCCGAT CTATC CAACACG GAT ACG tag gcggaca tccc tcta cGCG G
CCCGATCTACGCGTTGGTCT CTAC ||||| ||||||| ||| ||| ||| ||||||| |||| |||| ||||
GCGTTGGGCAGGGATGTTTG GATAG GTTGTGT CTA TGT ATC TGTTTGT AGGG GGGT GCGT G
TGTACTACGGTGTTTATCGG TT GG TT GGC ATG - AC T CT
TGTGTTGTTGATAGA

GAM776 TCATTGTACAAGAAACATTG 557 TACAAGAAAC 3627 t g- tgcatga cG T T
CATGAAAGACGATGATTATT ATTGCATGAA TCATTG acaa aaacat aaga A GATTA T
TTAATCTTATCTTACCTATG AGAC |||||| |||| |||||| |||| | |||||
TTTAATTGTTTAATGA AGTAAT TGTT TTTGTA TTCT T CTAAT /
T AA TCCA--- AT - T

GAM777 GGCCCGGCGCTCCACGCCGG 544 CGCCGGGTCT 3614 C CAC G TT--- AAAA
GGTTCCCGGCGGCGGAAAAG TGTCGCGGCC GGCCCGG GCTC GCCG GG CCCGGCGGCGG G
CGCGACCGCCGCCGGGTCTT GGGC ||||||| |||| |||| || ||||||||||
GTCGCGGCCGGGCCCGGGCC CCGGGCC cggg cggc ct gggccgcCGCC C
- c-- g gttct AGCG

GAM778 CAGTTTCTGAAGCAAAAGCA 545 ACAGAAGTCT 3615 - AAA AAA GG- A AA TGC
AAAGAGGCTATAGGGATAAT GAGTATGCTT CAGT TTCTGAAGCA GC AGA CT TAGGGAT TGC A
GCTGCAATTGCAATCTCTAC CGGA |||| |||||||||| || ||| || ||||||| |||
AGAAGTCTGAGTATGCTTCG GTCA Gaggcttcgt tg tct ga aTCTCTA ACG /
GAGAACTG A a-- ag- gaa c -- TTA

GAM779 AAGCGCGATACAAATCGACA 546 TTCGTACCGC 3616 GATACAAAT A C TTT C
TCTGGTTTTCGAGACCCGCG ATGCCGGCGC AAGCGC CG CAT TGGT CGAGAC C
TTTCGTACCGCATGCCGGCG TT |||||| || ||| |||| ||||||
CTT ttcgcg gc gta gcca gcttTG G
--------- c c t-- C

GAM780 GGGGAGAAAGGGGCGGTAGG 547 ATCATCCTCC 3617 AGAAA C A AGC - A
GGGAAGCGACGAGACCGATC ACCTCCCCCA GGGG GGGG GGT GGGGGA GA CG G
ATCCTCCACCTCCCCCACCC CCCC |||| |||| ||| |||||| || ||

C cccc cccc cca cctcct ct GC A
ac--- t - a-- a C

GAM781 TGGCTGGAGATAGCACTGAG 548 TAGCACTGAG 3618 C At- ac- - a c
CGTCTAGGCAGGCCCAGAAT CGTCTAGGCA TGG TGGAG agc tgagcgt ct gg a
GCTCATTAGCTTTACTTCAA GGCC ||| ||||| ||| ||||||| || ||
CTA ATC ACTTC TCG ACTCGTA GA cc g
A ATT ATT A C g

GAM782 GGATCAACATGTCACTCACC 551 TCTCTCGGTA 3621 AACAT A C - C ---- T
AGAGCGTCCACGTCCTCGTG GGACCACGGG GGATC GTC CT ACC AGAG GT CCACG C
GCAGAACTCTCTCGGTAGGA ATCC ||||| ||| || ||| |||| || |||||
CCACGGGATCC cctag cag ga tgg tctc CA GGTGC C
ggcac - - c t AGAC T

GAM783 TAATTGTTATTGGCCGGGAC 552 TTGTTATTGG 3622 t t cc cg--------- tg GA
GAAGTGGGATTACTGCTTAT CCGGGACGAA TAAt gttat gg ggga aag g T
TATTTTAATTCTCATCGTAA GTGG |||| ||||| || |||| ||| |
TTATTA ATTA TAATG CT CTCT TTC C /
T - A- TAATTTTATTA GT AT

GAM784 CCTGTGAGATTGTTTGTAAA 553 GATTGTTTGT 3623 T - taaagaat - A- - AA
GAATGAGCCCCACCCTGCCA AAAGAATGAG CC GTGAgatt gtttg gagc ccc CCC TGCC C
ACAAGGTGCGGGAAGGGCGC CCCC || |||||||| ||||| |||| ||| ||| ||||
TTTAGACTAATCTCATCGG GG TACTCTAA CAGAT TTCG GGG GGG GTGG /
C T -------- C AA C AA

GAM785 TATTTAGATATCTGGAACAC 554 TCAGTGGCCG 3624 AG GAACA - AGGA GGC
CCTGACGACTTTGAGGAGTT CGGATATACA TATTT ATATCTG CC CTGACGACTTTG GTT
A
GGCAGTGGAATTGCAGGGTT AGTA ||||| ||||||| || |||||||||||| |||
GTCAGTGGCCGCGGATATAC atgaa tataggc gg gactGTTGGGAC TAA G
AAGTA ca gcc-- t GT-- GGT

GAM786 GTTGTAATTGGTACAACAAA 565 TGGTACAACA 3635 AT---- a -------- aatatt
CATGTAATATTGTATTCCAC AACATGTAAT GTTGTA tggtaca caa acatgt g
ATGTAAATATTATTGTGTAC ATTG |||||| ||||||| ||| ||||||
TATAGTTATACAAC CAACAT ATCATGT GTT TGTACA /
ATTGAT - ATTATAAA CCTTAT

GAM787 AATGATTCAGGAGTTATAAA 555 AAATGTTTGT 3625 T A- - ATTTA CC
ATTTATGGGCCAATTTTCAA AATCTTTCAG AATGA TC GGAG TTATAAA TGGG A
ATGTTTGTAATCTTTCAGAT ATTC ||||| || |||| ||||||| ||||

TCATT TTAct ag tttc aatgttt aCTT A
t ac t gtaa- TT

GAM788 GACGATTTGATAAACGTGGA 566 TACAAGTTTA 3636 CGA C G CATT TT TAAAAT
TTGTGTCATTACTTTTTGAA ACATAATCAC GA TTTGATAAA GTG ATTGTGT ACTT TGAA
C
TAAAATCTTTGCCTTTTACA ATTT || ||||||||| ||| ||||||| |||| ||||
AGTTTAACATAATCACATTT CT AAACTAttt cac taataca tgaa atTT T
ATCAAACCATC ACC a - att- c- TCCGTT

GAM789 GCACCTAATAAAAATCACTT 556 TACACATCCT 3626 C- AAA - TTA A T TGT T- T
AAC
AATAGCAATGTGCTGTGTCA GTCCAGCATT GCAC TAAT AAT CAC AT GCAA GTGCTG CAG
TGT TATTGG C
GTTGTTTATTGGAACCACAC TGCA |||| |||| ||| ||| || |||| |||||| ||| ||| ||||||
CCGGTACACATCCTGTCCAG CGTG ATTA TTA GTG TG cgtt tacgac gtc aca atGGCC
A
CATTTGCAGTGCGTGCATTG TT AG- C CG- a - ct- ct c CAC
AATTATTGTGC

GAM790 GGCTAGACTTCATGGCGCCT 558 TCAGCGAAAA 3628 TAGAC GG- CT---- CCG
GGCACCGAATCCTGCCTTCT TGAATAATTG GGC TTCAT CGC GGCA A
CAGCGAAAATGAATAATTGC CT ||| ||||| ||| ||||
T tcg aagta gcg CCGT A
ttaat aaa actCTT CCT

GAM791 GTTTCCATTGCGTCTGGGCT 559 GGATTAGACG 3629 TT GTC G TCATTGCG TGG
TGTCTATCATTGCGTCTCTA GGGCCACCAG GT CCATTGC TGG CTTGTCTA TCTCTA T
TGGTTTTTGGAGGATTAGAC TAAT || ||||||| ||| |||||||| ||||||
GGGGCCACCAGTAATGGTGC CG GGtaatg acc gggcagat ggAGGT /
T- acc g ta------ TTT

GAM792 CCGCCTTAAACTACAGACAG 560 TCAAAACCTC 3630 AAACTACAGACA CA AA
GTCCCAGCCAAGTAGGCGGA AAAAAGGCGG CCGCCTT GGTCC GCC G
TCAAAACCTCAAAAAGGCGG ||||||| ||||| |||
ggcggaa ctAGG CGG /
aaactccaaaa- -- AT

GAM793 GGAGCAGCAGTGGCCGGGGG 572 AGTGGCCGGG 3642 A Ca -- g ca--- - a
CCCAGACGGGAGTCCGCGTC GGCCCAGACG GG GCAG gtggc cggg gcc gacg gg g
GCCCTGGCGCTCGTCGCCGC GGAG || |||| ||||| |||| ||| |||| ||
CTTTGCCC CC CGTT CGCCG GCTC CGG CTGC CC /
- TC CT G TCCCG G T

GAM794 TTATATCATTACTTACAAAT 561 TAGAATATTT 3631 - ACA GTA aa --- aaaa a
GTATATAGAATATTTAGAAA AGAAAATAAT TTATATCATTA CTT AAT TAtag tatt tag taata a
ATAATAAAATTATTAAAGGC AAAA |||||||||| ||| ||| ||||| |||| ||| |||||
TATTGGATAACTATGAAATT AATATAGTAAT GAA TTA GTATC ATAG ATC ATTAT a
AAAAGATAATGATATAA A AA- AA- A- GTT GGAA T

GAM795 GCCTTTCTCCGGCAGGTAGC 562 TACACGTACC 3632 C C-- A AGC a a -- a
CTACACGTACCTCACTATGG TCACTATGGC GC TTT TCCGGC GGT Ct cacgtacctc ctatggc cat
A
CCATAAAGATGCAGCCATAG CATA || ||| |||||| ||| || |||||||||| ||||||| |||
AGAGGTACGTGAAGAAGACC CG AGA AGGCTG CCA GA GTGCATGGAG GATACCG
GTA A
CGTCGGAATCAGAAGC A CTA C GAA A A AC G

GAM796 ATTATCACCTTAATCTCTTC 563 TACATTCTGA 3633 - TA CT CGA- AATAA
AGGCGAACATAAATAACTCC GGATCGGGGT ATTATC ACCT ATCT TCAGG ACATA C
AGCTGTGTACATTCTGAGGA AGAT |||||| |||| |||| ||||| |||||
TCGGGGTAGATAAT TAAtag tggg tagg agtct tGTGT T
a gc -- taca CGACC

GAM797 GGGTTAAGGCCTCGGGGTTA 564 AGGGGCCCGG 3634 AA GGGGTTA - GGC
GGGTCTCAGGCGGCGTTTGG GGTTAGGACC GGGTT GGCCTC GGGTCTC AGGC G
CTTAGGGGCCCGGGGTTAGG T ||||| |||||| ||||||| ||||
ACCT tccag ttgggg cccgggg TTCG T
ga ------- a GTT

GAM798 TTGCTTCTGATTCCGACGGG 573 TACGTGTAGG 3643 CTGA A CT T T CAT
TCTTCTTCACGTACCTCTCT CTACCTGCCG TTGCTT TTCCG CGGGT TCT CACGTACCTC
CTATGGCTG C
ATGGCTGCATCTTTATGGCC GAGA |||||| ||||| ||||| ||| |||||||||| |||||||||
ATAGTGAGGTACGTGTAGGC GGCGGA gaggc gtcca gga gtgcatGGAG GATACCGGT T
TACCTGCCGGAGAAAGGCGG Aa-- c tc t T ATT

GAM799 TTTTAAAGATCCGTGGGCTG 574 TTAAAGATCC 3644 t gg-- t T ATTCTC
GAGCTTTAAAATTCTCTATT GTGGGCTGGA TTttaaaga ccgt gc ggagctt AAA T
GTTCTTTCAAGTTCTGCAAA GCTT ||||||||| |||| || ||||||| |||
AATGGTTTTTAAAG GAAATTTTT GGTA CG TCTTGAA TTT A
- AAAA - C CTTGTT

GAM800 GCCTTTAGGGGTAGTGTCGT 575 TAGGGGTAGT 3645 ag-- g ttg g tTAG G AG-- G
T
TGTCGGGGTTAGGCCTGTAG GTCGTTGTCG GCCTTtaggggt t tcg tcgg g GCCT TAGGGGT
T TCG T
GGGTAGTGTCGTTGTCGGGG GGGT |||||||||||| | ||| |||| | |||| ||||||| | |||

TTAGGCCTTTAGGGGTAGTG CGGGGATTTCCG G GGC GGCT T TGGG ATTTCCG G GGC G
TCGGGGTCGGGGTTAGGCCT GATT G TGG G GA-- G GATT G T
TTAGGGGC

GAM801 GAACCAGCCCTGCGCGCTTG 567 ATCGCGCATG 3637 CAGCC C T TATATA-- C
CGCTATATACGCCCTGCGCA CGCACAGACG GAAC CTG GCGC TGCGC CGC C
CTCATCGCGCATGCGCACAG TTC |||| ||| |||| ||||| |||
ACGTTC cttg gac cgcg acgcg GCG /
ca--- a t ctaCTCAC T

GAM802 TCCATTGATCTGCTCACGAC 568 TGCACAGCCA 3638 AT AT T GA- A TAGAA
TGTAGCACTTAGAATCGCAC GTGAGCTGGC TCC TG C GCTCAC CTGT GCACT T
AGTGCACAGCCAGTGAGCTG CACA ||| || | |||||| |||| |||||
GCCACAGGA AGG ac g cgagtg gaca cgtGA /
ac cg t acc - CACGC

GAM803 CCGAGCTTAAAAAATATTTT 569 AGATCTGGGA 3639 AAA TAT CGG AA CA- ATC
ATTGGCGGTCAAAGCATGCT AATCATGGAT CCGAGCTT AAATATTT TGG TC AG TGCT C
ATCCTTCAGCAGATCTGGGA GTTT |||||||| |||||||| ||| || || ||||
AATCATGGATGTTTGGAGGC GGTTCGGA tttgtagg act ag tc aCGA /
TTGG GG- t-- aa- gg tag CTT

GAM804 GAGCGCAGAGCTATTACCGA 576 TCGCATGGAC 3646 A ATTA AA- TC CCCC
AGAAGTCTATCCCCCCAAAA CAGGTATTGC GAGCGCAG GCT CCG GAAG TATCC A
TGGATATTTTCGCATGGACC GCTC |||||||| ||| ||| |||| |||||
AGGTATTGCGCTC ctcgcgtt tgg ggt ctTT ATAGG /
a acca acg T- TAAA

GAM805 CACGTTGTGCGTTCTCCGTT 570 TTCGGGCGGA 3640 TG TC TGA TTT G G TA
GACCTTTGAAAAGGCGCGTG TTACGCGTTA CACGT TGCGT TCCGT CC GAAAA GCGC TGG T
GTATTTCTCGGTGTGTTTTT CGTG ||||| ||||| ||||| || ||||| |||| |||
CGGGCGGATTACGCGTTACG gtgca gcgca aggcg gg ttTTT TGTG GCT T
TG tt tt --- c-- G - CT

GAM806 GATCGTCAGAGCACGGATGA 571 TCAGAGCACG 3641 tc c agc ag ACT
GCGAGCAGCCGGACTCACCG GATGAGCGAG GATCG agag acggatg gagc cCGG C
CCGGAGCTCTATCCGTCTCT CAGC ||||| |||| ||||||| |||| ||||
CCTGGTC CTGGT TCTC TGCCTAT CTCG GGCC A
CC - --- A- GCC

GAM807 CCCGTACTCCGTTCGTTTTG 577 AGCCGTTTGC 3647 CCGT G ATCag- ccc- g cgg CA

GACATCAGCCGTTTGCCCGT CCGTGGTGCC CCCGTACT TCGTTTT GAC ccgtttg gt gtgc agCG T
GGTGCCGGAGCGCATTTTGC GGAG ||||||||| ||||||| ||| ||||||| || |||| ||||
TGCACGACTTTCCGAACGGA GGGCATGG AGCAAAG CTG GGCAAGC CA CACG TCGT /
CCCTGGTCGGAAACGATTTG TTT- G GTCCCA CTTT G --- TT
GTACGGG

GAM808 TTGGATCTTGTCCATCAAAG 586 TGGTCAGATT 3656 ----- TC - A CT TG A
TTTCTCTGGATACATGTCTG CTGTATGTCC TTGGATCTT G CAT CA AGTTT C GAT C
GTCAGATTCTGTATGTCCGT GTTC ||||||||| | ||| || ||||| | |||
TCTGAGGTCCGA AGCCTGGAG c gta gt ttaga g CTG A
Tcttg ct t c ct gt T

GAM809 TTTTGCTAGGCAAAATGGTG 578 TGTGCCTACA 3648 AGGCA ---- A- A
TGACACGACTTGGATACCAA TTAGCCATTT TTTTGCT AAATGGT GTG CACGACTTGG T
GTTGTGCCTACATTAGCCAT CAGA ||||||| ||||||| ||| ||||||||||
TTCAGAAGCAAAA AAAACGA tttaccg cat gtgtTGAACC /
agac- atta cc A

GAM810 GCGGCAGAGGCGGAGATCGA 579 CGGCTCCGAT 3649 AGAGG A G CA C GT TC
GGTCCAAGTCCAGGTCGCGG CTAGATCCCG GCGGC CGG GATC AGGTC AGTC AG CGCGG G
TCGAGGTCGCGGTCTCGGCT GTCG ||||| ||| |||| ||||| |||| || |||||
CCGATCTAGATCCCGGTCGC Cgctg gcc ctag tctag tcgg TC GCGCT A
----- - a cc c TG GG

GAM811 GGCCGTGGGGGGAGCAGGGG 587 CCCCCACCTC 3657 G- CA AC TCA
GAGACGGTCATCCTCCACCT CTCCAAACGG GGCCGT GGGGGAG GGGGGAG GG T
CCCCCACCTCCTCCAAACGG TC |||||| ||||||| ||||||| ||
TC ctggca cctcctc cccccTC CC /
aa ca CA TCC

GAM812 GCGTACCTTTTTTTCATCCG 580 TGCCATGATG 3650 CCTTTTTTT C CCTGCCG AT A- TTT- TC
ATCCCTGCCGGGTAATACGT ATCGATGTCA GCGTA CATC GATC GGTA ACGTCCC AGA GC C
CCCAAGATTTGCTCCATGTT TATG ||||| |||| |||| |||| ||||||| ||| ||
GTTTCTGCGGGGCGTTGCCA Cgtat gtag ctag ccgt TGCGGGG TCT TG /
TGATGATCGATGTCATATGC act------ - tagta-- -- CG TTGT TA

GAM813 GCCGATACCTTTTCATTAAT 581 TACCTTTTCA 3651 At attaa acac CTAA - AT
ACACACAGGGCTAACGAAGT TTAATACACA GCCG acctttc tac aggG CGAA GTCAGG G
CAGGATGTCCCTGATATTCG CAGG |||| |||||||| ||| |||| |||| ||||||
ATTTCCCTCACGTACCCGGA TGGT TGGAAAAG ATG TCCC GCTT TAGTCC /

AAAGGTTGTGGT GT GCCC- CAC- TTTA A CT

GAM814 AGCGACACGGGGCGCGTCGT 582 CCCCTGCAGC 3652 C TGTAAA TTAA TTTC A--
ATAT A A
GTAAACCATGTTAAACATTT GTGAAGGCAG GT G CCATG ACA AAACTGCTTTCGC GCA
GGGAA AT A
CAAACTGCTTTCGCAGCAAT TTTC || | ||||| ||| ||||||||||||| ||| ||||| ||
ATGGGAAAATAAATGTATTC TA C GGTAT TGT tttgacggaagtg cgt ccCTT TG A
CCCCTGCAGCGTGAAGGCAG T ------ TC-- Cc-- cga cc-- A T
TTTCCTGTCTTATGGCTATG
TGCTTTGGCT
GAM815 TAGGGCTGCTGATAGCTAGC 588 TCCGGTGCCT 3658 G T CTA C---- TT- T G
GCTGCACTTAAAAATGGGGT GTCGTAGACC TAGG CTGC GATAG GCGCTG AC AAAAA
GGG T
AGCCCTTTTTCTTGTAAATC TG |||| |||| ||||| |||||| || ||||| |||
CGGTGCCTGTCGTAGACCTG gtcc gatg ctgtc cgtggc TG TTTTT CCC A
a - --- ctAAA TTC - G

GAM816 GGGTGGCTATCTATCCATAG 583 GTGCATTGGA 3653 --- CTA- TAGGCAG T CG
GCAGGCATCCGGCGTCTTTG GATAGTAGCT GGGTG GCTAT TCCA GCA CCGG T
GTGCATTGGAGATAGTAGCT TTCA ||||| ||||| |||| ||| ||||
TTCACCC CCCac cgatg aggt cgt gGTT /
ttt atag ta----- - TC

GAM817 CGAGGAATAATAAGAACAAA 584 TTTCACAGTA 3654 A-- C AATGC A A AACA A TG
GA-- CA
GTAATGCCTGTAAAAATAAA GATTTTATTC AATA GAA AAAGT CTGT AAA TA TCAAC T
TAT TGGT T
CATCAACATTGTATGATGGT CGGT |||| ||| ||||| |||| ||| || ||||| | ||| ||||
CATTAAACCAATTAGTATGA TTGt ctt tttta gaca ttt AT AGTTG A ATG ACCA T
CGTTGAACTAATTTCACAGT ggc a gat-- c A CA-- C GT ATTA AA
AGATTTTATTCCGGTGTTAT
CCTCG
GAM818 GTGGCCCAACCTCTGCTCCC 585 CTTGAGGTCA 3655 ACCTCT T CTCTATTCT--- TT
TTA CC
CTCTATTCTCCTCTTGCGTT TACGTTTTAG GTGGCCCA GC CCC CCTC GCG TCT A
ATCTCCAATAGAATTTGCTT GGTG |||||||| || ||| |||| ||| |||
GAGGTCATACGTTTTAGGGT CGCCGGGT Cg ggg ggag cGT AGA /
GCTCGACCTGGGCCGC CCAGCT t attttgcatact tt TTA TA

GAM819 TGTCGGAGAGTAAACATTGA 589 TCGGAGAGTA 3659 -- - aaacat a taAAAC
CGGATAAAACAAAAATGCTC AACATTGACG TGtc gg agagt tg cgga A
CGCATAACTCTACCATGGCA GATA |||| || ||||| || ||||
ACGG CC TCTCA AC GCCT A
TA A AT---- - CGTAAA

GAM820 CGATTTCGAGAAATAATAAG 590 TGTAAAGATA 3660 ATAA AATGC - gata--- a ac t AATC
AATAAAGTAATGCCTGTAAA AACATCAACA TA GAATAAAGT Ctgt aaa aac tca attg TTGGT A
GATAAACATCAACATTGTTT TTGT || ||||||||| |||| ||| ||| ||| |||| |||||
GGTAATCATTAAACCAATTA GT CTTATTTTA GACA TTT TTG AGT TGAT AACCA /
GTATGACGTTGAACTAATTT GAC- GAT-- C AATCAAG C A- T AATT
CACAGTAGATTTTATTCCAG
TGTTATCCTCG
GAM821 TCCACATCGGCAGATGCGAC 591 CATCGGCAGA 3661 --- gc a g
GACATACGATTGTGTGCCGT TGCGACGACA TCCAcatc ggcagat gacg catac A
TTAATCTGCCTCGGGTGTGG TACG |||||||| ||||||| |||| |||||
A AGGTGTGG CCGTCTA TTGC GTGTG T
GCT AT C T

GAM822 CTGGGTTTGTGTGCCGACTT 592 ACCCTTTGAT 3662 TT TGCC CT CTTTTaccctt cttact cct- CTG
GTTCCTTTTACCCTTTGATG GACTTACTGC TGGGT GTG GA TGTTC tgatga gc gAC A
ACTTACTGCCCTGACCTGAC CCTG ||||| ||| || ||||| |||||| || |||
CCGTCTACCGCCTCCTCATC ACCCG CAC CT ACAAG ACTACT CG CTG /
ACCTTTAGAACACTCCCTCA -- TCC- C- ATTTCC----- CCTC-- CCAT CCC
CGCCCAG

GAM823 ACATAGCCCAAATGGACACT 593 AAATGGACAC 3663 A Caa g a- agg
TGCGGTTAGGACAAAACCGC TTGCGGTTAG ACAT GCC at gac cttgcggtt a
AAGCGGTCGATAGGCCATGT GACA |||| ||| || ||| |||||||||
TGTA CGG TA CTG GAACGCCAA /
C A-- G GC Aac

GAM824 CTCTTATTTTTAAATTAATG 3024 CAGAAATTAG 6094 TTTTTA AA CCCAATTA
TGTCCCAATTAGAAACCCAA TTGAGAG CTCTTA AATT TGTGT G
GCGCAGAAATTAGTTGAGAG |||||| |||| |||||
gagagt ttaa acGCG /
tga--- ag AACCCAAA

GAM825 GGCTTGAGCTACACCCCCCA 3025 TAACTAGGGT 6095 TT --- C ----- C C C
GTTCCCGCGTCGGTAACTAG TAAAGGTTTG GGC GA GCTA ACC CCC AGTT CCG G
GGTTAAAGGTTTGGCAGATT GCAG ||| || |||| ||| ||| |||| |||
TTGCC CCG TT cggt tgg ggg tcaa GGC /
TT Aga t aaatt a t T

GAM826 GCCCCTAAAAAGGATCCTTA 3026 TTAGATCAGT 6096 -- TC GAT TGTATTTT GG -- --- CAA

TGATGGCCTTGTATTTTGGG TTCCTTTGGG AAAGGA CTTAT GGCCT GGGA
TTGATTTAAA GGA A
AGGTTGATTTAAAGGACAAA CCGT |||||| ||||| ||||| |||| |||||||||| |||
CTATCCACAGATTTAGATCA TTTTCT GAAtg ccggg tcct gactagattT CCT /
GTTTCCTTTGGGCCGTAAGT CG TT --- tt------ tt AGACA ATC
TTCTTTTGCAACTGGGT

GAM827 CCAGGCACATCTGCTAATAG 3027 CTCCTACTCC 6097 CACAT TG AT A CTCTTACCA
TAGGAACACTCTTACCAGCT TAGTGGCTCC CCAGG C CTA AGTAGGA CA G
ACATCTATGCTCCTACTCCT CTGG ||||| | ||| ||||||| ||
AGTGGCTCCCTGG ggtcc g gat tcatcct GT /
ctc-- gt cc c ATCTACATC

GAM828 TCAGAAAGAGGTTTAATATT 802 TCCATCAGAA 3872 G G T A G GACCA AAG
AGA
TTTGTGAGACCATCGAAGAG AGAGGTTTAA TCA AAAGA GTT AAT TTTTT TGA TCG
AGAGAAAG T
AGAAAGAGATAAAACTTTTT TATT ||| |||||| ||| ||| ||||| ||| ||| ||||||||
TTACGACTCCATCAGAAAGA AGT TTTtt taa ttg agaaa act AGC TTTTTTTC A
GGTTTAATATTTTTGTGA G a t g g acctC A-- AAA

GAM829 TTTTTTACGACTCCATCAGA 3028 CATCAGAAAG 6098 - CTCca g g t a G GACCA AAG
AGA
AAGAGGTTTAATATTTTTGT AGGTTTAATA CGA tca aaaga gtt aat ttttT TGA TCG
AGAGAAAG T
GAGACCATCGAAGAGAGAAA TTTT ||| ||| ||||| ||| ||| ||||| ||| ||| ||||||||
GAGATAAAACTTTTTTTACG GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTTC A
ACTCCATCAGAAAGAGGTTT A ACCAG G A T G G ACCTC A-- AAA
AATATTTTTGTGAGACCATC
GAAGAGAGAA
GAM830 CTTTTTTACGACTCCATCAG 3029 CATCAGAAAG 6099 A CTCca g g t a G GACCA
AAG AGA
AAAGAGGTTTAATATTTTTG AGGTTTAATA CGA tca aaaga gtt aat ttttT TGA TCG
AGAGAAAG T
TGAGACCATCGAAGAGAGAA TTTT ||| ||| ||||| ||| ||| ||||| ||| ||| ||||||||
AGAGATAAAACTTTTTTTAC GCT AGT TTTTT TAA TTG AGAAA ACT AGC
TTTTTTTC A
GACTCCATCAGAAAGAGGTT - ACCAG G A T G G ACCTC A-- AAA
TAATATTTTTGTGAGACCAT
CGAAGAGAG
GAM831 ACCTCTTTCTGATGGAGTCG 803 TGATGGAGTC 3873 TTTCT TG TC AAAG CT TC
TCTTC T CTCACAA
TAAAAAAAGTTTTATCTCTT GTAAAAAAAG C GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
TCTCTCTTCGATGGTCTCAC TTTT | || ||| |||||| |||||| ||| || || |||
AAAAATATTAAACCTCTTTC G CT TTC TAtttt aaaatg gag ag CT CCA A
TGATGGAGTCGTAAAAAAAG CTTCT CT TC gaaa ct gt tCTTT - AATTATA

TTTTATCTCTTTCTCTCTTC
GATGGT
GAM832 ACCTCTTTCTGATGGAGTCG 804 TGATGGAGTC 3874 TTTCT TG TC AAG- CT TC TCTTC T CTCACAA
TAAAAAAGTTTTATCTCTTT GTAAAAAAAG C GA GAG GTAAAA TTTTAT CTT TC GA GGT A
CTCTCTTCGATGGTCTCACA TTTT | || ||| |||||| |||||| ||| || || |||
AAAATATTAAACCTCTTTCT G CT TTC TAtttt aaaatg gag ag CT CCA A
GATGGAGTCGTAAAAAAAGT CTTCT CT TC gaaa ct gt tCTTT - AATTATA
TTTATCTCTTTCTCTCTTCG
ATGGT
GAM833 TCTCAATAAAGAAATAAATA 805 AGAAATAAAT 3875 T A aa tcttt aT
TATCTTTGTTAAATATGTTA ATATCTTTGT TC CAATA agaaata tata gttaa A
ACTTTTTGTATATTTCTATA TAAA || ||||| ||||||| |||| |||||
TTGTGA AG GTTAT TCTTTAT ATGT CAATT /
T A -- TTTT- GT

GAM834 TATGAGGTTCGACCAGCGGC 806 AGCGGCTGCT 3876 A a gaaga- ga A AG AA CG
TGCTGGAAGAGGGCGACGAG GGAAGAGGGC TATG GGTTCGACC gcggctgctg gggc cg GG GATG GTGAC T
GAGGATGAAGTGACCGTGAT GACG |||| ||||||||| |||||||||| |||| || || |||| |||||
GTCGCCGTCACCCGAGCCCG GTGC CCGAGCTGG CGCCGACGAC CCCG GC CC CTGC CGCTG G
TGCAACAGCAGCCGCCGGTC - C AACGTG A- - A- -- TA
GAGCCCGTG

GAM835 CTATATGAACTTATGTGCCT 807 TGTGGACAAC 3877 TGAAC GCC- ATGC C
GTCATGCCAGCCAGAGTTGT AAACATAATT CTATA TTATGT TGTC CAGC A
GGACAACAAACATAATTATT ATTA ||||| |||||| |||| ||||
ATAG GATat aataca acag gtTG G
tatt- aaca gt-- A

GAM836 GTGGTTGTAACAGTTGCTTC 808 CGTTCAGTCC 3878 T A TG--- - T ATTA T TA AATC
GAGTTGTGAATTAGAATCGT GATATCGGAG GTGGTTG AAC GT CTTCGA GTTG GA GAA CGT CA T
TACAAATCTTACGTGCGACG AAAG ||||||| ||| || |||||| |||| || ||| ||| ||
TTCAGTCCGATATCGGAGAA CACCAGT TTG CA gaggct tagc ct ctt gcA GT /
AGTACCGTTTGACCAC - C Tgaaa a - ga-- - GC GCAT

GAM837 GCGTTCCGTTGAGAGTGACT 809 TCCAAGTTCA 3879 - C- TG ----- GTATT CC
GTATTCACCCTTATGTCCAA CTGACTCTTG GC GTTC GT AGAGT GACT CA C
GTTCACTGACTCTTGATAAG ATAA || |||| || ||||| |||| ||
AGCTGC CG CGAG ta tctca ttga GT T
T aa gt gtcac acct- AT

GAM838 GATACATCGATGTGGACAAC 810 CCATATGCTA 3880 A- GACAACA --- CT- ATAATA C
CT TACT
AACTGGGCCCTCTTTATAAA AAAGTTATGG TGTG ACTGG GCC CTTTATAA AGCG
TGT GGA G
TAATAAGCGCTGTCTGGATA AGTA |||| ||||| ||| |||||||| |||| ||| |||
CTGAATTCTCCCATATGCTA ACAT TGACC CGG gaggtatt tcgt ata cCT A
AAAGTTATGGAGTACGGCCT AG ------- GTC Cat gaaaa- - c- CTTA
GCCAGTTACAGACGAAGTAT
T
GAM839 TATGCTTCCTTTAAACAGGT 811 TCTCACACCA 3881 CT- TAAACA T TGG
GTTGGATTCTGATGGCTTTT GGGACAACAT TATG TCCTT GGTGT GGATTCTGA C
TAGAATCTCACACCAGGGAC A |||| ||||| ||||| |||||||||
AACATA atac aggga ccaca tctAAGATT /
aac ------ c TTT

GAM840 AGTTGGCTTTCTACCCCTCT 813 TAGTTTGTGT 3883 CT- CCCT- T ACAA A
TTACAGACAAGGAAAGGTTC GGGATCTCCA AGTTGG TTCTAC CT TACAG GGAA G
CCTGTATAGTTTGTGTGGGA ACT |||||| |||||| || ||||| ||||
TCTCCAACT tcaacc agggtg ga ATGTC CCTT /
tct tgttt t ---- G

GAM841 TTTACCTGTCCAATTGTCTG 819 TACCTGTCCA 3889 t t at- ------ CTATAATCA
CCAAAAA
TGAGGTCTATAATCAGACTT ATTGTCTGTG TT acc gtcca tg tctgtgaggt GACTTT T
TCCAAAAATATAAAGAAAAA AGGT || ||| ||||| || |||||||||| ||||||
GTTAATCTTACAGAAATTAC AG TGG CAGGT AC AGACATTCTA TTGAAA A
CATAATGGACTGGTTGA T T AAT CATTAA A-------- AAGAAAT

GAM842 GTCTCGGTCAGCGTGCCATA 820 TGGCATGCTG 3890 C TAAACGAATATTATA C T
A
AACGAATATTATATGGTACG ACCGAAC GT TCGGTCAGCGTGCCA TGGTA G CGA C
TCGAACATTCGCTTATCATG || |||||||||||||| ||||| | |||
GCATGCTGACCGAAC ca agccagtcgtacggt ACTAT C GCT A
- ---------- T - T

GAM843 GGGCACAATTTCTTGCACGT 812 TATACAGGCT 3882 CAATT C- G CA A
GTGCATATACCAAAGGGTAT ATGCAAGGTC GGGCA TCTTGCA GT TG TATACC A
ACAGGCTATGCAAGGTCATA ATAT ||||| ||||||| || || ||||||
TGTCC CCTGt ggaacgt cg ac atatGG A
atact at g -- G

GAM844 ATGTTTGTGGAGTGATATAC 814 GGAGTGATAT 3884 TT Tg - tata tgtgct tt
TTGTGCTGCTTATTTGCTTT ACTTGTGCTG ATGT G ga gtga ct gc a
TGGCTTTCGCATTTGCCTGC CTTA |||| | || |||| || ||

AT TACG C TT CGCT GG CG T
TC GT A TTC- TTTT-- TT

GAM845 ACATGGTGGTATTTGACAGA 815 TTTGACAGAC 3885 T- TG tt a tg - g
CATGATGTTGGGTTACTAGG ATGATGTTGG ACA GG GTA tgacag ca atgt tgg t
CATATTGTTGTTACTTATTG GTTA ||| || ||| |||||| || |||| |||
CTCTTGT TGT TC TAT ATTGTT GT TACG ATC t
TC GT TC - TA G a

GAM846 GCAAGTGCTACTACTTTTCG 816 AGTGAAGCCG 3886 AA G TAC-- AG GAG A
GAGTCAGAGTCCAATTGGAG AAAAATTTTG GC GT CTAC TTTTCGG TCA TCC A
TGAAGCCGAAAAATTTTGTA TAGA || || |||| ||||||| ||| |||
GACAGC CG Ca gatg aaaagcc agt aGG T
A- - tttta ga g-- T

GAM847 TTTCAAATAATATATGCTAA 817 TAATATATGC 3887 AA-- aaa catTAAAAT A
AATTAGTTCATTAAAATTTA TAAAATTAGT TTTCA taatatatgcta ttagtt TTATAG T
TAGATAACTATGATATATCT TCAT ||||| |||||||||||| |||||| ||||||
TTAACTAAAGTAGCATATGT AAAGT ATTGTATACGAT AATCAA AGTATC A
TACTCATGAAA ACTC GA- TTTCTATAT A

GAM848 CTCCTCCACTAATTCGCGGA 818 GTGCATCGCC 3888 TAA---- TA TG T T - TTAT
T
TACGTTGCCTTATGGCTGAG ATGGGTGACG CTCCTCCAC TTCGCGGA CGT CCT ATGGC
GA GC TGG T
CTTATTGGTTCCCCATGGTG ACTC ||||||||| |||||||| ||| ||| ||||| || || |||
CATCGCCATGGGTGACGACT GGGGAGGTG AGGTGCct gca ggg taccg ct cg ACC C
CCGTGGAGGGTTTTGTGGAG TTTTGGG ca gt - - a tgGT C
GGG

GAM849 TGACCCCGCCCCTCGGACTT 821 CCTCGGACTT 3891 CC Ccctc ctt ---- t
TGACCGTTCCCACGCCACGT TGACCGTTCC TGAC CGC gga tgac cgt c
CATTTTCCCACGCGACGTCA CACG |||| ||| ||| |||| |||
ACTG GCG CCT ACTG gca c
CA CAC-- TTT CACC c

GAM850 AATAATATAGATAGCAGATT 826 TAATATAGAT 3896 a - gc ta ----- AA
ACTTAAAATATTTATAAAAA AGCAGATTAC AAt atata gata agattact aAATA TTTAT A
ATAAAACTTTTATTTCTGGT TTAA ||| ||||| |||| |||||||| ||||| |||||
AGTTTTGTATCATATATGAT TTA TATAT CTAT TTTGATGG TTTAT AAATA /
T G A GT TC TTTCA AA

GAM851 GCGCTCATGTCGCTGGGAGT 834 TCGCTGGGAG 3904 C T c g c acc
ACACCCGGACCCGGGCCTGG TACACCCGGA GCG TCA Gt gctgg agtaca ccgg c

ATGTACTCCAGCACCTGATC CCCG ||| ||| || ||||| |||||| ||||
GC CGC AGT CA CGACC TCATGT GGTC g
T C - - A CGG

GAM852 ATTGATAATTATATGAGTGA 835 TGAGTGAATT 3905 - ------ tg a g acaca- CA
ATTTAATGATAACACATCAC TAATGATAAC ATTGATA ATTATA tgag a tttaat ata tCA T
ATCCTGAATTTAATATAGTT ACAT ||||||| |||||| |||| | |||||| ||| |||
AAAGTTGCTCAAAAACGTGT TAACTAT TAATGT ACTC T AAATTG TAT AGT /
AATATATCAAT A GCAAAA GT G A AATTTA CC

GAM853 CGCATTAATAATTTACCCAC 822 CTTGCGAATC 3892 A A- CCC - GA C-- T CTC
AGTGAAGCTTGCTAAGCAGG CTAAACTTGT CGCATT ATA TTTA ACA GT AG TTGC
AAGCAGG T
CTCTACCCCTGCTTGCGAAT AAAT |||||| ||| |||| ||| || || |||| |||||||
CCTAAACTTGTAAATAAAGC GTGTAG TAT AAAt tgt ca tc agcg ttcGTCC /
TATAGATGTG A CG aaa t aa cta - CCA

GAM854 CCGCCGTCTCGTAGACCGAA 823 TTTGATGAGG 3893 C C TAGA GA C- ACG
TCCAGACGACGCAGCCCGTC ACGTCGAAAT CCGC GT TCG CC ATC AGACG C
TTTGATGAGGACGTCGAAAT TGTG |||| || ||| || ||| |||||
TGTGG Ggtg ta agc gg tag tCTGC A
t a tgca ag tt CCG

GAM855 CAAACCGGGTGCAATATCAG 824 TGGTATGAAG 3894 - GCA TC - - TA
CTCCTGTCGCTATTAGTCGG CCTAGGTTTG CAAACC GGGT ATATCAGC CT GTCG C T
CGAGTGGCTGGTATGAAGCC |||||| |||| |||||||| || |||| |
TAGGTTTG gtttgg tccg tatggtCG GA CGGC G /
a aag GT G T AT

GAM856 GTAACGGGGATCGCGAGCGG 825 ACGGGGATCG 3895 Aa tcgcga g ag GAC T
TCGAGTCGGGACCCTGCAGG CGAGCGGTCG GT cgggga gc gtcg tcGG CC G
CGACCGAACGGCAGCAGATC AGTC || |||||| || |||| |||| ||
TTCCCCGCAAC CA GCCCCT CG CGGC AGCC GG C
AC TCTAGA A A- AGC A

GAM857 AGGGTGTCAATTACATTGCT 827 TTCCCGGGAC 3897 ACATT- -------- T CTA GTA
T
GATCGTGATGTGATAACTAC TTATCTCGTC ATT GC TGATCGTGATG GATAA CTGGGG
ATATTGGTG T
TGGGGGTAATATTGGTGTTA ACGA ||| || |||||||||||| ||||| |||||| |||||||||
ACATCAATATTCCCGGGACT TAG CG GTTagcactgc ctatt ggccct tATAACTAC A
TATCTCGTCACGATTGTTCT CTACAT TAATTCTT t cag --- A
TAATGCTACATCGATTGGTC
CCCT

GAM858 CGTGCTGCCATTAGCTCTTA 836 TGCCATTAGC 3906 Ct c---- t ttc A
TGCTCATTCCGCTGATTCAG TCTTATGCTC CGTG gccattag tctta gctca CGCTG T
CGCCTTGGGCTGAGAATGTT ATTC |||| |||||||| ||||| ||||| |||||
CTAGTGGTCCCATG GTAC TGGTGATC AGAGT CGGGT GCGAC /
CC TTGTA - TCC T

GAM859 GGTGAGCGGACGAACAGATA 837 TGAGCGAGCG 3907 A GA AC-- C G A G AGT
GCCGCGCGCACACGCGAGTC ACTGTCTCGA GGTG GCG CGA AGATAG CGC CGC CAC CG
C
TCCCGGTGAGCGAGCGACTG GTCG |||| ||| ||| |||||| ||| ||| ||| ||
TCTCGAGTCGCACGCACACC CCAC CGC gct tctgtc gcg gcg gtG GC /
A AC gagc a a a - CCT

GAM860 TTTTGTTAATAAAGTATGTA 838 TAAAGTATGT 3908 - t ttcattT TG - GACTAAG
TGTCC
TGGAGGTTTCATTTGTGGTT ATGGAGGTTT taaagt atgta ggaggt GTGGT CAC CCTGT
GTGT C
GCACCCTGTGACTAAGGTGT CATT |||||| ||||| |||||| ||||| ||| ||||| ||||
TGTCCCTGTTTTACATATAA ATTTTA TACAT CCTTTA CATTA GTG GGATA TACA
T
TAGGAGTGTGATTACCAACA A - CAAC--- GT A ATA---- TTTTG
TTTCCTACATAATTTTATGC
CCTACCCTAAG
GAM861 GAGGTGCTTGCATGGAGCCA 828 TATTGGATAA 3898 TG GC A A g--- c caa t
TTG
TCTCTATTGGATAAACAGCA ACAGCAAAGG GAGG CTT ATGG GCC TCTCtatt gataaa ag agg
gaa G
AAGGTGAATTGGCATTTTCC TGAA |||| ||| |||| ||| |||||||| |||||| || ||| |||
CCTCTTTTTATCAAAAGATG CTTC GAA TGTC CGG AGAGGTAG CTATTT TC TCC
CTT C
GAGAGGCCTGTAAAGTCCTT CT A- - - AAAA T --- C TTA
C

GAM862 TTCACATGGTTGTGAATCTT 829 TGTGAATCTT 3899 --- g ct cac ct
GGCACAGGCCTTAAAGTTTT GGCACAGGCC TTCAC ATGGTt tgaat tgg aggc t
CCACGTTCAGAGCCATACAG TTAA ||||| |||||| ||||| ||| ||||
TGGG GGGTG TACCGA ACTTG ACC TTTG a
ACA G C- T-- Aa

GAM863 GCACGTCCGCGGGCGCGTAG 842 GCGCGTAGGC 3912 C -- g cagcac a a AG CA
GCCAGCACCTGAGCCAGCAG CAGCACCTGA GCA GTCCGCG Ggcgcgta gc ctg gcc GC GT
A
GTCAAAGTGCTCGCCGGCCA GCCA ||| ||||||| |||||||| || ||| ||| || ||
GCAGCGTGCGCGCCAGCGCG TGT CGGGCGC CCGCGCGT CG GAC CGG CG CG A
GGCATGT A GA G AC---- - C CT TG

GAM864 CTCAAATTACTTCAGAGCTT 830 TACTTCAGAG 3900 Ttac a tcatttta A CCTC
TCATTTTAAAAAATTACATC CTTTCATTTT CTCAAA ttcag gctt aaa ATTACAT T
CTCTTCCTGTGTAATGTTTG AAAA |||||| ||||| |||| ||| |||||||
AGTGCTGAATTTTTGAG GAGTTT AAGTC TGAG TTT TAATGTG /
TT-- G -------- G TCCT

GAM865 CCAGAGCCTTCAAAAATTGC 831 CAACTGTATG 3901 ----- - AAAAT- TGAGT-- GAA
TGAGTGCTTCTGAAACTGAG AACCTGAAGA CCAGAG C CTTCA TGC GCTTCT A
AAGCTCCAACTGTATGAACC GTAA |||||| | ||||| ||| ||||||
TGAAGAGTAACTCTCTGG GGTCTC g gaagt atg CGAAGA /
TCaat a ccaagt tcaacCT GTC

GAM866 ACAGTAGTTTTCACGGTATT 832 TTAAATCGGG 3902 - CACG- -- T
TTTTGAAATTAAATTTTAAA TACATGATAA ACAGTA GTTTT GTATTT TTTGAAAT A
TCGGGTACATGATAAAGCAT AGCA |||||| ||||| |||||| |||||||
GCTGT TGTCGT cgaaa catggg aaattTTA /
a tagta ct A

GAM867 TCGTCGTCCACCTCAGGTAC 839 TATTATTTTA 3909 CG A-- GTAC-------- TA
AATAGTATATTATATATATA ATAAACTTAT TCGT TCC CCTCAG AATAGTATAT T
TTATTTTAATAAACTTATTG TGAG |||| ||| |||||| ||||||||||
AGGACGGGAGAACGA AGCA AGG Ggagtt ttattatATA /
AG GCA attcaaataatt TA

GAM868 TTACAACTTTCATTTTAAAA 840 TAGCGTCTTA 3910 TC - T GT TC
GTCGCGTCTTCTTCCGGTAG TTAAAGTTTA TTACAACTT ATTTTAA AAG CGC CT T
CGTCTTATTAAAGTTTAAGT AGTT ||||||||| ||||||| ||| ||| ||
TGTAG GATGttgaa tgaaatt ttc gcg GG T
tt a t at CC

GAM869 AAAATTATGTGTAAGCCTAG 843 CATTGTGTTT 3913 TT GTAA C CGT C - A
CGTGAGTGCGCACAGTCAGA ACTTTATTTA AAAA ATGT GC TAG GAGTG GCACAGT CAG T
TTCTTGCATTGTGTTTACTT GCAA |||| |||| || ||| ||||| ||||||| |||
TATTTAGCAATAACATCTTT TTTT TACA cg att ttcat tgtgtta GTT T
TT TC ATaa - tat t c C

GAM870 ATCTCTTTCAGTATGTGAAT 833 TATGTGAATA 3903 TCAGt-- - ta t
AGATAGGTATTTTATCTCTA GATAGGTATT ATCTCTT atg tgaataga ggta t
TTCATCATCGAATTTAAGAG TTAT ||||||| ||| |||||||| ||||
AT TAGAGAA TAC ACTTATCT Ctat /
TTTAAGC T -- t

GAM871 GAGCTGGAAGCTATCCTAAG 841 TATCCTAAGG 3911 AA a ct caa-- c ca

GTCAATCCGACTCCAACGTG TCAATCCGAC GAGCTGG GCt tc aaggt tc gactc A
GGTCAGAGCCATACCTTTCG TCCA ||||||| ||| || ||||| || |||||
AAGTGTCAGTTC CTTGACT TGA AG TTCCA AG CTGGG C
G- - CT TACCG A TG

GAM872 ATTTTAGGAACTACGTTCAT 844 TTCATCTTTT 3914 CG TCA TCCT GC
TATTAAAACTATC T
GGTATCCTGGCGAATATTAA ATCACCATAT ATTTTAGGAACTA T TGGTA G GAA
AATGATA G
AACTATCAATGATATGATTA AGTT |||||||||||||| | ||||| | ||| |||||||
TCGTTTTCATCTTTTATCAC TAGAATCTttgat a actat c ctt TTGCTAT A
CATATAGTTTCTAAGAT at cc- ttt- ta ---------- T

GAM873 TGGGCTACACTGATAGGCTG 845 CACCTGATTT 3915 G C ---------- C G C
CCCGTTCTGAAGGGGCACCT ACAAAACAGA TGG CTACA TGA TAGG TGCCC TT T
GATTTACAAAACAGACTTTA CTTT ||| ||||| ||| |||| ||||| ||
TTGTGGGCCA ACC GGTGT Att gtcc acGGG AA /
G T tcagacaaaacattta - G G

GAM874 GGCGTCTAAGATATTCTTCC 846 TCTAAGATAT 3916 - gatat a--- cttATT
ATCAACTTATTAACATTTTT TCTTCCATCA GGCGtc taa tcttcc tcaa A
GACTAGGGAAGATACATTAT ACTT |||||| ||| |||||| ||||
GACGTC CTGCAG ATT AGAAGG AGTT /
T ACAT- GATC TTTACA

GAM875 GGCCTGGAGGACGCGGGCCA 847 CACGAGCTGG 3917 G CGC A A T G GCCT
GCACGTGAAAGTGAGGTGCC CCCTCCTGCG GGCCTG AGGA GGGCCAGC CGTGAA G GA GT
C
TCTTTGACGTCCTTCACGAG GGCC |||||| |||| |||||||| |||||| | || ||
CTGGCCCTCCTGCGGGCC ccgggc tcct cccggtcg gcacTT C CT CA /
g --- a - - G GTTT

GAM876 GGCCACCTGCTTTCACCCCT 848 GGGCTTCACC 3918 T- TCAC---------- CTA
TCTACTTCAAGGGCTTCACC TCCAACCACC GGCCACC GCTT CCCTT C
TCCAACCACCTGAGCTCGGT TGAG ||||||| |||| |||||
GGCC CCGGTGG Cgag gggAA /
CT tccaccaacctccacttc CTT

GAM877 ATGTTTTTTATCTCTTTCAG 849 TATGTGAATA 3919 T -- TCAGt-- - ta t
TATGTGAATAGATAGGTATT GATAGGTATT ATGTTT TT ATCTCTT atg tgaataga ggta t
TTATCTCTATTCATCATCGA TTAT |||||| || ||||||| ||| |||||||| ||||
ATTTAAGAGATCCGATAAAC TACAAA AG TAGAGAA TAC ACTTATCT Ctat /
AT T CC TTTAAGC T -- t

GAM878 TGGGATTTTACTTAATATAA 2939 TTAGAAATGC 6009 A ATATAATAT CC TA
TATTATTTCCCGTAATAAAT CAAATCTATA TGGGATTTT CTTA TATTTC GTAA A
TTTATTAGAAATGCCAAATC AGAA |||||||||| |||| |||||| ||||
TATAAGAAAAGTCCTA ATCCTGAAa gaat gtaaag tATT A
a atctaaacc at TT

GAM879 CGGGTTTTTTATCTCTTTCA 2940 TCGAATTTAA 6010 TCTCT AGT - TA T
GTATGTGAATAGATAGGTAT GAGATCCG CGGGTTTTTTA TTC ATG TGAATAGA GGTA T
TTTATCTCTATTCATCATCG |||||||||| ||| ||| |||||||| ||||
AATTTAAGAGATCCG gcctagagaat aag tAC ACTTATCT CTAT /
tt--- c-- T -- T

GAM880 GAGTATTTAGGGTTAAGTTA 2941 TAACACAGTA 6011 TAT A------- C ATC-- TA
CCTGATCCCAATAAATTTGG TATGATCCTA GAG TTAGGGTTA GTTA CTG CCAA A
CCTTCCAGATAACACAGTAT ACTC ||| ||||||||| |||| ||| ||||
ATGATCCTAACTCTC CTc aatcctagt caat GAC GGTT /
tc- atatgaca A CTTCC TA

GAM881 ATTTTAGGAACTATGTTCAT 2942 TTCATGGTAT 6012 tca tcct gc tattaAAACTATC
T
GGTATCCTGGCGAATATTAA CCTGGCGAAT ATTTTAGGAACTATGt tggta g gaa
AATGATA G
AACTATCAATGATATGATTA ATTA |||||||||||||| ||||| | ||| |||||||
TCGTTTTCATCTTTTATCAC TAGAATCTTTGATATA ACTAT C CTT TTGCTAT A
CATATAGTTTCTAAGAT CC- TTT- TA ---------- T

GAM882 TGTATGTGTGCATGTTGTAT 2943 TGTGTGCATG 6013 tt tttt- TT
GTTTTGTATTGTTTGCCTGT TTGTATGTTT TGTAtgtgtgcatg gtatg gta G
TTGTATGTTGTGTATATGTA TGTA |||||||||||||| ||||| |||
CA ACATGTATATGTGT TATGT CGT /
TG TTGTC TT

GAM883 ATGTGTGGTTGCACCCAATG 2945 TTCTTTGTCC 6015 TGCACC T ---- TAC
AGTAAGGTACTGTCCCTTTA TTATTACACA ATGTGTGGT CAA GA GTAAGG T
TTGTTTCTTTGTCCTTATTA T |||||||||| ||| || ||||||
CACAT tacacatta gtt ct TATTTC G
ttcct- t tTGT CCT

GAM884 GACCCCAACCGCGGTACCCA 2946 AGGAACTGCG 6016 CC-- A CACTGA C
CTGATCTTTATCTTTATGAA GTTGCCCCGT GAC CAACCGCGGT CC TCTTTAT T
GAAAAACAGGAACTGCGGTT T ||| |||||||||| || |||||||
GCCCCGTT ttg gttggcgtca gg AGAAGTA T
cccc a aCAAAA T

GAM885 GGTGTTGTGCCCCCTCCCTC 2944 CACAAGTTTA 6014 T T CCCTCca tta a----------
t
CACAAGTTTAGATGATACCT GATGATACCT GGTG TG GCCCCCT caagt gatg tacc a
ATAGGTACTTGCAGTCTCGC ATAG |||| || ||||||| ||||| |||| |||| |

GAM891 GCACTTATTTCATGAATTTC 2951 TTCATGAATT 6021 ca ttcat aa
ATTTTTAGAACTCATTAAAA TCATTTTTAG GCACTTATtt tgaat ttttag c
TAGTATTTGAAAAATAAGTG AACT |||||||||| ||||| ||||||
T TGTGAATAAA GTTTA AAAATT t
AA TGAT- AC

GAM892 GCCCACAGATCGCACCTTCA 2952 TGGAAAGTGT 6022 ACA T ACC CG AA-- --- TCT
ACCGATAAGAGTCTCTAGAT TCGGGGGC GCCC GA CGC TTCAAC AT GA GTC A
GACAAATCGACAGTTAGTTG |||| || ||| |||||| || || |||
GAAAGTGTTCGGGGGC cggg ct gtg aggtTG TG CT CAG /
gg- t aa- AT ACAG AAA TAG

GAM893 TCATTGAGTTTAGTGGCAAA 2954 TAGATGCCGC 6024 TTG TA AACG ACAGA
CGACAAACAGACAAAAATTG CAGCTAGTTG TCA AGTT GTGGCA ACAA C
TAGATGCCGCCAGCTAGTTG A ||| |||| |||||| ||||
A agt tcga cgccgt tGTT /
tga c- aga- AAAAA

GAM894 GTCGGGGCACTTTTTCCTTC 2955 GGGGGTTACA 6025 AC-- g a a aaat c
CCTCGGGGGTTACAACTAAA ACTAAATTCG GTCGGGGC TTTTTCCTTCCCTC ggggtt ca ct tcgt a
TTCGTCAGTACGATACAGTG TCAG |||||||| |||||||||||||| |||||| || || ||||
AACTCCGGGGGGAAGGAGAA CGGCCTCG AAAGAGGAAGGGGG CCTCAA GT GA AGCA g
AAACCGCTCCGGC CCAA G - - CAT- T

GAM895 TTTTTATGAGTATTTTTACA 2925 TGAGTATTTT 5995 ttt aaaa a
AAAATGCATAAAGTGTATGT TACAAAAATG TTTTTAtgagtat tac atgcat A
CGTATGTATATTTATAAAAA CATA |||||||||||| ||| ||||||
AAAAATATTTATA ATG TATGTG /
TGT CTG- A

GAM896 CCCTGGCAGTTGTGTGTATT 2926 TGTGTGTATT 5996 CA tg ttccccttctc -- C TTACTTC AT
CCCCTTCTCCCAGTGGCTCT CCCCTTCTCC CCCTGG GT tgtgta cca gtGGCT TATTA TG T
ATTATTACTTCTGATTCTCA CAGT |||||| || |||||| ||| |||||| ||||| ||
ATTATTTAATAAGCCATATT GGGACC CG ATACAT GGT TACCGA ATAAT AC /
GGTTACATAAGGCCCAGGG -- GA T---------- TA - TTATTA- TC

GAM897 ACGTATACGTAGTAAGAAAT 2927 TACGTAGTAA 5997 - ---------- G T GTTT GG TTT
AATATGTTAGCACATATATG GAAATAATAT ag aaata atatgtta CACA ATATGTAT GTATGTAT T G

TATGTTTGTATGTATGGTTT GTTA || ||||| |||||||| |||| |||||||| |||||||| |
TGTATGTTGTATGTATGTAT TT TTTGT TATATAGT GTGT TATGTATG TATGTATG
G /
GTATTTGTGTGATATATTAC G TTTATGTCAT - T ---- TT TAT
TGTATTTTGTTTGTTTGCGT
GCGTGTATGT
GAM898 CCTAAAGGAAAAATTTTCCT 2928 TCGAAAGTTT 5998 A GG CT TTT C
CCGATTTGGATCAATATCCC TTAGTTCAGG CCT AA AAAAATTTTC CCGA GGAT A
CTTGGTCGAAAGTTTTTAGT ||| || |||||||||| |||| ||||
TCAGG gga tt tttttgaaag GGTT CCTA A
c ga ct CC- T

GAM899 GAGTTGTCAGCACTGATGAT 2956 TGTCAGCACT 6026 GT a c tt t CG
TATGTGTCTCGCACAAGCAT GATGATTATG GA tgtc gca tgatga atgtg cT C
ATTTTATCATGCAGGCAGTT TGTC || |||| ||| |||||| ||||| ||
C CT ACGG CGT ACTATT TATAC GA A
TG A - T- - AC

GAM900 ACGGTAACTCGTATATTTTT 2957 ACTCGTATAT 6027 TAact ta- cg-- taAA
ACGTACAATAAAGCGATTTG TTTTACGTAC ACGG cgta ttttta tacaa G
TAAAAATAAAAACTTTACGT AATA |||| |||| |||||| |||||
AATCCGT TGCC GCAT AAAAAT ATGTT /
TAAT- TTC AAAA TAGC

GAM901 GGCGAGGAATTTGATTTGCA 2930 TGGTATGAAT 6000 TT T G TATT T T AATTTA --
-- T
GTTTATTTTCCAGTTATGTG GCTACGTTAC T GA TT CAGTT TTCCAGT ATGTG TATT ACTA
CAGA GGT A
TTATTAATTTAACTACAGAG TGGA | || || ||||| ||||||| ||||| |||| |||| |||| |||
GTTATGGCCTATCTGCATGG G TT AA GTCAG Aaggtca tgcat gtaa tggt GTCT CCG T
TATGAATGCTACGTTACTGG GC T G ---- t c gta--- AC AT G
AAGACTGGAATTTCGGTTCC
TTGCC
GAM902 TAATATAATCCTAATTCATC 2929 TAGCATAGGT 5999 T- ATTCATCT-- C
TTTTTTATCGTATAAAAATT TTTATATTG TAATATAA CCTA TTTTTAT G
CTATAGCATAGGTTTTATAT |||||||| |||| |||||||
TG gttatatt ggat AAAAATA /
tt acgatATCTT T

GAM903 CAAAATGGTGTTTGAAAAAT 2931 CACCGTTTAT 6001 A- -- A A T AA
AGGTGTACAACACGTCACCG CAGGTACGCC CAAA TGGTGT TTGA AAAT GGTG AC C
TTTATCAGGTACGCCGAGTT GAGT |||| |||||| |||| |||| |||| ||
TG GTTt gccgca gact tttg ccac TG /
ga tg a - - CA

GAM904 TGTCGTCTTTATCCTTCAGG 2932 TACCTTTAAC 6002 TATCCTTC - TAATT
ACCATGTAATTCTTCAAGTA AAGACGACA TGTCGTCTT AGG ACCATG C
TGGTACCTTTAACAAGACGA ||||||||| ||| ||||||
CA acagcagaa tcc tGGTAT T
caatt--- a GAACT

GAM905 GAAACGCGAGATCGATCAGA 2933 TTAGTCTGTA 6003 CGC- -- ------ AAC C
AACGTTCTAGAATTAGTCTG ATATGTCGAT GAAA GAGA TCGAT CAGA GTT T
TAATATGTCGATATCTCCAT ATCT |||| |||| ||||| |||| |||
ATTTC CTTT Ctct agctg gtct tAA A
ATAC at tataat gat G

GAM906 GACGCAAATACTCCTCCATT 2934 CCAGAGGGGA 6004 ATA-- CAT---- CG
AACGCGTTTACGTTACTTAC CACGTTGTGT GACGCAA CTCCTC TAACG T
CAGAGGGGACACGTTGTGTC C ||||||| |||||| |||||
ctgtgtt ggggag ATTGC T
gcaca accATTC AT

GAM907 GTGTACTAGACGGGAACATG 2935 TACGTGGATA 6005 GACG A C-- TGA--- CA--
ACCC
TCCGGTCCTTTGAGCGTCAA CGAGGATCGT GTGTACTA GGAAC TGT CGGTCCTT GCGT
AGAC A
GACACCCAAAACGTCTGTAT TTGC |||||||| ||||| ||| |||||||| |||| ||||
ACGTGGATACGAGGATCGTT CATATGGT TCTTG Acg gctaggag tgca TCTG /
TGCAGTTCTATGATGGTATA AGTA - ttt catagg tATG CAAA
C

GAM908 GTTCGTCGTTCCGTGTCCAG 1549 TGTTGCTTTC 4619 C TCCG---- C GG TCC - G C
GGGGAGCGTCCCAGCCGGCG CCTGACGAAC GTTCGT GT TGTC AGGG AGCG CAGC
CG CGA G
ACGTTTTGACGAGCTGTTGC CTTC |||||| || |||| |||| |||| |||| || |||
TTTCCCTGACGAACCTTCTG TAAGCA CG gcag tccc tcgt gtCG GC GTT T
CACGAAT - Tcttccaa - tt t-- A A T

GAM909 CCGTGTCCTCGCTTTCTTCT 1550 CACGGGGTTA 4620 CCT CTC CCGCTT C T-- GT
CTT
CTCTCCGCTTCCCCGCGATC GAAAAAGAGA CCGTGT CGCTTTCTT TCT CCCCG GA
CCG C C
CGGTCCTTCGTTCGGTCGGC GCGT |||||| ||||||||| ||| ||||| || ||| |
TTTCACGGGGTTAGAAAAAG GGCGCG gcgagagaa aga ggggc cT GGC G G
AGAGCGTGCGCGCGG CGt aa- tt---- a TTC TG CTT

GAM910 CTGGGTAGCGCTACCGAGGG 2936 TCTGTGCGTA 6006 GTA - - - C GCTCA
TGCGTGCTCATCTCTAACCG GTGTCCAG CTGG GCGCTAC CG AG GGTG GT T
CCTCTGTGCGTAGTGTCCAG |||| ||||||| || || |||| ||

gacc tgtgatg gt tc CCGC CA /
--- c g t - ATCTC

GAM911 GGCCAGCCGATGGGTGCCGG 2937 AGCCGATGGG 6007 ag atg c- tt C
TTTGGCGGCCGCGGTCGCCG TGCCGGTTTG GGCC ccg ggtg cggt ggcggC G
CCGTCCACCAACGGGAGGCC GCGG |||| ||| |||| |||| ||||||
CCGG GGC CCAC GCCG CCGCTG C
AG AA- CT -- G

GAM912 AGGAGCGGCGACGCGAAGAC 2938 GCTCTCGGCG 6008 CGA CGA T AG
ACAA------- C
GACGGTGAGTCGAGCGGTCG CCGCGTT AGA CGGTGAG CG
CGGTCGGTCGGTCGGTCGGTC CGCG G
GTCGGTCGGTCGGTCACAAC ||| ||||||| || |||||||||||||||||||| ||||
GCGCGTCGCGGTCGTTTGAC tct GCCGCTT GC GCCAGTCAGTCAGTCAGTCAG
GCGC /
TGACTGACTGACTGACTGAC --- cg- - CA TCAGTTTGCTG T
CGACCGTTCGCCGGCTCTCG
GCGCCGCGTT
GAM913 TAGAATACGGGGATATAGAT 1551 CTAGAACATT 4621 TAC G- ------- - AA
GTTTTACAAACAAATGCTAG TTTGATTAAT TAGAA GGG ATAT AGATGTTTTA CA C
AACATTTTTGATTAATATAG ATAG ||||| ||| |||| |||||||||| ||
CCTTTCTA ATCTT TCC tata tttacaagat GT A
--- ga attagtt c AA

GAM914 GGCGGTAACAAATTCAGAGT 1552 TACACGTACT 4622 ACAAATTC C- - AA
ACGCTATACGTAATAAAACG TTTCAAATAC GGCGGTA AGAGTACG TATA CGT T
ATGTACACGTACTTTTCAAA CGCC ||||||| |||||||| |||| |||
TACCGCC ccgccat tttcatgc atGT GCA A
aaact--- ac A AA

GAM915 CAATTTGCAAAACAGTTTTT 1554 TGGCAGGAAG 4624 AAACAGT TG TTT TC
CTGCTGATTTGGATCAGTTT TTTTTAATGC CAATTTGCA TTTTCTGC A GGA A
CCTCTTGGCAGGAAGTTTTT AGGT ||||||||| |||||||| | |||
AATGCAGGTTG GTtggacgt gaaggacg T CCT G
aattttt gt CT- TT

GAM916 GGCTTCGTTGCGTATGGCCA 1553 TGGCACCAGC 4623 TT GTATG ACCACGTT
CCACCACGTTAAAGAGAGAC TCGAAGCC GGCTTCG GC GCCACC A
GGTGGCACCAGCTCGAAGCC ||||||| || ||||||
ccgaagc cg cggtGG A
t- acca- CAGAGAGA

GAM917 GGCGACATGGTTGATATTGG 1555 TACAGGAATC 4625 G GG A G- CC GATT

GTTTGGTGCCATGGATTTTA TAAATCAGAT GGC ACAT TTGAT TTGGGTTT GTG ATG T
AAACATTACAGGAATCTAAA GTGC ||| |||| ||||| |||||||| ||| |||
TCAGATGTGCC Ccg tgta gacta aatctaag cat TAC T
- -- - ga -- AAAA

GAM918 GTGCTTAAGTGCTATCGCTT 1556 TAAGTGCTAT 4626 taag----- tc ---------- g
TCGGGAACGCAAAAAAAAAA CGCTTTCGGG GTGCT tgcta gcttt cg g
GAGGCTTAGTAAAATATTAT AACG ||||| ||||| ||||| ||
AGTAC CATGA ATGAT CGGAG gc a
TATTATAAA T- AAAAAAAAAAC a

GAM919 GAGCACAGACAACAATTCAT 1557 TAGGACTATG 4627 -- ---- A ATt tgaaa cac
TAGGACTATGAAATTACCAC AAATTACCAC GAGC ACAGA CAACA TTC aggacta ttac c
CTACAGTAGATTGGTCTTTA CTAC |||| ||||| ||||| ||| ||||||| ||||
GGAAATGTTGATGATCTGTA TTCG TGTCT GTTGT AAG TTCTGGT GATG t
AGCTT AA AGTA A GAT TA--- Aca

GAM920 CCAACAGATGCATATGTAAA 1559 TGTAAAGCGC 4629 AT- T aa gca aa att
GCGCACCAATATATTTTATC ACCAATATAT CCAACAG GCA Atgt agc cc tat t
ATGCAGGCAGCTCACGTTTG TTTA ||||||| ||| |||| ||| || |||
CTTGCTGTTGG GGTTGTC CGT TGCA TCG GG GTA t
GTT T C- AC- AC CTa

GAM921 CTGGGGTAAACATTTTGGGA 1558 TTTTGCCCAA 4628 TAAACATT AC-- C TGG
CAACCTCCTATGGCATTTAG TTTCCCAG CTGGGG TTGGG AACCTC TA C
AGGTTTTTGCCCAATTTCCC |||||| ||||| |||||| ||
AG gaccct aaccc tTGGAG AT /
tt------ gttt - TTA

GAM922 GTTGACATGTGGAGCCACTG 1560 ACGACAATAA 4630 ACAT CACTGGCG-- A
GCGCGTTGCCGACAACGGCG CCCGCTCCGC GTTG GTGGAGC CGTTGCCG C
ACGACAATAACCCGCTCCGC CACG |||| ||||||| ||||||||
CACGCAGC CGAC cgcctcg gcaGCGGC A
gcac cccaataaca A

GAM923 CAACACACAAGCCAATATGT 1561 TTTGTGCTTT 4631 A CA TG TGCTAA CC C-
TCATT
GCTGCTAACACACCTATATA GCGTGTGTGT CAACACACA GC ATA TGC CACA TATATA
CTGTAA A
CCTGTAATCATTATTCCTTT GTGT ||||||||| || ||| ||| |||| |||||| ||||||
TATAGTTTATGTGTTTGTGC GTTGTGtgt tg tgt gcg gtgt GTGTAT GATATT T
TTTGCGTGTGTGTGTGTGTG g -- gt tttc-- tt TT TTCCT
TTG

GAM924 GCGGGCGTGGGGACCCGGGG 1562 GGGGATGGTA 4632 - GG CGGGGAGA AG T -
-- - G
AGAGACCACCAGGCCTCGCC GGGATTGGTG GCG TGG ACC GACCACC GCC
CGCCGGTTT TC TCTCTCTCC T
GGTTTTCTCTCTCTCCGTTG GGTG ||| ||| ||| ||||||| ||| ||||||||| || |||||||||
GGGGGGGGGATGGTAGGGATT TGT ACT TGG TTGGTGG tgg gtggttagg gg
aggggGGGG T
GGTGGGTGAGGTGGTTGTGG T GA TG------ Ag - gat t G
TAGTCATTGTGAGT

GAM925 TGGTCTCATAAAAAAAGTTT 1563 TGATGGAGTC 4633 AAAA TTTTAC T- T
TCTCTTCAAT CTCACAA
TACAAAAATATTTTTATTCT GTAAAAATAT T AAAG AAAAATATTTTTAT CTCT TC GGT
A
CTTTCTCTCTTCAATGGTCT TTTT | |||| |||||||||||||| |||| || |||
CACAAAAATATTAAACCTCT A TTTC tttttataaaaatg gagg ag CCA A
TTCTGATGGAGTCGTAAAAA GTC- TCTTA- ct t tCTTTCT--- AATTATA
TATTTTTATTCTCTTTCTGA
TGTCTCAACTA
GAM926 CCGAGCGGGGGAGAGCGGTA 1564 TACAGGGGAG 4634 GG- AGC- A GAA G G GG AG
GA- GAG GTG
GGGGAAACGCCGCCTGGGAT TGTACCCACC GGAG GGT GGG AC CC CCTG ATG TGG
CC TAGTGT A
GAGTGGGACCGAGTAGTGTG AAAA |||| ||| ||| || || |||| ||| ||| || ||||||
TGATAGGCACTAGAGGGCGC CCTC cca ccc tg gg ggac tGC ACC GG ATCACG /
CAGCGTACAGGGGAGTGTAC CAA aaaa - atg a - a- G- GCG AG- GAT
CCACCAAAACTCCAACACCA
CGG
GAM927 TTTTTCTTTGGTACAAAATT 1565 TCTTTGGTAC 4635 t tt cacaa ---- CA A
TCACACAAGTTTTTATACAG AAAATTTCAC TTTTtctt ggtacaaaa tca GTTTT TATA GACAA T
ACAAATTCTTGTCCATATAT ACAA |||||||| ||||||||| ||| ||||| |||| |||||
TTTAAAACATTGACTTTTGT AAAAAGAA TCATGTTTT AGT CAAAA ATAT CTGTT T
ACTAAGAAAAA - C- TA--- TTTT AC C

GAM928 AAAATATTTTTATTCTCTTT 1566 AATATTTTTA 4636 t- t tctctTCAAT CTCACAA
CTCTCTTCAATGGTCTCACA TTCTCTTTCT AAaatatttttat ctct tc GGT A
AAAATATTAAACCTCTTTCT CTCT |||||||||||| |||| || ||| |||
GATGGAGTCGTAAAAATATT TTTTATAAAAATG GAGG AG CCA A
TT CT T TCTTTCT--- AATTATA

GAM929 TGGGAAGTACAATATGGGGG 1567 TCAGATTGTT 4637 ACA TA AA-- A A G TG C AT -
A- A A
CAATGTAATTGATTGTAATG AGACAGCTAC A TGGGGGC TGTA TTG TT TAA A TCT GT GC
GTACC GTG C
ACTCTATGTGCAGTACCAGT AACA | ||||||| |||| ||| || ||| | ||| || || ||||| |||
GACGACACGGTATCCGCTAC T ACCTCCG acat gac ag att t aga CA CG TATGG CAC
G
TCAGATTGTTAGACAGCTAC GC- GC Caca c - - gt - ct T CC - A

AACACGCCTCCACGTCGACC
CCCA
GAM930 ACCTCTTTCTGATGGAGTCG 1568 TATTTTATTC 4638 TCT--- T TC t- t tctcttcaAT
CTCACAA
TAAAATATTTTATTCTCTTT TCTTTCTCTC GA GGAG GTAAAAtattttat ctct tc GGT A
CTCTCTTCAATGGTCTCACA TTCA || |||| |||||||||||||| |||| || |||
AAAATATTAAACCTCTTTCT CT TCTC TATTTTATAAAATG GAGG AG CCA A
GATGGAGTCGTAAAATATTT TTCTCT T T- CT T TCTTTCT--- AATTATA
TATTCTCTTTCTCTCTTCAA
TGGT
GAM931 ATAAAAAAGTTTTACAAAAA 1569 TCATAAAAAA 4639 A ACA A TCT- TTCTCT
TATTTTTATTCTCTTTCTCT GTTTTACAAA ATAAAAA GTTTT AAAAT TTTTTAT CT C
CTTCAATGGTCTCATAAAAA AATA ||||||| ||||| ||||| ||||||| ||
AGTTTTACAAAAATATTTTT TATTTTT taaaa ttttg aaaaata GG /
AT a aca a ctCT TAACTT

GAM932 AAAATATTTTTATTCTCTTT 1570 AATATTTTTA 4640 tatt t tctctTCAAT CTCACAA
CTCTCTTCAATGGTCTCACA TTCTCTTTCT AAaatatttt ctct tc GGT A
AAAATATTAAACCTCTTTCT CTCT |||||||||| |||| || |||
GATGGAGTCGTAAAATATTT TTTTATAAAA GAGG AG CCA A
T TGCT T TCTTTCT--- AATTATA

GAM933 TACATATGCATGCTTTACAC 1571 TAATGTACAG 4641 T-- TGCTT CACC TACTAta g
t a
ACCATACAATAATTACTATA TACAGTGTAA CA ATGCA TACA ATACAATAAT atgtaca
tacag gta c
ATGTACAGTACAGTGTAACA CATA || ||||| |||| |||||||||| ||||||| ||||| |||
TACCTGTGATGTGCATGTTG GT TATGT ATGT TATGTTGTTG TACGTGT GTGTC
Cat /
TTGTATTTTTGTATTTTTGT TTT TTTT- TTT- ------- A - a
ATTTTTGTA

GAM934 AAAATATTTTTATTCTCTTT 1572 AATATTTTTA 4642 t- t tcgctTCAAT CTCACAA
CTCGCTTCAATGGTCTCACA TTCTCTTTCT AAaatatttttat ctct tc GGT A
AAAATATTAAACCTCTTTCT CGCT |||||||||||| |||| || |||
GATGGAGTCGTAAAAATATT TTTTATAAAAATG GAGG AG CCA A
TT CT T TCTTTCT--- AATTATA

GAM935 CCGTGGTGTTGGAGTTTTGG 1573 TCGGTCCCAC 4643 TT TTT TAC- T - TACGC-- C
CTC CCTA
TGGGTACACTCCCCTGTACG TCATCCCAGG TG GGAG TGGTGGG AC CC CCTG TGG
GCC TAGTG T
CTGGCGCCCTCTAGTGCCTA CGGC || |||| ||||||| || || |||| ||| ||| |||||
TCACACACTACTCGGTCCCA GC CCTC GCCATCC TG gg ggac acc tgg ATCAC /
CTCATCCCAGGCGGCGTTTC CC TC- CCTT c c cctactc c ctC ACAC
CCCTACCGCTCTCCCCCGCT
CGG

GAM936 GAATTATTATTATTCTTATT 1574 TGAGCTCGTC 4644 TA TTATTA TCC AG AG CT-
CCTGAAC
ATTCTTATTCCACGAGAGTA TGTAAGAGCC AT TTC TTCTTAT ACGAG TATG CTCGT
GTAAGAG G
TGAGCTCGTCTGTAAGAGCC TGAA || ||| ||||||| ||||| |||| ||||| |||||||
TGAACGATGATTATTCTTAT TA aag gagaatg tgctc gtAT GAGCA TATTCTT /
TTCACGAGAGTATGAGCTCG GC tcc--- tc- ga GA CTT ATTAGTA
TCTGTAAGAGCCTGAACGAT
GATTATTC
GAM937 GCGGGCTGGTCATCGGCATT 1575 TCTGGCGCAC 4645 G AT- t - a- g ctcctC CTT
T
CTGGCGCACCGGTGCGCGCT CGGTGCGCGC GCGGGCT GTC CGGCAT ctg gcgc ccg tgcgcg
CC GG C
CCTCCCCTTGGTCTTCCCGG TCCT ||||||| ||| |||||| ||| |||| ||| |||||| || ||
CAACCCCGCGCACGGCCGCG CGCCCGA CAG GCCGTG GGC TGCG GGC ACGCGC
GG CC T
TGCGGCGTGCCGTGGGACGA G GGT C G CC - CCCAAC C-- T
GCCCGC

GAM938 TATTCTTATTTCATGAGAGT 1576 TTCATGAGAG 4646 ttc tgagc - t- G
ATGAGCTCGTCTGTGAGAGC TATGAGCTCG TATTCTTAT atgagagta tcgt c gT A
CTGAACGATGATTATTCTTA TCTG ||||||||| ||||||||| |||| | ||
TTTCATGAGAGTA ATGAGAGTA TATTCTTAT AGCA G CG G
CTT TAGT- A TC A

GAM939 CCGTGATCGATCCCCTCCCG 1577 TTTCAACGGA 4647 ATCGATCC CCC G CC- - AG
CCCGGTGGCCCCGAAACGAG CGCCCCGGGA CCGTG CCTCCCG GGTG CC GAAA CG
G
GGTCGATTTCAACGGACGCC GGAA ||||| ||||||| |||| || |||| ||
CCGGGAGGAAAAAATGCACG GGCAC ggagggc ccgc gg cttt GC /
G GTAAAAaa c-- a caa A TG

GAM940 TATTCTTATTTCATGAGAGT 1581 TGATCATTCT 4651 TTC - GCTAGTCT GA TG
ATGAGCTAGTCTGTGAGAGC TATTATCATT TATTCTTAT ATGAGAGTA TGA GTGA GCC A
CTGAACGGTGATCATTCTTA ATTC ||||||||| ||||||||| ||| |||| |||
TTATCATTATTCTTATTTCA ATGAGAGTA TATTcttat act tact tGG /
TGAGAGTA CTT t attattct ag CA

GAM941 ATGAAGTTAATGATACACAC 1578 TTAATGATAC 4648 t ata c ac gAATT
TACACTGTCGAATTTGATAG ACACTACACT ATGAAGt aatg ca actac tgtc T
GGACAAAGTAGTTGACGCGT GTCG ||||||| |||| || ||||| ||||
TTATTTCAT TACTTTA TTGC GT TGATG ACAG G
T GCA - AA GGATA

GAM942 TGGCCTTCCAGATGCTAACT 1579 TAACTTTTAT 4649 CT GA a- ac cac C TG
TTTATGACCCTAACACACAG GACCCTAACA TGGC TCCA TGCt acttttatg cctaa acaG GCCT T

CGCCTTGTGTGGGCCTGTTT CACA |||| |||| |||| ||||||||| ||||| |||| ||||
AGGCGTGGAGGTGGGGCGTG ACCG AGGT GCGG TGGAGGTGC GGATT TGTC
CGGG /
GACAGCCA AC -- GG -- --- - TG

GAM943 CCTCCACAGTTACTACACCA 1580 TCCACAGTTA 4650 - actacaccatataat G
TATAATAATGAGAGTTTTAA CTACACCATA CCtccaca gtt AAT A
AGAGTACCTGCGACATGTGG TAAT |||||||| ||| |||
AGG GGAGGTGT CAG TTG G
A CGTCCATGAGAAATT A

GAM944 TAAGGGCAGGGAGGAGATAC 1582 TGCAAAAGCG 4652 AG-- A- AC At a ------ g ac--
ggtCA
GTATGCAAAAGCGGGGGGGA GGGGGGACTG AGGGC GGAGG GAT GT gc aaa gcggg
ggg tgc A
CTGCGGTCAACAATAAGTAA CGGT ||||| ||||| ||| || || ||| ||||| ||| |||
AAACCCGCCCGCCACATCTT TTTCG CCTCC CTA CA CG TTT CGCCC CCC ATG
C
TCGCCACAATCGGCCTCCAG GAGA GG A- C- C CTACAC G AAAA AATAA
AGGCTTTTA

GAM945 TAACGTTGCTTATATTTATG 1583 ACGTTGCTTA 4653 t t t ttgt- CC
TTGTTGTACCCAGTGTGCAT TATTTATGTT TAacgt gc tatat tatg tgTAC A
GATTTATGTATGTGTGCATG GTTG |||||| || ||||| |||| |||||
TTG GTTGTA CG GTGTA GTAT ACGTG /
- T T TTAGT TG

GAM946 CAAAACCACAACACTGCTAA 1584 AACCACAACA 4654 A acac taatcctct--- TT
TCCTCTGGCTTCCTGCCTCT CTGCTAATCC CA aaccaca tgc gGC C
CCTACTGCTGCATACCTGTG TCTG || ||||||| ||| |||
GTTGTG GT TTGGTGT ACG CCG /
G CCAT TCGTCATCCTCT TC

GAM947 CTGAAATACCCGTAAACGGG 1586 TACCCGTAAA 4656 A - aaac- ta aaCG
GATGTATAAACGCAAAATGC CGGGGATGTA CTGA Atac ccgt ggggatg ta C
CCGTCCCTCCCGAATGGCGT TAAA |||| |||| |||| ||||||| ||
ATATTAG GATT TATG GGTA TCCCTGC GT /
A C AGCCC CC AAAA

GAM948 AATCCAACCCTCTTTGTACA 1587 TTGCATAGTT 4657 CT-- A-- A- TT --- C C
AAATGCTTTTGGCAGTACAT GGCCACAATT AATCCAACCCT TTGT CAA ATGC TTGGCA
GTA ATTT T
TTCTAAGAGTTACTCATGCT TCAG |||||||||| |||| ||| |||| |||||| ||| ||||
AATTGCATAGTTGGCCACAA TTAGGTTGGga aaca gtt tacg AATCGT CAT TGAG A
TTTCAGGGTTGGATT cttt ccg ga tt ACT - A

GAM949 TGGGCATATGTTTTTATGCA 594 TAAGCCAAGT 3664 GC T T- CAA TT TT GT
GGTGTTTGCAATATATTTTG ATCTGTCTTG TGG ATATGTTT TA GCAGGTGTTTG TATAT TG
GGC G
TTGGCGTGTAGCCCTTATTG CAAA ||| |||||||| || |||||||||| ||||| || |||
TATAAGCCAAGTATCTGTCT ACC TGTATaaa gt tgtctatgaac atATG AT CCG /
TGCAAATATGTAACCA AA c tc cga TT TC AT

GAM950 TGGTCTGTGTTAAATCCCTT 1585 CCCTTCTATA 4655 T TAAATccc t t t
CTATATTATTATTGATGTAT TTATTATTGA TGGTCTG GT ttctata ta tat g
TGTTGTAGAAAACTATTACT TGTA ||||||| || ||||||| || |||
TAGACCA ACCAGAT CA AAGATGT GT atg a
T TTATCAA- T T t

GAM951 AAGTTTGGCCTTCCTGATCC 1588 TCTTTCTATA 4658 T -- A- tctttctataat ac aa TT
ATCTTTCTATAATCCTGACC ATCCTGACCA AAG TTGGCCTT CCTG TCCA cctg cagg
CGT G
AGGAACGTTTGGTATGGGCC GGAA ||| |||||||| |||| |||| |||| |||| |||
TGTGTAGGTTTGGAGGTAGG TTC AACTGGAG GGAT AGGT GGAT GTCC GTA /
CCGAGGTCAACCTT C CC GG TT---------- GT GG TG

GAM952 GCAGAAGGTAGCTCCCTCGA 595 GAAGGTAGCT 3665 t tc-- c c gtgACA
CTGGGTGACAAGAAGAAACC CCCTCGACTG GCAgaagg agc cct ga tgg A
ATTCAGGAAGTGCTTCCTTC GGTG |||||||| ||| ||| || |||
TGC CGTCTTCC TCG GGA CT ACC G
T TGAA - T AAAGAA

GAM953 GTTCGTGCGCCAGGCCTGCA 596 GTACATGGGC 3666 G G C------- C AC - GCT
AA
AGATCTCCAACGTGGAGCTG ATCTTGCACG GTTC TGC CCAGGC TGCAAGAT TCCA GTG
GA GACC C
ACCAACCTGGTCTCGTACAT AGAA |||| ||| |||||| |||||||| |||| ||| || ||||
GGGCATCTTGCACGAGAACC CAAG ACG GGTCCG acgttcta gggt cat CT CTGG /
GCCTGGGGCAGAAC - G CCaagagc c a- g --- TC

GAM954 AGATCTATTATGTCTGTTAT 602 TATTATGTCT 3672 Cta c tatt tcT- CACT
TTGAGATTCTTCATCACTAC GTTATTTGAG AGAT ttatgt tgt tgagat TCAT A
TTAATGGCATTATCTCGTCA ATTC |||| |||||| ||| |||||| ||||
CAATGTAACCAATCT TCTA AATGTA ACA GCTCTA GGTA /
ACC - CT-- TTAC ATTC

GAM955 GGAAGGAGTGTGGCTAATGC 603 TCAGTACAAT 3673 A T AA---- --- G
TGGTAAGGCACCTTTCTATC CAAGCCCATT GG AGGAGTG GGCT TGCTGGTA AG C

AGTACAATCAAGCCCATTCC CCTC || ||||||| |||| |||||||| ||
TCCC CC tccttac ccga atgactAT TC A
c - actaac CTT C

GAM956 GAGGTGTGTGGCTCAGCACG 604 TAATAGGACA 3674 - G- CA- C GTGAC
TAGAGTGACAAGTAAATCTA CAACACCTC GAGGTGT GTG CT GCA GTAGA A
CTGTAATAGGACACAACACC ||||||| ||| || ||| |||||
TC ctccaca cac ga tGT CATCT A
a ag taa - AAATG

GAM957 GGAATTGTATATTAGCCTTG 605 AATTGTATAT 3675 -- agccttg AG- TCTAG T A
CTAAGGGAGACATCTAGTGA TAGCCTTGCT GGaat tgtatatt ctaaggG ACA TGA
ATAAGTGTG A
TATAAGTGTGAACTACACTT AAGG ||||| |||||||| ||||||| ||| ||| |||||||||
ATCTTAAATGTTGTAACTCC CCTTA ACATATAA GATTCCT TGT ATT TATTCACAT /
TTAGGATAATCAATATACAA AA CTAATAG CAA TGTAA C C
AATTCC

GAM958 GCTGGGCTCGAGCATGACGG 1589 GAGCATGACG 4659 C - a c - acta a- G
CGACTACCTCCACCTGAGCG GCGACTACCT GCTGGGCT ga gc tga g gcg cctcc cCT A
GGGGGGAGGACGCGCTCATC CCAC |||||||| || || ||| | ||| ||||| |||
AAGCATCTGGCCCGGC CGGCCCGG CT CG ACT C CGC GGAGG GGG G
T A A A T GCA- GG C

GAM959 ACATCTGGGACAGTTCTGCC 597 GTGCAGGGGT 3667 - T TTCT-- G AC ATACG
GCTTGACCCATATACGTATT TCCATTCTGT AC ATC GGGACAG GCC CTTG CCAT T
TAATGGTGCAGGGGTTCCAT TCTG || ||| ||||||| ||| |||| ||||
TCTGTTCTGATCGT TG TAg tcttgtc tgg ggac gGTA /
C - ttacct - gt ATTTA

GAM960 CGGCTGGACGTTGGTCCGCA 606 AAGCCGTTGG 3676 A T G GC G - AA- C
GGCGGTCGCGGAGGAACCCC CGACCTTGAG CGGCTGG CGT GGTCC CAG GGTCGC GA GG
CC C
GGGAAGCCGTTGGCGACCTT GACC ||||||| ||| ||||| ||| |||||| || || ||
GAGGACCCGCGCCCGGTCG GCTGGCC GCG ccagg gtt ccagcg tt cc GG /
C C a -- g g gaa G

GAM961 GCTGAGGAGGCCGGAGTCGT 607 TGAAGCCCTC 3677 G- GA - - TGC A- GAAG
CGGCCTGCTCGTGCGGCACG GGGCCAGGCC GCTGAGGAG CCG GTCGTC GGCCTG CTCG
GGC CGCC A
CCGAAGACGAAGGTGAAGCC AGGC ||||||||| ||| |||||| |||||| |||| ||| ||||
CTCGGGCCAGGCCAGGCGAC CGGCTCCTC GGC CAGcgg ccggac gggc ccg gtGG /
AGCGGAACTCCTCGGC AA GA a c tc- aa AAGC

GAM962 GCTATTAAACAGTATGGAGA 598 TGAGAAACTT 3668 A ----- TG--- A TTAA- g ctta a t a

CATTGATCTATTATTTAATG AAAGTAGACT TGGA GACAT ATCT TTAT tga aaa aagtag c ccg T

AGAAACTTAAAGTAGACTCC CCGA |||| ||||| |||| |||| ||| ||| |||||| | |||

GATTCGGGACTATTTGACTT ATCT TTGTA TAGG AATG ACT TTT TTTATC G GGC /

TGTCAACTTTGTAAAGGATA - TAGTG TAGTA A TTTCA G CAG- A - T

TGATATGTTGTGATTCTAGA

ATAGTAGTAGC

GAM963 TTGAAACTCCGCCCCTTACT 599 TGAAATGTTT 3669 AC CGCCCCTT - AAAAA

TTTATTAAAAATCTTCAAGA ACAATAGAAA TTGAA TC AC TTTTATT T

TGAAATGTTTACAATAGAAA TTCG ||||| || || |||||||

TTCGA Agctt ag tg aaagtAG C

aa ataacatt t AACTT

GAM964 GCCGGTTAGTATGACTTACT 608 TAAGACACAG 3678 T-- GA TA-- A---------- TA

TGTATAATAAGTATAGTTTT AAATACTATA GCCGG TAGTAT CT CTTGTATA TAAG T

AAACTGATTTTAGCAGAATA TCCG ||||| |||||| || |||||||| ||||

TATAAGACACAGAAATACTA CGgcc atcata ga gaatATAT ATTT A

TATCCGGC tat aa caca AAGACGATTTTAGTCAA TG

GAM965 GTTGTTTTCATTGTTGATGG 600 TTGATGGTAA 3670 TG TT tt tg ---- t t A G T

TAAGGATTCTTATTTTGAAG GGATTCTTAT GT TT CATTG ga gtaagg attc tattt gA GT GTTTT C

TGGTTTTTCAGAAGATAACT TTTG || || ||||| || |||||| |||| ||||| || || |||||

CTAAATATGAATTATGCCTT CG AG GTAAC TT TATTCC TAAG ATAAA CT CA TAGAA A

ATTGTTTTCAATGTTGATGG GT TT TT GT GTAT T T - A G

C

GAM966 ATTGACTTCGAAGAAAGATG 601 TTACATGGAG 3671 TG TT AAA C - TT GATT TGG TAAG

CGTCTTTTGGATTTGTAATG GAACACATTA AT AC CGAAG GATG GT CTT G TGTAATGAC GCCT T

ACTGGGCCTTAAGTTCATAG CTTT || || ||||| |||| || ||| | |||||||| ||||

GTGTTATTACATGGAGGAAC TA TG Gtttc ttac ca gga t acattATTG TGGA /

ACATTACTTTGGTTGAT GT -- a-- a a gg ---- --- TACT

GAM967 GGGGCAAGCAATGATGTCTT 610 TGGCAAAAGT 3680 AG- GTC TTGGT T C A ATTT -- C

TTCGTTGGTCATTTTTTCCA GTTTCGAGAA CAATGAT TTTTCG CATTTTT CCA AT CGAATT GG TCAG A

CATACGAATTATTTGGTCAG ATTA ||||||| |||||| ||||||| ||| || |||||| || ||||

CACATTGAATCCTTCAAATT GTTatta aagagc gtgaaaa ggt TA GCTTAA CC AGTT C

CGATATGGCAAAAGTGTTTC AAA --- ttt-- c A - ACTT TA A

GAGAAATTATTGAAACGCCT

C

GAM968 GCGGAAGTGACGCAAGCGGA 611 AACCCGCCCA 3681 A-- A- CA-- C AA GA--- A A A- - A AGC GA

AGGGGAGGAGCAGGAAGGGG CTAACCCGCC GG AGTG CG AG GG GGG GG GC GG AG GGG GG AG C

AGGAGCAGGACCCACTAACC CACT || |||| || || || ||| || || || || ||| || ||

CGCCCACTAACCCGCCCACT CC TCAC GC TC CC CCC cc cg cc tc ccc cc TC C

AACCCGCCCACTAACCCGCC CAA CC CCAA A CG AAtca - c aa a g caa AC

CACTAACCCGC

GAM969 CCTGCCTTTCAGCAGCTGGT 609 CAGCAGCTGG 3679 CTTTca g -- a ggatc

TAGCAACGGGATCTTTGAAC TTAGCAACGG CCTGC gcagct gt tagca cg T

GTGTTACAATGAGCTGTGCA GATC ||||| |||||| || ||||| ||

GG GGACG TGTCGA TA ATTGT GC /

------ G AC - AAGTT

GAM970 GCCGCTCTTAGCACAAAATC 618 TAGCACAAAA 3688 CTtagcacaaaa aacaaatctA---- C

AAAAACAAATCTAGCCACCG TCAAAAACAA GCCGCT tcaaa GC A

CAGTCTGTAGAGACTTTTGA ATCT |||||| ||||| ||

GTTGAAAAAGTAAGCGGC CGGCGA AGTTT CG C

ATGAAAAAGTTG TCAGAGATGTCTGA C

GAM971 TTTCAATAACTCTCACTTTT 619 TCAATAACTC 3689 Tt tca---------- tt

TTGCTAGAGGCAGGCTCAAC TCACTTTTTT T caataactc cttt t

AATGTCTGGAGTTGTTGGGG GCTA | ||||||||| ||||

G GTTGTTGAG GAGa g

GG GTCTGTAACAACTCGGACG tc

GAM972 AATGGTGCTATTAGAATTTA 612 TATTAGAATT 3682 T t agaa- aac-- t

CAAAACTGGTAATCCACATA TACAAAACTG AATGG GC att tttacaa tgg a

GTTGTAAAGTTAAAATTGTT GTAA ||||| || ||| ||||||| |||

CCGTT TTGCC TG TAA AAATGTT ACC a

T T AATTG GATAC T

GAM973 GTCGCTCATGCGGACAGTCA 613 TCTCTCACAG 3683 C ---- C CA ATTAA

AACATTCATTAACACGCAGG CATGATGAC GTCG TCATGC GGA AGT AACATTC C

ATGTTGCATTCTCTCACAGC |||| |||||| ||| ||| |||||||

ATGATGAC cagt agtacg tct tTA TTGTAGG /

- acac c CG ACGCA

GAM974 GCGTTCATATTAGACTACAA 614 TATTAGACTA 3684 - ---- acaaacct--- aATA

ACCTAATGATAATAACAAAA CAAACCTAAT GCGTTCA tatt agact aatgat A

ATCATTTATATTTTACAAGT GATA ||||||| |||| ||||| ||||||

TTTAACAATATTGAACGC CGCAAGT ATAA TTTGA TTACTA C

T CAAT ACATTTTATAT AAAA

GAM975 TTCGAATCGCCCCTTTTCCA 620 TCAAACCTTG 3690 CCCC-- C- AACA T AC
AAACATGTGAAGACCTTCTT ACAAAACCTA TTCGAATCG TTTT CAA TG GAAG C
CTCAAACCTTGACAAAACCT TTTG |||||||| |||| ||| || |||| /
ATTTGATTCGAG GAGCTTAgt aaaa gtt ac CTTC /
ttatcc ca ccaa t TT

GAM976 GCGAAATGTATTCAGATTCG 621 AATGTATTCA 3691 tcagattcgttt C---- - C AA TCA
TTTTCAGGTCCGAACGCCAC GATTCGTTTT GCGAaatgtat tcaggT CGA ACG CAC AC A
AAACTCAACAACGTAAGTGT CAGG |||||||||| |||||| ||| ||| ||| ||
CGTCTCGATTACGCCTGATT TGCTTTACATA AGTCCG GCT TGC GTG TG C
ATACATTTCGT TT---------- CATTA C T AA CAA

GAM977 TCGTCGAGATCGTGATTTGG 615 TCTGCAATTC 3685 G T T T G ATATAA TG A- ACT
AGAATATAACGTTGGAAGCA CGTGTCGATG TCGTCGA A CG GA TTG AGA CGT G AGC A
CTAACAGTTCCCTGGCGTCT A ||||||| | || || ||| ||| ||| | |||
GCAATTCCGTGTCGATGA agtagct t gc ct aac tct GCG C TTG /
g - - t g ------ GT CC ACA

GAM978 CGCGTTACCAACAATTGTGT 616 AATTGTGTGA 3686 ACCAACaa ---- c ac
GATCTCGTTACTGAAATCGG TCTCGTTACT CGCGTT ttgtgt gatct gtt t
ATTTAAAGCGCAAATATCAA GAAA |||||| |||||| ||||| |||
ACGTG GTGCAA AACGCG TTAGG Taa /
ACTATA-- AAAT C ag

GAM979 TGCATATTTGGACGCTCATC 617 TCCATGAATC 3687 TTGGACGCTCAt t ctac tga AAT
CATGAATCTACGAAGCTTGA TACGAAGCTT TGCATAT cca gaat gaagct ttAT C
TTATAATCCCCAGTAGATGG GATT ||||||| ||| |||| |||||| |||| /
CTTCCAAATTCCTGGCTAAC ACGTATA GGT CTTA CTTCGG GATG C
TATTACTATATGCA TCATTATCAATC C AAC- TA- ACC

GAM980 CGTAAATGCAGGGGTTAATC 622 AGGGAGCGCG 3692 TAATC G G CA Ca ggaa---- ag
g TGAA
GGGCGGATGGGGACCAGCGC GAAGGAGTCC GGGCG ATG GGAC GCG gggagcgc gg
tcct ctC A
AGGGAGCGCGGAAGGAGTCC TGCT ||||| ||| |||| ||| |||||||| || |||| |||
TGCTCTGAAAAAAATGAGGG TTCGC TAC CTTG CGC CCCTTGCG CC AGGG
GAG A
GGAACCGTGAGAAAGCGTTC TTC-- - G A- -- AAAGAGTG A- G TAAA
CCCGCAGTTCGCATCGCTTC
TTGCCCCCCG
GAM981 TGAGAGATTCCTCTGTGTGT 623 TACCATAAAA 3693 TTCC - TTTTt ---- tt tcCCATT
AT
TTTTTACCATAAAAAGAGTT AGAGTTATTA A TC TGTGTGT accataaaaaga gtta agt
TGAG T

ATTAGTTCCCATTTGAGATT GTTC | || ||||||| |||||||||||| |||| ||| |||| TACTTATTTTACTCTTAACT T AG ATACATA TGGTGTTTTTCT CAAT TCA ATTC /

TCTTCTTTTTGTGGTTTACC TC-- T CCATT TCTT TC TTTT--- AT ATACATATGACTTTTTTCA

GAM982 GGGAGAGAAATACCGACGGC 626 TCACGCCAAC 3696 AATACC GCC- ACA AATTATTA CGGACAGAGCGAATTATTAA ACGTCCCACC GGGAGAGA GACG GG GAGCG A GCACCCAACGCTCACGCCAA TCTT |||||||| |||| || ||||| CACGTCCCACCTCTTTCCC CCCTttct ctgc cc ctCGC / ccacc- acaa gca AACCCACG

GAM983 ATGAAGTTAATGATACACAC 624 TTAATGATAC 3694 t ata c ac gAATT TATACTGTCGAATTTGATAG ACACTATACT ATGAAGt aatg ca actat tgtc T GGACAAAGTAGTTGACACGT GTCG ||||||| |||| || ||||| |||| TTATTTCGT TGCTTTA TTGC GT TGATG ACAG G T ACA - AA GGATA

GAM984 CGCTCCCGCGGCCCCGCCCC 625 CCGCGGCCCC 3695 Ccc- c- a cc C CGCCGCC ACC CCACGCCCGCCGCGCGCGCG GCCCCCCACG CGCT gcggccc gcccccc cg cgC GCGCGCGCGCA CGG G CACGCCGCCCGGACCGCCGC CCCG |||| ||||||| ||||||| || ||| |||||||||| ||| CCGCCTTTTTTGCGCGCGCG GTGG CGTCGGG CGGGGGG GC GCG CGCGCGCGCGT GCC C CGCGCCCGCGGGGGGCCCGG ACAC CC C CC - TTTTTCC CGC GCTGCCACAGGTG

GAM985 GCCCCTCGCCCCCTCCCGCC 634 CCTCGCCCCC 3704 CCCTC CCCCTCCC CCCTC CCC CCTCGCCCCCTCCCGCCCCT TCCCGCCCCT GC GC GC GC C CGCCCCCTCCCGCCCCTCGC CGC || || || || cg cg cg CG T ctccc ccctcccc ctccC CCC

GAM986 GCATATGGAACGGTACTGGA 627 TATGGAACGG 3697 a ac a g---- a T TGTAGAACACTTGTGTGTCT TACTGGATGT GCAt tgga ggt ctg atgtaga CAC T ATATGATAACAGAGCTTCCA AGAA |||| |||| ||| ||| ||||||| ||| ATGC CGTA ACCT TCG GAC TATATCT GTG G - -- A AATAG - T

GAM987 TTCGGCATTTACTTCTAATA 642 TCTAATATAA 3712 G- CT-- aa aa - aaa c C TAAGGACGTTAAATACTCCA GGACGTTAAA TTC GCATTTA tct tat gg acgtt ta tCCAAATG A AATGCATTTATTTGGAATAC TACT ||| ||||||| ||| ||| || ||||| || |||||||| GAGCGTACCGAGTAGCGGAC AAG CGTAGAT AGG ATG CC TGCGA AT AGGTTTAT T TTTTAGATGCGAGAA AG TTTC CG AG A GC- A T

GAM988 TAGAAATATATTTTTGTTCA 628 TTCAGGTATA 3698 T TT ttc atc aaatg AAA T
A
GGTATATCAACAAATGTATA TCAACAAATG GAAA ATATT TG aggtat aac tataTGATGG ATA
ATATTT A
TGATGGAAAATATATATTTA TATA |||| ||||| || |||||| ||| |||||||||| ||| ||||||
AAAAAATATTTATACCATCA CTTT TATAA AT TTCGTA TTG ATATACTACC TAT
TATAAA A
TATAATATAGTTAAATGCTT - TT TT- AA- ATATA A-- T A
TTTATTAATATTTTCTA

GAM989 GTTGGGAAGTGCATGTTAAT 629 CTCCTGTTAC 3699 - T A T G - CTA
GAGGACACTATCTTTGCTCC TAGCTCTTCG GTTGG GAAG GC TG TAAT AGGA CA T
TGTTACTAGCTCTTCGCCGG CCGG ||||| |||| || || |||| |||| ||
C Cggcc cttc cg at attg tcct GT /
g t - c - c TTC

GAM990 CATATGGTATTTTATCGGTA 630 TATTTTATCG 3700 - t atataaatct AC- TA CA A
TATAAATCTAATAAACTATG GTATATAAAT CATATGG tatttta cggt aaTAA TATGTG
TTTTTTA GC T
TGTATTTTTTACAGCATTTG CTAA ||||||| ||||||| |||| ||||| |||||| ||||||| ||
CCATAGGAAAATCATATATA GTATATC ATAAAAT GTTA TTATT ATATAC AAAGGAT
CG T
ATTATTTCTTCCATTGTTAA T T CCTTCT---- AAT TA AC T
AATATCTATATG

GAM991 TATAAAATCGTAATACTAGT 631 ATTCTGGTGT 3701 TCG- TAT---- ATA
ATATCATAATGAGATTTTAA TAATATTTTT TATAAAA TAATACTAG ATC A
TTCTGGTGTTAATATTTTTA ATA ||||||| ||||||||| |||
TA atatttt attgtggtc TAG /
tata ttaATTT AGT

GAM992 GCCGCGCCTGACTAGAGTAC 635 TACTACTAGG 3705 - ACTA- A ACTATAAA
ACACTATAAATTCCATTCCG CGCTGGC GCC GCGCCTG GAGT CAC T
GTGACTTACTACTAGGCGCT ||| ||||||| |||| |||
GGC cgg cgcggat tTCA GTG T
t catca - GCCTTACC

GAM993 CAGTCTTTTGTCCAATAGTG 632 TCTTTTGTCC 3702 g gt---------- aa
TCGAATAAGCGTTCTATTTC AATAGTGTCG CAGtctttt tccaatagt cg t
TAGTAGTGCTATTGGAAAAA AATA ||||||||| ||||||||| ||
GACTG GTCAGAAAA AGGTTATCG GC a
- TGATGATCTTTATCTT GA

GAM994 AATTCACCACGCCCGGGAGA 633 TTTTATGGGT 3703 TT -- G TCG- C C-- AG

TTTCGAAATTGCTATTTCCG GTTCGGTGTT AA CACC ACGCCCG GAGATT AAATTG TATTTC
GTGC T
TGCAGTTCCGCATTCCGAAG TT || |||| ||||||| |||||| |||||| |||||| ||||
TACAATTTAACCGGTTTTAT tt gtgg tgtgggt ttttGG TTTAAC ATGAAG TACG T
GGGTGTTCGGTGTTTT tt ct a CCAA - CCT CC

GAM995 GCGGTTTTCGGTCTCTCCTC 636 AAGCTGCAGA 3706 TT-- CCTC---- G ATGAC G
ACTCGGCAGATGACTTCGGA GTTCGTCTCC GCGGT TCGGTCTCT ACTC GCAG TTC G
AGAGAAGCTGCAGAGTTCGT GGAG ||||| ||||||||| |||| |||| ||| |||
CTCCGGAGACCGGCCTCGCC CGCCG GGCCAgagg tgag cgtc GAG A
GC CTCC cctctgct a gaa-- A

GAM996 GCGCTGGTCCCCATCCGCCC 637 TCCCCATCCG 3707 cccc - gatta ccct AT
GATTAACCCCTGCATTTACG CCCGATTAAC GCGCTGGt atccgc cc ac GC T
CCCCTGTAAGGAGCGGATCG CCCT |||||||| |||||| || || ||
CCAGTGC CGTGACCG TAGGCG GG TG CG T
C--- A AA--- TCCC CA

GAM997 TCTTAAAGCGGCCATCGTTC 638 TGGCATGGTG 3708 T GC TT---------- A
AGTACTTGCTGGCATGGTGA ACATGAGTGA TC TAAAGCG CATCG CAGT C
CATGAGTGATGATGCTTTAT TGAT || ||||||| ||||| ||||
GA AG ATTTCGt gtagt gtCG T
T a- gagtacagtggtacg T

GAM998 GCGTGTAATACGCTGGTGTC 639 TGGTGTCTCA 3709 Ctgg cattatata T
TCATTATATACTAGCGTTGC TTATATACTA GCGTGTAATACG tgtct ctagcgt G
AGCGCTAGGACTACCTAAGA GCGT |||||||||||| ||||| |||||||
CAACCGTATTATACGT TGCATATTATGC ACAGA GATCGCG C
CA-- ATCCATCAG A

GAM999 ACAGTAGTTTTCACGGTATT 640 TTAAATCGGG 3710 - CA G- --- A
TTTGAAATTAATAAATTTTA TAAATGGTAA ACAGTA GTTTT CG TATT TTTGAAATT A
AATCGGGTAAATGGTAAAGC AGCA |||||| ||||| || |||| |||||||||
ATGCTGT TGTCGT cgaaa gt atgg aaattTTAA T
a tg aa gct A

GAM1000 GTTATAATCCATAAGCTTTG 650 AAGCACTAGT 3720 GAAAG- GG----- - AAAAGG
-- TT
AAAGATCTGCTAGTGTGGAT AGGTAACTAA TAAGCTTT ATCTGCTAGTGT AT ACC
CTGTCG TGG C
ACCAAAAGGCTGTCGTGGTT GAGG |||||||| |||||||||||| || ||| |||||| |||
CGCCCAGTCGACGGATGAGG ATTCggag tggatgatcacg TA TGG GGCAGC ACC /
TCATAAACGAAGCACTAGTA aatcaa aaGCAAA C AGTA-- TG CG
GGTAACTAAGAGGCTTAGGG

ATGAAGCAAC
GAM1001 ATGATGTGTACTTGTGGCTT 641 TGTGTACTTG 3711 g --- t ctt t TA
AAATTTATTTTACTTAATTA TGGCTTAAAT ATGAt tgt act gtgg aaattta TT C
AATTTTATCGCAGTTTAATA TTAT ||||| ||| ||| |||| ||||||| ||
AATCAT TACTA ATA TGA CGCT TTTAAAT AA /
A ATT - AT- T TT

GAM1002 TCATCCCGGCGCGCCCGACA 651 GCGCTCGGCG 3721 C C CATCCC ATCA
TCCCTGCGCGATCAGCTAGC CGCCGAGATG TCATC CGGCGCGCC GA TGCGCG G
GCGCGCTCGGCGCGCCGAGA A ||||| ||||||||| || ||||||
TGA agtag gccgcgcgg ct gcgCGC /
a - c----- GATC

GAM1003 GTAATGAATCGCACAGAATT 657 TCGCACAGAA 3727 ------ aat C CTC-- C T
ATTG A
ATGGACATCGATACCGTCTC TTATGGACAT acag tatggacatcgatAC GT GAAT TT
GCTGTGT TG A
GAATCTTTGCTGTGTATTGT CGAT |||| |||||||||||||| || |||| || ||||||| ||
GAATTCAAAAACACGGTTGA TGTC ATATTTGTAGTTGTG CA CTTA AG TGGCACA
AC T
ATTCTATTTACGTGTTGATG CAAAAT --- - TTTAT - T AAA- T
TTTATACTGTTAAAACATGC
GAAGCATTAT
GAM1004 GCGCACAATTGCCTGTAGTA 643 AGCGTGAATC 3713 CAAT T AGTag gaatc ga ag
GCGTGAATCCCGAGAGTCAG CCGAGAGTCA GCGCA TGCC GT cgt ccga gtc g
GAGGACGTTGGTAGCGAAGA GGAG ||||| |||| || ||| |||| |||
TCGGCATGCGT TGCGT ACGG TA GCG GGTT CAG /
---- C GAA-- AT--- G- ga

GAM1005 TTGTTTGCTCATCTCATATT 644 TGGAAAACCG 3714 T T CT - cg- c c- tcatCC- C
TGGAAAACCGGAACGTCAGC GAACGTCAGC TTGTT GC CAT CATATTt ggaaaac gaa gt agc
GA C
TCATCCGACCCGTCACTATA TCAT ||||| || ||| ||||||| ||||||| ||| || ||| ||
TGTTCAACTTCAAAGTTTTC GACAG TG GTA GTATAAA TCTTTTG CTT CA TTG CT
C
TGAAATATGCATGGTCGACA C - C- G AAA - AC TATATCA G
G

GAM1006 ACTTGGTTACTAAATACCCT 645 TTAGTCCATT 3715 T --- ACC T
AATGGAACTGAGTTCTATTA CGATAGTAAT AC TGGTTACTA AAT CTAATGGAAC G
GTCCATTCGATAGTAATCAT CATG || ||||||||| ||| ||||||||||
GT Tg actaatgat tta gattATCTTG /
t agc cct A

GAM1007 TATTATTTTTGTACCGGATT 646 TGAGATAGGA 3716 A - GG CG- G TTTTCGGG
A

CGCTTGTCTTGTGTTCTTTT CAGGAAAAGT TATT TTTTTGTA CC ATT CTTGTCTTGT TTC GTCGGG G

CGGGGTCGGGAGAGTTCGAC AAGG |||| |||||||| || ||| |||||||||| ||| ||||||

AGTTTATGAGATAGGACAGG ATAA GAAAATAT gg tga ggacaggata gag CAGCTT A

AAAAGTAAGGATATAAAAGA A A aa aaa - tATTTGA- G

AATA

GAM1008 TTCTTCGGATACGCCGTTTT 658 ACGCCGTTTT 3728 GATa ttta cgtcgctt A - GA

ACTCGCCGTCGCTTGGCAAC ACTCGCCGTC TTCTTCG cgccgt ctcgc GGCA CGC CT A

GCCTGAAGAAAGAGCGTGCC GCTT ||||||| |||||| ||||| |||| ||| ||

GCGAGCCTACGGCGCTATGA AAGAAGT GCGGCA GAGCG CCGT GCG GA G

AGAA ATC- TCC- -------- - A AA

GAM1009 CTGATATCATAATGAAGACA 647 TATCATAATG 3717 t ------ a - C CAC T

TTTTAGAGCACCACATCGTC AAGACATTTT CTGAtatca aatgaa gac tttta gag AC ATCGTC A

TATTGACGGTTGTCTCATGA AGAG ||||||||| |||||| ||| ||||| ||| || ||||||

AACGTCGAATTGTTCGTTTG GGCTGTAGT TTGCTT CTG AAAGT CTC TG TGGCAG T

ATGTCGG - GTTAAG C A - T-- T

GAM1010 TTTTTACGTTGGGATGCTCG 648 TACGTTGGGA 3718 ggga tcgtcg- T

TCGATGTCTGTGACATAACA TGCTCGTCGA TTTTtacgtt tgc atgtc G

ATTGCAGTAAAATGTAGGAG TGTC |||||||||| ||| |||||

GAGGATGTAA ACG TACAG /

AATG TTAACAA T

GAM1011 CTCCTGTAGCCCCCAGTAAA 649 TAAATGGATT 3719 - - CC C ta attt g a

TGGATTTCAGGGAGGGACCG TCAGGGAGGG CTCCT GT AG CC AG aatgg cag gaggg c

TCCTTGCTGTCATTCTCTTG ACCG ||||| || || || || ||||| ||| |||||

GACTAACGAGGAG GAGGA CA TC GG TC TTACT GTC TTCCT c

G A A- T TC ---- G g

GAM1012 GTGGGTCCATTCTTAATGGT 659 TATGTCCCAC 3729 - T- TAAT TG A-- C AAGA AATTA CA

GGAGAGCAGCTTGGAAGAGG ATCAGGTTCT GTGG GTCCAT CT GG G GAG AGCTTGG GGA TGC T

AAATTATGCCATTTCGCAAT CAGA |||| |||||| || || | ||| ||||||| ||| |||

ATGTCCCACATCAGGTTCTC CACC CAGGTA GG CC C ctc ttggact cct ACG T

AGACTGCCCCCTGGTCATGG T CT TCCC GT aga - acac gtatA CT

ACTCCAC

GAM1013 GTAGAACACGTGGGATAGGG 652 TGGCAAGGCG 3722 CAC AG-- A A ----------

TT

GATGACCTTGTCGACCGTTT CCCATTGGTT GTAGAA GTGGGAT GGG TG CCTTGTC

GACCG T

GTCGGTCCCCTGCTCCTTAG CTAC |||||| ||||||| ||| || ||||||| |||||

AGCTGGCAAGGCGCCCATTG CATCTT catcttg ccc gc ggaacgg CTGGC /

GTTCTACATTTCTAC TA- gtta - - tCGAGATTCCTCGTCCC TG

GAM1014 CGGTACGCCTGCCTGATGGC 653 TAGGGCTGCT 3723 C GC AT TGA GG G
TTGATAGTAGGGCTGCTGGG GGGCTGCTAG CGGTA GCCT CTG GGCT TAGTAG CTGCTGG
C
CTGCTAGTAGGGCTGCTGGG TAGG ||||| |||| ||| |||| |||||| |||||||
CTGCTAGTAGGGCTGCTG GTCGT CGgg gat tcgg gtcgtc gatGATC T
- at cg --- gg G

GAM1015 AGTAGGCCTGCTTGCTCGCT 665 TGGCTTGCTA 3735 G T TC TG CT - AG
GGCCTGCTTGCTGAGGGGAC GTAGGGCTGC AGTAG CCTGCT GC GC GC GCT TGCTG G
AGTAGGGCTGCTGGCTTGCT T ||||| |||||| || || || ||| |||||
AGTAGGGCTGCT tcgtc ggatga cg cg CG CGG ATGAC G
g t tt gt T- G AG

GAM1016 GGCCTGCTTGCTTGCTCGCT 666 TCGCTGGCCT 3736 T TT TT tc t t tt tt tc T T TT TT
TC TG
GGCCTGCTTGCTTGCTCGCT GCTTGCTTGC C GC GC GC gc ggcc gc gc gc gc GGCC GC
GC GC GC G
GGCCTGCTTGCTTGCTCGCT TCGC | || || || || |||| || || || || |||| || || || ||
GGCCTGCTTGCTTGCTCGCT G CG CG CG CG CG CCGG CG CG CG CG CCGG CG CG
CG CG CG C
GGCCTGCTTGCTTGCTCGCT T CT TT TT T T CT TT TT T T CT TT TT TC
GGCCTGCTTGCTTGCTCGCT
GGCC
GAM1017 CTAGTAGGGCTGCTGGGCTG 667 TGCTAGTAGG 3737 -- T- TG -- gct t t- G
CTAGTAGGGCTGCTGGGCTG GCTGCTGGGC CTAGTAG GGC GC GGCt gctagtagg gc gggc
gctAGTAGG C
CTAGTAGGGCTGCCTGCTGG TGCT ||||||| ||| || |||| ||||||||| || |||| |||||||||
CTTGCTTGCTTGCTTGCTAG GATCATC CCG CG CCGG TGATCGTTC CG TTCG
CGGTCGTCC T
TGGGGCCGCTTGCCTGCTAC GT TT -- GG GTT - TT G
TAG

GAM1018 GGCAGCGTCATACCATGTCG 668 TACTGTTTGG 3738 - CATA TGT T- TT AC
CCTGCTTGTGGCACTGAGCT CGTTTTGGGG GG CAGCGT CCA CGCC GC GTGGC T
ACTGTTTGGCGTTTTGGGGG GCAC || |||||| ||| |||| || |||||
CACGCTGACC CC GTCGca ggt gcgg tg catCG /
A cggg ttt tt t- AG

GAM1019 GTGGAGATCCAGTGCGGGCC 654 CGGTCAGTCC 3724 G GTGC CT GA A
TTGGACGGTAAAAGCCGGTC TTTGTGGATC GTG AGATCCA GGGC TG CGGT A
AGTCCTTTGTGGATCTGCAC TGCA ||| ||||||| |||| || ||||
Cac tctaggt cctg ac gcCG A
g gttt -- tg A

GAM1020 AATACCACTGACATACTCGT 655 CCACTGACAT 3725 c c- c at- aG- TT
AATCGTCAGTGTATTTCTTT ACTCGTAATC AATAc actga atact gta cgtc TGTA T
ACGACGGACGTAATATCAGT GTCA ||||| ||||| ||||| ||| |||| ||||
ATTTTCGGTTGTATT TTATG TGGCT TATGA TAT GCAG GCAT C
T TT C AAT GCA TT

GAM1021 GTTGTCTAAAACCTACACGT 656 TGCCACGGGA 3726 T A TACA AAT C AC
GGAATGACGATTCACAAAGA TTTAGCAAT GTTG CTAAA CC CGTGG GA GATTC A
GTCTCTGCCACGGGATTTAG |||| ||||| || ||||| || |||||
CAAT taac gattt gg gcacc CT CTGAG /
- a ---- gt- - AA

GAM1022 TAAATGTTAGGTTTGCTGGA 660 TTGCATGGTG 3730 TAGGTT A TTTAA T---
AG TAA
GATAAGTTTAAAGGCATTAT TTTACTTTCT TAAATGT TGCTGGAG TAAG AGGCATTATGT
CGA C T
GTTCGAAGCTAATACCTGTC TAAC ||||||| |||||||| |||| |||||||||| ||| |
TTGTCTTGCATGGTGTTTAC GTTTACA ATGATTTc attc tttgtggtacg GTT G A
TTTCTTAACTTTAGTAACAT ------ a tttca ttCT CT TCC
TTG

GAM1023 AAACTGTTCATATTGTGAGC 661 TTCATATTGT 3731 - ----- tgtga - a
CACAGTAGACATTGTTGGCC GAGCCACAGT AAAC TGt tcatat gcca cagt g
TGTATGTGATCATAACATGT AGAC |||| ||| |||||| |||| ||||
TT TTTG ACA AGTGTA CGGT GTTA a
T ATACT TGTC- T c

GAM1024 CATTATGCTGGAACCTGAAG 669 TGTAAGGTTA 3739 - GG- GAA TT G TGTGT G
TGTTTTCTAGAGTGTGTTTA TAAGATATAA CATTATG CT AACCT GTG TTCTA AG
TTAAATG G
AATGGGGTATTTGATTTATC TG ||||||| || ||||| ||| ||||| || |||||||
TGTGGAATTATGTAAGGTTA gtaatat ga ttgga tAT AAGGT TC AGTTTAT /
TAAGATATAATG a ata atg T- G TATTT G

GAM1025 GACAGTGTGAGTGTGGTAGC 670 TAACTGAGGA 3740 T T A AG A T AA - CC GT
AGTCATCTAGAACTTCGTCC GCTGAGAAGT GACAG GTGAG GTGGT GC TC TC AG CTTC GT
CATT G
CATTGTGCTAAATGTAACTG GACC ||||| ||||| ||||| || || || || |||| || ||||
AGGAGCTGAGAAGTGACCAC CTGTC CATTC CAcca tg ag ag tc ggag ca GTAA C
CTTACCCTGTC C - g a- - - ga t at AT

GAM1026 ATATTAAATAATTTTCTAGC 673 GCGAATAGAG 3743 ATAA aa-- a
GAATAGAGAAATTAAATCGT AAATTAAATC ATATTAA TTTTCTAgcg tagagaaattaa t
TAGTTTTTCTAGACGCGTTA GTTA ||||||| |||||||||| ||||||||||

GAAAAAGGATTAATGT TGTAATT AAAAGATTGC ATCTTTTTGatt c
AGGA GCAG g

GAM1027 GTCTTTTATGGCTGGTAAGT 662 TTTCAGCGTG 3732 TTTT AAG CAT GC
GCTGACATCAGGCCCCCTGT GCCAGCCATC GTC ATGGCTGGT TGCTGA CAG C
TTCAGCGTGGCCAGCCATCG GCTG ||| ||||||||| |||||| |||
CTGAC CAg taccgaccg gcgact GTC /
tcgc gt- tt- CC

GAM1028 GTGGCACGTCACCATCAAAA 674 CTTGATATAA 3744 ACGT ----- AAACATT AAC
ACATTGCCCAACAACACGGG AGGTGGCCAT GTGGC CACC ATCAA GCCC A
CTTGATATAAAGGTGGCCAT ||||| |||| ||||| ||||
taccg gtgg tagtt cGGG A
---- aaata ------- CAC

GAM1029 GAATATCGCAGTTATCAAGG 663 TATCGCAGTT 3733 tatc gttatc tta C T
TTAGTTATACCTGTTTATAC ATCAAGGTTA GAA gca aaggttag TA CTGT T
AGTTAACCCTAATCTTTGCT GTTA ||| ||| |||||||| || ||||
TTTC CTT CGT TTCTAATC AT GACA A
TT-- ------ CCA T T

GAM1030 GATGATGATTTATGAATTGA 664 TGATGATTTA 3734 tg tt-------- att-- g - C
TTCCGGAAGATCGCTATCGT TGAATTGATT GA atgat atgaattg ccg AAGAT CG T
ATTTTGTGGTTCCACAATTC CCGG || ||||| |||||||| ||| ||||| ||
ATTTCCATACATGTTATTGT CT TATTG TACTTAAC GGT TTTTA GC A
C GT TACATACCTT ACCTT G T T

GAM1031 TTGATTTTGCATGGTTGTAG 671 TGGAAGCTTG 3741 T A TTT TG TTTAATAATAT
tgggg g agtg
CTTTTTTGGTTTTAATAATA GGGGCAGGTC GGT GT GC TT GT ATGTGtggaagct gcag
tc T
TATGTGTGGAAGCTTGGGGG AGTG ||| || || || || |||||||||||| |||| ||
CAGGTCAGTGTAAGAGGCTG CTA CA CG AG CG TACGTATCTTTGA TGTC GG
/
TAGTTTCTATGCATGCTGGA - A TT- GT ---------- ----- - AGAA
TTGCAACATCAGGCAGGACC
AA
GAM1032 AGCCGCTGAGTGGTAAACAA 675 CCGCTGAGTG 3745 c ----- caaca- AG
CAGAACAGATAGTTTATTAT GTAAACAACA AGc gctgag tggtaaa gaac A
CTTTACCAACACCCTCAGCC GAAC ||| |||||| ||||||| ||||
GCT TCG CGACTC ACCATTT TTTG /
C CCACA CTATTA AT

GAM1033 TATAAATAATCTGATCTTTT 672 TAAATAATCT 3742 aat ga ttttc - AA

TTCATGTTCAAAAAAATGAA GATCTTTTTT TAtaaat ct tctt atgTT CA A
ACATATAAGAAAAGTAATTT CATG ||||||| || |||| ||||| ||
ATA ATATTTA GA AGAA TACAA GT A
AT- AA TA--- A AA

GAM1034 TCACGCCTACCAATAAGACA 676 TAAGACAAGC 3746 CC CCAAta ag c tt t
AGCCCTATATTTACTTGTTG CCTATATTTA TCACG TA agaca cc tatat ac t
CATTTTACTCGTCAGAAGAA CTTG ||||| || ||||| || ||||| ||
ATCACAGAGT TGAGA CT GACTG CA TTTTA GT g
CA AAAGAA CT - C- T

GAM1035 GCACATACAATTAACTTTTT 677 TATAAAAACT 3747 A AA C TTC --- TT
TTCATCACCTTTAAGGTTAA TAGGTATGGT GC CATAC TTAA TTTTT ATC ACC T
GATATAAAAACTTAGGTATG || ||||| |||| ||||| ||| |||
GT tg gtatg gatt aaaaa tAG TGG /
- -- c ta- AAT AA

GAM1036 AAATATATGTCTTAAAATAT 678 TCAATATTAT 3748 CT----- AA- c t-- - tg TTT
CAATATTATGATATAAATAT GATATAAATA AAATATATGT TA ATAt aatatta gatataa ata aaG
T
GAAGTTTTTTCGTTTTGTAT TGAA |||||||||| || |||| ||||||| ||||||| ||| |||
ATTATATCTTTTAATATTCA TTTATATACA AT TATA TTATAAT CTATATT TAT TTT T
TATCAGTATCTATAAACATA AATATCT GAC C TTT A GT GCT
TATTT

GAM1037 GCGGCCGGTCATTCGAGTGA 679 TCTCGTCGGC 3749 G AT G AT A AG
ATTCATTTTCCAGGGCGGAG GGACGGGTCG GCGGCC GTC TCGA TGA TC TTTTCC G
AAGATCTCGTCGGCGGACGG T |||||| ||| |||| ||| || ||||||
GTCGT tgctgg cag ggct gct AG AAGAGG /
g gc - ct - CG

GAM1038 ATTAATTTTAATATCTTTTT 680 TTTCAAATTC 3750 T TTTTC TA---------- AT
CTGATAAATAAATATATAAC AGATTTAAAA ATTAATTTTAA ATCT TGA AATAAATAT A
ATATTTATTAAATATTCTTT TTAA |||||||||| |||| ||| |||||||||
CATTTCAAATTCAGATTTAA Taattaaaatt taga act TTATTTATA /
AATTAAT - cttaa ttACTTTCTTATAAA CA

GAM1039 TCTCGCGATCGAAGGTCGGC 682 AGGAGTCGGC 3752 G GAAG-- G G G- G
GCGTGGGCCTGCGACGCAGG GGCGACGATG TCTCGC ATC GTCG CGC TGG CCTGC A
AGTCGGCGGCGACGATGGAG GAGA |||||| ||| |||| ||| ||| |||||
ATGGCGAGA AGAGCG Tag cagc gcg gct ggaCG /
G aggtag g - ga C

GAM1040 CTAGGACGGATTCTGTCGCT 681 TCTGTCGCTT 3751 C Ttc-- -- -- tttt

TCTTCGCCCGTTTTGGTCCT CTTCGCCCGT CTAGGA GGA tg tcgcttcttc gcccg g
GGGCTGGGAGAGGCGAGTCA TTTG |||||| ||| || |||||||||| |||||
AACCTTCCCTCTTGG GGTTCT CCT AC AGCGGAGAGG CGGGT /
C TCCAA TG GT CCTG

GAM1041 GAGGTGTGTGGCTCAACACG 683 TAATAGGACA 3753 - G- CA- C GTGAC
TAGGGTGACAAGAAAATCTA CAACACCTC GAGGTGT GTG CT ACA GTAGG A
CTGTAATAGGACACAACACC ||||||| ||| || ||| |||||
TC ctccaca cac ga tGT CATCT A
a ag taa - AAAAG

GAM1042 TGTCCACCGGACGAGTGGCG 684 CCAGCACCAG 3754 ---- AC- - C - AG
CGGCGAAGACGTCGCCAGCA CTTCTGTCGG TGTC CACCGG GAG TGG GC GGCGA A
CCAGCTTCTGTCGGTGTCAT TGTC |||| |||||| ||| ||| || |||||
GACA ACAG gtggct ttc acc cg ccGCT /
TAct gtc g a a GC

GAM1043 GTATTATCGTCCCGTTCCCA 685 AGGAGTATGC 3755 A C C------ Aag atg gt t c
GAAGGAGTATGCGTCGTTGG GTCGTTGGGT GT TTATCGTCC GTT CCAG gagt c cgt gggt
g
GTCGGAGCCCATGGTGGCAC CGGA || ||||||||| ||| |||| |||| | ||| ||||
TCACTGGCATTCTAAACAGG CG AATAGCAGG CAA GGTC CTCA G GTA CCCG g
ACGATAAAGC A A ATCTTAC A-- CG- TG - a

GAM1044 GGTCATGTCGGCCGAATCAT 689 TCTGCCGGCC 3759 C GTC AAT TCT ATC A GCAA-
--- A
CTATAGCATCATGGATCGCA AAAATACC GGT AT GGCCG CA ATAGC ATGG TC
TGAGA T
ATGAGAATTTTTTAGAAAAC ||| || ||||| || ||||| |||| || |||||
AAGACCATTAGCTATCTGCC cca ta ccggc gt tATCG TACC AG ATTTT /
GGCCAAAATACC - aaa c-- c-- AT- - AACAAAAG T

GAM1045 TCTCTAATTTTTGCCGGGTT 690 TGCCGGGTTA 3760 TT---------- gg a gacac- T
TAAAAATA
AAAACATAGACACAAAAGAC AAACATAGAC tgcc gttaaa cata aaAAGACAG ATAA
G
AGTATAATAAAAATAGAACA ACAA |||| |||||| |||| ||||||||| ||||
CCATTTTATTTTGTCTTTTT ATGG CAATTT GTGT TTTTCTGTT TATT A
TCCAATGTGTTTAACAAGGT CTATCCCGCTTCT AA - AACCTT T TTACCACA
ATCTTCGCCCTATCAGTTTG
AGA
GAM1046 TATTAGCTATGCTCACTAAA 686 ACTTCATTAA 3756 T T - T tc at ct attt TT
CTTCATTAATCAAGCTTAAT TCAAGCTTAA TAT AGC ATGCT CAC AAact atta caag ta tTTTAT
G
TTTTTTATTTGTTATAAAAT TTTT ||| ||| ||||| ||| ||||| |||| |||| || ||||||

ATATACTTGTAGTAGTTTGT GTG TTG TATGA GTG TTTGA TGAT GTTC AT AAAATA /
GCAGTATGTTTGTG T - C - -- -- AT AT-- TT

GAM1047 AGTTTACTATTTAGCTACAA 687 CAAGTTTCTT 3757 CTAT- tt
GTTTCTTAAAAACAATATTT AAAAACAATA AGTTTA TTAGCTAcaagtttcttaaaaacaatat t
TGTATATTGTTTTTAAGAAA TTTT |||||| ||||||||||||||||||||||||||
CTTGTAGCTAGTTTTTTGAA TCAAGT GATCGATGTTCAAAGAATTTTTGTTATA /
CT TTTTT TG

GAM1048 CTTTATTACTTAAATTTTGT 688 GAGCATTGCT 3758 TT T TT AAT TACAAA TA
TTAAATAGCTACAAATTTAT TTATAAACAA CTTTA ACT AAA TTGTTTA AGC TTTAT A
TAAGCATAGAGCATTGCTTT TTTT ||||| ||| ||| ||||||| ||| ||||| |||||
ATAAACAATTTTTAGTTTTA GAGAT TGA Ttt aacaaat tcg agATA /
GAG TT - tt att ttacg- CG

GAM1049 AACAAAGAAATGGAAATCGT 691 TATGTTCAAC 3761 AG T---------- A
AATACCAGTTATGTTCAACT TTTGAAATTG AACAA AAATGGAAA CGTAAT C
TTGAAATTGTTTTTTATTTT TTTT ||||| ||||||||| ||||||
CTTGTT TTGTT TTTATTttt gtatTG C
CT tgttaaagtttcaactt A

GAM1050 AGTTGTCGCAACAGGGTAGC 692 TATATTGTAC 3762 CAAC AGC-- GTAAACTT C
AGAC GT
TCGTAAACTTTAATGTATAA CAAAGATTTA AGTTGTCG AGGGT TC TAATGTATAA AG
ATCT A
CAGAGACATCTGTAAAAAGA AATC |||||||| ||||| || |||||||||| || ||||
TAAACTTTATATATTGTACC TCGATAGT TCcta ag gttatatATT TC TAGA A
AAAGATTTAAATCCTAATTT TTAA aattt aaaccat- - AAA- AA
GATAGCT

GAM1051 TGCAACCCCCTGATTTTGCA 693 CCCCTGATTT 3763 C tg ca a- gA GAAG
GTTCACCCAGAAGGGAAGAC TGCAGTTCAC TGCAA cccc attttg gttc ccca AGG A
AAGCCTCTTGGGACGGACCT CCAG ||||| |||| |||||| |||| |||| |||
AAGATATGGGGATTGCG GCGTT GGGG TAGAAT CAGG GGGT TCC /
A TA C- CA TC GAAC

GAM1052 CGTGTGTATATTATTTTTTT 694 TGTATATTAT 3764 tg-------- G GCG - ---------- G T
GT
TTTTTGTGTGTGTTTGCGCC TTTTTTTTTT tttttt tgT TGTTT CC CC CGTGT TC AAT G
CCCGTGTGTCTAATGTGCTG TGTG ||||||| ||| ||||| || || ||||| || |||
TTTGAAACACGTAAAGTAGC AAAAAAA ATA ACAAG GG GG GCACA AG TTG
/
TGGTGGAAGAACAGATAAAC TAATTTCCAA G AA- T TCGATGAAAT A T TC
CTTTAATAAAAAAAAAAGTA
TGTGCTCCCG

GAM1053 GTCCAGGCTAAACGACCGCC 695 TCTAGAACAA 3765 A TAAA---------- G TTtcta caaaa ga ag
TTTTCTAGAACAAAAAGGAG AAAGGAGGAA GTCC GGC CGACC CCT gaa ag gga a
GAAGAACATCCAACTGATTT GAAC |||| ||| ||||| ||| ||| || ||| TCATCTGGGGGGTCGGCATC CAGG CCG GCTGG GGG CTT TC CCT a TATAGTAAAAATGCCAGGAC A TAAAAATGATATCTACG G TCTA-- TTAG- AA Ac

GAM1054 GTTGATGCACATGGTAGACT 696 TTGCGCACGC 3766 CA CT CTG--- C AACA TG C
GTGTGTCTGTGTCATTCAAC TTTTTACCGT GTTGATG CATGGTAGA GTGTGT TGT ATTC G CTTTG G
AGTGCTTTGCGACGAAGTGT GGAC ||||||| ||||||||| |||||| ||| |||| | ||||| GGGAATAATAAATTGCGCAC TAGCTGc gtgccattt cgcacg ATA TAAG T GAAGC / GCTTTTTACCGTGGACGTCG ag tt cgttAA A GG-- GT A AT

GAM1055 GGCATTACCTCTGTACTCAA 701 TTTGATGTTT 3771 - -- C TGTA- A GTCAGT
CGTGTCAGTTTCTATAAACG AATCGCC GGC ATT AC TC CTCA CGT T ATGAGGATTTGATGTTTAAT ||| ||| || || |||| ||| CGCC ccg taa tg ag GAGT GCA T c tt t tttAG A AATATC

GAM1056 TAATTTGTTACTAATTTCTT 55 TTTGTTACTA 3125 t -- atcc TTAGA GT
TATCCACATATTCGTTAGAA ATTTCTTTAT TAAt tgttac taatttcttt acATATTCG ATT C TTGTCATGAGTGAATTCGAA CCAC |||| |||||| |||||||||| ||||||||| ||| TGTGTAAGGAGGTTGCTGTA ATTG ACAATG GTTGGAGGAA TGTGTAAGC TGA A ACACGTTA C TC ---- TTAAG GT

GAM1057 AAGTGATCACAGCCTGAGAA 697 AGGAGGCCAC 3767 - C-- GAAa a aagg--- g CCC
AGGAGGCCACAGCGAAGGCC AGCGAAGGCC AAGTGATCA CAGC TGA ggaggcc cagcg ccgc tGC G
GCGTGCCCCGAGCTGCAAGT GCGT ||||||||| |||| ||| ||||||| ||||| |||| ||| GGAGAAGGATGCTGGGCCTT TTTATTGGT GTTG ATT CTTCCGG GTCGT GGTG ACG A
CAGGATTAAATGTTGTTGGT T TAA AGGA - AGGAAGA A TCG TATTT

GAM1058 GTCTTGTTTGTAACATGGAT 698 TTAATATATT 3768 TTGTT C ATA T- CT A TT TT- C
ATCATTAACTAGATTGTATA ATAATAGTTT GTC TGTAA ATGG TCA TAA AGATTGT TAT TATATT ATAT T
TTTTATATTTTATATCTTCA TCTT ||| ||||| |||| ||| ||| ||||||| ||| |||||| |||| TATCTTAATATATTATAATA CAG ATATT TATC AGT Gtt tttgata ata atataa TATA T GTTTTCTTGTTTGAGCCTAT TTACT - CG- TT ct - tt ttC C TTATATCATTGAC

GAM1059 GTGGTAGCGGCACAGAATCT 699 CTACTGTCCC 3769 ---- C C AATCTTTCC T
TTCCAGGGCTTTAAAGTCCT ACTATATACC GTGGT AG GG ACAG AGGGCT T
ACTGTCCCACTATATACCAC AC ||||| || || |||| ||||||
cacca tc cc tgtc tcCTGA A
tata a c a-------- A

GAM1060 TGTTAAAAGAGGAATGAGTT 700 TGAGTTCTAG 3770 AAA-- G g g - t- a
CTAGCAAGCTCTAAATAAAT CAAGCTCTAA TGTT AGA GAAt agttcta caag ctc aaat a
ATTTCTGAGACTTGGTGGAA ATAA |||| ||| |||| ||||||| |||| ||| ||||
CTGGTTTGTCTATGTGAACA ACAA TCT TTTG TCAAGGT GTTC GAG TTTA A
GTGTA G G G A TC T

GAM1061 TCCAGGAGGACAGCGCCTCA 702 TGTCCAGGAC 3772 - A C-- AGC GA C AAAG
CC
GCGAGGACCTGCGCAGAAAG TCATCGGGGT TCCAGG AGG CAG GCCTC GAG CCTG GCAG
ATG C
ATGCCCTCCATAGTTGTCCA TCAT |||||| ||| ||| ||||| ||| |||| |||| |||
GGACTCATCGGGGTTCATTG AGGTCC TCC GTt tgggg ctc ggac tgtT TAC /
CCTGCCTGGA G - act cta a- c GA-- CT

GAM1062 TATAGCTTATTATCTGTTTG 703 TAGCTTATTA 3773 t- gcta ATCAAATATAC A TA--
AGATTA
TGCTAATATAATATCAAATA TCTGTTTGTG tgt tgt aTATAAT TCTTGTT TCGT GTTGGG
A
TACTCTTGTTATCGTTAGTT CTAA ||| ||| ||||||| ||||||| |||| ||||||
GGGAGATTAATATTACATCC ACG GCA TATATTA AGAATAG AGCA TAACCT
T
AATATATACGAGATAAGACA TT AC-- C---------- - TATA ACATTA
TTATATCAACGTTGCACGCT
ATAAGCATTA
GAM1063 CGCTTATGTGTACAGTTTCC 704 TGTACAGTTT 3774 TT--- t -- ttcct- ac
TTAGTACCCTGCTATATAAT CCTTAGTACC CGC ATG gtaca gt tagt c
GCCATGTACTCATTTTACGC CTGC ||| ||| ||||| || ||||
G GCG TAC CATGT CG ATcg /
CATTT T AC TAATAT tc

GAM1064 GAATAGCGCCACATATGATA 705 TAATAACACT 3775 CACAT ATAATATATTGTA TCT - C
TAG TATCTT
TATAATATATTGTAGATATC TACGTTTTTA ATGATAT GATA GACG AA TGTT ATAAT
C
TGACGAACTGTTTAGATAAT TCGA ||||||| |||| |||| || |||| |||||
TATCTTCTTCTTTTATTATA TACTGTA ctat ttgc tt acaa tATTA T
ATAACACTTACGTTTTTATC ACT-- CAAATTCCTTAag tt- a c taa TTTTCT
GAATTCCTTAAACATGTCAT
TCAATGCTTC

GAM1065 ATTCTCACCCCAGGACTAAA 56 TCTCACCCCA 3126 - gactaaa ag C TCT
AGAGAGGCTGTCTCACTTAC GGACTAAAAG ATtctca ccccag ag agG TG C
CCTAGCTGTTTTACTGGGGT AGAG ||||||| |||||| || ||| ||
TGGGAAT TAAGGGT GGGGTC TC TCC AT /
T ATTTTG- GA C TCA

GAM1066 GTAGTTTCCATGGGACTATA 63 TTACTACATA 3133 CCA C T T CCTC A
TAATTTTGTGGCCTCGAATA GTTATCTATC GTAGTTT TGGGA TA ATAATT TGTGG GAAT C
CAAATTTTACTACATAGTTA TTAA ||||||| ||||| || |||||| ||||| ||||
TCTATCTTAAAGACTAT TATCAGA attct at tattga acatc tTTA A
a-- - c t at-- A

GAM1067 CACCGCCATGCTTCCCCTCT 64 ACAACGGGTT 3134 GCCAT T CTCT ACTC- CTCCT
CCCACTCTTGAAACTCCTTT GGGCAGCCCA CACC GCT CCC CCC TTGAAA T
CTCTTTTCAAACAACGGGTT AAGG |||| ||| ||| ||| ||||||
GGGCAGCCCAAAGGTG GTgg cga ggg ggg AACTTT /
aaacc c tt-- caaca TCTCT

GAM1068 GTCGAGTAAGGAATCAGTCT 706 AGTAAGGAAT 3776 agt atc t tgt gt A
GTTCTGGTCTATCTGGGTCA CAGTCTGTTC GTCG aagga ag c tctg CT T
GAGTCTTGTCCTTCCACGGC TGGT |||| ||||| || | |||| ||
CGGC TTCCT TC G AGAC GG C
ACC GT- T --- TG T

GAM1069 GTGGGAGGCGTACCTGTTGT 707 TGTTGTTAAG 3777 TACC - aa ---- gg ga
TAAGTACGAGGGAGGAGCTA TACGAGGGAG GTGGGAGGCG tgt tgtt gtacg ag ag g
CTTTCTAGAGTGTGCAGACA GAGC |||||||||| ||| |||| ||||| || ||
CACGTCATCGTCTTCCAC CACCTTCTGC GCA ACAG CGTGT TC TC c
TACT C A- GAGA TT AT

GAM1070 AGTGCGTTTGATAAAAGTTT 708 TGCGATGTTC 3778 TTGATAAA TG A TTC T- TTT-
TCTTTT
GGCAATGCTTCGCATGGTTT AGCTGCACGT AGTGCGT AGTT GCA TGC GCA GG GGT
C
GGTTCTTTTCCCTGTCTGCC ACT ||||||| |||| ||| ||| ||| || |||
TTTTCCTTTGCTGCGATGTT tcatgca tcga tgt gcg CGT CC CCG C
CAGCTGCACGTACT cg------ ct a t-- TT TTTT TCTGTC

GAM1071 GTTATGTTTCTTAACTTCTT 57 TTTCACACAC 3127 TTTCTTAACTTCTTC -- TCTT-- GG -
GTACC AAT
CAGGTAGAACGTCTTTGGGA TCGTCCTCTA TATG AGGTAGA ACG TG AC ATCC
GT A
CATCCGTACCGTAATACAAA CCTC |||| ||||||| ||| || || |||| ||
CCCGAAGGATCGTTTCACAC ATGC tccatct tgc ac tG TAGG CA /

ACTCGTCCTCTACCTCCCGT Cc---------- cc tcacac tt C AAGCC AAC
AAC

GAM1072 ATACCCGTGCATTTTACCCT 65 ACCCGTGCAT 3135 Ta tttac gttaaT- TGAAG
CGTTAATCATCTGAAGTTGT TTTACCCTCG A cccgtgcat cctc CATC T
GCGGTGTTCCATAGAGGATC TTAA | ||||||||| |||| ||||
GTGTGTACGGGCGT T GGGCATGTG GGAG GTGG /
GC TGCTA ATACCTT CGTGT

GAM1073 GGCCTCGGCGAAGGGGCGTT 66 TGCCCTTGAG 3136 - GA ---------- A
CCAGCATGACGGCATGCTGG CGTGGGGCC GGCCTCG GC AGGGGCGT TCCAGCATG
C
ACGAGGCGCGCGATGCCCTT ||||||| || |||||||| |||||||||
GAGCGTGGGGCC ccggggt cg ttcccgtA AGGTCGTAC G
g ag GCGCGCGGAGC G

GAM1074 TCCGGCGCGCCAACGCGAAG 709 CACCGCGCTT 3779 C - C TA C
CGCGGCGTCTAGCCCCGGGC GCGCTTGGCG TCCGGCGCGCCAA GCG AAGCGCGG GTC
GCC C
CCGGCACCGCGCTTGCGCTT CGCC |||||||||||| ||| |||||||| ||| |||
GGCGCGCCGGG GGGccgcgcggtt cgc ttcgcgcc cGG CGG /
- g a CC G

GAM1075 TCTATTTTTAAACTATTTTT 58 TGTGAAAAAT 3128 TTT TCTTATTT TA CACCt--
aaatcg t ta
AATTTTCTTATTTAATATAT CGAAATCGTT TATT AATTT AATATAT GC gtgaa aaa cgt
a
TAGCCACCTGTGAAAAATCG AAGA |||| ||||| ||||||| || ||||| ||| |||
AAATCGTTAAGACACGCTTT ATAA TTAAA TTATATG TG TACTT TTT GCA g
AATCGGTTCATTAAATACGT T-- TTCT---- TA CATAAAT GGCTAA C Ca
ATGTATATTTCTTAAATTTA
ATAGTTATAGG
GAM1076 AGTTCGTATATTTTTATATA 59 TTTGTAAAAA 3129 ---------- A T ACA
TAACAATGATATTTGTAAAA AATAAACTTA AGTTCG TAT TTTTTATA ATA A
AAATAAACTTAACATATTGA ACAT |||||| ||| |||||||| |||
ACT TCAAGT ata aaaaatgt tAT /
TAtacaattcaa a t AGT

GAM1077 ATGAAAATCTTGCTAATGGG 60 TTCCTCTATC 3130 TCTT ---------- A
AATATAATTATATTTCCTCT GTATAAATAA ATGAAAA GCTAAT GGGAATAT A
ATCGTATAAATAATTAGCTC TTAG ||||||| |||||| ||||||||
TTTTTTCAT TACTTTT Cgatta ccttTATA T
TTCT ataaatatgctatct T

GAM1078 GTCCTTCGCGGACGCCTCGG 61 GTGGAGGTGG 3131 C GA G GC- G

CCGCCTGCGGGTACCAGGGG TCATGAGGGA GTCCTTCG G CGCCTC GCCGCCT GG T
GTGGTGGAGGTGGTCATGAG C |||||||| | |||||| ||||||| ||
GGAC cagggagt c gtggag tgGTGGG CC /
a tg g GGA A

GAM1079 ATAAAAATATTTTTGTAAAA 62 GAAGAGAGAA 3132 AAAA--- A GA
CTTTTTTATGAGACCATCGA AGAGAATAAA ATAAAAATATTTTTGT CTTTTTT TGA C
AGAGAGAAAGAGAATAAAAA AATA |||||||||||||||| ||||||| |||
TATTTTTGT TGTTTTTataaaaata gagagaa gCT /
agagaaa - AC

GAM1080 ATTGCCCATGCACAAACGAT 67 TAAGTTTTTT 3137 C--- CAA GA tctc---- cc
AAGTTTTTTCTCATCTCCCT CTCATCTCCC ATTGCC ATGCA AC taagttttt atct c
TAAGATTATTATATAAAAAT TTAA |||||| ||||| || ||||||||| ||||
TTAGGTATTGTATACTCGGC TGACGG TATGT TG ATTTAAAAA TAGa t
AGT CTCA TA- G- TATATTAT at

GAM1081 CTGCACCCCGGGCTCGTGTA 68 CACCGGGCCG 3138 C----- GC- CCG - C AAC
CCGCCTGCTGAACCCCACCG ACCTGCAG CTGCA CCCGG TCGTGTA CC TG TG C
CCACGGACCTACGCGAACAC ||||| ||||| ||||||| || || ||
CGGGCCGACCTGCAG gacgt gggcc AGCGCAT GG AC GC C
ccagcc acA CCA C C CAC

GAM1082 GAGAAAGAGAATAAAAATAT 69 AATATTTTTG 3139 AGA- aaaa--- - A
TTTTGTAAAACTTTTTTTAT TAAAACTTTT GAGAAAG ATAAAaatatttttgt ctttttta TG G
GAGACCATTGAAGAGAGAAA TTTA ||||||| |||||||||||||||| ||||||||| ||
GAGAATAAAAATATTTTTGT TTTTTTC TGTTTTTATAAAAATA GAGAGAAGT AC A
AAAACTTTTTT AAAA AGAGAAA T C

GAM1083 GAGAATAAAAATATTTTTGT 70 AATATTTTTG 3140 - aaaa--- - A
AAAACTTTTTTTATGAGACC TAAAACTTTT GAG AATAAAaatatttttgt ctttttta TG G
ATTGAAGAGAGAAAGAGAAT TTTA ||| |||||||||||||||| ||||||||| ||
AAAAATATTTTTGTTACTC CTC TTGTTTTTATAAAAATA GAGAGAAGT AC A
A AGAGAAA T C

GAM1084 GAGAATAAAATATTTTACGA 71 TGAGACCATT 3141 AA- CGA CA-- AGAAA - A T
CTCCATCAGAAAGAGGTTTA GAAGAGAGAA GAG TAAAATATTTTA CTC TC GA GGTTT
ATA T
ATATTTTTGTGAGACCATTG AGAG ||| |||||||||||| ||| || || ||||| |||
AAGAGAGAAAGAGAATAAAA CTC ATTTTATAAAAT gag ag tt ccaga tGT T
TATTTTACGACTC AGC AA- aaag agaag a g T

GAM1085 TTTTTCTTAGTACAAAAGTC 72 TGTGAAATTT 3142 A- G- AT--- AAAA G

AATGTTTTAAAATATATGGA TGTACCAAAG TTTTTCTT GTACAAAA TCA GTTTT
TATATGGACAA A
CAAGAATTTGTCTGTATAAA AAAA |||||||| |||||||| ||| ||||| ||||||||||
AACTTGTGTGAAATTTTGTA Aaaaagaa catgtttt agt CAAAA ATATGTCTGTT A
CCAAAGAAAAA ac aa gtGTT ---- T

GAM1086 GTGGGGCGACCTGCTCTTCT 73 CGACGAGCGA 3143 G C T T TCT -- C - A
CGCCGCCCGTCGCGACGACG CGCGCCCGGC GT GGG GACC GC CT CGC CGC CGTCG CG
C
ACGACGAGCGACGCGCCCGG GCGG || ||| |||| || || ||| ||| ||||| ||
CGCGGTCCCCGAC CA CCC CTgg cg gg gcg gcg gcagc GC G
G - - c ccc ca a A A

GAM1087 GAAAGAGAATAAAAATATTT 74 TAAAAATATT 3144 AA AA- tgtaaaa-- - A
TTGTAAAACTTTTTTTATGA TTTGTAAAAC GA GAG taaaaatatttt ctttTTTA TG G
GACCATTGAAGAGAGAAAGA TTTT || ||| |||||||||||| |||||||| ||
GAATAAAATATTTTTACGAC CT CTC ATTTTTATAAAA GAGAGAAGT AC A
TCCATC AC AGC TAAGAGAAA T C

GAM1088 GCGGGCTGCACGACCGGCTC 75 GAGCAGATGC 3145 - C AC A T AG G C C
GAGCTGCTGCACGGCAACCT GCCGGCGCAC GC GGG TGC G CCGGC CG CTGCT CA GG A
GGAGCAGATGCGCCGGCGCA CCAG || ||| ||| | ||||| || ||||| || ||
CCCAGC Cg ccc acg c ggccg gt gacga GT CC /
a - -- - c a- g - A

GAM1089 GAGTGTCTGGCCGAGGCCAA 76 CGCCCGGGCC 3146 G AGGCCAA AG C---- TC
TGAC C
GAAGTTCGTGCACGCGTCGG CGACGCCGAT GTGTCTG CCG GA TTCGTGCA
GCGTCGG GCCC GCGGC G
TCGCCCTGACGCGGCCGGAG CTGC ||||||| ||| || |||||||| ||||||| |||| |||||
CCGCCCGGGCCCGACGCCGA CGCAGAC GGC CT AAGCGcgt cgcagcc cggg
cgcCG G
TCTGCGCGAAATCCGGCAGA - ------- A- ctagc -- cc-- A
CGCTC

GAM1090 CTATACGTATCGTATAGATA 77 TCGTATAGAT 3147 A t a - g gta
GGGTCGAGTATCCCGTCGAT AGGGTCGAGT CT TACGTA cgt tagat ag gtcga t
GTTCGTCTAACGTACGTAAA ATCC || |||||| ||| ||||| || |||||
G GA ATGCAT GCA ATCTG TT TAGCT c
A - - C G GCc

GAM1091 CATTCGTCCTCCACGTCTCG 78 TTACGTGTCT 3148 - CTC- CT AGCCCCT
TAGCCCCTCTAACAAAAACG TGACGTAGTG CATT CGTC CACGT CGT C
TTACGTGTCTTGACGTAGTG |||| |||| ||||| |||
gtga gcag gtgca GCA T

t ttct tt AAAACAA

GAM1092 AAGGACCGACGCCGCGCGGA 79 CAGCCCTCCC 3149 CC - C ATC--- AC-- CCGTT
TCGGCACCGCGGCGCCGTTT ACCGCCGCGC AAGGA GACGC CG GCGG GGC
CGCGGCG T
ATATTCGCCGCGAACAGCCC GTTT ||||| ||||| || |||| ||| |||||||
TCCCACCGCCGCGCGTTTCC TTCCt ttgcg gc cgcc ccg GCGCCGC /
TT -- c - accctc acAA TTATA

GAM1093 GTATTAGGAAGAGATAATAT 80 TGGCAAATTT 3150 A GAGATAATATGAGA GGGA GA
GAGAGAATTGGGAATAGGAT AGAAGAAAAG GTATT GGAA GAATT ATAG T
TAATTATGGCAAATTTAGAA AAAA ||||| |||| ||||| |||| |||
GAAAAGAAAATTCCCAGTAC CATGA CCTT tttaa tATT T
C aaaagaaaagaaga acgg AA

GAM1094 TCGTCGCGGGAGACCGCGGA 81 TCGCGGGAGA 3151 g c aaa -- - G
AAACGACGGATGTGGCCACA CCGCGGAAAA TCGtcgcgg aga cgcgga cgac GGAT GT G
ATCCACGTCGATATTCGCGA CGAC ||||||||| ||| |||||| |||| |||| ||
TCTGCCGCGACGA AGCAGCGCC TCT GCGCTT GCTG CCTA CA C
G A ATA CA A C

GAM1095 GCTTCCGGGTACGTAGTAGG 82 TAGCTTACCT 3152 TACGT gct --- t G
TAGCTTACCTAGTACGGTAT AGTACGGTAT GCTTCCGGG AGTAGGta tacct agtacgg atgctg
G
GCTGGGGTAGCATTCCGTAC GCTG ||||||||| |||||||| ||||| ||||||| ||||||
TTCCGGGTATACCTACTTCC CGAAGGCCC TCATCCAT ATGGG TCATGCC TACGAT /
CGGAAGC T---- --- CCT T G

GAM1096 TATAGTTCAACAATGTGATG 83 AGGCAGTAAT 3153 CAA---- TGA G AAGAAAATAAAA
AG C
TGTGTCAAGAAAATAAAATG AAAAGGGGCA TATAGTT CAATG TGTGT TC TGCCT
TA A
CCTAGTACATTAAGAGGCAG TAGA ||||||| ||||| ||||| || ||||| ||
TAATAAAAGGGGCATAGACC ATATCAG GTTAC atacg gg acgga AT /
ATTGGCAAGTAGACTATA ATGAACG Cag g aaaataatg--- GA T

GAM1097 GAAACATGTAACAATATTAG 87 ATGAGCCATA 3157 A ACAA AGA - AGATG TTTACA
ATATAGGAGATGCATATTTT TAGACAATAT GAA CATGTA TATT TATA GG CATAT A
ACAATACCATTATATGAGCC ACAT ||| |||||| |||| |||| || |||||
ATATAGACAATATACATGCT TTT Gtacat ataa atat cc gtaTA T
TT C ---- cag a ga--- TTACCA

GAM1098 GAAAACCGGACCCGGAAGAT 88 TCGCCGGGCT 3158 CCG AGA A C TA A AGT

CGATACGTACGGACGAAAAG AACGGGGATC GAAAACCGGAC GA TCG TA G CGG CGAAA
G
TGCCCTTTCGCCGGGCTAAC ACCG ||||||||||| || ||| || | ||| |||||
GGGGATCACCGTCCGGTTTT CTTTTGGCCTg ct ggc at c gcc gctTT /
C cca agg a - gg - CCC

GAM1099 TAATGTATCAAAAATATCAA 84 TGTATCAAAA 3154 aaa tc cc GT
TATCCAATGTCCAATTAATG ATATCAATAT TAAtgtatca ata aatat aaT C
TTTTTATATCTGATATGTTA CCAA ||||||||||| ||| ||||| |||
ATTGTATAGT TAT TTGTA TTA /
CTA TT A- AC

GAM1100 AAGAAGTTAATATAGATAGT 85 AGTAAAGATA 3155 T GATa- a- tt ttat -- A
AAAGATATTTTTTTAGATTA TTTTTTTAGA AGAAGT AATATA gtaaag tattt ttaga
AGATTTTTTAT AC C
TAGATTTTTTATACACATGT TTAT |||||| |||||| |||||| ||||| ||||| |||||||||| ||
TAATAGAAGATCTTCTAACA TTTTTA TTATAT TATTTT ATAAA AATCT
TCTAGAAGATA TG A
AATAGGTTTTATGAAAATAT - AAAAG GG C- ---- AT T
ATTATTTTTT

GAM1101 AGGATGGAAGTTGAGTCCCT 86 TTAAGGGATT 3156 GAA- --- C A AATTTA
CAGTGTATCAATTTACAATG GGATAGCGAA AGGATG GTTG AGTCCCT AGTGT TC C
CAAGAAATATTAAGGGATTG ACAT |||||| |||| ||||||| ||||| ||
GATAGCGAAACATCCT TCCtac cgat ttaggga ttATA AG A
aaag agg a A AACGTA

GAM1102 ATGTTTTTATATCTAATGTC 95 TCTAATGTCC 3165 TTTT c gtcca - tttt C GT
CAATTAATGTTTTTATATCT AATTAATGTT ATGT ATAt taat atta atgt aTAT TAAT C
AATGTCCAATTAATGTTTTT TTTA |||| |||| |||| |||| |||| |||| ||||
ATATCTAATGTCCAATTAAT TATA TGTA ATTA TAAT TATA TGTA ATTA /
GTTTTTATAT TTTT - ACCTG C TTTT - AC

GAM1103 GTAAAAAAGGTTTCTATTTC 96 TTAGCATGTT 3166 A TTT T A- TA- C GAT
TATAGTAATGTTAACAAGTG CTAGAAGACA GTAAA AAGG CTAT TCT TAG ATGTTAA AAGT
A
ATAACAAATTTTTAGCATGT TAGT ||||| |||| |||| ||| ||| ||||||| ||||
TCTAGAAGACATAGTTTTTT CATTT TTTT gata aga atc tacgatt TTTA A
ATTTAC A Tt- c ag ttg - AAC

GAM1104 TAATGTATCAAAAATATCAA 97 TGTATCAAAA 3167 aaa tc c AC
TATCTAATACCCAATTAATG ATATCAATAT TAAtgtatca ata aatat taaT C
TTTTTATATCTGATATGTTA CTAA |||||||||| ||| ||||| ||||
ATTGTATAGT TAT TTGTA ATTA /
CTA TT - AC

GAM1105 TAATGTATCAAAAATATCAA 98 TCAATATCCA 3168 AAA tc ccaa tcca - TT ATC AAAT

TATCCAATGTCCAATTAATG ATGTCCAATT TCA ATA aatat tg atta atgTT TAT TGATATGTTA A

TTTTTATATCTGATATGTTA AATG ||| ||| ||||| || |||| ||||| ||| ||||||||||

AAATATCAATAATGTATCAA AGT TAT TTGTA AC TAAT TATAA ATA ACTATGTAAT /

AAATATCAATATCTAATACC CTA TT ACTA CCA- C CT AAA AACT

CAATCAATGTTTTTATATCT

GATATGTTA

GAM1106 TATGCATATGAATTTATGAG 102 CAATACAGGC 3172 A A GA-- AA--- ATGAAGAAG

AAGAAATTGGGATGAAGAAG TAGAATTATG TATGCAT TGA TTTATGA AG ATTGGG T

TTATAAAGAACCCAATACAG AAAT ||||||| ||| ||||||| || ||||||

GCTAGAATTATGAAATTAGT GTACGTG ATt aagtatt tc taacCC /

GCATG - a aaga ggaca AAGAAATAT

GAM1107 AGCCGTTTTCCCCCAACTCT 89 TCGCTGCTGG 3159 TT CCAAC --- ---- c cca atA C- T

CGCTGCTGGCGACCAACTTC CGACCAACTT G TTCCC TCtc gct gctgg ga acttca AGTA CGCA C

AATAAGTACCGCATCACTGC CAAT | ||||| |||| ||| ||||| || |||||| |||| ||||

GCTTACTGTGAAGTACTCAC T GAGGG AGAG CGA CGACC CT TGAAGT TCAT GCGT A

CAGCGTGTAGCTTCGAGACC GG TAACC CTT TGTG A CA- G-- TC C

AATGGGAGGGTGGCT

GAM1108 CTGTGGTGGGCGAGTTGTTT 90 AGTTGTTTAT 3160 ----- G a---- t- a c

ATACAGTACACGATTGTGCT ACAGTACACG CTGTGG TGG CG gttg ttat cagtaca g

GAGTGACCCAACCAAGACGG ATTG |||||| ||| || |||| |||| |||||||

CCAAAATTTCACAG GACACT ACC GC CAAC AGTG GTCGTgt a

TTAAA G AGAAC CC A t

GAM1109 GGTGCATTATAGTGCGGGGC 91 TATAGTGCGG 3161 G Ttat c gcac t g

ACGGTTGAAGGTGGCTTCAC GGCACGGTTG GGT CA agtg ggg ggt gaag T

CAAACCCACACTTATTGGAC AAGG ||| || |||| ||| ||| ||||

C CCA GT TCAC CCC CCA CTTC G

G TAT- A AAA- - G

GAM1110 GTCATACCCCAAGGGAGAAA 92 TAAAAAGCAT 3162 CATA A AGAA G- CAA AA A

ATTTGCACAATTAATATTAA GGAAAATTGG GT CCCC AGGG AATTT CA TT TATT A

TGGATAAAAAGCATGGAAAA AACC || |||| |||| ||||| || || ||||

TTGGAACCCTGGGGGGAAAG CG GGGG TCcc ttaaa gt aa atAG T

C AAAG G aagg ag acg aa G

GAM1111 ATGGTTCAGGTCCGCATAGG 99 GTTCAGGTCC 3169 a ---------- cag
TTCCCAGCAGAGGAACTTGT GCATAGGTTC ATGgttc ggtccgc ataggttcc C
TATTTGATACCGGGGCGGAC CCAG ||||||| ||||||| |||||||||
CGAACTAT TATCAAG CCAGGCG TGTTCAAGG /
\- GGGCCATAGTTTAT AGA

GAM1112 TCAAACAATGAATTTAGTAA 100 ATGAATTTAG 3170 AA- gaa ----- a g
CAGATAGTAGATATGCATTT TAACAGATAG TCA CAat tttagtaa cagat gta a
GAATTTTTATTAAGAAATTG TAGA ||| |||| ||||||||| ||||| |||
GGATGA AGT GTTA GAATTATT GTTTA CGT T
AGG AA- TTTAA - A

GAM1113 GTGACGAAGCAGCCTACCCC 93 AAGCAGCCTA 3163 Ga g - -- aa gt T GT --- -- TT
GAAGGTGGTTCGTGTGAGTG CCCCGAAGGT agca cct acc ccg ggtg tCGTG GA GCTCCCG CC GCGGT C
CTCCCGCCGCGGTTTCATAC GGTT |||| ||| ||| ||| |||| ||||| || ||||||| || |||||
CGTGAGGTCACGGGAGCTCC TCGT GGA TGG GGC TCAC AGCAC CT CGAGGGC GG TGCCA /
ACGAGTCACTACGGCTGGTA AG - A TC A- TG - -- ACT AG TA
AGGTGCTGACACAC

GAM1114 GGAAGTGTCATGGCGTCCAG 94 AACCCCGTTG 3164 CATG T - C CT TA ATAT
GGGCGTTCGTCTTTATGCAT GCGCGACGCG GGAAGTGT GCG CCAG GGG GTTCGT T TGC G
ATGAGCGGCGCGATCACGAA CTTC |||||||| ||| |||| ||| |||||| | |||
CCCCGTTGGCGCGACGCGCT Ccttcgcg cgc ggtt ccc caaGCA A GCG /
TCC cag- - g - CT GC GCGA

GAM1115 GTTCAGCCGCCTGGCCACGT 101 CAGCCGCCTG 3171 c - - tcct - G GCA
CCTGGTGCCTGCTGCAGAAC GCCACGTCCT GTT agccgcct ggcc acg ggtgC CT CT G
AAGGAGCGCGCCCTGTGGGC GGTG ||| |||||||| |||| ||| ||||| || ||
CGAGGCGGCTAAGC CGA TCGGCGGA CCGG TGT CCGCG GA GA A
A G G C--- C G ACA

GAM1116 GCTTCTTCGTGTGCCCGCCG 103 CCGTGCCCTG 3173 T CCCG TC G A---- T TC T C
CCCTCGGGCGCCACGGTGGT AGTACGGGCT GCT CTTCGTGTG CCGCCC GGGC CC CGG GG CGGC CGCG C
CCGGCTCGCGCCCGCGCGGC CGGG ||| ||||||||| |||||| |||| || ||| || |||| ||||
CGTGCCCTGAGTACGGGCTC CGG GAGGCACAT GGCggg ctcg gg gtc cc gccG GCGC C
GGGCGGAACTACACGGAGGG - CAA- -- - catga - gt - G
C

GAM1117 CAACCGCCTAGGTTCCGCCC 104 CTCTCTCGAC 3174 - A -------- CA- - AA

AGAGAAGCCAAATCGGCTCT GGCAAGTTCT CAACC GCCT GGTTCC GCC GAGA AGCC A
CTCGACGGCAAGTTCTTGGG TGGG |||||| |||| |||||| ||| |||| ||||
ACCGAGGCTGGTTG GTTGG CGGA CCAggg cgg ctct tcGG /
T G ttcttgaa cag c CT

GAM1118 TTTACAAAAACGTGATCGTG 105 ACGGACCGCG 3175 AAAAA- G A CGA GG
AGCACGT - AT- AA
ACCACGACCTGGGCGGGCAG TGCCCGTGGG CGTGATC TG CCA CCT GCGGGC
ACGCGG CC TAC A
CACGTACGCGGCCATTACAA CATG ||||||| || ||| ||| |||||| |||||| || |||
ACCAGTACACGGACCGCGTG GCACTAG GC Ggt ggg tgcccg tgcgcc gg ATG C
CCCGTGGGCATGGGCGAGAT GTCCAG A G ac- -- ------- a caC AC
CACGGACCTGGTGGA

GAM1119 GCTGCTGGCGACCCGGCTGA 106 CGAGCGCCGC 3176 CG - TGAC A - T
CGCAGCTCGCGCTTCGGCGG CGGAGTACCA GCTGCTGG AC CCGGC GC GCTCGC GC T
CGAGCGCCGCCGGAGTACCA GCAG |||||||| || ||||| || |||||| ||
GCAGC Cgacgacc tg ggccg cg cgagcG CG C
a- a c--- - G G

GAM1120 TCTTGGAAAGCTTACCCGCT 2996 AAGCTTACCC 6066 Aa accc t g ct TT
CTTGGCACTCCTTCTTCGGC GCTCTTGGCA TCTTGG agctt gc ctt gca cc C
TTGCGGAGGTAAGAGCTCCC CTCC |||||| ||||| || ||| ||| ||
CGGGG GGGGCC TCGAG TG GAG CGT GG T
CC AA-- - G TC CT

GAM1121 CGGGTGCCAATAATAAATTT 2997 TGCCAATAAT 6067 G c aattt gaaTCT
TGCGCGAATCTTATTTAAGT AAATTTTGCG CGG tgc aataata tgcgc T
GCACACCGTGTTATTTGCGG CGAA ||| ||| ||||||| |||||
CTG GTC GCG TTATTGT ACGTG /
G T GCCAC AATTTA

GAM1122 TTATTGATATTGGCAATTTA 107 TATGATATAT 3177 - TGG ATT-- -- T
CATTCAGATATATTTGAATA CTAATAA TTATT GATAT CA TACAT TCAGA A
TGTATTATATGATATATCTA ||||| ||||| || ||||| |||||
ATAA aataa ctata gt ATGTA AGTTT T
t ta- atATT TA A

GAM1123 TGTCTCCTATAGTACCCCTA 108 TAGTACCCCT 3178 TC--- A a ccta ta---- a C
AACTTTATAGAATCCGAGGA AAACTTTATA TGTC CT tagt cc aactt taga tC G
TCTGGACAAAGAGTTGGACT GAAT |||| || |||| || ||||| |||| ||
AAAGCGTACGACA ACAG GA ATCA GG TTGAG GTCT AG A
CATGC A - ---- AAACAG - G

GAM1124 CATGGGTAGTTTTCTGCGAG 109 GTTTTCTGCG 3179 G ttt ga ga gc TC
GGTGGGATCGGCGGCCTCCA AGGGTGGGAT CATG GTAg tctgc gggtgg tcg GGCC C
TGGCCACGACCGCCTCGGCA CGGC |||| |||| ||||| |||||| ||| ||||
GACTTGCGCATG GTAC CGTT AGACG TCCGCC AGC CCGG /
G C-- GC -- A- TA

GAM1125 GCTTCTCGACGGCAGACTCT 110 GGAGGAGAGT 3180 - G - TG
TTCTCCTCTGCTGTGAGGGG CTGCGTTGAC GCTTC TCGACG CAGACTCTT TCTCCTC C
AGGAGAGTCTGCGTTGACGG GGGG ||||| |||||| ||||||||| |||||||
GGC Cgggg agttgc gtctgagag aggGGAG T
c - g TG

GAM1126 ACTGGGTATAAAGAGTATAT 111 AAGAGTATAT 3181 ATAa- g a g ta
CTTTGGGTATAGATACAAAG CTTTGGGTAT ACTGGGT aga tat tctttg g t
AAATAGTCTGAAAGATTTAG AGAT ||||||| ||| ||| |||||| |
T TGATTTA TCT ATA AGAAAC t a
GAAAG G A A ag

GAM1127 TCTCTTGATGTCACATTTTG 112 TAAGGAAAAA 3182 TTG T - TACT A A CGTA- A
AA
GGTACTCGGAGATGAGTTCG AATGCAATTC TCTC ATG CAC ATTTTGGG CGGAG TG GTT
CC TATAG T
TACCATATAGAATAACTATA CGCC |||| ||| ||| |||||||| ||||| || ||| || |||||
AGGAAAAAAATGCAATTCCG AGAG TAC GTG TAAAATcc gcctt ac taa gg atATC /
CCTAAAATAGTGCATAGTGA TGA - A ---- a g aaaaa a AA
GA

GAM1128 CAAAGTCCATAACAGAGTTT 113 TGCACAAATG 3183 TAA--- G - - TT TA
TGTGTGTTTGCCATAGTTTT CTGTGGTGAT CAAAGTCCA CA AGT TTTGTGT GT GCCA G
GGTTGCTGCACAAATGCTGT TTGG ||||||||| || ||| ||||||| || ||||
GGTGATTTGGATTTTG GTTTTAggt gt tcg aaacacg CG TGGT T
ttagtg g t t T- TT

GAM1129 GAAAGGTCTTCCGACGTGGC 3000 AAGGTCTTCC 6070 tctt t aa ct- TGGA
AAGTCTGGACTACGTGGACA GACGTGGCAA GAaagg ccgacg ggc gt GGACTACG C
GAGTCGTAGTCCCCCACGAG GTCT |||||| |||||| ||| || ||||||||
CTTGTCGGCCTTTT TTTTCC GGCTGT TCG CA CCTGATGC A
---- - AG CCC TGAG

GAM1130 CGGGGGGGTCCCCCGTTGGG 2998 ATGCATCTTA 6068 T- CC G- G GA GCG
CAGGGAGAGGGCGCTGACGA TCAATTGCCC CGGGGGGGG CC CGTTGG CA GGA GG C
TGCATCTTATCAATTGCCCC CGTA |||||||| || |||||| || ||| ||
GTAGGGA AGGGatgc cg ttaact tc acg GC /
cc -- at t ta AGT

GAM1131 GAAGTCGTTGGAGATGCGGC 3001 CGTTCATGCC 6071 --- AG-- GG G GC
CCATGAGCTGCGAGAAGGCG CGCCTCGTTC GAAGTC GTTGG ATGC CCCATGA CT G
TTCATGCCCGCCTCGTTCCA CAGA |||||| ||||| |||| ||||||| ||
GACGCGG GGCGCa cttgc cccg acttgcG GA A
gac tccg t- - AG

GAM1132 CCTGCGTCGCCGGCGGCGCA 3006 CTCGATGGTC 6076 G G GGCGC - G CGA
CGGGCAGACGGTCGATGAAG TCGCCGCGCC CCT CGTCGCCG C ACG GGCA ACGGT T
CGCTCGATGGTCTCGCCGCG GGCG ||| |||||||| | ||| |||| |||||
CCGGCGT Tgc gccgcgcc g ctc ggta ctcGC G
g - ----- t g GAA

GAM1133 AGAAGAATCGCCAGGGTTGC 3007 CAGGGTTGCG 6077 GAA c cgtt -- gc
GTTGCGGTGTGCCCCGGTTC TTGCGGTGTG AGAA TCGC agggttg gc ggtgt c
GAGGCCGGCCGGATTCCGCG CCCC |||| |||| ||||||| || |||||
GCTAA AATC GCCT TAGGCCG GG CTTGG /
GGC - GCC- AG cc

GAM1134 GGAGTGTGACAACATATTAT 2999 TTATTGGAAA 6069 - ------- ATAT---------- TC
CATTTATTATTGGAAACAAA CAAAGTTGTC GGAG TGT GACAAC TA A
GTTGTCTCTGAGTACATCTC TCTG |||| ||| |||||| ||
C CCTC ACA ctgttg AT /
T TGAgtct aaacaaaggttatt TT

GAM1135 GGGCTTTATTCATAAACAAT 3002 ACTTACTTAA 6072 T TAAACAATAAA TAC CTG
AAAAGGTGTACTGACCCTGA AACACTTGAA GGGCT TATTCA AGGTG TGACC A
ATTTGGTCACTTACTTAAAA TATA ||||| |||||| ||||| |||||
CACTTGAATATAGCCT TCCGa ataagt ttcat aCTGG A
t tcacaaaa--- tc- TTT

GAM1136 CCACTGATGTCTCGTGCGAG 3010 ACTGATGTCT 6080 ct ct - - GG C
GGCTTGGGGGCCTGGGTACC CGTGCGAGGG CCa gatgt cgtgcgaggg ct tgGG C T
CGCAGCCCCTTGCGCGCGCA CTTG ||| ||||| |||||||||| || |||| |
TCTGG GGT CTACG GCGCGTTCCC GA GCCC G G
-- C- C C AT G

GAM1137 CTGTGTCCAAAGTTTTAAGT 3003 TCCAAAGTTT 6073 G a ttta ac----- AT
ACGGACCGCTATGTCCAGCG TAAGTACGGA CTGT tcca agt agtacgg cgcT G
TACCAACCTGTACTATTATG CCGC |||| |||| ||| ||||||| ||||
GAGGCAG GACG AGGT TTA TCATGTC GCGA T
G A ---- CAACCAT CC

GAM1138 CCTCCTATTGGGGAGCACTG 3004 TATTGGGGAG 6074 a --- - - - g
GGCCAAGGGTACTGTGTGCT CACTGGGCCA CCTCCt ttgggg agcactgg gc ca ag g
CTAGTGTTGTGCCTCAGCAG AGGG |||||| |||||| |||||||| || || ||
GGGG GGGGGA GACTCC TTGTGATC CG GT TC T
C GTG T T G A

GAM1139 AATGGTATTTGTTGGTTTAA 3005 TTTGTTGGTT 6075 ttt - atg---------- tgt
TGAGTTGTTTGTTACTGTGG TAATGAGTTG AATGGTA gttggt tta agt t
TGGATACCACCCGTAGTACC TTTG ||||||| |||||| ||| |||
AACCTTACCATT TTACCAT CAACCA GAT TCA t
TC- T GCCCACCATAGGTGGTG TTg

GAM1140 GCGTCCATTTTGAGTTCAGC 3011 GTCCATTTTG 6081 t tt tt c - TTTC
GACCGGTTTCGGTCTCCCGC AGTTCAGCGA GCg ccat tgag cag gac cgg G
GTTTTTGTTTTTGTTATGGC CCGG ||| |||| |||| ||| ||| |||
GC CGC GGTA GTTT GTT TTG GCC G
- TT TT T C CTCT

GAM1141 CGTGGCCAGCGCCCTCTATA 3008 TTCATTTTCA 6078 G-- - - - T AA TT TTAAT
AAAGATTTAGGATTAATATC GTTGACGGAG CGT GCCAG CGC CC TC AT AAGAT AGGA A
ATTTCCTTCATTTTCAGTTG CGAC ||| ||||| ||| || || || ||||| ||||
ACGGAGCGACTGGTAAAGCG GCG TGGTc gcg gg ag tg tttta tCCT /
AAA a a c t ac ct TTACT

GAM1142 TTACGATCCCGCGTCGTGGG 3012 TAGGATCTTT 6082 CGTG GGGT G A CAC - a
tt ccg ct
CCGGGGTCGGGGACTCTGCA CCCGGCCTCT CGT GGCCG CG GG CTCTG CTC CCTTt
ggatct c gcct a
CCTCCCTTTAGGATCTTTCC ACCA ||| ||||| || || ||||| ||| ||||| |||||| | ||||
CGGCCTCTACCAGGGCAAGG GTA TCGGC GC CC GGGAC GAG GGGGG CCTAGA
G CGGG c
GAGATCCGGGGGCGAGACCC ---- AT-- G - CCA C - GG AA- ac
AGGGCCGCGTACGGCTATGC
GGGCCCCGTGG
GAM1143 CCTCTCCGAATAATTGAAAC 3013 CTAGTTGTTT 6083 T ATT - AAT
ACTAGTAAATAAGGTACTAG CCCATATTTG CC CTCCGAATA GAAACA CTAGTA A
TTGTTTCCCATATTTGGAGT GAGT || ||||||||| |||||| ||||||
GG GG gaggtttat ctttgt gatcAT /
t acc t GGA

GAM1144 GGCGACGTGAGGGTGACGGA 3015 TTGCAAACAT 6085 - --- A--- GTAAAG
CGTAAAGTTTAACCAGTTTG CCTCAGTTCG GGCG ACG TGAGGGTG CGGAC T
CAAACATCCTCAGTTCGTGC TGCG |||| ||| |||||||| |||||
GCC CCgc tgc actcctac gttTG T
g ttg aaac ACCAAT

GAM1145 AAAATATTTCTTCGGTTTTA 3016 TGGGTAGGTT 6086 T TTT TCA TT TAGTTT A
ATCAGGCCTTTCTCTAGTTT GTTTGTTCTG AAAATATTTCT CGG TAA GGCCT CTC GTATA
A
GTATAAAGTTATATGGGTAG TGGA |||||||||| ||| ||| ||||| ||| |||||
GTTGTTTGTTCTGTGGAAAT TTTTATAAagg gtc gtt ttgga ggg tATAT G
ATTTT t tt- tg- t- ------ T

GAM1146 GAAGTTTTCCTGCTCTCGGT 3017 TGTCAAGGAT 6087 TTCC CTCG AAGT- - TG
CATA AT
AAGAAGTTCCTGGTGATGTT GTGGCTTGCA GAAGTT TGCT GTAAG TCCT GG
ATGTTAAA ACAAA A
AAACATAACAAAATAGTCTT AGCA |||||| |||| ||||| |||| || |||||||| |||||
TGTCTTTGACGTTGTCAAGG CTTTAG acga cgttc agga ct TGCAGTTT TGTTT G
ATGTGGCTTGCAAGCACGAT C--- a--- ggtgt a gt C--- CT
TTC

GAM1147 CCTCCAGAAGTTGTGTATCT 3009 AGTAAACGCG 6079 T AA- ----- Tag-- cg a --
cTAA
AGTAAACGCGATAATAGATA ATAATAGATA CC CCAG GT TGTGTATC taaa cg taatagat
agtg A
GTGCTAAACGAATTACTGAA GTGC || |||| || |||||||| |||| || |||||||| ||||
TCTATTACTGACTTTAATAT GG GGTC TA ATACATAG ATTT GT ATTATCTA TCAT
C
TGATACATACATTAATGACC T CAG ATTAC TTATA CA C AG TAAG
TGGTGG

GAM1148 GTTAAAATCTTTGCCAAGTC 2078 AAACATTAGC 5148 T C A CAA - A A C-- TTC CC
GAA C
CCAACACAAGGTCAATGATG CCTGATGCAC T G CA GTCC CACAAGG TCA TG TGGTT CATC
GGCT TG GG C
GTTCCATCTTCGGCTCCTGG GACT | | || |||| ||||||| ||| || ||||| |||| |||| || ||
AAGGCCTGCCAAACATTAGC A C GT CAGG GTGTTCC AGT GC Atcag gtag ccga ac
CC T
CCTGATGCACGACTACGTGA - T C CTC T - - cac tc- tt aaa G
TCCTTGTGCTCGGACCTGTC
AAGAAGTACC
GAM1149 CTGATGATCTGCGTTGACGA 2079 TGCGTTGACG 5149 - t tt cga caaa AG
CGGAAGTGTCAAAGACAAGA ACGGAAGTGT CTGA TGATC gcg ga cggaagtgt GACA A
TTCTGTCCTACATTTCCGAG CAAA |||| ||||| ||| || |||||||| ||||
TTCTCCGTCGGTCACTCAG GACT ACTGG TGC CT GCCTTTACA CTGT T
C C CT TGA TC-- CT

GAM1150 GCTTAAGGTTTCGCCCTTCC 3014 ATCAGCTTCT 6084 TT- - CTTCC TCCATAC CAC
GAGAATCCATACTCCATCAC CGGCGAGCAC GC AAGGT TTCGCC GAGAA TCCAT C
CCCAATGGATCAGCTTCTCG CTTT || ||||| |||||| ||||| |||||
GCGAGCACCTTTTCGC CG ttcca gagcgg ctctt aGGTA /

CTt c ----- cgact-- ACC

GAM1151 AGGTCAAGTACCTCACTGAA 3018 TACCTCACTG 6088 aag - C- C T TG GA
TTAC TA
GCGGGGATTGGCCTTACTGC AAGCGGGGAT cctcactg cggggattg gc TTACTGC G GA GCG
GGCGAG CG A
CGTGATGGCGGAGGCGAGTT TGGC |||||||| ||||||||| || ||||||| | || ||| |||||| ||
ACCGTAAGACGTTCTCGTCC GGAGTGAC GCTCCTAGT CG AGTGATG C CT TGC
CTGCTC GC /
ACGTTCTCCCGTAGTGACCG CCG G CC - C CT AC TT-- AG
CGTGATCCTCGGCCCAGTGA
GGCGCAGACCT
GAM1152 GAGTCGGCGACTCCCACGCC 3020 ATCGAGTACC 6090 GC - C- ta- cc ac
ATCGAGTACCCAACCTTACA CAACCTTACA GAGTCG GACT CCCA GCCatcgag cccaa tt a
AGAACATTGGGACTCTCGAT AGAA |||||| |||| |||| ||||||||| ||||| ||
GGCTCTGGGCAGTCAACGGC CTCGGC CTGA GGGT CGGTAGCTC GGGTT aa /
TC AA C CT TCA AC ga

GAM1153 GTATGTAATTTAAAAATGTG 2080 TTTCTTGGTG 5150 A A---- GA T ATAA
TGGATATTTGTATAAAAAAG AATAACATAC GTATGT ATTTA AAATGTGTG TAT TGT A
ACATATACATACATTTCTTG |||||| ||||| ||||||||| ||| |||
GTGAATAACATAC cataca taagt tttACATAC ATA ACA /
a ggttc -- T GAAA

GAM1154 TATCAAGATGTGTATGTTTG 2084 CAGCACAAAT 5154 - ---------- AAAA G
TGAAAATTGTGGAGACATAG CAAAGGTATT TATC AAGATGTGTAT GTTTGTG TTGTG A
CAGCACAAATCAAAGGTATT AATA |||| |||||||||| ||||||| |||||
AATACATGTCTTAGATG GTAG TTCTGTACata taaacac GATAC G
A attatggaaac gac- A

GAM1155 TTTTTAAAAAAGGCCACTTT 3019 GCCACTTTTT 6089 A- G ctttttttta- - A
TTTTTACAAAAGTGAAAAAA TTTACAAAAG TTTTTA AAAA gcca caaa agtgaa A
ACAATTTTTTCCACTCCAAA TGAA |||||| |||| |||| |||| ||||||
TATTTTAAAGAGGCCACTT TTCACC AGAA TTTT CTTT TTAACA A
GG A ATAAACCTCAC T A

GAM1156 TTTACAAATGAACTACATGT 3021 TGAACTACAT 6091 At a c tt tcaaa
TGTATTCTCAAATTGCCCGG GTTGTATTCT TTTACAA ga cta atg gtattc T
ATACTTGTATAGATCTATTG CAAA ||||||| || ||| ||| ||||||
TGAA AAGTGTT CT GAT TGT CATAGG /
AT A A T- CCCGT

GAM1157 CTAATTATTAATTAATAATT 3022 TAATTTAATA 6092 ATT Ata t tcc ta
TAATAGTTCCTAATTTATAT GTTCCTAATT CTAATT AATTA atttaa agt taattta T

ATATCTGGAAATGTATAATT TATA |||||| ||||| |||||| ||| |||||||
ATTTGGAATTTAGGAATTTA ATTTAA TTTAA TTATTA TAT AAGGTCT A
GGA GGT A GTA AT

GAM1158 AGATGTACAATTAATTGGAA 3023 TGTACAATTA 6093 g att- t---- TTTACA
TTTTGGAATTTACAATTTTA ATTGGAATTT AGAt taca aattggaat ttggaA A
TTAACTTTTTGTAATAAATT TGGA |||| |||| ||||||||| ||||||
TCCAAGATGTAGAA AAGA GTAG TTTAAATAA TTCAAT /
T AACC TGTTT TATTTT

GAM1159 CTTACCAAACAAAAACAGCT 2081 TGAGTAGTTT 5151 CC ACA T TT-- TA
CAGAGTGGTTATTATAATTT TGTTTATAAG CTTA AAACAAAA GCTCAGAG GG ATTA A
TAATTTTTCCTTTCTGAGTA |||| |||||||| |||||||| || ||||
GTTTTGTTTATAAG gaat tttgtttt tgagtCTT CC TAAT T
a- ga- T TTTT TT

GAM1160 CTTTATTTAATGTTACTGAA 2082 TGAGTACATA 5152 - TAC AAA ACC TCA
AATGTGCTCATACCTAACAG CAAACGCGTA CTTTATTTA ATGT TG ATGTGCTCAT
TAACAGTT A
TTTCAACTTAACTGTTACAG TGGA ||||||||| |||| || |||||||||| ||||||||
ATGAGTACATACAAACGCGT GGAATaggt tgcg ac tacatgagtA ATTGTCAA /
ATGGATAAGG a caa a-- GAC TTC

GAM1161 ATTGATCGTATTCAAGGCGT 2083 TTCAAGGCGT 5153 TC A- cg ac- tt
TATACAGGGTCTTAATGACT TATACAGGGT ATTGA GT ttcaagg ttat agggtc a
CTCTAATAGACCTTGAAAAA CTTA ||||| || ||||||| |||| ||||||
CTTTCAAT TAACT CA AAGTTCC GATA TCTCAG /
TT AA A- ATC TA

GAM1162 GAGATAAATAACAAAATCCA 2085 TAAATAACAA 5155 - ca caaac T
AACATTACATATCTGTGGTC AATCCAAACA GAGAtaaa taa aaatc attacA A
TGATTTCTTTATTTTATCTC TTAC |||||||| ||| ||||| ||||||
CTCTATTT ATT TTTAG TGGTGT T
T TC TC--- C

GAM1163 GACATCTTTGTTGTACAAGG 2092 TACAAGGTGA 5162 TTGta tgaata gt att
TGAATATGGTCTTAATTATT ATATGGTCTT GACATCTTTG caagg tg ctta A
ATAAGGTTAACCCTTGCGAA AATT |||||||||| ||||| || ||||
GATGTC CTGTAGAAGC GTTCC AT GAAT /
----- CA---- TG ATT

GAM1164 GAAATCTACCAGCAATTTGA 2093 TCTACCAGCA 5163 - ca tt -- acA A
CGCCATACAAGCAAATGCTC ATTTGACGCC GA AAtctaccag at gacg ccat AGC A

AAGTGGATCGTCTTATAACT ATAC || |||||||||| || |||| |||| |||
GGTAGATTGTC CT TTAGATGGTC TA CTGC GGTG TCG A
G AA TT TA AAC T

GAM1165 CTATTAGGTACTCCTTTTGT 2094 TAACCATACC 5164 ACTCC A AC- CA
GGTAATGGACGACATGTTCT GCAAAATGCA CTATTAGGT TTTTGTGGTA TGG GA T
AACCATACCGCAAAATGCAC CCTA ||||||||| |||||||||| ||| ||
CTAATGG GGTAatcca aaaacgccat acc CT /
cgt-- - aat TG

GAM1166 ACTTACGCCACGGATTTGTT 2086 ACGGATTTGT 5156 A Ca-- ttt a aca A AT
GACAATCAACAAGACGCATA TGACAATCAA ACTT CGC cgga gttg caatca ag CGC A
CACGCGCTTGGTTGCCAACT CAAG |||| ||| |||| |||| |||||| || |||
ACTCTGATACGCGGAAGT TGAA GCG GTCT CAAC GTTGGT TC GCG C
G CATA CAT C --- - CA

GAM1167 TGCAGCGGTATCTGCGTGGA 2087 CAGCGGTATC 5157 tatct g t gG GG
TTCCTGGGGTAGGGTGTCTG TGCGTGGATT TGcagcgg gcgtg at cct GGTAG T
CCAGAGGGTGTACGTTTGTT CCTG |||||||| ||||| || ||| |||||
GCA ACGTTGTT TGCAT TG GGA CCGTC /
----- G - GA TG

GAM1168 GTGGTCACTCTCAGCTGCTA 2088 CAGGCTCTGA 5158 T- CTGCTAA T ATG
ACCTGTGCAGATGGAAACTG GAGTGTTTCA GTGG CACTCTCAG CCTG GCAG G
TCAGGCTCTGAGAGTGTTTC C |||| ||||||||| |||| ||||
AC cact gtgagagtc ggac TGTC /
tt tc----- - AAA

GAM1169 TAGGAAGACAAGGATGATCG 2089 ACAAGGATGA 5159 Gaca g a ga G
CCAAACTGATTGACAAGGGG TCGCCAAACT TAGGAA ag atgatcgccaa ct tt A
GTTGGCGATTATACTGCATT GATT |||||| || |||||||||| || ||
CCTG GTCCTT TC TATTAGCGGTT GG GA C
ACG- A - GG A

GAM1170 TTGGAAGGGGATGAGTGGAC 2090 TTAGCAAAAT 5160 -- G- A - - CAA-- C ATGGGA
G TAG
TACACATAGTCAACAGGATT CAATCCTGCA TGA TGG CTA CACAT AGT CAGGATT GT
GT AGCAACT T
CGTATGGGAGTGAGCAACTT AAAG ||| ||| ||| ||||| ||| ||||||| || || |||||||
AGTAATGGTTGTTAGCAAAA ACT ACC GAT GTGTA TCg gtcctaa ta cg ttGTTGG /
TCAATCCTGCAAAAGCTAAT GG AA - C A aaaac c aaa--- a TAA
GTGCTAGCCAAATCAGGAGA
TCCTACAA
GAM1171 GTGTGACGTGAGTCTGATCC 2095 TGACAAGCCT 5165 -- AG - A AACAC T T
CAG TT

AACACTGAACGCTTTCGTCG GACGAGAGCG TGA CGTG TC TG TCC TGAACGCTTTCGTCG GTTT TCATG CT T
TGTTTTTCATGCAGCTTTTA TTCA ||| |||| || || ||| |||||||||||||| |||| ||||| ||
CAGACCATGACAAGCCTGAC ATT GCAT AG AC GGG acttgcgagagcagt cgaa agtAC GA /
GAGAGCGTTCATCGGGGCAT AC GA T - GCT-- c c CA- CA
GAAGTACGCATTACAC

GAM1172 GGAACGGAGGAGGCTTTCGC 2096 TGTGACGATG 5166 C AG TT C CT--- A G
CACACCTATCCTGAAAGCGT TCTTTACCAT GGAA GG GAGGC TCG CACACCTATC GAA GC T
TGCATTCTTTATGATAGGTG TCC |||| || ||||| ||| |||||||||| ||| ||
TGACGATGTCTTTACCATTC cctt cc ttctg agc gtgtGGATAG CTT CG /
C a at t- a TATTT A T

GAM1173 GCGTGATGATGACATTCATC 2097 CATACGGTTT 5167 AT ACATTCA TT- ATTCA TAC
ATGTATTTCCATTCACACAT ATATATGACC GCGTG GATG TCATGTAT CC CACA C
ACCTTTTGTGCATACGGTTT ATCC ||||| |||| |||||||| || ||||
ATATATGACCATCCACGC CGCAc ctac agtatata gg GTGT /
-- c------ ttt catac TTT

GAM1174 GTTCGTTGTCGCCCCTGTGA 2098 TGTGAGTGTG 5168 TT CCCtgt - - gc at
GTGTGGAGCTAATCATATTA GAGCTAATCA GTTCG GTCGC gagt g tgga taatc a
GGTTATATCCAGCAACTCTG TATT ||||| ||||| |||| | |||| |||||
AACGTGACCGAGC CGAGC CAGTG CTCA C ACCT ATTGG t
-- CAAGT- A G AT At

GAM1175 CAATGGCTGATTTTGGATTG 2099 CTTTGTACCA 5169 A T--- GA T T GA ATA
TTACAATGCGAGGATACATT ACAGGGTCTT CA TGGC GATTTTG TTG TACAA GC GG C
CCCGGGCTTTGTACCAACAG ACGC || |||| ||||||| ||| ||||| || ||
GGTCTTACGCCAATG GT ACcg ctgggac aac atgtt cG CC A
A catt -- c t GG CTT

GAM1176 GCGATTAACAACATTTTTCA 2100 TCACTAGTGC 5170 TT A TT A C ----- A- T C----- G T
ATACGGCGTTGAACTATTGC CAACGAGTCT GA AACA CATT TCA TA GG CGTTG ACTA TG TACCTG C A
TACCTGGCTAATGCAGGTAT CCAT || |||| |||| ||| || || ||||| |||| || |||||| |
AAACTCACTAGTGCCAACGA TT TTGT GTAG GGT At cc gcaac tgat ac ATGGAC G A
GTCTCCATAATGGTGATGAT T- A T- A a tctga cg c tCAAAT - T
GTTTTTGC

GAM1177 ATCAGTCCGTATTTTTAATG 2091 TTAATGGCTG 5161 A - t- gga aggt G ACA
GCTGGACTAGAGAAGGTGTT GACTAGAGAA ATC GTC CGTATTTt aatggct ctagaga gTT CTATT A

GCTATTACAAACAAATGGGA GGTG ||| ||| |||||||| ||||||| ||||||| ||| |||||
ACTTTCTAGAGCTGTTCCAA TAG TAG GTATAAAA TTGTCGA GATCTTT CAA GGTAA
/
AATATGAGATAGAT A A CC --- ---- G ACA

GAM1178 CAAATAGACTTAAATCACAC 2101 CATCACAGCA 5171 GA AAATCACA T ------- G
TGTTGTTGACTATGGAAATA GCATAAAAAA CAAATA CTT CTGTTGT GA CTAT G
GAGCTACATCACAGCAGCAT AGAA |||||| ||| ||||||| || ||||
AAAAAAAGAATATTTG GTTTAT gaa gacgaca ct GATA A
aa aaaaatac - acATCGA A

GAM1179 GGGTGATGGTGCAGTAGTAG 2102 TGATGGTGCA 5172 G a aatgaTGA
TTAATGATGAAGGAAAGGGA GTAGTAGTTA GG tgatggtgcagtagt gtt A
ATAATTGCTGTACCATTAAC ATGA || |||||||||||||| |||
C CC ATTACCATGTCGTTA TAA /
A A GGGAAAGG

GAM1180 TTAGACATGGTAAAGAATCC 2106 GACATGGTAA 5176 ga gtaaagaa aa c GATGT
AACCCTTAATGATGTGCAAA AGAATCCAAC TTA catg tcc cc ttAAT G
AATTAATGGGGAATATAACA CCTT ||| |||| ||| || |||||
TGGATGA AGT GTAC AGG GG AATTA /
AG AATATA-- -- T AAAAC

GAM1181 TCAAGTTCCTCCTAATAGCT 2107 TGGCAAAACA 5177 -- ------ GGATGG C GAA
TTGGATGGGTCACTGGGAAA GGGGTTATTA TCAA GTTCCTCC TAATAGCTTT GTCA TGG
A
TCATCAATGGCAAAACAGGG ATTA |||| |||||||| |||||||||| |||| |||
GTTATTAATTAATGGAGGAA AGTT TAAGGAGG attattgggg cggt ACT /
TAATTGA AA TAatta acaaaa A ACT

GAM1182 GATGTGAGTGCAGGTTCAGA 2112 TACAATATGC 5182 G GCAGGT GAAA- A CTA
AAATAATGTGTTTCTATCAC ATATGATAAG GATGT AGT TCA ATA TGTGTTT T
AAATACAATATGCATATGAT CTAC ||||| ||| ||| ||| |||||||
AAGCTACGTC CTGca tcg agt tat acatAAA /
- aat--- atacg a CAC

GAM1183 ACAGTCGGAGTCGAGTTTCT 2103 AGGCACCAAC 5173 - GTC TC ACAT TC
TGGTGACATTGGCTCTTTGT AACTCATCCG ACA GTCGGA GAGTT TTGGTG TGGC T
CAGGCACCAACAACTCATCC ACAT ||| |||||| ||||| |||||| ||||
GACATGT TGt cagcct ctcaa aaccac aCTG /
a a-- c- gg-- TT

GAM1184 CAGGACGAGACGCGGTTCCA 2104 CGACCGGACG 5174 A - A ------- - C CC

CACGGCCATGACCGTCTGGC CCCCGCTGCG CAGG CG AG CG CGGTT CCA ACGG A
GACCGGACGCCCCGCTGCGC CCTG |||| || || || ||||| ||| ||||
CTG gtcc gc tc gc gccag GGT TGCC T
- g - cccgcag c C AG

GAM1185 AGTCGGCATGTTTTGACTAC 2105 TGTTTTGACT 5175 - t ------ ctacttct gtca TCCC
TTCTGCCGTCATTCTCCCCC ACTTCTGCCG AGTC GGCA gttt tga gcc tTC C
TCATGAAAAGGCTCTTCTAT TCAT |||| |||| |||| ||| ||| |||
CATCCTTTGAACTGCCTGAC TCAG CCGT CAAG ACT CGG AAG C
T T - TTTCCT ATCTTCT- AA-- TACT

GAM1186 GGAGTGCATGCGCGAGATCT 2108 CCACGCAGGA 5178 AG CAT A ACAACC A ACA-
A
GCGACAACCTGACGAAGTAC CTCGCGCTTC GG TG GCGCGAG TCTGCG TG CGAAGT
CG A
ACGAACTCGATCGACTTCGC CAGA || || ||||||| |||||| || |||||| ||
CACGCAGGACTCGCGCTTCC CC ac cgcgctc ggacgc ac GCTTCA GC C
AGACC ag ctt a ------ c GCTA T

GAM1187 GATCATGTTCGCCACCAACC 2109 GCCGCTGGGC 5179 A-- CACCAA A T CT
CGACGTGCCACCTGGCGTGG GAGAGCGAAC GATC TGTTCGC CCCG CG GCCAC G
CCGCTGGGCGAGAGCGAACA ACGA |||| ||||||| |||| || |||||
CGAGATC CTAG acaagcg gggt gc cgGTG /
agc agagc- c - CG

GAM1188 AGGTTCCGCTGCGTGCTGAA 2113 TTCCGCTGCG 5183 a- gaaa----- GTA CG G - G
T C G
GTGAAAGAGCGGTAGCTCCG TGCTGAAGTG gtgctga gt gAGCG GCTC GCTGC TG TCG
TC GGTG AG A
GCTGCGTGTCGGTCTGGTGC AAAG ||||||| || ||||| |||| ||||| || ||| || |||| ||
AGGATCTCGCCGACGGCCAG CGCGACT CA CTCGC CGAG TGATG AC GGC AG
CCGC TC /
GTAGTGAGCGGCGCTCGACT GG GATGTTCAG GG- -- G C - - - T
TGTAGACGGTCAGCGCGCAG
TGCCCCT
GAM1189 GCAGCCGGATGATGGTGCGG 2114 TGTGCAAGCG 5184 A TGC- AGTGAG GAA TT-
AC- AGA- T
TTAGTGAGCCGGAAGCCCGT CACCTGCGAC G TGG GGTT CCG GCCCGTT GGTGCG
GCACGG ATT G
TTTGGTGCGACGCACGGAGA GGGC | ||| |||| ||| ||||||| |||||| |||||| |||
ATTTGAAGGTCCGGTTGTGC C GCC CCAG GGC cgggcag ccacgc cgtgtT TGG A
AAGCGCACCTGCGACGGGCG A TTTC GAGGA- GG- cgt gaa GGCC A
GCGGAGGAGGACCCTTTCCG
ACAGCGGGTGT
GAM1190 TTATATGATATCTTACAAAA 2110 TATGATATCT 5180 - c c- aAA TT TT- TTCTG
TATATTAAATCTTTCTTTAG TACAAAATAT TTAtatgat at tta aaaatatatt TC TC TAGTTAT A

TTATTTCTGATAACTTATAA ATTA |||||||||| || ||| |||||||||| || || |||||||
CTATTTGACGAAGGATATGT AATATATTA TA AAT TTTTGTATAG AG AG ATCAATA T
TTTTTTAATATAATTATATA A T TT GA- C- TTT TTCAA
A

GAM1191 TGTCTTATTTTTTATTTTAT 2115 TAATTAGCAG 5185 - TT- T T ---- AAT
ATGGATTATTATTAATAAAA TTCTTATAAC TGTCT TATTTT AT TTATA GGATT ATTATT A
CAATAATTAGCAGTTCTTAT ATCA ||||| |||||| || ||||| ||||| ||||||
AACATCATAAAATATAGATA ATAGA ATAAAA ta aatat cttga taatAA A
T Tac c t cgat CAA

GAM1192 GTAAAAGGATTATTGCATTT 2119 TAAGTATTAA 5189 A T-- CATT ta-- tc t TTT
ATTAAGTATTAAAACATTAT AACATTATCT GTA AAGGAT ATTG TATtaagtat aaacatta ta atA
T
CTATATATTTTGAATTATTT ATAT ||| |||||| |||| |||||||||| |||||||| || |||
ACTAATGTTTGAATATATTT CAT TTCCTG TAAC ATAATTTATA TTTGTAAT AT TAT
G
AATACAATTTTGTCCTTGTA G TTT ---- TAAG C- T TAA
C

GAM1193 GGATTTTTGCAATAATATGA 2120 TTATATGTTT 5190 TTT- TA--------- TTTT
TGTTTTATTTTTATTATATG TAATTTTTTG GGAT TGCAA ATATGATG A
TTTTAATTTTTTGCATATTA CATA |||| ||||| ||||||||
TCC CCTA acgtt tatattAT /
TTat ttttaattttg TTTT

GAM1194 TAGAATATAAAAATACATTC 2125 TACGATATTT 5195 TATA-- CAT C AAGATA - A
GCTATAGAAGATATAGTATC TAAAATTTTC TAGAA AAAATA TCG TATAG TAGT ATC A
AAAAGATAACTACAAGCTAT TA ||||| |||||| ||| ||||| |||| |||
ACGATATTTTAAAATTTTCT atctt ttttat agc atATC ATCA TAG A
A ttaaaa --- - GAAC-- A A

GAM1195 GAGTATACAATACAAAATGT 2126 TACAATACAA 5196 Atac- a t c TTTTCTG T
AGCATATATTTTTCTGTACA AATGTAGCAT GAGT aatacaaa tg ag atatat TACAA A
ATATATTGTAATATATACTT ATAT |||| |||||||| || || |||||| |||||
TATTTGTATTTAATAACTT TTCA TTATGTTT AT TC TATATA ATGTT T
ATAAT - T A ------- A

GAM1196 CCTGTGCAGAAAGTGACTCG 2111 CTACCGCGAG 5181 T AA T -- A ----- - - C
GCTGAGTGCTCCGGTGGCCC GTTTCCACCC CCTG GCAG AG GACTC GGCTG GTG CTC
CGGT GGC C
TTGCCTACCGCGAGGTTTCC AGCC |||| |||| || ||||| ||||| ||| ||| |||| |||
ACCCAGCCTCGGGTCTCTAC GGAC CGTC TC CTGGG ccgac cac gag gcca cCG T
TGCCAGG - A- T CT c ctttg c t T

GAM1197 CATGTGAGTAAATGGAAATC 2116 TGGAAATCAA 5186 AG AA a aata gac aa
AATAGCTGACTGTAAAAAAC TAGCTGACTG CATGTG TA tgga atc gct tgt a
ATAAGGCCGATATCCACGTG TAAA ||||||| || |||| ||| ||| |||
ATACATG GTACAT GT ACCT TAG CGG ACA /
A- GC A C--- AAT AA

GAM1198 GTAAACAGTATTGTTGGACA 2117 ACAGTATTGT 5187 tat acgtct---- T
CGTCTTCCTCAAGGATTTTT TGGACACGTC GTAAacag tgttggac tcc C
AAATAGTCCAGCATTGTTTA TTCC |||||||| |||||||| |||
C CATTTGTT ACGACCTG AGG A
--- ATAAATTTTT A

GAM1199 GATCCTAAAGAGCATGTTCA 2118 TTTGAAAAAA 5188 ---- T CAA---- AGAAAAAGTG
TTT GGCA
ACAATTAGAAAAAGTGTTTC TCAGAAATTG AAGA GCA GTT CAATT TTTCAAA
TACTACA G
AAATTTTACTACAGGCAGGA GTCA |||| ||| ||| ||||| ||||||| |||||||
TATGTAGTATCTTTGAAAAA TTTT TGT CAA gttaa aaagttt ATGATGT /
ATCAGAAATTGGTCAAAAAA AAGA - AAAactg agactaaa-- CT- ATAG
CTGTAGAATTTTTAGGATT

GAM1200 GAGCGAAAGGTGCCTGTGGA 2121 TGAAAGAGGA 5191 AAA GC T-- TT GAAAA G -
----- TG
GTTTTGGAAAATCCTCTTTG CATGCTCCTC GAGCG GGT CTG GGAGT TG TCCTCTTT AT
GGC T
ATGGCTGTGTCGCCCTGGGA TCAG ||||| ||| ||| ||||| || |||||||| || |||
GTGAAAGAGGACATGCTCCT CTCGC CCG gac cctcg ac aggagaaa tG CCG G
CTCAGAGGCCGGGCGCTC GGG GA tct t- ----- g AGGGTC CT

GAM1201 AATAGTAAGAGTCAATTTTT 2122 TAAATAGCAG 5192 AT TA TC T TA--- At a caaa
gaat
GTATTATAAATAGCAGTTCA TTCAAATGTG A AG AGAG AATT TTG TT aaat gcagtt tgt a
AATGTGAATAAAAAACAGGC AATA | || |||| |||| ||| || |||| |||||| |||
TGCAGTTTTCAAGCATCCAA T TC TCTC TTAA AAC AA TTTG CGTCGG ACA /
CAATTCCTCTCTCTTCT CT TC C- C CTACG CT A ---- AAAA

GAM1202 GATAATATGCTAATAGTAGG 2123 TAATATGCTA 5193 aatag gtaa A TA A CTAA- GAAA--
GGTA- AG
TAAACCCAGACTATGCCATC ATAGTAGGTA ct tag accC GAC TGCC TC TGTT CC
GGC A
CTAATGTTGAAACCGGTAGG AACC || ||| |||| ||| |||| || |||| || |||
CAGAGAAGCCGTTTAGGGGA GA GTT TGGG TTG GCGG AG GCAA GG CCG
G
GTAAACGAAGTTGAAGGCGC AGCTA AA-- A TC A TTGAA ATGAGG ATTTG AA
TGTTAGGGTAATTGATCGAA
GCAGAAAATC

GAM1203 AGGGAATGGTCCTTTTCCGC 2127 TGTCTAGTTT 5197 A TCCTT C TTA ------
GGCG
ACTGGTTAACGGTACTGAGG GGAATCTCCA AGGGA TGG TTCCG ACTGG ACGGTACT
GAGGA T
AGGCGTTGAAATCTTTAGGA ATTC ||||| ||| ||||| ||||| |||||||| |||||
AAGGTGCTGTCTAGTTTGGA TCctt acc aaggt tgatc tgtCGTGG TTTCT T
ATCTCCAATTCCT a tct-- t --- AAAGGA AAAG

GAM1204 TGTAGGTACTGGTGGATTTT 2128 TGAGTTCCTG 5198 CT GA- t t t tct cg
ATGAGTTCCTGCTCTATGTT CTCTATGTTC TGTAGGTA GGTG TTTTA gag tcc gc atgtt g
CGGTTTGACATGTGGATTTC GGTT |||||||| |||| ||||| ||| ||| || |||||
CTAAAGGAATACCTCTACCT ACGTCCAT CCAT GAAAT CTT AGG TG TACAG t
GCA CT AAG C T - --- Tt

GAM1205 AGCCACTCTTTTAAAAATTG 2775 TGGCCAAATA 5845 - AAAAATT--- A TT
CCAACCTTTATTGGTGGCCA TGAGAAAGGA AGCCAC TCTTTT GCCA CC T
AATATGAGAAAGGATGTGGT TGTG |||||| |||||| |||| ||
T TTGgtg aggaaa cggt GG A
t gagtataaac - TT

GAM1206 GAGGCGCTGATCTGCAGCTG 2124 CGTGCAGCCG 5194 --- TGA - A CG
CACGGCCGTGGAGTCGTGCA CATGAGACGT GAGG CGC TC TGC GCTGCACGGC T
GCCGCATGAGACGTGATACC GATA |||| ||| || ||| ||||||||||
TC CTCC gtg ag acg cgacgtgcTG G
ata cag t c AG

GAM1207 TTTTGATCGAGGCACCAAGA 2129 CATCGTTGAT 5199 TC GGCACCAA TC AAATT
TTCTGCCAAATTCCCCAAGG ATAATCTTTC TTTTGA GA GAT TGCC C
CATCGTTGATATAATCTTTC AAAG |||||| || ||| ||||
AAAG gaaact ct ttg acGG /
tt aatatag- ct AACCC

GAM1208 GATAACTACCGTTCATGCTG 2130 TACCGTTCAT 5200 C cgttc - ca tTA
TATGCATCATTATAATCTGA GCTGTATGCA GATAA tac atg ctgtatg tca T
CATATAGACATCTGTAATTA TCAT ||||| ||| ||| ||||||| |||
TC CTATT ATG TAC GATATAC AGT A
A TC--- A -- CTA

GAM1209 TCTGGTATACACCCGTCTCG 2776 CCGGACGGAT 5846 TATA C C A- AA TA
TGGTACGAAGTAGAGCGCGG GCAGTCCAGA TCTGG CA CCGTCT GTGGT CG G G
CACCACCGGACGGATGCAGT ||||| || |||||| ||||| || |
CCAGA agacc gt ggcagg cACCA GC C /
tgac a c CG G- GA

GAM1210 CGTAGTCTTAAAAATTTGAT 2777 TTAAAAATTT 5847 A C a---- taactacc c ----
ATCATT
AACTACCATTCATGCTATAT GATAACTACC CGT GT ttaa aatttga att ATG CTATATGT A
GTATCATTATAATCTGACAT ATTC ||| || |||| ||||||| ||| ||| ||||||||
ATAGACTTCATTAATTATTT GCA CA AATT TTAAACT TAA TAC GATATACA T
TTTCAAATTCATTCTTAATA - T CTTAC TTTTTAT- T TTCA GTCTAA
CACG

GAM1211 AATACCTCAATGTCTTCTAT 2781 TACCTCAATG 5851 ---- t- cta--- c AATT C AT
GGGCGTCGAATTCGTATGCG TCTTCTATGG AAtacct caa gtctt tggg gtCG CGTATG GTATA
C
TATAATCGGTATACACGTGC GCGT ||||||| ||| ||||| |||| |||| |||||| |||||
GCATGATTTCCAGATAAAAA TTATGGA GTT TAGAA ACCT TAGT GCGTGC CATAT
/
GATCTTTGTACTAGGTATT TCAT TC AAATAG T AC-- A GG

GAM1212 ATTAGTATTTAATATTTATT 2778 TTTAATATTT 5848 t ttatttattt c
TATTTTTTTACAACTAAAAT ATTTATTTTT ATTAGTAtt aatat tttta A
CAACAATTATATTAATGCTA TTAC ||||||||| ||||| |||||
AT TAATCGTAA TTATA AAAAT A
- TTAACAACT- C

GAM1213 GGTTTCAGCCGAGGCAATGT 2779 CAGCCGAGGC 5849 TTc- c- at tac CCTGGT -
TTT
TTACATAGTCCTGGTGCTTA AATGTTTACA GGT agc gaggca gtt atagt GC TTAA C
ATTTCCATTTTAATGCTTGT TAGT ||| ||| |||||| ||| ||||| || ||||
ATACTGTTTGACTGTCTCCA CCA TCG CTCTGT CAG TGTCA CG AATT C
GCTTTTCACC CTTT AC -- TT- TATGTT T TTA

GAM1214 GGGTAATAACTTTCCCAATC 2780 TCAACGGGCC 5850 TA T C C TTGT A TG TT
GGGTTGTGCTCGTAGATGAT CCCTTATTGT GGGTAA ACT TC CAAT GGG GCTCGT GA A T
TTGACTTGTCAACGGGCCCC GACG |||||| ||| || |||| ||| |||||| || |
CTTATTGTGACGGTGCTTAC CCCATT TGg ag gtta tcc cgggca ct T G
CC CG c t t cc-- a GT CA

GAM1215 CCCACATCACACATCAGGAA 2782 TCACACATCA 5852 c------ tc - tgaa GACGA -
AC
GTTGAAACCAATGACGATGG GGAAGTTGAA CCCACAt acaca agg aagt accaAT TGGT
GGC A
TGGCACAATGCCAACCGGTT ACCA ||||||| ||||| ||| |||| |||||| |||| |||
GGTACTTACCTACTGTGTAT GGGTGTG TGTGT TCC TTCA TGGTTG GCCA CCG
/
CTCAAGTGTGGG AACTCTA CA A ---- ----- A TA

GAM1216 TAATTATCATGTCAAGGATG 2783 TCAAGGATGT 5853 T C g tcata t aTCG
TCATAGACATTGTCATCGTC CATAGACATT TAAT AT ATGtcaa gatg gaca tgtc T
ATAGACACTGTCATCGTCAT GTCA |||| || ||||||| |||| |||| ||||
TGACATTGTCATTA ATTA TG TACAGTT CTGC CTGT ACAG /
C T A TA--- C ATAC

GAM1217 CAATATCAATATTGGTATAA 2787 TATAAAATAT 5857 TCAATA aa aaa aa GAC
AATATATAAAACATAAACTA ATAAAACATA CAATA TTGGtata atatat acat actA T
GACTTTTATAGTATGTAAAT AACT ||||| |||||||| |||||| |||| ||||
ATATCATATATCAAAACATT GTTAT AACTATAT TATATA TGTA TGAT T
TATTG TTACAA AC AA- -- ATT

GAM1218 ATATCAGATATAAAAACATT 2788 TATTTTGTGA 5858 A A-- C TGG T T
AATTGGGTATTAGATATTGA TATCAGATAT ATATC GATAT AAAA ATTAAT GTATTAGA AT G
TATTTTTGATACATTATTGA ||||| ||||| |||| |||||| |||||||| ||
TATTTTGTGATATCAGATAT tatag ctata tttt tAGTTA CATAGTTT TA A
a gtg a TTA T T

GAM1219 CTATGTTTATTGTCATGGCG 2789 TGTTTATTGT 5859 tg tt- c- -- T
ACAGTGTTGATACACTTTGT CATGGCGACA CTA ttta gtcatgg gaca gtgt G
TTCCCGTGACTCTTAAAATT GTGT ||| |||| ||||||| |||| ||||
AG GAT AAAT CAGTGCC TTGT CACA A
TA TCT CT TT T

GAM1220 GGAAGCAATGATTTTTACAT 2790 TTGGATAGTA 5860 ATGATTTTT AGT AAATTTTA
C- T- TT
AGTGTTCCTGCAAATTTTAA TCGCAGGAAC GGAAGCA ACAT GTTCCTGC ATAC TCT
CAAG C
TACCTCTTCAAGTTCACTTT TCGG ||||||| |||| |||||||| |||| ||| ||||
GTTGGATAGTATCGCAGGAA TCTTTGT TGTg caaggacg tatg agg GTTT /
CTCGGTGTTGTTTCT --------- gct c------- at tt CA

GAM1221 GATTATTATATTCATCTCGC 2791 TATTATATTC 5861 tatt a c- ac TG
ACCACGAAGTGATTCTTTAA ATCTCGCACC GAT atattc tctcg acc gaAG A
GGTTTCGAGAGAATATTTAT ACGA ||| |||||| ||||| ||| ||||
C CTA TATAAG AGAGC TGG TTTC /
TT-- - TT AA TT

GAM1222 ATTATGTCCTGTTTGGTGTC 2784 TATGTCCTGT 5854 tg g aaa- TCCCCCC - CTA
GCGA CT
CAAAATGGAGACTCTCCCCC TTGGTGTCCA t gt tcca tGGAGACTC AGAGCT TGG CC
GATATCC A
CAGAGCTTGGCTACCGCGAG AAAT | || |||| |||||||| |||||| ||| || |||||||
ATATCCCTAGAGGATGTCGG A TA AGGT ATCTTTGAG TTTTGA GCC GG
CTGTAGG /

ACTCCGTAGTTTTGAGTTTC GT G GGAG ------- T TCA ---- AG
TAGAGGTGGAGATTGAGAAT
AGGGGCAAAGT
GAM1223 TCTGGCATTTTCCCAAATTT 2785 TGGCTTGGGA 5855 T TT ATTTTTT GTT T C
TTTGCCATGTTTTTTGTACA ATTGCTTGG TC GGCA TTCCCAA GCCAT TTTTG ACAA A
ACAGTTGTTTAAAAATGGCT || |||| ||||||| ||||| ||||| ||||
TGGGAATTGCTTGG gg tcgt aagggtt cggtA AAAAT TGTT /
t t- ------- --- T G

GAM1224 GGACAGGTTTGACATCATAG 2786 TGAAAATGAG 5856 -- - ACA AGA - GA
ACACTTCTGATGAAGAAGAT ACAGACCGTG GG ACA GGTTTG TCAT CA CTTCT T
GAAAATGAGACAGACCGTGT TAAC || ||| |||||| |||| || |||||
AACC Cc tgt ccagac agta gt GAAGA /
aa g ag- aaa A AG

GAM1225 CGTCTCCTCTGGGCTACCTC 2792 TCTGGGCTAC 5862 c acct ----- T
ATTTTGACCCCGTTTATGGG CTCATTTTGA CGTCTCCt tgggct catttt gaccccG T
GTTGTTAAGAAGTGTGAGCC CCCC |||||||| |||||| |||||| |||||||
TATGGGGGGCG GCGGGGGG ATCCGA GTGAAG TTGGGGT T
T GT-- AATTG A

GAM1226 AGGTTAACCCATCTTGGATC 2793 TAGGACAGGA 5863 TAA- TCT AT ATC - T-
GCGA
CATCTCCTGCCTACTTCTCC ATCGGCCATT AGGT CCCA TGG CC TCCTG CCTACTTC
CCT T
TGCGATAAATAAGGTTGAAG TTGG |||| |||| ||| || ||||| |||||||| |||
TAGGACAGGAATCGGCCATT TCCA Gggt acc gg aggac ggatGAAG GGA A
TTGGGCAGTACCT TGAC ttt -- cta a TT ATAA

GAM1227 GGAAATCCAAATTTGTCTTT 2794 TACAGCTTTA 5864 CCAAATT GTC GA TC A
GTCAAAGGAGTTCACGGAAT AAAGGACAAT GGAAAT TGTCTTT AAAG GT ACGGAAT A
AAAATTCTGTTACAGCTTTA TTCC |||||| ||||||| |||| || |||||||
AAAGGACAATTTCC ccttta acaggaa tttc ca TGTCTTA /
------- aa- ga t- A

GAM1228 ATGTTATGTCCGGACAACAT 2799 TATGTTGTCC 5869 TTA - - TC- CTAG-- A
TCTTGGAAGACTAGGGATTT GTGGTCAATC ATG TG TC CGGACAACAT TTGGAAGA GG T
CACATTTTCTTTTAATCTAT AT ||| || || |||||||||| |||||||| ||
GTTGTCCGTGGTCAATCAT tac ac gg gcctgttgta AATTTTCT CT /
ta- t t tCT TTTACA T

GAM1229 CCAGGGTGGATGGTATTTGT 2800 TTGATGGGGC 5870 G - A TG TG ATAC
TGACAAATACATCTATTGTT TATGCCACCT CCAGG TGG ATGGT TT T ACAA A
GATGGGGCTATGCCACCTGG GG ||||| ||| ||||| || | ||||

ggtcc acc tatcg gg a tGTT /
- g - gt gt ATCT

GAM1230 GGTGTCTTATATGTATCCAC 2795 TATATGTATC 5865 T a at taa taCCA TAT TTTA
CA
TAATTGATGTACCAGATATG CACTAATTGA GGTG CTt tatgt ccac ttgatg GA GTT GACG G
TTTTTAGACGCAGTTCGTCC TGTA |||| ||| ||||| |||| |||||| || ||| ||||
AATTTTTCATCGTCAGACGT CCAT GAA ATATA GGTG GACTGC CT TAA CTGC /
GGGCATATACAAGTTACC T C CG CA- TA--- TTT C--- TT

GAM1231 AAACACAATCCCGACTCGGA 2796 TTGGTAAATC 5866 C - - C A- ATA-- G
ATATATATATGATAATAAAT CCAGTTCGGG AAACA AAT CCCGA CT GGA TAT TAT A
TGGTAAATCCCAGTTCGGGT TATT ||||| ||| ||||| || ||| ||| |||
ATTTTGTTT TTTGT tta gggct ga cct atg ATA T
T t t c aa gttAA A

GAM1232 TCTTCGTCTGAGGAGCTATT 2797 TATTGCTAGT 5867 - T G tat---- - tgt tg
GCTAGTGGGTGTGCACTGAC GGGTGTGCAC TC TTCGTC GAG AGC tgcta gtggg gcac a
GGTGCTTCCGCGTGGCATCC TGAC || |||||| ||| ||| ||||| ||||| ||||
GTTTGCTGCTTGACGGGTGA AG GGGCAG TTC TCG ACGGT CGCCT CGTG /
T - G TTTGCCT G T-- Gc

GAM1233 AAACACAATCCCGACTCGGA 2798 GTAAATCCCA 5868 C - - C ATATATATA AA
ATATATATACGATAATAAAT GTTCGGGAAT AAACA AAT CCCGA CT GGA CGAT T
TGGTAAATCCCAGTTCGGGA TTTG ||||| ||| ||||| || ||| ||||
ATTTTGTTT TTTgt tta gggct ga cct GTTA /
t a t c aaatg---- AA

GAM1234 CTAGGGAAAACATAAGAATA 2801 GGGAAAACAT 5871 A aaa g agaa GAG T AAA
AGA
GGAAGAAACCGAGGTTTGGG AAGAATAGGA CT ggga cataagaatag a ACC GT TGGGAGA
GCTG T
AGAAAAGCTGAGATAAAATA AGAA || |||| |||||||||| | ||| || ||||||| ||||
GCGCATTTTCCATACAGAGG GA TCCT GTGTTTTTGTT T TGG CA ACCTTTT CGAT
A
TTGTTGTTTTTGTGGATCCT A AG- G ---- AGA T ACG AAA
AAG

GAM1235 TCTGCTCTGGTTGAGCGCGT 2802 TGAGAACTCG 5872 G TT C A-- G G CTT
CATTCGCGACATACCTTTAT GCTGCTCCCA TCT CTCTGG GAGCG GTC TTC C ACATAC T
AAGTATGTGAGAACTCGGCT GAGG ||| |||||| ||||| ||| ||| | ||||||
GCTCCCAGAGGAGA AGA gagacc ctcgt cgg aag g tGTATG A
g -- - ctc a - AAT

GAM1236 AGGTAATGATAAAACTATTG 2803 TTACACGATC 5873 TAAT AACT- - CT A T
GTCTAGATATGTAATCAAAT TAAATTATCC AGG GATAA ATTG GT AGAT TG A
CTTACACGATCTAAATTATC CATC ||| ||||| |||| || |||| ||
CCATCCT TCc ctatt tagc ca tCTA AC A
tacc aaatc a t- A T

GAM1237 CATAGAAGTTCAAGTAAACC 2804 TTCAAGTAAA 5874 ttc-- aaa ct at C - T - -
AAGA
CCTCATGGATTAGCCTCTTA CCCCTCATGG AGAAG aagt ccc catgg taG CTC TTAGG GGC
TC TCTC T
GGTGGCTCTCTCAAGATAAA ATTA ||||| |||| ||| ||||| ||| ||| ||||| ||| || ||||
CGGAGATGACGCCTCTAATG TCTTC TTCG GGG GTGTC GTC GAG AATCT CCG AG
AGAG A
AGTCTGCTGTGTTGGGAAGC TTATT AA- TT -- T T - C T GCAA
TTTTATTCTTCTGTG

GAM1238 TATGACTAATCTAGATATGT 2805 TGACTAATCT 5875 --- aat ATG
TAATTAGATATGACTAATCT AGATATGTTA TAtgactaatcta gatatgtt taGAT A
AGATATGTTAATTAGATTAG ATTA |||||||||||| |||||||| |||||
TCATA ATACTGATTAGAT TTGTATAG ATCTA /
TAA --- ATC

GAM1239 GTGAGAGTGAAGTGTAATGA 2808 AAACAGAAAT 5878 G A TGTAA CG Gaa taagttt
ttTATT
CCACGTGAAACAGAAATAAG AAGTTTAACT GT AG GTGAAG TGACCA T acagaaa aacttt
A
TTTAACTTTTTTATTATTTT TTTT || || |||||| |||||| | ||||||| ||||||
TTTAAGGTTTGTTTTTTTTG CG TC CACTTC ATTGGT G TGTTTTT TTGGAA T
TATGTATGGTTAGTCTTCAC - - TG--- AT TA- TTTGT-- TTTTTT
CTGC

GAM1240 GTGTATTATTATAAAGTCCA 2809 TATAAAGTCC 5879 TA- tcc - tta
TATCGGAGTTACTTTTCTCT ATATCGGAGT GTGTAT Ttataaag atatc ggag c
AGGTATTTTTTATAACTTAT TACT |||||| |||||||| ||||| ||||
ACAC CACATA AATATTTT TATGG TCTC t
TTC T-- A TTT

GAM1241 TCCCACAATCTCATTGGTCC 2812 TCATTGGTCC 5882 ca-- cc -- --- --- G C A -- A
AGAGCCCTCTCAGCCGCGCT AGAGCCCTCT attggtc gagc tc tcag cC GC CT TG
TTGGTCGAGA GCT G
CTGATTGGTCGAGAGCTAGC CAGC ||||||| |||| || |||| || || || || |||||||||| |||
TGGCCCTCTCGACCAACCAT TAACCGG CTCG AG AGTT GG CG GA AC
AACCAGCTCT CGG C
AGGCCAGGGATTTTGATTGA CCGC AC TT TTA GAC - T C CC T
CAGCTCCGCCGGCCAATGAG
AACGCAGGGA
GAM1242 AACAAAGAAATGGAAATCGT 2806 TGGAAATCGT 5876 AG t taatacc t

AATACCAGTTATGTTTAACT AATACCAGTT AACAA AAAtggaaa cg agtta g
TTGAAATTGTTTTTTATTTT ATGT ||||| ||||||||| || |||||
CTTGTT TTGTT TTTATTTTT GT TCAAT t
CT T TAAAGTT T

GAM1243 TGAGTTGTTAAATCTTTACA 2807 TAAAACAACT 5877 TAAA- CAGG AG TT
GGTGTTTAGATTTTTCAGAT AGAGAAAAGT TGAGTTGT TCTTTA TGTTT ATT T
AAAACAACTAGAGAAAAGTA ATAA ||||||||| |||||| ||||| |||
TAACTCA ACTCaata agagat acaaa tAG /
tgaaa ca-- a- AC

GAM1244 CCTCCCCTCCCTCTCCCTCG 2810 TGAGGAGGAG 5880 TCCC C G GG A
TCCTGGTCGGAAAAGTCTGA AAGGAGAATG CCTCCCC TCTCC TC TCCT TCGGA A
GGAGGAGAAGGAGAATGGGG GGGA ||||||| ||||| || |||| |||||
AGG GGagggg agagg ag agga agtCT A
ta-- a - gg G

GAM1245 TCCCGGCACACATCCTGGAT 2811 TCCGTGGAGT 5881 G - A - TGC C C
GCCCTCCACGACGCTCTTTA AGTGGCGGGG TCCCG CAC AC TCC TGGA CCTCCA GACGCT
T
GCGTCTGGAGGTCCGTGGAG ||||| ||| || ||| |||| |||||| ||||||
TAGTGGCGGGG ggggc gtg tg agg gcct GGAGGT CTGCGA T
g a - t --- - T

GAM1246 TGGGCGAAGGCCTGCAGCTG 2894 AGCTGGTGAT 5964 C Cagc tg tc cta -- CCA
AT
GTGATTAGTTCCACTAGACG TAGTTCCACT TGGG GAAGGCCTG tgg attagt ca gac GGGCA
CGG C
GGCACCACGGATCCTACCGA AGAC |||| ||||||||| ||| |||||| || ||| ||||| |||
TGCCCAAGTTATTTGCCACT ACCC TTTTCGGAC ACC TAGTCA GT TTG CCCGT
GCC C
GATGTCCATCCAGGCTTTTT T CT-- TG CC TTA AA A-- AT
CCCA

GAM1247 GATCTAGATTCTATTGTTAA 2813 TCTATTGTTA 5883 CT- ttaaaag aaa TC AAT
AAGGAAAAATGTATCGATAA AAAGGAAAAA GAT AGATtctattg gaa tgta GAT A
TAAACCATTTTTACAGAGTT TGTA ||| |||||||||| ||| |||| |||
CAGCATCGGTGGAATCTTAA CTA TCTAAGGTGGC CTT ACAT TTA A
ATC AAT TACGA-- GAG TT CCA

GAM1248 GTCCGCCGTCTAGGTAAGTT 2814 TCTAGGTAAG 5884 C C-- aagttt a -- tC A- CC
TAGAGCTCAGGTCGAGACCG TTTAGAGCTC GTC GC Gtctaggt ag gctc agg GAG CCGGG
T
GGCCTTTGTCCGGCGCTCCC AGGT ||| || |||||||| || |||| ||| ||| |||||
TTGGAGCCTACCTAGACTCA CGG CG CAGATCCA TC CGAG TCC CTC GGCCT T

GCCGGC C ACT ------ - GT -- GC GT

GAM1249 GGGAAACGAAAACAAGGAAG 2891 ACGAAAACAA 5961 AA aaa aaga ag-- aT
ATGTAGCAATGTATGAAAAG GGAAGATGTA GGG acga caagg tgt ca G
CAAGGGTCTTGAGATCGTAC GCAA ||| |||| ||||| ||| ||
CTC CTC TGCT GTTCT ACG GT /
CA AGA GGGA AAAA AT

GAM1250 GAAAAAAGATGACTGGGAAG 2892 AAGATGACTG 5962 A at ct c-- GT
CTATCCGTATTGTGTTTGAT GGAAGCTATC GAAA aag gactgggaag atc gtaTT G
ACATAGATTCTTCTCGGTCC CGTA |||| ||| |||||||||| ||| |||||
TTGTTTT TTTT TTC CTGGCTCTTC TAG CATAG T
G -- T- ATA TT

GAM1251 GATGCAGGATTACCATTAAT 2815 CTAAAGCTAT 5885 CA- CCATTAATC AC
CTTAGGAAACAACTTCCTAA ATAATCCGTT GATG GGATTA TTAGGAA A
AGCTATATAATCCGTTCATC CATC |||| |||||| |||||||
ctac cctaat aatcCTT /
ttg atatcga-- CA

GAM1252 TCTTGCTCGACGTGCCGCGT 2816 CGAGATGGGC 5886 T T -- GGAGAA -- A
TC C
CTGGAGAACTATTTTCTTTG GAGGAGATGC TCT GC CGACGTGCC GCGTCT CTATTT
TCTTTGTC AG TGT T
TCAAGTCTGTCTTTACGAGC TGGG ||| || ||||||||| |||||| |||||| |||||||| || |||
TGGACGAGGACGAGATGGGC AGG CG GTTGTACgg cgtaga ggtaga AGGAGCAG TC
GCA T
GAGGAGATGCTGGGCATGTT C - gt ggagcg gc G GA T
GGCCGGA

GAM1253 TAGCCTTGCATATATTGATG 2817 TTGATGATAT 5887 T A TAt ataa ac
ATATAATTGTTTTTACTAAG AATTGTTTTT TAGCCT GC TA tgatgat ttgttttt t
GGAACAAAAGATTATCATCT ACTA |||||| || || ||||||| ||||||||
TAAGCAGGTTG GTTGGA CG AT ACTATTA AACAAGGG /
- A TCT GAA- Aa

GAM1254 TCTGCGACCCCGCCATAATC 2818 CTCTCCTCGG 5888 GAC GCCATA GT GGA TA
GTCCTGGACAACTACACCAA CTAACGGCCT TCTGC CCC ATC CCT CAAC C
GTGGCTCTCCTCGGCTAACG CGT ||||| ||| ||| ||| ||||
GCCTCGT tgctc caa ctc ctc GAAC /
cgg tcgg-- ct GGT CA

GAM1255 ATCTTCACAGCTGTTACCCG 2893 TCGGCCCGGT 5963 A GCTGTTACC CTTTA A GACC
CACCTTTAACGAACGACCCC GCTCCCCTTT ATCTTC CA CGCAC ACG AC C

ACTGCGATCGGCCCGGTGCT GAAG ||||||| || ||||| ||| ||
CCCCTTTGAAG gaagtt cc gtggc ctA CG /
t cctc----- ccgg- G TCAC

GAM1256 GACGACGTGGTTTTTGCTTC 2895 CAGCGGTCGT 5965 -- TTT TT GA TTT
CGAGCTGTGTTTTTATTGCA TTTAACCGCA GACGAC GTGGTT GC CC GCTGTG T
GCGGTCGTTTTAACCGCAGG GGTC |||||| |||||| || || ||||||
TCGTC CTGctg cgccaa tg gg cgacGT /
ga ttt ct -- TAT

GAM1257 GTGATTTATTGATATTAACT 2896 TGGCAGTACC 5966 TTAT TT ACAG-- TAGTGA A-
G
ACAGATGCTAGTGATACTAC TAATGCATAC GTGAT TGATA AACT ATGC TACT
CATGGGGA C
ATGGGGAGCAGTCCTTATGG GAAG ||||| ||||| |||| |||| |||| ||||||||
CAGTACCTAATGCATACGAA CACTG ACTAT TTGA tacg atga gtATTCCT A
GAGTTTTTATCATTTGTCAC TTT- TT gaagca taatcc cg G

GAM1258 CACCGTTCGCCAAACTTCCA 2897 ATGATCGTGA 5967 CGCCAAACTTCCACCTTC CAC -
T GC
CCTTCCCCCACACATTCCGC TTTTGTTACG CACCGTT CCC AC AT CC T
TCTCCTATGATCGTGATTTT GT ||||||| ||| || || ||
GTTACGGT tggcatt tta ct gt TC C
gtt---------- gtg a a CT

GAM1259 GAGTATTGAAGTTCAAATCA 2898 TGTTGGGTAG 5968 TT TTCAAATCA T- A AG Ct t -
- taa tt
ACCCTTCATGGATAAGTCTG CTCCCTTAAG GAAG ACCCT CATGG TA T gttggg agc tc cct
g a
TTGGGTAGCTCCCTTAAGTT TTAA |||| ||||| ||||| || | |||||| ||| || ||| |
AAACGTAGGTGATGCTTCCA CTTC TGGGG GTGTC GT G TAACCT TCG AG GGA
C /
ATGAGTCTGCTGTGTTGGGG -- C-------- TT - CT AG - T T TG- Aa
TCCTTCTACTC

GAM1260 GGCTATCAAGAGTGGACCTA 2899 TAAGATCGAT 5969 TA - TG A AC G
CTACTATTGGTTTTGGTTGT GGTGAGGACT GGC TCAA GAG G CCT TACTATTGGTTTTGGTT
T
AGAACTAAGATCGATGGTGA GCTT ||| |||| ||| | ||| ||||||||||||||||
GGACTGCTTATTGACTGCC CCG AGTT ttc c gga gtggtagctagaatCAA A
TC A gt a -- G

GAM1261 GGTAGAGGTAAGGCTAAACT 2900 AGAGGTAAGG 5970 Ta aa- aaa g aag G --- ---
C
TGGTAAGCGTGAGTTCGCTT CTAAACTTGG GG gaggt ggct ctt gt CGT AGTTC GCTTG
GATT C

GGATTCCAGAATCAGGCAAG TAAG || ||||| |||| ||| || ||| ||||| ||||| ||||
TACTGGGCTGATGAGGATGA CC CTCCA TCGA GAA TA GTA TCGGG TGAAC
CTAA A
AGATGAGCTGCCACCTCCTC TC CCG GTA G GGA G TCA GGA G
C

GAM1262 TGTGCCACGGTATCTAATTT 2901 CACGGTATCT 5971 c atc ttat- C
ATAATTAGACAGTTTTAATT AATTTATAAT TGTGC acggt taat aattaga A
TATCCATTACAATTGTGTAC TAGA ||||| ||||| |||| |||||||
A ACATG TGTTA ATTA TTAATTT G
- AC- CCTAT T

GAM1263 TTATCTAACAAAAAACGTGT 2902 TCTAACAAAA 5972 - --- cg t- cgT
GGTAGCGTCAACCTTACCTT AACGTGTGGT TTAtcta aca aaaaa tg ggtag C
CATATTTTTTAATGTCTGGA AGCG ||||||| ||| ||||| || |||||
TAA AATAGGT TGT TTTTT AC CCATT A
C AAT AT TT CCA

GAM1264 TTTAAACATTTTTCCATAGT 2903 TTTGCATTAC 5973 - TTCCATA - CT T
ATGTACTTTCTGTAGAATTT AATTACTAAA TTTAA ACATTT GTA TGTA TTC G
GCATTACAATTACTAAATGT TGTA ||||| |||||| ||| |||| |||
ATTAAA AAATT tgtaaa cat acgt AAG T
a tcattaa t tt A

GAM1265 GGTTAGTATATACTTGATCA 2905 TACTTGATCA 5975 GTATA t ga a- tacG TC
TCGATTCAATGTACGGCTCA TCGATTCAAT GGTTA tac tgatcatc ttca tg GC A
AGGTAATCAACTGAAGAGAT GTAC ||||| ||| |||||||| |||| || ||
GATTATGTGGATAACC CCAAT GTG ATTAGTAG AAGT AC TG /
AG--- T AG CA TAA- GA

GAM1266 GGGTCGTAGCGACTGACCTT 2904 TGGGATGTTG 5974 GT -- TGA TT- CAGAA
TTTTAA T
GTTCAGAAGCGTGGTTTTAA CTCTGCGCTC GG CGT AGCGAC CC GTT GCGTGG AGA
G
AGATGGTTCTCCGCGTGTGT C || ||| |||||| || ||| |||||| |||
AGCTCTGGGATGTTGCTCTG cc gcg tcgttg gg CGA TGCGCC TCT G
CGCTCC tc tc tag tCT TGTG- ------ T

GAM1267 AAGTATACGAACTTTCCGTT 2906 TAACAATAAT 5976 T AC CGTt aatt tttatttaaTAA
ATAA
AACAATAATTCAATTTTATT TCAATTTTAT AGTA ACGA TTTC aacaat caat AGTATTTTT
A
TAATAAAGTATTTTTATAAA TTAA |||| |||| |||| |||||| |||| |||||||||
CATCAGAAATATTAACATCT TCAT TGCT AAAG TTGTTA GTTA TTATAAAGA /
TTATATTGTTCAATTGTTTT - AC ATT- ACTT TATTTCTACAA- CTAC

AGAAACATCGTTACTT

GAM1268 GGCCCTCGACCAGCCCAGCA 2907 TGTCCAGGCT 5977 C A- - GCAC- AGGC TT --
TATCT
CGAAGCAGGCGATTTGCGTG TTCCAGATGG GGCCCT GACC GC CCA GAAGC GAT GC
GTGGCG T
GCGTATCTTTTGTTTGCCAC AGCA |||||| |||| || ||| ||||| ||| || ||||||
CTGCTTGTCCAGGCTTTCCA TCGGGA TTGG cg ggt tttcg ctg CG CACCGT /
GATGGAGCACGGTTAGGGCT - Ca a agacc gac- tT TC TTGTT

GAM1269 ATGAGTGTTGCTGGGGATGG 2908 CCTTCCATCC 5978 TGTT T CACGAAG
TGGGCCGCACGAAGATGTTA CTAGTTCTCG ATGAG GCTGGGGATGG GGGCCG A
AAATGGCCTTCCATCCCTAG T ||||| |||||||||||| ||||||
TTCTCGT tgctc tgatccctacc tccGGT T
t--- t AAAATTG

GAM1270 CTTCTGGCAACCTCGCCCGG 2909 TGGCAACCTC 5979 Ct aa cc t g GC
ATGGCTGTCTAGCCAATAGA GCCCGGATGG CTT ggc cctcg cgga ggct tCTA C
AGCCTTCGTCGAGGGCTTTG CTGT ||| ||| ||||| |||| |||| ||||
AG GAG TCG GGAGC GCTT CCGA AGAT /
TT -- T- - - AA

GAM1271 CGTTTGTGCGTAGGGGGTTG 2910 CTTTCGGGTC 5980 G G G C------ CT TT
CCCCGGAAGCTCTTGAAGTA TCTTCCAGCC CGTTT TGC TAGG GGTTG CCCGGAAG C G
CTTTCGGGTCTCTTCCAGCC GTTT ||||| ||| |||| ||||| |||||||| |
GTTTAGCGGAAATG GTAAA GCG Attt ccgac gggctttc G /
G - g cttctct AT AA

GAM1272 CTCTTCCTGTTCGGGGTCGT 2913 TGTCGTAGAC 5983 CT TC TC - G
CTGCGTAGCGGAACTGTTGT TCTCCTCACT CTCTTC GT GGGG GTCTGCG TAGCG A
CGTAGACTCTCCTCACTGAA GAAG |||||| || |||| ||||||| |||||
GGG GGgaag ca cctc cagatgc gtTGT A
t- ct t- t C

GAM1273 CGCGATCGGCTTTTTCTTTG 2914 TTCGTGACGT 5984 CTTTTTCTT GA -- t tc c
agcG AT
GCGAGGATGTTTTTCGTGAC AGTCGGCACA TGGCGAG T GTTTttcgtgacg ag gg acat
TTTTCC T
GTAGTCGGCACATAGCGTTT TAGC ||||||| | |||||||||||||| || || |||| ||||||
TCCATTCCGGAAAAACAATG ACCGCTC G CAGGAGGTACTGC TC CT TGTA
AAAAGG /
TTCATCTCGTCATGGAGGAC CCT------ AG TC - TA - ACA- CC
CTGGACTCGCCATCCCCGGT
TGTG
GAM1274 CCGGTTGAGCTCCTCCACGT 2915 CATTCCGTGG 5985 G GA C A G TAAA- G

GCTGCGCGGTAAATTTTGGA GGCATGGGGT CCG TT GCTC TCC CGTGCT CGCGG TTTTG A
TCTAGGGGCATTCCGTGGGG GGGT ||| || |||| ||| |||||| ||||| |||||
CATGGGGTGGGTGAGGGCGG GGC GG tggg ggg gtacgg gtgcc GGGAT T
G AG t - g ttacG C

GAM1275 GGGCCAGCTTTTGGGTGACG 2916 TGTCGTACTG 5986 TTTTG A - GA T- A AGTA
CGGACGTCCTGCATGCAGTA CTGGCCC GGGCCAGC GGTG CG CG CGTCC GC TGC T
TTCGAGGCACGCTTGGACGA |||||||| |||| || || ||||| || |||
TGTCGTACTGCTGGCCC cccggtcg tcat gc gt GCAGG CG ACG T
----- - t A- TT C GAGC

GAM1276 AAGGGATATTGAGCTGTTAG 2911 TTAGTGATTC 5981 A A -- A--- -- TT TTG
AGTACGAAACTGACATTTCT GGTTCATTTT AAGGG TATTG GCTGT TAGAGT CGAA
ACTGACA TC A
TGACCTTGGTTGTTAGTGAT GAAG ||||| ||||| ||||| |||||| |||| ||||||| ||
TCGGTTCATTTTGAAGCAGC TTCTC ATGAT CGACg gtttta gctt tgattGT GG C
GTAGTAACTCTT A G aa cttg ag T- TTC

GAM1277 TTCAGGACACTCTGAGTCAG 2912 TCAATACTTC 5982 CACTCT------ ATCT-- C
ATCTTTGGTTGTCCCTGCAA CTGACTCCCA TTCAGGA GAGTCAG TTGGTTGT C
TCAATACTTCCTGACTCCCA ACTC ||||||| ||||||| ||||||||
ACTCCAAAATCCTGAA AAGTCCT ctcagtc aactAACG C
AAAACctcaacc cttcat T

GAM1278 GATATGTTTATTCATAAACG 2917 TCGCTAAGGA 5987 TTT A ------ -- AATT
CGTCAAATTTTTCATGAATC GTTTAAGAAT GATATG ATTC TAAAC GCG TCA T
GCTAAGGAGTTTAAGAATCT CTCA |||||| |||| ||||| ||| |||
CATGTC CTGTac taag atttg cgc AGT /
tc- a aggaat tA ACTT

GAM1279 TTTTCAAATCCATTTGTGAG 2918 TACCTTTTCT 5988 CAT- TC- GC
AAGTCTATCGCCTTAGATAC CGTAGTCGAG TTTTCAAATC TTGTGAGAAG TATC C
CTTTTCTCGTAGTCGAGGTT GTTT |||||||||| |||||||||| ||||
TGAAGA AGAAGtttgg gatgctcttt atAG T
agct tcc AT

GAM1280 CAGGCTTACGCGCATGAATC 2920 CGCATGAATC 5990 GCTTACGc- atc cccatgCCAA
TCA C AA
TTCCATCACCCATGCCAAAA TTCCATCACC CAG gcatga ttccatca AAACC TCT C C
ACCTCATCTCCAACATGAAG CATG ||| |||||| |||||||| ||||| ||| |
AATGGTTTTGATGGAATCAT GTC TGTACT AAGGTAGT TTTGG AGA G /
GTCTTCTCTCACTG ACTCTCTTC --- ---------- TA- A TA

GAM1281 CTGTCTTGTTGCCCTCACCC 2921 CACCCGCAGC 5991 C T CTcaccc ccgca tct
GCAGCCGCACTGGCGTCTAC CGCACTGGCG CTGT TTG TGCC gcag ctggcg a
TTCGTCGGCAATCTGCACCT TCTA |||| ||| |||| |||| ||||||
GGCATCAAACAG GACA AAC ACGG CGTC GGCTGC /
- T TCCA--- TAAC- TTC

GAM1282 GTCTCACTAAGCCAACCCAC 2922 TGTCCTAGTT 5992 CCA- CCACCTCCCCC C--
CTACCAA
CTCCCCCCTCACATCCCTAC TCCAACCCTG GTCTCACTAAG AC CT ACATCC C
CAACCACTCCCTGGATGTCC TGCT |||||||||| || || ||||||
TAGTTTCCAACCCTGTGCTC CAGAGTGGTTC tg ga tgtAGG C
CTTGGTGAGAC Ctcg tcccaaccttt tcc TCCCTCA

GAM1283 AACACGGCGAGGCTGTGGTC 2923 TCATTCAGCT 5993 GGC C T TCC A- TT - TGCG
CCTCT
CTGGAATGTTTGAAGATGCG CCACTCCCAC AACAC GAGG TG GG TGGA TG TGA AGA
CCG C
CCGCCTCTCCATCCCGGACT CTCA ||||| |||| || || |||| || ||| ||| |||
CTCTCATTCAGCTCCACTCC TTGTG ctcc ac cc acct ac act TCT GGC /
CACCTCAAGTGTT Aa- - - tc- cg tt C CA-- CCTAC

GAM1284 GGCCACCCCATTCTGATCTC 2924 CACACCGCCC 5994 CCCCATTCT TCTCA A ACT CC
AGGCGATGACTCCGTCCTTT CCTTCTCCAC GGCCA GA GGCG TG CCGT T
GCGGCACACCGCCCCCTTCT TTTG ||||| || |||| || ||||
CCACTTTGGCC CCGgt ct ccgc ac GGCG /
ttcacct-- tccc- c ac- TT

GAM1285 GAAGATCGAGAAGAGAAAAG 410 GACTATGTAT 3480 G GAA AAA-- AT GA TAATA T
TACAATGTGAAGTAATAGCT TGGTAGCTCC GAA ATCGA GAG AGTACA GT AG GC A
ACTGCCCTGGACTATGTATT TGTC ||| ||||| ||| |||||| || || ||
GGTAGCTCCTGTCGATATTC CTT TAGct ctc ttatgt ca TC CG C
A gtc gatgg at gG C---- T

GAM1286 GAAGTAGCGAACCTCTGCTC 411 TGAGCAGGAG 3481 T - CT G C
ACTGCCCGGGCCCTCCGGGA TTGCGCTTTT GAAG AGCG AAC CTGCTCACT CCCGGG C
GGTGAGCAGGAGTTGCGCTT C |||| |||| ||| ||||||||| ||||||
TTC cttt tcgc ttg gacgagtGG GGGCCT /
- g ag A C

GAM1287 CCCTACAGAAAAGATAATGG 412 TGAAGGCCTT 3482 C AAA AAT- AC ---- AC
CTACCATCCACAAGGGATTA AGATCTGAGC CCCTA AG AGAT GGCT CA TCC A
CTGAAGGCCTTAGATCTGAG TTGG ||||| || |||| |||| || |||
CTTGGGG GGggt tc tcta ccgg gt AGG /
- gag gatt aa CATT GA

GAM1288 GGGGACCAGTTCTGATAGTG 413 TGATAGTGAC 3483 AC g- a aga t
ACAGATAGTAATTATGTTGC AGATAGTAAT GGGG CAGTTCt at gtgac tagtaat a
TAAGAGTTATAATGAAGAAT TATG |||| ||||||| || ||||| |||||||
TGCCCT TCCC GTTAAGA TA TATTG ATCGTTg /
-- AG A AGA t

GAM1289 GCGGCACACCAGAAACTTGC 414 TTGCCCAAGT 3484 C CAGAAAC AAACTC - A
ACAAACTCCGGATTCAGCAG GCAACACCGT GCGG ACAC TTGCAC CGGATT C G
AAATTTGCCCAAGTGCAACA GTCC |||| |||| |||||| |||||| |
CCGTGTCCGC CGcc tgtg aacgtg gttTAA G C
- ccac--- aaccc- A A

GAM1290 AGAGGGGGAGTGTGTGGTCT 418 GATCGGCAGA 3488 TGTGT A GA A
GTAGAGAGACATGAGTTGAT CCCCCTCTCC AGAGGGGGAG GGTCTGT GA GAC T
CGGCAGACCCCCTCTCCCCC CCCT |||||||||| ||||||| || |||
TCT TCtccccctc ccagacg ct TTG G
tccc- g ag A

GAM1291 TCTCACCCTGACAGCTGTCA 419 CCTGACAGCT 3489 CC---------- AG
GGGGTTACATGAGAGAACTT GTCAACCTAA TCTCAC
TGACAGCTGTCAGGGGTTACATGAG A
CATGTAACCCCTGACAGCTG TCCT |||||| ||||||||||||||||||||||||
TCAACCTAATCCTGACCGTG AGAGTG actgtcgacagtccCCAATGTACTT /
AGA CCAGtcctaatcca CA

GAM1292 GCATTGTTTACAGCAGATGT 420 CAGCAGATGT 3490 ATT gc ag cttgaA AC
CGTAGACATCTTGAAGGACA CGTAGACATC GC GTTTAca agatgtcgt acat GGACAT C
TACCAAATGTTCAGGTATAT TTGA || ||||||| ||||||||| |||| ||||||
GTGGATGACGTCTATGTGAG CG CGAGTGT TCTGCAGTA TGTA CTTGTA /
CTCAGC ACT A- GG TATGGA AA

GAM1293 GACACTTTGCCAGCGGTTGT 421 TTTGCCAGCG 3491 Ct cc t-- atttatcA
AGATTTATCATATTTCTCCA GTTGTAGATT GACA ttg agcgg tgtag T
CTACATATCCGTTACAATTT TATC |||| ||| ||||| |||||
GTT TTGT AAC TTGCC ACATC A
TT A- TAT ACCTCTTT

GAM1294 GTAAGGGTACTCTCATCACC 422 AAGGGTACTC 3492 --- --- t t aAATTAAT
AATGTAAATTAATATGTAGC TCATCACCAA GTaa gggt actctca caccaa gt A
AAACTTTGGTGTGGGAGTCC TGTA |||| |||| ||||||| |||||| ||
TACCCCTTTTGC CGTT CCCA TGAGGGT GTGGTT CA /
TTC TCC - T AACGATGT

GAM1295 AGGGCAATGCTCTAGCAGAT 423 TAGCAGATAA 3493 AA t agataaa- a -- --------- - A
AAACAAGCTGTTTCAGGAAG ACAAGCTGTT AGGGC TGCTC agc ca gct gtttca gGAAG
CT T
CTATAAGGTCTTCTCAAATG TCAG ||||| ||||| ||| || ||| |||||| ||||| ||
AATTGAAACCCAGCCTGGAT TCCTG ACGAG TCG GT CGA CAAAGT TCTTC
GG A
GCAGAGCTTGAGCAAGTCCT A- T AGACGTAG C CC TAAGTAAAC T A

GAM1296 GGCCAGGGTAGCTCAATCGG 2919 TTCTCGGTTC 5989 A--- C- GT - - C
TAGAGCAGCGGTTCCTGGAG AAGCCCGAGC GGCCAGGGT GCT AATCG AGAGC AGCGG
TTC T
TCCGCTGGTTCTCGGTTCAA CCTG ||||||||| ||| ||||| ||||| ||||| |||
GCCCGAGCCCTGGTT TTGgtcccg cga ttggc tcttG TCGCC GAG /
agcc ac -- G T G

GAM1297 TCTGAATAAAACATCAATGT 415 TAAAACATCA 3485 Ataa--- caat ---- a G
CGCAATTTGTATTGTCCAAT ATGTCGCAAT TCTGA aacat gtc gca tttgtATT T
ACAGAATGTCTATGATTCGT TTGT ||||| ||||| ||| ||| ||||||||
GTTAAAACCATCGGA AGGCT TTGTG TAG TGT AGACATAA C
ACCAAAA CT-- TATC A C

GAM1298 AGAGACTGTGATGGGGCAGC 416 ACTGTGATGG 3486 t a tac cgA CTCGACAACTA GT
TA A G
CTACTCCGAAGACCCCTCGA GGCAGCCTAC ggggc gcc tc AGACCC AGGGA TCC
GGG CGGCAG C
CAACTAAGGGAGTTCCTAGG TCCG ||||| ||| || |||||| ||||| ||| ||| ||||||
GACGGCAGGCTTCTGTCGCC CCCCG CGG AG TTTGGG TCCCT AGG TCC
GCTGTC T
TCTGGATCCCTGGGTTTGCA C A TAA ACG ---------- -- TC - T
GAAATGGCAGCCCCCTTGTA
CCCTCT
GAM1299 TTTGTATTTCCCTGTGTCGT 417 AAAGATGAGA 3487 CC- T - TGG CG T
TCGTGGTCTCGTTCGTGATT GTTGAAATGC TTTGTATTTC TGTG CGTT CG TCTCGTT TGA T
TTTTAAAGATGAGAGTTGAA TACA |||||||||| |||| |||| || ||||||| |||
ATGCTACATATGAAATATAG AGATATAAAG acat gtaa gt agagtag aTT T
A TAT c a tg- aa T

GAM1300 GGCATATATTCCTGATCCGC 424 ATAGAGAAAT 3494 TCCTGATCCGC GA A TA
CAATGATTCAATCCTTAGGA TGTACCTGTA GGCATATAT CAAT TTC ATCCT G
TGGGATAGAGAAATTGTACC TATG ||||||||| |||| ||| |||||
TGTATATGTT TTgtatatg gtta gag taGGG G
tccat------ aa a TA

GAM1301 TATATACGATAAGATATGTT 425 TAAGATATGT 3495 C --- ttt a g CAA-- TT
TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GAtaa gatatg attc taaac cGT ATTT C
TTTTCATGAATCGCTAATGA ACGC |||||| ||||| |||||| |||| ||||| ||| ||||
GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG GTA TAAG /
ATTGTCCTATATA C AAA TC- A A ATCGC TA

GAM1302 GCTGTCATTAAATATTTATC 426 TAAACTGTTC 3496 CATTAAATA C Cta - aa- ta a-
CT
ATCTAAACTGTTCTAATTGT TAATTGTATA GCTGT TTTAT AT aact gttct ttg tactt CTAA G
ATACTTACTAACTGTATTAG CTTA ||||| ||||| || |||| ||||| ||| ||||| ||||
AGGAGTAGCCAAAGGAGAAC CGACA AAATG TA TTGA CAAGA AAC ATGAG
GATT /
AAGTTATCATAGTAAAACAG --------- A CTA A GGA CG GA AT
C

GAM1303 AATGGTAGCGCATCTTTAAC 427 TTTGATCGAG 3497 C CTTT - TT CT
TCGTCAGTTAGCTCTTTCTT TTCGTCGCTA AATGGTAGCG AT AACTCG TCAG AG C
TTGATCGAGTTCGTCGCTAC CTAT |||||||||| || |||||| |||| ||
TATT Ttatcatcgc tg ttgagc agtt TC T
- c--- t t- TT

GAM1304 TAGGGGACCTCGGATATCGG 428 TTTGCCAGAA 3498 -- CG C---------- CAA
GCCTCGGCCAAGAAAGCCCA ACAGGTCAAG TAGGGGA CCTCGGATAT GGCCT GGC
G
AATTTGCCAGAAACAGGTCA TATC ||||||| |||||||||| ||||| |||
AGTATCTGGGGTATCTTCTA ATCTTCT GGGGTctatg ctgga CCG /
AT aa caaagaccgtttAAAC AAA

GAM1305 CTGAGGAGGGGCTGCAACAT 429 TCTTACGGAC 3499 A CAACATGACTG T C T -
AAG C
GACTGCCTTGACATCTTGGC CAGCCTCTCC CTG GGAGGGGCTG CC TGA ATCT GG CTG
CC A
TGAAGCCCACGGAACTAGAC CAG ||| |||||||||| || ||| |||| || ||| ||
CAGATCTTACGGACCAGCCT gac cctctccgac gg att tAGA CC GAT GG /
CTCCCAG - ca--------- c c - A CAA C

GAM1306 GTTACTATTATTTATAACTG 430 TATTATTTAT 3500 at--- taa a c
ATGTAACCCACGTAACATTA AACTGATGTA GTTACtatt tta ctgatgt ac c
GAATTAATTATCGATAGTAA ACCC ||||||||| ||| ||||||| ||
T TAATGATAG AAT GATTACA TG A
CTATT TAA A C

GAM1307 CGCGCACATCTGCCGTCTGC 431 TGCTGTTGGG 3501 ACAT C - - AA - C T GT
GCAACACCGCGTCCGTCAAG GCGCAAGAGC CGCGC CTG CG TCT GCGC CA C GCG CC C
GTGCTGTTGGGGCGCAAGAG GACA ||||| ||| || ||| |||| || | ||| ||

CGACAGCGAGCGCG GCGCG Gac gc aga cgcg gt g cgt GG /
AGC- a g a gg t t - AA

GAM1308 GAGACTGTGATGGGGCAGCC 432 TGTGATGGGG 3502 - a tac cga CTCGACAACTA GT TA A G
TACTCCGAAGACCCCTCGAC CAGCCTACTC ggggc gcc tc aGACCC AGGGA TCC GGG CGGCAG C
AACTAAGGGAGTTCCTAGGG CGAA ||||| ||| || |||||| ||||| ||| ||| ||||||
ACGGCAGGCTTCTGTCGCCT CCCCG CGG AG TTTGGG TCCCT AGG TCC GCTGTC T
CTGGATCCCTGGGTTTGCAG C A TAA ACG ---------- -- TC - T
AAATGGCAGCCCCCTTGTAC
CCTCTC
GAM1309 GGCGGCGATCTTCCACGCGC 433 ACGCGCTCCT 3503 ATCTT cgcg aacg- a ac
TCCTCAACGCCACGACGTAC CAACGCCACG GGCGGCG CCa ctcctc cc cg g
CGGGACCTGGAGGAGGACTG ACGT ||||||| ||| |||||| || ||
GCGCCGCC CCGCCGC GGT GAGGAG GG GC t
----- CAG- GTCCA - CA

GAM1310 TATATACGATAAGATATGTT 434 TAAGATATGT 3504 C --- ttt a ------ -- AATT
TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GAtaa gatatg attc taaac gcG TCA T
TTTTCATGAATCGCTAAGGA ACGC |||||| ||||| |||||| |||| ||||| ||| |||
GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG CGC AGT /
ATTGTCCTATATA C AAA TC- A AGGAAT TA ACTT

GAM1311 AGCGGTTGTAGATTTATCAT 435 TAAGAATTTA 3505 T T ATAT CC TACATATCC
ATTTCTCCACTACATATCCG GATACATCTA AGCGGT GTAGAT TATC TTCT AC G
TTACAATTTGTTAAGAATTT TATT |||||| |||||| |||| |||| ||
AGATACATCTATATTGCT TCGtta tatcta atag aaga TG /
- c attt at TTTAACATT

GAM1312 CTGGGGCCTTGGCGTCGGCC 441 TGGCGTCGGC 3511 - CTt c g t ct- CAAA
GGTGGCCTACCTGTCCAAAA CGGTGGCCTA CTG GGGC gg gtcg ccggtggcc ac gTC A
AGCTAGACCCAGTGGCCGCT CCTG ||| |||| || |||| ||||||||| || |||
GGGTGGCCCCCTTGCCTACG GGC TCCG CC CGGT GGTCGCCGG TG CAG A
G A TTC C G - ACC ATCG

GAM1313 CTGAGGAGGGGCTGCAACAT 442 TCTTACGGAT 3512 A CAACATGACTG T C T - AAG C
GACTGCCTTGACATCTTGGC CAGCCTCTCC CTG GGAGGGGCTG CC TGA ATCT GG CTG CC A
TGAAGCCCACGGAACTAGAC CAG ||| |||||||||| || ||| |||| || ||| ||
CAGATCTTACGGATCAGCCT gac cctctccgac gg att tAGA CC GAT GG /
CTCCCAG - ta--------- c c - A CAA C

GAM1314 GTTTAAAAAATCCAAAATTC 436 TCCAAAATTC 3506 A c--- a t a
TTAATAGAAATTTATTGTGA TTAATAGAAA GTTTA AAAAtc aaa ttc taatag a
AATTTAAAAGATTTTGTAAA TTTA ||||| |||||| ||| ||| ||||||
T TAAAT TTTTAG TTT AAG GTTatt a
G AAAA A T t

GAM1315 CCGCAGAGTGTTCCGGATTG 437 TCCACAACAA 3507 - CC G ----- G
CAGGTTTGGGCAACCTGTAT CTCTGCGG CCGCAGAGT GTT GGATT CAGGTTT GG C
GAATTTGGAGTCCACAACAA ||||||||| ||| ||||| ||||||| ||
CTCTGCGG ggcgtctca caa cctGA GTTTAAG CC A
a ca G TATGT A

GAM1316 TCAACAATGGAGATGACAAC 438 AGACAGGAAC 3508 - GAGA - ACG A TCCG-
AGTGG
GTCCTGATCTGTCCGGCAGT TGTACAGACA TCAAC AATG TG ACA TCCTG TCTG GC A
GGAGGTAGGCAGAGTCAGAC TTGG ||||| |||| || ||| ||||| |||| ||
AGGAACTGTACAGACATTGG AGTTg ttac ac tgt aggac agaC CG /
TTGA g ag-- a ca- - TGAGA GATGG

GAM1317 GAAATATTCCCAAGATTCGG 439 TCCCAAGATT 3509 A- Tt agat g cag
GATGCCACAGGTATTGGGTT CGGGATGCCA GAA TA ccca tcgggat cca g
CCGATAATGGGCCTGCCTTC CAGG ||| || |||| ||||||| |||
CTT GT GGGT AGCCTTG GGT /
CC CC AAT- - TAT

GAM1318 AGAGTGGCTTGGGGTGCAGT 443 CGGCACCCCA 3513 -------- AGTCTCG C
CTCGGCGCACACGTGCGCGG AACTCCGTAG AGAGTGGCT TGGGGTGC GCGCA A
CACCCCAAACTCCGTAGCCA CCAC ||||||||| |||||||| |||||
CTTT TTTcaccga accccacg cGCGT C
tgcctcaa g------ G

GAM1319 TAGTGGTGTTTGAGCGTGGT 444 TTTGAGCGTG 3514 TG Gttt tg - t
GATGTAGGTCTTTTTACTAT GTGATGTAGG TAG GT gagcg gtgat gtagg c
TATTTTGCTTTTAATTGTTA TCTT ||| || ||||| ||||| |||||
ATT TA TTCGT TATTA CATTT t
GT ATT- TT T t

GAM1320 CGAGAGACGTTTCTCGCTTA 445 TGAGAAAGCG 3515 - ACGT - A - - - CA
CTATACAGGGCCAAAGCGCA GTGAATTCCC CG AGAG TTC TCGCTT CT ATACA GG GC A
CCATGTATGAGAAAGCGGTG TCTA || |||| ||| |||||| || ||||| || ||
AATTCCCTCTACG GC tctc aag ggcgaa ga tATGT CC CG A
a cctt t a g A A CG

GAM1321 GAGACCTAGCAGACTTCCGG 446 CAGCACCCAG 3516 - A---- A TC-- TCc ac act - ctg AG

ATCCAGCACCCAGACTTGAT ACTTGATCCT GAG ACCT GCAG CT CGGA agc ccag tga tc ctaC T

CCTGCTACAGTACGTGGATG GCTA ||| |||| |||| || |||| ||| |||| ||| || ||||

ACTTACTGCTGGCCGCTACT CTC TGGA CGTC GA GCCT TCG GGTC ATT AG GGTG /

TCCGAACTAGACTGCCAACA A ACAAC A TCAA TCA CC GTC C TA- CA AGGTACTC

GAM1322 CCGACTATTATGAAAGGTTA 447 TGAAAGGTTA 3517 AT g ------ ---- t a GACATATT

CTCGGTTGAACAGATTGGAA CTCGGTTGAA CCGACT TAt aaa ggttac tcggt gaac gaTTGGAA G

GACATATTGAGAACGCGTTC CAGA |||||| ||| ||| |||||| ||||| |||| ||||||||

CGATCGTTCACCGATCCAGT GGCTGA GTA TTT CCGGTG AGCCA CTTG CTAGCCTT /

GGCCATTGGATTTGATGCAA AC G AGGTTA ACCT - - GCGCAAGA GTCGG

GAM1323 GCTGAGTACCACATGTCCAA 440 CTCGCCTCCG 3510 T AC-- T AAT-- - T

TGGCAGTTTTCCAACTCGCC AGGTCATCCC GCTGAG ACC ATG CC GGC AGTT T

TCCGAGGTCATCCCAGGTCC AGGT |||||| ||| ||| || ||| ||||

TCAGC CGACTC tgg tac gg ccg tcAA C

C accc t agcct c C

GAM1324 TTTTTGGTCCACTTTTCCAT 448 AGGGATAGAT 3518 TTTTCCAT- TA------- - CC TT CG TT C TA

ACGTTTATATTCTTTTAATC CTTGCAAGTT ACGTT TATTCT TTTAAT TGCG ATC T C GT T

CTGCGTTATCCGTTTCCGTT AAAT ||||| |||||| |||||| |||| ||| | | ||

ATATACAGGGATAGATCTTG TGTAA GTAAGA aaattg acgt tag a g CA /

CAAGTTAAATAGAATGCTCT TTTTTTTAC TAAATTCTC t a- tc at gg a TA

TAAATAATGTCATTTTTTTA

TCCGCTAAAAA

GAM1325 CGAAGTTGAAAACTTTGGCT 449 TTTGGCTTGA 3519 T A tt c-- t

TGAGCACCGATCATTTGACC GCACCGATCA CGAAGT GAA AC tggcttgagca cga c

TGCTTAAGCTATCGTCTTCA TTTG |||||| ||| || |||||||||| |||

CTTCG GCTTCA CTT TG ATCGAATTCGT Jtt a

- C CT CCA t

GAM1326 TGTTATTTATAGTTTATAGA 450 TTTATAGTTT 3520 - tt t g ttt gaTTA

CATTTGGGATTATTATAACC ATAGACATTT TGT TA tatag ttata aca gg T

TGTATATAACCTGTATTTGT GGGA ||| || ||||| ||||| ||| ||

ACA ACA GT ATGTC AATAT TGT CC /

T TT C A --- AATAT

GAM1327 TATATACGATAAGATATGTT 451 TAAGATATGT 3521 C --- ttt a gcGTCAA-- TT
TATTCATAAACGCGTCAAAT TTATTCATAA TATATA GAtaa gatatg attc taaac ATTT C
TTTTCATGAATAGCTAAGGA ACGC |||||| ||||| |||||| |||| ||||| ||||
GTTTAAGAATCTCATGTCAA ATATAT CTGTT CTGTAC TAAG ATTTG TAAG /
ATTGTCCTATATA C AAA TC- A AGGAATCGA TA

GAM1328 AATGGTAACGCGTCGTTAAC 452 ACGCGTCGTT 3522 ac t tt - ttaaCT
TCGTCGGTTAACTCTTTCTT AACTCGTCGG AATGGTA gcg cg aactcg tcgg C
TTGATCGAGTTCGTCGCTAC TTAA ||||||| ||| || |||||| ||||
TATT TTATCAT CGC GC TTGAGC AGTT /
-- T -- T TTCTTT

GAM1329 AGCGGTTGTAGATTTATCAT 453 TAAGAATTTA 3523 T T ATAT CC CACATATCC
ATTTCTCCACCACATATCCG GATACATCTA AGCGGT GTAGAT TATC TTCT AC G
TTACAATTTGTTAAGAATTT TATT |||||| |||||| |||| |||| ||
AGATACATCTATATTGCT TCGtta tatcta atag aaga TG /
- c attt at TTTAACATT

GAM1330 TATATATGACATAATAAATT 454 TATATGACAT 3524 t cataata TC- G
GGTAAATCCTAGTTCTGGTA AATAAATTGG TAtata ga aattggtaaa CTA T
TTTTACTAATTACTAAATCT TAAA |||||| || |||||||||| |||
GTATA ATATGT CT TTAATCATTT GGT T
- AAATCA- TAT C

GAM1331 CCAAATACATCGACTGCTAC 455 CTAAAGCAGT 3525 C ACT T GGT CTA
TGCTGGTGGACCTATCGTTG TGCCGATTTA CCAAATA ATCG GC ACTGCT GGAC T
TCCTAAAGCAGTTGCCGATT TTTG ||||||| |||| || |||||| ||||
TATTTGG Ggtttat tagc cg tgacga cCTG C
t --- t aat TTG

GAM1332 CGGTCGGCGCCGATTTCCGG 456 CCGGTCCAGA 3526 T GC --- G CG
CCCGGCGCGTCCCCGCGGGG TCGCGGTCGC CGG CGGC CGATTT CCGGCCC GCG T
CCGGTCCAGATCGCGGTCGC CCG ||| |||| |||||| ||||||| |||
CCG gcc gctg gctaga ggccGGG CGC C
c gc cct G CC

GAM1333 GATCCGGATTTGAAAGAAGT 457 TGAAAGAAGT 3527 Ttgaaa a - ga
TACTGTTGGTGATCAAACCA TACTGTTGGT GATCCGGAT gaagtt ctg ttggt t
GTCAGCAATTTCCTTATTTG GATC ||||||||| |||||| ||| |||||
GATC CTAGGTTTA CTTTAA GAC GACCA c
TTC--- C T AA

GAM1334 GCTTGCTCTTCCCTGATCAT 458 TCCCTGATCA 3528 T- T cc at--- tc -- act
CTCCTCAAGTACTACTCGGC TCTCCTCAAG GC TGC CTt ctg ca tcct caagt A
TTGCTGGGATTTGTTCTGCA TACT || ||| ||| ||| || |||| |||||
GAAAGTGCACTGC CG ACG GAA GAC GT AGGG GTTCG C
TC T A- GTCTT TT TC GCT

GAM1335 CTCCTTCCAATCCTAGCTCA 114 GGAGGTCAAT 3184 CCAA GC ----- TTCT TACA
ATTGACCTTCTTCCGACTAC TTCGAAGATA CTCCTT TCCTA TC AATTGACC TCCGAC G
AGAAGATGTTGGAGGTCAAT TGGG |||||| ||||| || |||||||| ||||||
TTCGAAGATATGGGACCTGA GAGGAG Agggt ag ttaactgg aggTTG A
GGAG TCC- at aagct ---- TAGA

GAM1336 ATTCATCCGGGCGTTCAGAA 459 CATCCGGGCG 3529 -- cgttcagaag g ATAAT
GAGTGGGAGCTATAATACAT TTCAGAAGAG ATTc atccggg agt ggAGCT A
CAAGCTCCAACTCCCGGATC TGGG |||| ||||||| ||| ||||||
CGAGT TGAG TAGGCCC TCA CCTCGA /
CC ---------- A ACTAC

GAM1337 TTTTTGGTCCATTTTTCCAT 466 ATCGTGCAGG 3536 TTTTCCAT- TA------- - T TT CG TCCGTTA
ACGTTTATATTCTTTTAATC TTAAATAGAA ACGTT TATTCT TTTAA CCTGCG ATC TT T
CTGCGTTATCCGTTTCCGTT TGCT ||||| |||||| ||||| |||||| ||| ||
ATATCCAGTGATAGATCGTG TGTAA gtaaga aaatt ggacgt taG AG /
CAGGTTAAATAGAATGCTCT TTTTTTTAC TAAATTCtc t - gc AT TGACCTA
TAAATAATGTCATTTTTTTA
TCCGCTAAAAA
GAM1338 GTGGGGCAGAGGAAAATTTG 467 GGGCAGAGGA 3537 c ggaaaatt cttcCT----- G
TGGCTTCCTTGCGAAAGTAT AAATTTGTGG GTGggg aga tgtgg TGC A
TTCAAACTAACCACATCTCC CTTC |||||| ||| ||||| |||
CCAC CACCCC TCT ACACC ATG A
- -------- AATCAAACTTT A

GAM1339 TAACTACCCTCCGGGAGCTC 468 CGGGAGCTCG 3538 ACCC a c c g
GGGGCCGTGGCCACGCAGTC GGGCCGTGGC TAACT TCcggg gct ggggc gtg c
TCCAGCCCTGGACCGAGTTG CACG ||||| |||||| ||| ||||| |||
GTTGA AGGTCC CGA CTCTG Cgc c
GCC- - C A a

GAM1340 CAGGCACTACTTTTTAGCCG 469 ATGACATTGA 3539 CTACTTTTT CGTTT a a tt t - gg
TTTTCTCGGATGACATTGAG GTATTTCTGG CAGGCA AGC TCTCGG tg ca gag att tct a
TATTTCTGGAAAAAGACAAT AAAA |||||| ||| |||||| || || ||| ||| |||
CTTCCTGCCACCCGAGAGCT GTCCGT TCG AGAGCC AC GT TTC TAA AGA a
TCTGCCTG CT------- ----- C C CC - C aa

GAM1341 CTTCTTTACTCGTGGTTAGT 470 TACCAGGAGA 3540 G-- TA GATCCG C
CGATCCGGTGCTACCACAAA GTAAAGAAG CTTCTTTACTC TGGT GTC GTG T
AGATACCAGGAGAGTAAAGA |||||||||| |||| ||| |||
AG gaagaaatgag acca tAG CAC A
agg -- AAAA-- C

GAM1342 TGATCTTGTGACGCATGCGG 115 ACGCATGCGG 3185 A T ac tgc g ggca g
CGCAGGCAGGCCGTTAGGCC CGCAGGCAGG TG TCT GTG gca ggc ca ggcc t
CATGAGCTTCTGCAGCACAG CCGT || ||| ||| ||| ||| || ||||
ACA AC AGA CAC CGT TCG GT CCGG T
- - GA CT- A AC-- A

GAM1343 GACAAAGAGCTGCTCGCTCA 116 TCGCTCAGGC 3186 AAAGA cg - - gtgaatagTA TG GTAG
GGCTGTTCTGTGAATAGTAC TGTTCTGTGA GAC GCTGCt ctcaggc tgt tct CAC GGGT G
ACTGGGGTGTAGGAGAGGGC ATAG ||| |||||| ||||||| ||| ||| ||| ||||
CCTGGTGAGACACGTGTCTG CTG CGGCGG GGGTCTG GCA AGA GTG CCCG A
GGAGGCGGCAGTTGGTC GTTGA A- T C ---------- GT GGAG

GAM1344 CGAGGCGTTGTGGCACAAAC 117 CGTTGTGGCA 3187 g- a- aa- g- A C G AG- CGA
AAAACAGGCGGAAGCCCTCG CAAACAAAAC CGAGGc ttgtggc caaaca aca gcGGA GCC TC TC GCCG G
TCAGGCCGCGAGAGGATGGC AGGC |||||| ||||||| |||||| ||| ||||| ||| || || ||||
ATCGAGGATGGCCTCCGCAA GTTCCG AACACCG GTTTGT TGT CGCCT CGG AG AG CGGT A
TGTCAGTGTTTGAGGCCACA GG GA GAC AA C T G CTA AGG
AGGGCCTTG

GAM1345 GTCGGGGCGGGAGAGTTCAC 460 TCCGTGCTTG 3530 A A C C C -- T
TCGGCACGCATGCACGTGTA CCTAGCGAAC GTCGGGGCGGG GAGTTC CT GGCA GCATG AC GTG A
ACCGCCAGTCCGTGCTTGCC TCAC |||||||||| |||||| || |||| ||||| || |||
TAGCGAACTCACCCGTCCCG CGGCCCTGCCc ctcaag ga ccgt cgtgc tG CGC A
GC a c t t c AC C

GAM1346 CGTGACATGGAGAAACTGGG 461 AGCTGTTGCC 3531 - A AA- --- A T CA g cag- g at
GGAATTTGTCTTCTGGCACA AGGGTGCTCA GG GA CTGGG GGA TTTGTC TCTGG Cagct ttgc ggt ctc g
GCTGTTGCCAGGGTGCTCAT TGAG || || ||||| ||| |||||| ||||| ||||| |||| ||| |||
GAGCGAGGGCCAGATGCAGG CC CT GACCC CCT GAGCAG GGACC GTCGA GACG CCG GAG a

AGCTGACCCAGGCGACGAGA T - GTA GGA A C CA G TAGA G Cg
TCCAGGCCCAGATGTCCCTC
TATCATG
GAM1347 GGGCGTGGCCGCTATTATAA 462 TTAGGACAAA 3532 T
AAAAAGTGAGAACGCGAAGC GTGCGAACGC
GGCCGCTATTATAAAAAAAGTGAGAACGCGAAGCGTTCGCACTTTGTCCTAATAATA A
GTTCGCACTTTGTCCTAATA TTCG ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
ATATATATATTATTAGGACA
CCGGCGATAATATTTTTTTCACTCTTGCgcttcgcaagcgtgaaacaggattATTAT T
AAGTGCGAACGCTTCGCGTT A
CTCACTTTTTTTATAATAGC
GGCCACGCCC
GAM1348 CCGCCCGCCCGACCCCCGAA 463 TAAACCACAC 3533 C CCGACCCCC ccac a t t
TAAACCACACAAGGCGGTAC AAGGCGGTAC CCGC CGC GAAtaaa ac aggcgg acg t
GTTTTCGTCTGTCTCGTTCT GTTT |||| ||| ||||||| || |||||| |||
TTATTTCTCACACACGCGCG GGCG GCG TTTATTT TG TCTGTC TGC t
CGG C CACACACTC CT-- C - T

GAM1349 CCGCGCAGGAAGGGGAAGGC 464 TGTGAGGTCA 3534 - G G AA CT---- -- A-
GCAGC
CTCCTCCGCCGGCAGGTGCA GCCGCTTCTT CC GC CAGGAAG GG GGCCTC CCGC CGGC
GGT G
GCGTCAGAACCAGGCCGCAG GGGC || || ||||||| || |||||| |||| |||| |||
CGGCTCTGTGAGGTCAGCCG GG cg gttcttc cc ctggag GGCG GCCG CCA /
CTTCTTGGGCAGG A g g ga tgtCTC AC GA AGACT

GAM1350 GGTGCTCCAAGATTACTAGT 118 TGGTAGGTGT 3188 T AAGAT- AG GG
ATTACCTTGGCGTAGAGGTG GGAAGGGCGC GGTGC CC TACT TATTACCTT C
GTAGGTGTGGAAGGGCGCGC GCC ||||| || |||| |||||||||
C ccgcg gg gtgg atggtGGAG G
c gaaggt -- AT

GAM1351 GGGTACGCGCGAGCGAGCGC 119 CAGTGCGTAG 3189 G A-- G G T - -------- TG
TC
CGGGGCTCTGCGCAGCGTGC CCGTTCTGCG GGTACGC CG GCGAGC CCGGG C CTG
CGCAG CG CTGGCGT G
TGGCGTTCGTTCGCGCCAGT TCAG ||||||| || |||||| ||||| | ||| ||||| || |||||||
GCGTAGCCGTTCTGCGTCAG TTATGCG GC CGCTTG GGCCT G gac gcgtc gc
gacCGCG T
TGTCCGGGTTCGCCACCGGC - CAC - - T t ttgccgat gt CT
GTATTC

GAM1352 GCGGCGAGACGAAGTCCAGC 120 AGGCACGCGC 3190 AGAC TCCA GG AA
ATG
ACGCGCGCGTGCGGGAAGCG GCGTGTCTTC GCGGCG GAAG GCACGCGCGCGTGC G
GCGC A
CATGACCAGCGTCAGGCACG CAGC |||||| |||| |||||||||||||| | ||||

CGCGCGTGTCTTCCAGCCGC CGTCGC cttc tgtgcgcgcgcacg C TGCG /
TGC cgac ---- ga -- ACC

GAM1353 ACACACCTACAAATTTACAT 121 TAAAATTGTT 3191 C CT A - - A- A
CTACAGGATTGCCTGAGAGA TGTCTGT ACA AC ACAA TTTA CA TCT CAGG T
CTGCTAAAATTGTTTGTCTG ||| || |||| |||| || ||| ||||
T tgt tg tgtt aaat GT AGA GTCC T
c tt a C C GA G

GAM1354 TTTATCCTGCAAGACTGTGG 122 TATTTTGGGG 3192 TGCAA T A- TTA A TC
ATATT
CCAGCTTACCAAAAAATTCT TGCCCGGTCC TTTATCC GACTG GGCC GC CCAAAA AT
TCTAG G
CTAGATATTGACAAACTGGA AGTC ||||||| ||||| |||| || |||||| || |||||
AGATATTTTGGGGTGCCCGG AGATAGG ctgac ctgg cg ggtttt tA AGGTC /
TCCAGTCCTGGATAGA TC--- - cc tgg a GA AAACA

GAM1355 CTTCTGGCGGGCAGCTCTGC 130 TGGCGGGCAG 3200 tg c ctc- ATCCT
TGGCAGGCATCCTTGGCTCG CTCTGCTGGC CTTC gcggg ag tgctggcaggc T
GCTTGCCGGCGTCCTCTTCC AGGC |||| ||||| || ||||||||||
CGCGGAG GAGG CGCCC TC GCGGCCGTTCG G
-- T TCCT GCTCG

GAM1356 ACAGCATTTAATACATATTC 123 TTCATTATTT 3193 G TT CATATT C AT TA
TAAATCTAAGTAATATAATT AATTTAGTTT ACA CAT AATA CTAAAT TAAGTAAT AATT T
TATATAATTCATTATTTAAT TATT ||| ||| |||| |||||| |||||||| ||||
TTAGTTTTATTCGGTGATGT TGT GTG ttat gattta atttatta ttAA /
A GC ttt--- - c- TA

GAM1357 AGTGGACTCTCCACTTCTCT 124 TAGAATGTCA 3194 CTC C CTTC T- C TA
TCTCGAGTATTCCCTATAAG AGTCCACT AGTGGACT CA TTCT TCGAGTA TC C T
TGATTTACTTGATAGAATGT |||||||| || |||| ||||||| || |
CAAGTCCACT tcacctga gt aaga AGTTCAT AG G /
act - t--- TT T AA

GAM1358 CAATGAGATCGATGTTGAGA 125 GATGTTGAGA 3195 GAGA ga a gaa aga-- AG AGA
CTGAAGCAAGAAGAAGGCTA CTGAAGCAAG CAAT TC tgttgag ct gca aga GCT T
GATGTCGGCAGTCTAAGCAT AAGA |||| || ||||||| || ||| ||| |||
GCAGAGGCTCGACGAGAATG GTTA AG GCAGCTC GG CGT TCT CGG /
AATTG AGTA A- - AGA ACGAA GA CTG

GAM1359 TAATACGATCGTTTGAACAT 126 GATCGTTTGA 3196 C --- ttcg a TCAA
TCGTTGGGTAGTAAATCAAT ACATTCGTTG TAATA gatcgtttga aca ttgggt GTAAA T

TAATTTTTGCAATTTAGATT GGTA ||||| |||||||||| ||| |||||| |||||
GTTTTTCAAGCGGTTCTATT ATTAT TTGGCGAACT TGT GATTTA CGTTT T
A C TTT TA-- A TTAA

GAM1360 AAGAAAACACCGATTAAATT 127 ATTAAATTAG 3197 ACACC tt g c tacatt AT TT
AGCATCAGCTACATTTAAAT CATCAGCTAC AAGAAA Ga aaatta cat agc tAAAT TC T
ATTCTTTTAGATAATTTATA ATTT |||||| || |||||| ||| ||| ||||| ||
ATTTGCTTATGTAATTTTTT TTCTTT TT TTTAAT GTA TCG ATTTA AG /
TAATATTTCTT ATAA- TT - T TTTAAT AT AT

GAM1361 TGATGTTTTATTATATTTCT 131 TGTTTTATTA 3201 t- tatttctc gcTTCTTTTAATAAT TTT
CAAATGCTTCTTTTAATAAT TATTTCTCAA TGAtgt ttatta aaat TCTTCT T
TCTTCTTTTTCATTAGAAGA ATGC |||||| |||||| |||| ||||||
TAAACTATCAAATAATTTTA ATTACA AATAAT TTTA AGAAGA C
TATTTTTAATAACTACATTA TC TTTTATAT ATAAACTATCAAAT- TTA

GAM1362 TCCTTGTGGTGGTGTCGTTA 132 TGTCGTTATA 3202 TT GGt ag a at
TACAGGTAATACATAACGTA CAGGTAATAC TCC GTGGT gtcgttatac gta tac a
TACGTATAGTGACTAACTAC ATAA ||| ||||| |||||||||| ||| |||
TTGGA AGG CATCA CAGTGATATG CAT ATG /
TT AT- -- - Ca

GAM1363 GATTCTGATATATAAATAGT 138 TATAAATAGT 3208 TC ta-- gtatttttt a ATGT CAA
ATTTTTTTCATTATATGTTA ATTTTTTTTCA GAT TGATA taaata tc ttat TAGACTCGG A
GACTCGGCAAAATACCGGGT TTAT ||| ||||| |||||| || |||| |||||||||
CTATTAATAAGGTCTTCATA CTA ACTAT ATTTAT GG AATA ATCTGGGCC /
TTTAGATTTATCATCATC CT TTAG ACTTCT--- - ATT- ATA

GAM1364 TATAGCAATATGAATTTTTT 139 TATTAAATAT 3209 A-- TTTTT T tat t tctaaa
TATTATTAAATATTAAATTA TAAATTATCT TATAGCA TATGAA TTA tattaaa taaa ta t
TCTAAATCCATTTTATTTTA AAAT ||||||| |||||| ||| ||||||| |||| ||
TATTTTAATATTAATTTTTC ATATTGT ATACTT AAT ATAATTT ATTT AT /
ATAGACTGTTATA CAG TTT-- T TAT T TTTACC

GAM1365 GATCTAAATAATCTCCGTTC 140 GTAGATCAAC 3210 G AAATTGT - ---- ----------
TA
AAAATTGTTTTACATTCTTC TACATTCATT TTCA TTTACATT CTTC TTTTAAT
TCTATAAT A
TTTTAATTCTATAATTAACT AAAA |||| |||||||| |||| ||||||| ||||||||
GTTGTAGATCAACTACATTC AAGT AAATGTAA GGGG aaaatta agatgTTG /
ATTAAAATTTTGGGGTAATG - ------- T TTTT cttacatcaact TC
TAAATGAAAACTTTGTTTAA
TT
GAM1366 GGCATACTATGGTGATGCGA 465 ACTATGGTGA 3535 Tac- tgatg - gg---- T-
GCTACAAAT

GGGCATTATTCAGTGCTACA TGCGAGGGCA GGCA tatgg cg ag cattat CAGT T
AATTCTTTTTTCAATTGCTA TTAT |||| ||||| || || |||||| ||||
TAATGATACAACTACGAACC CCGT ATACC GC TC GTAATA GTTA /
TCCATACATTTGCC TTAC TCCAA A AACATA TC ACTTTTTTC

GAM1367 AATGTTTACATATAGCGGAT 128 GTAGATCAAG 3198 CATATA G- A AT AAGAGAAA
CAACATACAAGAGAAAAATA CAACTTTTAA AATGTTTA GC GATC AC AC A
TAATACGTTAGTAGATCAAG ATAT |||||||| || |||| || ||
CAACTTTTAAATATT Ttataaat cg ctag tg TG A
tttcaa aa a AT CATAATAT

GAM1368 CTATCGAATCCAGGCCCCTG 129 TCGAATCCAG 3199 ---- gGATT
ATTGGTGGATTGCTGAAAGC GCCCCTGATT CTAt cgaatccaggcccctgattggt G
CAATCAGGGGCCTGGATTTG GGTG |||| ||||||||||||||||||||
CCCAATAG GATA GTTTAGGTCCGGGGACTAACCG C
ACCC AAAGT

GAM1369 TAGCTACTACACACCATCGA 133 TATGTTAGAT 3203 ACACA AAAAA TC A t- gg---
TTT
AAAAATCTCCATTTATGTTA GCGGGGGAGT T CCATCG A TCC TTtatg tagatgcg
ggagtatgtA T
GATGCGGGGGAGTATGTATT ATGT | |||||| | ||| |||||| |||||||| ||||||||||
TTTACCTATGTGTTTCGGAA G GGTAGT T AGG GAATAT ATTTATGT
CTTTGTGTAT T
ATGTATTTATTTATAAGGGA GTTAA A---- GA - TT AAAGG CCA
AGTATGATGGAATTGGGTTC
TG
GAM1370 GAGGTTGTTGACCACGTACA 134 CAGGTGCTCG 3204 A TGTT A TAc cgt a g a
GGTGCTCGTCGTAGGTGAGA TCGTAGGTGA G GGT GACC CG aggtgct cgt ggt ag c
CTCTGGCCCACGTCCAGCAT GACT | ||| |||| || ||||||| ||| ||| ||
TTCGCGGTCCTGCCC C CCG CTGG GC TTTACGA GCA CCG TC /
- TC-- C --- CCT C G t

GAM1371 GACCTTCTGCAGATAGGCGC 135 TCTGCAGATA 3205 tc ca ag g aC G CT CGC
GCTTGCGCACGTTGACCTCG GGCGCGCTTG GACCT tg gat gc cgcttgcgc GTT AC CG G
CGCGTGACGTTGTGGACGCG CGCA ||||| || ||| || ||||||||| ||| || ||
CGAGCGGGCGTCCAAGGGGT CTGGG AC CTG CG GCGAGCGCG CAG TG GC /
C GA -- -- G -- G TT AGT

GAM1372 GACTATAACCTCCGAAGTAC 136 TATAACCTCC 3206 C ccgaag --- a---------- A TA
GGGACCAGTAGGTAAAATCC GAAGTACGGG GA tataacct tacggg acc GT GG A
GACAAGGAATATATTCGTTC ACCA || |||||||| |||||| ||| || ||
CGGTATATCCGTAAACAGGT CT ATGTTGGA ATGCCT TGG CA CC A
TGTACTC C CAA--- ATA CCTTGCTTATATAAGGAA G TA

GAM1373 GCTATCGACAGCTACGACGT 141 ACTGGATGAG 3211 A TAC-- A ATac at - - agt
ATTAATACTGGATGAGGTAA GTAATGTCAG GCTATCGAC GC GACGT TTA tgg gag gtaat gtc
g
TGTCAGTGATTGGACAATTA TGAT ||||||||| || ||||| ||| ||| ||| ||||| |||
TACTCCCCCACAATGAGACG CGATAGTTG CG CTGCA AGT ACC CTC TATTA CAG
a
TCTTTCCGCGGTTGATAGC G CCTTT G AAC- CC A A GTt

GAM1374 AATAAAATCAGAATCTATAT 142 TTAGAATATC 3212 A ATCT-- GAAAT TAG
TTGAAATAGTTAGAGAGTGC CTAAATCTGA AATAAA TCAGA ATATTT AGT A
TTAGAATATCCTAAATCTGA CTTT |||||| ||||| |||||| |||
CTTTATT TTAttt agtct tataag tCG G
c aaatcc at--- TGA

GAM1375 GCTGTCGGTGAAGCGCAACT 143 TCGGTGAAGC 3213 - aa caactc- cg G
CCACCGTGTGATGGCGGTCG GCAACTCCAC GCTGt cggtg gcg cac tgTGAT G
CAGTGATCCAAACGCAGCAC CGTG ||||| ||||| ||| ||| ||||||
CGTACGGT TGGCA GCCAC CGC GTG ACGCTG C
T GA AAACCTA -- G

GAM1376 TCTCAAATTATCGCGATGGA 145 TATCGCGATG 3215 AAATtat ---- gcta- TC
TGCTACAGTAAACTCGCAGT GATGCTACAG TCTC cgcgat ggat cagtaaaC G
TTATTGATTTAATCTCCGGA TAAA |||| |||||| |||| ||||||||
TTGCGTGGAGA AGAG GCGTTA TCTA GTTATTTG /
GT----- GGCC ATTTA AC

GAM1377 AACTAGCACTACGATTACAA 146 TAGCACTACG 3216 a ---- tacaat- c - A
TGTGGGCATAACATCTGTAT ATTACAATGT AACtagc ct acgat gtggg ATA AC T
ATTTTCATCAACTTTATCGT GGGC ||||||| || ||||| ||||| ||| ||
TTTCGGAGCTAGTT TTGATCG GG TGCTA TACTT TAT TG C
A CTTT TTTCAAC T A T

GAM1378 TGGGGGCGTGTATACGAATA 147 GGCGTGTATA 3217 Gg cgaatacc -- TG A
CCTGAAGCGTTGGAAGCATT CGAATACCTG TGG gcgtgtata tgaa gcGT GA G
TGACGTATTTCAAAAAATAT AAGC ||| ||||||||| |||| |||| ||
ACACGCACTA ATC CGCACATAT ACTT TGCA TT C
A- AAAAA--- TA GT A

GAM1379 GCTTAGCGACGATGCACCCG 137 CACCCGTGAG 3207 TTA c c g gt t
TGAGGGAGGAGTCGTGAGCG GGAGGAGTCG GC GCGACGATG acc gtgagg agga cg g
TCCTCCTCACCGGTACATCG TGAG || ||||||||| ||| |||||| |||| ||
TCGCCACGC CG CGCTGCTAC TGG CACTCC TCCT GC a
CAC A C - -- g

GAM1380 TTTCCGCGGCCTCCATTGGC 144 TTCCCAGTCA 3214 GCCTC T CCTT GAC
TGGGACCTTTAACGACACAG TGTACGCGGA TTTCCGCG CAT GGCTGGGA TAAC A
GGTTATTCCCAGTCATGTAC GA |||||||| ||| |||||||| ||||
GCGGAGA agaggcgc gta ctgaccct ATTG C
at--- - t--- GGA

GAM1381 GTCTCCGGTCAGCCCGCTTC 148 CGAGGCTACC 3218 C A CC T AC T CCCATC
CCTCGACGGCCTCGTCGTCC GAGGGCAGTC GTCT CGGTC GC GCT CCCTCG GGCCTCG
CGT C
CATCCGTTTCGTACGCCGAG AGCC |||| ||||| || ||| |||||| ||||||| |||
GCTACCGAGGGCAGTCAGCC CAGA GCCGG cg tga gggagc tcggagc GCA G
GGCCGCAGAC C c ac c ca C TGCTTT

GAM1382 GCGGGGGGAGGAGCGGGGGG 149 GGGGAGGAGC 3219 GGGGGGAGGA GGGGGGAGGA
GGGGGGAGGA GGGGGGAGGA GGGG
AGGAGCGGGGGGAGGAGCGG GGGGGGAGGA GC GC GC GC GC G
GGGGAGGAGCGGGGGGAGGA GCGG || || || || ||
GCGGGGGGAGGAGCGGGGGG CG CG cg cg CG G
AGGAGCGGGGGGAGGAGCGG AGGAGGGGGG AGGAGGGGgg aggaggggg
aggaggggGG AGGA
GGGGAGGAGC

GAM1383 TGCCTTACGACCCGTTGAAA 150 ACCCGTTGAA 3220 T- Ga gttgaa a t ga G
GGATCTGGGAGAACAGTAAT AGGATCTGGG TGCC TAC ccc agg tc ggga aCA T
GTCATCCTTGACCCTGGGAG AGAA |||| ||| ||| ||| || |||| |||
TATCGGCA ACGG ATG GGG TCC AG TCCT TGT A
CT A- ------ C T AC A

GAM1384 GCTACGAGTTCCTGCGTGTC 151 TGGGCGGTTA 3221 - G - TG TC G - TT
GCTGGCTCGCCATTCACTGG CGTGGCGAGG GCTAC GA TTC C CGTG GCTG CT CGCCA C
TGTGGGCGGTTACGTGGCGA TCGG ||||| || ||| | |||| |||| || |||||
GGTCGGTGGC CGGTg ct gag g gcat tggc gg GTGGT /
g g c gt -- g t CA

GAM1385 GGGCTGGGGCCGGGGAGGGC 153 GGGCCGGGGA 3223 G G GGGGA G G G GGGGA G
G G GGGGA G G G GG
TGGGGCCGGGGAGGGCTGGG GGGCTGGGGC CT GG CC GG CT GG CC GG CT GG CC
GG CT GG CC G
GCCGGGGAGGGCTGGGGCCG CGGG || || || || || || || || || || || || || ||
GGGAGGGCTGGGGCCGGGGA GG TC GG TC GG TC GG cc gg tc gg cc gg TC GG
/
GGGCTGGGGCCGGGGAGGGC G G AGGGG G G G AGggg g g g agggg g G G
AG
TGGGGCTGGGGAGGGCTGGG

GCT
GAM1386 TCGGACATTGCTGATATCAT 154 TCCATGAGTA 3224 A G G A-- C------ GC
GGCCCAGGCTAGCTGGAAGA ATGAGAGTGC TCGG CATT CT AT TCATGG CCAG T
AATCCATGAGTAATGAGAGT CGA |||| |||| || || |||||| ||||
GCCGA agcc gtga ga ta agtacc GGTC /
- - g atg tAAAGAA GA

GAM1387 GTCGAACGTGTCGGGCTAGC 155 GGCTATGGAA 3225 - - TA - G T G TGGAG ---
TGA T
CATGGTCGGGCGTGTGCCCT CCGTCGCTGT CG GGC GC CAT GTCGGGCG GT CCC
AGCGATGG CGT CTGC T
GGAGAGCGATGGCGTTGACT ATGG || ||| || ||| |||||||| || ||| |||||||| ||| ||||
GCTTATGCGGCTATGGAACC GC TCG CG GTG CGGTCTGC CA Ggg tcgctgcc gta
ggCG A
GTCGCTGTATGGGAACCCGT T G TG T G C A tatg- aag tc- T
CTGGCGGTGTGCGTGCTGCG
TACATATCAC
GAM1388 TGTTCGTGGACAGAGCTTCT 159 TTCAATTCTC 3229 - AG TTCT A T A Ctt - c ttg
gTC
TTGCGGTAGATTATGATGAC AACATACGTT CAG C TTGCGGT GAT ATG TGA caattc tcaa
atacg ct A
TTCAATTCTCAACATACGTT GCTG ||| | ||||||| ||| ||| ||| |||||| |||| ||||| ||
GCTGTCACAGAAGATTGTGT GTC G AACGTCA CTA TAC ACT GTTAAG AGTT TGTGT
GA C
TTGAGGAATTGTTTCAGCAT G CT TAT- A - G TT- G - TA- AGA
ATCAACTGCAATATGTCCTG
GACCCGAACA
GAM1389 TCCTTGTGGTGGAGTTGTTA 160 AGTTGTTATA 3230 TT Ga g agta at
TACAAGTAATACATAATGTA CAAGTAATAC TCC GTGGTG gtt ttataca atac a
TATGTATAAGGACGCACCAT ATAA ||| |||||| ||| ||||||| ||||
TCGGA AGG TACCAC CAG AATATGT TATG /
CT G- G A--- Ta

GAM1390 GCCGTGGACCAGCCCTGGTC 152 GACCGGGCCA 3222 G C ---------- CT-- CTT C
GCCTCGCTTACCTGGGTCGC TCTCCCTGCT GCCGT GA CAGC CCTGGTCGC CG AC T
CGTTTCGTGACCGGGCCATC GTTT ||||| || |||| ||||||||| || ||
TCCCTGCTGTTTGACGGC CGGCA tt gtcg gggccagTG GC TG G
G t tccctctacc CTTT CGC G

GAM1391 GACGCACCAAGAAGGCATCC 156 ATTGTCCCGC 3226 GCACC AG- ATCCT TG AA
TGATGGTGTTTAAAAAAAAT ACATCTTTAA GAC AAGA GC GA GTGTTT A
ATTGTCCCGCACATCTTTAA GGTC ||| |||| || || ||||||
GGTC ctg ttct cg ct taTAAA /
gaat- aca cc--- gt AA

GAM1392 GTACGTTCATCGCCCTGAAC 157 GCCCTGAACC 3227 - - C c- c at

CTGTCGTTTATAGAGAACAT TGTCGTTTAT GTAC GTTC AT gccctgaa ctgt gttt a
AGATTTCAGGGTCATCGAGC AGAG |||| |||| || |||||||| |||| ||||
TGTAC CATG CGAG TA TGGGACTT GATA CAAg /
T C C TA - ag

GAM1393 AAAGAATTAGATTGTAAATA 161 TTAATTTAAA 3231 A-- AATAT AAA A GG AA
TACAAAAATTAATTCTTTAA AGAATTAGAT AAAGAATTAG TTGTA ACAA TTAATTCTTT AAA
AATAG A
AAGGAATAGAAAATATTATT TGTT |||||||||| ||||| |||| |||||||||| ||| |||||
AATTTAAAAGAATTAGATTG TTTCTTAATT AACAT tgtt gattaagaaa ttt ttATT A
TTCTGATACAAAAATTAATT AAA AGTCt a-- a aa AT
CTTT

GAM1394 TTTTTGTAGACAAAGAAGAG 162 TTACTGCAGA 3232 ACAAAGA ACACC CT - ---
ATTT AA
TACACCCTCTCATGGGCCCA TGGGCTCACT TTTTTGTAG AGAGT CT CA TGGGCCCA
GCA AGA C
GCAATTTAGAAACATCTCTT GGAA ||||||||| ||||| || || |||||||| ||| |||
ACTGCAGATGGGCTCACTGG AAAAATATC TTTCG Ga gt actcgggt cgt tCT A
AAGAGCTTTGATAATGCTAT GTAATAG A---- ag c aga cat- CT
AAAAA

GAM1395 GGGGGGTCTGTTTCTCCTGT 163 AGCCGTTAAC 3233 - TTTCTCC Ca aa--- c ta------
c
GGCAGCCGTTAACGCCGCTA GCCGCTAAGC GGGGGGT CTG TGTGG gccgtt cgc gc
agc t
AGCCTAGCTGACGAGATGCG CTAG ||||||| ||| ||||| |||||| ||| || |||
CGAATTAAACGGCACCACGC CCCCCCA GAC GCACC CGGCAA GCG CG TCg
/
CAGCACCCCCC C C------ A- ATTAA - TAGAGCAG a

GAM1396 GCACTGGTGTCCCATAATAA 164 ACTGGTGTCC 3234 - t- ccataataa --- A ATT
AGTGTATGACTCATTGTAAG CATAATAAAG GCact gg gtc agtg taTG CTC G
AGCATGTTGTACTGACTTCC TGTA ||||| || ||| |||| |||| |||
TGGTGT TGTGG CC CAG TCAT GTAC GAG /
T TT --------- GTT - AAT

GAM1397 GAGCCTCCGCACGTCCACCC 166 CCCCCCGGTC 3236 CCGC CCACC ATC TA
CGGGGATCTGCTACTCGCGC ACGTTCAGGT GAGCCT ACGT CCGGGG TGC C
CCCCCGGTCACGTTCAGGTT TC |||||| |||| |||||| |||
C cttgga tgca ggcccc GCG /
ct-- ct--- cc- CT

GAM1398 AAACACAAAAATGTATGTTC 158 AAATGTATGT 3228 CAA- -- acc-- a
AACCTTTTATTATACAATAA TCAACCTTTT AAACA aaatgtat gttca ttttatt T
AACTTTGTGAACTTATACAT ATTA ||||| |||||||| ||||| |||||||

TTGCTTTGTTT TTTGT TTTACATA CAAGT AAAATAA A
TTCG TT GTTTC C

GAM1399 AAACCTAATCAGAAATTCAG 165 TGTTAGGGAT 3235 TC- AAA - AAATT - ACAG - - TTCA
AAAACTATCTTGAAATTGAC GGTCTACAAG AAAT AGA CTAT CTTG GAC ATCC GGC TAGT GATATC A
ATCCACAGGGCTAGTGATAT AATA |||| ||| |||| |||| ||| |||| ||| |||| ||||||
CTTCAATATCTGATATCAAC TTTA TCT Gata gaac ctg tagg ttg ATCA CTATAG T
TATGTTAGGGATGGTCTACA TCT AAA a at--- g ga-- t A TCTA
AGAATAGAAATCTTCTATTT
CTGAAAGAAAT
GAM1400 GCAGATGTAAAGGCCTGGTG 167 TAACCTGTCA 3237 A GTAAAGG GT- GC TC A AGGA A
AGGCGAGTGTCTAGATTACA CTTCACTCCA GC GAT CCTG GAG GAGTG TAG TTAC GACTA T
GGAGACTAATATAGTCGGTA ACAG || ||| |||| ||| ||||| ||| |||| |||||
ACCTGTCACTTCACTCCAAC CG CTG Ggac ctc ttcac gtc aatG CTGAT /
AGGATCAGTCAGC A ACTA--- aac ac t- c G--- A

GAM1401 CTGTCGTCCCCCGATGCCGA 168 TTCGTGATAG 3238 TC- CC ATG A CG -- A
TCTCGCACACAGAGGCTGTT AACGGACGGT CTG GTC CCG CCG TCT CAC ACAG G
CGTGATAGAACGGACGGTGA GACT ||| ||| ||| ||| ||| ||| ||||
CTTCCAG GAC cag ggc ggc aga gtg tGTC /
CTt t- a-- a ta ct G

GAM1402 ATGTAGATGACGCGGAACAC 169 TAGATGACGC 3239 g c ac a cAGATAACTAATG CACA GG- AAA
ATATCTCAGATAACTAATGA GGAACACATA atgacg gga acat tct ATGTATCTA AAC GA A
TGTATCTACACAAACGGGAA TCTC |||||| ||| |||| ||| ||||||||| ||| ||
AAAGAAATCAGAGTTAGATA TACTGC CCT TGTA AGG TACATAGAT TTG CT G
GATACATGGAAATGTATCCT A T A- A ---------- AGA- AGA AAA
CGTCATAGATAT

GAM1403 GGAATGTTTGGAATATCCAA 170 TATTGTTTTA 3240 A CAA ----- A --- TAAT GT GAT
AGGCAGATTTTCTAACATTA AATTTTAAGT A TATC AGGCAG ATTTTCTAAC TTAG TTAA AT CATTT G
GTTAATAATATGTCATTTGA TAGA | |||| |||||| |||||||||| |||| |||| || |||||
TGTAAAAAATGGTATTGTTT T ATAG TTTGTT TAAAagattg aatt aatt ta GTAAA T
TAAATTTTAAGTTAGAAAAT A A-- AAATA - tta ttgt tG AAA
ATAAATTGTTTAGATAATCC
AAATATATC
GAM1404 GTTTTGCCCCATCGGCTATC 171 TAGGTGCCGC 3241 - T T CTCC- A
TGCTCCCAAAAAGTTGTAAT TGGGTGCGAA GTTTTGC CCCA CGGC ATCTG CAA A

ATAGGTGCCGCTGGGTGCGA AT ||||||| |||| |||| ||||| |||
AAT taaagcg gggt gccg tggat GTT A
t c - ATAAT G

GAM1405 CGATTTACGTAATCTATATA 172 GCAGAGTATC 3242 A A A CAA A- GAGA
CAAGATATATGCGAGAGAAT ATATAGAGAA CGATTT CGTA TCT TATA GATAT TGCGA A
GATATCGCAGAGTATCATAT TGCG |||||| |||| ||| |||| ||||| |||||
AGAGAATGCGAGGTCG GCTGGA gcgt aga atat ctatg acgCT T
- a g a-- ag ATAG

GAM1406 CGGTTACTATCAATATTATT 2855 TGATTATGAT 5925 A ATAT T - TATGAAAAT
CATCTAGTGATTATGAAAAT AGAACTG CGGTT CTATCA TA TCATC TAGTGAT T
TATAATGAATATTATTATGA ||||| |||||| || ||||| |||||||
TGATTATGATAGAACTG gtcaa gatagt at agtAG ATTATTA /
- ---- t T TAAGTAATA

GAM1407 TATTACTAACATAAAGATAA 2856 TACGTAAACT 5926 AACATAAAG a aaact ta ----------
--- G
TACGTAAACTACTTAATCTT ACTTAATCTT TACT ATAAt cgt act atctt agca A
AGCAGACATGCTCCACATAA AGCA |||| ||||| ||| ||| ||||| |||| |||| |

ATAAGGTTATCGATGCCGAA |||| ||||||||| || ||||||||| ||| ||
ACTTCTATCAGTGATTATTA taac ttattagtg ct TTCAAAGCC TTG GA T
CAAT a a atC GTAGCTA - A

GAM1412 GAGTTTAGATCTGAATTGAT 2863 TACAATATGT 5933 CTGA-- A -- AA
ACTGTCCAATCAGGATCTAG TTATCTAAGC GAGTTTAGAT ATTG TACT GTCC T
TACAATATGTTTATCTAAGC TT |||||||||| |||| |||| ||||
TT ttcgaatcta taac atGA TAGG /
tttgta - TC AC

GAM1413 GGAATGTTTGGAATATCCAA 2864 TATTGTTTTA 5934 A CAA ----- A --- TAAT GT
GAT
AGGCGGATTTTCTAACATTA AATTTTAAGT A TATC AGGCGG ATTTTCTAAC TTAG TTAA
AT CATTT G
GTTAATAATATGTCATTTGA TAGA | |||| |||||| |||||||||| |||| |||| || |||||
TGTAAAAAATGGTATTGTTT T ATAG TTTGTT TAAAagattg aatt aatt ta GTAAA T
TAAATTTTAAGTTAGAAAAT A A-- AAATA - tta ttgt tG AAA
ATAAATTGTTTAGATAATCC
AAATATATCT
GAM1414 GCACAGTATCAAGGATCAAC 2865 AAGGATCAAC 5935 A- - aa caactc ct
TCTGTTTATCTAGACATGAA TCTGTTTATC GCAC GTA TC ggat tgtttat a
TACTTCAATCCCAGGCTACC TAGA |||| ||| || |||| |||||||
CGTGT TGTG CAT GG CCTA ATAAGTA g
CC C AC ACTTC- Ca

GAM1415 GTTGCCGCTCTGATACTCCT 2866 TGCGGTAGCT 5936 CT CTC - G - A
CCGGGATGAGCCACATGGTC GTCCTGGTGG GTTGCCGCT GATA CT CCG GATGAG CC C
TCGTTGCGGTAGCTGTCCTG TAAC ||||||||| |||| || ||| |||||| ||
GTGGTAAC caatggtgg ctgt ga ggc tTGCTC GG A
tc c-- t g T T

GAM1416 CAGCTCCTTCTGATAGGTAA 2872 TAGGTAAACA 5942 - CT At aaac gaac ta
ACACGTCGAACGTGTAAGGC CGTCGAACGT CA GCTC TCTG aggt acgtc gtg a
ACGATGTTGGCCTTGTAGAT GTAA || |||| |||| |||| ||||| |||
GAGCATG GT CGAG AGAT TCCG TGTAG CAC /
A T- GT GT-- ---- GG

GAM1417 GGGCCCTAAGGAGGATAGCT 2859 AGGAGGATAG 5929 CCTA a ta t t c tcTCTA
GTGCCGGTGGTCTCTACACT CTGTGCCGGT GGGC agg gga gc g gc ggtgg C
GTTCCCACCCGCCGCTCCCC GGTC |||| ||| ||| || | || |||||
TAGCCC CCCG TCC CCT CG C CG CCACC A
A--- - -- - - C CTTGTC

GAM1418 CCTGGCCATGGCCGCTTCAG 2860 CGAGAGCGCC 5930 - CA -- CA AAAGA

AGTTCAAAGAGACCCCCGAA GTCAGAGCCA CC TGGC TGGC CGCTT GAGTTC G
CTCGAGAGCGCCGTCAGAGC TGG || |||| |||| ||||| ||||||
CATGG gg accg actg gcgag cTCAAG A
t ag cc ag CCCCC

GAM1419 ACACTGTTCTCAGCTAATAT 2867 CTGTTCTCAG 5937 t- agctaata cATCAC
CGATGCCATCACAAGCCTCA CTAATATCGA ACAc gttctc tcgatgc A
GCATCGGGGGAGAACTCGTG TGCC |||| |||||| |||||||
T TGTG CAAGAG GGCTACG A
CT GG------ ACTCCG

GAM1420 TGGGAGCCTAGCAGTGACGA 2868 GCAGTGACGA 5938 AGC ca atcc t- aa A
TCCACGGTGGCAACTATCCA TCCACGGTGG TGGG CTAg gtgacg acgg ggc cT T
GGGGCCCTCCGTCCCGTCAC CAAC |||| |||| |||||| |||| ||| ||
ACTAGTAGCCTA ATCC GATC CACTGC TGCC CCG GA C
GAT A- CC-- TC GG C

GAM1421 GGCGACACTTGGGTGCACAG 2873 AAGCTGCCGC 5943 CA -- CA-- TG CGT- AC
ACC
GTGGCCGTAGGTGTCACGTG GATGTACCCC GGCGA CTT GGGTGCA GG GC AGGTGTC
GTG T
ACCTTTTCCGCCGGCACCTT CGGG ||||| ||| ||||||| || || ||||||| |||
TAAGCTGCCGCGATGTACCC CCGCT ggg cccatgt cc cg TCCACGG CGC T
CCGGGGATCGCC AG cc agcg gt aaTT C- CTT

GAM1422 TTGTGATTCCAACCAGCGAG 2874 TGGTCAGGCG 5944 GATT AC- GCGA AA A
AATCACAT AAC- ATA
ATAACCCAGCCAATCACATC GGGGATCAGA TTGT CCA CA GAT CCC GCC CCATCA
TGGAG G
CATCAAACTGGAGATAGTAA TGTC |||| ||| || ||| ||| ||| |||||| |||||
CCTCCAAAAGTGGTGGTCAG AACG GGT gt cta ggg cgg ggtGGT ACCTC T
GCGGGGGATCAGATGTCATG ACT- Act aga- gg - act----- GAAA CAA
GTCAGCAA

GAM1423 CCGTGGTCCCAATAGATGGT 2875 TGTCCAAAGA 5945 GG-- -- AT CT AC---- AT
GTCTGGGACGACAGCATTAT CCCCATACCT CCGT TCCCA ATAG GGTGT GGG GACAGC
T
GCTGTCCAAAGACCCCATAC CCTA |||| ||||| |||| ||||| ||| ||||||
CTCCTATTGTGGGAAGCAGC GGCG AGGGT Tatc ccata ccc ctgtCG /
GG ACGA GT ct c- agaaac TA

GAM1424 GCCACCCCAAGCCTTCATAG 2876 TATGAAGTCA 5946 - AGC---- GAAGT
ACGAAGTCGCCAAAGTCTAT ACCATGGGCG GCCAC CCCA CTTCATAGAC C
GAAGTCAACCATGGGCGTGG TGGC ||||| |||| ||||||||||
C cggtg gggt gaagtatCTG G

c accaact AAACC

GAM1425 AGCCAAAACCCAATGTTCCA 2877 TGTCTCTGAT 5947 AAA C T - ACA C- - TG
ACACAGAGACCCCCTGGTCG GAGGACCTTG AGCC AC CAA GTTC CA CAGAGAC
CCCTGGTC GGT G
GTTGGGCCGCTGGATCAGGG AGTG |||| || ||| |||| || ||||||| |||||||| |||
CTGTCTCTGATGAGGACCTT TCGG tg gtt cagg gt gtctctg GGGACTAG TCG G
GAGTGAGGCT Ag- a c a a-- tC G CC

GAM1426 CCACACCCCCAGGATCTTCC 2869 TGAGGAAGCA 5939 CCCC ------ TA- CCCCC
TCTAAGGCCCCCACCAAACC TCTGGTCCTA CCACAC AGGAT CTTCCTC AGG A
TGGTGAGGAAGCATCTGGTC AGAG |||||| ||||| ||||||| |||
CTAAGAGTGTGG GGTGTg tcctg gaaggag TCC /
agaa gtctac tGG AAACC

GAM1427 TGGTTTAGAGCTAAATTTGT 2870 TAGAGCTAAA 5940 TTta aaa c--- tt
GAACTCTTTAAGAAAACTTT TTTGTGAACT TGG gagct tttgtgaa tc t
ACAAAATCAGCTCATCTCCA CTTT ||| ||||| |||||||| ||
ACC CTCGA AAACATTT AG /
TCTA CTA CAAA AA

GAM1428 ACCTGAAAATTGGATTGATA 2871 TGGATTGATA 5941 AAAATt-- t caaa aa C--- TA
ACAAAGAGTTAAAGTTCTGT ACAAAGAGTT ACCTG gga tgataa gagtt agTT TGT C
TACTGTACAAAAAAACTAGG AAAG ||||| ||| |||||| ||||| |||| |||
ATTTAGAATTATCACTCCTT TGGAC CCT ACTATT TTTAG TCAA ACA T
TGCCTGCAGGT GTCCGTTT C AAGA GA AAAA TG

GAM1429 GAAGATTTAAATGGTTTATT 2878 TAAATGGTTT 5948 Ttaa a ccttg T TTC
AGACCTTGCTGCTATTGATT ATTAGACCTT GAAGAT atggttt ttaga ctgC ATTGA A
CAACATTCAATGTAGATAAT GCTG |||||| ||||||| ||||| |||| |||||
CTAAAAGACTGTGTCTTC CTTCTG TGTCAGA AATCT GATG TAACT A
---- A AATA- - TAC

GAM1430 GACGTCCCCGTGGTTACCGT 2881 TCCCCGTGGT 5951 -- a- --- a tC
GACAAGCTCCACGCTAGTCA TACCGTGACA GACGtcccc gtggtt ccgt gac agc C
CAGCGGACAACTACAGGGGG AGCT ||||||||| |||||| |||| ||| |||
GCGTC CTGCGGGGG CATCAA GGCG CTG TCG /
GA CA ACA A CA

GAM1431 GTAATGATATCTCCATACTA 2879 AAGGAGCTCA 5949 TAT--- AT-- --- GT CA A
GTAGGTCCACCCAACTGGGA TTTCATTAC GTAATGA CTCC ACT AGTAG C CCC A
AGGTCTACTATCAGTCAAAG ||||||| |||| ||| ||||| | |||
GAGCTCATTTCATTAC cattact gagg TGA TCATC G GGG C

ttactc aaAC CTA TG AA T

GAM1432 CCACAAACAGAGCAAACTCG 2880 GAGCAAACTC 5950 AAACA a tc a cgc
ATGAAGGCCGCTACCGCCTC GATGAAGGCC CCAC gagca ac gatga ggc t
ATCATGTCTGTTTCCTTGGT GCTA |||| ||||| || ||||| |||
GG GGTG TTTGT TG CTACT CCG /
GTTCC C TA - CCa

GAM1433 GCGAGACAGATCAGCATTTG 2882 ACTGCACAGA 5952 A AGCA- - C AA
GCAGCCTAAACGGAGACTGC ATCGAGATCG GCGAGAC GATC TTTG GCAG CT A
ACAGAATCGAGATCGTTTTG TTTT ||||||| |||| |||| |||| ||
C CGttttg ctag agac cgtc GA C
- agcta a a GG

GAM1434 TAGTATGGTTTAGAGCTAAG 2883 CTTTACAAGA 5953 TTA G TAACG-- C
TTTGTTAACGCCCTAAGGAA TTAGTTCATC TAGTATGGT GAGCTAA TTTGT CC T
GCTTTACAAGATTAGTTCAT ACCA ||||||||| ||||||| ||||| ||
CACCATATTG GTTATacca cttgatt gaaca GG A
cta a tttcGAA A

GAM1435 AACTGGGAGAAGTTTGTAGT 2884 AGAAGTTTGT 5954 Ga ta acatc-- ac
ACATCAGACCATCTAAAAAG AGTACATCAG AACTGG gaagtttg gt ag c
GGCCCCAGACTTTATCAGTT ACCA |||||| |||||||| || ||
TTGACT TTTCAGAC CG TC /
A- CC GGAAAAA Ta

GAM1436 GGGTTCCCTCCACATTGTGG 2885 TTGGCCAACC 5955 G CCA TG- G C TG
GCAACCGTTGTAGGCGTTGG ATGCAGGGGA G GTTCCCT CAT TGG CAAC GT T
CCAACCATGCAGGGGAATGT ATGT | ||||||| ||| ||| |||| ||
t taagggg gta acc gttG CG /
g ac- cca g - GA

GAM1437 TTCTAACACATGTGTGGGCA 2886 ACAGGACTGG 5956 AACAC G A---- ATA CA C
ACAGATATCCTCATGCCAAT CACATGCTCA TTCT AT TGTGGGCA CAG TCCT TGC A
GCAACAGGACTGGCACATGC CGGA |||| || |||||||| ||| |||| |||
TCACGGATACAGAA AAGA Ta gcactcgt gtc agga ACG A
CA--- g acacg --- ca T

GAM1438 GGGTCTGCAAAACCCTCTGA 2887 CTCGTTCTTC 5957 TGCAAAACCCTC- ACACAG
GAATACACAGCATTAAAATT CTCAAATGAC GGGTC TGAGAAT C
CTCGTTCTTCCTCAAATGAC CC ||||| |||||||
CC cccag gctcTTA /
taaactccttctt AAATTA

GAM1439 TTTGAGAATAATGTACTGGT 2888 TAATGTACTG 5958 gta tg a t GAGACGG-- - T ---
- G
GTACAAAGTGCTGAGACGGG GTGTACAAAG AAtaat c gtgt caaag gct GAGA GTCCC CA
AC CGT A
AGAGTCCCTCAACCGTGAAA TGCT |||||| | |||| ||||| ||| |||| ||||| || || |||
ATGTGTGTTTGTGGGACTTC TTATTA G CACA GTTTC CGA CTCT CAGGG GT TG
GTA A
TCATTATGCAAAGCCTTTGA AC- GT - - AACGTATTA T T TTG T A
CACTGGCAATTATTTCTTCA
GA
GAM1440 GATATTGGCTCGTCTCACCT 2131 TTGGAGGTAA 5201 -- TG TC C CG AC
TCAACCGGTTACAGAAGATG GATATGTTGA GATA T GC GTCT ACCTTCAAC GTT A
TTGGAGGTAAGATATGTTGA CTTA |||| | || |||| ||||||||| |||
CTTATC CTat a tg taga tggaggttG TAG G
tc gt ta a -- AA

GAM1441 CATTCCGGTCAACAAGGCCA 2132 TACATGGCTA 5202 CAA A AAAT--- CT
AAATGCTCTATAAGCTTATA TGAACCGGAA CATTCCGGT CA GGCCA GCT A
CATGGCTATGAACCGGAATG TG ||||||||| || ||||| |||
gtaaggcca gt tcggt CGA /
a-- a acatATT AT

GAM1442 CTCTGGATATATAGGTACTG 2138 TAGGTACTGA 5208 TG- ------- g ttttta GTTT
AATATTTTTAAGCTATAGGT ATATTTTTAA CTC GATATAtag gtact aata agctaTAG A
TTACATATTGTGGCTGTGTA GCTA ||| ||||||||| ||||| |||| |||||||
TTATTGAGTATTTTTTAGCT GAG TTATGTGTC TATGA TTAT TCGGTGTT /
GTGTATTATTGAG TTA GATTTTT G TATGTG ATAC

GAM1443 TAGCTGTGTATTATTGAGTA 2139 TGAGTATTTT 5209 TAT G TTTTT TGTAT G TTTTT
T--- A
TTTTTTAGCTGTGTATTATT TTAGCTGTGT TATT AGTA TAGCTG TATT AGTA TAGCTG
GTATT T
GAGTATTTTTTAGCTGTGTA ATTA |||| |||| |||||| |||| |||| |||||| |||||
TTATTGAGTATTTTTTAGCT ATGA TTat gtcgat atga tTAT GTCGAT TATGA T
GTGTATTATTGAGTATTTTT TTT G tatgt ttttt g TATGT TTTT G
TAGCTGTGTATTATTGAGTA
TTTTTTAGCTG
GAM1444 GCACTAGTAGCATTTAACCC 2889 TGGCACTAGT 5959 A ATTTAACCCCtg - a atttaacccctG
- A ATTTA
CTGGCACTAGTAGCATTTAA AGCATTTAAC GT GC gc actagt gc GC ACTAGT GC
A
CCCCTGGCACTAGTAGCATT CCCT || || || |||||| || || |||||| ||
TAACCCCTGGCACTAGTAGC CA CG CG TGATCA CG CG TGATCA CG C
ATTTAACCCCTGGCACTAGT - GTCCCCAATTTA A - GTCCCCAATTTA A -
GTCCC

AGCATTTAACCCCTGGCACT
AGTAGC
GAM1445 CGACGAGAGGAGATCGACTT 2890 CTACAGGATT 5960 GA A -------- -- TA
TCCTGGGATAACTTCCTACA TCAAACAGGC CGACGAGAGGA TCG CTT TCCTG GGA A
GGATTTCAAACAGGCGGTCC GGTC |||||||||| ||| ||| ||||| |||
TCTCGTTG GTTGCTCTCct ggc gga aggac cCT /
-- - caaacttt at TC

GAM1446 CGGCCGCATTCATATTCTCG 2133 GCCGCATTCA 5203 c --- attc tttct G
ATTTCTTGTGCAAACACCCG TATTCTCGAT CGgc gcat tcat tcga TGT C
TTCGAAATGATCCATGCGCC TTCT |||| |||| |||| |||| |||
G GCCG CGTA AGTA AGCT ACA A
- CCT A--- TGCCC A

GAM1447 ACGTAGTATCTATCTTGATA 2134 TATCTTGATA 5204 G A - - aa a c
AGGCTATGCGAGCAGGCCCC AGGCTATGCG AC TAGT TC tatcttg at ggct tg g
ATCCGGGATATGAGCTAGGT AGCA || |||| || ||||||| || |||| ||
TG ATCG AG ATAGGGC TA CCGG ac a
G - T C CC - g

GAM1448 CAGGTCGATGAGTCACTGCG 2146 TGAGTCACTG 5216 --- - gatccc g
ATCCCCACGGGCGACCGTGG CGATCCCCAC CAGGTCG Atg agtcactgc cacgg c
CAGTGGCTGCGTTGGCGGCC GGGC ||||||| ||| ||||||||| |||||
TG GTCCGGC TGC TCGGTGACG GTGCC G
GGT G ------ A

GAM1449 GGAGCGGAACCCATTGAATA 2147 TACGTTAACC 5217 - CCCA-- AATAATGT A
CTATCA
ATGTCGTGTATGAGTCTATC CGCAGCATTT GGAGC GGAA TTG CGTGTATG GT A
AATATTTCACCGTATACGTT TTTC ||||| |||| ||| |||||||| ||
AACCCGCAGCATTTTTTCCA CCTCG Cctt gac gcatATGC CA /
GCTCC A ttttac gcccaatt - CTTTAT

GAM1450 GTGATACGGACAGTCCCCGG 2148 TCCCCGGATA 5218 --- Gtcc t gt t a aAT
ATATGGTCATCGACTTAATA TGGTCATCGA GTGA TACGGACA ccgga atg ca cg ctt A
AAAAAGCCGTGTACATCTCC CTTA |||| |||||||| ||||| ||| || || |||
GGTGTCTGTAAACTCGC CGCT ATGTCTGT GGCCT TAC GT GC GAA /
CAA ---- C AT - C AAA

GAM1451 GACTGGAACTTTGGTATAAC 2135 ACTTTGGTAT 5205 --- tg aacc - c C
CCCCCCAGCTACAAGTAGTT AACCCCCCCA GACTG GAactt gtat cc cc agcta A
TGGAGGACACATATAGGTTT GCTA ||||| |||||| |||| || || |||||
GTACAGTC CTGAC TTTGGA TATA GG GG TTGAT A
ATG -- CACA A T G

GAM1452 GGGTCGCAAGTTTTTACTAC 2136 TCGCAAGTTT 5206 c a ttac CCTAC AC
AGGCTGGCCTACGTGCACGT TTACTACAGG GGGt gca gttt tacaggctgg GTGC G
CCGCGCCTTCGGCCTGTAAA CTGG |||| ||| |||| |||||||||| ||||
GCGTGCAGCCC CCCG CGT CGAA ATGTCCGGCT CGCG T
A G ---- TC--- CC

GAM1453 TCTGGCAACCACCCTCTGTG 2140 TTAGCCCACC 5210 AA CCCTCT A - C CT
CCCAG
GACCTGGTGGCCTGACCTTA ATGGACCATC TCTGGC CCA GTGG CC TGGTGG CTGAC
TAC A
CCCCAGATTTATGTATGTTA TTAT |||||| ||| |||| || |||||| ||||| |||
GCCCACCATGGACCATCTTA AGATCG GGT tacc gg accacc gattG ATG /
TTGGGGGCTAGA GG tattc- a t c T- TATTT

GAM1454 CCAGTTTCTAAGGTTGTCAG 2149 TCTAAGGTTG 5219 T- ag ca cg aa A CG
CACGGATGAATATGTGACTC TCAGCACGGA CCAGT tcta gttgt gca gatg TATGTG CT C
GCACAAGCATATACTATCAT TGAA ||||| |||| ||||| ||| |||| |||||| ||
GCAAGCAGCTCTAGATTATT GGTTA AGAT CGACG CGT CTAT ATATAC GA A
GG TT CT AA A- C- - AC

GAM1455 TGTTCGAAATCGTTAGGGAA 2150 AAACATGACT 5220 AAAT T GG --- C G
TGTCTGGGGTACCCCAAACA TTCTTACGTT TGTTCG CGT AG A ATGT TGGG T
TGACTTTCTTACGTTGGTGA GGTG |||||| ||| || | |||| ||||
ATA ATAAgt gca tc t taca aCCC A
ggtt t tt cag a C

GAM1456 GCTTCACAAGACCAACAAAA 2137 TAACTCAAGA 5207 AACAA-- - ACAACG---- C --------
--- TT
GGTGGTGAACAACGTTTTGA ATTAAGAACT ACC AAG GTGGTGA TTTTGA TC
GTCTA G
CTCGTCTATTGCCTGGATTA TTAA ||| ||| ||||||| |||||| || |||||
CTAACTCAAGAATTAAGAAC TGG TTC CACCACT agaatt ag TAGGT /
TTTAAAAGTCACCACACTTG GTAGACG A GAAaatttca a aactcaatCAT CC
CAGATGGGTCTGTGAAGT

GAM1457 TCTAGACTACTTGCAGTGGG 2141 AGTGGGTAAT 5211 C GCag atccctatttcccta AA
TAATCCCTATTTCCCTATTA CCCTATTTCC TCTAGA TACTT tgggta tTAG A
GAAAAGCTAACAAAACTATT CTAT |||||| ||||| |||||| ||||
GTACCCAAGGTATCTGGA AGGTCT ATGGA ACCCAT AATC /
- ---- GTTATCAAAAC---- GA

GAM1458 AACGTGCTGCAAGTACATCT 2142 TGCAAGTACA 5212 Ct- g c gc- c A TAAA GGT
GGA

ACAGCCACACCTACACGTAA TCTACAGCCA AACGTG gcaa tacat taca cacac TAC CG AA TAAAC A
AAAGGTTAAACGGAAATAGT CACC |||||| |||| ||||| |||| ||||| ||| || || |||||
TTATAATTGTGTTGGTATGT TTGTAT TGTT GTGTG ATGT GTGTG ATG GT TT ATTTG /
GTGTTATGTATGTGTGTTGT ATT - T ATT T - TGTG AAT ATA
TTATATGTT

GAM1459 CAAACATTACCATCGACACT 2151 TCGACACTTC 5221 - TA tc-- cacaa gaac
TCACAATGCTGAACTGGTGG ACAATGCTGA CAAA CAT CCA gacactt tgct t
AGCAAAGTGTCACTCTGGCT ACTG |||| ||| ||| ||||||| ||||
GTGCTTTG GTTT GTG GGT CTGTGAA ACGA g
C TC CTCA ----- GGTG

GAM1460 TTGTGTCTTCTGAGGCCCAG 2152 TACACAAGGC 5222 T A CA T TTAATA TT
TTGTTTAATAAACCTTACTG CCAGGGACAC TTGTGTCT CTG GGCC GT GT AACC A
GTTACACAAGGCCCAGGGAC AA |||||||| ||| |||| || || ||||
ACAA aacacagg gac ccgg ca ca tTGG /
- - aa - ------ TC

GAM1461 GAGATAGTTTTCTCTATTCT 2143 TGAAATAATT 5213 TTT - A ------- ctagaaacat A A
GAAATAATTAGAACTAGAAA AGAACTAGAA GT CT CT TTCtg aaataattagaa GTTTAGAAA AA C
CATGTTTAGAAAAAAACGAT ACAT || || || ||||| |||||||||||| ||||||||| ||
TATTTCTGAATTATTCTAAT CA GA GA AGGAC TTTATTAATCTT TAAGTCTTT TT G
TATTTGAACAAACAGGAAAG TAT A A AAACAAG AT-------- A A
AAGTATACTATCGTC

GAM1462 GCGAAGATGACTCTCAAATT 2153 TATTACACTT 5223 AAG ACT- AAA t tac cgt
ATTACACTTACGGCATTCGT ACGGCATTCG GCG ATG CTC Ttat acact ggcatt t
TAACCAATGCCTATGGTGTC TTAA ||| ||| ||| |||| ||||| ||||||
ATAAACGAGTATCCGTATCC CGC TGC GAG AATA TGTGG CCGTAA a
GC CTA CTAT CA- C TAT CCa

GAM1463 GAGTGTTTATCCAGGGAAAT 2154 AGGGAAATCA 5224 CCag a c gaa aa
CAAAGAAGAAGTTAATATAG AAGAAGAAGT GAGTGTTTAT gga at aaagaa gtt t
ACAATTCTTTTGTATTCATA TAAT |||||||||| ||| || |||||| |||
GACACTC CTCACAGATA CTT TG TTTCTT CAG A
---- A T AA- AT

GAM1464 AGGAACAGATGTTTGCCAGA 2160 TTTCCCAGGA 5230 - G C A T- - G- -- A GG
CATTTTTTTAATAGGGCTGG TCTGGTTATT AGGAACAG AT TTTGC AG CATTTTT TAAT AGG CTGG AAC GTT T
AACAGTTGGTGAGGACGTTT AAAA |||||||| || ||||| || ||||||| |||| ||| |||| ||| |||

CCCAGGATCTGGTTATTAAA TCCTTGTC TA AAATG TC GTGaaaa attg tct gacc ttG CAG
G
AGTGCTAGTAAAAATACTGT A A A - tt g ag ct - GA
TCCT

GAM1465 ATTTATTGGTATAATTTCAG 2144 TATTGGTATA 5214 t a c tattc-- ATAC
TATTCGCATACTCTTCGGCA ATTTCAGTAT ATTtattgg at attt ag gc T
AACTTTCTCAAATCATCTAA TCGC |||||||| || |||| || ||
TGAAT TAAGTAATC TA TAAA TC CG C
- C C TTTCAAA GCTT

GAM1466 GTGGCGGGCCACCAATGGAG 2145 TGGAGGACCT 5215 - - A A a a tcacg ag
GACCTGATCACGGGCAAGAC GATCACGGGC GTGG CGGG CC CCA tgg gg cctga ggca a
ATGCCTCAGGGCCACCAATG AAGA |||| |||| || ||| ||| || ||||| ||||
GAGGACCTGATCAC CACT GTCC GG GGT ACC CC GGACT CCGT /
A A A A A G ----- AC

GAM1467 GGCATACAACAAACGATACA 2155 TGATTGCTGG 5225 ACA AAACGA T tg - tac
gaaca
TATATGATTGCTGGTACTCC TACTCCCGGA GGCAT AC TACA ATA attg ctgg tcccg t
CGGAACATACCGCACGGGAA ACAT ||||| || |||| ||| |||| |||| |||||
CGTCAGTTAATTGTATTGTA TCGTA TG ATGT TAT TAAT GACT AGGGC A
GAAGAAGTCGATGCT GC- AAGAAG - GT T GCA ACGCC

GAM1468 ATACAATACAAAATACAACT 2156 TACAAAATAC 5226 - acaact a AC---- G
CTTCGCATGTAAGAACTGGA AACTCTTCGC ATACAAta caaaat cttcgc tgtAAGA TGGA A
GATATCCAAACATATCTTAC ATGT |||||||| |||||| |||||| ||||||| ||||
ACGCGGGGGTTTTGTTATTG TATGTTAT GTTTTG GGGGCG ACATTCT ACCT T
TAT T ------ C ATACAA A

GAM1469 TCCCCTCCTACGGGAGCAGC 2161 ACTATGCTTT 5231 CAGCATACC c t cg aatggaCA
GCTA AAG
ATACCGCTCGACACTATGCT ACGAAGGTAA AG GCTCGACa ta gcttta aaggt CC
GGTGC G
TTACGAAGGTAATGGACACC TGGA || |||||||| || |||||| ||||| || |||||
GCTAGGTGCAAGGCAAGGCA TC TGAGCTGT AT CGGAAT TTCCG GG
TCACG C
CTGCAAGGAGAGGCCTTACT --------- C - CA GAGA---- AACG GAA
AAGGCTACTGTCGAGTCTCC
TGAGAGGTAA
GAM1470 GGCACCGATACGCGTGTTGT 2168 TCAAAGCGTT 5238 ACC - GTGTT A - TA
TTTACAGAACTCTATGAGAG GTTACAGCC GGC GATA CGC GTTTT CAGAA CTC T
TTTCTGGAGACTCAAAGCGT ||| |||| ||| ||||| ||||| |||
TGTTACAGCC ccg ttgt gcg CAGAG GTCTT GAG /
aca t aaact - T AG

GAM1471 CAAATTACGTATAATATAGG 2169 AATTACGTAT 5239 att ataata ga G ------- A ATAAT
GGAGTGGCTTTAGCATAATA AATATAGGGG CAa acgt taggg gtg CT TT GC A
TTTAAGCAGAAACAAACAGG AGTG ||| |||| ||||| ||| || || ||
CACCTCTCTACCAAGACGTT GTT TGCA ATCTC CAC GA AG CG /
GTTG GT- GAACC- TC G CAAACAA A AATTT

GAM1472 ATCTAGTTAGTCCTTTGACG 2157 CGATTTGTCA 5227 T CCT--- GA- AA
AGGATGAAAAGAGTCACGAT ACATCAAACT ATC AGTTAGT TTGACGAG TGA A
TTGTCAACATCAAACTAATT AATT ||| ||||||| |||||||| |||
GAT TAG ttaatca aactgttt ACT G
- aactac agc GA

GAM1473 ATAATTAGAACTAGAAACAT 2158 ACGATTATTT 5228 AAACAT - ---- ---- aaatta
aaTTATTT
GTCTAGAAAGAAACGATTAT CTAAATTATT G GTCTAGA AAGAA acgat tatttct ttcc G
TTCTAAATTATTCCAATTAT CCAA | ||||||| ||||| ||||| ||||||| ||||
TTGAACAAACAGGAAAGAAG C TAGATCT TTTTT TGCTA ATGAAGA AAGG /
TATACTATCGTCATTTTTTT GACC-- C TTAC TCAT ------ ACAAACAA
CTCTAGATCCAGCTACGATT
GATAAT
GAM1474 CCGCCGCGCTCGGTCTCGGT 2159 TCGGTGCCGC 5229 - CT GG t tg gcg g T
GCCGCGGGGTCGAGGCCGGT GGGGTCGAGG CCG CCGCG C TC cgg cc gg tcgaggccgg T
TATCCGGTTTCGGGCCAGGA CCGG ||| ||||| | || ||| || || ||||||||||
GTCGGAGAGGTCGCGGACGG GGC GGCGC G AG GCT GG CC GGCTTTGGCC A
A TG AG - GA A-- G T

GAM1475 CTTTATCTATTCTGAATCAT 2162 TCTATTCTGA 5232 c c atca gag GT
GGAGCAGCTGGTTCTACAGC ATCATGGAGC CTTTAt tatt tga tg cagctG T
TGAACAACTATCAAAATATA AGCT |||||| |||| ||| || ||||||
TAGAG GAGATA ATAA ACT AC GTCGAC C
T A ATCA AA- AT

GAM1476 TTTAAAAAATGGTGTGGTAA 2163 TATATGCCAA 5233 AAA GT- - ACT
GTTATACACTAAAAGTATAG AGTTTAAA TTTAAA TGGTGTG AAGTT ATAC A
ACTTGTATATGCCAAAGTTT |||||| ||||||| ||||| ||||
AAA aaattt accgtat TTCAG TATG /
gaa atG A AAA

GAM1477 GGGTGAGAACGTTCCAGAGT 2170 AGGGAAATCA 5240 CGTT A CCag a c gaa
aa
GTCTATCCAGGGAAATCAAA AAGAAGAAGT GGGTGAGAA CC GAGTGTCTAT gga at aaagaa
gtt t
GAAGAAGTTAATATAGACAA TAAT ||||||||| || |||||||||| ||| || |||||| |||
TTCTTTTGTATTCATAGACA CTTATTTTT GG CTCACAGATA CTT TG TTTCTT CAG A

CTCGGTTTTTTATTC T--- - ---- A T AA- AT

GAM1478 GGGCGCCCCGAGCATCGGCG 2171 TCTCTCGGTC 5241 C C C TGTC A
GTGTCTCTCGAGAGCTTTCG CTCGGGGCCC GGG GCCCCGAG ATCGG GG TCTCGAG G
AGATCTCTCGGTCCTCGGGG C ||| |||||||| ||||| || |||||||
CCCC ccc cggggctc tggct tc AGAGCTT C
- c c t--- T

GAM1479 CGCCGCTGGCTCGGAGCCAA 2172 CTCGCCCACG 5242 CT - A C GCC T-- AT
GTGCGCCGGCGGCCGGGCTC CTGCTGCACT CGCCG GGCTCGG AGCC AGTGCG CGGCG
GGGC CGG C
GGATCGCTCGCTCGCCCACG CGGC ||||| ||||||| |||| |||||| ||||| |||| |||
CTGCTGCACTCGGCTCCCGG GCGGC CCGGGCC Tcgg tcacgt gtcgc cccg GCT /
GCCCTCGGCG TC C c c a-- ctc CG

GAM1480 GTCTAGAAAATATAACGCAA 2164 TAACGCAATA 5234 GA aacg atgtt- aa
TATGTTAGTTAAAAATGTAA TGTTAGTTAA GTCTA AAATAt caat agtta a
CTTGTTAGATTGATATTTCA AAAT ||||| |||||| |||| |||||
TGGGC CGGGT TTTATA GTTA TCAAT a
AC ---- GATTGT Gt

GAM1481 ATAGACGCTATTTATCCGGG 2165 TGAGAACGTT 5235 ATTTATCC GTA- AA
CGGTATACCCAAAAGGGGTG CCAGAGTGTC ATAGACGCT GGGCG TACCC A
AGAACGTTCCAGAGTGTCTA TAT ||||||||| ||||| |||||
T tatctgtga cttgc gtGGG /
gac----- aaga GA

GAM1482 GAGTGTCTATCCAGGGAAAT 2166 TAATTCTTTT 5236 CCAG A C GAA AA
CAAAGAAGAAGTTAATATAG GTATTCATAG GAGTGTCTAT GGA AT AAAGAA GTT T
ATAATTCTTTTGTATTCATA ACAC |||||||||| ||| || |||||| |||
GACACTC CTcacagata ctt tg tttctt tAG A
---- a t aa- AT

GAM1483 GTGTCGGTGACGCCGTGTGG 2167 TCGGTGACGC 5237 - -- cc - acg-- ACCAGA G
GTACGCCGGCACCAGACTAA CGTGTGGGTA GTG tcggt gacg gtgt gggt ccGGC CTAA A
GAACTTAGAACCCCGCTGGA CGCC ||| ||||| |||| |||| |||| ||||| ||||
AAGGACCCTACACCGTCCTG CAC AGTCG CTGC CACA CCCA GGTCG GATT A
CTGACCAC C TC -- T GGAAA CCCCAA C

GAM1484 ATAATTAGAACTAGAAACAT 2173 TAGAAAGAAA 5243 AAAC Ct --- ---- gaaTTA
AATTATTT
GTCTAGAAAGAAACGATTAT CGATTATTTC TAG ATGT agaaagaa acgat tatttct TTCC
G

TTCTGAATTATTCCAATTAT TGAA ||| |||| |||||||| ||||| ||||||| ||||
TTGAACAAACAGGAAAGAAG ATC TATA TCTTTTTT TGCTA ATGAAGA AAGG
/
TATACTATCGTCATTTTTTT GACC TC TAC TCAT ------ ACAAACAA
CTCTATATCCAGCTACTACT
GATAAT
GAM1485 AGAGACTGTGATGGGGCAGC 2174 ACTGTGATGG 5244 t a tac caA CTCGACAACTAA
GT TA A G
CTACTCCAAAGACCCCTCGA GGCAGCCTAC ggggc gcc tc AGACCC GGGA TCC GGG
CGGCAG C
CAACTAAGGGAGTTCCTAGG TCCA ||||| ||| || |||||| |||| ||| ||| ||||||
GACGGCAGGCTTCTGTCGCC CCCCG CGG AG TTTGGG CCCT AGG TCC
GCTGTC T
TCTGGATCCCCGGGTTTGCA C A TAA ACG C---------- -- TC - T
GAAATGGCAGCCCCCTTGTA
CCCTCT
GAM1486 CTGAAGAGGGGCTGCAACAT 2175 TCTTACGGAC 5245 AA CAACATGACTG T C T -
AAG C
GACTGCCTTGACATCTTGGC CAGCCTCTCC CTG GAGGGGCTG CC TGA ATCT GG CTG
CC A
TGAAGCCCACGGAACTAGAC CAG ||| ||||||||| || ||| |||| || ||| ||
CAGATCTTACGGACCAGCCT gac ctctccgac gg att tAGA CC GAT GG /
CTCCCAG c- ca--------- c c - A CAA C

GAM1487 GATACCCATTCAAGTGAAAG 2176 TGAAAGGCTA 5246 AG - -------- a - CTA ----
A
GCTATTATAGTTAGGAGGGC TTATAGTTAG TCA tgaa agg ct ttatagtt aggaggG GCA
ATATAAG A
TAGCAATATAAGAAAACTTA GAGG ||| |||| ||| || |||||||| ||||||| ||| |||||||
TATTCAATGTATTTTTTTTT AGT ACTT TCC GA AGTATCGA TTTTTTT TGT
TATATTC A
AAGCTATGAAAGTAAAGATA GA A ATAGAAAT A A TTA AACT A
CCTATTCAAGTGAAAGGCTA
TT
GAM1488 GTATAAAAAACTTAAGGTTT 2180 AAGAAACTGA 5250 AAAA A- AAA--- CCATA
AAA
ATTTAAAAGTCCATATTTTA ATAGAAATAG GTATA ACTTA GGTTTATTT AGT TTTTAT A
TAAAAGTTAATGAAAAAGAA ATTG ||||| ||||| ||||||||| ||| ||||||
ACTGAATAGAAATAGATTGA CGTAT TGAAT ttagataaa tca AAAGTA G
TAAGTCCATATGC ACC- Ag gataag aagaa ATT

GAM1489 TGTCTAGAAAGAAACGATTA 1722 ACGATTATTT 4792 - ---- ---- gaatta aaTTATTT
TTTCTGAATTATTCCAATTA CTGAATTATT TGTCTAGA AAGAA acgat tatttct ttcc A
TTTAAACAAACAGGAAAGAA CCAA |||||||| ||||| ||||| ||||||| ||||
GTATACTATCGTCATTTTTT ATAGATCT TTTTT TGCTA ATGAAGA AAGG /
TCTCTAGATA C TTAC TCAT ------ ACAAACAA

GAM1490 GGCAGCGCCGCCCGCCCGCA 1723 TGCCGAGGCG 4793 CGC--- - - ---- T
GCGGCGGTCCCCCGCCCTCG GCCCATCGTG GGCAGCGC CCGCC CG CAGC GGCGG C
GCTGCCGAGGCGGCCCATCG CTGC |||||||| ||||| || |||| |||||
TGCTGCC Ccgtcgtg ggcgg gc gtCG CCGCC C
ctaccc a c GCTC C

GAM1491 AGAGTTGCATGAAGATATTG 1729 CACTGCACTG 4799 GAAGATA GAAA- C - AG TG CG
ATC-- A
TTGAAATTCTCCGCAGAAGG TGGCCCAATT TTGTT TTCT CG CAGA GGGT CA GCAG
AATCCAG C
GGTTGCACGGCAGATCAATC TGAC ||||| |||| || |||| |||| || |||| |||||||
CAGACACTGGATTCCGCACT AACAA AAGA Gc gttt cccg gt cgtc TTAGGTC /
GCACTGTGGCCCAATTTGAC AGGAA-- AGAGA A a aa gt ca acGCC A
GAAGAAAGAGAAACAAAAGG
AATGCAATTCT
GAM1492 GATGACTGGTTTCTATTTGG 1730 TTTCTATTTG 4800 G--- tt- a gt
TGACAGTCGTTCTGACTGTA GTGACAGTCG GATGACTG tttctat ggtg cagtc t
CCTATGTAGAAAATAACGGT TTCT |||||||| ||||||| |||| |||||
CATC CTACTGGC AAAGATG CCAT GTCAG /
AATA TAT - tc

GAM1493 GGGACCGCTCCAATGAGTTC 1731 TGCTGGGGGA 4801 CG--- AA G TAT A G
TCCTATGGCAAGCGGTCGCT GTCAGGAGAC GGGAC CTCC TGA TTCTCC GGCA GC G
GCTGGGGGAGTCAGGAGACA ACCG ||||| |||| ||| |||||| |||| ||
CCGTCCC CCCTg gagg act aggggg tcgt CG T
ccaca -- g --- - C

GAM1494 GGTGGAGATGGCAGAGGCTG 1732 AGAGGCTGTC 4802 Ca tc c c
TCGCCGCGCCCGAGGTGCTG GCCGCGCCCG GGTGGAGATGG gaggctg gc gcgcc g
CCCAGCCTCCCCGTCTCCAT AGGT |||||||||| ||||||| || |||||
C CTACCTCTGCC CTCCGAC CG CGtgg /
C- C- T a

GAM1495 GCCGCCTGTCCCCGGATCAC 2177 TCCCCGGATC 5247 C -- ca- c gatc ACGC
CCCGTGATCGTCCGACGCCA ACCCCGTGAT GCCGC TGtccc cggat ccc gt gtcCG C
CTACCGGGCCAACTGGGCCA CGTC ||||| |||||| ||||| ||| || |||||
GTCTGAAGGGACGCGTGGC CGGTG GCAGGG GTCTG GGG CA CGGGC A
C AA ACC T AC-- CATC

GAM1496 GTGGTGATTTAGAAATAGGA 2178 TGATTTAGAA 5248 aaata aga c AGGATG
GACCTACCGCAGGATGATGA ATAGGAGACC GTGGtgatttag gg cctac GC A
GGAAGCGTGGGCCGAGCTAA TACC |||||||||||| || ||||| ||
GTTACCAC CACCATTGAATC CC GGGTG CG T
GAG-- --- - AAGGAG

GAM1497 CAAAGAAACACCTACTTCTT 2179 TTCGTACCGT 5249 GA C -- G--- TG C- T C
CAGACATGTGCACGATAATA GTGTAGAATG CAAA AACAC TAC TTCTTCA ACA TG ACGA
AATAG A
GCATCTATTTTCGTACCGTG AAGG |||| ||||| ||| ||||||| ||| || |||| |||||
TGTAGAATGAAGGGTTGTAT GTTT TTGTG ATG Gggaagt tgt gc tgct TTATC /
GTGTTGATTTG AG T TT aaga gt ca t T

GAM1498 GACAGCGACGAGGTGCTGGT 2181 CGGCGCGTGC 5251 AGC- - --- TG AC------- CC
G GG
GCTGGGCACGCGCCCCAGGC GCGCCCACCT C GACG AGGT GCTGG CTGGGC GCGC
CA GCGCCGCT A
GCCGCTGGACGGGGCGGCGC ACCG | |||| |||| ||||| |||||| |||| || ||||||||
GTGCGCGCCCACCTACCGCC G CTGC TCCG CGACC GGCCCg cgcg gt
cgcggcGG C
CGGTGCCAGCCTCGCCTACG GGCC A CTC GT ccatccacc c- g GG
TCCCGGGTC

GAM1499 TTGGCTTGACCTCGACCCAA 2182 TGTGTAATTC 5252 GA G AA-- t t ga at---- gC
T T
AGTTGTGTAATTCAGGAAAG AGGAAAGATT T CCTC ACCC AGTtgtg aa tcag aag ttcc
AAAGAG GG A
ATTTCCGCAAAGAGTGGTAA TCCG | |||| |||| ||||||| || |||| ||| |||| |||||| ||
CTCTCTCTTTAGGAGTTTTC G GGAG TGGG TTAACAT TT AGTC TTC GAGG
TTTCTC CT A
ACTTCACTGATTTTTACAAT AG - CATA T T AC ACTTTT A- T C
TATACGGGTGAGGGAGACCA
A
GAM1500 GCCGCCCCTAGCCCCGCGGC 2183 CTCCGCGCCG 5253 C TA C G TCC CGCA
GGTCCAGCCGGCGCATCATT GGCGGGCCGG GCCG CCC GCCC GCG CGG AGCCGG T
CTGGCTCCGCGCCGGGCGGG C |||| ||| |||| ||| ||| ||||||
CCGGC cggc ggg cggg cgc gcc tcGGTC /
c -- c - --- TTAC

GAM1501 GGCGCCCGCGGCGGTTCCGG 2184 CCCGCGCGCG 5254 C - TC T CTCCCCCA
TGCCTCCCCCAGCCCCTCCA CCGCGTGCGC GGCGC CGCGGCG GT CGG GC G
GCCCCGCGCGCGCCGCGTGC C ||||| ||||||| || ||| ||
GCC ccgcg gcgccgc cg gcc CG /
t g c- c ACCTCCCC

GAM1502 GCTCCACGCTTTGGCACGCG 2185 GGTCATGGGC 5255 C TT A G g gggc ga gaa
GCCGGTCATGGGCACTTGGA ACTTGGAGCG GCTCCA GCT GGC CGC GCCg tcat acttg gc a
GCGAAATCGGCACGAGTCAG AAAT |||||| ||| ||| ||| |||| |||| ||||| ||
ATGAACGGCGGCGCGCTCAG CGAGGT CGA TCG GCG CGGC AGTA TGAGC CG /
CTGGAGC - C- C G A GAC- A- GCt

GAM1503 TTGCCTCCGGGGTCCACGGT 2186 TCCACGGTGC 5256 CT - ccct cg aA
GCCCTGGACGTGGCCAACCA CCTGGACGTG TTGC CCGG GGtccacggtg gga tggcc C
GGCCGTCTCCCACGCCGTGG GCCA |||| |||| |||||||||| ||| |||||
ACCGCCGGTGCAA AACG GGCC CCAGGTGCCGC CCT GCCGG /
T- G AC-- CT AC

GAM1504 TTAATCTGTGTGTCCTGTTC 1724 TACAATATAC 4794 TCT CC TCC CC A-- A-- G
TTATG
CACCCCATGAGTAAGTGTTG AACATATGTA A GTGTGT TGT AC CATG GTA GTGTTGTA
TATTGTGTG T
TAGTATTGTGTGTTATGTCT CAGC | |||||| ||| || |||| ||| |||||||| |||||||||
GGTGTATACAATATACAACA T TACACA ATA TG GTAC cat tacaacat ataacatAT C
TATGTACAGCCATGTTGTTT TT- AA TTT TT cga gta - GTGGT
TATAAAACACATTTTTAA

GAM1505 TAAAGGGGGCACATGTGGCT 1725 AAGGGGGCAC 4795 -- gtggctat AA
ATAGTAGAATCTCTACTCAA ATGTGGCTAT TAaagggggc acat agtaG T
TATAGTGTCCGCCCCCTTTA AGTA |||||||||| |||| |||||
ATTTCCCCCG TGTG TCATC /
CC ATATAAC- TC

GAM1506 CAGGCTGATGAGTCACCGTA 1733 TGAGTCACCG 4803 --- - attccc g
TTCCCCACGGGCGACCGTGA TATTCCCCAC CAGGCTG Atg agtcaccgt cacgg c
CGGTGGCTGCGTTGGCGGCC GGGC ||||||| ||| ||||||||| |||||
TG GTCCGGC TGC TCGGTGGCA GTGCC G
GGT G ------ A

GAM1507 GTTTCTATAACAACCTCCCC 1734 TCTATAACAA 4804 T caac cccc--- cc- A
CAGGTCCAGTTATGAACTCC CCTCCCCCAG GT tctataa ctc aggt AGTT T
CACCTTACACCAGAGATATT GTCC || ||||||| ||| |||| ||||
ATGGATGC CG AGGTATT GAG TCCA TCAA /
T ATA- ACCACAT CCC G

GAM1508 GAAACTAGACATAAAATAAA 1737 AGAGAAGTTA 4807 ACT A AATATTTA--- TTGGA TT
AAG- GAA
TATTTACCAACTTGGAACTT GGTGTTTGTT AGACATAA ATA CCAAC ACTT ACTTC
TCAT G
TTACTTCAAGTCATGAAGAT GGGA |||||||| ||| ||||| |||| ||||| ||||
AGTGGAAGAGAAGTTAGGTG TCTGTATT TAT ggttg tgga tgaag GGTG /
TTTGTTGGGAGCCTTGAAAT CTT C AAAGTTCCGag tttg- t- agaA ATA
ATCTTATGTCTTTCCTC

GAM1509 TAATAGTACAGAATATAAAC 1742 TACAGTTTAT 4812 G ------ AAT---------- C
AATACATGCGACATGTTGAG GTTTCAATTA TAATA TACA GAATATAAAC ACATG G
GAGTTTGACTTACAGTTTAT TGTA ||||| |||| |||||||||| |||||
GTTTCAATTATGTAGTATTA ATTAT atgt tttgtatttg TGTAC /

G attaac acatTCAGTTTGAGGAGT A

GAM1510 AAAACGTCCTGCATCTGCAG 1743 TAGGAAGAAG 4813 TCCT C AGCC A CC TAA CA
CCACTTCATCCTCCAGTAAA TAGTATGTGT AAAACG GCAT TGC ACTTC TCCT AG ACC A
CCCAAACGGTCTAGGAAGAA TATT |||||| |||| ||| ||||| |||| || |||
GTAGTATGTGTTATTGTTTT TTTTGt tgtg atg tgaag agga tC TGG /
tat- t a--- a -- --- CA

GAM1511 CCTTTTGCTTGTTCACTGTG 2187 ATGCTGCGCA 5257 T G C ACATT
CGGCATTATTACATTTACAC TGAAAGAGCG CC TTTGCTT TTCA TGTGCGGCATTATT T
CGGTAATGCTGCGCATGAAA AACG || ||||||| |||| |||||||||||||
GAGCGAACGG Gg aagcgag aagt acgcgtcgtaATGG /
c a - CCACA

GAM1512 GGAGGAGATAAATATCTTAC 1726 TGAGCTGAGG 4796 A AAAGA GA-- AC CAA GG- AAAA GT
GCAAAGAAGCGCTTGAGCTA TTACAGATTT TCTT CGC AGCGCTT GCT AGAAA GTGAC AGC GGCT T
CAGAAACAAGTGACGGAGCA CTAA |||| ||| ||||||| ||| ||||| ||||| ||| ||||
AAAGGCTGTTGTGGCTGAGC AGGA GCG TCGCGGG CGa tcttt cattg tcg tCGG /
TGAGGTTACAGATTTCTAAG C A---- ACAA a- aga gag ag-- TG
CAACAGGGCGCTAGCGCAGG
AACTACCTCT
GAM1513 CGAGGGGAACGGGGGATGGA 1735 TGGAAGGACG 4805 A AA A ac aa ga tcc AT
AGGACGGGAAGTGGAAGTCC GGAAGTGGAA CG GGGG CGGGGG tggaagg ggg gtg ag TG A
TGATACCCATCCTACACCCC GTCC || |||| |||||| ||||||| ||| ||| || ||
CCTGCCTTCCACCCTCCGGC GC CCCC GCCTCC ACCTTCC CCC CAC TC AC /
CCCCCG - CG C GT CC A- CT- CC

GAM1514 GCTTTTCACGCCACGCGTAT 1736 TACCAGGCTG 4806 T C C --- ACGAGTTTT
AAACGAGTTTTCAGTCATAA GCATGGAAGC GCTTT CA GCCA GC GTATAA C
ATTGTACCAGGCTGGCATGG ||||| || |||| || ||||||
AAGC cgaag gt cggt cg catGTT /
- a - gac AAATACTGA

GAM1515 GACCCACGTACTCCAAGAAG 1738 TGCCTGGCTC 4808 C CTCCA A- TGTCC CCC
GCATGTGTCCCACCCCGCCT TCTATGCTTG GACCCA GTA AG AGGCATG CAC G
GTGTTTTTGTGCCTGGCTCT GGTC |||||| ||| || ||||||| |||
CTATGCTTGGGTC ctgggt cgt tc tccgtGT GTG /
t atctc gg TTTT- TCC

GAM1516 AGAATGCCTGGGAAATGATA 1744 TGAGTACGAA 4814 ATG-- GAAA TAG A --- GAA- AGAAA

GAGAAAGAGAGACTGAAACT GTCAATTCTC AGA CCTGG TGA AG AAGAGA GACT
ACTTAGTGC A
TAGTGCAGAAAAGAACCGCG TTAC ||| ||||| ||| || |||||| |||| |||||||||
CTGAGTACGAAGTCAATTCT TCT GGACC ACT Tc ttctct ctga tgagtCGCG /
CTTACTTCAGCCAGGAATAG GATAA G--- --- a taa agca CCAAG
TCT

GAM1517 GACTTAAACGCATACGGGTA 1727 TCCACCCTCC 4797 A-- -- AC- ATA CA
TAGACTATCACGCAATGGTC GTGCTGGTTA GACTT AAC GCAT GGGT GACTAT C
CACCCTCCGTGCTGGTTACC CCGA ||||| ||| |||| |||| ||||||
GAGTC CTGag ttg cgtg ccca ctGGTA G
cca gt cct c-- AC

GAM1518 CTCAAGAGCTGTGGTCAGCG 1728 CAAGAGCTGT 4798 a- a t c------- caacACTCT
CTCAACACTCTAATGCCTCT GGTCAGCGCT CTc ag gctg ggt agcgct A
AAGCGCTCTCACCTCACCCA CAAC ||| || |||| ||| ||||||
GCCTCCGAG GAG TC CGAC CCA TCGCGA /
CC - - CTCCACTC ATCTCCGTA

GAM1519 TAGAAACTGATGACTCATGC 1739 ATCTCTTTCC 4809 A ATGACTCATGC CCCAATC ACC
GCTGGCCCAATCTCCACCTT AGCCAGTTAC TAG AACTG GCTGG TCC T
CCAGGATCTCTTTCCAGCCA TA ||| ||||| ||||| |||
GTTACTA atc ttgac cgacc aGG T
a ---------- tttctct ACC

GAM1520 GACTTCTTTCCAGAGATTGT 1740 TAACTGCCCC 4810 C--- A----- TTCCAA
CTTCCAACTCAACATGATAA TCTGACAAAA GACTTCTTT CAGAG TTGTC C
CTGCCCCTCTGACAAAAAGA AGAA ||||||||| ||||| |||||
AGTT TTGaagaaa gtctc aatAG T
aaca cccgtc TACAAC

GAM1521 TCCTATCCTGCTGAACTTTA 1749 TTCAGCTAGT 4819 C TG T A T
GCAGAAACTCTAGCGAGTTT GTTGTATGAT TCCTATC TGC AAC TTAGC GAAACTC A
CAGCTAGTGTTGTATGATAG AGGA ||||||| ||| ||| ||||| |||||||
GA aggatag atg ttg gatcg cttTGAG G
t -- t a C

GAM1522 ATACCCGGCGATTTTCCCAA 1750 ACCCGGCGAT 4820 gg -- accacc- TCTAACA
CCACCCCTCTAACAACGATA TTTCCCAACC ATaccc cgattt tccca cC A
TACGGCATTCCCTGGGACCA ACCC |||||| |||||| ||||| ||
GGTCGAGGGTGT TGTGGG GCTGGA AGGGT GG C
A- CC CCCTTAC CATATAG

GAM1523 ATAATTAGAACTAGAAACAT 1741 AAACAGGAAA 4811 AC AAAC TT --- ----
GAATTATTC--- T

GTTTAGAAAGAAACGATTAT GAAGTATACT TAG ATGT AGAAAGAA ACGAT TATTTCT
CAA T
TTCTGAATTATTCCAATTAT ATCG ||| |||| |||||||| ||||| ||||||| |||
TTGTCCAAACAGGAAAGAAG ATC TATA TCTTTTTT Tgcta atgaaga GTT A
TATACTATCGTCATTTTTTT TC GACC TC TAC tcat aaggacaaaCCT T
CTCTATATCCAGCTACTGCT
GATAAT
GAM1524 GAATGTTCCAGAGTGTTTAT 1745 TTCCAGAGTG 4815 tt--- a ccag a T GAA AA
CCAGGGAAATTAAAGAAGAA TTTATCCAGG GAATG cc gagtgtttat gga aT AAAGAA GTT T
GTTAATATAGACAATTCTTT GAAA ||||| || |||||||||| ||| || |||||| |||
TGTATTCATAGACACTCGGT CTTAT GG CTCACAGATA CTT TG TTTCTT CAG A
TTTTTATTC TTTTT - ---- A T AA- AT

GAM1525 TAAAGCTGATTGTATAAATT 1746 AAGCTGATTG 4816 ---------- c ATACCTA
TACTATTAATACCTAATTGA TATAAATTTA TAaagctgattgtat aaattta tatTA A
CCACTAATAATAAATTTTTT CTAT |||||||||||||| ||||||| |||||
ATCATTAATATAATTAGTTT ATTTTGATTAATATA TTTAAAT ATAAT T
TA ATTACTATTT A CACCAGT

GAM1526 GGCTGCGGGACAGTGATGGA 1747 ATGGAGATGA 4817 ----- - at g at-- - a
GATGATGGTGGCCCAGAGGG TGGTGGCCCA GGCTGC GGGACA GTG gga atg ggtgg ccc g
ACCACCTGCGCGTGTCCCAC GAGG |||||| |||||| ||| ||| ||| ||||| |||
GTGTCCCCCTTTGCGGTC CTGGCG CCCTGT CAC CCT TGC CCACC Ggg /
TTTCC G -- G GCGT A a

GAM1527 AGAAAGAAACGATTATTTCT 1748 ACGATTATTT 4818 --- ---- gaatta aaTTATTT
GAATTATTCCAATTATTTGA CTGAATTATT AGAAAGAA acgat tatttct ttcc G
ACAAACAGGAAAGAAGTATA CCAA |||||||| ||||| ||||||| ||||
CTATCGTCATTTTTTTCT TCTTTTTT TGCTA ATGAAGA AAGG /
TAC TCAT ------ ACAAACAA

GAM1528 GGATGACTCTCAAATTATTA 1751 TATTACACTC 4821 A TCAAA t cac cgt
CACTCACGGCATTCGTTAAC ACGGCATTCG GGATG CTC Ttat acact ggcatt t
CAATGCCTATGGTGTCATAA TTAA ||||| ||| |||| ||||| ||||||
ACGAGTATCC CCTAT GAG AATA TGTGG CCGTAA a
- CA--- C TAT CCa

GAM1529 GTCGCAGGCCCAGTAGAGCG 1752 GCCCAGTAGA 4822 CA a ga cg tc GGT
CCGGGTTCTCCGGGTCGAAC GCGCCGGGTT GTCG Ggccc gta gcgc ggttc cG C
GTGAGCCGTGTGTGCGGGCC CTCC |||| ||||| ||| |||| ||||| ||
CTTGAT TAGT CCGGG CGT TGTG CCGAG GC /
TC - G- -- T- AAG

GAM1530 GGCCCGCGCACAACAAATCG 1753 TGTGATAGAA 4823 GCGCACAACAA A CTTAAC T

CGGATTACTTAACTGCATCC TACGATAGGG GGCCC ATCGCGG TTA TGCA C
ATGCAAGCACTGACTGTGAT CC ||||| ||||||| ||| |||| AGAATACGATAGGGCC ccggg tagtgtC AGT ACGT C atagcataaga - CACGA- A

GAM1531 GCGTAATGGGCGTGGTCATC 1754 CTGCAGTTGG 4824 AATG T- - C ATATA GT
CTCGGCTATATAAGGGGGCG TGATCGACTT GCGT GGCG GGTC ATC TCGGCT
AGGGGGCGC C
CGTCGAGCGCTTCCTGCAGT CCGC |||| |||| |||| ||| |||||| |||||||||
TGGTGATCGACTTCCGCCAG CGCA Ccgc tcag tag ggttga tcCTTCGCG /
GGACGC GGGA ct c t cg--- AG

GAM1532 ATTTCTTCTCCGTGTTGCAG 1755 AGCCAAGACG 4825 TG C CTATGATA G ATG
ATCTATGATATTGGTGCGAT TTTACAAGTC ATTTCTTCTCCG TTG AGAT TTGGT CG G
GGTCACGAGCCAAGACGTTT GGAG |||||||||||| ||| |||| ||||| ||
ACAAGTCGGAGGAGGAGT TGAGGAGgaggc aac tttg aaccg GC /
tg a cag----- a ACT

GAM1533 CCCTCTCCTTCATGCGCCGA 1756 AAGAGGCTGT 4826 CCTTCAT C CGAC G
TACCCCGACTCGGTGACGAA CGGTGTCCCC CCCTCT GCGCCGATA CC TCG T
GAGGCTGTCGGTGTCCCCGT GTAG |||||| ||||||||| || |||
AGAGGG GGGAga tgtggctgt gg aGC G
tgcccc- c aga- A

GAM1534 AGAGCTGTCGCGAAGTATTC 1757 TCGCGAAGTA 4827 c tattc gtg TAA CG AAT
GCTCCGTGCGGGTAACGCCG TTCGCTCCGT AGAGCTGt gcgaag gctcc cggG CGC A A
AAATAGACTTAGCGCCCGAG GCGG |||||||| |||||| ||||| |||| ||| |
GAGTTTTCGTACGGCTCT TCTCGGCA TGCTTT TGAGG GCCC GCG T /
- ----- A-- --- AT CAG

GAM1535 GATGTAGTAGACGTTGGCGC 1758 TAGTAGACGT 4828 agt g---- tg c at-- a
GGATGGGATCTCCCTTGGCC TGGCGCGGAT GATGt agac t g gcgg ggg T
GCCTTGAAGTGGGTCTTGGC GGGA ||||| |||| | | |||| |||
ATC CTACG TCTG A T CGCC CCC C
GT- GGTGA GT C GGTT T

GAM1536 GTACGCGGTGAAGGTAAGTT 1764 TTCGTCTTTG 4834 A GT T CA TG--- T TGGGA
GTC-- GG
GCTTCCAAAAGGCGTGGGTG AAGTACTTGT G AAGT GCTTC AAAGGCG GGTGT GC
ATGGTGG GCA A
TTGCTGGGAATGGTGGGTCG CGTA | |||| ||||| ||||||| ||||| || ||||||| |||
CAGGAAAATGTTAAAGTCGC c ttca tgaag tttctgc CCGTA CG TGCCGCT TGT A
CGTGCATGCCGAGTTCGTCT g tg - -- ttGAG - ----- GAAAT AA
TTGAAGTACTTGTCGTAACT

GTCGTAC
GAM1537 GTCGCTGGGCGCGACGACTC 1765 TGGAAGAGGA 4835 GGGCGC-- - GCGC GA
G -- G TCCT
CTCGCGCCCACCTGTGAAGC CGTCGTTAAA GTCGCT GACGAC TCCTC CCACCTGT
AGCC CG TG GG T
CGCGTGGGGTCCTTTTTATC GAGG |||||| |||||| ||||| |||||||| |||| || || ||
GTAGTTGGGGTTGGGCAGGT CGGCGG ttgctg aggag ggtGGACG TTGG GT AT CT
/
GGAAGAGGACGTCGTTAAAG Aggagaaa c aa-- GG G TG G ATTT
AGGAGGCGGC

GAM1538 GGTTGTGTCATGACGGGCTT 1759 TCCACAGTGG 4829 T CA CG- - - AA TGC T
CTA
CAGTCCATTAAGTGGATGCT GCGTGGCAGC GGT GTGT TGA GGCT TCA GTCCATT GTGGA
TG CAC C
GTCACCTACTGAGTGCCACC CACA ||| |||| ||| |||| ||| ||||||| ||||| || |||
TTCCACAGTGGGCGTGGCAG CCA TACG ACT ccga ggt cgggtga cacct AC GTG /
CCACATCAAGCATACC - A- aca c g -- TCC C AGT

GAM1539 ACTACTTAGGCATGGCTGCT 1760 AGGCATGGCT 4830 TTa gc ct ccccta - CA
TTTC
GACCCCTATGGCGACAGCAT GCTGACCCCT ACTAC ggcatg tg ga tggCGA CAG TGTTTTTT
T
GTTTTTTTTTCTGCGTAGGG ATGG ||||| |||||| || || |||||| ||| ||||||||
AACAACTGTTTGCCAGGCAC TGATG TCGTGC AT CT ACCGTT GTC ACAAGGGA /
TTCTTTAATCGTGCTGGTGT TGG TA TT TCACGG T A- TGCG
AGT

GAM1540 CCTGGCAGTGCCATATACAG 1761 TGGCAGTGCC 4831 ataca- acACCTAG CATG AC
-- CAAATA
TCCCACACCTAGTGGGTCCA ATATACAGTC tgccat gtccc TGGGTC GTA GTC
TGAGGCT T
TGGTAACGTCTGAGGCTCAA CCAC |||||| ||||| |||||| ||| ||| |||||||
ATATTTAATAAGCCTTACTG ATGGTA CAGGG ACCCGG CAT CGG ATTCCGA
/
GCTACAGCAGGCCCAGGGAC ACAACA -------- ACGA -- TC ATAATT
ACAACAATGGTATATGCTGG
G
GAM1541 AAACAAGGTAGAAACCAACG 1762 TGGTATTTCC 4832 ----- A AC AC-- CC AGG
aagcatta- aa
GGGTCCTCAGGTGGTATTTC GGAAGCATTA A GGT GAA CA GGGGT TC tggtatttccgg
cc A
CGGAAGCATTACCAAATAAG CCAA | ||| ||| || ||||| || |||||||||||| ||
GCAACCTCAGCTGGGAATAC T CCA CTT GT CCCCA AG ACCATAAGGGTC
GG T
CAGCGGACTACCCCCAACTG TCCTC A AT CAAC TC GCG GACTCCAAC AA
TATTCAACCCTCCTTTGTTT

GAM1542 ACACAACTGTGCATTCTGGG 1766 AACACTGGGG 4836 ACT AT--- G C A CC

CTGTACGCCTCCCATGGGCG TAAGGGCACT ACACA GTGC TCT GG TGT CGCCT C
AACACTGGGGTAAGGGCACT GTGT ||||| |||| ||| || ||| |||||
GTGTGT TGtgt cacg ggg tc aca GCGGG /
gt- ggaat g - a TA

GAM1543 TAGGTTTGTAACATCCTCTG 1767 TTGGCCCCTA 4837 G - -- - ---------- TAA GT
CCATAACTTGTCAAAAAGAT CAGAAAAGCA TAG TTTGTA AC ATCCT CT GCCA CTT C
TTGGCCCCTACAGAAAAGCA GGAT ||| |||||| || ||||| || |||| |||
GGATCCGTATGCAAAGCTA ATC AAACGT TG tagga ga cggt GAA A
G A CC c aaagacatccc tTA AA

GAM1544 CACCCCAGGAGCCCCGGCAG 1768 CAGCACCCCA 4838 C- CA A CCA A C- CA A CCA A C- CA A C
CACCCCAGGAGCCCCGGCAG GGAGCCCCGG GC CCGG GC CC GG GC CCGG GC CC GG GC CCGG GC CC C
CACCCCAGGAGCCCCGGCAG CAGC || |||| || || || || |||| || || || || |||| || ||
CACCCCAGGAGCCCCGGCAG CG GGCC CG GG CC cg ggcc cg gg cc cg GGCC CG GG /
CACCCCAGGAGCCCCGGCAG AC C- A ACC A ac c- a acc a ac C- A A
CACCCCAGGAGCCCCGGCAG
CACCCCAGGAG
GAM1545 CTTTGTTGAACTTGCCGTAC 173 TGTTGTAGCC 3243 C CCG CAG T ATA AC C--- CTA T GC
CCGTCCAGCTTGATGTTATA GGTGGCGAAC GTAC TC CTTGA GTT CACCG GTTAC TTGTTAA TG AC C
CACCGACGTTACCTTGTTAA TCGG |||| || ||||| ||| ||||| ||||| ||||||| || ||
CTATGTACGCCCAGTCAAAA CATG AG Gggct caa gtggc cgatg AGCAATT AC TG /
TTAACGATGTTGTAGCCGGT T --- A-- - gcg -- ttgt AAA - AC
GGCGAACTCGGGAGAGTACT
GCTTGAGAAAG
GAM1546 AGGGTGTTTCGGGTGCGGTT 1763 CGGGTGCGGT 4833 GTTT---- - - tg- t cct
GCCTGACCCTAATAAGTTTG TGCCTGACCC AGGGT cgggtg c ggt cc gac a
GACTGCCTGACGCCCGCATA TAAT ||||| |||||| | ||| || |||
TATAACCCT TCCCA GCCCGC G CCG GG TTG a
ATATATAC A T TCA T AAt

GAM1547 CACCTCCAATGGGAGAGCAT 1769 ACAGGGCGAT 4839 - AAT---- ------ A TG CA AA---- C AA
TGGGGCAAGGGAACCCCGTG TGCCCTCCCC C TCC GGGA GAGC T GGG AGGG CCC GTGCAGG C
CAGGAACCCACCTGCACAGG TGGA | ||| |||| |||| | ||| |||| ||| |||||||
GCGATTGCCCTCCCCTGGAG G AGG CCCT TTCG g ccc tccc ggg caCGTCC C
CTTATAACTTCCCCTATTCA T ACTTATC TCAATA a gt c- gttagc a AC
GGATGGTG

GAM1548 GTGTTTTTGATTGTAGCGGA 1770 TTTTTGATTG 4840 att - aaa-- TA
AAAATGTAATAAATTTTACA TAGCGGAAAA GTGtttttg gtag cggaa tgtAA A

GACAGTTTTGCCTACTGAGA ATGT ||||||||| |||| ||||| |||||
ACAT TACAAGAGT CATC GTTTT ACATT A
--- C GACAG TT

GAM1549 ATAACTTTTGGTCACCCACC 1771 ACTTTTGGTC 4841 g- c cgaa - GT- C CGGA AA
TCGAACGTCGAGTAGTCGAC ACCCACCTCG ATAactttg tcacc acct cg TCGA AGT GA TGGTTG G
GGATGGTTGAAGCCCGGCCA AACG |||||||||| ||||| |||| || |||| ||| || ||||||
GATCCACTTCATCGAGCGCC TATTGGAGAC AGTGG TGGG GC AGCT TCA CT ACCGGC /
AGGGTGGTGAAACAGAGGTT AA - ACC- G ACT C AG-- CC
AT

GAM1550 TCCTGGATACAATACTCTCC 1772 TACAATACTC 4842 GAtac- cccTCC TC
TATTACGCCCCTCCGGTCAG TCCTATTACG TCCTG aatactctcctattacgc GG A
GCCCTCCCGCGTAATAGGAG CCCC ||||| |||||||||||||||| ||
GGTATTTCTTTATAGGG GGGAT TTATGGGAGGATAATGCG CC /
ATTTCT CCCTC- GG

GAM1551 CGTCGCCACAGAATACATGT 1773 TGTCTAGAGA 4843 A ACAtg ta tat- ccat aT
CTAGAGATATCAGGCCATTG TATCAGGCCA CGTCGCCAC GAAT tc gaga cagg tg T
ATTTTCACCTTGCTCTTCTT TTGA ||||||||| |||| || |||| |||| ||
CTGAAAATGGTTCGTGGCGA GTAGCGGTG CTTG AG TTCT GTTC AC /
TG - GTAAA TC TCTC C--- TT

GAM1552 GGGCGGGATAGCTCAGCAAA 1774 TACTATGTCG 4844 -- AGC AAA TG -- ----- T A CTCTCC A
CCTGGATGGGTCATCGTGTG TACACGTGAA GGAT TCAGC CC GA TGGG TCA CGTGTG GGCG GA G
AGGCGCTCTCCGAAGTCTCT ATCT |||| ||||| || || |||| ||| |||||| |||| ||
ACTATGTCGTACACGTGAAA CCTA AGTTG GG CT ACTC agt gcacat ctgt CT T
TCTCTCAAATCTGGGGTTGA TA --- --- GT AA tctaa - g atcat- C
ATCCATCGCCC

GAM1553 CTCCGGGAGGGAAAACGGCG 174 GGGAAAACGG 3244 Ag aa ggtagaaa C T GC
AGGGTAGAAACGAGCGGTGA CGAGGGTAGA CTCCGGG gga acggcgag cgAG GG GA A
GCAAAATCCCCTCGCTCGTC AACG ||||||| ||| |||||||| |||| || ||
GTCGTCCTCCTCGGAG GAGGCTC CCT TGCTGCTC GCTC CC CT A
CT GC -------- - - AA

GAM1554 GTCATCGGCGTACGTGGGGA 175 AAGAGTCCGG 3245 CG -- TA- C GAAA---- TG
TGTACCGCGACTGAAAGCTG GCCCATCAGC GTCATCGGCGTA TGGG GATG CCG GACT GC T
TTGGCGACGTAAGAGTCCGG CCAG |||||||||||| |||| |||| ||| |||| ||
GCCCATCAGCCCAGATATGT CAGTAGCTGTAT accc ctac ggc ctga CG /

CGATGAC Ag ga ccg - gaaTGCAG GT

GAM1555 TACAGCTACGAAGAGAATAT 176 ACGAAGAGAA 3246 - Tacg-- tat -- g
ATGTTATGTGAGAATGTTAG TATATGTTAT TACA GC aagagaa atgtt atgt a
ACATTTTTCTTTTAAATTTG GTGA |||| || ||||||| ||||| ||||
CTTGTA ATGT CG TTTTCTT TACAG TGTA G
T TTTAAA TT- AT A

GAM1556 ACCACAGCGCATGCGCCGGG 177 CGTTGTGGGG 3247 A- CATGC G g - c g
TTG T
CCGTTGTGGGGCCCCGGGCC CCCCGGGCCG ACC CAGCG GCCGG Cc ttgtgg ggccc gg
ccggggcCCC GG C
GGGGCCCCTTGGGTCCGCCG GGGC ||| ||||| ||||| || |||||| ||||| || |||||||||| ||
GGGCCCCGGGCCGGGCCGCC TGG GTTGC CGGCC GG GGCACC CCGGG CC
GGCCCCGGGG CC C
ACGGGGGCCGGCCGTTGGCG CG ----- - G G - G --- G
GT

GAM1557 CCAGCGGCCGGCCGGCGCTT 178 ACGCCCCTTG 3248 A CC - T GA-- AT
AGGGGGAGGATGTCGCCGAC GCCGCCCCGG CC GCGGCCGG GGCG CT AGGGG GG G
GCCCCTTGGCCGCCCCGGCT CTGC || |||||||| |||| || ||||| ||
GCAGG GG cgtcggcc ccgc gg tcccc CC T
A -- c t gcaG GC

GAM1558 TCTGCCTCTGCCGCTTGTGA 179 TGAGTGCGCG 3249 - G g g -- - TG --- G
G
GTGCGCGCGCCGGCTCTGCG CGCCGGCTCT CC CTTGtgagt cgc cgccggct ctgc gg TCG
GCGGCGGCTGC GC G
GTGTCGGCGGCGGCTGCGGC GCGG || |||||||||| ||| |||||||| |||| || ||| |||||||||| ||
GGCTGCGGCGGCCGCCGTGT GG GGGCGCTCA GTG GCGGCCGG GATG CT GGC
TGCCGCCGGCG CG C
TCGGTCTCGGTAGCCGGCCG C G G G CC G CT TTG G T
GCGGGTGGACTCGCGGGGGG
CCGGAGGGTGG
GAM1559 GGCAAAGCGGCGGGGCGGTT 181 AAGCGGCGGG 3251 aag ---- -- -- ---- - G ------
G
CGGGGGGGGGGGGGGGGGGC GCGGTTCGGG cggc ggggc ggt tcgggggggG GGG GGG
GGGC GG A
GGGAAACCAAGTAGGCCCGC GGGG |||| ||||| ||| |||||||||| ||| ||| |||| ||
CCATCCGCGGCCCCTCCCGG GCTG CCCCG CCG GGCCCTCCCC CCT CCC
CCCG CC A
CAGCCACGCCCCCAGCGTCG GG- CGAC CA AC GGCG A G GATGAA A
GGTGTC

GAM1560 TTGCCGCCGTGGGCAATCGG 1775 CCGCCGTGGG 4845 c aatcgg - CCA GC
TTGTTAGTCCCAGGTAGGCC CAATCGGTTG TTGc gccgtgggc ttgt tagTC GGTAG C
CACTATCGATTATGCAGTGG TTAG |||| ||||||||| |||| ||||| |||||

CCTACGGCAGCAA AACG CGGCATCCG GACG ATTAG CTATC /
A GT---- T --- AC

GAM1561 GTGCCGTTTAGATGGTCTCA 1776 TTGGGTCTAA 4846 G G AGATG C G G GAGG
GACCGGGATCGAGGTGCAAG GGCGGGAAGG GT CC TTT GTCT AGACC G ATC T
GTTGGGTCTAAGGCGGGAAG GGAT || || ||| |||| ||||| | |||
GGGAT ta gg aag cgga tctgg t tGG /
g g gg--- a g - AACG

GAM1562 CACGGTCGTTGTAGGCTTGT 180 TCGTTGTAGG 3250 c a ttgt gaGAAA
GATAGATGAGAAACATAAAC CTTGTGATAG CACGGt gttgt ggc gatagat C
GGTTTGTTCGCCACGATCGC ATGA |||||| ||||| ||| |||||||
CGTG GTGCCG TAGCA CCG TTGTTTG A
C - C--- GCAAAT

GAM1563 GTTTTAGAAAACCATCTACT 182 TTTGATATTT 3252 AACC- TACT TATG
ATATCATATGAAATACTGGT CTTTTAAAAC GTTTTAGAA ATC ATATCA A
ATTTGATATTTCTTTTAAAA ||||||||| ||| ||||||
C caaaatttt tag tATGGT A
cttta tt-- CATA

GAM1564 TCGCGAGGAGAACTCCGCCG 183 TAACGCGAGA 3253 - A A C AAA- GGA A
AACGGATG T
TAAACTCGGGACGTAACGGA AAGGCGTCGG TCG CG GGAG ACTCCG CGT CTCG CGT
ACGG CG C
ACGGATGCGTCTACGAACAA AGTC ||| || |||| |||||| ||| |||| ||| |||| ||
CTCCCGTAACGCGAGAAAGG GGC GC CCTC tgaggc gcg gagc gca tGCC GC T
CGTCGGAGTCCTCCACGACG A A c t gaaa --- a CTCAACAA A
G

GAM1565 GTGTATGAAATGGGCGGGAT 184 TATGAAATGG 3254 a tg- ggata tAC ACCAATTTG
T
ACTATCTACGTGGACCAATT GCGGGATACT GTGt tgaaa ggcg ctatc GTGG CATA T
TGCATATTATATGAAAACTA ATCT |||| ||||| |||| ||||| |||| ||||
ACCGCATGATGGCGCTATTT CACA ATTTT TCGC GGTAG CGCC GTAT /
TTTAAACAC A TTA ----- TA- AATCAAAA- A

GAM1566 CCTCCACCTCCTCTTCGAAG 185 TATTCCACTG 3255 --------- - T AA c- t------ c
taCTT
AATATTCCACTGTCCCCTTT TCCCCTTTTC TCC TCT CGAAG tatt cactg ccccttttt tc T
TCTCTACTTTTTAATGAAAA TCTA ||| ||| ||||| |||| ||||| |||||||| ||
AGGGGCAAATGTCAGTGATG AGG AGA GCTTC GTAG GTGAC GGGGAAAA AG
/
ATGAGCTTCGAGACGGACCA ACCAACACC C - GA TA TGTAAAC - TAATT
CAACCACCAACTGGAGG

GAM1567 AGGCTCTGACGTCTCTCCCT 186 TCTGACGTCT 3256 tct ctctccctaccc cTCC AA
ACCCTGGCTCCCGGAAAAAA CTCCCTACCC AGGC gacgt tgg CGG A
CCGAAAACCACCCATTTCCT TGGC |||| ||||| ||| |||
CATGTTTGCCT TCCG TTGTA ACC GCC A
T-- CTCCTTTACCC- AAAA AA

GAM1568 TTACATAATTTATATTAAGA 188 TAATTTATAT 3258 - tcaaat C CT AGAAT G
ATATCAAATATTCTATCTAA TAAGAATATC TTACAtaatttatat taagaata ATT TAT AAAC TC T
ACAGAATTCGTAAGATATAG AAAT |||||||||||||| |||||||| ||| ||| |||| ||
TTTTTGTATAATTATTTTTA AATGTGTTAAATATA ATTTTTAT TAA ATG TTTG AG A
TATATAAATTGTGTAA T ------ T TT ATAT- A

GAM1569 TTGTATGTGACGTTTCCGGA 189 TATGTGACGT 3259 t- tttcc - aaaaGG G T
ATAAAAAGGTTGATCCGTCG TTCCGGAATA TTGtatg gacg gga ata TTGATCC TCG G
TGAACGAAGGGTCGAATACG AAAA ||||||| |||| ||| ||| ||||||| |||
TGTCTCCAGCTCGTCTTCAT AGCATAC CTGC CCT TGT AGCTGGG AGC A
ACGA TT TCGA- C GCATA- A A

GAM1570 GTTGTCGCTTTCGTTGTAGA 190 TATCTCGACA 3260 - TTTC T CG A GTC
CGTATCGGAACGTCCATAGT CGCGCACGAC GTTGT CGC GTTG AGA TATCGGA C C
CCGATATCTCGACACGCGCA ||||| ||| |||| ||| ||||||| |
CGAC cagca gcg cagc tct atAGCCT G /
c ca-- - -- - ATA

GAM1571 GTTTTTTTTTATTGCTAATG 191 TTGCTAATGC 3261 A - tgcgtaaacc aTG AGTAC
CGTAAACCTGCCCCATGCCC GTAAACCTGC GTTTTTTTTT ttgc taa tgcccc CCCCC A
CCAGTACAAACAAGGGGGGG CCCA |||||||||| |||| ||| |||||| |||||
GGGGCACTAAAAATTTTTGC CAAAAAAAAA AGCG GTT ACGGGG GGGGG /
GCGAAAAAAAAAAC - C TTTAAAAATC GG- AACAA

GAM1572 GCTGGCCACGTGCCCCGAAC 196 CATCGATGGA 3266 C - C- ACA---- AT
ATCAGATTACCTGGGACCCC CGCGTTGTCA GCTGGC ACGTG CC CGA TCAG T
ATCGATGGACGCGTTGTCAG GC |||||| ||||| || ||| ||||
C cgactg tgcgc gg gct GGTC /
t a ta acCCCAG CA

GAM1573 CAAGCTTCGCGTTCAGCGGC 187 CAGCGGCTTC 3257 TTca-- g - gcaacaa AC- A TCT-
-- - TCA
TTCTGTTTGCGCAACAATCA TGTTTGCGCA gcg ctt ctgtttgc TC AT CGGAAT CT CCT
C
CATACGGAATTCTCTCCTTC ACAA ||| ||| |||||||| || || |||||| || |||
ACACTGGGCAGTTCTTCATT CGT GAG GACAAATG AG TA GCCTTA GA GGG
/

CCGCATAGCGAGCTTAAAGT CGATGG G T AAATTCG CGA C CTTCTT C TCA
AAACAGTGAGGTGCGGTAGC
CGCTTGTTTG
GAM1574 CGTCCGCGGCGACGGCGCCG 192 GGAGTGGGGT 3262 GGCGA C CC G G A G
A
TCGCCGCCGCGCTCGGAACG CGACGGCCCG CGTCCGC CGG GCCGTCG GCC CGCTC GA
CGTTC GA C
TTCGGAACGTTCGGAACGCT AGGA ||||||| ||| ||||||| ||| ||||| || ||||| ||
CGGAGTGGGGTCGACGGCCC GCAGGCG gcc cggcagc tgg gtgag CT GCAAG CT G
GAGGAAGCGGACG Aagga - -- g g C G T

GAM1575 ACGTGTTTTTTTTAAGTTAT 193 TAAGTTATTT 3263 -- - a act- t ccacC
TTTACTATTGAGCCACCTAT TACTATTGAG ACGTGTT TTTTTtaa gtt tttt at gag T
ACACTCTGTTACAAAAAAAA CCAC ||||||| |||||||| ||| |||| || |||
CATTGAAAAATAGATATGT TGTATAG AAAAAGTT CAA AAAA TG CTC /
AT A A ACAT T ACATA

GAM1576 GATATGTCAATACAACAGTC 194 TATGTCAATA 3264 aa - acag aatg C T A
AATGTTCTCAGGATTGCAAG CAACAGTCAA GAtatgtc ta ca tc ttCT AGGA TGC A
TGCGTTTTTAAGAAAAAGAA TGTT |||||||| || || || |||| |||| |||
ATATGATGAAGATATATC CTATATAG GT GT AG AAGA TTTT GCG G
AA A ATAA AAA- A T T

GAM1577 CGTGCGTGTTCTGTGCGTTA 195 GTGCGTTATA 3265 T C- tatataa - aa
TATAACCAGAACAAGCTGTG TAACCAGAAC CGTGCG GTT Tgtgcgt ccaga ac g
TCTGGACTTTGCGCGCAACG AAGC |||||| ||| ||||||| ||||| ||
ATCTGCACG GCACGT TAG ACGCGCG GGTCT TG /
C CA TTTCA-- G Tc

GAM1578 ACACCCACTTCCAGGGCGTA 197 CGAAAGTTCT 3267 A ACTTCCA C AACCc ag tcacc a
act
ACCCGAAAGTTCTCACCACA CACCACACCC AC CCC GGG GT gaa ttc ac ccc t
CCCACTTCCAGGGCGTAACC ACTT || ||| ||| || ||| ||| || |||
CGAAAGTTCTCACCACACCC TG GGG CCC CA CTT AAG TG GGG /
ACTTCCAGGGCGT C ACCTTCA A CCACT GA CCCAA C ACC

GAM1579 GGCGTGGCGATACGACGAAG 198 TGACCGTGTG 3268 C - ------ A- A G
CCGTGGAGATGGCTCTGACC TGAAACGACC GG GTGG CG ATACG CG AGCCGT G
GTGTGTGAAACGACCGCTCC GCTC || |||| || ||||| || ||||||
Cc cgcc gc tgtgc gt TCGGTA A
t a aaagtg ca C G

GAM1580 ACCACATGGTGGTTATCTGT 199 TATCTGTATA 3269 tat ataaact c - a AC------
ACC

ATAAACTGCACCTGTTAACG AACTGCACCT CATGGTGGT ctgt gcac tg tt ACGTGTA
TGCGCC A
TGTAACTGCGCCACCACAAG GTTA |||||||| |||| |||| || || ||||||| ||||||
GGCGTATATAAAAGTGCATG GTACTACCG GATA TGTG GC AA TGTACGT
ATGCGG C
TAAATCGAGTGTTTAAAAAA C-- AAAAATT A T A GAAAATAT GAA
TAGCGCCATCATGCGGT

GAM1581 CGGCTTGTGGAGGTAAGAGC 200 TGTGGAGGTA 3270 Ttgt ta tccc- gg- C TACC
TCCCGGGGGACGGCTTACCA AGAGCTCCCG CGGC ggagg agagc gg gA GGCT A
ACTTGGCTTCATACTTATCT GGGG |||| ||||| ||||| || || ||||
GCTCTCTTCTCCTTCGCTG GTCG CCTCT TCTCG TC CT TCGG /
CTT- TC TCTAT ATA - TTCA

GAM1582 CCTCTCAAATCTTGGGTTAA 201 TCTTGGGTTA 3271 T AAtc aaactcatc c A
ACTCATCACCGCGAAAATCT AACTCATCAC CCTC CA ttgggtt ac gcgAA A
TTGCCGTTCCAAACCCGAAT CGCG |||| || ||||||| || |||||
CCTGCGAGG GGAG GT AGCCCAA TG CGTTT T
C CCTA ACCT----- C C

GAM1583 GCTCGGGCGCATCCGCTCGC 202 TTCGACAGCA 3272 - ATC- C C CA- A T
TCGTCGACAACGAGCTCTGC GCGCCGCGCG GCTCGGG CGC CGCT GCT GTCGA ACG GC
C
GTGTACTTCGACAGCAGCGC CCCC ||||||| ||| |||| ||| ||||| ||| ||
CGCGCGCCCCGAGC CGAGccc gcg gcga cga cagct TGT CG /
c cgcc - - tCA G T

GAM1584 ATCTCGTCAATTCCATTCCG 203 CATCATGCCA 3273 ATT--- CC A ----------
GAA
ACTGCTACTGCCATGAATCA TCACGATCAG TCTCGTCA CCATT GACTGCT CTG
CCAT T
AATGGGACATCATGCCATCA CAGC |||||||| ||||| ||||||| ||| |||| |||| /
CGATCAGCAGCAGTCAAGGT AGAGTAGT GGTGG CTGAcga gac GGTA /
GGCACTTATGATGAGAT ATTCAC AA c tagcactaccgtactacAG AAC

GAM1585 GGCGACTACGATATACTAGT 204 ACTACGATAT 3274 c ata- t t AA
GTTGGACGAAGTTATGTCCA ACTAGTGTTG GGCGa tacgat ctag gt ggacg G
CCCTGGCCCAGTTGTATTCG GACG ||||| |||||| |||| || |||||
CC CCGCT ATGTTG GGTC CA CCTGT T
T ACCC C - AT

GAM1586 GTCACGTTGGGTGACTCTGT 205 ACGTTGGGTG 3275 ac t ctct-- a-- C
CGATCCACGCCTGGAAACCG ACTCTGTCGA GTC gttggg ga gtcg tcca G
ACCCACCTTCCCCCAACCCG TCCA ||| |||||| || |||| ||||
AC CAG CAACCC CT CAGC AGGT C

CC C TCCACC CAA C

GAM1587 TGCCAACTGTCCGCTTGGTG 206 TCTGCACCAC 3276 CAACT- CGCT- C- AACATTT
CACTGAACATTTCCGCCCAA CAATGATTAC TGC GTC TGGTGCA TG C
CCATCTGCACCACCAATGAT ACTG ||| ||| ||||||| ||
TACACTGCA ACg tag accacgt AC C
tcacat taacc ct CAACCCG

GAM1588 GATGATTCAGTCATTGTCGG 207 AGTCATTGTC 3277 TTCa- a tc ct ccca TC
CACTCCACCCATCTCCCCGA GGCACTCCAC GATGA gtc ttg ggca cca tC C
ATTGGCCTGCCATCAAAGAC CCAT ||||| ||| ||| |||| ||| ||
CTCCTTCATC CTACT CAG AAC CCGT GGT AG /
TCCTC A TA CC TA-- CC

GAM1589 TGGAAATAGTATATAAGGAT 208 TAGTATATAA 3278 g gttt---------- GTAC - TT- A CT
AGTTTCTAGATTGTACGGGA GGATAGTTTC tataa gata ctagaTT GGGAG CTC CACT CTCG G
GCTCTTCACTACTCGCTGCG TAGA ||||| |||| ||||||| ||||| ||| |||| |||| TCGAGAGTGTACGAGACTCT ATATT TTAT GGTTTGG CTCTC GAG GTGA GAGC C
CCAGGTTTGGTAAGAAATAT G ATTTTATAAAGAAT AC-- A CAT - TG
TTTATATTGTTATAATGTTA
CTATGATCCA
GAM1590 GGATTTGTATATTAGCCTTG 209 AGGGAGACAT 3279 -- AGCCTTG ag- tag t A
CTAAGGGAGACATCTAGTGA CTAGTGATAT GGA TTTGTATATT CTAaggg acatc tga ataagtGTG A
TATAAGTGTGAACTACACTT AAGT ||| |||||||||| ||||||| ||||| ||| |||||||||
ATCTTAAATGATGTAACTCC CCT AAACATATAA GATTCCT TGTAG ATT TATTCACAT /
TTAGGATAATCAATATACAA TA CTAATAG CAA TAA C C
AATTCC

GAM1591 GCGAGTCGCTATGACGCGTC 210 CACTATGGCG 3280 TC - A GTCCTT CCAG--- GA GTCG A
GAGGGTCCTTCGTCTCCAGA CGTCGATGGT GAG GCTAT GACGCGTCG GG CGTCT AGCCAG GA GC T
GCCAGGAGAGTCGGCATTGG CCCT ||| ||||| |||||||||| || ||||| |||||| || ||
CATCATCAACTGGCTGAACC Ctc tggta ctgcgcggt tc GCAGA TCGGTC CT CG T
CCAGACGCACTATGGCGCGT cc g a ac---- CCCCAAG AA ACTA G
CGATGGTCCCTCGT

GAM1592 GGAAGTGAAGAACCTCGTGA 212 TGAAGAACCT 3282 AGtg-- c a------- aa TC CTC
CCCAAATACTCCTGCTCCTC CGTGACCCAA GGA aagaacct gtg ccca tac CTG C
ATAGACGTACCTGGGATGAG ATAC ||| |||||||| ||| |||| ||| |||
AGACACAAGGTTCTTAAATT CCT TTCTTGGA CAC GGGT ATG GAT /
GTCC GTTAAA A AGAGAGTA CC CA ACT

GAM1593 GCAGCTCTAACTTGGCATCT 213 TGGCACGACT 3283 AACTT--- CTCTTTT G T CCT-- -
TT---- CT
CTTTTACAGTGGTTCTCCTG GTTCCTATAT GGCAT ACAGT GT CT GATTT GCTC
CGTG C
ATTTGCTCTTCGTGCTCTTC GCTC ||||| ||||| || || ||||| |||| ||||
ATGTCCACTGAGCAAGATCC tcgta tgtca ca gg CTAGA CGAG GTAC /
TTCTGGCACGACTGTTCCTA TCACGCTc tatcct- g c tCTTC A TCACCT TT
TATGCTCTCGCACTCTTGTT
GC
GAM1594 GGTTTGGGCAACAAAACTCT 214 CAAGCAAGAG 3284 TT ACAAA- AACCC C
TAACCCTTTGCGCGAATGCA TGGCTAATGT GGT GGGCA ACTCTT TTTGCG G
AGCAAGAGTGGCTAATGTCT CTGC ||| ||||| |||||| ||||||
GCC Ccg tctgt tgagaa gaaIGT A
-- aatcgg c---- A

GAM1595 GTGATGTTGCGATAACATCC 215 AAAGAGGTCT 3285 T AACAT GG -- C
TCTGGGATGCCAAGCAGATC TCATCGCACA GTGATGT GCGAT CCTCT GA TGC A
AAAGAGGTCTTCATCGCACA TCGC ||||||| ||||| ||||| || |||
TCGC cgctaca cgcta ggaga CT ACG /
- cttct aa AG A

GAM1596 TACTATAACAGGAAACATAG 216 TAACGGCAAT 3286 CAGGAAAC GAA GGA CC
AAGTTGCGGATAGAGCCTGG GATATTTATA TACTATAA ATA GTTGC TAGAG T
TTTCTAACGGCAATGATATT GTG |||||||| ||| ||||| |||||
TATAGTG gtgatatt tat taacg atCTT G
-------- ag- gca TG

GAM1597 TGCATGAAAATATCATTAAA 211 TGAAAATATC 3281 - tg a a- - CAA
TTGTTTTACAAATTTTAAAT ATTAAATTGT TGC A aaaat tc ttaaattgt ttta A
GCAATTTAAAAGAATTTTTG TTTA ||| | ||||| || |||||||| ||||
TAGCA ACG T TTTTA AG AATTTAACG AAAT /
A GT - AA T TTT

GAM1598 TGTATTTTTCTTTGCAGAGA 217 TGGAGAGCTT 3287 TTTT - GA-- t - ttata tg gga
TGTATGGAGAGCTTATATTG ATATTGGGGG TGTAT CTTTG CA GATGTA gg agagc t gg a
GGGGAAAATACCTGACTGTT AAAA ||||| ||||| || |||||| || ||||| | ||
CTGCCTATATTCGAATGTTG ACATG GAAGT GT TTATAT CC TCTTG A CC a
AAGTATGTACA TAT- T AAGC - G TC--- GT ATa

GAM1599 GGGTGTGATGTACAGGAAAA 218 TACAGGAAAA 3288 A--- a--- aaaa aag a - AC
TGACGAAGATGAAGGAACCA TGACGAAGAT GGGTGTG TGtac gg tgacg atg ag GA C
ATCGCTGCATAACGTTAAAC GAAG ||||||| ||||| || ||||| ||| || ||
CGCAAGTGCAGAAATACACC CCCACAT ACGTG CC ATTGC TAC TC CT /

C AAAG AACG AA-- AA- G G AA

GAM1600 TATATATTTTGGGTTCTGGC 220 TATTTTGGGT 3290 t-- ttct cta TAC C - T T ATAATC
TACTGTATATACAGGTACTG TCTGGCTACT tggg gg ctgtatA AGGTA TGTGGTA CA TGGAT GTT A
TGGTACATTGGATTGTTATA GTAT |||| || ||||||| ||||| ||||||| || ||||| |||
ATCACACAACCAGCCATCTA ACCC CC GACATGT TCCAT ACATCGT GT ATCTA CGA C
CTGCTGCTACACTACCTTGT CAT CTT- CC- --- C C C C CCAACA
ACAGCCCCTTCCCCATACAG
TATGTA
GAM1601 GGTTCCACCTGCCTTCTTTC 228 TCCACCTGCC 3298 cct c - aatcaa----- G
AATCAATGCGAAAGCACACC TTCTTTCAAT GGTtcca gc ttc tttc tGC A
CCCTACCGAAATGGATGCCT CAAT ||||||| || ||| |||| |||
GGAACC CCAAGGT CG AGG AAAG ACG A
C-- T T CCATCCCCCAC A

GAM1602 GCAATGTTAAAGTGACTCCT 219 TTAAAGGTAA 3289 - TAAA CT- AGAT- ACCTA
CCAGATTACTCACCTATAAT GAGTTATGAC GC AATGT GTGACTC CC TACTC T
CGCGAGTATTAAAGGTAAGA GCAT || ||||| ||||||| || |||||
GTTATGACGCATTAGC CG Ttacg tattgag gg ATGAG A
A cag- aat aaatt CGCTA

GAM1603 AAGTAAAGATTTCAAAGATG 221 TAAAGATTTC 3291 ttcaaa--- --- tg
TTTTCTGTCAGAAAATACCA AAAGATGTTT AAGtaaagat gatg ttttc T
TCCAAGTCAATATCTTTACT TCTG |||||||||| |||| |||||
T TTCATTTCTA CTAC AAAAG /
TAACTGAAC CAT AC

GAM1604 GGTTTAGTATCTCAATTGTC 229 TGAGTATTTG 3299 A - ATTGTCTG AAG TTA- ---- T
TGTCTTAAGTTCCATTACAA GATTTGGAAA GGTTT GTAT CTCA TCTT TTCCA CAAATAT AC A
ATATACTAACGTCTGAGTAT AGAA ||||| |||| |||| |||| ||||| ||||||| ||
TTGGATTTGGAAAAGAAAAT CTAGA TATA GAGT agaa aaggt gtttatg TG A
TTGTGAGTATATCAGATC C T GTTTAAa- --- ttag agtC C

GAM1605 TAATATTTGTAATTATTTTT 222 TTATTGTTAT 3292 T T TT- AAT TATA
TTAATAAAATATAATACTAT TTAAAATAAT TAA ATTTG AATTATTTT TAATAA ATAATAC T
ATCATTTGTATTATTATTGT TCTA ||| ||||| ||||||||| |||||| |||||||
TATTTAAAATAATTCTAAAT ATT TAAat ttaataaaa attgtt tATTATG C
TTTA T c ttt at- TTTA

GAM1606 AATATTGAATGTATTATTGA 223 TTGAATGTAT 3293 t ---- att T
TTTTATTAATATATTTATTT TATTGATTTT AATAttgaatgta tat tgatttt aATA A
AAAAAATCATTATATATTAC ATTA |||||||||||| ||| ||||||| ||||
ATTTAATATT TTATAATTTACAT ATA ACTAAAA TTAT T
T TATT AAT T

GAM1607 ACTTTCATTAATAATATTTT 224 TCATTAATAA 3294 Ttc ta--- ttaTC TT
TAAATTTATCAGAGTTTACA TATTTTTAAA ACT attaataa tttttaaat AGAGT A
TATTCTCCGTTTAAAAAATT TTTA ||| |||||||| ||||||||| |||||
TTTTATTAATTCTGGT TGG TAATTATT AAAAATTTG TCTTA C
TCT TTTTA CC--- TA

GAM1608 TGATATAGATTTAATATTTG 225 TATAGATTTA 3295 ttaatat ttt - TTA
TTTATCATATTTATCATATA ATATTTGTTT TGAtatagat ttg atc aTAT T
TAGATTCAATCATAGTATCT ATCA |||||||||| ||| ||| ||||
ATATCA ACTATATCTA AAC TAG TATA /
TGATACT T-- A TAC

GAM1609 GATATAATATTTACTAATTT 226 TATATAATTT 3296 TAATATTT ---------- A
ATCATCTGATATATAATTTT TTAATATAAT GATA ACTAATT TATC T
TAATATAATTAGTTAATTTA TAGT |||| ||||||| ||||
TC CTAT tgattaa atAG C
TTAAT--- tataatttttaatat T

GAM1610 GTATTGAATTCATAAATTAT 227 TATATATTCT 3297 TCATA t ctatttc taaa
ATATTCTATTTCGCTTAAAA ATTTCGCTTA GTATTGAAT AAT atatatt gct a
TTTTAGTTATTAATATATCA AAAT ||||||||| ||| ||||||| |||
TTACTATATTTAATAT TATAATTTA TTA TATATAA TGA /
TATCA C TTAT--- TTTt

GAM1611 TTTATTAGATATTATATTAA 230 TATTAGATAT 3300 t tatt ttcat TATT
TTTCATCATATATTCCTGCT TATATTAATT TTtattaga atta aat CATA C
ATGTTTTCATTTTTTGATTC TCAT ||||||||| |||| ||| ||||
TAATAAA AAATAATCT TAGT TTA GTAT /
- TTT- CTTTT CGTC

GAM1612 TAAAACATCTAAAGATGATA 231 AAGATGATAG 3301 C aa ----- t----- tttCA
GATGTGTATTAATTTCATCT ATGTGTATTA TAAAA ATCTA gatga tagatg gtattaa T
TGTTTAATATTTATATCATC ATTT ||||| ||||| ||||| |||||| |||||||
TATTTTTTCATCAATAGATT ATTTT TAGAT CTACT ATCTAC TATAATT /
TTTTA T AA TTTTT TATATT TGTTC

GAM1613 TAATAATATCATGTATATAA 232 TCATGTATAT 3302 c- ta tt ttATA AT TTG

TTTTTTATATTTATATTAAA AATTTTTTAT TAATAATAt atgtata attt tatat TTAA TC A
TTCTTGATCTGATCTTAAAC ATTT |||||||| ||||||| |||| ||||| |||| ||
TATATATCAAATCTTGTACA ATTATTATA TACATGT TAAA ATATA AATT AG /
TTTATATTATTA TT TC CT TCA-- CT TCT

GAM1614 ATACGAAACATTGTCGGCTC 2844 AACATTGTCG 5914 a ctcaaaaactccc ATG A
AAAAACTCCCACAGATGTCC GCTCAAAAAC ATACGAa cattgtcgg ACAG TCCATCG C
ATCGACGTCGATGGAACTGT TCCC ||||||| |||||||| |||| |||||||
TTGGCAATGCTTTGTGT TGTGTTT GTAACGGTT TGTC AGGTAGC G
C ---------- A-- T

GAM1615 ACTTTGAAAAAGCTTCTGTT 233 TGAAAAAGCT 3303 g ttc tg- AG---------- AT
TATGCATGTAGGTTATTTAA TCTGTTTATG ACTTt aaaaagc tgttta catgT GTT T
ACAGTTTTATAACGAAAAAA CATG ||||| ||||||| |||||| ||||| |||
AATATGATTTAGATAAATGT TGAAA TTTTTTG ATAGAT GTATA CAA /
TTTTTAAAAGT A TAA TTA AAAAAAAGCAATATTTTGA AT

GAM1616 GCTCTTATAATATTGGACTC 234 TGAGAACAAC 3304 AATA- GA CACCATA A
CACCATAGGAAACTTCCGAA CACAATAAGA GCTCTTAT TTG CTC GGA A
ATTGAGAACAACCACAATAA GC |||||||| ||| ||| |||
GAGC cgagaata aac gag CCT C
acacc aa tTAAAG- T

GAM1617 GTCTGTACAAAAGTTTGAGA 2845 TAGAATGGGG 5915 ACAAA TTG- - AG GGCTA
GT
TTTTCAGATTCTGCGGCTAT AACATCTACT GTCTGT AGT AGAT TTTC ATTCTGC
TAGAGAA A
AGAGAAGTATAATTCTTTGG TACT |||||| ||| |||| |||| ||||||| |||||||
TAGAATGGGGAACATCTACT CGGATA tca tcta aagg taagatG GTTTCTT T
TACTGGAAAATAGGC AAAGG ttca c gg ----- AA

GAM1618 GAGACGTCCATATCTGATTA 2846 TTGATCCGGG 5916 CGTCC -- T GATGA AAAA
TTATGATGAGGTAAAAAATA GTATTATATT GAGA ATATCT GATTA TAT GGT A
AACCGTTTAATATTGATCCG TTC |||| |||||| ||||| ||| |||
GGGTATTATATTTTC cttt tatggg ctagt ATA CCA /
tatat gc t ATTTG AATA

GAM1619 GGAAGACACATTATTTGACG 2849 TAGAACGATC 5919 ACAC T C - AA CT
ACGAATTATACTCTATTATA TTTCGATGAT GGAAG ATTATT GA GA CG TTATA C
GAACGATCTTTCGATGATAA AAAT ||||| |||||| || || || |||||
ATTTCC CCTTt tagtag tt ct gc gatAT T
aaa- c t a aa TA

GAM1620 CACGAAACTCTTAATGTTTC 2847 TTTGTCCTTA 5917 TAATGTTT- CTTA A
TCCTTAGGATTTCTGCCAGA GAGTTTTGTG CACGAAACTCT CTC GG T
GTTTGTCCTTAGAGTTTTGT |||||||||| ||| ||
G gtgttttgaga GAG TC T
ttcctgttt ACCG T

GAM1621 GCAAGCGCATTATATGTTTT 2848 TGATATACAA 5918 A GCA T TG AAt caaagtt a
TGATATCTTAATGATATACA AGTTTGCAAG GC AGC TTATATGTT T ATATCTT gatata tgc a
AAGTTTGCAAGCGCATTATA CGCA || ||| ||||||||| | ||||||| |||||| |||
TGTTTTCAAGATGTTGATGA CG TTG AATATGTAG A TGTAGAA TTGTAT acg g
TGTATAAAAGTTGC - AA- T GT CTT ATT---- c

GAM1622 CTGCAGATCCGAAGTATTCG 2850 AGACACCTTC 5920 TCCGAA C TAT GCTCAA
TGTA
GAGTATAGGGCTCAACTGAT CTTCAAGTAC CTGCAGA GTATT GGAG AGG CTGA T
GTATTATTTCAGACACCTTC TCTG ||||||| ||||| |||| ||| ||||
CTTCAAGTACTCTGCAG GACgtct catga cttc tcc gaCT /
------ a ct- aca--- TTAT

GAM1623 GCCGTCAGGATCAAGGATCG 2851 TCGCTCCGCC 5921 A---- ATCAA- AT ACC-- A
GAGACCCCCAACAGGGACTC CCAGACCGCC GCCGTC GG GG CGGAG CCC A
GCTCCGCCCCAGACCGCCCG CGAC |||||| || || ||||| |||
ACCGACGGC CGGCAG cc cc gcctc GGG C
Ccagc gccaga cc gctCA A

GAM1624 GGCGTTCAGGCCTTAATACT 2819 CAGCATGTAT 5889 CA TA TA--- - TCT
AGCCGCATCTTACCTGTCGG CGGGGCTCCG GGCGTT GGCCT ATAC GCCG CA T
CAGCATGTATCGGGGCTCCG ACGC |||||| ||||| |||| |||| ||
ACGCC Ccgcag tcggg tatg cGGC GT /
cc gc tacga T CCA

GAM1625 CGCCGAAAAATGCTTGTCTG 2820 CACTTTTTTG 5890 AAAA CTT CT T-- T CG
GCTGAGGTTGGTGTCGCTAA TCTCGCTTCA CGCCGA TG GT GGC GAGGT GGTGT C
TGCCACTTTTTTGTCTCGCT ATGT |||||| || || ||| ||||| |||||
TCAATGTCGGTG GTGGCt ac cg ctg tttca cCGTA /
gta- tt- ct ttt - AT

GAM1626 GCCAGGTTTCCATTGCCACC 2852 TTTCCATTGC 5922 t- att-- c g gaa
CGGGCGAAAACAAGCCGGGT CACCCGGGCG GCCAGGt tcc gc acccgg c a
AGTTTCAGGGGTCATCTGGC AAAA ||||||| ||| || |||||| |
CGGTCTA GGG TG TGGGCC G a
CT GACTT A - AAC

GAM1627 TTTTTCCTCTGTTTTTGCTT 2821 CCTCTGTTTT 5891 ct- tttt acgttcaaAT TCTTTAA
GACGTTCAAATTTTGGGTCG TGCTTGACGT TTTTTc ctgt gcttg TTTGGGTCG C
TCTTTAACCTGCTCTTGACT TCAA |||||| |||| ||||| |||||||||
TAAATAAGCTTCTACGGTCA AAAAAG GGCA CGAAT AAATTCAGT /
GAAAAA ACT TCTT ---------- TCTCGTC

GAM1628 GGAGCAAGCCATTTTAAAAT 2853 TTCGAAGTGC 5923 C CATTTT CC TACAG TCC
CTCCGTTACAGTTGAATGGT AGATTTTCCG GGAG AAGC AAAATCT GT TTGAATGG A
CCAAGTCTATTCGAAGTGCA CTTT |||| |||| ||||||| || ||||||||
GATTTTCCGCTTTCTCT TCTC ttcg ttttaga cg agcttATC /
t cc---- -- tga-- TGA

GAM1629 CGATATAGTACGCGCCTGCC 2854 TAGTACGCGC 5924 a ct cg- a ---------- AA
GGGAGAAACATCCCCTGAAC CTGCCGGGAG CGATAt gtacgcgc gc gg gaaacAT
CCCCTG C
CGCGGGGGTGACCGTATACT AAAC |||||| |||||||| || || ||||||| ||||||
ATGTTTCCTAGAGCCGTGCG GCTGTA CATGCGTG CG TC CTTTGTA GGGGGC /
TACCATGTCG C C- AGA - TCATATGCCAGT GC

GAM1630 TCCCCGTGGGCTCCACGCGT 2822 AACACCGTGA 5892 GC C C T -- C
TTTCCACCCTTTCCTGGAGG ATCCACGGGG TCCCCGTGG TC ACG GT TTCC ACCCTTT C
GGTCCGGAACACCGTGAATC A ||||||||| || ||| || |||| |||||||
CACGGGGA aggggcacc ag tgc ca aaGG TGGGGAG T
ta - - c CC G

GAM1631 AGTCTGGCCGAGCGGCGCCA 2823 CGAGTCCGCG 5893 A ---------- G - G AC
ACC
TCTTGGAGGAGGGGCGAGTC GTCGCCGCCT GCGCC TCT TGGAG AGG GGCGA
TCGCGGGC CGCCTCGGT C
GCGGGCACCGCCTCGGTACC GTTC ||||| ||| ||||| ||| ||||| |||||||| |||||||||
CCCTGGCCGAGGCGAGTCCG CGCGG AGA GCctt tcc ccgct ggcgcctg gcGGAGCCG
C
CGGTCGCCGCCTGTTCCGTG G TCCATCGTAGT g g - a- GTC
ATGCTACCTAGAGGGCGCTG
TCGAGGCGACT
GAM1632 TACTGTTTTATTGGTAGTTT 2824 TGGATGTATC 5894 TATT- T T CGA CTT CA
ATGTATCGACGCTTTCCCAA TATGCTACCT TACTGTTT GGTAGT TA GTAT CG TCC A
AATGGATCTGGATGTATCTA TGGT |||||||| |||||| || |||| || |||
TGCTACCTTGGTGGACAGTA ATGACAGG ccatcg at tatg gt AGG A
tggtt t c tag CT- TA

GAM1633 GCTTCACACGTTTCTACCAA 2825 TAGTAGGAAC 5895 T -------- CAA CAAGA
GCCCAAGATTCGATCGGTAG CCGCAATTGT GC TCACAC GTTTCTAC GCC T
TAGGAACCCGCAATTGTGTG GTGA || |||||| |||||||| |||
ACGT TG agtgtg caaggatg tGG T

C ttaacgcc a-- CTAGC

GAM1634 AGCTTGTTATTGGCTCCCGG 2826 TGCCATGTTG 5896 A G-- C--- GA
CCCAGTTGATGGAGCTGCCA GGAGAAACAA AGCTTGTT TTG CTCCCGGC CAGTT T
TGTTGGGAGAAACAAAGCAA AGCA |||||||| ||| |||||||| |||||
GTT TTGAacga aac gagggttg gtCGA /
- aaa tacc GG

GAM1635 GTTCAGGCGGCGGGGCTCGA 2827 AGGCGGCGGG 5897 ag - ------- - ga- acCGGA
A
CGACGGACCGGACGGTACAG GCTCGACGAC GTTC gcgg cggg gct cgac cgg CGGTAC G
TTGTACCGGAGCCGATAGTC GGAC |||| |||| |||| ||| |||| ||| ||||||
GTAGTAACTAGACCCGACCG CAGG TGCC GCCC TGA GCTG GCC GCCATG T
TGAGGAC AG A AGATCAA T ATA GAG--- T

GAM1636 CCCGTCGCGTTGGGTTGCAG 2828 TCGCGTTGGG 5898 - gttg tg ag---------- c
CCGCAAGCGGACGCTGGGGG TTGCAGCCGC CCCG tcgc ggt c ccg a
GAGCGGTGGCCAGAGCGAGC AAGC |||| |||| ||| | |||
GGG GGGC AGCG CCG G GGc a
G AGA- GT GCGAGGGGGGTCGCA g

GAM1637 GGGCGCCGCCACCCCCGACC 2829 TCGCCGGGCG 5899 CG A A G G GT
GGGGGAGCGGTCGTCGCTCG GGGGGGAAGC GGGCGC CC CCCCCG CC GG GAGCG C
CCGGGCGGGGGGGGAAGCGCC GCCC |||||| || |||||| || || |||||
C cccgcg gg gggggc gg cc ctCGC /
aa - - g g TG

GAM1638 TTCAGGGCCCCACAAATTTC 2830 ATAGAACTAA 5900 C ATT A--- C G CACCCCC TG
C-- CCCA A
ATATTTCCAGCAGCCTTTCC CTTGTGACAC AA TCAT TTTC AGCA CCTTTC CG AGT
TTC CAG A
ACCCCCCGTGAGTCTTCCCC AGAA || |||| |||| |||| |||||| || ||| ||| |||
ACAGAAACTGCATAGAACTA TT AGTG AAAG TTGT GGAaag gt tca aag GTC /
ACTTGTGACACAGAAAGGTG A GT- GACC T - acaca-- gt atc ataC A
TTTGAAACCAGGTGATGTTA
TGAAACTGAAG
GAM1639 GAAAAGGAGGAGAACACGGA 2831 TAGCGCTCAG 5901 GA--- A A tag ga tctc
aA
TAAAGTTAGCGCTCAGAATA AATATCTCAT GAAAAGGAG GAACACGG TA AGT cgctca ata
attca T
TCTCATTCAAATCCATGAAT TCAA ||||||||| |||||||| || ||| |||||| ||| |||||
AAACTATATGGGCGATATTC TTTTTCCTT TTTGTGCC GT TTA GCGGGT TAT
TAAGT C
TGCCGTGTTTAAAGATTCCT AGAAA - C TA- A- CAAA AC
TTTT

GAM1640 GGGATGAAACCTCTACTGCC 2832 TGGGATCTGA 5902 -- CCTCT - AAT--- - A- TAC
T
CTAGGAATGCCAGGCAGGTA GCCTGGGCTA GGGAT GAAA ACTGCCC TAGG GCC
AGGC GG CCCACC C
CCCCACCTCCGGGTGGGATC ATTG ||||| |||| ||||||| |||| ||| |||| || ||||||
TGAGCCTGGGCTAATTGTCT TCCTA CTTT TGATGGG ATCT cgg tccg tc gggtGG C
ACGGGTAGTTTCATTTCCAA AC ACTT- C gttaat g ag ta- G
TCCT

GAM1641 GTATATAGATGTCAATGAAG 2836 TAGATGTCAA 5906 taga atgaag ac CA T
AGTACACAGAAGCAGCTGCA TGAAGAGTAC GTATA tgtca agt acagAAG GC G
GCAACTTCTGTACTAGTGGC ACAG ||||| ||||| ||| ||||||| ||
AGATTGTGC CGTGT ACGGT TCA TGTCTTC CG C
TAG- GA---- -- AA A

GAM1642 CATGTTTGTCAGCATATTTG 2833 CTAGGTCAAA 5903 G T CATA- - ATT TGTT
CATTGCATGTTTCAAATTGC GTTCCCTGCC CAT TTTG CAG TTTG C GCA T
TAGGTCAAAGTTCCCTGCCA AAAA ||| |||| ||| |||| | |||
AAAATG GTA aaac gtc aaac g cGT C
a c ccttg t gat TAAA

GAM1643 CCAAACTTGCTTTTAGGCAC 2834 ACTTGCTTTT 5904 t t g acata tAC
ATAGTTTTACTGCATAAACA AGGCACATAG CCAAact gct ttag c gttt T
TTTAGCTAATAGCAGTTTGG TTTT ||||||| ||| |||| | ||||
GGTTTGA CGA AATC G CAAA G
- T - ATTTA TAC

GAM1644 GCCACAGAGGTCTCTGCTAG 2835 TGCTAGTTTG 5905 C G- tg agt cc gaa
TTTGGGCCAGCGAAACGGGC GGCCAGCGAA GC ACAGA GTCTC ct ttggg agc a
TATCCCGGTCCGGTGGAGGC ACGG || ||||| ||||| || ||||| |||
AGTCTGTCGC CG TGTCT CGGAG GG GGCCC TCG /
C GA GT CCT TA ggc

GAM1645 CTGAGGGGACCATGATATGT 1318 TACGCGGTTA 4388 CA- A- G AA G
ATAGGCGAAAGGCGGGGCTT GGAGTCCCCT CTGAGGGGAC TGAT TGTATAG CGA GGC G
CGGTTGTACGCGGTTAGGAG CAG |||||||||| |||| ||||||| ||| |||
TCCCCTCAG gactcccctg attg gcatGTT GCT TCG /
agg gc G -- G

GAM1646 CAGTGTTTCAAAAGTAGCAT 2837 CACTGGGTTG 5907 GTAGCATAAA CC----- A TAGAG
A- TT GGT
AAACACTATCCATTCCAAGT ATATTGGACT CACTAT ATTCCA GTCTG TAAC AGTGT
CA A
CTGTAGAGTAACAAGTGTTT GGGG |||||| |||||| ||||| |||| ||||| ||

CAGGTATAAATGCTGCACTG GTGATA Tggggt caggt gttg tcacG GT T
GGTTGATATTGGACTGGGGT AA-------- TAAAAAA - tata- gg TC AAA
AAAAAATATAGTGAATTTTG
AGACCTG
GAM1647 ATATTGTTTCCTAGATATGC 1319 TAAGTGCAAA 4389 TT C A---- CAG-
GATTTTAATT G
TGGCAGTTTGTATGATTTTA AAAATTAGCA ATA GTTTC TAGAT TGCTGG TTTGTAT
GTTG G
ATTGTTGGGAACAACTAAGT AAAG ||| ||||| ||||| |||||| ||||||| ||||
GCAAAAAAATTAGCAAAAGA TAT CAAAG ATTTA acgatt aaacgtg CAAC A
ATTTAGAAACCTTAT TC - Agaaa aaaa aat------- A

GAM1648 GACTTGGGTCTTGCAACGCT 2838 TGGCATGCGC 5908 ACGCT----- - AAT - ------ A--
G AAG
ACACTCTGGCAATCATCCAA TAGAGATGTT A ACA CTCTGGC CAT CCA ACAGAA
TTT TCTA A
CAGAAATTTGTCTAAAGAGC TTTT | ||| ||||||| ||| ||| |||||| ||| ||||
TCTAGAGGAAAGATTTTGTA T tgt gagatcg gta ggt TGTTTT AAG AGAT G
TAATATGGCATGCGCTAGAG ATTATttttt a c-- c ATAATA AGA G CTC
ATGTTTTTTTATTATGCAAG
GACCCAGTT
GAM1649 TTATTGTTGGAAAAATTTTA 2839 TAGAATGTGT 5909 G- G AAA CC----- T AT
GCCCAAAACATTGACATAGC TGAAAAAATG TTATT TT GA ATTTTAGC AAAACA TGAC A
GTCGTTGTTTTACACAATGT A ||||| || || |||||||| |||||| ||||
TAGAATGTGTTGAAAAAATG agtaa aa tt taagatTG TTTTGT GCTG /
A aa g gtg TAACACA T CG

GAM1650 AACCAATCTCAAAAGTTACT 2840 TCTCAAAAGT 5910 At ----- ac - aagtA
TGTGCTAAGTATTTCAAAGA TACTTGTGCT AACCA ctca aaagtt ttgtg ct T
TACAGAAGACTTTTTTCATG AAGT ||||| |||| |||||| ||||| ||
AGCTGGTT TTGGT GAGT TTTCAG GACAT GA /
C- ACTTT AA A AACTT

GAM1651 AGGACGCGGCCCCGACGGCC 1326 GCCCCGACGG 4396 - Ggc g - - a---------- aa
ACCCCGACGAAGAAACGGAC CCACCCCGAC AGGAC GC cccgacg cc ac cccg cg g
GACGCCGGCCGCGGCCCGGG GAAG ||||| || ||||||| || || |||| ||
AGTAGGCGTCGGGATAGCGG TCCTG CG GGGCTGC GG TG GGGC GC A
TCCT G ATA - A A CCGGCGCCGGCCGCAGCAG AA

GAM1652 CGGGTCTCGGCCACGGTGGC 2841 CGCCGGAGTG 5911 - G GG --- A C
GACCAGGGGCACCTCCCGGA GGCGACGACC CGGGTC TCG CCAC TGGCGA CC GGGG A
CCTCGCCGGAGTGGGCGACG CG |||||| ||| |||| |||||| || ||||
ACCCG gcccag agc ggtg gccgcT GG CCCT C
c g ag CCA - C

GAM1653 GCCGCGGCGCTCCATGAGGA 2842 TGAGGAGCCA 5912 C - t cca cc - aAG
GCCAGAGCCCGCCGGGGAAG GAGCCCGCCG GC GCGGCGC TCCA gaggag gagc gc cgggg
G
GCGGCCCCGTGCCGCTCCTC GGGA || ||||||| |||| |||||| |||| || |||||
CTCCTCCTGGAGGCGCCGCC CG CGCCGCG AGGT CTCCTC CTCG CG GCCCC /
GC C G C CTC C- T GGC

GAM1654 TAATGTTGGTTCATGAAGAT 1327 TGAAGATAAA 4397 CAt aag t caa - --- TAA A
AT A
AAAGTGTGCCAAAGAAACTT GTGTGCCAAA GTT gaagata tg gc agaa aCT TTTA ACA
ATGATTA GT G
TTATAAACAAATGATTAATG GAAA ||| ||||||| || || |||| ||| |||| ||| ||||||| ||
TAGGTGCTAGTCGTGTGTAC CGA CTTTTAT AC CG TCTT TGG AAAT TGT
TGCTGAT CG G
TTAAACAGGGTATTCTATAG TAT GA- - ATA A GAC TCA G -- T
CCAAGTATTTTCTATAGCCA
GTATTA
GAM1655 CGCCGTGGACAGGTTTAGCG 2843 ACAGGTTTAG 5913 G Gaca c tttttctc CCGT
CTTTTTCTCGCCGCGCCGTC CGCTTTTTCT CGCC TG ggtttag gc gccGCG C
ACTTCGCGGTCTTATCACGC CGCC |||| || ||||||| || ||||||
TTTAGACCACAGGGCG GCGG AC CCAGATT CG TGGCGC /
G A--- T CACTATTC TTCA

GAM1656 CGACAACGTCGGGCGCGTTC 1320 TAAAATCACA 4390 T-- G- T AGAG TGT T- C CTG-
CAC T T
AGAGTCCTGTACCGTGTGCG CCTCGGTGGA ACG CG GCGCG TC TCC ACCG GTG GA
AGA GTAG GT C
ACTGAGACACGTAGTGTTCA AAGA ||| || ||||| || ||| |||| ||| || ||| |||| ||
AACTCTACCTTCTAAAATCA TGC GC CGTGC ag agg tggc cac ct tCT CATC CA A
CACCTCGGTGGAAAGATCGT TAT GG T aa-- --- tc a aaaa TC- T A
GCGGCGTATCGTTGTCG

GAM1657 GGAAACGGGACACAATGGAC 1321 TTACTGCATA 4391 AAC ACAAT CTT AC T GTC
TTTGCAACGTATATGTCTTT TCCGTCTTTT GGA GGGAC GGA TGCA GTA AT T
GATTTACTGCATATCCGTCT ATCC ||| ||||| ||| |||| ||| ||
TTTATCC cct ttctg cct acgt cat TA /
att ----- at- -- t GTT

GAM1658 AGACATACGAGCCAGTGTAC 1322 TTTCAAAGTA 4392 C CAGT AGCGTAT TC
AGCGTATTGTCTCTCCATTT CTGTTGTTCG AGA ATACGAGC GTAC TG T
CAAAGTACTGTTGTTCGTAT TATC ||| |||||||| |||| ||
CTCT TCT tatgcttg catg AC C
c ttgt aaacttt CT

GAM1659 GTTGTCATGTATCGTTGTGT 1323 TGTCATGTAT 4393 at tcgt ggctGATATTG GC
TTGGCTGATATTGTGACGGG CGTTGTGTTT GTtgtc gta tgtgttt TGACGG G

CGAACTGTCAAAAAAAAACA GGCT |||||| ||| ||||||| ||||||
CATATTAGACAAC CAACAG TAT ACACAAA ACTGTC /
AT ---- AAAAA------ AA

GAM1660 TCCGGCCGGGTCACTTGTTC 1338 TCACTTGTTC 4408 - c tt tcataaa tcTAT
TCATAAAAGCGGTCTATCTC TCATAAAAGC TCCGG CCGGGt ac gttc agcgg C
CACTCCGCTCAGCCGGACCG GGTC ||||| |||||| || |||| |||||
TACCCGGACCGGA AGGCC GGCCCA TG CAGG TCGCC T
A - C- CCGAC-- TCACC

GAM1661 GTCGCAAAGCGCGCGGGCAG 1324 TCGCGATGGC 4394 C AA --- AGCCA - AG
CCACGGCCCAGACTGCGGTC CCGGAGCGCG GT GC AGCGCGC GGGC CGGCC C A
GCGATGGCCCGGAGCGCGCT CTCG || || ||||||| |||| ||||| |
CGCCAC CA Cg tcgcgcg cccg gctGG G /
C c- agg gtagc C TC

GAM1662 GGGAGACGGCGCAGCCAGTG 1339 CACGTGGTCT 4409 CG- - - TAAAG
TTTTTAAAGATAAAACAAGG GTGCGGCTCT GGGAGA GCGCAG CCA GTGTTTT A
CACGTGGTCTGTGCGGCTCT CCC |||||| |||||| ||| |||||||
CCC ccctct cgtgtc ggt cacGGAA T
cgg t g CAAAA

GAM1663 GATAACGGCACTAATATTAA 1325 CGGCACTAAT 4395 AAc a atattaact c GCT
CTTATCTAAAGGGCTAACAC ATTAACTTAT GAT ggc cta tat taaAGG A
CTTTACATATAGCGCCCAAA CTAA ||| ||| ||| ||| ||||||
TC CTA CCG GAT ATA ATTTCC /
AAC C --------- C ACA

GAM1664 TATAGAGATTATCAGTATCC 1328 TAGAGATTAT 4398 a tatcag c ac TAAT
AAGACACTAATAAACACGTA CAGTATCCAA TAtag gat tat caag aC A
GCTTGTATAACTATTACTAT GACA ||||| ||| ||| |||| ||
A ATATC TTA ATA GTTC TG A
A TCA--- T GA CACA

GAM1665 TACGTTTTTCATTCTTCTAG 1329 TTTTTCATTC 4399 tt- c agaaaca ACT
AAACATTTGAACTATTATTA TTCTAGAAAC TACGt ttcatt ttct tttGA A
GACAATGGAGAAAAGTGAAT ATTT ||||| |||||| |||| |||||
ATACGTA ATGCA AAGTGA AAGA AGATT /
TAT A GGTAAC- ATT

GAM1666 GATGAGACAGGTTTACTTTA 1346 TTTAGATAGC 4416 CAG TAC ga - ac at
GATAGCGGTACTGATGTCCA GGTACTGATG GATGAGA GTT ttta tagcg gt tg g
CACGCGTTAGATAAATATAA TCCA ||||||| ||| |||| ||||| || ||

TAAATCTCATC CTACTCT TAA AAAT ATTGC CA ac /
AAA TAT AG G C- ct

GAM1667 ACCGCAAACTCCCGTCGAAG 1330 TCGAAGCTGG 4400 G AC- C-- ga gag g gc
CTGGAGCCGTGTGCAAAACA AGCCGTGTGC ACC CAA TCC Gtc agctg cc tgt a
GGATGTAGCTAGGCAGCGGA AAAA ||| ||| ||| ||| ||||| || |||
CCGTTGGGT TGG GTT AGG CGG TCGAT GG ACa /
- GCC CGA A- GTA - aa

GAM1668 CTTCGAAATCTTCAACCCCG 1331 TCGAAATCTT 4401 aa aa--- - gga AAAAC
GAGGCGGCAAAACACACGCG CAACCCCGGA CTtcga tcttc cc cc ggcgGC A
CCGTCGAAGGAGGAACAAGA GGCG |||||| ||||| || || ||||||
AGAAGTCGAAG GAAGCT AGAAG GG GG CTGCCG /
GA AACAA A AAG CGCAC

GAM1669 CTCTTAGAGTATCGCCACCG 1333 ACGGCAGTCG 4403 ---------- t
ACGACGACGACGGCAGTCGA AGCGCGGCTT
TTAGAGTATCGCCACCGACGACGACGacggcagtcgag cgcggc t
GCGCGGCTTCGCCGCGGCAG CGCC |||||||||||||||||||||||||||||||||||| ||||||
CTTCGCTGCCTCGACTGCCG AATCTCATAGCGGTGGCTGCTGCTGCTGCCGTCAGCTC
GCGccg /
TCGTCGTCGTCGGTGGCGAT CGTCGCTTCGACG c
ACTCTAAGAG

GAM1670 GAGACAGCAACATGAGTGAA 1340 TGAGTGAAAG 4410 --- C tg-- gagata aaCAAACC
AGAGATAGCATGAAAACAAA AGATAGCATG GAG ACAG AACA agtgaaa gcatgaa T
CCTTGAAATAATTTATGCGT AAAA ||| |||| |||| ||||||| |||||||
AATTTTATTATCTTGTTATT CTC TGTT TTGT TTATTTT CGTATTT /
GTGACCTC CAG A TCTA AATG-- AATAAAGT

GAM1671 GATTATAACACTACTTGGAC 1332 TATAAGCATA 4402 C CTAA TACT T CCAATT TTta
tatact t
TAACTGATACTACATATGTT TACTGTATCT A TTGGA CTGA ACA ATGTT TG taagca
gtatc t
CCAATTTGTTTATAAGCATA TCTG | ||||| |||| ||| ||||| || |||||| |||||
TACTGTATCTTCTGATATTT T AACTT GACT TGT TACAA AC ATTCGT TATAg c
GCTTAGCTTCATTTAACATT C TTAG ---- T TTT--- TTCG T----- t
TGTTCAGGATTTTCAACTAC
ATATTTTAATT
GAM1672 AAAACTCGTACCAACGGCAA 1341 TTATTTGTAT 4411 A --- AAAA-- GAA T A- G AC
TC A
AAATTTCGAAGATTAGAGGA GATTCAGACT CA C GGCA TTTC GAT AGAGGAG TGAAT
CG ACA TGGTG T
GATGAATGCGACACATCTGG CTTT || | |||| |||| ||| ||||||| ||||| || ||| |||||
TGATTTTATTATTTGTATGA GT G TCGT AAAG CTG Ttttctc actta gt tgt attAT T
TTCAGACTCTTTTGTCCAGA A TTT AATATA AC- - ag - a- tt T

AAATATAATGCTTTTGATGG
TATCGGGTGT
GAM1673 CTTACAAAAAAATTGGATTC 1342 AAAAATCCAA 4412 ACAAAAAAA CAATA G
AATATTATTGGAGACGATAA GAAACAAGAA CTT TTGGATT TTATTG A
AAAATCCAAGAAACAAGAAG G ||| ||||||| ||||||
gaa aacctaa aATAGC G
gaacaaag- aa--- A

GAM1674 TGCCTTTCCGGCAGAGCATC 1334 TTTGCAATCA 4404 CA CC T CATC C GC--- C
TC CTT
CCCTGGCATCGACACTCACG TATAGTGAGT TTCCGG GAGCAT CC GG GA ACTCAC GAT
GCAA AACTGA A
CGATCGCAATCAACTGACTT TCTA |||||| |||||| || || || |||||| ||| |||| ||||||
AATCCTCGGTTTTGCAATCA AAGGCC CTTGTG GG CC ct tgagtg cta cgtt tTGGCT A
TATAGTGAGTTCTACCCCTG CC CA T CCat - atata a -- CCT
GACGTGTTCCCCCGGAACTG
CA
GAM1675 CAAAATAGTAAGTACTTTTA 1335 AGTAAGTACT 4405 ATa-- tatc - tATACACT CC
AG C A
TCGTTTCGTTATACACTAAT TTTATCGTTT AA gtaagtacttt gt ttcgt AATG CAGG AG TCAG
T
GCCCAGGAGAGCTCAGATTT CGTT || |||||||||| || ||||| |||| |||| || ||||
TGACTGATCTGCACATTACG TT CATTTATGGGA CA AAGCA TTAC GTCT TC
AGTT /
AACACCCCAGGGTATTTACA GACCA CCC- C -------- AC AG - T
CCAGTTTG

GAM1676 CCACAATTAGCTATTCGTGT 1343 TAGCATCATC 4413 T T T AC - t ac---- cta
CTT
ACTAGCATCATCGGATACGC GGATACGCCT CCACAAT AGCTAT CG GT tagca tca cggat gc
tccTGCA A
CTATCCTGCACTTAAGCCTG ATCC ||||||| |||||| || || ||||| ||| ||||| || |||||||
CAGGACGCTATCAGGTCCGC GGTGTTG TCGATG GT TA ATTGT AGT GCCTG CG
AGGACGT A
TGACTGTTACCATTTGTGTA C T T CC C C GACTAT C-- CCG
GCTCGTTGTGG

GAM1677 TATAAATGATGTTTGTGAAT 1344 TAAATGATGT 4414 ttg tat- CTGATACATAATTAAA
C A
ATATATTATCTGATACATAA TTGTGAATAT TAtaaatgatgt tgaa atatTAT AATA CATCAT
G
TTAAAAATACCATCATAGCA ATAT |||||||||||| |||| ||||||| |||| ||||||
TGATGATATTGTAGTATTTT ATATTTATTATA ATTT TATGATG TTAT GTAGTA /
TTTTAAATATATTATTTATA TAA TTTT ---------- A C

GAM1678 TTATTATAAATTCTGTTGTA 1345 TCTGTTGTAT 4415 Ttc t t
TAATTATAATTATAATTATA AATTATAATT TTATTATAAA tgttg ataattataat a
ATTATTAATACATTTTATAA ATAA |||||||||| ||||| ||||||||||

TAA AATAATATTT ATAAT TATTAATATTa t
TAC - a

GAM1679 TCTCATTGTTATGTAGTTGT 1353 TATTAAACAT 4423 - AT A -- Ttat c ttttta T- T
GATTTATTAAACATATTTTT ATTTTTTATA TCTC ATTGTT GT GTTGT GAT taaa atat taactc
AG A
TATAACTCTAGTATTCTCCG ACTC |||| |||||| || ||||| ||| |||| |||| |||||| ||
AGTTACTTATATATTTATTT AGAG TGATAA TA TAACA CTG ATTT TATA ATTGAG
TC T
GTCAGACAATAATGCAATAG G CG A GA TTT- A TTC--- CC T
TGGAGA

GAM1680 TATTGTACTGTTTAGGAAAA 1336 TAGGAAAAAC 4406 C TTta aaa ------ tca
ACTGATTTTTCAAATATAAA TGATTTTTCA TATTGTA TG ggaa ct gatttt a
ATCTATAATAGAAGTTCCGG AATA ||||||| || |||| || ||||||
TCACTACAATA ATAACAT AC CCTT GA CTAAAA a
C TGG- GAA TAATAT Tat

GAM1681 CTGGAGCCAAGGGGATGGAG 1337 TGAATTCTTT 4407 - T GA A G
ATGGCATCGTGTGGGCTGAA CTCTTGGTTT CTG GAGCCAAGGGGA GGA TGGC TC T
TTCTTTCTCTTGGTTTGCAG GCAG ||| |||||||||||| ||| |||| ||
gac tttggttctctt ctt gtCG GG G
g t aa - T

GAM1682 CCTTATTTTATAAAATATCA 1347 TAAAATATCA 4417 T a- tgac gaag
TGACGATTGGGAAGCTGTTA TGACGATTGG CCTTATT TAtaaa tatca gattgg C
TTAATCAATTGGTAGATTTA GAAG ||||||| |||||| ||||| ||||||
TACGATGAGG GGAGTAG ATATTT ATGGT CTAATT T
C AG TAA- ATTG

GAM1683 GGTGGCATCCCTTCATATCG 1348 ATAAGGCTCG 4418 --- - TA GC----- A- AGT AG
G G
CCCCTAGGTCTAGTTCACTG AGGGTTGGAA CA TC CCTTCA TC CCCT GGTCT
TCACTGG TTG ATGGA A
GAGTTGGATGGAGAAGTTCG AGAA || || |||||| || |||| ||||| ||||||| ||| |||||
TGCAACCGGTGATAAGGCTC GT GG GGAAGT ag ggga tcgga aGTGGCC AAC
TGCTT A
GAGGGTTGGAAAGAACTGAA TAA A Ca aaaggtt gc at- -- G G
GGAGGAATTGCTGACACACC

GAM1684 CCTATGATACATATGCTCTT 1349 TAATGTACTT 4419 - A CTCTtaa c tt t ta GCA
AATGTACTTGTTTACTGTTT GTTTACTGTT CCT ATGAT CATATG tgta ttg tac gtt taC C
ATACGCACCCAAGTAACAAC TATA ||| ||||| |||||| |||| ||| ||| ||| |||
TGTATTTAATTATAACCTAT GGA TACTA GTGTAT ATAT AAT ATG CAA ATG C
GTGAATCATAAGG A A CCA---- T TT T CA AAC

GAM1685 GTAGCGAGCGTGAGGAAACA 1350 TGACTAAAGT 4420 A A G AAA- AAA - ACTGTG------ AC
AAATAGCGTCACTGTGGCCA GGAAGCCTGA GT GCG GCGT AGG CA TAG CGTC GCC C
CCATGGCATAAATGACTGAA CGCC || ||| |||| ||| || ||| |||| |||
CGATGACTAAAGTGGAAGCC CA TGc cgca tcc gt atc gtAG CGG /
TGACGCCGTGAC G - g gaag gaa a CAAGTCAGTAAATA TA

GAM1686 TCCATACGTTTTTGGGAAAG 1361 TTTTTGGGAA 4431 A t-- aaa----- t
TTGGGCTCGGCCCAACGCAA AGTTGGGCTC TCCAT CGt tttggg gttgggc c
CAGACCTAGGCACACGATGG GGCC ||||| ||| |||||| |||||||
A AGGTA GCA GGATCC CAACccg /
- CAC AGACAACG g

GAM1687 TCATTAAGCAAGACAGCGTC 1362 TGCGGCAACA 4432 AAGCAAGAC AGA AC--- AAAAGA-- T A
AGACGCACGCTGGAAAAGAG CCAGCCAGCA TCATT AGCGTC CGC GCTGG GCTGC CC A
CTGCTCCAACCGGTGCGGCA AAAG ||||| |||||| ||| ||||| ||||| ||
ACACCAGCCAGCAAAAGGCG AGTAG TCGCAG GCG cgacc cggcg GG C
CAGACGCTCATAAGGATGA GAATAC--- AC- gaaaa gaccacaa t C

GAM1688 CATCGCGCGGGGCACGCACT 1363 TGCCGTGGGC 4433 GCGC ACGCACTTCAC A
TCACGCCGCGCGCCCACGGC GCGCGGCGCC CATC GGGGC GCCGCGCGCCCACGGCAGCGTCCG G
AGCGTCCGAGGGCGGGCGCT CCCA |||| ||||| ||||||||||||||||||||
GCCGTGGGCGCGCGGCGCCC GTAG ccccg cggcgcgcgggtgccgtCGCGGGC G
CCAGATG ac-- ---------- G

GAM1689 CACCAGAATGGATAGAAAGA 1351 AGACAAACAC 4421 GAA AAaga c-- acaa ta
CAAACACAGTTACAACATAG AGTTACAACA CACCA TGGATAG caaa acagtt ca g
CTTTGAGGACTGTCAATTTG TAGC ||||| ||||||| |||| |||||| ||
AACTATCTAAAATGGTG GTGGT ATCTATC GTTT TGTCAG GT c
AAA AA--- AAC GA-- TT

GAM1690 TTCTCATCGCTTTTCTTACT 1352 TAAAATGTTA 4422 TCTTACT GA AAATAAA A AC C TG GAAA TG
TAACAGATTGCAAAAATAAA CTGTGATGAA TAACA TTGCAA ACA TATT CG T TTGAT ATTG A
ACAATATTACCGCTTGTTGA GAA ||||| |||||| ||| |||| || | ||||| ||||
TGAAAATTGTGAATTAATGC attgt aatGTT TGT ATAG GT A AATTG TAAT /
TAGTTAATGATGAGATATGT ------- aa GATG--- - A- - GT ATCG TA
GTAGTTGTAAAATGTTACTG

TGATGAAGAA
GAM1691 GCTTGTGTTGCAACAGCGCT 1354 TGTGTTGCAA 4424 Ttg c gctaaaaa A C AG
AAAAAATGAGAACAAGAGAG CAGCGCTAAA GC tgttgcaa agc atG GAA AAG A
ACTTTTTACATAATAGCTTT AAAT || |||||||| ||| ||| ||| |||
TGCAATAAATGC CG ATAACGTT TCG TAC TTT TTC /
TAA T ATAA---- A - AG

GAM1692 GAATTAACCAATAGAGACAC 1355 TTGCTGACGG 4425 TA C ----- A -- A
GTTTGACACAGAAGCTGTGT TCTATATTCT GAAT AC AATAGA GAC CGTT TGACACAG A
TGCTGACGGTCTATATTCTG GTTT |||| || |||||| ||| |||| |||||||| TTTGTATTC CTTA TG ttgtct ctg gcag gttGTGTC /
-- t tatat - tc G

GAM1693 TTGTTTGTGTTCTGAAGCTT 1364 TAGATTGTTT 4434 G C - TT AGT T T
ATCAGTTATTATATAAGAAA ACGAAGCAGA TTGTTT TGTT TG AAGC ATC TATTA ATAAGAAA
G
TGCCTTTCTTATTGATAGAT AGCA |||||| |||| || |||| ||| ||||| |||||||| TGTTTACGAAGCAGAAGCAG Gacgaa acga gc tttg tag atAGT TATTCTTT C
g a a t- --- - C

GAM1694 ATATCTGTAAGTTGTATTCT 1368 TGTAAGTTGT 4438 tgtaag ta tcg A- T
TTTTATCGAAGCAGAGTTTC ATTCTTTTTA ATATC ttg ttcttttta aAGC GAG T
CTCCGGTTTAGTTAGGAAGA TCGA ||||| ||| ||||||||| |||| ||| AGTTAAATGATGT TGTAG AAT AAGAAGGAT TTTG CTC T
TA---- TG TGA GC C

GAM1695 GGAGACTCACCTTGGGGATC 1356 TCGGCACCTC 4426 C ATCCATCCTCTCCA CC TT
AC TT-- T AC
CATCCTCTCCAAGCGGCCTC CTGAACTGCT ACCTTGGGG AGCGG TCGG GAG GCC
CCG GGG C
GGTTGAGACGCCTTCCGTGG CCTC ||||||||| ||||| |||| ||| ||| ||| |||
GACCGTCTCCCGGCCTCGGC TGGAACCct tcgtc agtc ctc cgg GGC CCT G
ACCTCCTGAACTGCTCCTCC A cc---------- a- -- ca ctCC - CT
CAAGGTAAGTCTCC

GAM1696 CCCAAGGTAAGTCTCCTCTC 1357 TCCCCGAGGG 4427 AA AA ------ A TC TC CC
AGGTCGAGCTCGGCTGCCCC TCTTTAGAGA CCC GGT GTCTC CTCTC GG GAGC
GGCTGCC T
TTAGGTAGTCGCTCCCCGAG CACC ||| ||| ||||| ||||| || |||| |||||||
GGTCTTTAGAGACACCCGGG GGG cca cagag gggag cc ctCG CTGATGG /
C- -- atttct c -- -- AT

GAM1697 CCTAGCGCTGAAAAACAAGG 1365 TCAAAATAAA 4435 A GAAAA-- AA - GACG ACCCC
CC TAA
CTCTGACGATTACCCCCTGC AGATGCCGAG CCT GCGCT AC GGC TCT ATT CTG CA
A

CCATAAAATTTGCCTAGTCA TCTA ||| ||||| || ||| ||| ||| ||| ||| ||
AAATAAAAGATGCCGAGTCT GGA CGCGA tg ccg aga taa GAT GT /
ATAAAAGCGCAAGG A AAATatc ag t aaa- aact- CC TTA

GAM1698 AAGAATCTGTTATATGGTAT 1358 TCTGTTATAT 4428 Atct tat a- gg ATAAAACATTAAA CC- A
AGGGAGAGTATAAAACATTA GGTATAGGGA AAGA gtta ggtat g agagt TGC GTACTT T
AATGCCCGTACTTATTAAAG GAGT |||| |||| ||||| | ||||| ||| ||||||
TATTCAGTAGCCAATCCTAA TTCT TAAT TCATA C TCTCA ATG TATGAA T
CTCTTTCGAATACTTATTAA CGT- TAT AG TT ATCCTAACCG--- ACT A
TTGCTCTT

GAM1699 TTGTTTTAAATTGTTGATTT 1366 TGATTTATTA 4436 T T ----- ------- t
ATTAAAGAATATAGTTTGGC AAGAATATAG TTGTTTTAAA TG tgattta ttaaaga atatagtt g
AACTATATAAATGAATTTTT TTTG |||||||||| || ||||||| ||||||| ||||||||
GAGAATTTAAGTCATTATTT AACAAAGTTT AT ACTGAAT AGTTTTT TATATCAA G
TGAAACAA T T TTAAG AAGTAAA C

GAM1700 TGAGTCAATTGGTAGAGTTT 1359 AGTCAATTGG 4429 ag - tt- aa-------- GCTAA- GGC
TATAACGAGGTCGCTAACTG TAGAGTTTTA TG tcaattg gtagag ttat cGAGGTC CT T
GCTGTTAAGAGATGAGACCT TAAC || ||||||| |||||| |||| ||||||| ||
CGCCTATTCCTGATAACTTC AC AGTTGAC TATTTC AATA GCTCCAG GA G
TTTATACAGTTGAAACA AA A TTC GTCCTTATCC AGTAGA ATT

GAM1701 GATTTCTAAGTTACTTCTGC 1367 AGTTACTTCT 4437 TT Aag ct gcat cta G
AGCATATAACTAAACACGTT GCAGCATATA GA TCT ttactt gca ataa AACAC T
AGTGTTCTTTATTGTTTGGG ACTA || ||| |||||| ||| |||| |||||
TAAAACAGATTTC CT AGA AATGGG TGT TATT TTGTG T
TT CAA TT ---- TC- A

GAM1702 TTTCTCGAATATACGGGCCA 850 TCGAATATAC 3920 ata gccaagttagaa C A----------C
AGTTAGAATCTCCAGTAACT GGGCCAAGTT TTTCtcgaat cgg TCTC AGT ACTA C
ACCATAGTGGGATATCATCC AGAA |||||||||| ||| |||| ||| ||||
AGCAGCTAGAGACCGCCAAT AAAGAGCTTA GCC AGAG TCG TGAT /
TCGAGAAA ACC ---------- A ACGACCTACTATAGGG A

GAM1703 TCCATATTTCCTGACTTGTG 858 TGGGATGGGG 3928 TT TG----- G - G GA
TCTTGACTTGCGTCGATTGG GTGTGGGATG TCCATAT CC ACTT TGTCTTG ACTT CGTC T
GATGGGGGTGTGGGATGGGG GGGG ||||||| || |||| ||||||| |||| ||||
GTGTGGGATGGGGGTGTGGG GGGTGTg gg tggg gtagggt TGGG GTAG T
gg tagggtg g G G GG

GAM1704 TCCAGTGTAAGCAAGTCGAT 1360 TGAATGACAT 4430 AA-- AGT - ----- tag g aaa
TTGAATGACATAGGCGACAA AGGCGACAAA TCCAGTGT GCA CGATTt gaa tgaca gc ac g
AGTGAGGTGGCATTTGTCAG GTGA |||||||| ||| |||||| ||| ||||| || ||
AAGTTTCAAAGTCGTGTAAG AGGTTACA TGT GCTGAA CTT ACTGT CG TG t
AACATTGGA AGAA --- A TGAAG TTA G Gag

GAM1705 TGCACTACCTATCTGCTCAT 1369 TAGTGTTGAG 4439 ACCT CA ---- TT TT GTGTTT
T
TCGTTGTTTCGGTTCTGTGT GTAATTCTAG TGCACT ATCTGCT TTC GTTG TCGG CT
GTCTGA T
TTGTCTGATTCTTAGATAGT AAAG |||||| ||||||| ||| |||| |||| || ||||||
GTTGAGGTAATTCTAGAAAG ATGTGA TAGGCga aag taat agtt ga tAGATT /
CGGATTGAGTGTA GT-- -- atct gg gt ------ C

GAM1706 GGGTAAATGACAATGGGGGT 1370 AATGACAATG 4440 aa aatg aca- G G
AAATGACAATGGGGCGCTTG GGGGTAAATG GGGTA tgac ggggtaaatg aT GG C
GTGACACATTTGCCCCACCG ACAA ||||| |||| |||||||||| || ||
TCGCCTGCCC CCCGT GCTG CCCCGTTTAC TG TT G
CC CCA- ACAG G C

GAM1707 TTTCTCGAATATACGGGCCA 1371 TCGAATATAC 4441 at gccaagttagaa C A----------
C
AGTTAGAATCTCCAGTAACT GGGCCAAGTT TTTCtcgaat acgg TCTC AGT ACTA
C
ACCATAGTGGGATATCATCC AGAA |||||||||| |||| |||| ||| ||||
AGCAGCTAGAGACCGTCAAT AAAGAGCTTA TGCC AGAG TCG TGAT /
TCGAGAAA AC ---------- A ACGACCTACTATAGGG A

GAM1708 TCAGAGATTATTGTCTTATA 859 TATAAATTTA 3929 A- TC- CTTTCT
TTCTTTCTTGTTATCCGATA ATAAGACTTT TCAGAG TTATTG TTATATT T
TAAATTTAATAAGACTTTGA GA |||||| |||||| |||||||
agtttc aataat aatatAG G
ag tta CCTATT

GAM1709 GATATAATCTAAACGACGTA 1372 TAAGCTGCAA 4442 A--- ---- A A AGGCG ----------
ACT
GAAGGCGTGTTTCCTTGGAA AATAGGTGAA TA TCTA AACG CGT GA TGTTTC
CTTGGA A
CTACTATCTAAGCTGCAAAA ACAA || |||| |||| ||| || |||||| ||||||
TAGGTGAAACAAAAAGTCAC AT AGGT TTGC GCA CT acaaag gaatCT /
GCGTTACACTGGAAGCGTAT GCGA CACA - - GAAAa tggataaaacgtc ATC
ATC

GAM1710 GAAATTAGAGTTTGTACATT 1373 TGGCTACAAA 4443 TT-- ACATTA A GTC
AAGCAACATGTCTTTAAATG CTTTTCCTTT GAAA AGAGTTTGT AGC ACAT T
TGGCTACAAACTTTTCCTTT TC |||| ||||||||| ||| ||||
TC cttt tttcaaaca tcg tGTA T
tcct ------ g AAT

GAM1711 ATTGTTTGTATTCATTCAAT 865 TTTGTATTCA 3935 tt - aatgt ct T
GTCTCTTTTTCAGAAATTAG TTCAATGTCT ATTGt gtattc attc ct ttT C
TTTAGAGTCGAATACTGCAA CTTT ||||| |||||| |||| || |||
T TAACG CATAAG TGAG GA AAA A
T- C ATTT- TT G

GAM1712 TAGAGTTAAGAGAGATTAGA 1374 TGGCTACAAA 4444 GTTAA-- ATT ACATTA A
GTC
GTTTGTACATTAAGCAACAT CTTTTCCTTT TAGA GAGAG AGAGTTTGT AGC ACAT T
GTCTCTAAATGTGGCTACAA TCCA |||| ||||| ||||||||| ||| ||||
ACTTTTCCTTTTCCACATCA ATCT ctttt tttcaaaca tcg tGTA C
TCTA ACTACac cct ------ g AAT

GAM1713 ATTGTTTGTATTCATTCAAT 851 TTTGTATTCA 3921 tt - aatgt cc T
GTCTCCTTTTCAGAAATTAG TTCAATGTCT ATTGt gtattc attc ct ttT C
TTTAGAGTCGAATACTGCAA CCTT ||||| |||||| |||| || |||
T TAACG CATAAG TGAG GA AAA A
T- C ATTT- TT G

GAM1714 TAGAGTTAAGAGAAATTAGA 852 TGGCTACAAA 3922 GTTAA-- ATT ACATTA A GTC
GTTTGTACATTAAGCAACAT CTTTTCCTTT TAGA GAGAA AGAGTTTGT AGC ACAT T
GTCTCTAAATGTGGCTACAA TCCA |||| ||||| ||||||||| ||| ||||
ACTTTTCCTTTTCCACATCA ATCT ctttt tttcaaaca tcg tGTA C
TCTA ACTACac cct ------ g AAT

GAM1715 AACATCCTAATACTTTATTT 853 TAACAATATC 3923 TAATACTTTAT TT AG AT
GTTTTAAAGCTATTAAAGAG ATTTTTGGAT AACATCC TTGTT AA CT T
TTCTAACAATATCATTTTTG GTT ||||||| ||||| || ||
GATGTT ttgtagg aacaa TT GA /
tttttactat- tC GA AA

GAM1716 AGGTTTACCTATTTTATCAC 854 TATTGTGTAC 3924 T- CC ----- - AT
GATTGATATCTGATTATATT AAGTAAAATA AGGT TA TATTTTAT CACGAT TGAT C
GTGTACAAGTAAAATAATTA ATTA |||| || |||||||| |||||| ||||
CTACCT TCCA at ataaaatg gtgtta ATTA /
TC ta aacat t GT

GAM1717 TCAGAGTATAAATTTTAGAA 872 TGCGTTGATG 3942 TAAATT AA- TTAG
ATAACATTAGCAAATTGTTG TCGTTATTCT TCAGAGTA TTAG ATAACA C
TGCGTTGATGTCGTTATTCT GA |||||||| |||| ||||||
GA agtcttat agtt tGTTGT /
tgctgt gcg TAAA

GAM1718 CTTACGAGGATCTCCTTAAA 855 TGACGGGAAG 3925 AC ATC TAA TCCAG
TTCGAGTCCAGTAATTCCTT CCTTACGAG CTT GAGG TCCT ATTCGAG T
TGAGTGACGGGAAGCCTTAC ||| |||| |||| |||||||
GAG gag ttcc aggg tGAGTTT A
ca ga- cag CCTTA

GAM1719 CCCTTGTTAAGATATGATGC 873 TATGATGCAA 3943 TT TAAGAt- a aaata cgac A
AATAAATACACGACATGAAA TAAATACACG CCC GT atg tgcaat ca atGAA C
CTTTCATTTATTGACGAATT ACAT ||| || ||| |||||| || |||||
GCACCATTTAAACTATTTGG GGG TA TAC ACGTTA GT TACTT /
G TT TCAAATT C AGCA- TATT T

GAM1720 AAAACTTTTACGGTGGAGAA 856 TACGGTGGAG 3926 TTt- gagaattat AC
TTATTAAATTACTAAACATA AATTATTAAA AAAACT acggtg taaattacTAA A
TTAGTAATTTATACTGTTCA TTAC |||||| |||||| ||||||||||
TAGTTTT TTTTGA TGTCAT ATTTAATGATT /
TACT --------- AT

GAM1721 TGCGTAAATTTCGCAACTAA 866 TTTTTCGTTT 3936 T TTT C CT T AA
TGAGATAAATTGGAAATTCC TTTTCGTTTT TGCG AAA CG AA AATGAGA AAATTGG A
AATTTTTTTCGTTTTTTTCG TTTC |||| ||| || || ||||||| |||||||
TTTTTTTCGCA ACGc ttt gc tt ttgcttt tTTAACC /
t ttt t tt t TT

GAM1722 CTGAGGGGACCATGATGTGT 857 TACGCGGATA 3927 -- ATGA G TC G
ATAGGCGTCAAGCGGGGCTT GGAATCCCCT CTGAGGGGA CC TGTGTATAG CG AAGC G
CGGTTGTACGCGGATAGGAA CAG ||||||||| || ||||||||| || ||||
TCCCCTCAG gactcccct gg gcgcatGTT GC TTCG /
aa atag G -- G

GAM1723 GATGGCGTCTTCCCTGTTTT 860 TAAGGCAGGC 3930 - C ----- C A - GGA
GCCCTTAGACTATTCGAGTT AAGACAGCTA GATGGC GTCTT CCTGTTTT GCC
TTAGACTATTCG GTTGCCTCT GT T
GCCTCTGTGGATTAGGGCTG TT |||||| ||||| |||||||| ||| |||||||||||| ||||||||| ||
GAGGCAGCACGGATAGTCTG ttatcg cagaa ggacggaa CGG AGTCTGATAGGC
CGACGGAGG CG T
ATGGCCAAATAAGGCAGGCA a c tAAAC T A T GGA
AGACAGCTATT

GAM1724 TTGTAATTTCCAATTTACAT 861 TTAATTGGAA 3931 T TTTACA C AAATA T
AACTAATTGAAATAATTTTA TTTTGGAATT TTGTAA TTCCAA TAA TAATTG ATTT A
CAAGATGAACAATTAATTGG TACA |||||| |||||| ||| |||||| ||||
AATTTTGGAATTTACAA Aacatt aaggtt gtt attAAC TAGA C
t ttaag- a AAG-- A

GAM1725 AATTGGAATTTTGGAATTTA 862 TAATAATTTT 3932 GA- T---- TTTTAT
CAATTTTATTAACTTTTTGT CCAAGATGTA AATTG ATTTTGGAA TTACAA T
AATAATTTTCCAAGATGTAC CAAT ||||| ||||||||| ||||||
AATT Ttaac tagaacctt aatGTT /
atg ttaat TTTCAA

GAM1726 AAGAAAGCTTTAAAGTTAAA 863 AAGCTTTAAA 3933 a aaagt--- -- g AC T
TATCCTGCAGATACGATTTT GTTAAATATC AAGA agcttt taaatatc ct cAGAT GA T
TCCATCTGAAGTTGGTATTT CTGC |||| |||||| |||||||| || ||||| ||
GTTATAGAAAAAGTTATCTT TTCT TTGAAA GTTTATGG GA GTCTA CT T
A AAGATATT TT A C- T

GAM1727 TATCTATCGTTGGCATTTCA 867 TCTATCGTTG 3937 a t- tcaagttcc CAC
AGTTCCGATACACATTTTAT GCATTTCAAG TAtct tcg tggcatt GATA A
TCCATAAATAATGCTATTTG TTCC ||||| ||| ||||||| ||||
AAGATA ATAGA AGT ATCGTAA TTAT /
- TT TAAATACC- TTT

GAM1728 TAGCTTTTATTGAATCCAAA 874 TTGAATCCAA 3944 TTAt aaaacatc aac
ACATCAGTTAACAAACAAGC AACATCAGTT TAGCTT tgaatcc agtt a
TACCAAAGGATTTGTCATAA AACA |||||| ||||||| ||||
GTTG GTTGAA GTTTAGG TCGA A
TACT AAACCA-- ACA

GAM1729 GTATGAAACTTTATGAGGAA 864 AACTTTATGA 3934 - ttatgagg g aa
CTGGTGAGAAATAACTTACG GGAACTGGTG GT ATGAaact aactg tgag A
GTTATGATTTCGGTTTCGTC AGAA || |||||||| ||||| ||||
GC CG TGCTTTGG TTGGC ATTC T
C CTTTAGTA - AA

GAM1730 CACAAAATGATTAGATGCTT 868 TATACTTAAC 3938 A A GC- AC TTA Ctat ct act-
actAAACTT
AACTTACTTAATAACTATAC TATACTTATA TT GAT TTA TTAC ATAA acttaa at tatag A
TTAACTATACTTATAGACTA GACT || ||| ||| |||| |||| |||||| || |||||
AACTTAACTTATCAACTATA AA CTA AAT AGTG TATT TGGATT TA ATATC /
CTTAATTTTTAGGTCCTTAT C - ATA CA TAA CC-- TT ATTC AACTATTCA
AATGTGAACTAAATAATCAA

CTGTTTTGTG
GAM1731 TCTCAGTAGTAGTAAGTCTC 880 TCTTGCTGAA 3950 T A- --- CAC TG T ACA- TGCA-
T TTTT
ACTGGTGATGGGATACAAGT TAGGCTATCT C CAGT GTAGTA AGTCT TGG A GGGAT AG
AGT CC C
GCAAGTTCCTTTTCAAATGG ACTA | |||| |||||| ||||| ||| | ||||| || ||| ||
TGCTCAAATCTAAGGATCCT G GTCA Tatcat tcgga gtc t tCCTA TC TCG GG /
CTTGCTGAATAGGCTATCTA - CG cta taa gt c GGAA TAAAC T TAAA
CTATGCACTGGA

GAM1732 GTAATAATGTTGTATACAGT 869 TATTATGGCA 3939 TAA- - GTAA GT- T- T
AAGTTGGTTAACATGTTGGT ATGTATTACA GTAA TGTTGTA TACA GTTG TAACATG TGGT
T
TTTTATTATCCATGTTATTA ACAG |||| ||||||| |||| |||| ||||||| ||||
TGGCAATGTATTACAACAGC CATT acaacat atgt cggt atTGTAC ATTA T
ATTTAC TACg t aa-- att CT T

GAM1733 ATTGTACATACTATATTGTA 881 TGCTATGTGT 3951 TG A AA- AC- CAA
AAACAACCAGCCAATACTGC ATATAGTGAG AT TACATACT TATTGTA ACA CAGC T
TGCTATGTGTATATAGTGAG GTAT || |||||||| ||||||| ||| ||||
GTATGTATGGT TG ATGtatgg gtgatat tgt gtCG /
GT a atg atc TCA

GAM1734 TGCACTGCGGTCATCGTCTC 882 TCCACGGTCC 3952 C- TCG c - t ctcctcaa T A
C CAC
CACGGTCCACTCCTCCTCAA ACTCCTCCTC A TGCGGTCA TCt cac gg ccactc gcTCT TGGC
GA GG A
GCTCTTTGGCAGACGGCACA AAGC | |||||||| ||| ||| || |||||| ||||| |||| || ||
TACTCATCGGCCGCGGGGCG T GTGCCAGT AGA GTG CC GGTGAG CGGGG
GCCG CT CT /
TAGAGTGGCCAGTGTAGAAT CT TA- T A - ATG----- C G A CAT
TGACCGTGTCTGTA

GAM1735 GGTTCTCTGTTAATGACTCA 870 TTAATGACTC 3940 T T taat a cca- gg- T
TCCCATAAGTGGTGGTCTGG ATCCCATAAG GGT C CTGt gactc tc taagt tGGTC G
TGACCAAGAACTTAGTCTGA TGGT ||| | |||| ||||| || ||||| |||||
AGGGTCACAGCGACC CCA G GACA CTGGG AG ATTCA ACCAG G
- C ---- A TCTG AGA T

GAM1736 CACTTTCTGTGGTGCCTTAT 875 TCTGTGGTGC 3945 TTtct tg ctt cCT CT
GAATCAGACCTAGCTACACT CTTATGAATC CAC gtgg c atgaatcaga AG A
TTTCTGATTCATGTGCTACC AGAC ||| |||| | |||||||||| ||
TCTGTG GTG CATC G TACTTAGTCT TC /
TCTC- GT --- TT- AC

GAM1737 TATGGGAATATTCTGGTAAA 871 AAAGTGCATG 3941 GG TC- a- - gtatcaat tc

AGTGCATGTATCAATTTTAG TATCAATTTT TATG AATAT TGGTAaa gtg cat tttag G
TCGTTTTTGGATTTCTGTAA AGTC |||| ||||| ||||||| ||| ||| |||||
TGTTACGATTTGCTATGTGT GTAC TTATG ATCGTTT CAT GTA AGGTT T
ATTTTCATG TT TGT AG T ATGTCTTT TT

GAM1738 GCGGGGCCGAAAGCCACGTT 876 TCTCTGAACC 3946 GC A C Ttc--- c- tgtgtgc CC CA
CTCTGAACCTTGCGTGTGTG TTGCGTGTGT GCGGG CGAA GC ACG tctgaa cttgcg aa CCAG C
CAACCCCAGCACGGTAATAC GCAA ||||| |||| || ||| |||||| |||||| || ||||
TGTCATGAAACACACTTTAA CATGG AGAG TC ACA TTTCAC AAAGTA GT TAAT /
GGTAACACTGAGACTGGTAC TC - - ATGGAA AC CT----- CA GG

GAM1739 TGTAGTTTTAGTGTATAGAT 883 TATACAGATT 3953 T TT T ATAT -- tt- t tc
ATTATACAGATTTGATTTAT TGATTTATCT TG AGT TAGTG ATAG tataca ga tgat ta t
CTATTATATCGCTTTCCATG ATTA || ||| ||||| |||| |||||| || |||| ||
TGTATAAGCTATTTACTATT AC TTA ATCAT TATC ATGTGT CT GCTA at /
ATTCCA C TT T GAAT AC TTC T ta

GAM1740 GATTAGTTATATTCTATGTA 887 TCTATGTAAT 3957 TT A tc t-- gattacatG TACTATTT
ATAATAACGATTACATGTAT AATAACGATT GA AGTT TAT tatgtaa aataac TATATAACATA C
ATAACATATACTATTTCTAT ACAT || |||| ||| ||||||| |||||| ||||||||||
TTTCTTATGTTATATAAAAA CT TCAG ATA ATACATT TTATTG ATATATTGTAT /
AGTTATTTATTTACATAATA TT A -- TAT AAAAA---- TCTTTTAT
AGACTTTTC

GAM1741 GTCCGCCGTCTAGGTAAGTT 888 TCTAGGTAAG 3958 C C-- aagttt a -- tC A- CC
TAGAGCTCAGGTCGAGACCG TTTAGAGCTC GTC GC Gtctaggt ag gctc agg GAG CCGGG T
GGCCTTTGTCCGGCGCTCCC AGGT ||| || |||||||| || |||| ||| ||| |||||
TTAGAGCCTACCTAGACTCA CGG CG CAGATCCA TC CGAG TCC CTC GGCCT T
GCCGGC C ACT ------ - AT -- GC GT

GAM1742 GCCGCCCTACCTGAGGCCGC 895 CTGCCGCCTC 3965 CCTACCT C CATCC C TT
CATCCACGCCGGTTGAGTCG CCGCCTGTGG GCCGC GAGGC GC ACGC GG G
CGTTCTGCCGCCTCCCGCCT T ||||| ||||| || |||| ||
GTGGT tggtg ctccg cg TGCG CT /
tccgcc- c tcT-- - GA

GAM1743 GAATATGAATTCTATATCTA 877 TACATTGAAC 3947 TTC TCT TCT TAG-- T TA
CAGCATTTTCTTTATAGTTA AATTGATATA GAATATGAA TATA ACAGCATTT TTA TTAATGT GTAAT T

ATGTTGTAATTATCGGTTAT AGTG ||||||||| |||| ||||||||| ||| ||||||| |||||
ACATTGAACAATTGATATAA CTTATACTT GTGT TGTTgtgaa agt agttaca tATTG /
GTGTTGTTTTGTGCTTTTCA TTC TT- tat taaca - GC
TATTC

GAM1744 CCTGTGCTTCGCCCGGATGG 878 TGGCGTCCTC 3948 G CCC- A A-- - C
ACGAGAGCCTCACCTCCGTG GCCGTCCAGC CCTGT CTTCG GGATGG CGAG GCC TCAC T
ATGGCGTCCTCGCCGTCCAG ACGA ||||| ||||| |||||| |||| ||| ||||
CACGAAGAACAGG GGACA GAagc cctgcc gctc cgg AGTG C
A acga - ctg t C

GAM1745 TTTCCATATCATCATTGTGT 879 TGTGTAAACT 3949 C ATt aaac- aa tt
AAACTAAATAACGTTTTCTA AAATAACGTT TTTCCATAT ATC gtgt taaat cgt t
TGGCATTTAATAAGGCATTG TTCT ||||||||| ||| |||| ||||| |||
GATATGTGGAAA AAAGGTGTA TAG TACG ATTTA GTA /
- GT- GAATA CG tc

GAM1746 AGATCTGCGGCACGCACTGC 884 TACAGGGAGG 3954 T GCA ---- A- G-- --- - TC
ATCACCGGCCTCTCGGTCAC TGCAGATCAT AGA CTGCG CGCA CTGCATC CC GCC TCT
CGG A
GTCGAAGAACAGGTACAGGG GCGC ||| ||||| |||| ||||||| || ||| ||| |||
AGGTGCAGATCATGCGCACG TCT GACGC gcgt gacgtgg gg tGG AGA GCT /
CAGCTCT C Ac- acta ag aca ACA A GC

GAM1747 TTTTTCTTATTGTCTTCAGA 885 TCAGATTATA 3955 ---------- CT A CCTTAT
TGAGCCTTATTACTTCATCT AATTTTCTAA TTTTTCTTA TTGT TC GATGAG T
CATCAGATTATAAATTTTCT TAAA ||||||||| |||| || ||||||
AATAAATTAAGAAAAA AAAAAGAAT aata ag ctACTC A
Taaataatctttta tt a TACTTC

GAM1748 CTGTTGTTTAAAAGAAAGTA 886 TAAAAGAAAG 3956 aa- a gacag-------- a- - T
GACAGTGATACGGTGAACCA TAGACAGTGA CTGTTGTTtaa ga agta tg tac gG G
GTAGCCAAAACAAAATTTAA TACG |||||||||| || |||| || ||| ||
TATTATCAGATTAAACAGCA GACGACAAATT CT TTAT AC ATG CC A
G AGA A AATTTAAAACAAA CG A A

GAM1749 TTGAAGCTTTTATATTAAAC 903 AATCAACCCT 3973 TTTATATTAAACA aa accc gc--
aca
ATGCGATCTAATCAACCCTA AGGCAAACAC TTGAAGCT TGCGATCT tca tag aaac c
GGCAAACACACTAAGTTTAA ACTA ||||||| ||||||| ||| ||| ||||
GACTAAAACTGAAGAGATCG AATTTCGG ACGCTAGA AGT ATC TTTG /
CAGGCTTTAA ---------- GA CAAA AGAA Aat

GAM1750 TTGCTCCCAAACCTCAGCGC 2334 AAATATGGAA 5404 CCAAACCTC- - CTCCCAAAAGA
CC- CA

CTCCCAAAAGACATATTTCC CATTCCCAGC TTGCTC AGC GC CATATTT TG G
TGCAGATTCACTCAAATATG TGCT |||||| ||| || ||||||| ||
GAACATTCCCAGCTGCTACA AGCGAG tcg cg gtataaa AC A
ACAAACAGAGCGA ACAAACAACA t acccttacaag CTC TT

GAM1751 ATACAGCTTTGATTCTTCTG 889 TAGCTTTGAT 3959 T TG TT T AT- - CG
ATCGTCTTGACGGTGTTCAC GTTGTAT ATACAGC T A CT CTG CGTCT TGA G
GGGCGCGGTGGTAGCTTTGA ||||||| | | || ||| ||||| |||
TGTTGTAT tatgttg a t ga GGT GCGGG ACT T
t gt tc t GGC C TG

GAM1752 GCGTCTGCAGCATTGTCTGC 896 TCTGCAGCAT 3966 c - ------- ct tcaT
CTGGTCATCACCTTCCTGCA TGTCTGCCTG GCGt tgcagcatt gtc tgc gg C
GCTCATCGACTGGTGCTGCG GTCA |||| ||||||||| ||| ||| ||
CGCGC CGCG GCGTCGTGG CAG ACG CC A
C T CTACTCG T- TTCC

GAM1753 TTTTGCTTATGCAGAGTCGG 904 TATGCAGAGT 3974 TG agtcg gg
CAAGCTTTGGAAAGGAGCTT CGGCAAGCTT TTT CTtatgcag gcaagcttt a
GCGCCGCTGCGTAAGTGAAG TGGA ||| ||||||||| |||||||||
GAA GAATGCGTC CGTTCGAGG /
GT GCCG- AA

GAM1754 CATACGAATATACGATAGGA 890 GGAGGAAAGA 3960 AATATACG A ---- - gg
GGAAAGAAGTTCCTGGTCAA AGTTCCTGGT CATACG AT ggaggaaaga agt tcct t
GGATGCTTGGGTTTTTCCTC CAAG |||||| || |||||||||| ||| ||||
TAATAAAAGAGTGTATG GTATGT TA TCTCCTTTTT TCG AGga /
GAGAAAA- A GGGT T ac

GAM1755 ATTAATCACTGATTCCTTTT 897 TCACTGATTC 3967 a ttccttt--- t cg AG
TCGATGCCGGACAATAGCAC CTTTTTCGAT ATTAAtc ctga ttcga gc GACAAT C
AATTGTTTAGCTTTGGACTC GCCG ||||||| |||| ||||| || ||||||
TATGTATTCAGGATTAAT TAATTAG GACT AGGTT CG TTGTTA A
- TATGTATCTC T AT AC

GAM1756 CGCCTTACAGGGGTGTGGTA 891 CGGCAAGACC 3961 ACA---- T AG A CT
GTGCAGGGTCTGCCTGCTCG GCTCCCCGGC CGCCTT GGGG GTGGT TGC GGGT G
GCAAGACCGCTCCCCGGCAA AACC |||||| |||| ||||| ||| ||||
CCGAGGCG GCGGAG cccc cgcca acg cTCG C
ccaacgg t ga g TC

GAM1757 AAACCATCCAATCCACTACC 892 TGGCATATTA 3962 ATCCACT--- GCt- - t - a tat
TTTTATACA

AATAGCTGGCATATTAAGTG AGTGTAGTTA ACCAATA ggca tat aag tgt gt attATT A
TAGTTATATTATTTTTTATA TATT ||||||| |||| ||| ||| ||| || ||||||
CAATATTCTCGTAATAATTC TGGTTGT TTGT ATA TTC ACG TA TAATAA /
TATAGCATCTTCATACTGTT GAATATTTTT AATT C C T A TCT TGCTCTTAT
TTAATGTTGGTTTTTTATAA
GATGATGGTTT
GAM1758 ACCACTGGAAAGCTTCTACC 893 TGGAAAGCTT 3963 t aa- tc cct--- ca T
TCTGGACATGTGTTATATAC CTACCTCTGG ACCAC gga gct ta ctgga tGTGT A
AATCCAGTCATACTGAGAGT ACAT ||||| ||| ||| || ||||| |||||
GAGTCTTGTGGT TGGTG TCT TGA GT GACCT ACATA /
T GAG GA CATACT A- T

GAM1759 AACCTGTTAAGCTGAGATGG 894 TGTTAAGCTG 3964 g----- agat tt GA
CTGCATTTTTGGAGAAATAA AGATGGCTGC AACCt ttaagctg ggctgcat TTG G
TGTGCAGCTTAGCTTGAATT ATTT ||||| |||||||| |||||||| |||
TTAAGGTT TTGGA AGTTCGAT TCGACGTG AAT A
ATTTTA ---- T- AA

GAM1760 TATTTGTTTTAAGTACATCA 2338 TTTAAGTACA 5408 t a c- cca tcTT- T TT
CCAAAAATTTCTTTATAATT TCACCAAAAA TATTTGTt ta gta atca aaaatt TATAAT CATT A
CATTTTATTAATGTATTATA TTTC |||||||| || ||| |||| |||||| |||||| ||||
TTTTCAATTTTATGATTTTA GTAAATAA AT TAT TAGT TTTTAA ATATTA GTAA /
TATATAATAAATG T A TT A-- CTTTT T TT

GAM1761 GCGCAGTTCCCGAGGGGTCA 898 TTCCCGAGGG 3968 c g a tt atcaTAA
TTTCTTATCATAAAATAATA GTCATTTCTT GCGCAGttcc ga gggtc t ctt A
AAAAGGGGGACCTGTCCGGA ATCA |||||||||| || ||||| | |||
GCTGCGC CGCGTCGAGG CT TCCAG G GAA A
C G - GG AAATAAT

GAM1762 TTGGTTCTTTGAACATCTTG 899 TCTTTTGATT 3969 CTT ---- ATCTT AG TA
GTCGAAAAGTAGGTATTTTC TATCCGTACA TTGGTT TGA AC GGTCGAAA TAGG T
TATCTTTTGATTTATCCGTA CTCG |||||| ||| || |||||||| ||||
CACTCGTGTAGCCAG GACCGA gct tg ttagtttt ATCT /
TGT caca cctat ct TT

GAM1763 CGTCTGAATATCCAAAGTTA 900 TCTGAATATC 3970 c-- tatccaa t ggtC - AATC AAAAT
TCAGGTCTAGTGTAATCTAC CAAAGTTATC CGt tgaa agt atca TAG TGT TAC C
AAAATCAGAACAGTAATTGG AGGT ||| |||| ||| |||| ||| ||| |||
CATCTAAATGATCACTACAA GCA ACTT TCA TAGT ATC ACG ATG A
ACTTTCATGTACG TGT TCAAACA C AA-- T GTTA ACAAG

GAM1764 ACTTGATTCAAAGTCGGGAT 2335 TCAAAGTCGG 5405 - Ttca g gat t - AA
TTTTTCGGTTGAATTTCGTA GATTTTTTCG AC TTGA aa tcgg ttt tcggt tg T

TCGACAAATTACTGAGTTCG GTTG || |||| || |||| ||| ||||| ||
TTCAATGT TG AACT TT AGTC AAA AGCTA GC /
T TGC- G ATT C T TT

GAM1765 GCCATTCTCTACAAGGTAAA 2339 TGTAAGCATA 5409 CTACAA --- Ctgtaagc tag cat
T AC
GACCCGGGAGTCTGTAAGCA TAGATGACAT GGTAAAGAC CCGGGAGT ata atga
aatgG ATC A
TATAGATGACATAATGGTAT AATG ||||||||| |||||||| ||| |||| ||||| |||
CACAATGATCCGTTTCATAA CTATTTCTG GGCCTTTA TAT TACT TTGCC TAG
/
TTATTAGAAAATATTTCCGG CTTAGG ACA TAAAAGAT TAA --- - TA
ACAGTCTTTATCGGATTCTT
TATTGC
GAM1766 TCCGTCTAAAACATAACTTT 2340 TCTAAAACAT 5410 cataactttct--- TA T TT AGAA----
AC
CTGTACCATAGGGTATCTTT AACTTTCTGT aaa gtacca GGG ATCT TGTAAATCA
TAGA C
TGTAAATCAAGAATAGAACC ACCA ||| |||||| ||| |||| ||||||||| ||||
CGGTCTAAACGATAATGATT TTT CATGGT CTC TGGA ACGTTTAGT ATCT C
TGCAAGGTTCTCCTGGTACT TTTTTAAGCATTAT C- T -- AATAGCAA GG
ATTACGAATTTTTTTTTAGC
TTCGGG
GAM1767 CAATATAAATAAATTATCTT 2336 TAAGTTAAAA 5406 AAT--- AT-- T TTTC
TTATTATTTCTTTTTTAATA TTTTACCAGT CAATATA AAATT CTT TATTA T
TAAGTTAAAATTTTACCAGT ATAT ||||||| ||||| ||| |||||
ATATTG GTtatat tttaa gaa ATAAT /
gaccat aatt t TTTT

GAM1768 AAAGGTAACGTGTAATCGCC 901 TAATTTGTGT 3971 C T C T AC TTG
ATATATTGCAACCATTGATT GTTTGCGCTT AAAGGTAA GTGTAA CGC ATA ATTGCA CA A
TTTGTGTAATTTGTGTGTTT TGCT |||||||| |||||| ||| ||| |||||| ||
GCGCTTTGCTTTT TTTtcgtt cgcgtt gtg tgt taatGT GT T
t t - t -- TTT

GAM1769 GCTGCGCCCCCTAACTATAC 902 TACAAGCACG 3972 CCCCCTAACTAta-- g c aac-------
-------- aA
AAGCACGCAGGTGCAAACCG CAGGTGCAAA CTGCG caa cacg aggtgca cg A
AAAACCGTAGCGTTTCCACG CCGA ||||| ||| |||| ||||||| ||
ACTTATGTACCTCCGTGGTT GACGT GTT GTGC TCCATGT GC /
GGAACACGAAAGCAACTGCA CAACGAAAGCACAAG G C
ATTCAGCACCTTTGCGAT CA
GT

GAM1770 GTCAGGCATGTTTGCGCATA 2341 TTAAAACAAA 5411 GG-- TTGC T AAACATACAACAT
G T
TATAAAAACATACAACATAC TTGTATTGTA GTCA CATGT GCA ATATAA ACAC TAA T

ACGTAATTTTTTGGTGTTTA CATG |||| ||||| ||| |||||| |||| |||
AAACAAATTGTATTGTACAT CAGT gtaca tgt tatgtt TGTG GTT T
GAAATTGAC TAAA ---- - aaacaaaatt--- - T

GAM1771 CCACGTCGTTATCAGCGTGC 905 CAAGATCGAC 3975 CG - A- - TGT--- C - C CAG
TGTGTCACGCCGTCTCGGCC GTGACTATTT CCA TCGTTA TC GCGT GC GTCACG CG TCT
GGC C
AGCAGCGTCAAGATCGACGT TGCA ||| |||||| || |||| || |||||| || ||| |||
GACTATTTTGCAACGCAAGA GGT AGCAGT AG CGCA cg cagtgc gc aga cTG /
TTGACGAGATGG AG T AA a ttttat a t a CGA

GAM1772 GGGTAATACGAATTTTGAAT 906 TGGGAGTATC 3976 A- AATTTTGAAT ga atctg- tatat
TTTGGGAGTATCTGTCAAGT TGTCAAGTAT GGGTA TACG TTtgg gt tcaag t
ATATTCAACTCTTGAATAAC ATTC ||||| |||| ||||| || |||||
CACGACCAGGCGTAGCTATC CCTAT ATGC GGACC CA AGTTC /
C CG ---------- AG CCAATA TCAAc

GAM1773 CGCTATACCGTCCTTTAAAT 907 TTTAAATTAG 3977 - -- ttta gaca gcgcg
TAGACAAGGTGCGCGTCTCT ACAAGGTGCG CGCT ATACCGT CC aatta aggt t
AAACCTATAATTCCCGGTAG CGTC |||| ||||||| || ||||| ||||
CGGTATAAGCG GCGA TATGGCG GG TTAAT TCCA c
A AT CCC- A--- AATCT

GAM1774 GGCGACCGTTGTGTGGAGTT 2342 GACCGTTGTG 5412 ac t g agaaaagA A
AGAAAAGAGCACGGACACCG TGGAGTTAGA GGCg cgttgtg gga tt GCACGG C
TGCAGGGTCCCTACAGCGCC AAAG |||| ||||||| ||| || ||||||
GCC CCGC GCGACAT CCT GG CGTGCC /
C- C G A------- A

GAM1775 GCAGATCTGTTAACGCCTGT 908 TTAACGCCTG 3978 A --------- c acaatg A A
AGAACAATGGACTATTATTA TAGAACAATG GC GATCTGttaac gc tgtaga gact TT T
AAAAGTCATTATTTACAAGC GACT || |||||||||| || |||||| |||| ||
TTTACAAAAGTTGATGGATT CG TTAGGTAGTTG CG ACATTT CTGA AA T
AGC A AAAACATTT A ATTA-- A A

GAM1776 TCAAATTGAAGATCATCCAA 909 TGCAAAAGAT 3979 AGA - CAACA T T
CAGCGTATCATTTTTTAATG AGAGGCTTAA TCAAATTGA TC ATC GCGTA CATT T
TATGCAAAAGATAGAGGCTT TTTG ||||||||| || ||| ||||| ||||
AATTTGA Agtttaatt ag tag cgtAT GTAA T
cgg a aaaa- - T

GAM1777 TGTTGAGATATGTACATTAA 2337 TTATATTATT 5407 A- TGTACAT-- AAT TC TC
TAAATATATTCCAGAATCAT ATCCAAAGTC TGTTG GATA TAATA ATAT CAGAA A

TTTTTGTTATATTATTATCC TATC ||||| |||| ||||| |||| |||||
AAAGTCTATCCCCAACA ACAAC ctat attat tata GTTTT /
CC ctgaaacct --- tt TT

GAM1778 GTTTTTTTTGTATTTATATA 2344 TATAGTGTTT 5414 T T- TACAAC - -- ACT
CAACAACACATAGTTTGTAC TTTATAAATA GTT TTTT GTATTTATA AACAC ATAG TTTGT A
TAATGACAGAGTTTATAGTG TCTA ||| |||| ||||||||| ||||| |||| |||||
TTTTTTATAAATATCTAAAA CAA AAAa tataaatat ttgtg tatT AGACA /
TAAC T tc ttt--- a TG GTA

GAM1779 ACCTCTTTCTGATGGAGTCG 910 TGATGGAGTC 3980 TTTCT TG TC AG CT TC
TCTTC T CTCACAAA
TAAAAAGTTTTATCTCTTTC GTAAAAAGTT TC GA GAG GTAAAA TTTTAT CTT TC GA
GGT A
TCTCTTCGATGGTCTCACAA TTAT || || ||| |||||| |||||| ||| || || |||
AAAATATTAAACCTCTTTCT AG CT TTC tatttt aaaatg gag ag CT CCA /
GATGGAGTCGTAAAAAGTTT CTTCT CT TC ga ct gt tCTTT - AATTATAA
TATCTCTTTCTCTCTTCGAT
GGT
GAM1780 TTTCTAAGAATTTACAATCT 2355 TAATTCTATT 5425 --- A TAA--- TACAT C
AAAATAGTACATGATTCACA AATGTTGATG TTTCTAAG AATTTAC ATC AATAG GATT A
ATTTAATTCTATTAATGTTG GTAA |||||||| ||||||| ||| ||||| ||||
ATGGTAAATTACATTTAGAA AAAGATTT TTAaatg tag ttatc TTAA /
A ACA g ttgtaa ttaat C

GAM1781 GATGTGATAAATACAGCGAT 2343 TGTCATAGTT 5413 AAA --- TTTGT - CCGAG
CA
ACCATTTGTGGGCATTGTCC GTAGAGGTCA GATGTGAT TACAGC GATACCA GGGC
ATTGT TGACG T
GAGTGACGCATTCACGTCAA CATC |||||||| |||||| ||||||| |||| ||||| |||||
TATATAATCGTTCTCCTTGG ctacactg atgttg ctgtGGT CTTG TAATA ACTGC T
TGTCATAGTTGTAGAGGTCA gag ata TCCT- C TATA- AC
CATC

GAM1782 TCTTGATTATTAATACAAAT 2345 AACAAGAATT 5415 A- -------- A-- A C GA
TCATTGTCTATGAAATGTGA AAAGTGTTGT TCTTG TTAT TAATAC AATTC TTGT TAT A
ACAAGAATTAAAGTGTTGTA AAAC ||||| |||| |||||| ||||| |||| |||
AACTATGTAAGCCAGGA AGGAC AATG gttgtg ttaag aaca GTG /
CG TATcaaat aaa - a TA

GAM1783 CATATTACAAAATCGATTCC 2361 TCGATTCCGT 5431 TAC c ccaag aaaaACA
GTCCAAGATGATAAAAACAT CCAAGATGAT CATAT AAAAt gattccgt atgat T
TTACCGGCATCATAAACACG AAAA ||||| ||||| |||||||| |||||
GAGTTTATTTTATATG GTATA TTTTA TTGAGGCA TACTA T
--- T CAAA- CGGCCAT

GAM1784 TCTTTCTGCATGTAGTTTTA 2346 CATGTAGTTT 5416 - c tttaaaaaa a
AAAAAGCAGAACTTTGTAAA TAAAAAAGCA TCTTT CTG atgtagt gcag a
ATATATACTATATCTGGAAA GAAC ||||| ||| ||||||| ||||
AGA AGAAA GGT TATATCA TGTT c
A C TATATAAAA T

GAM1785 GCGGGGGGTCTGGGGCTCTG 2347 TCAGGTGGCC 5417 T G -- GA CA
ACCTGAGTGCAGGTTACGAA CGAGCCCCCC GCGGGGGG CT GGGCT CTGACCT GTG G
GGTCAGGTGGCCCGAGCCCC CGC |||||||| || ||||| ||||||| |||
CCCGC cgcccccc ga cccgg gactGGA CAT /
c g tg AG TG

GAM1786 TTTTCTCCGTACAAGAAATG 2348 TACAAGAAAT 5418 C acaagaaa ac- ctt CAGACA TT C- CAC
GACGTCACTTGAGCAGACAC GGACGTCACT TTTTCTC Gt tgg gtca gag CAG TCAT GAC G
AGTTTCATCGACCACGACAG TGAG ||||||| || ||| |||| ||| ||| |||| |||
TCTCATGATCTGACTACCTC AAAAGAG CA ACC CAGT CTC GTC AGTA CTG /
TGACCCGCCAACGAGAAAA - -------- GCC --- CATCA- T- CT ACA

GAM1787 GGGGCGGCGCCCGCGGGGGA 2349 GCGCGCGGGG 5419 G GGGGGA G GG-- GGGG
GCGGCCGGCTCCGGGGGAGG CTGCCCT GGGGCGGC CCCGC GCG CC CTCCG A
GACGGGGAAGGGGGCGCGCG |||||||| ||||| ||| || |||||
GGGCTGCCCT tcccgtcg gggcg cgc GG GGGGC /
- ------ g GGAA AGGG

GAM1788 CCCGTCTCCCTCTGTGGTCG 2351 CTCTCGTCTC 5421 G G-- TGGT A GA
TGGGTGGTGCGAGAGTACAC GGGGGACCAC CCC TCTCCCTCTGTGGTC TGGG GCGAGAGT CAC T
GATGGGTGGCTCTCGTCTCG AGGG ||| |||||||||||||| |||| |||||||| |||
GGGGACCACAGGGGGAGGGG GGG GGAGGgggacaccag gctc tgctctcG GTG /
GG G ggg ---- - GG

GAM1789 GGCATGTCGGCCGACAAATC 2356 TGTAGCAGTT 5426 CAT C A-- C--- CTTC
GCAGCTGTCTTCGCCGCCGC AACGTCGCCG GG GTCGGC GAC AAT GCAGCTGT G
AGCTGTAGCAGTTAACGTCG GCCT || |||||| ||| ||| ||||||||
CCGGCCTCC CC cggccg ctg ttg tgtCGACG C
tc- - caa acga CCGC

GAM1790 CATCTTTTACCAACACAAAG 2350 TCTTTTACCA 5420 ct acacaaa aTATTT TT - GATAAT ACA
GGTGGATATTTGTTCATTGG ACACAAAGGG At tttacca gggtgg G CATTG GAGTT AATAC C

AGTTGATAATAATACACACA TGGA || ||||||| |||||| | ||||| ||||| |||||
AAGTATTTGGATTCACGGTG TA AGATGGT TCCATC T GTGGC CTTAG TTATG
/
GGTTACGACTACCTCAGACT AG CAGAC-- AGCAT- GG A GT---- AAA
GGTAGAGAATG

GAM1791 GTACGCGTGTCGATTCATCA 2352 ACGCGTGTCG 5422 -- ------ a-- at
AGGTATATAAACCTGGGGAT ATTCATCAAG GTacgcgt gtcga ttcatc aggt A
GAGGCTACCTCGACATACGT GTAT |||||||| ||||| |||||| ||||
GTGC CGTGTGCA CAGCT GAGTAG TCCA T
TA CCATCG GGG AA

GAM1792 GACCAGTCAGCCGCGAACGG 2353 AGTCAGCCGC 5423 Cagt cgaa- a ac--- - A
AAATAACGCCGAATCGAGCT GAACGGAAAT GAC cagccg cggaa ta gC CG A
CCTCTAATTCCGATAACCGG AACG ||| |||||| ||||| || || ||
CTGTTGTC CTG GTCGGC GCCTT AT CG GC /
TT-- CAATA A CTCCT A T

GAM1793 GGCTTGGCCCATCAACTGCT 2354 TTAGAAGGCA 5424 CCA AAC AAA TTA GACTT
AAACTGATTAGGGAGACTTT CGGGAGACGC GGCTTGGC TC TGCT CTGA GGGA T
AAACATCCCCTTAGAAGGCA CGAG |||||||| || |||| |||| ||||
CGGGAGACGCCGAGCT TCgagccg ag acgg gatt CCCT /
cag ggc aa- C-- ACAAA

GAM1794 TTACATAAGGTTTTTACAAA 2357 TATAATATTT 5427 GTTT- C---- CTTGT - CA-
ACATA
TATTGACTTGTTATTTATTA ATTCAATATT ATAAG TTA AAATATTGA TATT TATTAAA
AATGGG T
AACAAATGGGACATATAACA TTTT ||||| ||| ||||||||| |||| ||||||| ||||||
CTTTCATTAAATTTAATATA TATTC AAT tttataact ataa atAATTT TTACTT A
ATATTTATTCAATATTTTTT AATTT ATttt tattt t AAA TCACA
TATAATTTAACTTATGTAA

GAM1795 GGGTACACGAAAACAGCTAA 2358 ACGTTGGGCC 5428 A Aac- aacaaga C TAAGCA-
C- G
CGTTGGGCCAAACAAGATAT AAACAAGATA AAAC GCT gttgggcca tatctg GG GTTT
GGCCCCG C
CTGCGGTAAGCAGTTTCGGC TCTG |||| ||| ||||||||| |||||| || |||| |||||||
CCCGGCCCGGGGCCAAGAAC TTTG CGA CAACCCGGT ATAGAC CC CAAG
CCGGGGC /
AGATGGTCCCCAGATATGGC A CTCC ------- C TGGTAGA AA C
CCAACCCTCAGCAGTTTCTT
AAGACCC
GAM1796 GGTTAGTTCAATTTGTTAAA 2368 TTAGTCCTGA 5438 -- CAAT--- AA A CTCAGT C
GACAGGATCTCAGTAGTCCA CTCAACAATA GGT TAGTT TTGTT AG CAGGAT AGT C
GGCTTTAGTCCTGACTCAAC CCAC ||| ||||| ||||| || |||||| |||
AATACCACCAGCTAAAACC CCA ATCGA aacaa tc gtcctg TCG A

AA Ccaccat c- a att--- G

GAM1797 GTTTTATATGTTTTGATATA 2371 TATGTTTTGA 5441 TTT t atataacca - TATCT T
TATAACCAATCTAATCTATC TATATATAAC GT Atatgttt gatat atCT AATC TTAAT T
TTTAATTTTATTAATAAATG CAAT || |||||||| ||||| |||| |||| |||||
ATTCAGATAATGATTGATAT CA TATATAGA CTATA TAGA TTAG AATTA /
CTAGATATATTATAC TAT T GTTAGTAA- C TAAAT T

GAM1798 ATAGAAAATCAAAAACAATG 2359 TGCGTAGCAC 5429 AAATCAAAAACAAT A C
AATGGTGCTAAGCACCACAT CATTTTCATA ATAGA GAATGGTGCTA GCACCACAT C
CCGGATGTGGTGCGTAGCAC ACAT ||||| |||||||||||| |||||||||
CATTTTCATAACATTAATCT TATCT tttaccacgat cgtGGTGTA G
AT AATtacaatact-- g G

GAM1799 GAGCAGAACAAACCACATCA 2360 CAAGATGTTA 5430 CAG AAA-- ---------- AA A
AGTGCATAGCACAAGATGTT GCATACTCCG GAG AAC CC ACATC GTGC T
AGCATACTCCGGAACTGGTT GAAC ||| ||| || ||||| ||||
ATCTC CTC TTG gg tgtag cACG /
TA- GTcaa cctcatacgat aa A

GAM1800 CCTAGCCCTAACCCTAGGGC 2369 GGGCTGCGGC 5439 CCCTAACCC ACCC
CCCTAA
TGCGGCCCTAACCCTAGCCC CCTAACCCTA CCTAG TAGGGCTGCGGCCCTA TAG C
TAACCCTAACCCTAACCCTA ACCC ||||| |||||||||||||| |||
GGGCTGCGGCCCTAACCCTA GGATc atcccggcgtcgggAT ATC C
ACCCTAGG ccaatccca CCCA CCAATC

GAM1801 CGCCCCCACTGGCAGCCAAT 2370 CCCCACTGGC 5440 cccca g ccaa-- tAAT
GTCTTGTAATGCCTTCAAGG AGCCAATGTC CGC ct gcag tgtcttg G
CACTTTTTCTGCGAGCCGCG TTGT ||| || |||| |||||||
GCG GA CGTC ACGGAAC /
CC--- G TTTTTC TTCC

GAM1802 GTGCTTTAACGTCAATGGTA 2362 AATGGTACAA 5432 aaattttatcct c T - T CTCT-------
AA
CAAATTTTATCCTCGCTTTG ATTTTATCCT ggtac cg tT GTGTAT CATAT CGT
AGTATA A
TGTATCATATTCGTCTCTAG CGCT ||||| || || |||||| ||||| ||| ||||||
TATAAAATTCTATATTCAAA CTATG GC AA CGCATA GTGTA GCG TTATAT T
TTATCATGCGATGTGTATAC ---------- - T T - TACTATTAAAC CT
GCTAACGGTATCAATAAACG
GAGCAC
GAM1803 GGATTCCTAATTTTAACATC 2363 TTCCTAATTT 5433 ttc att-- atcaaaact CAC
AAAACTTAAAGACACTGGAT TAACATCAAA GGA cta ttaac tAAAGA T

CTTTAGTTAATTCAATAGCT ACTT ||| ||| ||||| ||||||
TCC CCT GAT AATTG ATTTCT /
TC- AACTT --------- AGG

GAM1804 GAAAGGGGGCCCGGGGGATC 2364 TCCCCCGGTT 5434 C-- --- C- G
TCCCCCGCGGTAACTGGTCA ACCCCCTTTC GAAAGGGGG CCGGGGGA TCTCC
CCGCGGTAACTG T
CAGTTGCCGCGGACGGAGAT ||||||||| |||||||| ||||| ||||||||||||
CATCCCCCGGTTACCCCCTT ctttccccc ggcccccct AGAGG GGCGCCGTTGAC C
TC att ACT CA A

GAM1805 GGCCGGACCGTTGATTCCCT 2365 TCCCTGACGA 5435 G TTG c ag----- atgc
AG
GACGACTACGAGCACATGCA CTACGAGCAC GGCCG ACCG ATtccctgacga tacg cac
ATGAAGC A
TGAAGCAGAAGGCTTCATTT ATGC ||||| |||| |||||||||||| |||| ||| |||||||
GGTGACCCCGACGTGATCGT CCGGC TGGT TAAGGGATTGCT GTGC GTG
TACTTCG /
TAGGGAATAGTGGTCGGCC - GA- A AGCCCCA GTT- GA

GAM1806 CTGAGTGACGTCGGAGGGAG 2366 TACCCTACCG 5436 GACG - AGC CAC G
CTCCACGGCCGGGGGGCCAAG AGAACTCAG CTGAGT TCGG AGGG TC GGCC G
ATACCCTACCGAGAACTCAG |||||| |||| |||| || ||||
gactca agcc tccc AG CCGG /
ag-- a at- AA- G

GAM1807 CTAAATAGTTTAATCCAATA 2367 TTGCATTGCA 5437 AT ATC A---- GG
AATTGAGGATAATCAATTCT TAAACTCGTT CTAA AGTTTA CAAT AATTGA A
TGCATTGCATAAACTCGTTA AG |||| |||||| |||| ||||||
G gatt tcaaat gtta TTAACT T
gc ac- cgttC AA

GAM1808 GCAGCTGGGGTGGAAGTCTG 2303 TTAGTCTCCG 5373 C AGTCTGAAAAA AAA --- G
A AG
AAAAAGGGAAAGGGGAGGTG ACCCGCCGTC GCAG TGGGGTGGA GGG GGGGA G TG
GC A
AGCAGAGTGCCCAGTTAGTC CGCC |||| ||||||||| ||| ||||| | || ||
TCCGACCCGCCGTCCGCCCT TGTC ATCccgcct ccc cctct t AC CG /
ACTGT - gccg------- ag- gat G C TG

GAM1809 TATACTATCTGAAGAATATA 2304 TATCATACAA 5374 TATCTGA- - ------ ATT
TAATAACTGATATAGTATTA GGATTGTTAT TATAC AGAATATATAATAA CT GATATAGT A
TCAGCTATATCATACAAGGA ATAT ||||| |||||||||||||| || ||||||||
TTGTTATATATTTTCTAAAA ATATG TTTtatatattgtt gg ctatATCG /

ATGTATA TAAAAATC a aacata ACT

GAM1810 AGATCCTTGGTTATTATATT 2306 TCCTTGGTTA 5376 c- gtt-- ccttat - AA
CCTTATACTAGTAGAATAGT TTATATTCCT AGAt cttg attatatt aCTA GTAG T
TACTTAGTTAATGATGTAAT TATA |||| |||| |||||||| |||| ||||
TCTAACAAGAAATCT TCTA GAAC TAATGTAG TGAT CATT /
AA AATCT TAAT-- T GA

GAM1811 TCTGGCTCTGTTATTGTACC 2307 TATTGTACCC 5377 GT-- tg ccc- taac ta
CGATATAACGGTAATACTAA GATATAACGG TCTGGCTCT tat ta gata gg a
TTTATCTAAATATGATGTAT TAAT ||||||||| ||| || |||| ||
AAGAGTTAGA AGATTGAGA GTA AT CTAT TC /
ATAT GT AAAT TTAA At

GAM1812 AGCGATAAAAGTAATAGAAA 2372 TAGAAAACAC 5442 C AA- --- a- atacca- C AA GAT
ACACTATACCATGTCTACCG TATACCATGT G GATAA GTAAtaga aaac ct tgtctac GAT TATGAA T
ATAATATGAAGATTATATTC CTAC | ||||| |||||||| |||| || ||||||| ||| ||||||
ATAAAGTCGTAGATAATTAA C CTATT TATTATTT TTTG GA ATAGATG CTG ATACTT /
AGAGAAGTTTAAATTTATTA - AAA AAA AA GAAATTA - AA ATA
TAAATTATCCT

GAM1813 GTGAGATAGTCATGGAGACT 2308 CTTTGTGGAT 5378 GAT AG TA---- GA A TCG
ACATCAGATTACGAGGATGT GATGAACTAT GTGA AGTCATGG AC CATCA TTACGAGG TG T
CGTTTTTACTTTGTGGATGA GTAG |||| |||||||| || ||||| |||||||| ||
TGAACTATGTAGCCGTGACT TACT TCAGTGCC tg gtagt ggtgtttc AT /
CCATCAT ACC ga tatcaa a- - TTT

GAM1814 TGGAAGACTGTACAAGGAAT 2309 TGAGCGAAGG 5379 AA A A TCGATGATG ATACGGTAC AA AATTA
TGATGAAGTTCGATGATGTT AGACCACTAC GGA TTGATG AGT TTGCT TATGG TTGATAA A
GCTATACGGTACTATGGAAT ATCA ||| |||||| ||| ||||| ||||| |||||||
TGATAAAATTAATGAGATTA TCT Aactac tca agcga gtATC AGCTATT /
TCGAGGCTATGAGCGAAGGA -- - a ccagagga- --------- GG AGAGT
GACCACTACATCAATCTTAC
AGAAGTCCA
GAM1815 CAGTATCATTTAAACATTTA 2373 TCACAACTTT 5443 A TTT TTT C C T
ACTTGCGGGGTTGATCTCAC ATTGTTTTTG CAGT TCA AAACA AA TTG GGGG T
AACTTTATTGTTTTTGAACT AACT |||| ||| ||||| || ||| ||||
G Gtca agt tttgt tt aac ctCT G
- t-- tat c a A

GAM1816 AGATCCGTGAGAAATACGTT 2374 TGAGAAATAC 5444 Gtg ta tttagccg- tA
TAGCCGCCTTTAATAGAGGA GTTTAGCCGC AGATCC agaaa cg cctt A
AATCCCACCGCCTTTCTGGA CTTT |||||| ||||| || ||||
TCT TCTAGG TCTTT GC GGAG /
--- CC CACCCTAAA AT

GAM1817 GTTAATCTCACAACTTTACT 2310 TAGCATAGAT 5380 TAA AAC -- - C
GTTTTTGAACTGTTCAAAAT CCGTGAGAAA GT TCTCAC TTTA CTGT TTTTGAA T
ATAGCATAGATCCGTGAGAA TAC || |||||| |||| |||| |||||||
ATAC ca agagtg agat gatA AAAACTT /
taa cct ac T G

GAM1818 TAAAAAACGGCAGATTAAGT 2375 TTAGTGCGAT 5445 TT TTTCCACGACCCGCA G CG----
-- -- -- C
AGATTGCCCTTTCCACGACC TGCGATTATG GCCC GCCACCT AGCG CGCA
CGCA GAAC T
CGCAGCCACCTGAGCGCGCG TCCG |||| ||||||| |||| |||| |||| ||||
CACGCAGAACCTATGTTTAG CGGG CGGTGGA TCgc gcgt gcgt ttTG A
TGCGATTGCGATTATGTCCG -- ---------- - ctgtatta ta ga T
CTAGGTGGCGGGCTATTTTG
ATCCTGCCGCG
GAM1819 CCACCTGTTTTAACATATAA 2376 TAATAGGCAG 5446 TA T- -- ga t tatccgTCATTG-
CTTCTC A
TAGGCAGGAGATAGATATCC GAGATAGATA ACA Ataatag gcag ga aga CAATATTC
GT G
GTCATTGCAATATTCCTTCT TCCG ||| ||||||| |||| || ||| |||||||| ||
CGTAGGCACACAATCGAATA TGT TATTATT CGTC TT TCT GTTATAAG CA G
TTGATAAAATCTCCATTCTC -- TC TA TC C TACCTCTAAAATA CTAACA C
TTCTCTGCATTTATTATCTT
GTCTTGGTGG
GAM1820 CATGTAGTAAGTGTCGATTG 2311 TTAGGACAGA 5381 T A GA G A AAC
TAATAAGGAACTGATGCCTA TACTACTATT CA GTAGTA GTGTC TT TAATA GG T
TTAGGACAGATACTACTATT TG || |||||| ||||| || ||||| ||
TG gt tatcat catag ag attAT CC G
t - ac g - GTA

GAM1821 CTGTGTCCAAGGTAAAATCG 2312 TCCAAGGTAA 5382 caa aaa gtt tAG
TGTTTGTGTAGTTTTCACAA AATCGTGTTT CTGTGtc ggt atcgt tgtg T
TGATGCCATCATAGATATAG GTGT ||||||| ||| ||||| ||||
GATATAG CTA TAGTA ACAC /
ATA CCG --- TTT

GAM1822 GTCATTCATTTAGAATGGTT 2313 TATTATGTTT 5383 A TTAG G GG TCA TG T C
C
GTTGGGCTTTATCAAGTGTA AAAGATGACA GTC TTCAT AATG TTGTTG CTTTA AG TA
TAGTCAG AT A

TTAGTCAGCATCAGCATCTG ATAT ||| ||||| |||| |||||| |||||| || || ||||||| ||
GCTATTATGTTTAAAGATGA CAG AAGTA Ttat aacagt gaaat tt at atCGGTC TA G
CAATATTATTATGAAGAC - TTA- - a- --- gt t - C

GAM1823 TGAGAATATTGATGATTTTT 2305 TGATATTTAC 5375 AT- TTTTTTTAAGA---- c ttat CATTACAGA
TTTAAGATGATATTTACTTT TTTTTATATG TGATGAT tgatattta ttt atgcttg A
TTATATGCTTGCATTACAGA CTTG ||||||| ||||||||| ||| ||||||| /
ATAATATTCACAGGTATTAT ACTACTA GCTATGAGT AAA TATGGAC /
TAAAATGAGTATCGGAGCTA CCT TACCATTACATCGAG A TTAT ACTTATAAT
CATTACCATATCATCATCCA
TGCTCA
GAM1824 ATGGAGATACAACGTGAAAT 2314 TAATGTATCA 5384 CAA- A-- T ACTC
ACTTTATTACTCCATTAAAT CTTACGATAA ATGGAGATA CGTGA ATAC TTATT C
AATGTATCACTTACGATAAT TGTC ||||||||| ||||| |||| |||||
GTCTCTAT TATCTctgt gcatt tatg aatAA /
aata cac t ATTA

GAM1825 AAGATGATAAAAACACGTTT 2315 AACACGTTTA 5385 T cgttt tt gtcaacCA
ATTTTATATGTCAACCATTA TTTTATATGT AAGA GATAAAaaca at tatat T
CTAAAAAATATATTGTTCTG CAAC |||| |||||||||| || |||||
TTTTTGTTTTCTT TTCT TTGTTTTTGT TG ATATA T
T CT--- TT AAAAATCA

GAM1826 TGGGAACTTCAGGAGCTGAC 2316 CAGGAGCTGA 5386 ca c ac ga tat TATCT- CT
TTAGAAAATATTGTTTTATC CTTAGAAAAT TGGGAACTT ggag tg tta aaa tgTTT CTTGGG G
TCTTGGGCTGCATTCAGGTT ATTG ||||||||| |||| || ||| ||| ||||| ||||||
TTTTAGGCATTTTTGATAAA ATTCTTGGG CCTT AC AAT TTT ACGGA GGACTT /
CATTTCCCCGGGTTCTTA CC T A- AG TT- TTTTTT AC

GAM1827 GAGATTGTACTATTTGTATA 2317 GATTGTACTA 5387 t- at- a cg t-- A
CGCATCTTTAATAAAAGTTT TTTGTATACG GAgat gtact ttgt ta ca cTTT A
TGAATAAACAATTGAGTACT CATC ||||| ||||| |||| || || ||||
TGTTTC CTTTG CATGA AACA AT GT GAAA T
TT GTT A AA TTT A

GAM1828 AAGTGATATAAGGGGAATAC 2318 TAAGGGGAAT 5388 TAtaa atacacat atcAAAA
ACATGAGTAATCAAAACCCA ACACATGAGT AAGTGA gggga gagta C
GCACATACTCTCCTCGAATT AATC |||||| ||||| |||||
CATTT TTTACT CTCCT CTCAT C
TAAG- -------- ACACGAC

GAM1829 CCCAGCACATACTCTCCTCG 2322 TGAGTCGACG 5392 CACATACTC- C A TT CC

AATTCATTTCTCCTACCAGT ACCATCGCCT CCCAG TC TCGA TTCAT CT T
TGTGAGTCGACGACCATCGC ACTG ||||| || |||| ||||| ||
CTACTGGG GGgtc ag agct gagtG GA A
atccgctacc c - TT CC

GAM1830 GCCCTTAGTCATCCATGCTG 2319 TCCATGCTGT 5389 TTA Atc- gc - ca aa- CCAC-
G
TGGCCGGTGCAGGAAAGACC GGCCGGTGCA GCCC GTC cat tgtggccg gtg gg AGA CCT
A
ACCCTGATTAGGCAATTTCT GGAA |||| ||| ||| |||||||| ||| || ||| |||
ACACCAACACTCGGCCACGA CGGG CAG GTA GCACCGGC CAC CC TCT GGA T
ATGCTCAGACGCTGGGC TCG ACTC A- T AA ACA TTAAC T

GAM1831 GAACAGAAAAGGGGGAGAAT 2320 CATAACGTTC 5390 AG-------- GG T CC G
TTTCCGTAAGACTTACATAA TTTTCAAAGC GAACAGAAA G GAGAAT TT GTAA A
CGTTCTTTTCAAAGCAGTTC AGTT ||||||||| | |||||| || ||||
TTTCTGTTT TTTGTCTTT c ttcttg aa cATT /
Cttgacgaaa tt c ta C

GAM1832 GTTGGATATCTTTTGTTTGT 2323 TCTTTTGTTT 5393 G ttgtttgtc aaat TT- AC G
CGGATGTAAATTCGTTGATT GTCGGATGTA GTT GATAtctt ggatgt tCG GATTTTA AT T
TTAACATGTAAATAGTGAGG AATT ||| |||||||| |||||| ||| ||||||| ||
TTTTCTGATGTGACGTCTAA TAA TTGTAGAA TCTGCA AGT TTGGAGT TA A
GATGTTGAAT G --------- GTGT CTT GA A

GAM1833 CGTTGTCGCGCGGCGACGCC 2321 CGGGCCGAGG 5391 C ---------- G
GGCGCGGCGGGCCGAGGACG ACGGACCGTT CGTTGTCG GCGGCGA CGCCG C
GACCGTTTCGCCGCTCGACG TCGC |||||||| ||||||| |||||
ACG GCAGCAGC CGCcgct gcGGC /
T ttgccaggcaggagccgg G

GAM1834 CTGGCGTCCCTCTCGGTGGC 2324 GCGCAGAGCC 5394 CT T aga - c gCTCC
GCAGAGCCTGCCGCCGCTCC TGCCGCCGCT CTGGCGTCC CTCGG Ggcgc gcctg ccgccgct cg
C
GGCTCCCGTTCGACGCGGCG CCGG ||||||||| ||||| ||||| ||||| |||||||| ||
GCGGTCGGGCGGGCGTCTCG GGCTGCAGG GGGCT CTGCG CGGGC GGCGGCGG
GC G
GGCGGACGTCGG C- - GG- T C AGCTT

GAM1835 GTCTCCTTAAAGCTTCTGAT 2328 TGATGGTAAC 5398 C TTAA Ct t ac-- t atgt
GGTAACTGTGTTACATGTGC TGTGTTACAT GT TCC AGCTT ga ggta tgtgt ac g
TCCGTCATACGTAAATGCCT GTGC || ||| ||||| || |||| ||||| ||
TCTTAAGCTATTTGGAAAC CA AGG TCGAA CT CCGT GCATA TG /
A TTTA TT T AAAT C CCTc

GAM1836 GCTCCCGCTCAGTCTGTTAG 2325 GCTCAGTCTG 5395 gttagt t a GAAT TTGCATATTC T
TT AAA A
TCCTCCTAGTTCGAATCCTT TTAGTCCTCC t cc cct gtTC CCTT TCTC CCCAC TTCA
TC A
TTGCATATTCTCTCTCCCAC TAGT | || ||| |||| |||| |||| ||||| |||| ||
TTTTCAAAATCAAAGAGGGT G GG GGA CAAG GGAA AGAG GGGTG AGGT
AG /
GGACTGTGGGGAGAAAGGGA ------ T - ---- ---------- - TC GGG A
ACAGGTGGGGACGACCGGGA
GC
GAM1837 GCCGTCCCGATTAACCGATT 2326 TAACCGATTC 5396 CC--- Tt c ccgca- agcac ACCA
CCCCGCACGGAGCACCGCGG CCCGCACGGA GCCGTC GA aac gattcc cgg CGCGG C
ACCACCCGACCGCGAGCCGA GCAC |||||| || ||| |||||| ||| |||||
CTCCTGGAGTTCGTTCCTCA CGGCAG CT TTG TTGAGG GCC GCGCC /
TTTCGACGGC CTTTA CC C TCCTCA GA--- AGCC

GAM1838 TGTAAAAAGAAAATGCGAGT 2327 TGGCATGAAG 5397 AAAAGA- GA- AAG TGT T GT
T AT TT
GCAAGAACTGTGGTTGGTTT CATTTACAAA TGTA AAATGC GTGC AAC GGT G TTCC
GCG ATCAG C
CCTGCGATATCAGTTCAACC AGTG |||| |||||| |||| ||| ||| | |||| ||| |||||
TGATTACGTGGAAGTCTACT ACgt tttacg tacg TTG TCA C AAGG TGC TAGTC A
TCTGTTGTGGCATGAAGCAT gaaaaca aag gtG TCT T TG - AT CA
TTACAAAAGTGCA

GAM1839 TCCGGCAACATCACCGCGGC 2329 TATGCCGTGC 5399 AACATCAC C -- -- C
CGTGCGGATGCTCCAAAGCC CGCCGGA TCCGGC CGCGGC GTGC GGAT GCT C
TGTCCACGTATGCCGTGCCG |||||| |||||| |||| |||| |||
CCGGA aggccg gtgccg tatG CCTG CGA A
cc------ - CA TC A

GAM1840 GCCCCCGTCTGTCGCCTCTC 2330 CCCGTCTGTC 5400 cc t tctcc ttTCC
CCTTTTTTCCCCCCCTCAAA GCCTCTCCCT GCC cgtctg cgcc cttt C
GAACGTGGTGTTGGGCGCCG TTTT ||| |||||| |||| ||||
GC CGG GCGGGT GTGG GAAA C
CC T TGCAA CTCCC

GAM1841 TTCTTTTAAATACGTATCAC 2331 TAATACTTAG 5401 AAT TC TT TGCTTTACTTA CT
TTTT
AGTTTAATGCTTTACTTATA TTAATACCTT TTCTTTTA ACGTA ACAG TAA TAAG TTGTA
T
AGCTTTGTATTTTTAGAATT TACT |||||||| ||||| |||| ||| |||| |||||
ATAATACTTAGTTAATACCT AAGAAAGT TGCAT TGTC att attc aatAT A
TTACTCTGTCTACGTTGAAA --- C- tc tccataattg- at TAAG
GAA

GAM1842 ATAATCAACATAACCTCATC 1777 TAATAGGGAT 4847 ACA - C- A -- A
ATCTATTAACTGATAACGGT AAAGGATTAA ATAATCA TAA CCT ATC TCTATTA ACTGAT A
TAGTTATAATAGGGATAAAG TGAT ||||||| ||| ||| ||| ||||||| ||||||
GATTAATGATTAT TATtagt att gga tag ggataat TGATTG C
a-- a aa - AT G

GAM1843 TACGAAACACCGATAAATTA 2332 TAAATTATAA 5402 ACACC a- - aa a
TAAAAGAAGCAGTGATTCCG AAGAAGCAGT TACGAA GAta attat aa gaagcagtg t
CTGTTTCAGTTAATAATACT GATT |||||| |||| ||||| || |||||||||
ATTTTCGTA ATGCTT TTAT TAATA TT CTTTGTCGC t
----- CA A GA C

GAM1844 ATCGTATTGTGGTTATATGG 1780 TGTGGTTATA 4850 ATtg t c a- TAA
CTACAATTTCATAATGAGTT TGGCTACAAT ATCGT tggttata gg tac atttca T
GAAGTCAGTGTCCTATGATC TTCA ||||| |||||||| || ||| ||||||
AATGACGAT TAGCA ACTAGTAT CC GTG TGAAGT G
GTA- - T AC TGA

GAM1845 ATGGAAAGGGGGGGCGAGGCA 1788 CCCCCGTTCG 4858 G A CA C -
GACGATGAGAGGATGGA A - GG
GGGCAGCGGGCGGGGGAGGA CCCACTACGA CGAG C GGG GCGGG GGGG GAG
CG GGGGG TCCC A
CGATGAGAGGATGGACGAGG GGTC |||| | ||| ||||| |||| ||| || ||||| ||||
GGGTCCCGGAGGAGGGAGCC gctt g ccc cGCCC CCCC CTC GC CCCCC AGGG
G
CCCCGCTCGCCCCACCCGCC - c -- A G ---------- - G AG
CCCGTTCGCCCACTACGAGG
TCTAT
GAM1846 TTAACTTCGCAATAATTTCT 1778 TCGCAATAAT 4848 CT caataattt t taa
GGTTAGATAACGCACTCTAC TTCTGGTTAG TTAA tcg ctggt aga C
CAGTCAAGTCAATGATATTA ATAA |||| ||| ||||| |||
G GATT AGT GACCA TCT G
AT AACTGAACT - CAC

GAM1847 CTACGTACCACCTATAATCA 2333 TGTAGGAAAA 5403 GT- - ATCATCtg aa- - at
TCTGTAGGAAAATGGAAGGT TGGAAGGTAT CTAC ACCACC TATA taggaa tgga aggt g
ATGTACATCTATCTACTGTT GTAC |||| |||||| |||| |||||| |||| ||||
CCTAATATCATATATGGTGG GATG TGGTGG ATAT ATCCTT ATCT TCTA t
TGTAGTAG ATG T ACTATA-- GTC A ca

GAM1848 AGCGCCGGCGGCTGGCGAGC 1796 CTCGCCGCGT 4866 - - - G
GGCGGCGGCCACGCGCGCTG TGCGCGGCGT AGCGCCG GCGGC TGGCGAGCGGCG GCG C
CTCGCCGCGTTGCGCGGCGT T ||||||| ||||| |||||||||||| |||
T ttgcggc cgttg gccgctcGTCGC CGC C

g c G A

GAM1849 TGCCGGAGATGCACGCCATC 1797 ACGCCATCTT 4867 A Cac c -- agtac---------- g
TTCGAGGAGTACCCGGACCT CGAGGAGTAC TGCCGG GATG gc atcttc gagg ccg A
GGAGCAGAAGTACCTGAGCC CCGG |||||| |||| || |||||| |||| |||
TCATGAAGATGCCCATCACC ACGGCC CTAC CG TAGAAG CTCC GGT C
GGCA A C-- - TA GAGTCCATGAAGACGA C

GAM1850 TTCCCACTCCCTCCTCCAGG 1798 CCTCCAGGGC 4868 - ---- c-- g- c ------ - CG
GCCTGCTTCGACGATCCCGC CTGCTTCGAC TTCC CAC TCCCTc tccagg cctg ttcg acg atcCCG G
GGGCCGGGATACGTGGCGCC GATC |||| ||| |||||| |||||| |||| |||| ||| ||||||
CGAACAGGGACCTGGAAACG AAGG GTG AGGGAG AGGTCC GGAC AAGC TGC TAGGGC /
AGGGACTCCGTGAGGAA A CCTC CAA AG - CCGCGG A CG

GAM1851 GGATTTTATATCTGATATCA 1779 TATCTGATAT 4849 c cacaaa t a A - CAAAA- - CCAAT AA
CAAAATATCAATAATGTATC CACAAAATAT t tgatat ata ca tA TG TAT ATATCA ATAT GTCC T
AAAAATATCAATATCCAATG CAAT | |||||| ||| || || || ||| |||||| |||| ||||
TCCAATAAAGGATTTTATAT A ACTATA TAT GT AT AC ATA TATAGT TATA TAGG A
CTGATATCACAAAATATCAA - AAAAC- - A A T AAACAC C TTT-- AA
TAATGTATCAAAAATATCAA
TATCTAATACC
GAM1852 AGGGAAGGTTTGACTCGCCT 1799 AAGAAGCGAC 4869 AA GAC C CCCA AGGAC
CTCCCAGCCCAGGACCAAAA AGAATCCGTC AGGG GGTTT TCGC TCT GCCC C
CGGGCGAAGAAGCGACAGAA CT |||| ||||| |||| ||| ||||
TCCGTCCT tcct ctaag agcg aga CGGG /
gc ac- a aG-- CAAAA

GAM1853 AACATACCAATGTCGATCTC 1800 TCTCATACTT 4870 T - C- c ctt-- ta caagT--- ACA
ATACTTATGGTAGGTTCAAG ATGGTAGGTT AACA ACC AATGT GAt tcata atgg ggtt CACG G
TCACGACAGGCCGCGTGTTA CAAG |||| ||| ||||| ||| ||||| |||| |||| ||||
CACACAACCCCCATTTCACT TTGT TGG TTACG CTA AGTGT TACC CCAA GTGC G
GTGAAATCCCGCATTCGGTT - C CC A CACTT C- CACACATT GCC
GTT

GAM1854 GCTATGATAAGCGGAGGAAA 1781 TATGATAAGC 4851 tat a --- aaa TG T
ACCTGCCTGATTCCTTGGGC GGAGGAAAAC GC gata gcg gagga cctgcC A T
GGGGATCCTTGTGCGCTGTC CTGC || |||| ||| ||||| |||||| |
TTGC CG CTGT CGC TTCCT GGGCGG T C
TT- - GTG AG- GT C

GAM1855 TAGGTTATCGTTGAGATTAA 1801 TGACAAAATT 4871 G AT G AA-- --- TTACG T T GAT
AAAGACTACGTTACGTTTTC TCGTAGTTAA TA GTT CGTTGA ATT AAA GACTACG TT TC CT G
TCTGATGACAAGTGACAAAA ATTT || ||| |||||| ||| ||| ||||||| || || ||
TTTCGTAGTTAAATTTCTAG AT TAA GTAACT TAA ttt ttgatgc aa ag GA /
AATGTCAATGTGAATGTA G GT G GATC aaa tttaa c t ACA

GAM1856 TAACTGTCCCGGCGTGCCTC 1802 TGGCATGAGG 4872 CGG TCCA - AG
CATCTGCTGAGTCCCGTGCA ATGGTTG TAACTGTCC CGTGCC TCTGC TG T
GACTGGCATGAGGATGGTTG ||||||||| |||||| ||||| ||
gttggtagg gtacgg AGACG GC /
a-- tC-- T CC

GAM1857 CGAGTTAAATTACATAAGTC 1782 TCCCGAGTTC 4852 - TACA A G TT AGA
CCGAGTTCTCGGGACAAGAT TAGGGACCTA CGAGT TAAAT TA GTCCC AG CTCGGGACA T
GGCGTGTCCCGAGTTCTAGG CTTG ||||| ||||| || ||||| || |||||||||
GACCTACTTGTTTGTACTTG GTTCA GTTTg at caggg tc gagccctGT G
T ttc- c a tt GCG

GAM1858 GAGGGCCGGGTGTCCGAAGC 1783 GAGGCCGTCG 4853 CG C AGC A AG G
CGACCTCCAGCGGTACCGGG ACACCGCCCT GAGGGC GGTGTC GA CG CCTCC CG T
AGGCCGTCGACACCGCCCTC C |||||| |||||| || || ||||| ||
ctcccg ccacag ct gc ggagG GC A
-- - --- c -- C

GAM1859 CCGCGCTCCTGCCCCCGGTC 1784 CCCCCGGTCT 4854 ----- C cc - tct cc T A ACG TACAT
TTCTACGAGCCCGTGGTGGA TCTACGAGCC CG CTC TG cccggt ct acgag cgtgG GG CT CGGCC C
CTACGCGGCCTACATCAACC CGTG || ||| || |||||| || ||||| ||||| || || |||||
TGGCCGAGCTCTACGTCTTC GC GAG AC GGGCCA GG TGCTT GCATC TC GA GCCGG /
GTCTGGTACCGGGACCACGA CTCTT C CA T TC- CT - - --- TCCAA
GTTCTCCGCGG

GAM1860 AACGCGCTGCCCGGCGAGCG 1789 TCGGACCCGC 4859 C - -- --- C C C - AG
GTCCGCGGCCGCCGCCGAGA GCTCGGACCG AACGCG TG CCCGG CGAGC GGTCCG GG CGC GC CG A
CCCGAGCCGCGTCCTCGGAC GGAC |||||| || ||||| ||||| |||||| || ||| || ||
CCGCGCTCGGACCGGGACGA TTGCGC Gc gggcc gctcg ccaggc CC GCG CG GC /
CGCGTT A a ag cgc t T C A CC

GAM1861 TTTGCGCCTGCGTCTGTATC 1785 CTAGATCTGT 4855 TG CCTG T- CT A A
TGTACTAGTTAGCTAACTAG ATCTGGCGGT TT CG CGTC GTAT GT CTAGTT G
ATCTGTATCTGGCGGTTCCG TCCG || || |||| |||| || ||||||
TGAA AA gc gcgg tatg ta gatcAA C
GT cttg tc tc - T

GAM1862 TGGGAGACGTCTCAGAGGCA 1786 TCTCAGAGGC 4856 AGACG g tcgg t
TCGGGGGCCATTTTTGTGGC ATCGGGGGCC TGGG tctcaga gca gggccat t
CCAATCTGTATCTGAGAACC ATTT |||| ||||||| ||| |||||||
CG GCCC AGAGTCT TGT CCCGGTG T
A---- A CTAA T

GAM1863 GAAGGATACGTGGTTCTATT 1787 TATTGGGCGG 4857 ATACGT tat c c cg
GGGCGGCGAGGGGCCGAAAC CGAGGGGCCG GAAGG GGTTC tggg gg gaggggc a
GCTCCTCTCCTCCATCTGAA AAAC ||||| ||||| |||| || |||||||
TTTTTGCTTTC CTTTC TTAAG ACCT CC CTCCTCG a
GTTT-- TCT - T ca

GAM1864 TGCTACCTTTAAACCTTATG 1803 TACCTTTAAA 4873 ctt ttatgt ct-- C AAA C TG
TAGACTGGGACAGTAAAGCA CCTTATGTAG TGCtac taaacc aga gGGA AGT GCA AGCT
G
CAGCTTGGGTCAGCTTGTCA ACTG |||||| |||||| ||| |||| ||| ||| ||||
CTTTTCTTTAATCTTTTTCC ACGATG ATTTGG TCT TCTT TCA TGT TCGA G
GGTTTAGTAGCA --- CCTTTT AATT T C-- - CT

GAM1865 GGGAAGATAATTTCAGTTGA 1790 TCAGAGCATG 4860 AA - AGTTGA AGAA G T
AGAAGAAGTTGTGAAGTACG GTCTAGAAAT GGG GAT AATTTC AGA GTT TGAAG A
TTTCAGAGCATGGTCTAGAA TCAT ||| ||| |||||| ||| ||| |||||
ATTCATTACCCC CCC Tta ttaaag tct cga actTT C
CA c a----- ggta g G

GAM1866 CGGGGCAGTTTGTGTACAAG 1791 TACAAGAACT 4861 A T G - t a gt
AACTGCGAGATGGTGCACAT GCGAGATGGT CGGGGC GTT GT tacaa gaac gcg gatg g
CGCGCCGTTCTTTGTAGCGG GCAC |||||| ||| || ||||| |||| ||| ||||
CGGCCCTG GTCCCG CGG CG ATGTT CTTG CGC CTAc /
G - - T C G ac

GAM1867 CCCTTTTCAGTACAAAGGCA 1809 TACATCAAGA 4879 GTA AAGG AC A T AATtaca a a
t - a AA
AACCCTATCTCGCTAATTAC AGAAAAGTCA CA CAA CCT TC CGCT tcaag agaa ag cac ag
TTC G
ATCAAGAAGAAAAGTCACAG CAGA || ||| ||| || |||| ||||| |||| || ||| || |||
ATTCAAGAAAGAGCTCGTGC GT GTT GGA GG GTGG AGTTC TTTT TC GTG TC
GAG A

CTATTTTGCTTGAATTGGGT AG- GAA- -- - T GTTA--- G A C C - AA
GTGGAGGTTGAAGTGGAGGA
GGAGGG
GAM1868 TCTGGCGGGTTATTGGTGGA 1792 TTGGTGGAAG 4862 GGC At gg caatg T G AT
AGGCTGTAACAATGTCTGTG GCTGTAACAA TCT GGGTT tggtggaa ctgtaa tc GT TC A
TCATAATCGAACTGAAAACT TGTC ||| ||||| |||||||| |||||| || || ||
TGCAGATTTTACCGCAACCT AGA TCCAA GCCATTTT GACGTT AG CA AG A
CAAGA AC- C- A- CAAA- T - CT

GAM1869 GGGCTTGTAGTTATACGTTC 1793 TACGTTCGAC 4863 gt cac taaaaaa G GTACA---
CTTT G G
GACACCATTAAAAAAGAAGG ACCATTAAAA Atac tcga cat gaAG CTATAT GA CATC
ATTG C
CTATATGTACAGACTTTCAT AAGA |||| |||| ||| |||| |||||| || |||| ||||
CGATTGGCATCAATGATGTA TATG GGCT GTA TTTC GATATA CT GTAG TAAC
A
TCTCAGATCAGAATATAGGC -- TA- ------- G AGACTAGA CTAT - T
TTTATGATTCGGGTATGTGC
AAGCCC
GAM1870 CGATTTAAAAAGGGGCAGTC 1794 CACCGCCTGT 4864 AA - CA AAGTT CG
TGCAAAGTTTATCGCGGGTG TAGGTTG CGATTTAA AGG GG GTCTGCA TAT C
TAATGTAGACACCGCCTGTT |||||||| ||| || ||||||| |||
AGGTTG gttggatt tcc cc cAGATGT GTG /
g- g a- AAT-- GG

GAM1871 TGTCGCAATCGTATCAAACT 1795 TGAGTGCGAT 4865 ATCAA C CA T A
CAGGCGGCAAGAGATACTGT TGTGACA TGTCGCAATCGT ACTCAGG GG AGAGA ACTGTT
G
TAGACAGCAGTTCTCTAACC |||||||||||| ||||||| || ||||| ||||||
TTCTGAGTGCGATTGTGACA acagtgttagcg tgagtCT CC TCTCT TGACGA A
----- T AA - C

GAM1872 CCGTTGTACGAGTCTCTCAT 1804 ATGAAGTCCT 4874 T T AGT Catga cctt- a g
GAAGTCCTTTGATACTAGAA TTGATACTAG CCG TG ACG CTCT agt tgat cta a
ATAGGATCATTGAAACTGAA AAAT ||| || ||| |||| ||| |||| |||
GAAGAGTCGCGTCCATCGG GGC AC TGC GAGA TCA ACTA GAt a
T C GCT AGAAG AAGTT G a

GAM1873 TCGAAACCTGTTATTTCCTG 1805 TATTACAGTG 4875 AAACCT TGGATCAC T CG G
GATCACCTGTTAACGTACGC GGAATAACTA TCG GTTATTTCC CTGT AA TACGC T
GTGGCGTATATTACAGTGGG AAAG ||| ||||||||| |||| || |||||
AATAACTAAAAGTGA AGT caataaggg gaca tt ATGCG /
gaaaat t------- - at G

GAM1874 TGGTGATAGATTAATCCTTG 1806 ATAGAGGAAC 4876 GATTAA GA- ACTTT

AAGTAACTTTTTTATATATT TAATATTACT TGGTGATA TCCTT AGTA T
ATAGAGGAACTAATATTACT A |||||||| ||||| ||||
A atcattat aggag TTAT /
aatca- ata ATATT

GAM1875 TATTACTGCAAGATTTTGAT 1807 TTCACATTGC 4877 CA----- TT--- TTTTTTAT TT CATAC T
TTTTTATTTGGTTTTGTCAT CAGCTTTTAC TATTACTG AGAT TGA TTGGT TGT AAGC T
ACAAGCTTTAGTTTTCACAT TTCA |||||||| |||| ||| ||||| ||| ||||
TGCCAGCTTTTACTTCATTC ATGATGAT TCTA act gaccg aca tTTG T
TCATCTGTATTATTAGTAGT TATTATG CTCTT tcattttc tt ct--- A
A

GAM1876 TCGGCGTTGTCGCAATCGTA 1810 TCAAACTTGT 4880 GTT CAAAC CTGC ACA TT
CCAAACACAAGCTGCGAGAG TAAGTGCGGT TCGGC GTCGCAATCGTAC ACAAG GAGAG CTG A
ACACTGTTAGACAGCAATTC TGTG ||||| |||||||||||| ||||| ||||| |||
TCAAACTTGTTAAGTGCGGT AGCCG CAgtgttggcgtg tgttc ctCTT GAC /
TGTGACGCCGA --- aat-- aaa- AAC AG

GAM1877 GACCGTTGCCATTAGAAGTC 1811 TGCCATTAGA 4881 tg - caa t
AAATTCAGCTTTTGCTGAGT AGTCAAATTC GACCGT ccattagaa gt attcagc T
GAGCTTTCTAATGGACATGG AGCT |||||| ||||||||| || |||||||
TT TTGGTA GGTAATCTT CG TGAGTCG T
CA T AG- T

GAM1878 TCGAAACCCCTTATTTCCTG 1812 TATTACAGTG 4882 A C C-- GGA-- C T CG TT
GATCACCTGTTAACGCACGT GGAATAAGTA TCGAA CC CTTATTT CT TCAC TGT AA CACG T
TTGACGTGTATTACAGTGGG AAAG ||||| || ||||||| || |||| ||| || ||||
AATAAGTAAAAGTGAGAGGT AGCTT GG GAGTgaa ga ggtg aca tt GTGC /
TCGA - A aat ataag - - at AG

GAM1879 GACCGTGGCCATCAGGAGTC 1808 TGAGTGAGCT 4878 G CA TCAA- T
AAATTCAGCTTTTGCTGAGT TTCCAGTGGA GACCGTG CCAT GGAG ATTCAGC T
GAGCTTTCCAGTGGACATGG CATG ||||||| |||| |||| |||||||
TC CTGgtac ggtg cctt tgagtCG T
a a- tcgag T

GAM1880 TGTCACAGTCGTATCAGACA 1817 TCGAACTTGT 4887 CAGAC CTG ATA TC
CAAGCTGCGAGAGATACTGT TAAGTGCGAT TGTCACAGTCGTAT ACAAG CGAGAG CTG A
CAGACAGCAATTCTCGAACT TGTG |||||||||||||| ||||| |||||| |||
TGTTAAGTGCGATTGTGACA ACAgtgttagcgtg tgttc gctCTT GAC /

aat-- aa- AAC AG

GAM1881 CCCCCAGGCATATTCAATAG 1818 TCGCATACTG 4888 -- T A GG- TT
GGACAGTGTTAATTTACTGT AATTGTTTGT CCCC CAGGCA ATTCA TA GACAGTG A
CGCATACTGAATTGTTTGTT TGGG |||| |||||| ||||| || |||||||
GGGG Gggg gtttgt taagt at ctGTCAT A
tt - c acg TT

GAM1882 TGCGGGGGCAACATATCCTT 1813 TCCACCACGG 4883 CAACATATCC GCC--------- TA
CACCCGCCGCTACCTGCTCT GGTGAACTTC TGCGGGGG TTCACCC GC C
TCCACCACGGGGTGAACTTC CCCC |||||||| ||||||| ||
CCCCGCA ACGccccc aagtggg CG /
ttc------- gcaccacctTCT TC

GAM1883 TGTCTTGCATTACTACCGTC 1819 CATTACTACC 4889 Gcatta a tc ctccaca CCCT
ACCTCCACAGCCCCTATTAC GTCACCTCCA TGTCTT ct ccg ac gc A
AGCCCGCAAGTCTCGGCAGA CAGC |||||| || ||| || ||
AAAAGACA ACAGAA GA GGC TG CG T
AAA--- C TC AACGCC- ACAT

GAM1884 GTTGTACTGAAATTCGTGAG 1814 TGCAATAGAT 4884 G AT- GTGA A ATA
TAATATATAAAACCATAATG CATTCAGTAA GTT TACTGAA TC GTA TAT A
CAATAGATCATTCAGTAAAA AAC ||| ||||||| || ||| |||
C caa atgactt ag cgt ATA A
a act ataa A CCA

GAM1885 AGGGACCTCTGATTCTCCTG 1815 TGAGGAACCG 4885 A T CTCCTGT G A- ATC G
TGACGCATGCCGATCCTATC GTATGGGTCG AGGG CC CTGATT GAC CATGCCG TCCT
GATT G
GATTGGAAATCTGAGGAACC ATCA |||| || |||||| ||| ||||||| |||| ||||
GGTATGGGTCGATCAGTGGC TCCC GG Gactag ctg gtatggc agga CTAA /
CCCT C T ------- g ca gt- A

GAM1886 ACCACATGACAATGAACAAA 1820 CATGACAATG 4890 -- - acct- a GA
CCTAAGACAGATTATGCTTT AACAAACCTA ACCAcatg acaatg aacaa aag cA T
ATGCTTGTTGTGTTGTAATA AGAC |||||||| |||||| ||||| ||| ||
TGTGGT TGGTGTAT TGTTGT TTGTT TTC GT /
AA G CGTAT - AT

GAM1887 GCCGCAGCTCACATGCCGCC 1816 TGAGAGGAGG 4886 ACAT G TC CT
TTCCGCGCTTGCCTAGGCGC CGGGTTGCGG GCCGCAGCTC GCC CCT CGCGCTTGC A
GAGTGTGAGAGGAGGCGGGT C |||||||||| ||| ||| |||||||||
TGCGGC cggcgttggg cgg gga gtGTGAGCG G

---- a ga CG

GAM1888 GGCCCGAGTCTGCCTGGCTG 1821 AGGTGCAAAT 4891 -- CCTG TGC GT - TCC
CTGCGTCTCGCTCCGAGTGC GCGACCAGAC GGCCCGA GTCTG GC TGC CTCG C G
CGAGGTGCAAATGCGACCAG TGTC ||||||| ||||| || ||| |||| |
ACTGTCGGGCC CCGGGct cagac cg acg gaGC G /
gt cag- taa tg C TGA

GAM1889 CGTCTCTCCGGAGAGCGGCT 1822 CTCCGGAGAG 4892 CTct g a ------ C
TGGTGCGGAGCTCCCGGGAG CGGCTTGGTG CGT cc gag gcggcttgg tgcggaGCTC C
CTCCGCGGAAGACCCAGGCC CGGA ||| || ||| |||||||||| ||||||||||
GCCTCGGGTGTAACG GCA GG CTC CGCCGGACC GCGCCTCGAG G
ATGT G - CAGAAG G

GAM1890 GGCCCGACAGTCTGGTCGCA 1382 ACGCAGCAGC 4452 CA-- C ATT AC G ACT
TTTGCACCTCGGCACTCGGA CAGGCAGACT GGCCCGA GTCTGGT GC TGC CTCG C C
GCGAGACGCAGCAGCCAGGC CGGG ||||||| ||||||| || ||| |||| |
AGACTCGGGCC CCgggct cggaccg cg acg GAGC G /
caga a --- ca - AGG

GAM1891 CGTTACACCCGAGGCGGCCT 1823 CACCCGAGGC 4893 Aca c - ctg cttcc C
GGGTCTTCCGCGGAGCTCCC GGCCTGGGTC CGTT cc gag gcggc ggt GCGGAGCTC C
GGGAGCTCCGCACCAAGCCG TTCC |||| || ||| ||||| ||| |||||||||
CTCTCCGGAGAGACG GCAG GG CTC CGCCG CCA CGCCTCGAG G
AGA C T AA- ----- G

GAM1892 TGGGCATTTTTGATTGCAGA 1375 AGAGAACAAG 4445 T A T--- - T AAAAA
AAAATTCAAA C A
TTTCCAGGTTTTCTGCAAAA GCGGAATACA TTGAT GC GAT TCCAG GT TTCTGC TCT
CTG TATT T
ATCTAAAATTCAAACTGCTA CTGG ||||| || ||| ||||| || |||||| ||| ||| ||||
TTATTAATACAGGTCCCAGA GATTA CG TTA Aggtc ca aaggcg aga GAC ATAA /
GAACAAGGCGGAATACACTG - A CAAT a t gaaca gaCCCTG--- - T
GATAACATTAGCATTAGAAC
CCA
GAM1893 TGTATTACAGTAGAAAGAAA 1376 TACAGTAGAA 4446 TATt ga tactcaa T TG C- TG
G
TACTCAAAGTGTTCAATGTA AGAAATACTC TG acagta aagaaa agTGT CAA TA CTG CG G
CCTGTGCGGGATCGTGCGGC AAAG || |||||| |||||| ||||| ||| || ||| ||
TTGTTTTGTATATTTTTCTT AC TGTCAT TTCTTT TTATA GTT GT GGC GC A
ATACTGTTTTCA TTT- A- ------- T TT TC GT T

GAM1894 ACTGGACTCGGTTTCGCTGT 1390 CTCCCAGAGC 4460 T GCT G TTCAA TGA
AGCTGTGGTTCAACCTGAAC TGCTAGGAAC ACTGGAC CGGTTTC GTAGCT TGG CC A

ATGGCTCCCAGAGCTGCTAG CGGT ||||||| ||||||| |||||| ||| ||
GAACCGGTCCAGT TGACCtg gccaagg cgtcga acc GG /
- at- g ctc-- TAC

GAM1895 TAATTAGTTCTGTAGTAATA 1377 TTAGTTCTGT 4447 t- a t----- t AT C --- A
TCTTTAATAATTGGCTATAC AGTAATATCT TAAttagttc gt gtaa atc ttaaTA TGG TAT AC T
ATCTGTTCAATACTATCTAT TTAA |||||||||| || |||| ||| |||||| ||| ||| ||
TGATGATTTCTTTTTACGGC ATTAATCAAG CG CATT TAG AGTTAT ATC ATA TG C
TTGAACTAATTA TT G TTTCTT T CT - ACT T

GAM1896 TATATGTTAATGTCATAAAA 1383 TATGTTAATG 4453 t aat aaa- t T T-- C TAA
ACTAATTGTTTGTTAGACGA TCATAAAAAC TA atgtt gtcata actaa TG TTGT AGA GATT T
TTTAATCTCAATCTCTTTTA TAAT || ||||| |||||| ||||| || |||| ||| ||||
CAATCATTTGGTGGAATATG AT TACAA TAGTAT TGGTT AC AACA TCT CTAA /
ATCAACATTTA T C-- AAGG T T TTT - CTC

GAM1897 CCCATACGTGATTCGTGATC 1384 AACCTTTCCA 4454 AC TG TC CTTTTTT--- TAG
TTTTTTGGTTTGTAGTATAG CTCTATCATA CCCAT G AT GTGAT GGTTTG T
TAAACCTTTCCACTCTATCA TTGC ||||| | || ||||| ||||||
TATTGCTCGTGGG GGGTG c ta tacta ccaaAT A
CT gt -- tctcaccttt GAT

GAM1898 GATTATACTATGTGGCTATA 1378 TACTATGTGG 4448 A-- t gctata aat TC
ATAAAATTACGTTCTTTACG CTATAATAAA GATT tac atgtg ataa taCGT T
TATTATACTACACACGTTGT ATTA |||| ||| ||||| |||| |||||
AACAAATC CTAA ATG TGCAC TATT ATGCA /
ACA T ACATCA --- TT

GAM1899 TATGAAAGGAATAGTATTTG 1379 TTAAAAATAG 4449 AAA AATA G a - atacgt AAT
TTAAAAATAGAACTGTATAC AACTGTATAC TATG GG GTATTT ttaaa atagaa ctgt atTA A
GTATTAAATACAAATGATCC GTAT |||| || |||||| ||||| |||||| |||| |||
ATTGATAGATTTTATGTTTA ATAC CC TATAAG AATTT TATTTT GATA TAGT C
AAGAATATAACCCATGCATA GTA CAA- A G A GTTACC AAA

GAM1900 ATGCTTAATATCTTTACTAC 1380 TGGCCATGAT 4450 C- TACTACAACC AA TA T
ACA
AACCCGAAAATGTACATTTA CGTATCAATA ATG TTAATATCTT CGA ATG CATT ATTAAA
A
TTAAAACAAGTATTTAATAA AGGT ||| |||||||||| ||| ||| |||| ||||||
TGGCCATGATCGTATCAATA TAC AGTTAtggaa gct tac gtAA TAATTT /
AGGTATTGAAACAT AA taactat--- ag cg - ATG

GAM1901 GAGTTGTTACGTCTGCGTCT 1381 TACGTCTGCG 4451 GT tctgc t aa t

TTGTAAGTTTTCTAAACAGA TCTTTGTAAG GAGTT tacg gtctt gt gttt C
TCAAGGCCTCGTATAAACTC TTTT ||||| |||| ||||| || ||||
CTCAA ATGC CGGAA TA CAAA /
AT TC--- C GA T

GAM1902 GACAGGCCCCGGCTATCGCG 1385 TATCGCGACA 4455 GG G ta------- g -- c
ACATGTCGGCGACCCACGGT TGTCGGCGAC GACA CCCC GC tcgcgacatgtc gc gacc a
CGGGTGGACGTGTCGCGACA CCAC |||| |||| || |||||||||||| || ||||
TGGACGTGCAGGGGGATGTT TTGT GGGG CG AGCGCTGTGCAG TG CTGG /
AG A TGCAGGTAC G GG c

GAM1903 ATACACTATGACCAACATAA 1397 AATGTTGTGG 4467 ATGACCAA-- AG AC
CAAGTAATACAAAATTAAAT TAACAAAAAG ATACACT CATAACA TAAT A
GTTGTGGTAACAAAAAGGTG GTGT ||||||| ||||||| ||||
TAT TAtgtgg gtgttgt ATTA /
aaaaacaatg aa AA

GAM1904 GAGAGTGATTGAGGAAGTGA 1386 TGTTAAGCAG 4456 GAA GAA CA GAAA a aa----
c ga A
AGCTAGAGCAATAGAAAGCT AACTCCTGCT AG GT GCTAGAG ATA GCtgtta gcag ct ctgct
ccT A
GTTAAGCAGAACTCCTGCTG GACC || || ||||||| ||| ||||||| |||| || ||||| |||
ACCTAAATAGGGAAGCAGTA TC CG TGATCTC TAT TGACAAT CGTC GA GACGA
GGA A
GCAGACGCTGCTAACAGTGA AGG AAG -- GAG- - GCAGAC T AG T
GTATCTCTAGTGAAGCGGAC
TCGAGCTCAT
GAM1905 ATTGTTTCATATTATTGCAT 1387 TCAATACCAT 4457 CA TC - A CGCAAT - C--- CCT
TGTTA
GTCCAACAACAACTGACGCA TTCGAAGAGT TG TG CAACAA C ACTGA TAC CTTCGA
GTAT ACGG T
ATTACCTTCGACGTATCCTA ATCA || || |||||| | ||||| ||| |||||| |||| ||||
CGGTGTTATTTAGTCTGTCA AC AC GTTGTT G TGact atg gaagct cata tGTC /
ATACCATTTCGAAGAGTATC -- CT T C ------ a ttac ac- TGATT
AGTCGTTTGTTGTCCACAGT
AAAAGCAAT
GAM1906 TTCCGGAATTAGGGTTGGCT 1398 AGGCAACCCC 4468 -- ACG C C
CTGGGCCAGCGCTTGGGGTT AAGCAAGCTG ATTAGGGTTGGCTCTGGGCCAGC
GCTTGGGGTTG TG CACTAAGACAAGCGG G
GACGTGCCACTAAGACAAGC GCCC |||||||||||||||||||| |||||||||| || ||||||||||||||
GGCGCGCCGCTTGTCTTAGT TAATCCCAACCGAGAcccggtcg cgaaccccaac AC
GTGATTCTGTTCGCC C
GTCAAGGCAACCCCAAGCAA aa gga T G
GCTGGCCCAGAGCCAACCCT
AATTCCGGAA
GAM1907 TGTTCCGCGTGAGAGCCATT 1399 TGTGGCTACA 4469 C GAG---- T AA- CAG AG
CTTAATCCAGTAGAGACGGC TGCAACGCAG TGTTC GCGT AGCCAT CTT TC TAG A

TAAAGAGAGGGGTGTGGCTA GACA |||||| |||| |||||| ||| || |||
CATGCAACGCAGGACA acagg cgca tcggtg GGG AG ATC C
a acgtaca t GAG AA- GG

GAM1908 TGTAATCGTCACGTGAACTC 1400 GGACACTGGA 4470 T C GTGAA AG - C
CAAGGTCGAGCTGACTCGGA GGTGAGTCAC TGTAA CGT AC CTCCA GTC GAG T
CACTGGAGGTGAGTCACGCT GCTT ||||| ||| || ||||| ||| |||
TGCA ACGtt gca tg gaggt cag CTC G
c c agtg- ca g A

GAM1909 AAGGAATCGTATTTATTAAA 1388 AATCGTATTT 4458 a a aat ---------- TA
AATAGAAATGTGTATATTTT ATTAAAAATA AAGGa tcgtattt ttaaa agaaaT GTGTA T
ACACACAAATGATGAATTAA GAAA ||||| |||||||| ||||| |||||| |||||
TAGATTTCTTATTTAAGGAG TTCCT AGTATGAG AATTT TCTTTA CACAT /
TATGATCCTT - G AT- GATAATTAAGTAGTAAACA TT

GAM1910 GCGACCCCAGCCACGCACGA 1401 TTTGCGGGAT 4471 CCAG A CG A - AA
ACAGAGTTTAACGGAAGCGT AAGGTTGT GCGACC CC CGCA AAC GA GTTT C
CGTTTGCGGGATAAGGTTGT |||||| || |||| ||| || ||||
tgttgg gg gcgt ttG CT CGAA /
aata - -- - G GG

GAM1911 TATATCTATTGTAATTTTAC 1389 TATTACTTTT 4459 TATT- TT T--- - A
AAGTTATAGGAATAATCGCT TGATGTA TATATC GTAAT TACAAG TATAG GA T
ATATTTTTTTGTATATTACT |||||| ||||| |||||| ||||| ||
TTTTGATGTA atgtag catta ATGTTT ATATC CT A
ttttt t- TTTT G A

GAM1912 TTTATATATTCATTACAGTA 1391 TAATATAGTT 4461 TT- TT A - GT - CAC
TAAT
AGATGGTGATAAATTAGTTA TATTATTCAT CA AC GTAAGATGG TGATAAATTA TATTA
CAACA AAAAATAT A
TTACAACACACAAAAATATT TTTA || || ||||||||| |||||||||| ||||| ||||| |||||||
AATAATATCATGTTTTTTGT GT TG Cattttact attatttgat ataat GTTGT TTTTTGTA A
TGATAATATAGTTTATTATT TTT TT A t -- A --- CTAT
CATTTTACAGTTTTGTTTTA
TATAAA
GAM1913 GCATTTATCGTCTCAATTAT 1392 TAATAGGAGA 4462 - CG---- AA A AC
AATATTACTAAAGTATAATA AAAAATATAT GCATT TAT TCTC TTAT ATATT T
GGAGAAAAAATATATAATGT AATG ||||| ||| |||| |||| |||||
Tgtaa ata agag gata tATGA /
t taaaaa -- a AA

GAM1914 TGATACATTGATTAATGAAA 1402 TCCAGTAGTT 4472 T - A AAA TTATAAT

GAACTTATAATGCCTCAAAT ACGTGTTTCG TGA ACAT TGATTA TG GAAC G
GTTCCAGTAGTTACGTGTTT ||| |||| |||||| || ||||
CG gct tgtg attgat ac ctTG C
t c g --- TAAACTC

GAM1915 TTTTTACACTATTAAGTTTT 1403 TATTAAGTTT 4473 C -- gtttt ta
ATTGCTACTAACCGTAGTAA TATTGCTACT TTTTTA ACt attaa attgctac a
TTTTATTAATGCAGTATAAA AACC |||||| ||| ||||| ||||||||
AA AAAAAT TGA TAATT TAATGATG /
A CG ATTT- cc

GAM1916 GGTTCACAATGTTAGTGATG 1393 TGGTAAGCAG 4463 TGA - GAAAGATG G --- TC ---- ----- T
GGGCGCTGAAAGATGCGTAG AAATCCAAGG TGGGGC GCT CGTA CTACC CT TGGA GCCACT C
CTACCCTTCTGGAGCCACTT GTAC |||||| ||| |||| ||||| || |||| ||||||
CCTGGTGGTAAGCAGAAATC ACCCTG CGA GCAT GGTGG gg acct tggtGG C
CAAGGGTACGGTGGTACGGT TCG A AAGGTG-- - cat ga aaagacgaa T
GGAAAGCAGTCCCAGCTCTG
CATTGGGAACC
GAM1917 AGTTGAAAGCATTGATGAAA 1394 TTGAAAGCAT 4464 ca t tcctta A
TCCTTAGGCATAGCCGGTAA TGATGAAATC AGttgaaag ttga gaaa GGC T
TTTTCTCGGGACTTTCGACT CTTA ||||||||| |||| |||| |||
TCAGCTTTC GGCT CTTT CCG /
AG - TAATGG A

GAM1918 CATGCGTGAAGAAGATAAGA 1404 TCCTATGTGT 4474 AAGA AGA AT TTT
GGGAATCCACTTTTCAGTAG CTAAAGCATG CATGCGTG AGATA GGGA CCACT C
TGGTCCTATGTGTCTAAAGC CGTG |||||||| ||||| |||| |||||
ATGCGTG gtgcgtac tctgt tcct GGTGA /
gaaa gta -- TGA

GAM1919 GCTTTTTCTATTATGGCATT 1405 TGGCATTTTG 4475 TTTTTCTA g t at- tgtCC
TTGTAATAATGCTCTGTCCA TAATAATGCT GC TTAt gcattt gtaata gctc A
CTATCGAGTCTGTATTATTA CTGT || |||| |||||| |||||| ||||
AGTGTGATAAGTGTGC CG AATA TGTGAA TATTAT TGAG /
TGTG---- G T GTC CTATC

GAM1920 ATTATCATCAATAAAATGTT 1406 TGTGAATAAC 4476 A AA TGtg- a ctctctt-- t
TGTGTGAATAACTCTCTCTT TCTCTCTTGT ATTATC TCAAT AATGTT tgaat act gtt c
GTTTCCAAACTCTCAAAATG TTCC |||||| ||||| |||||| ||||| ||| |||
GTAGTTCGATCCTAATATTA TAGTGG AGTTA TTATAA GCTTG TGG CAA c
AATTGAAGGTGAT A AA TCCTA A TAAAACTCT A

GAM1921 TTCCGGAATTAGGGTTGGCT 1395 TTAGTGGCAC 4465 TT CCT A C
CTGGGCCAGCTTGCTTGGGG GTCAACCCCA ATTAGGGTTGGCTCTGGGCCAGC
GCTTGGGGTTG TG CACTAAGACAAGCGG G
TTGCCTTGACACTAAGACAA AGCG |||||||||||||||||||||| |||||||||| || |||||||||||||
GCGGCGCGCCGCTTGTCTTA TAATCCCAACCGAGACCCGGTCg cgaaccccaac ac
gtgattCTGTTCGCC C
GTGGCACGTCAACCCCAAGC -- tgc g G
GCTGGCCCAGAGCCAACCCT
AATTCCGGAA
GAM1922 TTCCCGCCTTATGCAAATGG 1396 AGCCATTTTA 4466 T AAATGG ag g t ct
aATTTT
GCAGCCATTTTAAGTGTTTC AGTGTTTCAC TTCCCGCCT ATGC GC ccattttaa tgtt ca at A
ACTATAATTTTATTGGTCAG TATA ||||||||| |||| || ||||||||| |||| || ||
TTTTGTAACGGTTAAAATGG AGGGGCGGA TGCG CG GGTAAAATT GCAA GT TG
T
GCGGAGCGTAGGCGGGGA - AGG--- -- G T TT ACTGGT

GAM1923 GATCTTCTGCTCTATTCCAA 1407 AACACTGTGA 4477 C C A AA A----- ACC
CATCAGTCACAAGGCACCGA CTGATGGGGG GATCTT TG TCT TTCC CATCAGTCACA GGC
G
GCGCCGAACACTGTGACTGA AGAA |||||| || ||| |||| |||||||||| |||
TGGGGGAGAAGACCACAGGA CTAGGA AC AGa gagg gtagtcagtgt CCG /
TC C C a gg cacaaG CGA

GAM1924 TATCAAGATGTGTATGTTTG 1413 CAGCACAAAT 4483 - ---------- AAAA G
TGAAAATTGTGGAGACATAG CAAGGGTATT TATC AAGATGTGTAT GTTTGTG TTGTG A
CAGCACAAATCAAGGGTATT AATA |||| |||||||||| ||||||| |||||
AATACATGTCTTAGATG GTAG TTCTGTACata taaacac GATAC G
A attatgggaac gac- A

GAM1925 CCTAATTTATTAAGATCAGA 1408 TAAAATCTAT 4478 TT GATCA A AC T
TGGATTATAACATGTTTCTG TACAATTTTT CCTAATTTA AA GATGGATT TA ATGTT C
AATATCTAAAATCTATTACA AAAT ||||||||| || |||||||| || |||||
ATTTTTAAATTAGG GGATtaaat tt ttatctaa at TATAA T
tt aaca- a C- G

GAM1926 ATTTATATATATTTCTCTTT 1414 TATATATTTC 4484 tatat t ------ t CC TATT
CTATATAATATCCTCTATTT TCTTTCTATA ATTTA atttc cttt ctata aatAT TC T
TTTTCGAAAATATTTATAGC TAAT ||||| ||||| |||| ||||| ||||| ||
AACATAAGGTGGAATTTTAA TAAAT TAAGG GGAA GATAT TTATA AG T
AT TT--- T TACAAC - AA CTTT

GAM1927 GCCCCGAGTCGCGTGGATGA 1415 TGAGCAACGC 4485 C G -- At aac- t c a
GCAACGCTAAACAACAACCG TAAACAACAA GC CCGAGTC CG TGG gagc gc aaa aac a
TTTTTTCGCTACCGCTCCCC CCGT || ||||||| || ||| |||| || ||| |||

CAGCCGGGGCTCGGAGC CG GGCTCGG GC ACC CTCG CG TTT Ttg c
A G CG CC CCAT C T c

GAM1928 ACCACCCAAAACGAGTAACC 1416 TGGCTTCGTT 4486 CCCA TAA TAAAAACATCGTTG
CA
AATAAAAACATCGTTGACGG TATATGGT ACCA AAACGAG CCAA ACGG C
CACTCTCTGTAGTTTGGCTT |||| ||||||| |||| ||||
CGTTTATATGGT tggt tttgctt ggtT TGTC T
ata- c-- TGA---------- TC

GAM1929 TACATTATAATATAACTAAC 1417 TTAAAACTAA 4487 A TAACT-- A ATG
TGTTTAAACAATGATGGTGT ACTTGTTACA TACATTATAAT TAAC GTTT AACA A
TAAAACTAAACTTGTTACAT TTGT |||||||||| |||| |||| ||||
TGTGATGTA ATGTAGtgtta attg caaa ttGT /
c ttcaaat a GGT

GAM1930 TTATGTGGGGGATGTTCTTG 1409 TAACGCGAGG 4479 T C- TG GGC ATT
TTTC G AC
GGGATGCTTTGCGGGCCAGG GTTCCTTAAT GGGGGATGTT TTGGGGA CTTTGCG CAGGCG
TGGA GC GGTT T
CGATTTGGATTTCGCGGGTT AAAT |||||||||| ||||||| ||||||| |||||| |||| || ||||
ACTGGGACTGGTATTTCCGT TTTTCTGtaa aattcct ggagcgc GTTTGT GCCT TG TCAG
/
GTTTGTAACGCGAGGGTTCC - at tg aat --- TTA- G GG
TTAATAAATGTCTTTTCGTA
A
GAM1931 ACAGTAGAAAAAAATACACA 1410 AAGCGTACAA 4480 - A cgt aatg c
AAGCGTACAATGTACGTGTT TGTACGTGTT ACAGTA GAAAA AATACACAaag ac tacgtgtt a
CAGGAGCATGTGGTTTATTT CAGG |||||| ||||| |||||||||| || ||||||||
TGTGTGTTCTTTTTATATTG TGTTAT TTTTT TTGTGTGTTTT TG GTGTACGA g
T A C ATT ---- g

GAM1932 GATCAGAGGAACCGGATCTT 1418 TCTTCTGGTT 4488 AA TT AATC T
ATAATCGGAGCTCTTTCGAG TGGTTTGGAC GATCAGAGG CCGGATC AT GGAGCTCT T
AGCTCTTCTGGTTTGGTTTG CTCT ||||||||| ||||||| || ||||||||
GACCTCTGGTC CTGGtctcc ggtttgg tg tctCGAGA C
a- tt gtct G

GAM1933 GATCTTCTGCTCTATCTCAA 1411 TAGCTGGTGG 4481 C C A A TA----- ACA
CATCAGCTACTAGGCACAGA TGAGGAAGAA GATCTT TG TCT TCTCA CATCAGCTAC GGC
G
GCGCCGAAGTATGTAGCTGG CACA |||||| || ||| ||||| |||||||||| |||
TGGTGAGGAAGAACACAGGA CTAGGa ac aga ggagt gtggtcgatG CCG /
TC c a a g TATGAAG CGA

GAM1934 CCATTGCCGAAGGCACAACC 1419 AGCGCAATGC 4489 C - ------ - GC AGA- CC - G-
- CA
CGCCGCCGACGCAGAGCAGA GAGCCGCCAG AAC CCGCC GCC GAC AGAGC GCG GC
CGCA GCG TCGT A
GCGCCGCCGCAGGCGTCGTC AGCT ||| ||||| ||| ||| ||||| ||| || |||| ||| ||||
AAGCAACGAGCGCAATGCGA TTG GGCGG TGG CTG TCtcg cgc cg gcgt cgc aGCA
G
GCCGCCAGAGCTCTAGTCAG T C ATCGAC A A- agac -- a aa g AC
GTCAGCTAGGCGGCGTTTAG
CCAGGCGAGGG
GAM1935 AATTGCATCAACCACCCTGC 1412 TGTGTTATCT 4482 CAAC CCCT - TGA- TCAAAA
GCCCTAGTGTGACCTCAAAA GATGTGCGAT AATTGCAT CA GCGC CCTAGTG CC A
AAGAGCCTGGAACCTACTGG T |||||||| || |||| ||||||| ||
GTGTGTTATCTGATGTGCGA ttagcgtg gt tgtg GGGTCAT GG A
TT ta-- ctat t CCAA TCCGAG

GAM1936 AAGTGTCATTTGACCCTGAA 1420 TCATTGGTCA 4490 G T TT CTG AATAAA
TGACGAATAAAATAAAAGTG TCTGTCAGTT AA TG CA TGACC AATGACG A
TCATTGGTCATCTGTCAGTT || || || ||||| |||||||
tt ac gt actgg ttactGT /
g t ct --- GAAAAT

GAM1937 GAATATTATTATTGAAATTA 1421 TCTAATGTAG 4491 TT GAA T CC- CAAT TCA
TGTGAGCCACGTAGCAATCA ATAATTTTGT GAATA ATTATT ATTA GTGAG ACGTAG CAAG
T
AGTCATGTTTTTGTCACTAC TT ||||| |||||| |||| ||||| |||||| ||||
GTTTACTCATCTAATGTAGA tttgt taatag taat tACTC TGCATC GTTT /
TAATTTTGTTT tt atg c ATT ACT- TTG

GAM1938 AACAACTTATAACACGATGT 1427 TTAGTGTAAC 4497 A A CAC-- CCG AA
TACCCGAAGAAACCATTTTA ATTTAAGATT AAC ACTT TAA GATGTTAC AAGA C
GTGTAACATTTAAGATTAGA AGAA ||| |||| ||| |||||||| ||||
AGTAGTT TTG TGaa att ttacaatg ttTT /
A g agaat tga AC

GAM1939 GTCTTCGTTGAAAACTATGC 1422 TTTGCATATA 4492 T- T AA CA TAT TTTT
CGTTAAGTG- A
ATTTATATTGTTTTTTAACC CATATGCGGT TCG TG AACTATG TTTA TGTT AACCGC
GCGAAAG T
GCCGTTAAGTGGCGAAAGAT TTTA ||| || ||||||| |||| |||| |||||| |||||||
ACTTTTTGCATATACATATG AGC AT TTGATAC AGGT GCAa ttggcg cgtttTT A
CGGTTTTAACGTTTTGGACA TT T AC -- TTT tt-- tatacatata C
TAGTTCATATCGATTAAC

GAM1940 TTGTATTTTTCAAGACGTAT 2591 TTTGATGCGT 5661 T CAAG-- TTT TT TTTC

TTTTTGTTTTATTTCTTCTA ATTCAAAAAA TTG ATTTTT ACGTATT TGT TA T
TTGTCATATTTGATGCGTAT ATCA ||| |||||| ||||||| ||| ||
TCAAAAAAATCAA Aac taaaaa tgcgtag ATA GT T
- aactta ttt CT TATC

GAM1941 GCCACAGAACCGCACTGTGT 1423 TGACAAGCAA 4493 -- C CA TGTTCA T CAG G
T- AT
TCAGGTGTATACAGGCTGGT ATGTATTCCC GCCACA GAA CG CTG GG GTATA GCT
GTCAGT TGCTGC T
CAGTTTGCTGCATTGGGCAG CAGG |||||| ||| || ||| || ||||| ||| |||||| ||||||
CGCCGCTGACAAGCAAATGT CGGTGT CTT GC gac cc tatgt cga cagtCG GCGACG /
ATTCCCCAGGACGATTCATT TA A Ag c----- t aaa a CC GG
GTGGC

GAM1942 ATTAAATCATTAATTTCTTT 1424 TCATTAATTT 4494 tc tttc atC TG
ATTTGATAATCGTTTGACTG CTTTATTTGA ATTAAA attaa tttatttgata GTT A
GCATATCAAATAAATTTTTT TAAT |||||| ||||| |||||||||| |||
AATCCTTTAGT TGATTT TAATT AAATAAACTAT CGG /
CC TTTT A-- TC

GAM1943 TATTTTAGCTATATCTTTTC 2592 TAAAAGGTGA 5662 TT TA- TC T ATA TCACC
CTTTATAATATACTTCACCA ATTTGATTGT TAT TAGC TA TTT CCTTT ATATACT A
ATAGTAGTATATAAAAGGTG TATT ||| |||| || ||| ||||| |||||||
AATTTGATTGTTATTATA ATA attg gt aag ggaaa tATATGA /
tt tta tt t a-- TGATA

GAM1944 AGATACATACGTTCGCTATG 1425 TTGGTTGAGC 4495 TAA A --- - T
GACCAAGTGGTACCGGTTGG GCAACCAACC
GTTCGCTATGGACCAAGTGGTACCGGTTGGTTGC GCTCGA CAA GAC GGC A
TTGCTAAGCTCGAACAAGAC GGTA |||||||||||||||||||||||||||||||||| |||||| ||| ||| |||
GGCTAAGCCGGTCCGGTTGG CAAGCGATACCTGGTTCACCatggccaaccaacg cgagtt gtt
CTG CCG /
TTGAGCGCAACCAACCGGTA --- g GGC G A
CCACTTGGTCCATAGCGAAC
GTATGTATCT
GAM1945 TAATATGGTAGGTTAACTGT 2593 TGGTAGGTTA 5663 ggta- gt aaaaa-- TAG
AAAAAATAATAGAACTTTTG ACTGTAAAAA TAATAt g taactgta taa A
GAATAAATATAGTTAGTTGG ATAA |||||| | |||||||| |||
TTAATGTTA ATTGTA T ATTGATAT GTT A
ATTGG TG AAATAAG TTC

GAM1946 TATTGCTTTATTACTTCATT 1426 TAAAAAAGTA 4496 T- T CAT TAA
TTTATTATAAATAACTGATA CTACCAGCGA TATTGCT TA TACTT TTTTATTA A
AAAAAGTACTACCAGCGATA TA ||||||| || ||||| ||||||||
atagcga at atgaa aaaatAGT T
cc c --- CAA

GAM1947 TATAATAATATACAATAATC 2596 TAATATACAA 5666 ta- aataat- ttc GTA
TTTTCTGTGTGTAAGATAAC TAATCTTTTC TATAA atatac ctt tgtgT A
GCGTTTAAGTATATAAGTAT TGTG ||||| |||||| ||| |||||
ATAGTTTATA ATATT TATATG GAA GCGCA G
TGA AATATAT TTT ATA

GAM1948 TTAGCACCATATCCAAAATA 2594 TGTACATTTA 5664 CACCATATCCAAAAT ac--- aaa
ttAA T
ATTGTACATTTAAATATAAA AATATAAAAA TTAG AATtgt atttaaatat aatt GTTTT T
AATTTTAAGTTTTTTAAAAA TTTT |||| |||||| |||||||||| |||| |||||
CCAATAATTCATGTTTAAAT AATC TTAACA TAAATTTGTA TTAA CAAAA /
ATTAAACAATTTCTTTTCTT TTTTTTCTTTTCT-- AATTA C-- TAAC A
TTTTCTAA

GAM1949 AAAATAATTGTACATTTAAA 2597 TGTACATTTA 5667 AT ac--- aaa ttAA T
TATAAAAATTTTAAGTTTTT AATATAAAAA AAA AATtgt atttaaatat aatt GTTTT T
TAAAAACCAATAATTCATGT TTTT ||| |||||| |||||||||| |||| |||||
TTAAATATTAAACAATTTCT TTT TTAACA TAAATTTGTA TTAA CAAAA /
TT CT AATTA C-- TAAC A

GAM1950 GGGTGGTGTCTGCAGCAAAA 1428 TATTTTGCAT 4498 T TCT - GAG-- AC C
GAGGAACTTGCCCAGGCAGT GCCACCTCCC GGG GGTG GCA GCAAAA GA TTGC C
CAGTTATTTTGCATGCCACC ||| |||| ||| |||||| || ||||
TCCC ccc ccac cgt cgtttt CT GACG A
t --- a atTGA -- G

GAM1951 TGGGGGCTTCATGATCCCAC 1429 TTGAGATTCT 4499 TTCAT A -- CCGAT TGATGA --
----- CT
CGCCTTTCCCGATGATGATG GATGAGAGGC GATCCC CC GCCTTTC GA CAACCG
CGGCTGT G
ACAACCGCGGCTGTCTGAAG TTGG |||||| || ||||||| || |||||| |||||||
CGGCTGACGAAATCGGTTGA CTGGGG gg cggagag ct gttGGC GTCGGCG /
GATTCTGATGAGAGGCTTGG TTT-- G tt tagt- taga-- TAAAGCA AA
GGGGGTCTTTGCCCTCA

GAM1952 GAGTAAGTCTGAAGCCTTTA 1430 ATAACCCACC 4500 AG AA CTTTAT-- TATAAG CCC
TGGTGTATAAGCGGCCCGAA TTTACCCTGC GAGTA TCTG GC GGTG CGG G
TTTTGATAACCCACCTTTAC GACG ||||| |||| || |||| |||
CCTGCGACGGAGTGCTC CTCGT AGgc cg ccac GTT A
G- ag tcccattt ccaata TTA

GAM1953 TCGAGCTGTTCATTTGAAGA 1431 GAGCTGTTCA 4501 ga t- tt g tgaGA T
CACTGAGAGTGGTTAACCAT TTTGAAGACA TC gctgt cat gaa acac GTGG T
GTGTGTGTTCCTATGTTGCA CTGA || ||||| ||| ||| |||| ||||

GTAAGA AG TGACG GTA CTT TGTG TACC A
AA TT TC G TG--- A

GAM1954 ACGGGTCATCCGACAAACAT 1432 ATGATGTACC 4502 - TCCGACAAACAT ACTT- G G
GATGCACTTCGTGGTCAGGC CGCGTCTGAT ACGGG TCA GATGC CGT GTCAG C
AGCTGATGATGTACCCGCGT CCCG ||||| ||| ||||| ||| |||||
CTGATCCCGT Tgccc agt ctgcg gta taGTC A
t ---------- cccat g G

GAM1955 TCTGCTGGTACAAGGAATGG 1433 CGTTGATTTT 4503 C--- AG GGC CC
CCGTTACCGGTTGACGTTGA ATGTACTACC TCTG TGGTACA GAAT CGTTA G
TTTTATGTACTACCTACAGG TACA |||| ||||||| |||| |||||
GGac atcatgt ttta gcAGT /
atcc at gtt TG

GAM1956 GGCCACAGGATGTAGATCGC 1434 AAGCTGCAAT 4504 CA AT GATC ACA GAAAC AA
AGACACTGAAACGCTGAAAC ACCGCCGATG GGCCA GG GTA GCAG CT GCTG A
ACAGCATTAAGCTGCAATAC GCC ||||| || ||| |||| || ||||
CGCCGATGGCC ccggt cc cat cgtc ga CGAC /
ag gc aa-- --- aTTA- AC

GAM1957 ATGGCACGCGCCGCCAGCAA 2595 CGCCAGCAAA 5665 - Cc agt---------- tg CT
ATTTAAGTCCTGGTGGCTCA TTTAAGTCCT ATGGCA CGCG gccagcaaattta cctgg G C
CCTGCCAGGTAAACAAGGTT GGTG |||||| |||| |||||||||||| ||||| |
AAAGTGGGTTTGCTGGCCTT TACCGT GCGT CGGTCGTTTGGGT GGACC C /
GCGTTGCCAT T TC GAAATTGGAACAAAT GT CA

GAM1958 TTAATCATATCATAATTAAG 2598 TATTTAGCAA 5668 C C -- ATTTTTCTTTAT A T
TAATTTTTCTTTATCTAGAA TACAAATTCT TTAAT ATAT ATAA TTAAGTA CTAGA GTAAAT
C
GTAAATTCAATTTATATTTA ATTT ||||| |||| |||| ||||||| ||||| ||||||
GCAATACAAATTCTATTTGA AATTA TATA TATT AGtttat gattt tATTTA /
AATTATCATATTATTAA T C AA cttaaacataac a A

GAM1959 GTGCCCTTCTCGCCTTCATT 2600 AATTGTATGA 5670 C ---- -- CTT-- T T- G
TTCTTCTGCTGTCGAGCAGT GCTGGAGATA GTGC CT TCTC GC CA TTTCT CTGCT T
TAGGAATTGTATGAGCTGGA TAAG |||| || |||| || || ||||| |||||
GATATAAGTGCAC CACG ga agag cg gt aaGGA GACGA C
T atat gt agtat t TT G

GAM1960 TGGGTAAAAGGGTGGAAGGG 2599 TAAGGACCAA 5669 --- GGAAGG G GG- ATTC
A TT
TGGTTGGTTGGTATTCCCTT AAAAACAATA TGGGT AAAAGGGT GT GTT TTGGT CCTT
GAC G

AGACTTGATGTTAAGGACCA AAAT ||||| |||||||| || ||| ||||| |||| |||
AAAAAACAATAAAATCTTTT ATCCA TTTTTCta ta caa aacca ggaa tTG /
TAAAACCTA AAA aaa--- a aaa ---- - TA

GAM1961 TAGCTTGCCTTAAGCAGTCT 2601 AAGCAGTCTT 5671 -- CTT-- agt atat t ATT
TTATATCTTCTGTATATTAT TATATCTTCT TAGCT TGC aagc cttt cttctgta ATT T
TTTAAAGTTTATAGGAGCAA GTAT ||||| ||| |||| |||| |||||||| |||
AGTTCGCTTTACTCGCAATA ATCGA ACG TTCG GAAA GAGGATAT TGA /
GCTA TA CTCAT CTT C--- T AAT

GAM1962 GTGTGACTTGGATTGGAAAT 2602 TGACTTGGAT 5672 G - - -- g AAAAATC
GTGGAGAAAAAATCGGGACC TGGAAATGTG GT tg acttggattg gaa at tggaga G
CATTTCTAGGTTGTTCACAA GAGA || || |||||||||| ||| || ||||||
TCCAAGTACAGAC CA AC TGAACCTAAC CTT TG ATCTTT /
G A A GT G ACCCAGG

GAM1963 GAAAGATCATAACTAATAAC 2608 TTCAAATGTT 5678 CATAACTAA ACA AAT TACTATA
ATTACAAATAATCCTACTAT AATCTTTC GAAAGAT TAACATT AAT CC A
AATCAATACGGTGATTCAAA ||||||| ||||||| ||| ||
TGTTAATCTTTC ctttcta attgtaa ttA GG /
--------- ac- GT- CATAACT

GAM1964 GCCCTTCTAATTAAGAAAAA 2609 TAAGAAAAAA 5679 - AATt-- g a ---- c A - A
ATCGGCGATGAAGATTAAGC TCGGCGATGA GCCCTT CT aa aaa aatc gg gatgaagatTA GC
CG C
CGACAGTGAGCGTAATCTTC AGAT |||||| || || ||| |||| || |||||||||| || ||
ATCTCTCTTAGATTATTTGT TGGGGA GA TT TTT TTAG TC CTACTTCTAAT CG GT A
TTTCCAGAGTAGGGGT T GACCTT G A ATTC T G A G

GAM1965 GCTGCGAGGTGATCCACGTA 2604 TCCACGTAAG 5674 GC GAtc- aagc- agaa t
AGCCCTCAGAACCGTCTCGG CCCTCAGAAC GCT GAGGT cacgt cctc ccg c
AAGGAGGACCCCACGTGCTT CGTC ||| ||||| ||||| |||| |||
TAGCCTCAAAGC CGA CTCCG GTGCA GGAG GGC /
AA ATTTC CCCCA GAA- T

GAM1966 GGATCTTCTGCTCTGCACAA 2605 CGACATAGGT 5675 C C - A A----- ACA
CCAGCCACACGGCACAGTGC GGCTGGTGGT GGATCTT TG TCT GCAC ACCAGCCAC CGGC
G
GCCGACATAGGTGGCTGGTG GCTA ||||||| || ||| |||| ||||||||| ||||
GTGCTAGAACACAGGATCT TCTAGGA AC AGa cgtg tggtcggtg gcCG /
C A t g gataca CGT

GAM1967 TTGTGACGTAGCAATTATCG 2606 AGAGTTTAGT 5676 AG - TC T A- TCG

TATTGTGCATGTGTCGTTCA ATACTAATAT TTGTGACGT CA ATTA GTATTG GC TGTG T
TCACAGAGTTTAGTATACTA GAAG ||||||||| || |||| |||||| || ||||
ATATGAAGCGTCGCGA AGCGCTGCg gt taat tatgat tg aCAC T
aa a ca t ag TAC

GAM1968 GTCAACCAGGGCACCCTCCC 2603 CAGGGCACCC 5673 g c- ccca a gC
CCACCGAGTGCTTTAATGCG TCCCCCACCG GTCAACcagg cacc tcc ccg gt T
GAGAGGAATGGTGGCCTGGT AGTG |||||||||| |||| ||| ||| ||
TGAC CAGTTGGTCC GTGG AGG GGC TA T
G TA AGA- G AT

GAM1969 TTGTTTTTGAACATGTGGCA 2610 TCAGTGCCAC 5680 TT CA AC GCAAT C-
TGAAA TTC
CACGCTGCAATGTACTGCCA AATTTCATTA TTGTT TGAA TGTGGCAC GCT GTA TGCCA
GGTGG T
TGAAAGGTGGTTCTATATCC ACAA ||||| |||| |||||||| ||| ||| ||||| |||||
ACCACTTGGCGTCTGCCGAA aacaa actt acaccgtg tGA CGT GCGGT CCACC A
GTCAGTGCCACAATTTCATT tt ta ac AGC-- CT TCA-- TAT
AACAA

GAM1970 AATAACTGTATTTCTCACTC 2614 TCTTGCTCTT 5684 C - ctta tc-- -- AAT ATTAT
AGT
TTGCTCTTAGTTAGTCATTG AGTTAGTCAT TTTCT ACtct tgct gttag attgtg TCT AATT TAC
A
TGTCTAATAATTATTATTAC TGTG ||||| ||||| |||| ||||| |||||| ||| |||| |||
AGTACAAGGTATTATGAATT AAAGA TGAGA ACGA TAGTC TAACGC AGA TTAA
ATG C
CAAAGATACGCAATAAATCT - T CTA- TAAA AT AAC GTATT GAA
GATATCAGCATAGAGTAGAA
AATTGTTGTT
GAM1971 TCTTCCCCCCCATCACCCCG 2607 TCCCGGTTGA 5677 CA A- TG A A TTAA CATTA-
TT- TGG
CAATTTGCACCCAGCCTTTA TTTTTGGGTG CAT CCCCGC ATT C CCC GCCT CTA
AATTGGG CGAT C
ACTACATTAAATTGGGTTCG GGTG ||| |||||| ||| | ||| |||| ||| ||||||| ||||
ATTGGCAATGTTGTCTCCCG GTG GGGGTG TGG G GGG tggg ggt ttggccc GTTG /
GTTGATTTTTGGGTGGGTGG A- GG GT A g tg-- ttttag tCT TAA
GGAGTGGGTGGGTGGGGAGT
GGGTGGGTGGG
GAM1972 GTTATGAAAATTTTAATATT 2620 TGAAAATTTT 5690 A taatatt - tAC A CTA TTAA
TCTTCATTACAGTATATACC AATATTTCTT GTT tgaaaattt tcttc at AGTAT TAC AATCTA A
TAAATCTATTAAAATATTAG CATT ||| ||||||||| ||||| || ||||| ||| ||||||
ATTGTAGTGATACTAATATA CAA ATTTTTAAA AGAAG TA TCATA GTG TTAGAT /
GAAGATTTTAAATTTTTAGA G TTTT--- A TAA - ATG TATA
AC

GAM1973 TGGCAGAGCCTTGTTTCGTT 2612 TATAACACAA 5682 C - TT TC - --- G T ATC T
GTACATGCTGGGTGAATCGC TCTGGTCTCT TGG AGAG CC GTT GTTGTA CAT GCT GG GA
GC C

TCATGCAAGTCTTGAGCTCT CCA ||| |||| || ||| |||||| ||| ||| || || ||
ATGATATAACACAATCTGGT acc tctc gg taa caatat GTA CGA TT CT CG A
CTCTCCA - t tc ca A TCT G - GAA T

GAM1974 TTCCTGGTTGGTATTGCGCT 2611 TATTGCGCTA 5681 GG tgcg- ac -- ca
ACCGATTCTTCACAGACTGA CCGATTCTTC TTCCT TTGGtat ct cgat tcttca g
AGACTGTCGAGATTGTGTAC ACAG ||||| ||||||| || |||| ||||||
CAAAAAGGAG GAGGA AACCATG GA GCTG AGAAGT /
AA TGTTA -- TC CA

GAM1975 GCGGTTCTTGTTCTCCCTGA 2621 TCCCTGAGCC 5691 TTCT Ctcc c - agacA- AT
GCCACCATCACCTAGACACA ACCATCACCT GCGG TGTT ctgag cac catcacct CAG A
GATAGTCTGAAAAGGAGGTG AGAC |||| |||| ||||| ||| |||||||| |||
ATGCGTGTCTCGGAAAAACA CGCC ACAA GGCTC GTG GTAGTGGA GTC /
CCCGC C--- AAA- T C GGAAAA TG

GAM1976 CAAGTCAATAAAACACTATT 2622 TATTATGTTC 5692 A ------- C gttcaccc-- - cA
ATGTTCACCCTGAATCAATC ACCCTGAATC CAAGTC ATA AAACA tattat tgaat caat C
ACTCTGTTGCATTTATAACA AATC |||||| ||| ||||| |||||| ||||| ||||
AAAAAGTAATAATGTTTATG GTTCAG TAT TTTGT ATAATG ATTTA GTTG T
TAAATATAGACTTG A AAATGTA A AAAAAACAAT C TC

GAM1977 GTTTATACTACACTGCAGGC 2613 TACACTGCAG 5683 a - aggcgtatg - A
GTATGCACAGCGATAAAGGT GCGTATGCAC GTTTATACt ca ctgc cacagcg ATA A
GTATGTTGTGAACTTAAAAG AGCG ||||||||| || |||| ||||||| |||
CAGCTGAGTATAAAC CAAATATGA GT GACG GTGTTGT TGT G
- C AAAATTCAA A G

GAM1978 TAGAAAATTTATTTATTAGC 2615 TTTATTAGCT 5685 ------- ta gcta C---------- CT
TCGTTTAGTGCTAAATCATC CGTTTAGTGC agc tcgtt gt aaTCATCAT AACAA T
ATCAACAACTTCATTGTTTT TAAA ||| ||||| || ||||||||| |||||
CATCTTTTTTCTTTTTTATG TCG AGCAA CA TTAGTAGTA TTGTT /
ATGATTGATAACAACGATAT AAGATAT -- ATAG TTTTTTCTTTTTTCTACTT AC
AGAAGCTAATATTACAGAAG
GTCTA
GAM1979 TCATTAAATTCAGTTTTATA 2616 TCAGTTTTAT 5686 tc tttataatcttt- ttACCTCACA A
ATCTTTTTTTATTACCTCAC AATCTTTTTT TCATTAAAT agt tttta GC T
AGCATTCGCGTATCATTATT TATT ||||||||| ||| ||||| ||
AAAATTTCCAACTCATTATT AGTAATTTA TTA AAAAT CG T
ATTTAATGA -- TTACTCAACCTTT TATTACTATG C

GAM1980 GCTCGCCCTTTTTTGTAACA 2617 GCCCTTTTTT 5687 g tg acagatggcgaT A
GATGGCGATGGAACAGAGGT GTAACAGATG GCTC ccctttt ta GGAAC G
TCCTATGTGGGGGGGGGGGG GCGA |||| |||||||| || |||||

GC CGGG GGGGGGGG GT CCTTG A
G GT AT---------- G

GAM1981 CGAACTGCTTCCATTTTTTC 2618 TTAGATGCCG 5688 T- T T GC GT AT
CCTTACGGTGCCTGACGTCG TCAGGGAAAG CGAAC GCTTCCATTTTT CCCT ACGGT CTGAC
CGT T
TATTTTAACGGTTAGATGCC ATGG ||||| |||||||||||| |||| ||||| ||||| |||
GTCAGGGAAAGATGGGAGTT GTTTG TGAGggtagaaa ggga tgccg gattG GCA T
TGTTTG TT - c ta -- AT

GAM1982 CCGGCAAGCACTCGTCCGAA 2252 AAGCACTCGT 5322 aagc - tc gacac A-- CC
ATTC
GGAGGACACGCCACGCGACC CCGAAGGAGG CCGGC act cg cgaaggag GCC CGCGA CG
C
CGATTCCCAGCCGCTTCGCG ACAC ||||| ||| || |||||||| ||| ||||| ||
CCCGGCTACTTCTTCGCCTG GGCCG TGA GT GCTTCTTC CGG GCGCT GC /
CAGTCCGCCGG CC-- C CC AT--- CCC TC CGAC

GAM1983 CTCCCATCTTTCCCTGACGG 2253 TCTTTCCCTG 5323 C c- g ca a -- TA
CATCTAACCGTTAAAATACG ACGGCATCTA CT CCAt tttccct acgg tct ac cgT A
ACGTCAGGCACCGTAAGGGA ACCG || |||| ||||||| |||| ||| || |||
AAAAATGGAAG GA GGTA AAAGGGA TGCC GGA TG GCA A
A AA A AC C CA TA

GAM1984 CGCGGGGGAAGGTCGGTCCA 2254 TTGGAACAGA 5324 - T CCATTTC-- C A C C
TTTCGCTCCTATTCCGCACC AGCATTACAC CGCGGGGGAA GG CGGT GCT CT TTCCG AC
T
TTCGTTTGGAACAGAAGCAT ACAC |||||||||| || |||| ||| || ||||| ||
TACACACACCGCCATTTCCC GCGCCCCTTT CC GCca cga ga aaggt TG T
CGCG A - cacacatta a c K C

GAM1985 GGGCTGTGCTAGCACGCGCC 2255 TAGCACGCGC 5325 ------ Cta cacga gtc
ACGAGGAGGTCACGGCTCCG CACGAGGAGG GGGC TGTG gcacgcgc ggag a
CGCGTGCAAACGCAGACAAC TCAC |||| |||| |||||||| ||||
GCCC CCCG ACGC CGTGCGCG CCTC /
CAACAG AAA ----- GGc

GAM1986 GGTTGGTACTCCCGCGCGCC 2623 GCGCCGCGCG 5693 GTA CC C G GAGAAG
AA C
GGGGGAGAAGTGCGCGCGCG CGCAACCGCG GGTTG CTC GCG GCCG GG
TGCGCGCGCGGC CAA G
GCAACAACGCCTTGCGCCGC GCCG ||||| ||| ||| |||| || |||||||||||| |||
GCGCGCAACCGCGGCCGTCG CCAAC GAG Tgc cggc cc acgcgcgcgccg gTT C
AGAACAACC AA- C- - g a----- c- C

GAM1987 TGCAATAAAAATTAAATTAT 2619 TAAATTATGG 5689 AATAAAAA at g aacctt AA
GGAATAACCTTAATAGTAAA AATAACCTTA TGC Ttaa tat gaat aatagTA T
TAGATATTATTTTTTTAGTT ATAG ||| |||| ||| |||| |||||||
CAGTATATTAGGTCTCGCA ACG GATT ATG CTTG TTATTAT A
CTCTG--- AT A ATTTTT AG

GAM1988 CGTAAATGTGAAAAAGTATG 2624 AATGTGAAAA 5694 aa aaaaa g ACTC TT C
ACC
GGGAAAGAACTCATCTTAAC AGTATGGGGA CGTA tgtg gtatggg aaaga ATC AAC TCCC G
CTCCCACCGTTAGGGAGTTT AAGA |||| |||| ||||||| ||||| ||| ||| ||||
TGATTATCTTTTCTATACCA GCGT ATAC CATATCT TTTCT TAG TTG AGGG /
TAGATGCG AG ----- - AT-- TT - ATT

GAM1989 TTTTCCAATTTCGTAAGTCG 2256 GATGATAGGA 5326 A-- AA---------- CAAAAACAT
AA
TCTACAAAAACATATACAAA TTATTATGTG TTTTCCA TTTCGT GTCGTCTA ATAC
A
CTGTATCTAGATGATAGGAT GCGG ||||||| |||||| |||||||| ||||
TATTATGTGGCGGAACAATG AAAAGGT AAggcg tagtagAT TATG /
GAAAA AAC gtgtattattagga C-------- TC

GAM1990 GTATTGCCACCGACGACGAC 2257 ACGGCAGTCC 5327 ---------- g
GACGGCAGTCCCTGCCGGCG CTGCCGGCGA GTATTGCCACCGACGACGACGacggcagtccct
gccggc a
AAGCCGGCCGCCGCGAAGCG AGCC |||||||||||||||||||||||||||||||| ||||||
GCAAGGGACTGCCGTCGTCG CATAACGGTGGCTGCTGCTGCTGCCGTCAGGGA
CGGccg /
TCGTCGGTGGCAATAC ACGGCGAAGCGCCGC a

GAM1991 GACTGAATTTTCGCAGTCTC 2265 ATTACAGTGA 5335 AGTCTCTTTTC TTCCC T
CC
TTTTCCCTCTTCCCTTGTTA GGTTACACAG GACTGAATTTTCGC CCTC TTGT ATTC A
TTCCCATAGAATTACAGTGA GTGG |||||||||||||| |||| |||| ||||
GGTTACACAGGTGGAGATTC TTGACTTAGAggtg ggag gaca taAG /
AGTT gacacatt--- t---- t AT

GAM1992 ACGACGGCTACAGCTCGCGG 2258 GAAGATGAGC 5328 A A C-- GAA- - GCC AG
TCGAAGCCGTCGCCCGACAG GCGAGACCGT ACG CGGCTAC GCT GCGGTC GC CGTC
CGAC A
ATAGTCGAAGATGAGCGCGA ACAG ||| ||||||| ||| |||||| || |||| ||||
GACCGTACAGGTAGTAGTCG TGC GCTGATG TGg tgccag cg gtag gCTG /
ACGT A A aca agcg a aa- AT

GAM1993 TTGGATCCCAATGTCTTGTT 2259 ACTGCAGTCT 5329 - TC TTC AAT TA TTATA T
A- -- A
CAGAATGCTGCTAGATGCTT CGTGCTGCAT CCAA TG TTG AG GCTGC GATGC AGC
CGAGA GCAGT AC A
ATAAGCTCGAGAAGCAGTAC CGCA |||| || ||| || ||||| ||||| ||| ||||| ||||| ||
AAGAGTAAACTGCAGTCTCG GGTT AC AAT TC TGacg ctacg tcg gctct cgtca TG G
TGCTGCATCGCAGTCTACTA C C- TTA ATC -- ----- t ga AA A
TTTAACCACTTGGGGGCCAA

GAM1994 GATGAACTGTCCTCAACAAG 2260 CTTGTTGTTG 5330 A GTCCT TGAAAA T
TATGAAAAGCAATTATTTGT TAAGATTATT GATGA CT CAACAAGTA GCAA T
GAAGTTACTTGTTGTTGTAA ||||| || ||||||||| ||||
GATTATT ttatt ga gttgttcAT TGTT A
a atgtt TGAAG- T

GAM1995 CCTGCAGGCATTTTGTGAAA 2261 TTGATGAGAG 5331 T GCA AAGG ATGAAAGCTA
GAAA T
AGGGTAAAGTATGAAAGCTA CCTTAAAATG CC GCAG TTTTGTGAA GTAAAGT CTCTCA
AGTAC T
CTCTCAGAAAAGTACTTATG ACTT || |||| ||||||||| ||||||| |||||| |||||
TATTGATGAGAGCCTTAAAA GG CGTC AAAACACTT TATttca gagagt ttATG A
TGACTTTATATTCACAAAAC T --- A--- gtaaaattcc ag-- T
TGCTGG

GAM1996 CATTTGTAATAGAAAATTTA 2262 TAGAAAATTT 5332 GTA - a a gaaa
AGAGAAGAAAAAGAATTCCT AAGAGAAGAA CATTT Ata gaaaattt ag gaa a
AAAATTTTTATATGAAAGTG AAAG ||||| ||| |||||||| || |||
GTGAA TAT TTTTTAAA TC CTT /
AG- A A - AAga

GAM1997 TAGATTATAAACATAGACCT 2266 TATAAACATA 5336 -- ---- ctt at
TGCCTATTGAAAGGTCTAGT GACCTTGCCT TAGATt ata aacatagac gcct t
CTATGTTGAACTATTAGATC ATTG |||||| ||| ||||||||| ||||
TA ATCTAG TAT TTGTATCTG TGGA g
AT CAAG ATC AA

GAM1998 CGGGAAACTGCGTTTTGGAT 2263 TGCGTTTTGG 5333 AAACt- taa- a G
AATGTGCAGGACGTATGTTC ATAATGTGCA CGGG gcgttttgga tgtgc ggac T
GTACGGTCCTCCAGAACGCC GGAC |||| |||||||||| ||||| ||||
GCGTACCCG GCCC CGCAAGACCT GCATG CTTG A
ATGCGC CCTG - T

GAM1999 TATAACGTCTAACTTACAAC 2264 TAACGTCTAA 5334 ta act cg cA AA
ACGGTCATAATAGAATCCCT CTTACAACAC TA acgtcta tacaaca gt TAATAG T
ATTAACATGTTGTATATAGA GGTC || ||||||| ||||||| || ||||||

TGTCGTA AT TGTAGAT ATGTTGT CA ATTATC /
GC AT- A- -- CC

GAM2000 ATGATTTAGTTACTTTAATA 2267 TTCAGGTATT 5337 A CTTT A GTT AAATTGATT
ACCGTTAGACATAAAATTGA TAACGAATCA ATGATTT GTTA AATA CC AGACATA C
TTCTATGAAAACTGTGTTTC T ||||||| |||| |||| || |||||||
AGGTATTTAACGAATCAT tactaag caat ttat gg ttTGTGT /
- ---- - ac- CAAAAGTAT

GAM2001 CTAATATAGTTAATAGTGTA 2268 TAGTGTACTA 5338 a c caaaca TAAAAA----- C--
CCCAA
CTACAAACAGGCGATGGTAA CAAACAGGCG TAAt gtgta ta ggcgatgg GACT TTCGTCTT
A
AAAGACTCTTCGTCTTCCCA ATGG |||| ||||| || |||||||| |||| ||||||||
AAATGTTAGAGACGGAAATA ATTA CATAT AT CCGCTATC TTGA AGGCAGAG
A
GTTGTCAAGATTCTCTATCG C A C----- TCTTAGAACTG TAA ATTGT
CCCTAATATACCATTAAAAA
TTGTTAG
GAM2002 GTTCTTAAATAGCAGCCAGG 2269 TCTGTCAGTT 5339 --- ----- CT- --- T TCCTCT-
C G
GCCTTACCGACCAGTTTTCG GGTGTAAGCC GCAGC CAGGGC TACCGAC CAG
TTTCGTG TGG GCG C
TGTCCTCTTGGCGCGGCTCT CTGC ||||| |||||| ||||||| ||| ||||||| ||| |||
GCCTATATATGCCACGGAAT TGTCG gtcccg gtggttg gtc AAGGCAC ATC CGT T
CTGTCAGTTGGTGTAAGCCC TAG CTACc aat act t CGTATAT - C
TGCCATCGCTGTGATATTTT
TATTGCGTTGC
GAM2003 TCTGCTATTCGCCTACCTAG 2270 GGGAAACCTC 5340 GCT- - - - a tc aa-- cc
GGAAACCTCGAAAAAAATCC GAAAAAAATC TCT ATTCGCCTA C CT Aggg aacc gaa aaat t
TAAATTTAACGTTTTTGGTT CTAA ||| ||||||||| | || |||| |||| ||| ||||
GCCCTGAGTGTTGGGCGAAT AGA TAAGCGGGT G GA TCCC TTGG TTT TTTA /
TGAAAGA AAGT T T G G TT GCAA aa

GAM2004 GGAATTTTTCTTGGTTTTCG 2271 TTTTTCTTGG 5341 ttt gg tTT A AT
GGTGTGATTTTATATTCATG TTTTCGGGTG GGAA ttctt ttttcgggtgtga TAT TTC G
TAGAAAGTGTTTCACACCTG TGAT |||| ||||| |||||||||||| ||| |||
AGGAGAAGAATCTTTCC CCTT AAGAA AGGAGTCCACACT GTG AAG /
TCT G- TT- A AT

GAM2005 TCGAATTCAAACGTGCGACA 2272 TTCATGTTTC 5342 C G TG TATTGGTTC
GGAAC
GTGGCTATTGGTTCGGGCGA TGTGCACATT TCGAATTCAAA GTGC ACAG GC
GGGCGACC C
CCGGAACCCGTTAGGTCGTT TGAA |||||||||| |||| |||| || ||||||||
CATGTTTCTGTGCACATTTG AGCTTaagttt cacg tgtc tg cttGCTGG /

AATTCGA a - tt ta------- ATTGC

GAM2006 ACGCGCATGTTGAAGTCGAG 2273 TTGAAGTCGA 5343 C AT- tga cg- tc g
GTGTCCACACAAGTAGTTGT GGTGTCCACA ACG GC Gt agt aggtg cacacaa T
GTGTACCTAACGCTCTTGCC CAAG ||| || || ||| ||||| |||||||
CAGCACGT TGC CG CG TCG TCCAT GTGTGTT A
A ACC TTC CAA -- G

GAM2007 ATCGGCCCACTCTTGCATTT 2274 TGAAGGAGGA 5344 G CA--- GCA G A
CTTCGGGGACGTTTGTGAAG GAGAGGATAC ATC GCC CTCTT TTTCTTCG GG C
GAGGAGAGAGGATACGGCGG GGCG ||| ||| ||||| |||||||| ||
AT TAG cgg gagag gaggaagt TT G
g catag ag- G T

GAM2008 GTTCCCTTCTATGATAATGG 2278 TATGATAATG 5348 TTCtat aat ttt ttatg-- GTC ACA
ATTTGGCCTTATGGCTGTCG GATTTGGCCT GTTCCC gat gga ggcc GCT GGCA G
GCAACAGGCCTGCCAAAGTA TATG |||||| ||| ||| |||| ||| ||||
ATCATCGGCCCACTCTTGCA CAGGGG TTA TCT CCGG TGA CCGT /
TTTCTTCGGGGAC CTTCT- CGT CAC CTACTAA AA- CCG

GAM2009 GGATAAATAATCGTATTATT 2275 AATCGTATTA 5345 gt- t aat g aaT G GGG A
GGCA CT
GTAATAGGGAAATTTAGGGG TTGTAATAGG aatc atta tgt ag ga TTAGG GAG TTTCA TGGTG
GAG A
AGGGGTTTCAATGGTGGGCA GAAA |||| |||| ||| || || ||||| ||| ||||| ||||| |||
GAGCTAAACTTAACACCAAT TTAG TAAT ACA TC CT AATCC TTC AAGGT ACCAC
TTC /
GGAAAGCTTGCCTAATCGCT ATT T C-- G --- G GA- A AA-- AA
CACATTAATTTAGATTTTCG
ACTTGTGTCC
GAM2010 ACGCGACAACTTCGAGAACC 2276 CGAGATAGAC 5346 C AA- AACC G CCG- GA
TCGGGGTCTCCGCGGCCGAC CGCGACTCGG ACG GAC CTTCGAG TCG GGTCT CGGCC
C
CTGGCCGAGATAGACCGCGA AGGT ||| ||| ||||||| ||| ||||| |||||
CTCGGAGGTCGTCCGT TGC CTG gaggctc agc ccaga gcCGG /
- Ctg ---- g taga TC

GAM2011 GCGCACCGCCGCCGAGATCG 2279 TCAGAAGTCC 5349 C - C GAT G aa------- a c g
g
AGTGTCAGAAGTCCAAGCGC AAGCGCGTCG GCG AC CGCCG CGA CGAGT tcag gtcca g
gc tc t
GTCGTGGAGGCCCTGGACGT TGGA ||| || ||||| ||| ||||| |||| ||||| | || ||
CGTCATCCTGAAGCTCGTCG CGC TG GCGGC GCT GCTCG AGTC CAGGT C CG
ag /
TCGGCGAGTTCGC T A T --- A CTACTGCTG - C G g

GAM2012 CAAGATGAATCGGTGAAGTC 2277 GTGAAGTCTC 5347 AATC t t tag gcctt- TA
TCCATAGAGTGCCTTATTTG CATAGAGTGC CAAGATG Ggtgaag c cca agt aTTTG C
TACAGCAAGTTTCTAAATTA CTTA ||||||| ||||||| | ||| ||| |||||
CTTGGGTTTTCATCACAACG GTTCTGC CTACTTT G GGT TTA TGAAC /
TCTTG AACA T - TCA AATCTT GA

GAM2013 GGGGCGGGAGGGGGAAGGGG 2280 AGGGGGAGCC 5350 C a- cc cttt- cccgC-- CTC C A
GAGCCGGAGCTTTGGCCCGC GGAGCTTTGG GGGAGGGGGA gggggag ggag gg TCG GGCCGGCC GA T
TCGCTCGGCCGGCCCGAATC CCCG |||||||||| ||||||| |||| || ||| |||||||| ||
CTCGGCCGGCCCGAATCCCC CCCTCCCCTT TCCCCTC CCTC CC AGC CCGGCCGG CT C
TCCTTCCCCTCCCTCCCCTC T CC -- CCCTT TCCCCTA --- - C
CTTCCCCTCCCTCCCC

GAM2014 GATTTGGCCAAATGTATCCA 2281 TAACTAGTGT 5351 CC G CATCATAA--- GG ATAA G GTAAAC T
TCATAATCTGGGTTATAAAC AGAAAACAGA GG AAAT TATC TCTG TT AC GGT AAGAATATA G
GGGTGTAAACAAGAATATAT GATA || |||| |||| |||| || || ||| |||||||||
GTTTATATTTTTTAACTAGT CC TTTG ATAG agac aa tg tca TTTTTATAT T
GTAGAAAACAGAGATAGTAA TT - ATAAATGatag aa gatg a at---- T
ATAGATAGTTTTTCCAGATC

GAM2015 TTATGTAAACAAGTTTATAA 2282 TAAGTTGTGA 5352 AACAA-- t at ta
GTTGTGAAGAAGATAGTAAA AGAAGATAGT TTATGTA GTTTAtaagttg gaagaag ag a
TTTTCCTTTTTTTAATTTAT AAAT ||||||| |||||||||||| ||||||| ||
AGGCGAGCCCATACATGA AGTACAT CGGATATTTAAT TTTTTTC TT /
ACCCGAG - CT ta

GAM2016 AATATAGTACCTAAAGGATA 2283 TATAGTACCT 5353 acctaa ta a CAA
TTATTCTCAAATACAAGAAC AAAGGATATT AAtatagt agga tt ttcT A
AAGTTCCTGATAATTATATT ATTC |||||||| |||| || ||||
TTATATTA TCCT AA AAGA T
ATAG-- TG C ACA

GAM2017 GTAATTATATATAATATAAT 2284 TATAATATAA 5354 - t atc t TTAT TA
CTATATAATAATATTTATTT TCTATATAAT GTAAT TATA ataatata tatataa aataT TTATTGT A
ATTGTTAAATACAATAACAT AATA ||||| |||| |||||||| ||||||| ||||| |||||||
ATTTTATATATAATATATTA TATTA ATAT TATTATAT ATATATT TTATA AATAACA /
TTTATATATTAT T T AAT - C--- TA

GAM2018 GATTAGATCTAAGTTGCTAG 2285 TGACATAGCA 5355 TCTAAGT - CAC TT

TCATGCACGTTTTAAGCTCT TATTCTAGTT GATTAGA TGCTA GTCATG GT T
ATGACATAGCATATTCTAGT ||||||| ||||| |||||| ||
T ttgatct acgat cagtAT CG /
tat---- a CT- AA

GAM2019 TGACATAAGCCTTGGGATCT 2286 TTAGATCTAG 5356 ATA- TG TT TC TCT
TTGTGTCTGTCTAATGTCAC GCTACTGGTC TGAC AGCCT GGATCT GTG TG A
TGCTTAGATCTAGGCTACTG A |||| ||||| |||||| ||| ||
GTCA actg tcgga tctaga CGT AC A
gtca -- tt C- TGT

GAM2020 CGTCCGCCTGTACGCGGACC 2287 TTTCTGGTTT 5357 C - T A TC AGGCG T T
GATCACCAGAAGGCGGACAT TTGGACTGTG CGTC GCC TG ACGCGG CCGA ACCAGA
GACAT GGGC G
TGGGCTGTGGTTCATGTTTC TTCG |||| ||| || |||||| |||| |||||| ||||| ||||
TGGTTTTTGGACTGTGTTCG GCGG TGG gc tgtgtc ggtt tggtct ttGTA CTTG T
TGGTTGGCG T T t a tt ----- - G

GAM2021 GTATTTTATTGGGAATATTG 2298 TGTTTCGGAT 5368 TT- TT -- --- GA
GCGGGGATAAACCTGTTTCG GTTTACCCTT GTA TTA GGG AATATT GGCGGG T
GATGTTTACCCTTAATCTTA AATC ||| ||| ||| |||||| ||||||
C CAT aat ccc ttgtag ttgtCC A
Tct t- at gct AA

GAM2022 ACCGCGGAGCTTATAGCCGC 2288 TAGCCGCCTG 5358 C agcc ---- tt g ct
CTGCCTTGCTCGCTGCTGGA CCTTGCTCGC ACCGCGGAG TTAt gcct gcc gctc ctg G
CAGGAGCTCGGTTGTTGGGC TGCT ||||||||| |||| |||| ||| |||| |||
ACTGATAACTCCGTGGT TGGTGCCTC AATA CGGG TGG CGAG GAC /
- GTCA TTGT CT - AG

GAM2023 AAAGGTTGACGGGCATTCTT 2299 GGGCATTCTT 5369 TGAC ttct gctccT
AATTATGTTGCTCCTTTTAC AATTATGTTG AAAGGT gggca taattatgtt T
CAAATGTGGTTATGCTGCTT CTCC |||||| ||||| ||||||||||
TACTGCCTTT TTTCCG TTCGT ATTGGTGTAA /
TCAT CGT- ACCATT

GAM2024 GATGTACATTCCAACACTGC 2289 TGTACATTCC 5359 tccaac tg---------- TTT G
TGCCATATTTTTGGAGAAAT AACACTGCTG GAtgtacat actgc ccatAT TGGA A
TCAATATGGATATGATATTA CCAT ||||||||| ||||| |||||| ||||
TTTGCAGTATGTATATC CTATATGTA TGACG GGTATA ACTT A
------ TTTATTATAGTATA --- A

GAM2025 ACATTGAGTATCTAAATTAT 2290 TAAATTATAC 5360 AG Ct-- a aaa

ACAAGTATTAAAAATACTAG AAGTATTAAA ACATTG TAT aaattatacaagt tta a
ATTTGTGTAGTTTTAAAATA AATA |||||| ||| ||||||||||||| |||
AATAATGT TGTAAT ATA TTTGATGTGTTTA GAT /
AA AAAT - Cat

GAM2026 ACTAGTCACAAATCAGATCA 2291 TCCAAACTAT 5361 A ACAAATCA TC CAAA - T
ATGGTCAAAGATCTTCGGAA TACTCCAGGG ACT GTC GA AATGGT GAT C T
TCCAAACTATTACTCCAGGG ATAA ||| ||| || |||||| ||| |
ATAAGT TGa tag ct ttatca ctA G C
a ggac---- ca aac- A G

GAM2027 GATTAGTTAATATCGATGAT 2292 TTACATTAAA 5362 T GATG AAA CATAAG
TTAATAAAGGGAGCCATAAG TGATGTTATT GATTAGT AATATC ATTTAAT GGGAGC T
TGTTAAAGTTCTTACATTAA AGTC ||||||| |||||| ||||||| ||||||
ATGATGTTATTAGTC ctgatta ttgtag taaatta ttCTTG /
- ---- ca- AAATTG

GAM2028 GCGTTACTCTTCCCACTTAT 2293 TACTCTTCCC 5363 Tt cttccca t- tAGG
AATATTTTAGGAAAACAAAT ACTTATAATA GCG act ctta aatattt A
ATTTTTAAGCCAAAGTTTCG TTTT ||| ||| |||| |||||||
T TGC TGA GAAT TTATAAA /
TT AACC--- TT CAAA

GAM2029 TTTATTTATTAAATATAGAC 294 TATTTATTAA 3364 a aaa gat - AAA
GATCCCATAAAATATAATGA ATATAGACGA TTt tttatt tatagac cc cAT A
GGTTAGTTTATAGAATAGGA TCCC ||| |||||| ||||||| || |||
AGA AGA GGATAA ATATTTG GG GTA T
A G-- ATT A ATA

GAM2030 CGTGACTTCCGGTCATGTGA 2294 TCAGCCCAAT 5364 ----- A A CA
CTTCCGGTGACGTGTTTCCG AGTTAAGCCG CGGTCATGTGACTTCCGGTGACGTGTTTCCGGCT
GTT GGTTGACC CGCG T
GCTGTTAGGTTGACCACGCG GAAA |||||||||||||||||||||||||||||||| ||| |||||||| ||||
CATGCCGCGCGGTCAGCCCA GCCAGTACACTGAAGGCCACTGCACaaaggccga taa
ccgactGG GCGC /
ATAGTTAAGCCGGAAACACG attga c C CG
TCACCGGAAGTCACATGACC
GGAAGTCACG
GAM2031 GTATTTGGTGGAGTCGTAAA 295 AAGCTGACAG 3365 - T CG gacag tccc gc- GG
GCCCG
GCTGACAGAGTCCCTGGGTG AGTCCCTGGG GT AT TGGTGGAGT TAaagct ag tgggt gCT
GCT C
CGCTGGGCTGCCCGCACTGA TGCG || || ||||||||| ||||||| || ||||| ||| |||
AGTAAAGTTAAACTCACTCC CA TG ACCACCTCG GTTTTGG TC ACTCA TGA TGA
/

CTAGACAGGTTTTGAGCTCC A C A- ACAGA CCTC AAT AA AGTCA
ACCACGTAAC

GAM2032 GTTAGAGACGGAAATAGTTG 296 TAACATGGTA 3366 ----- AAGAT CG TAATA
TAAAA TA T
TCAAGATTCTCTATCGTCCT ACTGGAATAG AATAG TTGTC TCTCTAT TCC TACCAT
ATTGT GA T
AATATACCATTAAAAATTGT AGAT ||||| ||||| ||||||| ||| |||||| ||||| ||
TAGATTTTTCCGCAATAACA TTATT GATAG agagata agg atggta tAACG CT T
TGGTAACTGGAATAGAGATA GTCTA CCGAt -- tca-- caa-- C- T
GCCGATAGATCTGTTATTTC
AGTCGCTGAT
GAM2033 GAGAGGCTGGCAGATTGAGC 2300 TAGAGCCTGG 5370 G ATT - GGG CT A A
CCTGGGAGGTTCTCTCCAGC GTGTTCCCTG GAGAG CTGGCAG GAGC CCT AGGTTCT CC
GC C
ACTAGCAGGTAGAGCCTGGG CTAG ||||| ||||||| |||| ||| ||||||| || ||
TGTTCCCTGCTAGACTCTC CTCTC gatcgtc cttg ggg tccgaga GG CG T
A c-- t --- t- A A

GAM2034 CACGCTTGCTTGCTTAAAGC 2301 GCTTGCTTGC 5371 t aa-------- cctctt
CCTCTTCAATAAAGCTGCCA TTAAAGCCCT CACgct gcttgctt agc c
TTTTAGAAGTAAGCTAGTGT CTTC |||||| |||||||| |||
G GTGTGA CGAATGAA TCG /
T GATTTTACCG AAATAA

GAM2035 AAGACCCTGGTCTGTTAGGA 2302 TGTTAGGACC 5372 A ---------- accc g
CCCTTTCTGCTTTGGGAAAC CTTTCTGCTT AAG CCCTG GTCtgttagg tttctgctttgg A
CGAAGCAGGAAAATCCCTAG TGGG ||| ||||| |||||||||| ||||||||||
CAGATTGGCGCCTGAACAGG TTC GGGAC TAGACGATCC AAGGACGAAGCC A
GACTT A AAGTCCGCGGT CTAA A

GAM2036 TATTATGTAAATTTAAAAAA 2295 TGTAAATTTA 5365 a taaaaaa tagACCTG T A A A
T AAA
ATTAATTAGACCTGTTATAT AAAAAATTAA a att attaat TTATA ATA TG AAATAT TTAT
TAAT G
ATAATGAAAATATATTATTT TTAG | ||| |||||| ||||| ||| || |||||| |||| ||||
AATAAAGATACATTATATGA T TAA TAATTA AGTAT TAT AC TTTATA AGTA ATTA
A
AATATTTCCACTATTTATGA A TAGTAA- TAAAA--- T C C A T CAT
AAAATATTAATAATGATAAT
ATAAGTAATG
GAM2037 GCCATACAGTGGACCAATAC 2296 CAGTGGACCA 5366 Aca gga--- a- - t
GGGATAATGTTTGTCCTCGC ATACGGGATA GCCAT gt ccaat cg ggataa g
AATTGGATAGAAACGTAGTG ATGT ||||| || ||||| || ||||||
GC CGGTG CA GGTTA GC CCTGTT /
ATG AAGATA AC T t

GAM2038 TGGTTTGATATTTCATATAC 302 TATTTCATAT 3372 a t agatA C ATT AA-- A CT
TATTTATAAGATATCCATAT ACTATTTATA ttcat tactatt ata TCCATAT ATC GTGT ACTAAATA CGT T
CATCATTGTGTAAACTAAAT AGAT ||||| ||||||| ||| ||||||| ||| |||| |||||||| |||
AACGTCTTCTATGTATTTAG AGGTA GTGGTAG TAT AGGTGTA TAG TACA TGATTTAT GTA /
TAAGGACATTGGATATGTGG C - GAAA- - GT- GGAA - TC
AAAAGTATGATGGTGCATGG
AAGTTAGTACA
GAM2039 GTCCGCTGTTTCCGTTAATA 2297 TAATAGCACG 5367 CGCTG TAATAAT TT AA GC - C
ATACTATTTTCGTAACTGGC ATCGTGGTTA GTC TTTCCGT ACTAT TCGT CTG GGA TTATT A
GGATTATTCATAAATAACTC ACAA ||| ||||||| ||||| |||| ||| ||| |||||
TAATAGCACGATCGTGGTTA CAG AAAGGTA tggtg agca gat tCT AATAA T
ACAATATGGAAAAACTTGAC TTCAA Taacaat ct c- aa C A

GAM2040 GGTGGTGGATGGGTGATGAC 303 TGGTGGATGG 3373 gg g t a ttGGTAG
AGGGTTGGTAGGTCGTAAAT GTGATGACAG GGtggt at gg gatgac ggg G
CCCGGTCATCCTGGTAGCCA GGTT |||||| || || |||||| |||
CT TCACCG TG TC CTACTG CCC T
A- G - G TAAATGC

GAM2041 GGAAATGCGCCAGAGGGTGA 297 TGACAGGTAT 3367 TGCG A A- C---- - G
TGCTGGGTCGCACGGCGCCA CTACTGGACT GGAAA CCAG GGGTG TG TGG GTC C
ACTGACAGGTATCTACTGGA TTTC ||||| |||| ||||| || ||| |||
CTTTTCC Ccttt ggtc tctat ac ACC CGG A
tca- a gg agtCA G C

GAM2042 GTATAATCAGTTTGATGTTG 304 TGGCGGCAAA 3374 AAT T TGTG AATAC AT A C
TGCATTTAATACCCATCGCA TGATTACATT GTAT CAGT TGATGT CATTT CC CGCAGT TC A
GTATCCAAGGACACTGTGGC ACAT |||| |||| |||||| ||||| || |||||| ||
GGCAAATGATTACATTACAT CATG GTta attaca gtaaa gg gtGTCA AG A
TGCAGTAC AC- c tta- c---- cg C G

GAM2043 GTGCGGTGCACGTTGACATC 305 TGTGGACAAC 3375 G - - ACA A- A AGG
ATGTTCAAAGTAGGCGAGGC GAGCTGACGC GT CGGTG CA CGTTG TC TGTTCA AGT C
TGTGGACAACGAGCTGACGC TGAC || ||||| || ||||| || |||||| |||
TGACACCGGAT TA GCCAc gt gcagt ag acaggt tCG /
G a c cg- ca g GAG

GAM2044 CGTACTACTGAGATATACTA 298 TAGAGTATAA 3368 ACTA--- CTACCGA a ga gttac A

CCGATATAGAGTATAATGAT TGATTTAGTT CGT CTGAGATATA TAtagagt taat ttta ttTAAT A

TTAGTTACTTTAATAACCGT ACTT ||| |||||||||| |||||||| |||| |||| ||||||

TAGACATAAAATTGATTCTA GCA GACTTTGTGT GTATCTTA GTTA AAAT AGATTG C

TGAAAACTGTGTTTCAGGTA ATTTATG CAAAA-- - -- AC--- C

TTTAACG

GAM2045 AGGGTACGTCTATCGGTCCG 306 CCAGCACAGG 3376 TC TCC- G GAAA GGAT- GTTA CG AG

GCTGGCCCGAAAGGCGGTGG TGGTAATCGC G TATCGG GGCT GCCC GGCGGT CCTGTGT GGGTT T G

ATCCTGTGTGTTAGGGTTCG TATA | |||||| |||| |||| |||||| ||||||| ||||| |

TAGGTGGTAAATCCCAGCAC C GTGGCC TCGG CGGG tcgcta ggacacg cCTAA G /

AGGTGGTAATCGCTATAGGG CA CTAT A ata- atggt ac-- AT GT

CAGGCTTATCCCGGTGACCG

CTTCCCT

GAM2046 GGGGCCTCCGGTGTGAATAA 307 CCTCCGGTGT 3377 c - g ataagccct GA

GCCCTCGTCTGGAGCATCAG GAATAAGCCC GGGGc tc cggt tga cgtCTG G

ACGTTAAACTGAGACGTCCC TCGT ||||| || |||| ||| ||||||

CCCTG AG GTCA ATT GCAGAC C

C A A --------- TA

GAM2047 CCCCACGTATGGCAACGCCG 308 TATGGCAACG 3378 -- gg- g ttaaaa-- t

CTTAAAACCCTTCGGGGACA CCGCTTAAAA CCCCAC Gtat caac ccgc ccc T

GCTATGCGGGTTGACAATGC CCCT |||||| |||| |||| |||| |||

CAGTGGGG GGGGTG CGTA GTTG GGCG GGG C

AC ACA - TATCGACA G

GAM2048 GCGGCGCCGTGCTACAGGCG 309 GTGGCATTCC 3379 ---- TG A G G A AA- - - T

GCAAGGGGAAAAATCCTTCG CTCCCTTAGC GCGGC GCCG CT CA GC GC AGGGGA AAT CC TTCGGG G

GGTGACCCCGGGTGGCATTC AGCA ||||| |||| || || || || |||||| ||| || ||||||

CCTCCCTTAGCAGCATGAGT CGTCG TGGT GA GT cg cg ttccct tta gg gGGCCC A

GTGGTGGTAGCTGC ATGG GT - a a a ccc c t C

GAM2049 GGTCCGCTGCCTAGCTACAT 310 CGACGGGAGT 3380 GT - -- TA TACA TT- ACACG

CCTGTTTTGCACACGGCTCC TTGCGGTCAA G C CGCT GCC GC TCCTGTT GC G

AGCTTCGACGGGAGTTTGCG GCGA | | |||| ||| || ||||||| ||

GTCAAGCGAGGTC C G gcga tgg cg agggcag CG /

TG a ac -- tttg cTT ACCTC

GAM2050 GATATCTCATTATTTGATTA 299 TGTTATATTA 3369 TCTC- T- -- - CA

TGTAGCGCCAGGAGCTGTTA AGTCAATCTA GATA ATTA TTGATT ATGTAGC GC G

TATTAAGTCAATCTAATCAC ATCA |||| |||| |||||| ||||||| ||

TCTATC CTAT taat aactga tatattg CG /
CTCac ct at t AG

GAM2051 CTTTCAACCATAAATAATGT 311 ACCATAAATA 3381 A ---- taatg- ttt A
CGTTGTTTTAAATTTATATC ATGTCGTTGT CTTTC acca taaa tcgttg ta A
GATGAACTAATTTTAAATCT TTTA ||||| |||| |||| |||||| ||
GGTGGAAAG GAAAG TGGT ATTT AGTAGC AT T
G CTAA TAATCA TAT T

GAM2052 TTGTATATATTATAGTTTCA 312 TAACTGCAGA 3382 TATA A TCATTA C--- CATACC
CCTT- A
TTATGGGCATTTTATCATAC TGAAAAATAA TTG TATT TAGTT TGGG ATTTTAT
TCTGCA TC A
CTCTGCACCTTTCAACTGAC AATA ||| |||| ||||| |||| ||||||| |||||| ||
TAACTGCAGATGAAAAATAA AAC ATAG ATCGA ACCC taaaata agacgt AG C
AATATCACCCAAGCTAAGAT TATG A ------ ACTa aaaagt caatC T
AGTATCAA

GAM2053 TGCCCAGCAGCAGCAGTAGC 300 CGAGGAGAAC 3370 C --- AGCC T CCCAGT
CCCTCTGTGCCCAGTTCCAT TGCTGGCCCT TG CCAGCAG CAGCAGT CCTC GTG T
CATCGCCGAGGAGAACTGCT GCTG || ||||||| ||||||| |||| |||
GGCCCTGCTGGCCG GC Ggtcgtc gtcgtca ggag CGC C
C ccg aga- c TACTAC

GAM2054 CTCGTCGCTTGACAGCACCG 318 CAGCCGCAGC 3388 T A -- ACC------- A
CCGCAGCCGCGGCAGCCGCA CGCCATGACA CTCGTCGCT G CA GC GCCGC G
GCCGCCATGACAGCGACGAG GCGA ||||||||| | || || ||||
GAGCagcga c gt cg cGGCG C
- a ac ccgacgccga C

GAM2055 GGGACAGACCAGACCTAGGA 313 AGGCATGGAC 3383 ---------- GA A--- TC
GCTATTCTACCATAGCAGAA ATACTAATAT GGGACAGA CCA CCTAGG GCTAT T
CTTAGGCATGGACATACTAA CTGT |||||||| ||| |||||| |||||
TATCTGTCTT TTCtgtct ggt ggaTTC CGATA A
ataatcataca ac AAGA CC

GAM2056 ACAGGCCGGGTTTTAAAACT 314 TGTGAGGATC 3384 GG TAA---- ---------- G G TTT
TACTCAGGGGAATTGTTTTT TAACTCTAAG ACAGGCC GTTT AACTTA CTCA GG
AATTG T
TTTAGTTCTGTGAGGATCTA TTGA ||||||| |||| |||||| |||| || |||||
ACTCTAAGTTGACACATAAA TGTCCGG TAAA ttgaat gagt tC TTGAT /
TTAGGCCTGT AT TACACag ctcaatctag g - TTT

GAM2057 ATTAGAGAACCACGTAATTG 301 TCCACCAAGC 3371 A-- CGTAA GTCA C T

GGTCAACCCGTTAATACCGG CCTGGAAATC ATTAGAGA CCA TTGG ACC GT A
TCCACCAAGCCCTGGAAATC TCTA |||||||| ||| |||| ||| ||
TCTAGT TGatctct ggt aacc tGG CA A
aaa cccg- acc- C T

GAM2058 GATGTTAAATATTATTAGTC 315 TAATAGGCCC 3385 - AGTCTC A-- CGCAA GTCAAC CTA
TCATTAACAAACCACGCAAC TGGAAATTGT GATGTTA AATATTATT ATTAACAA CCA CTAT CCG A
TATGTCAACCCGCTAATACC TAAT ||||||| ||||||||| |||||||| ||| |||| |||
GGTCTAATAGGCCCTGGAAA CTACAAT TTATAATAA taattgtt ggt gata GGC /
TTGTTAATAAATAATATTGT G A----- aaa cccg- atCT-- CAT
AACATC

GAM2059 CATATATATGTAATAGTCTC 316 TATGTAATAG 3386 a a ctcat c-- CGCAA GTCAAT TTA
ATCACTAACCCACGCAACTG TCTCATCACT CATATAtatgt at gt cactaa cCA CTGT CCG A
TGTCAATCCGTTAATACCGG AACC |||||||||| || || |||||| ||| |||| |||
TCCAACAGGCCCTGGAAATT GTATATATACA TA CG GTGATT GGT GACA GGC /
AGTGGCAATAACATATATAT A A ----- AAA CCCG- ACCT-- CAT
G

GAM2060 CCGCTTCTATTTACTCCCGC 317 CCGCAGCACA 3387 C-- CTCccg-- ac a aa
AGCACAATGAACCAACACGG ATGAACCAAC CCGCTT TATTTA cagc aatga cc c
GCTCGTTTCGTTGATCACAT ACGG |||||| |||||| |||| ||||| ||
TTAGATAAAAAGGCGG GGCGGA ATAGAT GTTG TTGCT Gg a
AAA TTACACTA CT C gc

GAM2061 GTTAGGCAATGTATATTTAT 319 CAATGTATAT 3389 - ca tatttat aaATTTAAAACATATT CT
CCATCGTCAAATTTAAAACA TTATCCATCG GTTA GG atgta ccatcgtc TGAA T
TATTTGAACTTAACTTCAGA TCAA |||| || ||||| |||||||| ||||
TGATGGTGCATCCATAGC CGAT CC TACGT GGTAGTAG ACTT A
A -- ------- ---------- CA

GAM2062 ATATTTTTCTATAATCTGTC 320 TCCCTCATAG 3390 C ATC- - AAC T TCCACAAA
TTTTAAACGATGGATTTTCC AATGATACAC ATATTTTT TATA TGTC TTTTA GA GGATTT T
ACAAATGCGCCTCTCAAGTC GTAT |||||||| |||| |||| ||||| || ||||||
CCTCATAGAATGATACACGT TATAAAAA Atat atag aagat ct cctGAA G
ATAAAAAATAT - gcac t a-- c CTCTCCGC

GAM2063 CCGCTTCTATTTACTCCCGC 321 CCGCAGCACA 3391 - - CTCccg-- ac a aa
AGCACAATGAACCAACACGG ATGAACCAAC CCGC TTCT ATTTA cagc aatga cc c
GCTCGTTTCGTTGATCACAT ACGG |||| |||| ||||| |||| ||||| ||

TTAGATAAGAAGGCGG GGCG AAGA TAGAT GTTG TTGCT Gg a
G A TTACACTA CT C gc

GAM2064 CCGCTTCTATTTACTCCCGC 322 CCGCAGCACA 3392 C-- CTCccg-- c a aa
AGCACAATGAACCAACACAG ATGAACCAAC CCGCTT TATTTA cagca aatga cc c
GCTCGTTTTGTTGATCACAT ACAG |||||| |||||| ||||| ||||| ||
TTAGATAAAAAGGCGG GGCGGA ATAGAT GTTGT TTGCT Gg a
AAA TTACACTA T C ac

GAM2065 CGCTTCTATTTACTCCCGCA 326 TCCCGCAACA 3396 - - Ctcccg-- ac a aa
ACACAATGAACCAACACGGG CAATGAACCA CGC TTCT ATTTA caac aatga cc c
CTCGTTTCGTTGATCACATT ACAC ||| |||| ||||| |||| ||||| ||
TAGATAAGAAGGCG GCG AAGA TAGAT GTTG TTGCT GG a
G A TTACACTA CT C Gc

GAM2066 ACGGTAGAATTGATAATATA 323 TACCTCATAA 3393 TAAA-------- CA-- T- TCTGTG A
TT TA
AATATGAGCATTAGTATTTC AACAAAAAAG TAATA TATGAG TTAG ATT GATTAAT
GAT C G
TGTGGATTAATAGATTTCTA CTAT ||||| |||||| |||| ||| ||||||| ||| |
GTATGGGATCATTAATCATT ATtat atactc AATC TAA CTAATTA CTA G T
TCTAATCTCTAAATACCTCA cgaaaaaacaaa catA TC TCTTTA - GG TA
TAAAACAAAAAAGCTATTAT
CAAATACTGT
GAM2067 ATTATTAGACGAGTTACAAA 327 TGCGATCAGA 3397 A TACAAA AT G GA
CTATTTGGATAGACACATAT TATTTGCTAA ATTATTAG CGAGT CT TTG ATA C
GCGATCAGATATTTGCTAAT TAAT |||||||| ||||| || ||| |||
AAT taataatc gttta ga agc tAT A
- ta---- ct g AC

GAM2068 GCGGGTTCTTGTATTCCGTG 324 TTGGCTGGCA 3394 G A AT ATT
TGATAGATGGTTGGATTGAT TACGGAATAT GCGG TTCTTGTATTCCGTGTG TAG GGTTGG G
AATCGATTGGCTGGCATACG AGGA |||| |||||||||||||||| ||| ||||||
GAATATAGGAGGTCGC CGCT Gaggatataaggcatac gtc ttAGCT A
G g gg AAT

GAM2069 CTGAGGGGACCATAGCATGT 325 TAGCATGTAT 3395 CA- a- g aa g
ATAGGCGAAAAGCGGGGCTT AGGCGAAAAG CTGAGGGGAC tagc tgtatag cga agc g
CGGTTGTACGCGGTTAGGAG CGGG |||||||||| |||| ||||||| ||| |||
TCCCCTCAG GACTCCCCTG ATTG GCATGTT GCT TCG /
AGG GC G -- g

GAM2070 GGGTTTTATAAATGATTATA 328 TAAATGATTA 3398 T atga a aaa aAA
AGAGTAAAAAGAAAGTTGCT TAAGAGTAAA GGGTT TAtaa ttat agagta ag G

GATGCTCTCATAACCTTGTA AAGA ||||| ||||| |||| |||||| ||
TAACCC CCCAA ATGTT AATA TCTCGT TC /
T CC-- C AG- GTT

GAM2071 CTCAGTCCCTGTCTCTAGTT 334 TCCCTGTCTC 3404 - c ta-- tgt tcGA
TGTCTGTTCGAGATCCTACA TAGTTTGTCT CTCAG tccctgt tc gtt ctgt G
GTTGGCGCCCGAACAGGGAC GTTC ||||| ||||||| || ||| ||||
CTGAG GAGTC AGGGACA AG CGG GACA A
C - CCCG TT- TCCT

GAM2072 TGTAGCTAAAGCTAAAGCAT 329 GCTAAAGCTA 3399 A -------- aaa gtgct
GCAGTGCTATTGAAATGCAT AAGCATGCAG TGT gc taaagct gcatgca A
GTAGCTTTACAACAATTGCA TGCT ||| || ||||||| |||||||
ACA ACA CG ATTTCGA TGTACGT T
A TTAACAAC --- AAAGT

GAM2073 GTTTGGGGATGAACCATGGT 330 TATGTCAGAA 3400 GA- ACCA--- TT A
CTTTGCTTGACACAAGCTGG CCTAAAC GTTTGGG TGA TGGTCT GCTTG C
GACCGATATATGTCAGAACC ||||||| ||| |||||| |||||
TAAAC caaatcc act GCCAGG CGAAC /
aag gtatATA GT A

GAM2074 ACATTATGCATTGTGGTTTT 331 TATGCATTGT 3401 t tt tt tgt tg TTT
GTTGTGTGGTTTGTTTTTGC GGTTTTGTTG ACAT atgca gtggt tgt g G G
TTATATTGCTATGTTGCATG TGTG |||| ||||| ||||| ||| | |
TGT TGTG TACGT TATCG ATA C T /
- TG TT TT- GT TTT

GAM2075 GCCTATTTGTACGGGTCGAG 332 TACGGGTCGA 3402 ATTTG- gg--- tac tg AC
TACAAACGTGGCCATCACGA GTACAAACGT GCCT tacg tcgag aaacg gccATC G
TAGATGGTTCTGTTTTTCGA GGCC |||| |||| ||||| ||||| ||||||
ACAGATGTAAATCGGAGGC CGGA ATGT AGCTT TTTGT TGGTAG A
GGCTAA AGACA --- CT AT

GAM2076 CATCACGATAGATGGTTCTG 333 GTTCTGTTTT 3403 gt-- g -- -- t CG CGTC--
ACG
TTTTTCGAACAGATGTAAAT TCGAACAGAT GATG tct tttttcga aca gatg aaAT GAGG
GTGCAGT G
CGGAGGCGTCGTGCAGTACG GTAA |||| ||| |||||||| ||| |||| |||| |||| |||||||
GTAAACTGCACATCTATCCT TTAT AGA AAAAAGTT TGT TTAT TTTG CTCC
CACGTCA /
CTAGTTTCTATTGATGTAAT AACT - AA AG C AT TATCTA AAT
TGAAAAAAGATCAATATTTT
ACGATGATG

GAM2077 ATACACAGTACTTGTAATTT 342 TACATCAGTT 3412 A ---- -- T A TCT---------- TCG
CTTGAAACATCTCCTCGAAT GACACCGTGT ATACAC GT ACT TGTAATTTCT GA ACA
CC A
ATGGCATTAACTTTCTTTTT GT |||||| || ||| |||||||||| || ||| ||
GTATTTAGAGATTACATCAG tgtgtg ca tga acatTAGAGA TT TGT GG A
TTGACACCGTGTGT c cagt ct T A TTTTCTTTCAATTAC TAT

GAM2078 TGTTACGTCCCACTGGCACA 335 TGAGAGCAAT 3405 ACG CTG TTAAAAAAAATGGTA
GG TG AA- T
TTTAAAAAAAATGGTAAGAG CTGATGGAAT TGTT TCCCA GCACAT AGA GTTCT T
CAT T
GGTTCTTGTAACATTTGATG ATAT |||| ||||| |||||| ||| ||||| | |||
GGGATGAGAGCAATCTGATG ACGA AGGGT TGTGta tct cgaga A GTA /
GAATATATGTGTTGGGAAGC --- --- tataaggtag----- aa gt GGG G
A

GAM2079 GTTTGCTGCATGCACGCGAC 336 TTGCTGCATG 3406 a acaaacacGAGAT - - AAG A
AA A TT
AAACACGAGATTGTGCTCGA CACGCGACAA catgc cgcg TGT GC TCGATG GTT GTC
CG TTTAT G
TGAAGGTTAGTCAACGATTT ACAC ||||| |||| ||| || |||||| ||| ||| || |||||
ATTTGGTTATAAGCGGGGAT GTGCG GCGT ACA CG AGTTAC CAG TAG GC
GAATA G
AGACGCGCATTGATGCTACA - CAATTAAGTAT-- T T GCG A GG - TT
TATGAATTAACTGCGGCGTG
TTGGGGGTTAT
GAM2080 GCCCAACGGTGCCCCTTTAT 343 CAACGGTGCC 3413 Ccaac ccct cg-- GA
CGCCGTATGAATATGTGAAG CCTTTATCGC GC ggtgc ttatcgc taT A
AGCGATAACAGCACCCACGC CGTA || ||||| ||||||| |||
CG CCACG AATAGCG GTG T
CAC-- AC-- AGAA TA

GAM2081 TACCGATATACAGTATAATG 337 TATACAGTAT 3407 - t ata- - t ac--- A
ATTTAGTTACTTTAATAACC AATGATTTAG TACC GA atacagt at ga ttagtt TTTAAT A
GTTAGACATAAAATTGATTC TTAC |||| || ||||||| || || |||||| ||||||
TATGAAAACTGTGTTTCAGG ATGG CT TGTGTCA TA CT AGTTAA AGATTG C
TA A T AAAG T T AATAC C

GAM2082 GGGGGGGTGGGCCTCGTCCC 344 CGGGACCCGC 3414 G G CTC CA--- GA-- C
CACGCAGACCCGCGGGCAAA GCGCCTGCCT GGG GGGTG GC GTCCC CGCA CC G
TGCGAGAACGGGACCCGCGC ||| ||||| || ||||| |||| ||
GCCTGCCT tcc tccgc cg caggg GCGT GG C
g g cc- cAAGA AAAC G

GAM2083 ATATATTATGTGCACGAGCA 338 TATTATGTGC 3408 a cgagca ata ATT
GCATAAGACATATTATGAAG ACGAGCAGCA ATAtatt tgtgca gc agACAT A

TGTTTAAGCAGGATGCACAA TAAG ||||||| |||||| || ||||||
ATGTAT TATGTAA ACACGT CG TTTGTG T
- AGGA-- AA- AAG

GAM2084 GTGGCAGACAAAGCCAAAAC 345 TGTTACAGTG 3415 G G AAAG AAAC TG AAA
AATGTTTTAAAAAAAAAGGT GAGGTGTGGT GTG CA AC CCA AA TTTT A
GTTACAGTGGAGGTGTGGTA AC ||| || || ||| || ||||
C cat gt tg ggt tt GGAA /
g g ga-- gaca gt AAA

GAM2085 CACGCCGCTATGGGAGGCGC 339 CCGCTGCGAG 3409 CG ATG A - TTT
CGTGTTTTTCACCAACACGC ACGCGTG CACGC CT GG GGCGC CGTGTT C
GCGCCGCTGCGAGACGCGTG ||||| || || ||||| ||||||
gtgcg ga tc ccGCG GCACAA /
ca gcg g C CCA

GAM2086 TGTATTCAGTATTTTTGGAA 340 TCAGTATTTT 3410 Ttc g ca aA- A
TCATAAAAAATAAAAAAAGT TGGAATCATA TGTA agtattttt gaat taaaa TAAAA A
TTTACCATTTTAAAATTTAA AAAA |||| ||||||||| |||| ||||| |||||
AAAGTATTTACA ACAT TTATGAAAA TTTA ATTTT ATTTT A
--- A AA ACC G

GAM2087 GCGCTGCTGGGGGACAGGAG 346 TGCTGGGGGA 3416 g g ga a CAG GAGAC
GAGGGTTCGCAGCCCTGAGA CAGGAGGAGG GCGCt ct ggg cagg ggagggttcG CCCT T
CTTAAAGAAGGGGACGAGCC GTTC ||||| || ||| |||| |||||||||| ||||
CTCCGCCTGAACCTGAGGAG CGTGA GA TCC GTCC CCTCCCGAGC GGGA T
TGC G G AA G AG- AGAAA

GAM2088 GTGTGAGCCCTTCACGTCGG 341 TAAACAGCCC 3411 TG CT C G - G
GGGTGTTTGTGTGTTTGTGA CGATTTGACA G TGAGCC TCA GTCGGGG TGTTTGTG TGTTT T
AGCAGCATAAACAGCCCCGA GGTT | |||||| ||| ||||||| |||||||| |||||
TTTGACAGGTTCGTGC C GCttgg agt tagcccc acaaatAC ACGAA /
GT ac t g G G

GAM2089 GAACCTGTCAAATCGGGGCT 347 TGTCAAATCG 3417 A g aa c a c CTTC
GTTTATGCTGCTTCACAAAC GGGCTGTTTA GA CCt tca tcgggg tgttt tg tG A
ACACAAACACCCCCGACGTG TGCT || ||| ||| |||||| ||||| || ||
AAGGGCTC CT GGG AGT AGCCCC ACAAA AC AC /
C A GC C C - AAAC

GAM2090 ACGAACCTGTCAAATCGGGG 349 TGTCAAATCG 3419 g aa cta a c CTCC
CTATTTATGCTGCTCCACAA GGGCTATTTA ACGAACCt tca tcgggg ttt tg tG A
ACACACAAACACCCCCGACA TGCT |||||||| ||| |||||| ||| || ||

TGAAGGGTTCGT TGCTTGGG AGT AGCCCC AAA AC AC /
A AC CAC C - AAAC

GAM2091 GTTGGGCCAAACAGGATATC 348 GCCCGGGGCC 3418 AGGA C T G --- C- C AA AGA T
TGCGGTGAGCAGTTTCGGCC AAGAACAGAT TATCTG GG GA CA GTTT GGCCCCGG CCGGGGCC GAAC TGG C
CCGGCCCGGGGCCAAGAACA GGTC |||||| || || || |||| |||||||| |||||||| |||| |||
GATGGTCACCGCGGTTCGGC ATAGAC CC ct gt caag ccggggcc gGCCCCGG CTTG GCC /
CCCGGCCCGGGGCCAAGAAC ---- - - g aga aa c -- GC- A
AGATGGTCCCCAGATATGGC
CCAAC
GAM2092 CGCCACCCTGCGGGCGACCC 235 TACTTCGCCG 3305 - CT--- - ACC - TAGTC T C
GGGGGGTGCTCTGATAGTCT CCGCGACCCG CGC CACC GCGGG CG CGG GGGGTGCTCTGA TCGCG GCC A
CGCGTGCCCAAGGCCCGTGA CCAC ||| |||| ||||| || ||| |||||||||||| ||||| |||
TCGGGGTACTTCGCCGCCGC GCG GTGG cgccc gc gcc cttcatGGGGCT AGTGC CGG /
GACCCGCCACCCGGTGTGCG T CCcac a gcc g ----- C A

GAM2093 CCTCGTCTTTGGTTGGCTCC 236 CTCCGAATAC 3306 T--- - CAATCC- TC TC- C ATT GCA TTT
AATCCGATTCCGAGTCGTCC CTGTCGAATC TGG TG GCTC GAT CGAG GT CGA GG TCGGAGTC T
GAATTGGGCATCGGAGTCTT TCCT ||| || |||| ||| |||| || ||| || ||||||||
TTCCCTGGCTCCGAATACCT ACC AC CGAG CTG GCtc ta gct cc agcctcGG C
GTCGAATCTCCTCGTCGTCT CATC T CCTGCTT CT ctc a gt- ata TCC
TCGTCCGAGCTCACTACCCA
AAGATCGCGG
GAM2094 TCCGTCCATCGGCGTGGTGC 350 AAGCACCCCG 3420 G A G T C-- - TC
TCGATCCCGTCATTCGGTGA CGAAGGAGGA TCC TCC TCG CG GGTGCT GATC CCG A
TCTCAAGCACCCCGCGAAGG ||| ||| ||| || |||||| |||| |||
AGGA agg agg agc gc ccacga CTAG GGC /
- a - c aCT T TT

GAM2095 GCTATTACCGTATCTAATTC 243 TACCGTATCT 3313 acc ctaattccgagg AGA AA
CGAGGATGAAGAGCGAAATT AATTCCGAGG GCTATt gtat atga GCG A
CGTGATCGTAAAAATAAAAA ATGA |||||| |||| |||| |||
ATACAAGATAGT TGATAG CATA TGCT TGC /
AA- AAAAATAAAAA- AG- TT

GAM2096 GAGGCGGTCGGCGGAGGAGG 351 AGGAGGCGGC 3421 - C Ca - c- a cc ------ CT C
CGGCAGGAGGCGGCAGAGGA AGAGGAGGCC GG AGGAGG GG ggag gcgg agagg gg ggagGGCG TGGG GC C

GGCCGGAGGGCGTGGGCTGC GGAG || |||||| || |||| |||| ||||| || |||||||| |||| ||
CCTGGCCCCCCGTCGCGCCG CC TTTTCC CC TCTC CGCC TTTCC CC TCTCTCGC
GCCC CG T
CTCTCTCTCCCCTTTTCCCG C - TC T CT - TC CGCGCT CC G
CTCTCTCTCCCCTTTTCCCG
CCCGCCTGCCC
GAM2097 GGGTACCACAGGTGGGTGCT 352 TGGAAACTTG 3422 A AC- T TTt-- tgcc-- t cgt C
TTGGAAACTTGCCGGTCGCC CCGGTCGCCG GGGT CC AGGTGGG GC ggaaact gg cgc
gctC T
GTGCTCCTGTGAGCTTGCGT TGCT |||| || ||||||| || ||||||| || ||| ||||
CCCTCCCCGGTTTCCTTTGC TCCA GG TCCGCCC CG CCTTTGG CC GCG CGAG
G
GCTCCCGCCTTCCGGACCT - CCT T CGTTT CCCCTC T TT- T

GAM2098 GCCGAAAGCCGCGTGTCGGT 353 GGACATGACG 3423 G GG ACA T T AGA
TATA
GACACGTCGTCTTGAGACGG CGCCCAAGAC GCCGAAA CCGCGTGTC TG CG CGTC TG
CGGTGTCTTA T
TGTCTTATATATCTTCTTAA ACGT ||||||| ||||||||| || || |||| || ||||||||||
GACGCCGGACATGACGCGCC CGGTTTT GGtgcacag ac gc gcag ac gCCGCAGAAT C
CAAGACACGTGGATTTTGGC A a- cc- - t ag- TCTT

GAM2099 TATATTATATAATATTTTAT 244 TATTATATAA 3314 - a---- G T TT ATTCCAATT--
GT
AAAATTAGTATTTCTTTTAT TATTTTATAA atataatatt ttataa attA TA TTC TTATAT AATA A
ATATTCCAATTAATAGTAAA AATT |||||||||| |||||| |||| || ||| |||||| ||||
ATATTTATAAATATAGATAT TATATTATAA AATGTT TAAT AT AAG AATATA TTAT
A
AATTGAACTAATAATCTCTA C ATCTC A C TT GATATAAATAT AA
TTGTAACAATATTATATAAT
ATA
GAM2100 GTTTTTCTTGTCTACTGGTT 354 TTCCTGTAAA 3424 GTCTACT- CATATACA
AACATATACAACAACACAAT AGAAAAAC GTTTTTCTT GGTTAA A
TAACTTCCTGTAAAAGAAAA ||||||||| ||||||
AC caaaaagaa tCAATT /
aatgtcct AACACAAC

GAM2101 CGGGTGCTCCGCTCTTCGTA 251 TTTTTTGATT 3321 TCC CT- TACCTGT TT
CCTGTAGACTTGGATGTCTT TAGCTGCACC CGGGTGC GCT TCG AGAC G
TTTTGATTTAGCTGCACCCG CG ||||||| ||| ||| ||||
gcccacg cga agt tCTG G
t-- ttt tttt--- TA

GAM2102 CCGAGGTCGTCGGTTTCGAG 355 TTTAGACTTT 3425 - C TTC TATT C TTT GCAT -
TTC
TATTTCCACTTTGTGCATAC GTCGATTTTC CCG AGGT GTCGGT GAG TC AC GT ACCCC
CC A

CCCCCTTCATTCGGCGGGGT TACC ||| |||| |||||| ||| || || || ||||| ||
TTAGACTTTGTCGATTTTCT GGC TTTA CGGcca ctt ag tg ca tGGGG GG /
ACCGGCATTTACGG A - t-- tt-- c ttt gatt C CTT

GAM2103 TGTTGTTGCGTTCGAAACCG 237 AGAGGAATCA 3307 T C--- C Aa a-- tc ct
AAGAGGAATCATCGGAAGCT TCGGAAGCTG TGTTG TG GTTCGAAA CG gagg atca ggaag g
GAACTTCCTTTGGTATACCT AACT ||||| || |||||||| || |||| |||| |||||
CCACGATTTCGAATTAAACA ACAAT AC TAAGCTTT GC CTCC TGGT CCTtc /
TTAACA T AAAT A AC ATA TT aa

GAM2104 CGTAAAGTGACGTTTACGTT 238 TCGAAAACGG 3308 A TTA Tt gag c --- t TGT G T AA
CGAAAACGGAGTCCAACTAG AGTCCAACTA G CGT CG cgaaaacg tc aact agtg TCGGGA ATG AC CG C
TGTTCGGGATGTATGGACTC GTGT | ||| || |||||||| || |||| |||| |||||| ||| || ||
GAACAACGGTGCGTTTCTTC C GCG GT GCTTTTGC AG TTGG TCAT AGCCTT TGC TG GC /
CGACTACTTGTGGTTTGAAA - CG- T- AAA T TGT C CTT G - AA
ACGTTTTCGTTGGCGCGCAC
TGCG
GAM2105 CTTGTAGAATTACCGTGGAT 239 TGTAGAATTA 3309 ttaccg--- tcacaacTG
CACAACTGTTGCATATCTTC CCGTGGATCA CTtgtagaa tgga T
CAAAATATATCTTTTGCAAG CAAC ||||||||| ||||
GAACGTTTT ACCT /
CTATATAAA TCTATACGT

GAM2106 TAGACTTCCAAGTATTAATT 240 TCCAAGTATT 3310 Ttccaag gttaca tC T AA TCGC TT TATA
CGTTACAGATCCATGTATGA AATTCGTTAC tattaattc ga CA GTATGA CGAG TAA AGTG A
AACGAGTCGCTAATTAGTGT AGAT ||||||||| || || |||||| |||| ||| ||||
ATAATTTTCATTTTTTATAA ATAATTAAG CT GT CATACT GTTT ATT TTAC /
TTTTGTCATACTGCTCCAGA TATA--- AC---- C- - -- TAAT TT TTTT
ATTAATAATATCTCTA

GAM2107 GTTTCGGGGAAGGGGGAGGA 245 TACAGCACCA 3315 GG- GAGGAGAAG T G GAGG C ACACTC- T AT
GAAGGTTTCGGGGGAGGAGG GGTTCTCCAC A GG GT TC GGGGAG TGGA TTGTG GGGT ATC T
TGGACTTGTGACACTCGGGT AC | || || || |||||| |||| ||||| |||| |||
TATCATTAACGATACTTACA t cc ca GG CTTCTT ACCT AACGC TTCA TAG A
TCGGCGCAATTCCAAAATTC gga acga----- t G AAA- T GGCTACA - CA
TTCGGGTACAGCACCAGGTT
CTCCACAC
GAM2108 GCGGGGGGAGGAGCGGGGGG 241 GGGGAGGAGC 3311 GGGGGGAGGA GGGGGGAGGA GGGG
AGGAGCGGGGGGAGGAGCGG GGGGGGAGGA GC GC GC G

GGGGAGGAGCGGGGGGAGGA GC || || ||
GC cg cg CG G
aggaggggggg aggaggggGG AGGA

GAM2109 GGGGGGAGGAGCGGGGGGAG 242 AGACGCCGAA 3312 A AG GGGGGAGGA GGG AGGA GGGG
GAGCGGGGGGAGGAGCGGGG AACGGGCCCC GGGGGG GG CG GCG GG GC G
GGAGGAGCGGCCAGACGCCG CCCC |||||| || || ||| || ||
AAAACGGGCCCCCCCC ccccccc cc gc cgc CC CG G
- gg aaaagc--- aga GG-- AGGA

GAM2110 GCCCCCCCGCGGGCGCGCGCG 246 CGGGCGGCGT 3316 GG - AAAAAGG G
CGCGCAAAAAAGGCGGGCGG GCGCGCGCGC GCCCCCCCGCG CGC GCGCGCGCGCA CGGGC G
CGGTCCGGGCGGCGTGCGCG GGCG |||||||||| ||| |||||||||||| |||||
CGCGCGGCGGGCGTGGGGGG CGGGGGGTGC gcg cgcgcgcgcgt gcCTG C
C GG g gcggcgg G

GAM2111 GCGGGGGGAGGAGCGGGGGG 247 GGGGAGGAGC 3317 GGGGGGAGGA GGGGGGAGGA GGGGGGAGGA GGGG
AGGAGCGGGGGGAGGAGCGG GGGGGGAGGA GC GC GC GC G
GGGGAGGAGCGGGGGGAGGA GCGG || || || ||
GCGGGGGGAGGAGCGGGGGG CG cg cg CG G
AGGAGC AGGAGGGGgg aggaggggggg aggaggggGG AGGA

GAM2112 GAATTGTCCTTGAGCTTGTA 248 TGACACCGGG 3318 C ---- TTTA TAC C --- GGG - - TG
TACTCTGTTTACATACCACC CGGCCCTTAG TTGTATA CTCTG CA CAC TGAGGGT TCGG TA CT TCG A
TGAGGGTTCGGGGGTACTTC TGAT ||||||| ||||| || ||| ||||||| |||| || || |||
GTGATGCGGCAGATGACACC AACATAT GAGAC GT gtg attcccg ggcc gt GA GGC /
GGGCGGCCCTTAGTGATTGC - ACAA C--- ta- - gcg aca A C GT
CAGAGAACATATACAACCGA
AGACCTCGTTT
GAM2113 GGATTCTATAGATTTAATAA 249 TATTACAGAT 3319 -------- T AA - CAAC CTAC
ATCCAACTGATTCTACTATA TCTATAGATT GGAT TCTATAGA TT TAA ATC TGATT T
AAATCAACAGATATTACAGA TAAT |||| |||||||| || ||| ||| |||||
TTCTATAGATTTAATAAATC CCTA agatatct ag att tAG ACTAA /
C AAtaattt t ac a ACA- AATA

GAM2114 GAACTGAGCTTTTTAATTAA 250 AAAGTGAAGG 3320 A TTTTAATTaa aag c- - c
AGTGAAGGACCCGGGCCAAG ACCCGGGCCA GA CTGAGCT agtg gac cg ggc a
GCCTCGCCGTCATCTACTCG AGGC || ||||||| |||| ||| || |||
GCTCAGTC CT GACTCGG TCAT CTG GC Ccg a
- C--------- CTA CC T g

GAM2115 TATTTGCTTGCCCGTGATGT 259 TGTTTGTATG 3329 TGATG- TT- Ttg a - t gTAAAT CAC
GCTTTGTATTTGTTTGTATG TAGTGCTTTC GCCCG TGC TGTAT tttgt tgtag tgctt cttt GT A
TAGTGCTTTCTTTGTAAATG TTTG ||||| ||| ||||| ||||| ||||| ||||| |||| ||
TCACAGAAACTTCTAAAAGA TGGGT ATG ACATA AAATA ATATC ACGGA GAAA CA /
GGCACCTATAATAAAAATAT TAAAAA TCT TAA - C - ATCTT- AAG
ACATCTGTAAAAAATTGGGT
TTTGTGGTTAG
GAM2116 GGTATATATTTATAAAAAAG 252 TAACATCGTA 3322 ATAAAAAAG-- C CGCGGAA GACAC CATCAT
TTTTTGATTACGATGTCATA ATCAAAAGAA TTTTTGATTACGATGT ATA AGAG ATTAA A
CGCGGAAAGAGGACACATTA TTGC |||||||||||||||| ||| |||| |||||
ACATCATACATCAATTAATT gaaaactaatgctaca tAT TCTT TAATT /
ACATTCTTATAACATCGTAA TTTAAcgttaa a ------- ACAT- AACTAC
TCAAAAGAATTGCAATTTTG
ATGTATACC
GAM2117 TGTATTCAGTATTTTTGGAA 253 TCAGTATTTT 3323 Ttc g ca aaAA A
TCATAAAAAAATAAAAAAAG TGGAATCATA TGTA agtattttt gaat taaa TAAAA A
TTTTACTAATTTAAAATTTA AAAA |||| ||||||||| |||| |||| |||||
AAAAGTATTTACA ACAT TTATGAAAA TTTA ATTT ATTTT A
--- A AA AATC G

GAM2118 GTGGTTCTCTGCTTTTCCTC 254 TCTGCTTTTC 3324 Ctc c t c -------- CA
CAGAGGTCTGTGAGCACAGT CTCCAGAGGT GTGGTT tg tt tc tccagaggtctgt GAGCA G
TTGCTCAAGAATAAGCAGAC CTGT |||||| || || || |||||||||||| |||||
CTTTGGATGACAAACACAAA CACCAA AC AA AG AGGTTTCCAGACG CTCGT /
ACCAC AAC A C T AATAAGAA TT

GAM2119 GCGTACCCTGCTCGGGCTGG 260 ACCCTGCTCG 3330 --- -- - C---- - C C TCCA A
GTACCAGCAGCCGACGGAGA GGCTGGGTAC cgggctgg gtaccagcA GC CGA GG AGAAGCGG GGT GG GC G
AGCGGCGGTCGGTCCAGCAG CAGC |||||||| ||||||||| || ||| || |||||||| ||| || ||
ACGCCGTTCCCGCCCCGCTT GCCCGACC CATGGTCGT TG GCT CC TCTTCGCC CCG CC CG A
CTACCACTACTCGCGTAATG ATG AA C CATCA A - C TTGC C
CTGGTACGTACCAGCCCGAA
GAAGGAGACGT
GAM2120 GACGCCGTTAATAATTGGCA 255 TGTGCACACC 3325 G AATAA-- A A - GC- C TAG
GTAAACTGCGAAAGGGCGTA TTTCCGCGGT GAC CCGTT TTGGC GT AACTGCG AAAGG GTACATCG AG T
CATCGCAGTAGTGATTTTAC TCAC ||| ||||| ||||| || ||||||| ||||| |||||||| ||

GATGTGCACACCTTTCCGCG CTG GGCGA AACCG ca ttggcgc tttcc cgtgtAGC TT G
GTTCACCGCCAACAACAAAA - AAACAAC C c c aca A TTA
GCGGGTC

GAM2121 CGAATGTATCTAGTTCGTTG 261 TATCTAGTTC 3331 Gta-- tt tgaa- - aa
AAGTATGCAACTCGCATTGC GTTGAAGTAT CGAAT tctag cgt gta tgc C
AAGATACGTGTTAGAGAATA GCAA ||||| ||||| ||| ||| |||
GTTTG GTTTG AGATT GCA CGT ACG /
ATAAG GT TAGAA T CT

GAM2122 GGGCGCCGCCGCCACGAAGG 256 ACCCTGCGTT 3326 C- -- - ---- - accc ttttt aaaa--
T
AGACCCTGCGTTTTTTCTTC TTTTCTTCGT GC GC CGC CACGA AGG AG tgcg tcttcgt
CCAT C
GTAAAACCATTCAAATGGCT AAAA || || ||| ||||| ||| || |||| ||||||| ||||
CGCCGCGAAGATGTCTGTAC TG CG GTG GTGTT TCC TC ATGT AGAAGCG
GGTA A
CTACCTACAATTGTGAGTGT AA TT A AACA A C--- CTGT- CCGCTC A
TGCAAGTGTCC

GAM2123 GTATTTATACATATCGTCAA 262 CACTATGTGT 3332 - TC ATC TTTG AAT
TCGTCATTTTTGTGTAAAAT AAATTAC GTA TTTATACATA GTCA GTCATT TGTAA G
GATAATTACAAATGACAAAT ||| |||||||||| |||| |||||| |||||
GACACTATGTGTAAATTAC cat aaatgtgtat cAGT CAGTAA ACATT A
t ca AAA ---- AAT

GAM2124 AACCCTGCGAAAAGAAGCTG 257 AAGAAGCTGT 3327 GAAaa a cta- tat
TGCTACTATATTTTGCTAGG GCTACTATAT AACCCTGC ga gctgtg cta t
CAACATGGTATCAGCAGGGT TTTG |||||||| || |||||| |||
T TTGGGACG CT TGGTAC GAT t
A---- A AACG Cgt

GAM2125 GATATCAACCTGTGCCTGTA 263 TGCCTGTATT 3333 A- - a g tca
TTAGCTGTGTCAGAAGCCAA AGCTGTGTCA GATATCA CCTGt gcctgt ttagct tg g
AGCTAAACAGGCTATAGGAA GAAG ||||||| ||||| |||||| |||||| ||
TGGTATT TTATGGT GGATA CGGACA AATCGA AC a
AA T - A Cga

GAM2126 CTATCTAATAATATACCTTA 258 TACCTTATAC 3328 AATAtacc tgg g aaTA AA
TACTGGACTAGTGCCAATAT TGGACTAGTG CTATCTAAT ttatac acta tgcc TT A
TAAAATGAAGTGGGCGTAGT CCAA ||||||||| |||||| |||| |||| ||
GTGTAATTTGATTGGGTGG GGTGGGTTA AATGTG TGAT GCGG AA A
GTTT---- --- - GTG- GT

GAM2127 TGTAAGTTTGGGCGGATGAG 264 TGAGGAAGTG 3334 TTTG GA aa---- gg g g g

GAAGTGGGGCGCGGCGTGGG GGGCGCGGCG TGTAAG GGCG tgagg gt ggcgcg c tgg A
AGCCGGGCGCGCCGGATGTG TGGG |||||| |||| ||||| || |||||| | |||
ACGTTTTAGACGCCATTTTA ACATTT CCGC ATTTT TA CCGCGC G GCC /
CA TA-- AG GCAGTG GG - G G

GAM2128 AGCGGACGGTAGTGCTTTAC 265 TAGTGCTTTA 3335 G C ta-- a a aat T
TAAAAGATAATACTGTGGTC CTAAAAGATA AGC GA GG gtgcttt ctaaa gat ac G
GATCGTTTAGAAGGCATGAA ATAC ||| || || ||||||| ||||| ||| ||
TCCTTTGGCT TCG TT CC TACGGAA GATTT CTA TG T
G T TAAG - G GC- G

GAM2129 GTCGGATCGAGTTTTATTCA 266 TAACGTTGAC 3336 G TT AT A T T
AAGTTGTTATGGGTACTAAC GATTCTCGAT GTCG ATCGAG TT TCAA GTTG TA G
GTTGACGATTCTCGATGCGG GCGG |||| |||||| || |||| |||| ||
C Cggc tagctc ag agtt caat AT G
g tt c- g C G

GAM2130 GTATCAAAAATATCAATATC 267 TCAAAAATAT 3337 c c atctaataccCA CA - C----
CA
TAATACCCAATCAATGTTTT CAATATCTAA TAt aaaaatat aat AT ATGTTTTT ATAT
TGATAT C
TATATCTGATATCACAAAAT TACC ||| |||||||| ||| || |||||||| |||| ||||||
ATCAATAATGTATCAAAAAT ATA TTTTTGTA TTA TA TATAAAAA TATG ACTATA
A
ATCAATATCTAATACCCAAT - A ACCCATAATCTA AC C TAATA AA
TAATGTTTTTATAT

GAM2131 TGTTTTTATATCTGATATGT 271 TGATATGTTA 3341 C-- aa- caa AAA TC
CTAATA
TAAAATATCAATAATGTATC AAATATCAAT TTATAT tgatatgtta atat taatgTATCA ATA AATAT
C
AAAAATATCAATATCTAATA AATG |||||| |||||||||| |||| |||||||||| ||| |||||
CCCAATCAATGTTTTTATAT AATATA ACTATGTAAT TATA ATTGTATAGT TAT TTGTA
C
CTGATATGTTAAAATATCAA AAA AAC AA- CTA TT ACTAAC
TAATGTATCAAAAATATAAA
TAATCA
GAM2132 GGTAAAAGAAAGTTAGAAAT 268 TATGATGAAC 3338 G AGAA AAG A
TAAAGAAATTAGTGATTTAT AAGTTTTTTT GGTAAAAGAAA TT ATTA AAATT G
ATGATGAACAAGTTTTTTTT TACT |||||||||| || |||| |||||
ACT tcatttttttt aa tagt TTTAG /
g caag atA T

GAM2133 CGTCTGAATATGCATCTGAA 269 ACCAGTATAG 3339 AATA A --------- T A-- TT
ACTTGGACATTAGTTGACAC AAACTTTTAG CGTCTG TGC TCTGAA ACT GG CA A
CAGTATAGAAACTTTTAGAA AAGC |||||| ||| |||||| ||| || ||

GCGCTCCAGACG GCAGAC Gcg agattt tga cc GT /
CTC- a tcaaagata - aCA TG

GAM2134 TATATATTATAAAAAAGTTT 270 TATATTATAA 3340 taaa--- ag GAAAAAG-
CACATTAA
TTGATTACGATGTTATAAGA AAAAGTTTTT tatta aa tttttgattACGATGTTATAAGAG GA
C
GGAAAAAGGACACATTAACA GATT ||||| || ||||||||||||||||||||||| ||
TCATACATCAATTAACATTC GTAGT TT GAAAACTAATGCTACAATATTCTT CT
/
TTATAACATCGTAATCAAAA TTTAACG AA ACAATTAA ACATACTA
GAATTGCAATTTTGATGTAT
A
GAM2135 CTCAAAGCTCATCTCTTCTT 278 AAGCTCATCT 3348 Aa c c - tcac CA
CACTTGCGTCAACGAATGTA CTTCTTCACT CTC agct at tctt ct ttgcgT A
AATTAGTAAGAATAGCTAGA TGCG ||| |||| || |||| || ||||||
G GAG TCGA TA AGAA GA AATGTA C
A- - - T TTA- AG

GAM2136 ATATTTAAAGAATAAATTTT 272 TAAATTTTTA 3342 T - tata atA-- T
TTATTAAG
TATATTATAACAATATAATT TATTATAACA TATT AAAGAAtaaatt tttatat acaat ATTCT CTAAA
A
CTTCTAAATTATTAAGACTT ATAT |||| |||||||||||| ||||||| ||||| ||||| |||||
ATTCCTTTTAGAGAATCAAT ATAA TTTTTTATTTAA AAGTATA TGTTA TAAGA GATTT
C
GATTGTATATGAACAATTTA T C ---- GTAAC - TCCTTATT
TTTTTTTAATAT

GAM2137 ATATTAAAAAAATAAATTGT 273 TAAATTGTTC 3343 A A gttc ---- cat - ----- AT
TCATATACAATCATTGATTC ATATACAATC T AAA AAtaaatt atat acaat tgATTCT CTAAA
AGGA A
TCTAAAAGGAATAAGTCTTA ATTG | ||| |||||||| |||| ||||| ||||||| ||||| ||||
ATAATTTAGAAGAATTATAT A TTT TTATTTAA TATA TGTTA ATTAAGA GATTT
TTCT /
TGTTATAATATAAAAATTTA A C AAA- ATAT T-- A AATAA GA
TTCTTTAAATAT

GAM2138 ATTTGTTAATGGTCTCGATG 279 TTAATGGTCT 3349 G - ctcgat--- a g C
TAATCGTCGTAGCTGCTACG CGATGTAATC ATTT ttaa tggt gt atc tcgTAG T
AGATAACTTTTTTTCTGCCA GTCG |||| |||| |||| || ||| ||||||
TTTAAGAGAT TAGA AATT ACCG CA TAG AGCATC /
G T TCTTTTTTT A - G

GAM2139 TTGTTAGCCGCTTCCTTTTC 274 ACGGAGGAAA 3344 A CG- C-- A AATACAA
CATGAAATACAAATAATAAG CGAAGAATGC TTGTT GC CTTC TTTTCC TGA A
ATCACGGAGGAAACGAAGAA AACA ||||| || |||| |||||| |||

TGCAACAA Aacaa cg gaag aggagg aCT T
- taa caa c AGAATAA

GAM2140 TAAGTGTGCTAAACGCCGCA 275 TGTTTTGACT 3345 T TAAAC AG AT
GAGCAAAACGTTATAATAGA GTGGTGCCTA TAAGTG GC GCCGCAG CAAAACGTT A
TGTTTTGACTGTGGTGCCTA CTTA ||||||| || ||||||| |||||||||
CTTA attcat cg tggtgtc gttttgtAG A
c ----- a- AT

GAM2141 TCTGCAATTAAATTCTGTTA 280 TCTGTTATCG 3350 -- TT tc - --------- gggaa T
TCGAAGTGGGAAGATTTGTA AAGTGGGAAG TCTG CAA AAAT tgtta tcg aagt gatttG A
ATCAAATTAAAAACTTAAAA ATTT |||| ||| |||| ||||| ||| |||| ||||||
TATTACGATTAACAAGATTT AGAC GTT TTTA ACAAT AGC TTCA TTAAAC A
TTTGACCAGA CA T- GA T ATTATAAAA AAAA- T

GAM2142 CGTCACTGAAATACGCGCGC 281 TATCGCGCAC 3351 A AAATAC ----- A A CC
GAGGAACGCCCCGACGATCC AGGACAGCGA CGTC CTG GCGCG CG GGA CG C
CGGATATCGCGCACAGGACA CG |||| ||| ||||| || ||| ||
GCGACG gcag gac cgcgc GC CCT GC C
c aggaca tatAG - A AG

GAM2143 CATGGAATGATGCGGCACGG 282 CACCCGACGC 3352 A A GCAC C AGCGACG
CGCGACAGCGACGGGGAAAT ACCATCCATG CATGGA TG TGCG GG GCGAC G
GGTCGCACCCGACGCACCAT |||||| || |||| || |||||
CCATG gtacct ac acgc cc cGCTG /
- c agc- a GTAAAGG

GAM2144 GCGGTTCTTGTTCTCCCTGA 286 TGACAAGGAG 3356 TTCT CTCC C - ------- ACA
GCCACCATCACCCAGACACA GTGATGTGTG GCGG TGTT CTGAG CAC CATCACC
CAGAC G
GATAGTCTGACAAGGAGGTG ACTC |||| |||| ||||| ||| ||||||| |||||
ATGTGTGACTCGGAAAAACA CGCC ACAA GGctc gtg gtagtgg gtCTG /
CCCGC C--- AAA- a t aggaaca ATA

GAM2145 GGTTGCTGCACAACCGGGGC 276 TGAGGCCCTT 3346 CAACC TG ----- AT
TTTGCCCGGGGATTTCATCC GTAGTAACC GGTTGCTGCA GGGGCTT CC CGGGG T
CGTTCAAGGTGAGGCCCTTG |||||||||| ||||||| || |||||
TAGTAACC ccaatgatgt tcccgga GG GCCCT T
----- gt AACTT AC

GAM2146 TGATGAGAAAGTATTCTTCA 287 AAGTATTCTT 3357 GA---- a tcac- ac
CTGTAGACATGTTATATTAT CACTGTAGAC TGATGA aagt ttct tgtag a
CAGAAACTTCAAGAATTATC ATGT |||||| |||| |||| |||||

A ACTATT TTCA AAGA ATATt /
AAGAAC - CTATT gt

GAM2147 CGTTTGGATGAAGTGATTCC 277 TGTTAAAATT 3347 GA- TGA- - AATTCGAA G
AGAATTCGAATTAGTATCGA TTAGCTGAGA CGTTTG TGAAG TTC CAG TTAGTATC A
CCGATGTTAAAATTTTAGCT AGTA |||||| ||||| ||| ||| ||||||||
GAGAAGTATCTTCAGGATGA GCAAGT ACTTC aag gtc aattgtAG C
ACG AGG Tatg a gattttaa C

GAM2148 CATCTGTAATTAATAGGTTC 283 TAGGTTCCTC 3353 GTAA-- gt c ttaca- a
CTCGATTTACATCAAATTTT GATTTACATC CATCT TTAAtag tcct gat tcaa t
GAAAGACTGTTAGGACTGTT AAAT ||||| ||||||| |||| ||| ||||
GGGAAATAAGGTG GTGGA GGTTGTC AGGA TTG AGTT /
ATAAAG -- - TCAGAA T

GAM2149 TTGTAGGTGCGGATAGGTCT 284 TACAGTGGCT 3354 A T ATA - T TA A- -- T A TCC- A
CTCTACAGAGCTGTATAGGT GCGGCGACGA TGT GG GCGG GGTC TC C CAG GCTGTAT AGG GTG CGG GGG C
GTGACGGTCCGGGACACCCA CCCC ||| || |||| |||| || | ||| ||||||| ||| ||| ||| |||
AGCCCGCCGCCCCTGTGTAC ACA CC CGcc ccag ag g gtc tgacatG TCC CGC GCC CCC /
AGTGGCTGCGGCGACGACCC A T --- c c gc gg TG C C CGAA A
CGCTCCAACAA

GAM2150 CCCTGCTCACGTACGAGTTC 285 TACAGTGTTC 3355 ------ - G T TCTAATCTTC TG - - AG
GATCTAATCTTCGGGGTGCG CATTCGTACT CCCT GCTCA CGTAC AGT CGA GGGG C GTA TGCGA T
TATGCGAAGTTGTTGCGTTA GTAC |||| ||||| ||||| ||| ||| |||| | ||| |||||
CAGTGTTCCATTCGTACTGT GGGA CGAGT Gcatg tca gct cctt g cat GCGTT /
ACGTTGAGCGCTAATAGGG TAATCG T - t ta-------- gt a T GT

GAM2151 ACCGCAGGAGGTACCCGTAG 288 TGTGATCCTC 3358 C -- C-- T GAAAAA
TCGTTGAAAAATTGAAAGTG CTCCGGT ACCG AGGAGG TAC CG AGTCGTT T
GCGGCTCCGTATGTGATCCT |||| |||||| ||| || |||||||
CCTCCGGT tggc tcctcc gtg GC TCGGCGG T
c ta tAT C TGAAAG

GAM2152 TTTACATTTATTAAATTAAC 2743 TAAATTAACA 5813 TAT- aca tt------ aAAA T ACAAT
ATTATGTTTAATACAAAATC TTATGTTTAA TTACATT taaatta ttatgt aatac TCTA CATG T
TATCATGACAATTATTTACA TACA ||||||| ||||||| |||||| ||||| |||| ||||
TGTGGACAGTATTTATTTTT GGTGTAG ATTTAAT AATATA TTATG AGGT GTAC /

TATATAAAATAATTTATTAT TATT AA- TTTTTTAT AC-- - ATTTA
GATGTGGA

GAM2153 ACAAGTTATGGAAATAAAGA 2740 TATGGAAATA 5810 Tt- - aa-- cgca
AACTCGCATGTTTTAGTTTT AAGAAACTCG ACAAG atg gaaata gaaact t
AGTCTATTTCTCATTCTCTT CATG ||||| ||| |||||| ||||||
GT TGTTC TAC CTTTAT TTTTGA g
TCT T CTGA TTTT

GAM2154 GCCCATCGAACGCTCTTCGG 2744 AACCGTAGTA 5814 C-- AA - T--- G- AA -- CAT
GATTATAATTTCAATGTCAT GCCGTTGTAG GCC ATCG CG CTCT CGG ATTAT TTTCA
ATGT C
CCTCTACATCTTGAAACCGT AGTC ||| |||| || |||| ||| ||||| ||||| ||||
AGTAGCCGTTGTAGAGTCGC CGG TAGC Gc gaga gcc tgatg aaAGT TACA C
GCGATAATGGC TAA GC t tgtt ga cc TC TCT

GAM2155 GGAAGTCAAGTATTTATACA 2745 TCAAGTATTT 5815 AA attt g T TT
CGTTGAGTGTCATTTACATG ATACACGTTG GG Gtcaagt atacac ttgagtg CAT A
TGTCATTTAAGTGTGTCATT AGTG || ||||||| |||||| ||||||| |||
TGACCC CC CAGTTTA TGTGTG AATTTAC GTG C
-- C--- - T TA

GAM2156 TCACTTTCAGTTTTTAGTTT 289 CTTGAACACA 3359 TCAGTTT --------- C AT
CAACTCTTATTGCGAGACTT ATTCTACTAA TCACTT TTAGT TTCAA TCTT T
GAACACAATTCTACTAACTT CTTC |||||| ||||| ||||| ||||
CAATAAGTGA AGTGAA aatca aagtt AGAG /
TAActtc tcttaacac c CG

GAM2157 TAGATATAAAACTAGGTAAT 290 TATAAAACTA 3360 GA aa- g- c cac A
CTATACACACTAAAAAGTTT GGTAATCTAT TA tataa cta gtaat tata ACT A
TTATACATTACGATAGATAT ACAC || ||||| ||| ||||| |||| |||
TATGGATA AT GTATT GAT CATTA ATAT TGA A
AG ATA AG C TTT A

GAM2158 TATATAATACCTTTACACCA 2748 TATAATACCT 5818 ta - acac cg acT TG
CGCAACTACATATATTGCTT TTACACCACG TA taat accttt ca ca ACATATAT C
TGTATATGTTGTATGAAAGG CAAC || |||| |||||| || || ||||||||
TAATTACGTA AT ATTA TGGAAA GT GT TGTATATG T
GC A ---- AT --- TT

GAM2159 GGTCTGAGGAAGATTAAGAA 291 AGGAAGATTA 3361 C a --- t TGTTC TT
AAAGGCCTCGTGTTCACTTG AGAAAAAGGC GGT TGaggaag tta agaaaaaggcc cg ACTTGG G
GTTGCCGTCAAGTATCCTGT CTCG ||| |||||||| ||| |||||||||| || ||||||
GGTTTTTTTCTACCTAACTT CCG ACTCCTTC AAT TCTTTTTTTGG GT TGAACT C

CCTCATGCC T - CCA T CCTA- GC

GAM2160 GCATTGAGCACTGCTAATAG 2741 TTGTGCAGAT 5811 TGA CT AA T AC TAAA GAG
GTTTGTATCACGTTAAAGAT TTAAACTTGG GCAT GCA GCT TAGGTTTG ATC GT GATTTA T
TTAGAGTGTATGAATTGTGC GTTT |||| ||| ||| |||||||| ||| || ||||||
AGATTTAAACTTGGGTTTTG CGTA CGT tgg gttcaaat tag cg ttAAGT /
CCTTATGC TTC tt -- t a- tg-- ATG

GAM2161 TCTGTCCAATCGGAAGTGAA 292 GTCATTTTTA 3362 - AAT-- ---------- AAC T
ACCACATCTTTGTGTCATTT ATCAGCCCCG TCTGT CC CGG AAGTGA CACA C
TTAATCAGCCCCGTTAAAGG TTAA ||||| || ||| |||||| ||||
TACAGA AGACA GG gcc tttact gTGT T
T Aaatt ccgactaatt --- T

GAM2162 GCCGCCCTGCGACACAATCA 293 ACACAATCAC 3363 C- acacaatca c c- ttt
CCCGTCCGTGGTTTCGAATC CCGTCCGTGG GCCGC CTGCG cc gtc gtgg c
TACACGACAGGCCCGCAGAC TTTC ||||| ||||| || ||| ||||
GCGGC CGGCG GACGC GG CAG CATC G
CA CC------- A CA TAA

GAM2163 CTCTACCTCTGGACTTCAGG 2753 TCAGGACCTG 5823 AC AC-- a t ga tt
ACCTGCAGACTCTTAGTGAG CAGACTCTTA CTCT CTCTGG Ttcagg cc gca ctc a
CTTGTTGGCCCTGAAAATGC GTGA |||| |||||| |||||| || ||| |||
CGGAGAGGGAG GAGG GAGGCC AAGTCC GG TGT Gag /
GA GTAA C T TC tg

GAM2164 CACACATGCTTCCGTATGTC 2749 TATGATCGAC 5819 AT CC A T T C
GTATCTTGTTTAACTTTTTA AATAGAGCCA CACAC GCTT GT TGTCG ATC TGTTTAA T
AGTATGATCGACAATAGAGC GTGT ||||| |||| || ||||| ||| |||||||
CAGTGTG Gtgtg cgag ta acagc tag atGAATT T
ac a- - - t T

GAM2165 CAACGAGCTAGACTTTGTTA 2742 TAGACTTTGT 5812 GAGCtag - ---------- a
TGGAGAAACTCTAAAAAAAA TATGGAGAAA CAAC actttg tta tggag a
TTGTTAATTAAAGTAAATAG CTCT |||| |||||| ||| |||||
TTG GTTG TGAAAT AAT AKctc /
ATAAA-- T TGTTAAAAAAA a

GAM2166 TGTTGATACTTGATATTGAT 2746 TTGATAATTA 5816 ACT- t --- ag tagtataAT AT T
AATTAGTATAATTAGTATAA GTATAATTAG TTGAT TGATAt gata att tataat TAGTATA TAGTA A

TTAGTATAATTAGTATAATT TATA |||||| |||||| |||| ||| |||||| |||||||| |||||
ACTATGTATTATATTTCATT AATTA ACTATA CTGT TAG GTATTA ATTATGT
ATCAT A
ATTATGAGGATTTATGTCAT AAGT - ATT GA TTACTTTAT -- T
ATCATGAAATTAATA

GAM2167 TTATTATATACACAGCATAC 2754 CAGCATACAT 5824 ATACAcagcat- tat
ATAAGTGTATATTATTTACA AAGTGTATAT TTATTAT acataagtgta t
CTTATGTTTATAACTCGACG TATT ||||||| ||||||||||
TAATAA AATAATG TGTATTCACAT /
CAGCTCAATATT tta

GAM2168 GATGGACGGCCAGGCCTCCG 2747 TCAGCAGCAG 5817 A GCC C- GA- A A- AA - C
AGCAGCGCATCCTGCAACTG GAGCGTGCCG GATGG CG AGG CTCC GC GCGC TCCTGC
CTG CG G
CGCGTCCGTCAGCAGCAGGA CCAA |||||| || ||| |||| || |||| |||||| ||| ||
GCGTGCCGCCAAGGAGCTCC CTACC GT TCC GAGG cg cgtg aggacg gac GC T
TCGATGCCATC - AGC TC aac c cg ac t C

GAM2169 CACCGGAACCCACCAGAGGC 2750 CCGGAACCCA 5820 cc ca---------- a
GGAAGCCGCCTTCGCCCGTG CCAGAGGCGG CAccggaa cac gaggcgg a
AGGGTGCGTGTGTTTTCTGG AAGC |||||||| ||| |||||||
TG GTGGTCTT GTG TTCCGCc /
TT TGCGTGGGAGTGCCCGC g

GAM2170 AGATCTAGGTTATTTGATGA 2757 TAGGTTATTT 5827 g gacac gcagGAAC
CACCCGCAGGAACACATACA GATGACACCC AGATCtag ttatttgat cc A
ACAGGAGAATTAAATGAATT GCAG |||||||| ||||||||| ||
AGATCT TCTAGATT AGTAAATTA GG C
A AGA-- ACAACATA

GAM2171 CGTTAGCCCAAAGAGTGAAG 2758 AAGGATGCAG 5828 G CAA -- CTAT CTTTA -- T
AGT
TCTATTCCCTTTATTGAGTC CTTCGTGCTC CGTTA CC AGAGT GAAGT TCC TTGA GTC
CTG T
TCTGAGTTTTCCCAGCGATA TAGG ||||| || ||||| ||||| ||| |||| ||| |||
TTCAAAGGATGCAGCTTCGT GCAGT gg tctcg cttcg agg aACT TAG GAC T
GCTCTAGGTGACG - a-- tg acgt a---- TA C CCT

GAM2172 TGAAATGGACTATGTAAGCT 2759 GACTATGTAA 5829 AA ga a aag-- ggg-- ca
GGGGGCACATATATGTATAT GCTGGGGGCA TG ATG ct tgt ctg gca t
ACGGAGGAAACAAGGACATG CATA || ||| || ||| ||| |||
GCA AC TAC GA ACA GGC TGT a
GG AG - AAGGA ATATA AT

GAM2173 GCTGGGGCCATATATATGTG 2751 TACCTGGCAT 5821 G C ATA G A-- A
CAGGACATTAACGATGATAC AAGGTGCCCG GCT GGGC AT TATGT CAGG CATT A
CTGGCATAAGGTGCCCGGGC GGC ||| |||| || ||||| |||| ||||
cgg cccg tg atacg gtcc GTAG /
g - ga- - atA C

GAM2174 GCCACATTGGACCACAGGTG 2752 TATCACAGAC 5822 A T GA ACAG--- ACCA
GTGCCACCATTACAGGTATC TAAGGGACAT GCC CAT G CC GTGGTGCC T
ACAGACTAAGGGACATGAGG GAGG ||| ||| | || ||||||||
C Cgg gta c gg cactatGG /
a - ag aatcaga ACAT

GAM2175 TTATGTGTATAACACAGAAA 2755 TATAACACAG 5825 - acagaaa gaaa- g AAAG
AGGAAATATGGCTAAAGGTA AAAAGGAAAT TTATGT Gtataac ag tatg CT G
AAAGGCATGGTAGACTATAA ATGG |||||| ||||||| || |||| ||
AGGGTTGTACTATATGA AGTATA CATGTTG TC GTAC GA /
T GGAAATA AGATG G AAAT

GAM2177 AAACAGCTAACGTTGGGCCA 2761 ACGTTGGGCC 5831 A Aac- aacagga C T G ---
C- G
AACAGGATATCTGCGGTGAG AAACAGGATA AC GCT gttgggcca tatctg GG GA CA GTTT
GGCCCCG C
CAGTTTCGGCCCCGGCCCGG TCTG || ||| ||||||||| |||||| || || || |||| |||||||
GGCCAAGAACAGATGGTCCC TG CGA CAACCCGGT ATAGAC CC CT GT CAAG
CCGGGGC /
CAGATATGGCCCAACCCTCA A CTCC ------- - - G AGA AA C
GCAGTTT

GAM2178 ATGTTGTTTTACGATATAAT 2762 TGTAACATAT 5832 TTTACG A-- ----- A
ACAACTATAAAATATGGAGA ATAACAGTAC ATGTTGT ATATA TACAA CTATA A
TCTTGTAACATATATAACAG AACA ||||||| ||||| ||||| |||||
TACAACAT Tacaaca tatat atgtT GGTAT /
tgacaa aca CTAGA A

GAM2179 CCTTTCATTGTAAATGTATG 2763 TGGCACAAGA 5833 AAA--- A- ---- - ---------- T
GTTTGATAATGATGAAAGAA CTGAAGGG GT TGT TGGTT TGATAATG ATGAAA
GAAA T
ATTCTTTTCCTTATACCTGT || ||| ||||| |||||||| |||||| ||||
TGGGATTTTATATATTATCA ca ACA ACCAG ACTATTAT TATTTT CTTT C
AGATGACCAAAACAAATGGC cggtAA AA TAGA A AGGGTTGTCCATATTC T
ACAAGACTGAAGGG

GAM2180 GGGATACTGTTCGCTTTTTT 2756 TACTGTTCGC 5826 GG c cttt t TTA
CTTTCGTGTCTGTTTATCTT TTTTTTCTTT G Atactgtt gctttttt cg gTCTGT T
ATAGATCGTGCCGAGGAAGT CGTG | |||||||| |||||||| || ||||||

AGCAGTATTTC C TATGACGA TGAAGGAG GC TAGATA /
TT - CCGT - TTC

GAM2181 GGGAAATTTGTTCAACGCAT 2764 TGGAATCGTC 5834 A- TCA CATT TC
TTTTCAATTTCACGCAATTG ACGCAGATGC GGGA ATTTGT ACG TTTCAATT A
GAATCGTCACGCAGATGCTC TCTC |||| |||||| ||| ||||||||
TC ctct tagacg tgc aaggtTAA C
cg cac t--- CG

GAM2182 TTGATTTGAACATAGTCATA 2765 TCTAATAGAT 5835 A TAAG ATAAA A CT CT T T AT
CC CTG
AGGGGATAAATAATACTTTA AGCCCTGACT TAGTCA GGG TA TA TTATATTT GAT G GG
TGA CATT C
TATTTCTGATTGTGGATTGA AGAC |||||| ||| || || |||||||| ||| | || ||| ||||
CCCATTCTGCTTAAAATGCT atcagt ccc at at AGTGTAAA TTA C CC GCT GTAA T
TCGCCCATTGAAAATGTGAT - ---- gatag a ct AG - - -- TC AAT
CTAATAGATAGCCCTGACTA
GACAAATTAA
GAM2183 TCCAGAAAGCTCTCCAGACC 2766 ACAGTATACA 5836 AAGCTCTCCA CATTT AT
ATTTTACTGTTTATACACAA AGTCATTTTA TCCAGA GAC TACTGTTT A
ACAGTATACAAGTCATTTTA TGAA |||||| ||| ||||||||
TGAATCTGGA AGGTCT ctg atgacaAA C
aagtatttta aacat CA

GAM2184 GCTTTTCGTCTCTCCAAGGA 2771 CAAGGAACAC 5841 TC TCTCcaa a tg gct
ACACTGGGTCCGCTGAAAGG TGGGTCCGCT GCTTT GTC gg acac ggtcc g
GACCGTGTACCGACCAAAGC GAAA ||||| ||| || |||| |||||
CGAAA CAG CC TGTG CCAGG a
C- ------- A -- Gaa

GAM2185 TATGCTACTATTGATGTACA 2767 TACTATTGAT 5837 C tatt --- att cac
ATTTGACACACGCTTCATTA GTACAATTTG TATG tac gatgta ca tga A
TGAACTACATCCTGTACCAT ACAC |||| ||| |||||| || |||
G GTAC ATG CTACAT GT ACT C
C TC-- CAA ATT TCG

GAM2186 GGCCGTCTGGTTCGAGGATA 2768 GAGGATATGA 5838 C GT- a t- tg - c c
TGACCCCCGCCGAGCTGGAG CCCCCGCCGA GGC GTCTG TCg gga a acc cc gc g
GTTGTCTTCCCGACTACGGA GCTG ||| ||||| ||| ||| | ||| || ||
CGCC CCG CAGGC AGC CCT T TGG Gg cg /
- ATC - TC GT A t a

GAM2187 TCTAAACAGTTGGCGTTAAC 2769 TACAGCATTT 5839 - GG -- - TT A- AGATTT
TT

GCTTATGCATACATTCAGAT GCTGTTGTAA TCTAAAC AGTT CGTTA AC GC ATGC TACATTC
TATGTGC T
TTTATGTGCTTTATTGCATG CGGG ||||||| |||| ||||| || || |||| ||||||| |||||||
TACGAATGTACAGCATTTGC AGATTTG TCgg gcaat tg cg tacg atGTAAG ATGTACG A
TGTTGTAACGGGCTAGTTTA A -- gt t tt ac C----- TT
GA

GAM2189 AATGACCTATATGTTAATAC 2193 TAATACTCGA 5263 CC TGTta cg-- tg tg t
TCGATTGATATTGATATTGA TTGATATTGA AATGA TATA atact at atat ata t
TATTGATATTGATAATTAGT TATT ||||| |||| ||||| || |||| |||
GTATATTATATTTCATT TTACT ATAT TGTGA TA TATA TAT G
TT TATA- TTAA GT GT A

GAM2190 ATGTCTATCCAGTATATGCG 2772 TACAATATCT 5842 TATCCA -- AG A--- TA- T T
GT
AGTAAGTCTTATCTTGTCAT GTATAAGTAC ATGTC GTAT ATGCG TA GTCT TCT GTCA
TG T
TGGTTTACATTGATCAGAGT CCTT ||||| |||| ||||| || |||| ||| |||| ||
CAGATACAATATCTGTATAA TACAG catg tatgt at tAGA AGA TAGT AC /
GTACCCTTCCGACAT CCttcc aa ct aaca CTG C T AT

GAM2191 GTACTGGGTCTCTCTGGTTA 2194 TCTCTGGTTA 5264 C C a tct CT
GACCAGATCTGAGCCTGGGA GACCAGATCT GTA TGGGT tctctggttag ccaga gagc G
GCTCTCTGGCTAACTAGGGA GAGC ||| ||||| |||||||||||| ||||| ||||
ACCCACTGC CGT ACCCA AGGGATCAATC GGTCT CTCG G
C - - --- AG

GAM2192 CACGCTTGCTTGCTTAAAGA 2195 AAGCTGCCAG 5265 - A---------- A
CCTCTTCAATAAAGCTGCCA TTAGAAGCAA CACGCTTG CTTGCTT AAG C
GTTAGAAGCAAGTTAAGTGT GTTA |||||||| ||||||| |||
G GTGTGAat gaacgaa TTC C
t gattgaccgtcgaaATAAC T

GAM2193 ATCATTTATTTATTGTATAA 2196 TATTTTATTA 5266 TTA- ------- AA CA- ta aaaat ta
cT
TATTTCATATATTTTATTAA AAATTTACAT TTTA TTGTAT TATTT TA ttttatt t catatt A
AATTTACATATTCTAACAAA ATTC |||| |||||| ||||| || ||||||| | ||||||
TGTGCGATAACAATAAAAAT AAAT AATATA ATAAA AT AAAATAA A GTGTAA
A
TAGATAAATAGGATATAAAA CTCG TTAACAA GG TAG TA CAAT- GC AC
CAATTTAAAGCTCAGGAT

GAM2194 AAAATGGCATATTTTAATAT 2201 AATGGCATAT 5271 - tt- tatatat TT
ATATGATTTTTATAGTCTTT TTTAATATAT AAaatggc atat taa gaTT T
AATTTTATTTATATAGTCAT ATGA |||||||| |||| ||| ||||
TTT TTTTACTG TATA ATT CTGA /

A TTT TTAATTT TA

GAM2195 ATGATATAAAAGAGTGCTAA 2197 TGCAACAGTC 5267 TATAAAA CTAAATTTTT TAAACTt- - tccta tt ctc
ATTTTTGAGTAAACTTGCAA CTAACATTCA A GAGTG GAG gc aacag aca cac T
CAGTCCTAACATTCACCTCT CCTC | ||||| ||| || ||||| ||| |||
CGTGTGTTTGTGTCTGTTCG T CTCGC CTC CG TTGTC TGT GTG /
CCATCCCGTCTCCGCTCGTC CACTG-- ---------- TGCCCTAC C TG--- TT TGC
ACTTAT

GAM2196 TTTTTGGAGGTTCGCTTTTC 2198 TTGGAGGTTC 5268 - tt------ c ata t
TATATCTCATGAAGAAAGTC GCTTTTCTAT TTTttgg agg cg ttttct tc C
GCTGTTCGTCCTACTAAAAA ATCT ||||||| ||| || |||||| ||
AAAAATC TCC GC GAAAGA AG A
A TGCTTGTC T --- T

GAM2197 GAGCATGAGAGCGGCTTTAG 2199 TGAGAGCGGC 5269 g - g ag TC AT TTT- AA CCT A
CGTAAAGTTTTTCTCCGATA TTTAGCGTAA agagcggc ttta cgtaa ttTTTC CG AGT GAT AGGT TAAG A
GTTTTGATAAAGGTCCTTAA AGTT |||||||| |||| ||||| |||||| || ||| ||| |||| ||||
GAATCTTAACCTATCCCTTA TTTTGCCG AGAT GCGTT AAAAAG GT TCA CTA TCCA ATTC /
CTCTGATGAAAAAGATTGCG A C G AG TA C- TTCC -- --- T
GTAGACGCCGTTTTAGAAAT
C
GAM2198 CAGCTTCGAGGTATAACCTA 2773 ATGATGTTTT 5843 --- A CAACAC G -- T GAA CTT
CAACACGGAGGGGAAGGGGG GTCCCTCTGT TATA CCTA GGAGGG AAG GGGGGG ACAAAACGT ATTAGA T
GGTACAAAACGTGAAATTAG CTTA |||| |||| |||||| ||| |||||| ||||||||| ||||||
ACTTTTTTTTTAATGATGTT ATGT GGAT CCTTTC ttc tctccc tgttttgta taATTT /
TTGTCCCTCTGTCTTACTTT GGA C AC---- a tg - g-- TTT
CCCATAGGCTGTAAGGCCCT
CGAGGAAGAG
GAM2199 AAGACTGAGAAAACTCGATG 2202 GGTGCATAAT 5272 GAAA-- TCG --- C
TACTTCCGAGGATGTGGTGC GTCACACATC AAGACTGA AC ATGTACT TC G
ATAATGTCACACATCAGTCT AGTC |||||||| || ||||||| ||
T TTctgact tg tacgtgg AG A
acacac taa TGT G

GAM2200 GTTGAAAATAACTTTATAGA 2774 TAGAATTTTA 5844 ACTTTAta a tttctttatt CT
ATTTTAAAATTTTCTTTATT AAATTTTCTT GTTGAAAATA gaatttt aaat AAAAT T
AAAATCTTTTGTTTTTCTTT TATT |||||||||| ||||||| |||| |||||
TATTATTTCAAAATTTTGTT TAATTTTTGT TTTAAAA TTTA TTTTG /
TTTAAT -------- C TTATTTTCT- TT

GAM2201 GGTGTGAATATCAAGCAGGA 2200 AAGCAGGACA 5270 GAATATCaa- - ga- taacaag ga
CATAACAAGGTAGGATCTCT TAACAAGGTA GGTGT gc ag ca gtag t
ACAATACTTGGCACTAGCAG GGAT ||||| || || || ||||
CATTAATAACACC CCACA CG TC GT CATC /
ATAATTACGA A ACG TCATAA- TC

GAM2202 CACAATGGTAAGCCAGTGGT 2206 TACTATGTTA 5276 AAT A- CCA- GGTAT
AGTAAAGGTATAAGAAATTT CTGAACCTAG CAC GGT AG GTGGTAGTAAA A
GCTACTATGTTACTGAACCT GTG ||| ||| || ||||||||||
AGGTG gtg cca tc tatcatCGTTT /
gat ag attg AAAGA

GAM2203 GCTTACCAGTAGACAAAGAG 2203 TAGCTCCCTA 5273 ACC ACAAA AC - ACA----- -
CAA
CACAGCAGTACAAGCGCCAA TTTAAAGGC GCTT AGTAG GAGC AG CAGT AG CGC C
CAGCAGCGACTGACTACCCA |||| ||||| |||| || |||| || |||
CTGACTTAGCTCCCTATTTA cgga ttatc ctcg TC GTCA TC GCG A
AAGGC aat c---- at A CCCATCAG A ACG

GAM2204 ATGACTCGGCGCCGACTCGG 2204 TAGGTGGGTC 5274 GC GA GGC- G AAAA GGAT-
GACA GGTAG
CGACCGGCCAAAAGGTGGTG TTAAGAGAAG GCC CTC GACC GCC GGTGGT
GGGTGAT GGGTT G
GATGGGTGATGACAGGGTTG GTTA ||| ||| |||| ||| |||||| ||||||| |||||
GTAGGTCGTAAATCCCGGTC tgg gag ctgg tgg TCACCG TCCACTG CCTAA /
ACCTTGGTAGCCACTATAGG at aa aatt g atA- ATGGT GC-- ATGCT
TGGGTCTTAAGAGAAGGTTA
AGATTCCTCT
GAM2205 GCGGCGTGGATATATACTCC 2207 TGACTGGCGT 5277 C A A T C ------ TCA
AGCCAGAAAAGACTCAGATT ACATAGCCAT GCGG GTGG TAT TAC CCAG CAGAAA AGAC
G
GTCTCATGACTTTCTGACTG CCGC |||| |||| ||| ||| |||| |||||| ||||
GCGTACATAGCCATCCGC cgcc tacc ata atg ggtc gtCTTT TCTG /
- g c c a CAGTAC TTA

GAM2206 TGCTTGGTATGCATTGCTAC 2208 ATGCATTGCT 5278 TT T- -- cta- c tta
ACTTGCTTATGCTGCAACTG ACACTTGCTT TGC GG atg cattg ca ttgc t
CTTTCAATGAACATTCCCTT ATGC ||| || ||| ||||| || ||||
GCA ACG CC TAC GTAAC GT AACG /
TT CT AA TTTC C Tcg

GAM2207 GCCTGGGCTCGCTCGCGGTC 2205 TTCACTCGCA 5275 ----- - TCAG GAT
AGGGATCGATGACGGGTTCA GAGCACAGAG GCCTGGGCTC GCTC GCGG GGATC G
CTCGCAGAGCACAGAGAGTC AGTC |||||||||| |||| |||| |||||

CGGGC CGGGCctgag cgag cgct cttGG /
agaca a ca-- GCA

GAM2208 GACTTGATTACCGTCGACGG 2209 CGCCACGTCT 5279 CT C T CC- - T-- AGG
CCCGGGCTCTTCGAGGTCCA TCGTCGCTGC GA TGATTA CG CGACGG CG GGC CTTCG T
CGAAGTCCGCCACGTCTTCG TGAT || |||||| || |||||| || ||| |||||
TCGCTGCTGATCGTCTC CT GCtagt gt gctgct gc ccg GAAGC /
CT c c tct a cCT ACC

GAM2209 TAAAATTTGTGTGTGCAGCA 2210 AGGAATGTAA 5280 ATTTG TGC GACGAATT A
CGAACCAA
ATTGACGAATTTATTCCATG AATTGTTATC TAAA TGTG AGCAATT TATTCC TGA C
ACGAACCAACATAAATAATT ACAA |||| |||| ||||||| |||||| |||
TAAGGAATGTAAAATTGTTA ATTT acac ttgttaa gtaagg ATT A
TCACAATGGCTTTA CGGTa ta- aat----- a TAATAAAT

GAM2210 AAAGCAATCGTTACTTGATT 2211 AATCGTTACT 5281 aat - tt ttt- a ctTCT
TTAAAGACTTCTCAATTTCT TGATTTTAAA AAAGC cgt tac ga ta aga C
CTCTACATTTCCTGTATACG GACT ||||| ||| ||| || || |||
GCTTT TTTCG GCA ATG CT AT TCT A
--- T TC TTAC C CTTTA

GAM2211 GGTGAAATCTTCTGGGCTAG 2212 TAGTGCTCTC 5282 T TCTTC Ct g - tc-- ct
TGCTCTCACTCTCCTATCTG ACTCTCCTAT GG GAAA TGGG agt ct ctcac tcctat g
GCATAGGACTTCGTGAGTAG CTGG || |||| |||| ||| || ||||| ||||||
ACTTTCCCATTTCTTTTCTC TC CTTT ACCC TCA GA GAGTG AGGATA /
T T TCTTT TT - T CTTC Cg

GAM2212 GCAGATACTTCAAACAGGAT 2213 CTTTTTGGCG 5283 AT--- C---------- C
ACTGGTATCCTTTTTGGCGC CGCGCGCGAA GCAG ACTTCAAA AGGATA T
GCGCGCGAATTTTGAAGTTA TTTT |||| |||||||| ||||||
CCACTGT TGTC TGAAGttt tcCTAT G
ACCAT taagcgcgcgcgcggtttt G

GAM2213 CAACTTGTTCTGAGACGTCT 2214 TCCCTGGGGC 5284 T ACG GAT AT ----- TG----- TA
AAAG G
GGATCTGATCCCGACCGCTG TAGCAGAAAC GAG TCTG CTG CCC GACCGC TCGT
CTGCC AC A
TCGTTACTGCCAAAGACGAA TCTT ||| |||| ||| ||| |||||| |||| ||||| ||
AGTGGTAGGCGCGAACCGTT ctc agac gat ggg TTGGTG AGCG GATGG TG A
TGTGGTTTCCCTGGGGCTAG - aa- --- cg tccct TTTGCCA CG ---- A
CAGAAACTCTTTAGGTTG

GAM2214 GCAGAGACGAAAGAGGAGTA 2220 AGGAGTACTC 5290 GA AA- t gag g

CTCTTGAGTGCGCAGCGAGA TTGAGTGCGC GCAGA CG AGaggag actctt tgc c
AGAGTTTTCTCTCAGCGAAT AGCG ||||| || ||||||| |||||| |||
CTGC CGTCT GC TCTCTTT TGAGAA gcg /
AA GAC - GA- a

GAM2215 AAATCTATCTTATATACACA 2228 TTAGTGTTTA 5298 AT --------- A TTCTATCAA
TAATTATTCTATCAATTTTA ATAAAAATAT AAATCT CTTATAT ACAC TAATTA T
CCAATTAGTTAGTGTTTAAT GGGG |||||| ||||||| |||| ||||||
AAAAATATGGGGGATTT TTTAGg gggtata tgtg attGAT /
-- aaaataatt - TAACCATTT

GAM2216 TCCAATAGTACATTTTCCAG 2236 TTAGATATTA 5306 A- G TTCCAGAt t tgt attt ---- A
ATTAGATATTAATGTCGTAT ATGTCGTATT TCC ATA TACATT tagata taa cgt ga aCAG G
TTGAACAGAGCCTGTAACAT TGAA ||| ||| |||||| |||||| ||| ||| || ||||
CTCAATGTCTTTATTATCTA AGG TAT ATGTAA ATCTAT ATT GTA CT TGTC /
TAGCCAATGTAATATCCGGA CC A CCGAT--- T TCT ACT- ACAA C

GAM2217 TTATATATATACTAACATCT 2221 TATATACTAA 5291 G T---- C - G
ATACTACTAACCTAACTATG CATCTATACT actaacatctatactactaACCTAACTATG CCTAATG ATG
AGT GTCGGC T
GCCTAATGTATGCAGTGTCG ACTA |||||||||||||||||||||||||||||| ||||||| ||| ||| ||||||
GCGTCGCCGACAACTACATT TGATTGTAGATATGATGATTGGATTGATAC GGATTAT
TAC TCA CAGCCG /
ATATTATTAGGCATAGTTAG - TATAT A A C
GTTAGTAGTATAGATGTTAG
TATATATATAA
GAM2218 CCCTGAAAATCTTATGTCAT 2215 TTACCTGACA 5285 TGAAAA -- TA C GA
ATACTGTGTGGACATATATA GATGAGGACA CCC TCTTA TGTCA TA TGTGTG C
TATTACCTGACAGATGAGGA TATG ||| ||||| ||||| || ||||||
CATATGGG GGg ggagt acagt at ATATAT A
tataca ag cc t AT

GAM2219 TATGATATTTAAAATGGTTG 2216 TAATCTTTAT 5286 TAAAATGGTTGTTAT T- GCT
TTATATAAATTTACCGCTTA TCAGTATCAT TATGATATT ATAAA TTACC T
CAGGTAATCTTTATTCAGTA A ||||||||| ||||| |||||
TCATA atactatga tattt aatGG /
ct---------- ct ACA

GAM2220 AATATCATCTATTGAATATC 2222 AAGATTATTT 5292 C CT AT----- AAAT
TTTTTAAATTGCTAAAAAAG TGTTAATTCA AATAT AT ATTGA ATCTTTTT T
ATTATTTTGTTAATTCATTA TTAT ||||| || ||||| ||||||||
TATT TTAta ta taatt tagaaAAA /
t ct gttttat ATCG

GAM2221 TTATATTTTTTAAATATTTA 2217 TACAATATTT 5287 T- ------- TTAT TCTAT
TACATATTATATTTTATTTC ATTAAAATGT TTATATTTT TAAATATT TATACATA ATTTTATT
A
TATATCATATAATAAAATTT AA |||||||||| |||||||| |||||||| ||||||||
TGTGTATATCGTTACAATAT aatgtaaaa atttataa ATATGTGT TAAAATAA T
TTATTAAAATGTAA tt catTGCT TT-- TATAC

GAM2222 GGTATTTTTATCATATTTAT 2218 TCATATTTAT 5288 ATTTT c ttatt ttt
TTAATATTTTTTCATTAATA TTAATATTTT GGT TAt atat taatatt t
TTATCATATATAATATGACC TTCA ||| ||| |||| |||||||
CCA ATA TATA ATTATAA c
GT--- A TACT- TTa

GAM2223 CCCCCATCAGAAGGTTTAGG 2219 TTGTACATTC 5289 TCA TTTA TCCG TTAC ATC
TCCGGTATTTACGCCTTTAT CCTTCTGGGG CCCCCA GAAGG GG GTAT GCCTTTATC G
CATCGGTAGATGGAGGTTGT G |||||| ||||| || |||| |||||||||
ACATTCCCTTCTGGGGG gggggt cttcc ct catg tGGAGGTAG /
--- ---- ta-- t--- ATG

GAM2224 CTGCTGCCGAGGAACTGCTT 2223 TCGCCCAACT 5293 CGA AAC- T ATA A - C ACCTC
GATATGGACGGCCGCACCTC ACGCATACGC CTGCTGC GG TGC TG TGG CG G CGC A
AGAACAGCGACTCGCCCAAC CAGC ||||||| || ||| || ||| || | |||
TACGCATACGCCAGCAGCAG GACGAcg cc acg at acc gc C GCG /
a-- gcat c ca- c t A ACAAG

GAM2225 AACGCTTAATAGAAATTATT 2224 TATTGTACAT 5294 -- ATta cat-- tat t
GTACATTTTTCTATTAGTAT TTTTCTATTA AACGCTTA ATAGAA ttgta ttttc tagta G
GAGTGCTATGAAAATTTCCT GTAT |||||||| |||||| ||||| ||||| |||||
ACAAAAGTTCTGTTTTGAGT TTGTGAGT TGTCTT AACAT AAAAG ATCGT A
GTT TT GAA- CCTTT T-- G

GAM2226 CATAAATATTCTAAGCCAAA 2237 TTTGTTAGAA 5307 A GC TTTCTCGTG T C C T
T
TATTTTTCTCGTGATTAGTC TATCTGTG CATA ATATTCTAA CAAATATT AT AGT TG GT
AC T
TGCGTTACTTCTGTCACCAC |||| ||||||||| |||||||| || ||| || || ||
ACTCATATTTTTCATGGTAT gtgt tataagatt gtttATGG TA TCA AC CA TG C
TTGTTAGAATATCTGTG c -- TACTTTTTA C C - C T

GAM2227 ATGGCGGTTGTACTGTAATT 2238 TCACGGAGAT 5308 GG C ATT-- AAAT- TTTA
TCTCAAATCAAAGTTTTAAA ACTCTACACT ATGGC TTGTA TGTA TCTC CAAAGT A
GTATGCTTTGTCACGGAGAT ACGA ||||| ||||| |||| |||| ||||||
ACTCTACACTACGAAGTTAT TATTG agcat acat agag GTTTCG A
A- c ctcat gcact TATG

GAM2228 GTGACGGCCCCTGCGGTCGC 2225 CCGCACCATG 5295 - GC T C GCCT CTC -- CC- A
CTGACCTCCGTTGCCCGGGA TACGTCTTAG GTG ACG CCC G GGTC GAC CGT TGC GGG
C
CACCCACCGCACCATGTACG ACCA ||| ||| ||| | |||| ||| ||| ||| |||
TCTTAGACCACGGGTTCGTA CGC TGC GGG C ccag ctg gta acg CCC /
CGC A TT - a att- cat cc ccA A

GAM2229 GGTATTACCATAGACGCGGC 2229 TACCATAGAC 5299 Tta- ag g atag C AT
GTATAGTACCAGCGTATCTC GCGGCGTATA GGTA ccat acgcg cgt tacCAG GT C
ACCTGGTAGCGGCGCGTAGT GTAC |||| |||| ||||| ||| |||||| ||
GGATTTTGCC CCGT GGTG TGCGC GCG ATGGTC CA /
TTTA A- G ---- - CT

GAM2230 CAAAGCATTGAAGGTGGCTC 2226 TGAATGGGGT 5296 A TGAA G - AGAG GTTTCAG
GCCTAGAGCGGATTGTTTCA GAAGCAGCTA CA AGCAT GGT GCT CGCCT CGGATT T
GTAGTCCATAAATCTGAATG TGCT || ||||| ||| ||| ||||| ||||||
GGGTGAAGCAGCTATGCTGT GT tcgta tcg cga gtggg gtCTAA A
G G ---- a a gtaa ATACCTG

GAM2231 GCTCGTATGAGCCGGTGATT 2230 TCAATGGTGT 5300 AT - ATT AT TC CT A
CCGTTATCATTCTTGCTGCG ACTCGGTTCA GCTCGT GAGCCG GTG CCGTT CAT TTG
GCGTAT A
TATAACGTACGCTTAATTGT CGAG |||||| |||||| ||| ||||| ||| ||| ||||||
GTCAATGGTGTACTCGGTTC Tgagca cttggc cat ggtaa GTG AAT CGCATG /
ACGAGT -- t gt- ct TT T- C

GAM2232 TGACGAATTACGACATTATT 2231 TAGAGGACGT 5301 TACGACATTA a g tg- ac
TTAGAGGACGTGTGTGCGTA GTGTGCGTAC TGACGAAT TTTt gaggac tgtg cgt a
CATCAACGAGTCGCGGGTCC ATCA |||||||| |||| |||||| |||| |||
TTAAGAGGTTCGTCA ACTGCTTG GAGA TTCCTG GCGC GCA t
---------- A G TGA ac

GAM2233 CTTTCCACGTTGATCTTTTA 2227 TTGAAGCGTT 5297 C - TCTTTT---- TCT- T - T
TGTTTCTCTTCTGCGAGTTT GCAACATCTT CTTTC ACG TTGA ATGTTTC TC GC GAG T
ATTCAGTTGATTTTGAAGCG CGGC ||||| ||| |||| ||||||| || || |||
TTGCAACATCTTCGGCCGTT GAAAG TGC ggct tgcgaag AG TG CTT T
GAAAG T c tctacaacgt ttTT T A A

GAM2234 CTATCGCCACGGAACTCACT 2239 AGAGGACGTC 5309 CGCCA GAACTCAC A
TTATTTTa c c -- at
AATTATGACATTATTTTAGA TGTTCGTATA CTAT CG TAATT TGACA gagga gt tg ttcgt
a

GGACGTCTGTTCGTATATCA TCAA |||| || ||||| ||||| ||||| || || |||||
ACGAGTCTAAACTCCTTAAA GATA GC ATTGA ACTGT TTCCT CA AT GAGCa t
CGGTTTGTCAAGTTATACAA ATCA- AAAACAT- - TTGGCAAA - A CT ac
AACGACTAATAG

GAM2235 TAACAATATATTATTAGTTT 2244 TTAATAATAT 5314 ---------- TA
ATATTACTGAATTAATAATA AAAATTCCCA TAACAA TATATTATTAGTTTA T
TAAAATTCCCAATCTTGTTA ATCT |||||| ||||||||||||||
ATTGTt atataataattAAGT T
ctaacccttaaa CA

GAM2236 AAGGTTAGTGAGATTCCTAT 2245 TTAGTGAGAT 5315 tt ttcctattccaaaatCAT G T
TCCAAAATCATGAAGGAGTT TCCTATTCCA AAGG agtgaga GAA GAGT T
TGTATTCGTTTTTTCTCATT AAAT |||| ||||||| ||| ||||
TTCCTT TTCC TTACTCT TTT CTTA G
TT TT---------- G T

GAM2237 GCTCCACCCCGCCGACGAGC 2246 GGACGGTGGG 5316 CA- GA AG- GG G GC
CGGCCGCCGTCCGGGTGCGC GGACGCGGGG GCTC CCCCGCC CG CC CCGCCGTCCG
GT G
GGACGCGGACGGTGGGGGAC GCGG |||| ||||||| || || |||||||||| ||
GCGGGGGCGGGGCGCGAGC CGAG GGggcgg gc gg ggtggcaggC CA C
CGC gg gca g- G GG

GAM2238 ATCTATGAAAACAGACGACT 2247 ATCATACTAA 5317 - AAACAG G AAGAGA GCTAGCA
AA
ATAAAGAGATAGGCTAGCAA GTATAGTAGT ATCTA TGA AC ACTATA TAG ATTCT T
TTCTAATCGGGAATCATACT ATCA ||||| ||| || |||||| ||| |||||
AAGTATAGTAGTATCACATC TAGGT ACT tg tgatat atc taAGG /
ATTGGAT T ACacta a ga---- atac--- GC

GAM2239 TTCCCTAGTAAGGTGCGAGT 2232 TTAGGTGATC 5302 TAGTAA- GC- GTGA TT
GACTAGCAAGATTTACTCTT AAAACCGGTC TTCCC GGT GA CTAGCAAGA T
GTTAGGTGATCAAAACCGGT ATTG ||||| ||| || |||||||||
CATTGGGAG GAGGg cca ct gattGTTCT /
ttactgg aaa agtg CA

GAM2240 CTACTGGCAATACTAGATGA 2233 TGGCAATACT 5303 tg aa aga t g --- -- A
CTTGTTGTCTAGACTTGGGA AGATGACTTG CTAC gc tact tgact gtt tCTAGA CTTGGGAG
AGGC G
GAGGCAGCGCTTTCCTTCCA TTGT |||| || |||| ||||| ||| |||||| |||||||| ||||
AGTGATCTGGGGGCAGTCAA GATG CG GTGG ACTGA CGG GGGTCT GAACCTTC
TTCG /
AGGTGAGCTGGTAG GT A- AA- - - AGT CT C

GAM2241 ACGTTCCACTCGTCCAGATT 2234 TAAGTGTAGA 5304 G A C CCA aa ta ac a
AAGTGTAGACCTTTACGTTA CCTTTACGTT AC TTCC CT GT GATt gtg gaccttt gtt a
ATAACAAGAAGGTTGTCACG AATA || |||| || || |||| ||| ||||||| |||
CGATCAGTGCAAGCGGAAGG TG AAGG GA CG CTAG CAC TTGGAAG CAa /
T G C A TGA CG TG AA t

GAM2242 GTGGTCTATTCTTTTTCGTT 2235 CTGCGGGGTG 5305 G AT - GT TG T ATCC- C
TGCCTCTGATCCTGGGCGGT ATAGATAAAA GT GTCT TCTTTT TC T CC CTG TGGG G
CCGTACTGCGGGGTGATAGA GAAG || |||| |||||| || | || ||| ||||
TAAAAGAAGACAAC CA CAga agaaaa ag a gg ggc GCCT /
A -- t at gt - gtcAT G

GAM2243 AGAACAAAAAGTGTGTGTCT 2240 TGTGCAGTAG 5310 --- AA --- T CATT -- TT C
GACATTCACATTTATTTTTA AGTTGTGCCT AGAACA AA GTGT GTGTC GA CACA TTTATT
TACAAGA A
CAAGACAATTTTGTGCAGTA TCCG |||||| || |||| ||||| || |||| |||||| |||||||
GAGTTGTGCCTTCCGACACC TCTTGT TT CGCG CACAg ct gtgt agatga gtgtTTT /
CCGCGCCGTTCGCTGTTCT CGC GC CCC c tcc- tg c- A

GAM2244 TCTCTATCCAAGGATGTAAT 2248 TCCAAGGATG 5318 Atccaa t ttaaa tgA
TAAATGTTTGATCGATAACA TAATTAAATG TCTCT ggatg aa tgtt T
ATGTTTCCATCCATAGCAGA TTTG ||||| ||||| || ||||
GA AGAGA CCTAC TT ACAA C
CGATA- C TGTA- TAG

GAM2245 ACCGATTCTTCCTGTTTGAA 1435 ATCATGTTTT 4505 T TCCTGTTT CT-- TT
CGTCTATTTTTTTGTTAAGA TTCTCACAGT ACCGAT CT GAACGT ATTTTT G
ATTATCATGTTTTTTCTCAC ATCG |||||| || |||||| ||||||
AGTATCGGT TGgcta ga tttgta TAAGAA /
t cactcttt ctaT TT

GAM2246 GAAGTGCGGTTCCAGAAGGA 2241 GGCGTAGATG 5311 GG GAAGG ATAAAAC AG
G
GTAATAAAACCTGTGCCTCA TGCTGTGGAA GAAGTGC TTCCA AGTA CTGTGCCTC CGG
T
GCGGGTGACTGGGAGGCGTA AGCA ||||||| ||||| |||| ||||||||| |||
GATGTGCTGTGGAAAGCATT TTTTacg aaggt tcgt gatgcggAG GTC G
TT a- g---- gta---- G- A

GAM2247 GTATGTATGATAGTATATTT 2242 TGTATGATAG 5312 g g ag a TA
ATAAGATTAGTTTGTTATGT TATATTTATA GTAt tat at tatatttata gat G
AAGTATGTAGTAGTAAGTAT AGAT |||| ||| || |||||||||| |||
TATG ATG TG GTATGAATGT TTG T

A A AT A TT

GAM2248 TGCTAAAATACAATCTAAAC 2249 TGTTAAAAAA 5319 AT CTAAACA - -- G cag- cca G
AATAATGAATTGGTGTTAAA TCAGTATCCA ACAAT ATAAT GAA TTG tgttaaaaaat tat gcttAGC T
AAATCAGTATCCAGCTTAGC GCTT ||||| ||||| ||| ||| |||||||||||| ||| |||||||
GTGTGTTAAGTAATAAAGTA TGTTA TATTA CTT AAC ATAGTTTTTTA ATA TGAATTG G
TTTTTTGATAACAAATTTCT -- ------- T TA A TGAA A-- T
ATTATATTGTTAAGCA

GAM2249 GTAATGGGGAACCGAAAACT 1436 TGGGGAACCG 4506 -- aaac aa aaaTACAGA
GAACCAAATACAGAAATTAG AAAACTGAAC GTAAtggggaa ccga tg cc A
AAGAGGAACATCGGCTTTTC CAAA |||||||||| |||| || ||
CCGTTAT TATTGCCCTTT GGCT AC GG /
TC ---- AA AGAAGATTA

GAM2250 GATGGGTGGGAAATATAATA 2243 TACACGGTTA 5313 G GAAATATAATAAAGC AAAT CATAAAA
AAGCAACCGAAATGGTACAT CACCACCGAT GAT GGTGG AACCG GGTA A
AAAAACTAAAAATACCTACA C ||| ||||| ||||| ||||
CGGTTACACCACCGATC cta ccacc ttggc CCAT /
g aca---------- acat AAAAATC

GAM2251 CCCCCCTCCCCCTGTGGTCC 1442 CTCGCACCAC 4512 CC C CCCCGAGA-- C- CC
CCCGAGACGAGAGCCACCCA CCACGACCAC CCC CTCCC CTGTGGTC CGAGAG CAC A
TCGTGTACTCTCGCACCACC AGAG ||| ||||| |||||||| |||||| |||
CACGACCACAGAGGGAGACG GGG GAGGg gacaccag gctcTC GTG /
GG CA a cacccaccac AT CT

GAM2252 AGATCCTGCTGTCTCCTCAG 2250 TGGAATGGTG 5320 T C TC CT ------ ACA
CATCATTCCAGGCACAGGAC CTGTTGAATC AGA CCTG TG TC CAGCATCATTCCA GGC G
GCCAGAAAATGGAATGGTGC AACA ||| |||| || || |||||||||||| |||
TGTTGAATCAACAGGTTCT TCT GGac ac ag gtcgtggtaaggt CCG /
T a ta tt AAAAGA CAG

GAM2253 AGCGATTTATCTAAATTAAA 1443 TCTAAATTAA 4513 TAtc taaatta ttat tTTATAAC
TTACATTATGCTTTTATAAC ATTACATTAT AGCGATT taaat ca gct T
TTACCTACTAGCCTGCCCAA GCTT ||||||| ||||| || |||
CATTTACACGATCGTT TTGCTAG ATTTA GT CGA /
CAC- CAACCC- C--- TCATCCAT

GAM2254 AAATAGCTAACATTAAGTAG 2251 TAGCTAACAT 5321 t--- - caag -- C GA A CTAA TGA

TCAAGGAACGAAAACAGGAA TAAGTAGTCA taagt agt gaA CGAAAA AGGAA ATTTTTG TGT GGTG A

GAATTTTTGATGTCTAAGGT AGGA ||||| ||| ||| |||||| ||||| ||||||| ||| ||||

GTGAATTATTATCACAATAA ATTCG TCG TTT GTTTTT TTCTT TGAAAAT ACA CTAT T

AAGTGATTCTTATTTTTGAA TATT A AAA- AA A AG A ---- TAT

TTTAAAGCTAGCTTATTATT

ACTAGCCGTTT

GAM2255 AGTTCTACATACCAGTGATT 1444 ACGCCTTTTT 4514 TCTACAT TTTCC---------- tt tttac ct

TCCACGCCTTTTTGTTTATT GTTTATTTAC GT ACCAGTGA acgcc tttgttta gc T

TACGCCTTCCGCATTCTAAA GCCT || |||||||| ||||| |||||||| ||

TAAGTGGTGTTTTATAAATC CA TGGTTACT TGTGG GAATAAAT CG /

CCCTGCTTCATTGGTTTTAA CTAATTT TCGTCCCCTAAATATTT T- CTTA- CC

TCACT

GAM2256 CATGGGCGGCGATATAAAAT 1437 CATCGTAGTC 4507 GC ATAAAA AAG - CAAAAAATC- A

GCAAGGTGCTGCTCAAAAAA ATGCTCATG CATGGGCG GAT TGC GTGCT GCT AGGC A

TCAGGCAAAGCCTCGCGCAA |||||||| ||| ||| ||||| ||| ||||

AAAAGCAAGCACATCGTAGT gtactcgt ctg atg cACGA CGA TCCG /

CATGCTCATG a- ------ cta A AAAAACGCGC A

GAM2257 GGCCCGGGCTGCGCACGCCA 1438 TGAGTTCGCT 4508 C- A CCAGC A t a a---- --- TG

GCCGGGACGGGTGAGTTCGC AGGCAAGCAC GCTG GC CG CGGG CGGG gagttcgct ggca gcacg gac G

TAGGCAAGCACGGACTGGCG GGAC |||| || || |||| |||| ||||||||| |||| ||||| |||

GTTACACGTGCATGCGTGCC CGGC CG GC GCCC GCCC CTCAAGTGA CCGT CGTGC TTG /

GAGTGAACTCTCCCGCCCCG CT C A---- C T G GCGTA ACA GC

ACGCGCTCCGGCTCCGGGCC

GAM2258 GGGGGAGGGACGGGGAAGGG 1445 CCCGCCTTCG 4515 A A G G - C - T- CCTG

GGCGCGCGGGGCTGCCCTGC CGCCCCCCCC GGGGG GGG CG G AAGG GGGCG GCGG GGC GC C

CGCCCGCCCGCCGCCGCCGC C ||||| ||| || | |||| ||||| |||| ||| ||

CCGCCTTCGCGCCCCCCCCC ccccc ccc gc c ttcc cccGC CGCC CCG CG C

c - g - g - G CC CCCG

GAM2259 CACCCGTAGTTAACGCATCT 1449 TGAAGAGTAG 4519 ACGCA-- A CCATTACTG C AT

ACAGATCCATTACTGAAGTA AAATAATTAC CACCCGTAGTTA TCT CAGAT AAGTA AC T

CACATTAACGTTGCTTATCT GGGT |||||||||||| ||| ||||| ||||| ||

GAAGAGTAGAAATAATTACG Gtgggcattaat aga gtCTA TTCGT TG A

GGTG aaagatg a --------- - CA

GAM2260 GTGTTCCCCAGAGCGTCTGT 1439 CCCCAGAGCG 4509 cc gcgt t t TCTTT-
TTCCAAC
GTATTCAGTTTCTTTCTTGA TCTGTGTATT GTGTT ccaga ctg gta tcagtT CTTGAT T
TTTCCAACTTAATCGCATCG CAGT ||||| ||||| ||| ||| |||||| ||||||
AGCATCGCGGCTGATTGCCC CACAA GGTCT GGC CGT AGTCGG GAGCTA /
GGTAATCTGGACAACAC CA AAT- C T CGCTAC CGCTAAT

GAM2261 TTCGTAATACTTGATATACT 1440 TTCAGAGTCT 4510 ACTT-- TAT GTC G
CGTCAGAAAGCAGTTTCTTC TCCTGAAAGT TTCGTAAT GA ACTC AGAAA C
AGAGTCTTCCTGAAAGTTAC TACG |||||||| || |||| |||||
GAA AAgcattg ct tgag tCTTT A
aaagtc tc- act G

GAM2262 GACGCTAACCTCCTCCTTGT 1441 TGTACATATC 4511 C CCTCC-- GTCA- A C
CAGTGTACAACTGCACACGG AGAAGGATTT GA GCTAA TCCTT GTGTACA CTG A
CTGTACATATCAGAAGGATT ATAT || ||||| ||||| ||||||| ||| |
TATATTTGGCTC CT CGGTT aggaa tacatgt GGC C
- tatattt gacta C A

GAM2263 ATCTAGTTGTATGAGTTTAT 1446 TTCACGGTCT 4516 TT - TTT TT - AAT CTTTAA-----
---- AT
CGTTTACATAAGCAATTAAC TAGTATTTTT GTA TGAG ATCGT ACAT AAGC TAACGG
CAG G
GGCTTTAACAGATGATCTGA AGAT ||| |||| ||||| |||| |||| |||||| |||
GTAATAATATACCTCTGTTA tat attc tggca tGTA TTTG ATTGTC GTC /
TACGTTTAATGTTCACGGTC tt g --- ct A CAT TCCATATAATAATGA TA
TTAGTATTTTTAGAT

GAM2264 GTTTAATGTTCACGGTCTTA 1450 TTCACGGTCT 4520 T -------- ctta t
GTATTTTTAGATATCAATTG TAGTATTTTT GTT AATGt tcacggt gtatt t
TGATTTACACCATATTCGAC AGAT ||| ||||| ||||||| |||||
CAG TTATA AGTGTTA TAtag t
C CCACATTT AC-- a

GAM2265 AAAATAAATTAGAAGCTGTG 1447 TAGAAGCTGT 4517 AAATt ag ----- - atgAA- TT
GGTCATTGTTATGAATCTCT GGGTCATTGT AAAAT aga ctgtgg gtca ttgtt TCTC T
TTCAGAGGAATACAGACAAT TATG ||||| ||| |||||| |||| ||||| |||| |
TGACAAAATTCACAGACTCT TTTTA TCT GACACT CAGT AACAG GGAG /
CAAGATTTT GAAC- CA TAAAA T ACATAA AC

GAM2266 CCACCGCAATAGATCCTGTT 1451 TATCGCATTT 4521 C AA TCC TA - A C
AGATACATAGATCCTCGTCG TCTAACGTGA CCA CGC TAGA TGT GATA CAT GAT C
TGATATCGCATTTTCTAACG TGG ||| ||| |||| ||| |||| ||| |||
TGATGG ggt gtg atct acg ctat GTG CTG T

a ca ttt -- A - C

GAM2267 GCCGTCTTGCGAATCGTGAC 1448 TGTGTATGTA 4518 C TT AATCGT ---- A T---- - C-
- AT
GCTGGAGATGTTGCAACACC TAACTCATCC GC GTC GCG GACG CTGG GATG TGCA
ACAC TGC T
TGCATTGAGCAACTGTGTAT CGGA || ||| ||| |||| |||| |||| |||| |||| |||
GTATAACTCATCCCGGATAT TG CAG TGC TTGT ggcc ctac atgt tgtg ACG /
TGTTTCAACCGTTTGACTGT T TT CAACT- TATa - tcaat a tCA AG

GAM2268 GAGGAGAGACGCGACTTCTG 1452 TGGCATGCAG 4522 G ACTTC c - - ----------
g
GCATGCAGCCTGCTCCGGAC CCTGCTCCGG AG AGAGACGCG tgg at gcagcc tgc
tccg a
ACGGATTCCCAATTACCACC ACAC || ||||||||| ||| || |||||| ||| ||||
CCAAGCACGGCTGCTATTCT TC TCTCTGTGT ATC TA CGTCGG ACG AGGc
c
ATTTTATGTGTCTCTGCTT G ATTTT T T C AACCCCACCATTAACCCTT a

GAM2269 GCTCTCTACCTACAAGAATC 1453 TTTACAGCGC 4523 --------- ACC A ---- A TT T
ATTAGTGCTGAAGGTTCCTT TAGTATTAGA GCT CTCT TACAAGA TC ATTAGTGCTG
AGG CC T
TCGGGGTTTACAGCGCTAGT GTTT ||| |||| ||||||| || |||||||||| ||| ||
ATTAGAGTTTTGTAAGAGTT CGA GAGA ATGTttt ag tgatcgcgac ttt GG T
TATTATTAGC TTATTATTT --- g atta a GG C

GAM2270 AAAATAAATTAGAAGCTGTT 1454 TAGAAGCTGT 4524 AAATt ag tg----- - atgAA- TT
GGTCATTGTTATGAATCTCT TGGTCATTGT AAAAT aga ctgt gtca ttgtt TCTC T
TTCAGAGGAATACAGACAAT TATG ||||| ||| |||| |||| ||||| |||| |||
TGACAAAATTCACAGACTCT TTTTA TCT GACA CAGT AACAG GGAG /
CAAGATTTT GAAC- CA CTTAAAA T ACATAA AC

GAM2271 TTTATAGTTAGAAATGGATA 1455 TAATACCAAT 4525 AA--- - T TCTCtaa ataatcttaat--
A
ATTGAAATATTTTCTCTAAT AATCTTAATA AGA TGGATA ATTGAAA ATTT tacca
ataaa T
ACCAATAATCTTAATATAAA TAAA ||| |||||| ||||||| |||| ||||| |||||
ATCTTTTATCCTCATCTCAT TCT GCCTAT TAACTTT TGAG GTGGT TATTT C
CGTGGTGAATAAATGAGTCT ATAAA A C TAAATAA GCTACTCTACTCC T
TTCAATATATCCGAAATATC
TAACTCATGAA
GAM2272 AGTCGTTGAAACAATTGTTT 1456 TGCGTGGATA 4526 A--- TT AA CAA -- G T-----
C
AACAAACAACCCGTGTACGT AGGGATATTT AGTCGTTG AACAA GTTT CAAA CCC GT
TACGT GAGAG G

TGAGAGCGACTCTCCCATTT GGCA |||||||| ||||| |||| |||| ||| || ||||| |||||
GCGTGGATAAGGGATATTTG TCAGCAAC TTGTT TAGa gttt ggg ta gtgcg CTCTC /
GCAGATTTTGTTCTCGCAAC GCTC T- cg ata aa g tTTACC A
GACT

GAM2273 TTGCTGTTACAATAGTGGGC 1457 TGTTACAATA 4527 tg- a- ---- ccac ACT AA
CCACTGTGACTAGAAAGCCT GTGGGCCCAC TTGC ttac atagt gggc tgtg AG A
TCGCACAGCCCTGAGATTAT TGTG |||| |||| ||||| |||| |||| ||
AAGTAGACTGCAA AACG GATG TATTA CCCG ACAC TC /
TCA AA GAGT ---- GCT CG

GAM2274 AGTGGTCCTTCAAAGTTATG 1458 TATGTTGCAC 4528 CCTTCAAA a cactca gtacacA T
TTGCACTCATAGAAGTACAC TCATAGAAGT AGTGGT GTt tgttg tagaa CC C
ACCTCCGGCATCCATTCTGA ACAC |||||| ||| ||||| ||||| ||
AAAATAACAAAACACCACT TCACCA CAA ACAAT GTCTT GG /
-------- A AAAAA- ACCTAC- C

GAM2275 ATAAGTAGACTGCAACAACA 1462 TCTCGCGGTC 4532 T CT CAACATCGAAACC C A
TCGAAACCCCGCGACACAAA TTGCTCTCTT ATAAG AGA GCAA CCGCGA ACA A
TCTGTCTCGCGGTCTTGCTC AT ||||| ||| |||| |||||| |||
TCTTAT tattc tct cgtt ggcgct tGT T
- -- ct---------- c C

GAM2276 TAAGAATGCATTTGTTCTGC 1459 ATGCATTTGT 4529 - c - tagaaa AACT-- CAATTAT
ATCTT G
CAATAGAAACTTAAACTGAG TCTGCCAATA ca tttgtt tgc caa CTTA GAGC TATATA TG
A
CCAATTATTATATAATCTTT GAAA || |||||| ||| ||| |||| |||| |||||| ||
GGAAACGTGTATGTATTTGC GT AAATAA ATG GTT GAGT TTCG ATGTAT GC
A
TTTTTCTGTGAGAAACTTGA C A A CAAA-- GTCTTT TTT---- GT--- A
GTAAAATAAACTGCCACATT
CTTG
GAM2277 TATAATGTACTAGATAATAT 1470 TAATATTATA 4540 A T GA taaag- atttaaCCA
TATAAAGCCTTTATTTAACC AAGCCTTTAT TATA TG ACTA taatatta ccttt A
AACCTATCTTCAAAGGACCG TTAA |||| || |||| |||||||| |||||
TCTGATGTTAAATGGTTCGA ATAT GC TGGT ATTGTAGT GGAAA /
TATA A T AA CTGCCA CTTCTATCC

GAM2278 TGCATTTTATGCAAAAAAAG 1460 TGCAAAAAAA 4530 A aaaaaa--- atatg CTT TTACA
AAAATATGAGCAGGCTTGGA GAAAATATGA TGCATTTT tgc agaaa agcagG GGA A
TTACAACCTCTTCCTCCTGC GCAG |||||||| ||| ||||| |||||| |||
TAAGGTTTCTGAGCAAAAAG ACGTAGAA ACG TCTTT TCGTCC CCT /
CAAAAGATGCA A AAAAACGAG GGAA- T-- TCTCC

GAM2279 GCCCTGAGCTCGCGCCTCAA 1461 CCTCAATGTC 4531 A GCGcctcaa caaaa cA AG
TGTCAGCTGCAAAAAGTCAC AGCTGCAAAA GCCCTG GCTC tgtcagctg agt CTTA T
TTAAGTCCTGGGCCACTACA AGTC |||||| |||| ||||||||| ||| ||||
GCTGACAATTCAGAGCCAGG CGGGAC CGAG ACAGTCGAC TCA GGGT /
GC - ACTTA---- A---- CC CC

GAM2280 GTTATCGCGCCACCTTGTGG 1477 TATCGCGCCA 4547 a ttgt tTATATA A TTTCC
TACTTTCA CTAT
CTACATTATATAGCACGATC CCTTGTGGCT cc ggctaca GCACG TCAC ACGTTA
CGTA G
ACTTTCCACGTTATACTTTC ACAT || ||||||| ||||| |||| |||||| ||||
ACGTACTATGACTCATACGC GG CCGGTGT CGTGC GGTG TGCAAT GCAT
A
CTTAACGTCACGTGGCGTGC - ---- TAG---- - CAC-- TCC----- ACTC
GATTGTGGCCGGGGCTGAAA
AT
GAM2281 CGCAGTTCGGCGACACGCCC 1471 CTAAATCGCG 4541 C ---------- AC-- CC CAGC
AAT
GCGTCCCGACAGCAGAGGTA CGCGGGCTCA CG AGTTC GGCGAC GCCCGCGT CGA
AGAGGT C
ATCCCGAGCTTCTAAATCGC AGTC || ||||| |||||| |||||||| ||| ||||||
GCGCGGGCTCAAGTCGCCCT GC TCAAG CCGctg cgggcgcg gct tcTTCG C
TTTTGTCTCGAACTCG - CTCTGTTTTTC aact c- aaa- AGC

GAM2282 CATCTATATCATTTCTATAT 1463 TCTATATCAT 4533 c cat ataaaa T TTTAAAA
AAAAATTTTGCAATTTTAAA TTCTATATAA CAt tatat ttctat atTT GCAAT A
AAATGTACCATTGTCAAATC AAAT ||| ||||| |||||| |||| |||||
TAGCCATAGAATCATATATA GTA ATATA AAGATA TAAA TGTTA /
TG T CT- CCGATC C CCATGTA

GAM2283 AAGGTTTCATCTAATCCTTT 1464 TTTTTCTATA 4534 TTTCATCTAAT TTTCCA AC TTC
TTCCAATAACAAAAATTTTT TCTATAGGGC AAGG CCTT ATA AAAAATTT G
CGTTATAAATTTTTTCTATA ATAT |||| |||| ||| ||||||||
TCTATAGGGCATATAATATT TTCC ggga tat ttttTAAA T
CCTT TTATAAtatac tatcta ct TAT

GAM2284 GAGAGTGTGCCTTAGCTTGA 1465 TCTAGAGCTT 4535 TG G A- AA AC A T
AAGGCACTCTAAAGCTAATG CAGGTCAGAG GAGAG T CCTT GCTTGA GGC TCTA AGC A
CTCTAGAGCTTCAGGTCAGA GAGT ||||| | |||| |||||| ||| |||| |||
GGAGTGCTCTC CTCTC g ggag tggact tcg agat tCG A
Gt a ac -- -- c T

GAM2285 TGGTCCTGGCTACACACCCA 1478 CCTGGCTACA 4548 c c acccaa-- gTC
AAGGCACGTCAGACAGTGTC CACCCAAAGG TGGTc tgg tacac aggcac A
TCTAAATCAGTGTACCAAGA CACG ||||| ||| ||||| ||||||

CCA ACCAG ACC ATGTG TCTGTG G
A - ACTAAATC ACA

GAM2286 CTCTTGAAGACATAAATACT 1472 TAAGCGTTCT 4542 GA CATAAAT TAT ATATA CT
ATTAAGAAATATATGGACTT TATACGTTCT CTCTT AGA AC TAAGAA TGGA T
TATTCTAAGCGTTCTTATAC AAAG ||||| ||| || |||||| ||||
GTTCTAAAGAG GAgaa tct tg attctt atCT T
a- ------- cat gcga- TA

GAM2287 GGTTTGATTTAAGTAAATGA 1479 TTAGTTGTTT 4549 A TAA TG T TG TA GT
ATTGTTTAGTGATTTAAATT AGTGATTTAT GGTTTG TTTAAG ATGAAT TT AG ATT AATTTGA
T
TGAGTTTAATTAGATTAGTT AGTT |||||| |||||| |||||| || || ||| |||||||
GTTTAGTGATTTATAGTTTA TTAAAC AAATtt tattta ga tt tga ttAGATT T
AAGCAAATT G ga- gt t gt -- AA

GAM2288 CCCTCACAGTTGCTGTGGTG 1466 TGTGGTGTTG 4536 TCA- TG tg- g- attcc-------- t
TTGTGATTCCTCTTCTGCAG TGATTCCTCT CCC CAGT C tg tgttgtg tcttc g
AAGATATTAATAAAGTGTAT TCTG ||| |||| | || ||||||| |||||
AACAGACAAATGTGACTGGC GGG GTCA G AC ACAATAT AGAAG C
CTGGG TCCG GT TAA AG GTGAAATAATTAT A

GAM2289 CCTACCTACACTAATAAACT 1467 TAAAAAGAGA 4537 CTAATAAA TGA-- TATATTT
ATAACT CTAA
GGTGAGTACCTTTATATTTT TAAATAAGGT CTACCTACA CTGG GTACCTT TCTC
TTGT A
CTCATAACTTTGTCTAAATA ACAA ||||||||| |||| ||||||| |||| ||||
AAACAATAAAAAGAGATAAA GGTGGATGT GACC catggaa agag AACA /
TAAGGTACAAGATCCAGCAT AC------ TAGaa taaat-- aaaaat AAAT
GTAGGTGGG

GAM2290 TCCAGAGAACCATTTTAAAA 1480 TATGATGGTG 4550 A GA TTAAAAAAG ATAA
AAGGACCTATAAATGTGGAG ATCCGGA TCC GA ACCATT GACCT A
GTTATATATGATGGTGATCC ||| || |||||| |||||
GGA agg ct tggtag TTGGA T
c ag tatATA--- GGTG

GAM2291 GGACAAACCGTGAAAATGCC 1468 TGTCATAGGC 4538 CAAAC AAAAT CA A CTCAA------
----- A
CAATGAACGCCTCAAGGAAC TAAAACACGC GGA CGTG GCC ATGA CGC GG A
ACCAACGAGAATCATCCAAG TCTC ||| |||| ||| |||| ||| ||
TGTCATAGGCTAAAACACGC Cct gcac cgg tact gtG CC C
TCTCC ctc-- aaaat a- - AACCTACTAAGAGCAA A

GAM2292 TTCATGCTGTAGAAAAAATT 1469 TCGAAGATTC 4539 G TAGAAAAA G TT agattcaac--
ca
GCCATTGCTCTCGAAGATTC AACAGGTCCA TTCAT CTG ATT CCA GCTCtcga aggtc a
AACAGGTCCAAACGGCCTTA AACG ||||| ||| ||| ||| |||||||| |||||
ACATAACCATCGGGGGTGCT AAGTA GAC TGA GGT TGGGGGCT TCCGg /
GGAGTGAAGAAGCCAGATGA - CGAAGAAG - CG ACCAATACAAT ca
A

GAM2293 AGGGTACTTATCAGATTTTG 1473 TAGAATCACC 4543 A TATCAG TT - ACA A GA
G
TTACGACATTGATGAGATTA AGAGCCGATA AGGGT CT AT TGTTA CG TTG TGA
TTAAAAAAA A
AAAAAAGAACTTTTTTTAGA ACAT ||||| || || ||||| || ||| ||| |||||||||
ATCACCAGAGCCGATAACAT TCCCA GA TA acaat gc gac act gatTTTTTT A
ATATAGACCCT - TA---- t- a cga c aa C

GAM2294 CTGGCCGGGCTCGGGCTCGA 1474 CAAGGACACC 4544 G T G TGT TGTT AC - G
ACTT GA- TTT
GGTGTGCCTGTTTGCCACGG GCGGGCGTGC CG GC C AGG GCC TGCC GGC CGC CGCG
TGTCCT GCC T
CCGCGCGCGACTTTGTCCTG CCGG || || | ||| ||| |||| ||| ||| |||| |||||| |||
AGCCTTTTGGCGGCGCAAGG GC CG G TCT CGG GCgg ccg gcg gcgc acagga CGG
/
ACACCGCGGGCGTGCCCGGC G T - TT- TT-- c- t g c--- acG CGG
GTTGGCTTTCTGTGCGCGAC
GCCTGCTAG
GAM2295 GACCTTTCGTCCGGTGTCGG 1475 CTAGCGCTCC 4545 C G ---- CGC- AA CA A
CC
ACGCCTCAAGCATGCCAGGC GCGTGCGAGA GAC TTTC TCCG GTGTCGGA CTC GCATGC
GGCGC GGCG G
GCAGGCGCCGCCCTGCTAGC AGAT ||| |||| |||| |||||||| ||| |||||| ||||| ||||
GCTCCGCGTGCGAGAAGATC TTG AGAG AGGC CACAGCCt gag cgtgcg tcgcg tcGT C
CGACACTACTCGGAGAGACG C - TCAT agaa -- cc a CC
TT

GAM2296 CGCGGGCAGGGATCCTTCAC 1476 CTTCTGCTCG 4546 G TCCTTCACGCG T CCGC
C
GCGCGGGCCCGTGGTAGCCG GGCCCGACCT CGCG GCAGGGA CGGGCCCG GGTAG
GGG C
CGGGCCCTTCCTTCTGCTCG TTCC |||| ||||||| |||||||| ||||| |||
GGCCCGACCTTTCCTGCGCG GCGC CGTcctt gcccgggc tcgtc cCT C
CG G tcca------- - tt-- T

GAM2297 GCTCGCGCACACGCCGTACA 1484 TCGCGCACAC 4554 g acg cacact -- T
CACTGCAGCAGTTACTGTTC GCCGTACACA GCtc cgcac ccgta gcAG CAG T
TGCCCTCTACGGAGGTGCGG CTGC |||| ||||| ||||| |||| |||
GGC CGGG GCGTG GGCAT CGTC GTC /
- GA- CTCC-- TT A

GAM2298 TTGTTATTAATACTAGTTGA 1485 TAATACTAGT 4555 TATta - tg ttttcta T
TTTTTCTAGCATCTTTGTCG TGATTTTTCT TTGT atactag t at gca C
TGTTGATCTAGTATGTGTGC AGCA |||| ||||||| | || |||
AA AACG TATGATC A TG TGT T
TGTG- T GT TGC---- T

GAM2299 ATTTCTGGTCTCTAGACGCT 1486 TTTGTCGTTA 4556 GTCTCTA C- CAATA
GGTAGTTCAATAAATAAAAA CAGAGAT ATTTCTG GACG TGGTAGTT A
ACTATCATTTGTCGTTACAG ||||||| |||| |||||||| AGAT tagagac ctgt ACTATCAA A
attg--- tt AAAAT

GAM2300 AGAGGCGCGACTTTTGGCAT 1481 TTACCACCCC 4551 ACTTT----- A CC C ACACG T
GCAGCCTGCTCCGGACACGG GAGCACTGCA AGAGGCGCG TGGC TGCAG TGCTC GG GATT C
ATTTCCAATTACCACCCCGA GCTA ||||||||| |||| ||||| ||||| || |||| GCACTGCAGCTATTCTATTT TTTCTGTGT atcg acgtc acgag cc ttAA / TATGTGTCTTT ATTTTATCTT - -- c cacca C

GAM2301 GCTATAGAAATGACTCTTTA 1487 TTCTGAACAG 4557 T A GA T---- A --- ----- A CAC
TCTTAGTGGCCTCAGAGACT TGGTCTTTAC GCTA AGA AT CTCT TATCTT GT GGCC TCAGAG CT A
CACAATATGGTTCTGAACAG AAGA |||| ||| || |||| |||||| || |||| |||||| || TGGTCTTTACAAGATACTAG CGAT TTT TA GAGA ATagaa ca ctgg agtctt GG A CAGAGAAATCTTTTTAGC T C AA CGATC - ttt tgaca - TAT

GAM2302 TAATAAACGATTTAATTAAA 1488 TAAATTACTA 4558 CG T ATt tactata a CTA
TTACTATATATATATTTACA TATATATATT TAATAAA AT TA aaat tatatattt caA T
ACTATCCTTTGAAGTATATA TACA ||||||| || || |||| ||||||||| ||| ATTCAATATTTTGTATATTA ATTATTT TA AT TTTA ATATATGAA GTT / TTTATTA AT T GT- TAACTTA - TCC

GAM2303 GTGGTATCAGGAGTACATCT 1489 TCAGGAGTAC 4559 A ------- at-- acaact
TGCACAACTATTGACGGCAG ATCTTGCACA GTGGT tcagga gtac cttgc a
GCACCGTACATTTTAATCCT ACTA ||||| |||||| |||| ||||| GGACCAC CACCA GGTCCT CATG GGACG /
- AATTTTA CCAC GCAGTT

GAM2304 TATGGTGATATAGTAATGAG 1482 CTTGCACAAG 4552 A A CT AA TT AG TT AG TT C

TGCCTGCACAAGTGCTTGCA TGCTTGCACA AT TAGTAATG GTGC GCAC GTGC GCAC GTGC GCAC GTGC GCA A

CAGGTGCTTGCACAGGTGCT AGTG || |||||||| |||| |||| |||| |||| |||| |||| |||| |||

TGCACAAGTGCTTGCACAAG TA GTCATTAC CATG CGTG CACG Cgtg cacg cgtg cacg cGT A

TGCTTGCACAAGTGCCTGCA C A TT AA TC aa tt aa tt G

CAAGTGCTTGTACACATTAC

TGCATCGCCAA

GAM2305 AAGATAGTATTCATCTTCAT 1483 TAGTATTCAT 4553 catcttc ctat CTA

GCTATTTAATACATCTAATA CTTCATGCTA AAGAtagtatt atg ttaATACAT A

TATGTATTGGTCATTAAAAA TTTA |||||||||| ||| |||||||| /

ATATTATTTT TTTTATTATAA TAC GGTTATGTA /

AAAAT-- T--- TAT

GAM2306 TGTTGTGGTATCAGGAGTAC 1490 AGGCAGCATA 4560 --- A ------- CAT-- ACAACT

ATCTTGCACAACTATTGACG CATTTCAATC TGT TGTGGT TCAGGA GTA CTTGC A

GCAGGCAGCATACATTTCAA CTGG ||| |||||| |||||| ||| |||||

TCCTGGACCACATTGACA ACA ACACCA ggtcct cat ggaCG /

GTT - aacttta acgac GCAGTT

GAM2307 CATTTGTGCTAGATGAGCGG 1492 TGCTAGATGA 4562 G - g-- c a TC

CAAAGAACTCATCTTTCTGA GCGGCAAAGA CATTT tgctaga tga cgg aaaga ctcA T

GATTTTTCTGGGATTATTCT ACTC ||||| ||||||| ||| ||| ||||| ||||

GGTAAAAATG GTAAA ATGGTCT ATT GTC TTTTT GAGT T

A T AGG - A CT

GAM2308 TTGGTGCCCCCTTAGAGGCA 1491 TAGGTGCCCC 4561 CC - T A- A GAA

CATTATAGAACCAGGTATAG CTTAGAGGTA TTGGTG CC CT AG GGCAC TTATA C

GTGCCCCCTTAGAGGTACAC CACC |||||| || || || ||||| |||||

CAA AAccac gg ga tc ccgtg gatAT C

at a t cc - GGA

GAM2309 ATCTCAAGGAACTTAAATGA 1493 TAGAAAGTTT 4563 - AG AAATG GTTGT- AC

AGAGTTGTAGACAAACTTAG ATGAAGAT ATCT CA GAACTT AAGA AG A

TAATCTTATAGAAAGTTTAT |||| || |||||| |||| ||

GAAGAT taga gt tttgaa TTCT TC /

a a- agatA AATGAT AA

GAM2310 TAGTAAATGTGATTGTATGT 1500 AATGTGATTG 4570 - ----- a ttacattTCC CAAT A

TGTTACATTTCCATGTCAAT TATGTTGTTA TAGTAa atgt gattgt tgttg ATGT AGAGTTT T

AGAGTTTATAAAAATTTTTA CATT |||||| |||| |||||| ||||| |||| |||||||

TACATTATCTTCCAACAAGC ATCATT TGCA TTAACG ACAAC TACA TTTTAAA A

AATTGACGAACGTATTACTA A AGCAG A CTTCTAT--- TAT- A

GAM2311 GACTATACCTAGTGCTATTT 1501 TATACCTAGT 4571 c --- - c------- T TTCTT
TGACATACTCGTGTTCTTGT GCTATTTTGA GACtata ctag tgc tattttga ataC CGTG G
GTAATTGCGGTATCTATATT CATA ||||||| |||| ||| |||||||| |||| ||||
ATTAAAGTACGTAAATCTAG TTGATAT GATC ATG ATGAAATT TATG GCGT T
CTATAGTT C TAA C ATTATATC - TAATG

GAM2312 TTCCAGCAATATCATTTTTG 1494 TAAAGTATTA 4564 TCA TA--- a g at-- tcg GG
ATT
TACTTAAAGTATTATCCTGT TCCTGTAAAT A TTTTTG CTt aa tatt cctgtaaa tcATTGAT TATT
G
AAATCGTCATTGATGGTATT CGTC | |||||| ||| || |||| |||||||| |||||||| ||||
ATTGTAAGATAAATTAATGG T AAAAAC GAA TT GTGA GGACATTT GGTAATTA
ATAG /
TTTTTACAGGTAAAAGTGGT CAA TTAGA C G AAAT TT- A- AAT
TCAAGAGATTCAAAAAAACT
ATTATTGGGA
GAM2313 ACATTAGTATGTTTATTTCA 1502 TGTTTATTTC 4572 tg cataat a ATTTA TA- A
TAATGTCATTATTAGTATTT ATAATGTCAT ACATTAGTA tttattt gtc ttattAGT GTAGT GC A
AGTAGTTAGCAAGTGCCATA TATT ||||||||| ||||||| ||| |||||||| ||||| ||
TTACAACTAATAAGATCAAA TGTAGTCGT AAATAAA TAG AATAATCA CATTA CG G
AATAAAACTGCTGATGT CA AAC--- - A---- TAC T

GAM2314 GCTACCACACGGAGGCCGAT 1495 TCCGAACACT 4565 A- A G CGATACC C AA AA-
TCA AC
ACCGGGACGGCAACAAATTC GGCGCCTCCT GCT CCAC CGGA GC GGGA GGC CA TTCG
GCT A
GTCAGCTACAACGGTCCGAA CACA ||| |||| |||| || |||| ||| || |||| |||
CACTGGCGCCTCCTCACACA CGA GGTG GTCT CG tcct ccg gt aagc tGG /
GCATCTGGTGGCCAGC CC - A ACacac- - cg cac c-- CA

GAM2315 TAGCCGTCCTCGCCGCCGCA 1496 AAGGTGCGCC 4566 - GT C C C GCATAC-- GC
TCTGCATACGCTGCTCTGAG GCAAGGGTGC TAGC C CCT GC GC GCATCT GCT T
TCTCATTAAAGGTGCGCCGC GTTA |||| | ||| || || |||||| |||
AAGGGTGCGTTA attg g gga cg cg cgtgga TGA C
c tg a c - aATTACTC GT

GAM2316 AATATATATATAACGTTTTT 1497 TATATAACGT 4567 t a ttt---- taaa
TACGTAAAACATATTGTAAT TTTTTACGTA AATATA atat acgt ttacg a
TTAATCACGTGATGTTTATG AAAC |||||| |||| |||| |||||
TT TTGTAT TGTA TGCA AATGT c
T G CTAATTT TATA

GAM2317 GATGGCCCTCCAGGCTGTCG 1503 TCGACGCCCC 4573 T tc c ccctgttt T TG
ACGCCCCCTCCCTGTTTGTC CTCCCTGTTT GATGGCCC CCAGGCTG ga gcccct gtcgCC
GGC G

GCCTGGCTGGCCGCTCGGTG GTCG |||||||| |||||||| || ||||||| |||||| |||
GCTCCGGGGGGCTTCCGGCC CTGCCGGG GGTCCGGC CT CGGGGGG CGGTGG
TCG /
TGGGGGCCGTC - -- T CCT----- C CC

GAM2318 CTCGGGGGATAGTGAGGAAT 1498 TACGGGACCC 4568 GGG G AT- CAA- tac
aatga gg
TCTCAAGGGATACGGGACCC AATGACTGGA CTCG GATA TGAGGA TCT GGGA gggaccc
ct a
AATGACTGGATAAGAGAAGG TAAG |||| |||| |||||| ||| |||| ||||||| ||
GTTTTTCCCCGTAAGATGAT GAGT CTAT GCTCCT AGA CCCT TTTTGGG ga /
CCTCGTATCACATGAG ACA - AGT ATGC --- AAGA- at

GAM2319 GTACTATCAGTTAACCACTC 1504 TCAGTTAACC 4574 tc tta ctc tgcTCA
TTGAATATGCTCAATGACCC ACTCTTGAAT GTACTA ag acca ttgaata A
TATTCAACACTGGTGTCTCT ATGC |||||| || |||| |||||||
TAGTAC CATGAT TC TGGT AACTTAT /
TC TG- CAC CCCAGT

GAM2320 GAAATCGGATAACGGCACGC 1505 AAGGTCTCAG 4575 G aa t ca gac GTTTA CG
A A A
GGAAAGGTCTCAGCGAGTTG CGAGTTGGAC ACGGCAC CGGA gg ct gcgagttg acgtT GC
TCTCGA G GT T
GACACGTTGTTTAGCCGTCT ACGT ||||||| |||| || || |||||||| ||||| || |||||| | ||
CGAAGAGTATCTGCACTCGA TGCTGTG GCCT CC GA CGTTTAGC TGCGA TG
AGAGCT C CG C
GAAAGTAGCGTTGCGATTTG - CG T -- GT- ----- AA - A T
CAGTCCGCTCCGGTGTCGTT
CACCCAGTTAC
GAM2321 TCTTTGCTTGATTTACAATA 1506 TGCTTGATTT 4576 g - acaa ta C - GA
TGATATTTCTCTTAATAATG ACAATATGAT TCTTt ctt gattt tatga ttt TCTTAATA AT T
ATTAATATATTAAGAAAAAC ATTT ||||| ||| ||||| ||||| ||| |||||||| ||
TTATGACGAAGATTAAAGGA GGAGA GAA TTAGA GTATT AAA AGAATTAT TA /
GAGG G A AGCA C- A A AT

GAM2322 GCTTAACTAAGGGGACTATG 1507 TGGCATGTAT 4577 TAA-- A A- a- g ca g
GCATGTATAGGCGCAAAGCG AGGCGCAAAG GCT CT AGGGGACT tggc tgtatag cg aagc g
GGGCTTCGGTTGTACGCGGT CGGG ||| || |||||||| |||| ||||||| || ||||
TAGGAGTCCCCTCAGGATAT TGA GA TCCCCTGA ATTG GCATGTT GC TTCG /
AGT TATAG C GG GC G -- g

GAM2323 GAGATTGTATCAGTTTCGTA 1508 GATTGTATCA 4578 -- - t ta tgA G T
GTCTTGAGTATTGGTATTAC GTTTCGTAGT GAgattgta tc agt tcg gtct GTATTG TAT A
TATATAGTATATAGATGTCG CTTG |||||||||| || ||| ||| |||| |||||| |||
ACGCTAGATATACAGTCTC CTCTGACAT AG TCG AGC TAGA TATGAT ATA C

AT A C TG TA- - T

GAM2324 GGAGGTGGAGCTGGTAGAAA 1499 TGACAAGAAA 4569 ------- - AAATT- G A - AGAA
TTCTAGATATTTTATGTATT TATATAGTAG GGAG GTGGAGCT GGTAG CTA ATATTTT TGT ATTT A
TAGAAAAAGAAGATGACAAG CAGT |||| |||||||| ||||| ||| ||||||| ||| ||||
AAATATATAGTAGCAGTTGC CCTC TACTTCGG CCGTt gat tataaag aca tAGA /
CTGGCTTCATGATAATACTC ATAATAG T gacgat a a g AGAA
C

GAM2325 TGAGAAACTGAAGAAAGATG 1509 AGACCATAGT 4579 GAA A-- AGA ------- T--- ACAC T
GTTTTGAAGTTCTATGGACA AATGCTTTAT TGA ACTGA GAA TGGTTT TGAAGT CTATGG TTGG T
CTTGGTTTTCCAGACCATAG ATAA ||| ||||| ||| |||||| |||||| |||||| ||||
TAATGCTTTATATAAAAAAG ACT TGATT CTT GCCGAA atttcg gatacc gaCC T
CCGGGTTCAAATTAGTAGGT GGA AAA GG- AAaatat taat a--- T
CA

GAM2326 ACGTCGCTTGTACACGTCGT 1512 GGGTACGGGG 4582 ---- A TT GCCC
TCGTGGCCCAAAGACACGGG ACACGGCGT ACGTCG CTTGTAC CGTCG CGTG A
TGGCGGGTACGGGGACACGG |||||| ||||||| ||||| ||||
CGT tgcggc gggcatg gCGGT GCAC /
acag g GG AGAA

GAM2327 GGTACGACGAGAATCTTTAT 1510 ACGAGAATCT 4580 GT g ctttatacc GA AACT
ACCTTTCCTGGAATATCATT TTATACCTTT G ACGac agaat tttcctg ATATCATT G
AACTGTTGCCAATGATGTTA CCTG | ||||| ||||| ||||||| ||||||||
GGAAATATTCTGTTGTGTC C TGTTG TCTTA AAAGGAT TGTAGTAA T
TG - T-------- -- CCGT

GAM2328 CATTGTAAAAGAAATATATG 1513 TATGTGGTGT 4583 AAAG tg gttacagtta aa- GAG
TGGTGTTACAGTTAGGTGAA TACAGTTAGG CATTGTA AAATAtatg gt ggtg CAA A
CAAGAGATATATTGGAGCAT TGAA ||||||| ||||||||| || |||| |||
TGCTGCATATGTTTGAGTGC GTAACGT TTTGTATAC CG TTAC GTT T
AATG GAG- GT ---------- GAG ATA

GAM2329 GTCTTAGAACTAGTGCTTTG 1511 TCAATCATTT 4581 CTAGT TT tt a g G
TCAATCATTTAATGGCCAAG AATGGCCAAG GTCTTAGAA GC TGtcaatca ta tg ccaaggcaa G
GCAAGGCATTGTCTTGGGCA GCAA ||||||||| || ||||||||| || || |||||||||
CTATTTGATTGACATTGTGG CAGAATCTT TG ACAGTTAGT AT AC GGTTCTGTT C
TCTTTCTAAGAC TCTGG TT TT C G A

GAM2330 GGTAATACTTTTCTAAAAAC 1514 TCTAAAAACT 4584 A C t a at- ca at T

TAATCTCAAGTATTGTTTAC AATCTCAAGT GGTA TA TTT ctaaaa cta ct agt tgTT A
AAGCGACTGAAGTAATAGTT ATTG |||| || ||| |||||| ||| || ||| ||||
TTAGCAAAATAATACC CCAT AT AAA GATTTT GAT GA TCA GCGA C
A A C - AAT AG -- A

GAM2331 CAGTAAAGGTATTATTTTGC 1520 TATTTTGCTA 4590 G A T g - tta c CGC T
TAAAACTATTACTTCAGTCG AAACTATTAC CA TAA GGTA tatttt ctaaaa cta ctt aGT TTG A
CTTGTAAACAATACTTGAGA TTCA || ||| |||| |||||| |||||| ||| ||| ||| |||
TTAGTTTTTAGAAAAGTATT GT ATT CCAT ATGAAA GATTTT GAT GAG TCA AAC A
ACCATTAATG A A T A T TA- T T-- A

GAM2332 ACCAGGTATTAGTGCCCCCT 1515 TAAGTGCCCC 4585 -- A- CC - T A- A AACCAG A
- CCC
TAGAGGCACATTATATAACC CTTAGTGGCA GGT TTAGTG CC CT AG GGCAC TTATAT GT
TAG GTGCC T
AGGTATAGGTGCCCCCTTAG CACT ||| |||||| || || || ||||| |||||| || ||| |||||
AGGCACACTAACAATAGGTA CCA AAtcac gg ga tc ccgtg aatATG CA ATC CACGG T
TAAGTGCCCCCTTAGTGGCA CA CC ac t t cc - GATAA- - A AGA
CACTAACCACCACAATTGGT

GAM2333 CGGTGCCATTTTTCCAAATG 1521 TGGCTGATTC 4591 TTT AAA GG TG TAT AT T TG
CAG T TG
GGGGTTGCATTATGGATAGG TATCTCTCGT TTCC TG GGT CAT GGATAGGA TCG T CA
TTTGG GGT T
AATTCGTTTGCACAGTTTGG GTGG |||| || ||| ||| |||||||| ||| | || ||||| |||
TGGTTGTGATATCCCAAAAT AAGG AC CCg gtg tctatctt agt g GT AAACC CTA G
ATGTGGCTGATTCTATCTCT TT- A-- TA gt ctc -- c gt ATA - TA
CGTGTGGCCATCAAGGAATT
AGACGCCG
GAM2334 TCTCTACTCAGTCCCTGTCT 1522 TTGGCGCCCG 4592 A - C TA-- TGT TCGA
CTAGTTTGTCTGTTCGAGAT AACAGGGACC TCTCT CTCAG TCCCTGT TC GTT CTGT G
CCTACAGTTGGCGCCCGAAC TGAG ||||| ||||| ||||||| || ||| ||||
AGGGACCTGAGAGGGG GGGGA gagtc agggaca ag cgg GACA A
- c - cccg tt- TCCT

GAM2335 CACCATTGCTATGACCGTGC 1516 TTGATACCAT 4586 C - AT ---- TG CCCG- A GTA
CCCGGGTAATCAATAGTAGC TGCGTGCAAA CA CAT TGCT GACC G C GGTA TCAATA G
TATATTGATACCATTGCGTG AGGT || ||| |||| |||| | | |||| ||||||
CAAAAGGTTTCAGCACATGC GT GTA ACGA Ttgg c g ccat agttAT /
TG C C CT aaaa gt cgtta - ATC

GAM2336 TGACAGATAATAATATATTT 1517 TAATATATTT 4587 - AA------- - acc-- t aa
ACCGTGATTTTAATTAAACA ACCGTGATTT TGACAG AT taatat attt gtgat tt t
TCACATCCAAAGTAATATTA TAAT |||||| || |||||| |||| ||||| ||
AATTCGAAGATACTGTTA ATTGTC TA ATTATA TGAA CACTA AA /
A GAAGCTTAA A ACCTA C AT

GAM2337 AATATGTATATTATATGCTC 1523 TATTATATGC 4593 A - gc aaa aa T GAAT
AAACTAAGGTAGATATGGAA TCAAACTAAG AAT TGTAtatt atat tc ct ggtagA ATG A
TATTTACATTTTACCGAAGA GTAG ||| |||||||| |||| || || |||||| |||
AGATAATATAAATATACAAA TTA ACATATAA TATA AG GA CCATTT TAC /
TT A A AT AA- AG - ATTT

GAM2338 TGTGAATTCTATACTGTGAA 1518 CTTGAACATT 4588 GA TATAC - C T C
TGCTTTAGATCTGAGTCTTG TCACAAAATG TGT ATTC TGTGAA TG TT AGAT T
AACATTTCACAAAATGAATA AATA ||| |||| |||||| || || ||||
AACA ACA taag acactt ac ag tcTG G
Aa taaa- t a t A

GAM2339 CGCGGTTTCTTACGCGGGCT 1524 CCCCGGGGAG 4594 T T GGG GAG A GC
GAGCTCGGGAGTAGCGGATG AGGAGTGTTA CGCGGTT CT ACGC CT CTCGGG GTA G
CCCCGGGGAGAGGAGTGTTA GTAA ||||||| || |||| || |||||| |||
GTAACCGCG GCGCCaa ga tgtg ga gggccc cGT /
t t ag- gag - AG

GAM2340 TTCGTTTTTCAGAAAACTCA 1519 TTTTTCAGAA 4589 t aaact ttcaGTCA
AGTGTTCAGTCATATCAAGT AACTCAAGTG TTCGt tttcaga caagtg T
TCACTTGCCTCTGAAACACG TTCA ||||| ||||||| ||||||
AA AAGCA AAAGTCT GTTCAC /
C CC--- TTGAACTA

GAM2341 TGTTTATTTAGTATGGTAAC 1526 TAGTATGGTA 4596 T-- aac tatat cg TTA
TGTATATGACGGAATTAATG ACTGTATATG TGTTTAT tagtatggt tg ga gAA A
CTTCTATCTCTTCATAAACT ACGG ||||||| ||||||||| || || |||
ATATTATTTATAAATA ATAAATA ATTATATCA AC CT CTT /
TTT AAT TTCT- AT CGT

GAM2342 TATATCTAATATACTTGGAT 1527 TAATATACTT 4597 ta---- ct - taCAAG-- TT CG
TATTTCTGTACAAGAATTTA GGATTATTTC TATATC atata tggatt atttctg AAT AGCTATT T
GCTATTCGTAAAATAGTTTT TGTA |||||| ||||| |||||| ||||||| ||| |||||||
ATTATCAAATCTAGGAATCA ATATAG TATAT ACTTAA TAAGGAT TTA TTGATAA /
ATTCATATATATGCATACGA CATACG AT C CTAAACTA TT AA
TATA

GAM2343 ACTGGCCACTCACCCATGTT 1528 CTTTCTGCAC 4598 - C CCAT AT A---- CG
GTATTGCAACCAACGTTGTT CGCAATCCCG ACTGG CCA TCAC GTTGT TGCA CCAA T
TGGCTTTCTGCACCGCAATC TGAA ||||| ||| |||| ||||| |||| ||||
CCGTGAATGGTCCGGT TGGCC GGT agtg taacg acgt GGTT T
T a ccc- cc ctttc TG

GAM2344 GATTCTCATGTATGTGTTTT 1525 TAAAATACCT 4595 CT-- T CCT ATT
GTAACCTGACATTAAAAAGT GCATGTTGCA GATT CATGTA GTGTTTTGTAA GAC A
CTGTTTATAAAATACCTGCA ATC |||| |||||| |||||||||| |||
TGTTGCAATC ctaa gtacgt cataaaatATT CTG A
cgtt c TGT AAA

GAM2345 TAATATATGTATAATCTTAT 1534 ATCAGATTTA 4604 -- TAT T GTTAAAA
AGGTTAAAATAACACTAACT TCATTAATAT TAATAT ATG AATCT ATAG T
ATCAGATTTATCATTAATAT TA |||||| ||| ||||| ||||
TA attata tac ttaga taTC A
at tat c AATCACA

GAM2346 AAATAATTATCCTGATTTCT 1529 TCTATAGAAC 4599 ATTA-- c t aa ctttt--- a
CTATAGAACACTTTTTTGCA ACTTTTTTGC AAATA TCCTGATTTCt ta ag ca ttgc g
GCTGCAACTTATTTATGGAC AGCT ||||| |||||||||| || || || |||| |||
TTTGTGGGAATCAGGAATCT TTTAT AGGACTAAGGG GT TC GT AACG c
TGTATTT GTTCTA T T AG ATTTATTC t

GAM2347 GCATTAGATAACTGCAGAAA 1535 ACGCTGCGTA 4605 G AAC AAGa------ c gtt-- t
GACGCTGCGTATAGTTATGT TAGTTATGTA GCATTA AT TGCAGA cg tgcgtata atgtattc T
ATTCTTAGAATACGTCTGTA TTCT |||||| || |||||| || |||||||| ||||||||
TATACGCACGAACATATAAG CGTAAT TA ATGTCT GC ACGCATAT TGCATAAG /
TCTGTAAGAATGTAATGC G AGA GAATATACAA - ATGTC A

GAM2348 CTTACCCTTCCCCAACTTTC 1536 TGAGGCCGGT 4606 ---- A TT-- - G C ATATt-- gc tgta ag
TCTGTCGGTCGTGGTATATT GTATGTAGAG CCC AC TCTCTG TC GT GTGGT gag cgg tgtag a
GAGGCCGGTGTATGTAGAGA AGTC ||| || |||||| || || ||||| ||| ||| |||||
GTCTACGATCTTCGATCTCC GGG TG AGAGGC AG TA CACTA CTC GCT GCATc /
CTTCGGATCACATGGAGCGG GCTT A TTGT G G - GGCTTCC TA TCTA tg
AGATGTTGTAGGGTTCGAGA
GGGGTGAG
GAM2349 GCCTGGAGTGTGCATTGCAA 1530 TACAAAGTGT 4600 A GT-- GCAATACAAAG GG
TACAAAGCCCGGGAAATGGG TACAGCACCA GCCTGG GT GCATT CCCG A
ATACAAAGTGTTACAGCACC GGC |||||| || ||||| ||||
AGGC cggacc cg tgtga GGGT /
a acat aacatA----- AA

GAM2350 GGTCGTCTTTGCTCCGCGTC 1531 GAGCTGCGCA 4601 C- TTTC AA TT CTCC A---- CCGATTA A
AATTTCTGAACGCTTGGCTC CTTCTTGGCG C GCGTCAA TG CGC GGCTCTA GCG GGGA GGTC T

TACTCCGCGAGGGACCGATT CACG | ||||||| || ||| ||||||| ||| |||| ||||
AGGTCATTGACCGAAAATCC g cgcggtt ac gcg tcgagAT CGC CCCT CCAG /
CATCAACGCTAGAGCTGCGC ca cttc -- -- ---- AACTA AAAAG-- T
ACTTCTTGGCGCACGAGCTC
CTCGACC

GAM2351 GTAGTCGGTACTTAGGCTCA 1537 TGCCAGGCTC 4607 T C AG CAA C T GTC
AGCCGTTCCGCCGTCAAAAG AATTACTGCT GTAG CGGTA TT GCT GC GT CCGCC A
GCGGGCTGCCAGGCTCAATT AC |||| ||||| || ||| || || |||||
ACTGCTAC catc gtcat aa cgg cg CG GGCGG /
- t ct ac- t - AAA

GAM2352 GATTTATTGTGTATGGAAGA 1532 TGTATGGAAG 4602 Gt aagaa acc CAT ATA A - TA
AGTAACCATATTACATAATA AAGTAACCAT GATTTATT gtatgg gta atatta AAT TAC GGC TATT C
TATACAGGCTATTTACAAGA ATTA |||||||| |||||| ||| |||||| ||| ||| ||| ||||
TGCGCCGTACCGTTCGATGA CTAAGTAA CGTATC CAT TATAGT TTG ATG CCG GTAG /
TATAGTACGTACTATGCCAA AC ATG-- GA- AGC CC- - C AA
ATGAATC

GAM2353 CGTAGGAGATCTTGGCAATA 1538 TAGGAGATCT 4608 - t-- aata gCGGA
TTCTGGCGGATAAGAACGGA TGGCAATATT CGtagga ga cttggc ttctg T
AAAGCCAAGTATTCGTTCTA CTGG ||||||| || |||||| |||||
TG GTATCTT CT GAACCG AAGGC /
G TAT AA-- AAGAA

GAM2354 CTGATACGGATGATCTTGGT 1539 TGAAAACCGG 4609 A GATGA - A- GG- C TG
TTAGGTGGCAACGCTGAAAG GAACGCAGGA CTGAT CG TCTTG GTTT GGT CAA GC A
TTTGAAAACCGGGAACGCAG AAAC ||||| || ||||| |||| ||| ||| ||
GAAAACGAATCGG GGCTA Gc aggac caag cca gtT TG /
A aaa-- g gg aaa - AA

GAM2355 CGTAGTGGACTTTCGCTTTG 1533 TTACTCCATA 4603 CTT-- CT GAA- T T
AAGAGTTAATGTTAATATAT GATTCGATAT CGTAGTGGA TCG TT GAGT AATGT A
TTACTCCATAGATTCGATAT AATT ||||||||| ||| || |||| |||||
AATTTATTACG GCATTATtt agc ag ctca tTATA A
aatat tt atac t T

GAM2356 CACTAAAAAGACATATAGTA 1540 TATGACCTAC 4610 AAAA- CA --- CC T --- T
GTAGGTTACCTATTATCCTT GTTTATTATA CACT AGA TATAGTA GTAGGTTA TAT AT CC T
AAGGCTCATCATGTATGACC ATCT |||| ||| ||||||| |||||||| ||| || ||
TACGTTTATTATAATCTCGC GTGA tct atattat catccagt GTA TA GG A
CGAGTG GCCGC a- ttg at C CTC A

GAM2357 GAAGCTAAAGAATTAAGAAA 1541 AAGAATTAAG 4611 Aaa- a a--- c a -- A
ACAGTATCGCGATACGCAAG AAAACAGTAT GAAGCT ga ttaaga aa agt tc gcg T
AACTATTACCATTTTAATCG CGCG |||||| || |||||| || ||| || |||
GAGAGCTTT TTTCGA CT AATTTT TT TCA AG CGC /
GAGG - ACCA A - AA A

GAM2358 TTTTTTTTAATATAGAATAT 1542 TAGAATATAA 4612 AATAt acattt a TA
AACATTTTAAATAATATATT CATTTTAAAT TTTTTTTT agaatata taaata ta T
ATTAATATTTATATATTTTT AATA ||||||||| ||||||||| |||||| ||
TCAAAAAAAA AAAAAAAA TTTTATAT ATTTAT AT T
CTT-- ------ A TA

GAM2359 GGGAATGTGTTTAACCTTAT 1543 TACCTAGTAA 4613 T ACCTTAT--- A AA
CTATCTTAATAAAAGAAGTG ACATTTTTCC GGGAA GTGTTTA CT TCTT T
CTACCTAGTAAACATTTTTC ||||| ||||||| || ||||
C ccttt tacaaat GA AGAA /
t gatccatCGT - AA

GAM2360 CACCCAGACGCTCGGCACTT 1544 ACGCTCGGCA 4614 C ctc ct ct- g
AGCTCTCGAGTGATTGCCTG CTTAGCTCTC CAC CAGacg ggca tagct cga t
GCTGCTTGCCCCGTTTGCGT GAGT ||| |||||| |||| ||||| |||
G GTG GTTTGC CCGT GTCGG GTT G
C C-- TC TCC A

GAM2361 GCCCCGTTTGCGTGGAATGA 1545 GCCCCTGTTT 4615 C TG ATGA CA
GGCCAAACAAGCATTTGGCC GTCTAGACGG GCCCCGTTTG G GA GGCCAAA A
CCTGTTTGTCTAGACGGGGC GGC |||||||||| | || |||||||
cggggcagat t tt ccgGTTT G
c gt gtcc AC

GAM2362 GGGGCTTTGTGTTTTTCCCA 1546 GCTTTGTGTT 4616 c t ttcccacc cC -- C- G
CCCCTGCCCTTGCCCCTGGC TTTCCCACCC GGGg tttg gttt cctg CTT GCC CTGGCC C
CGCCTGGCCGGCCGGCTAAA CTGC |||| |||| |||| |||| ||| ||| ||||||
GTATAGGCCAGACCAAACCC CCCC AAAC CAGA GGAT GAA CGG GGCCGG C
CC C - CC------ AT AT CC T

GAM2363 GTAATAACCTTACAAAACAT 356 TAAGATATGA 3426 CT AAA ACAA-- G
ATACAACATTGGAAATGCAT ATGTGTGTTA GTAATAAC TACA CATAT CATT G
AAGATATGAATGTGTGTTAT TTAC |||||||| |||| ||||| ||||
TAC cattattg gtgt gtata GTAA /
t- aa- gaatAC A

GAM2364 GGTGATAAGTCTTATATAGC 1547 TACAATATAA 4617 TCTT GCAA GAA A- ---
ACAA CT

AATATAGAAGTAAACATAGG GTATATTAAT GTGATAAG ATATA TATA GTA ACATAG
GCAAA GTATT A
CAAAACAAGTATTCTAATAG TTTG |||||||| ||||| |||| ||| |||||| ||||| |||||
ATATTTTGCTAACTATGTAG CATTgttt tatat atat cat TGTATC CGTTT TATAG A
TACAATATAAGTATATTAAT taat ga-- aa- GA AAT ---- AT
TTTGTTACC

GAM2365 AATCTGACTTAGTTAAATAT 357 TTCATATAAT 3427 CTTA -- AG
GTGGATTTAGTTAAAAATTC TTTAATATTT AATCTGA GTTAAA TATGTGGATTT T
ATATAATTTTAATATTTCAG CAGA ||||||| |||||| ||||||||||
ATT TTagact taattt atatacttAAA T
tta- ta AA

GAM2366 ATTATTTGATAAGTTTACTA 1548 TAAGTTTACT 4618 --- actaa ttaaaATT TCG
ATAAATGGTTAAAATTAGAC AATAAATGGT ATTATTTG Ataagttt taaatgg AGAC T
TCGTTAATGTCTTCTTCACT TAAA |||||||| |||||||| ||||||| ||||
CATTTAAAACTTATAAACAA TAGTAAAC TATTCAAA ATTTACT TCTG T
ATGAT AAA ----- CACTTCT- TAA

GAM2367 GCCGTACGTGGGTTCACAGC 362 CGCAAGCACG 3432 T GT ACA TTTTTTTA GAG
TTTTTTTTTACCGAGATCAG GTCACGTCGG GCCG ACGTGG TC GCTT CC A
GGACACGCAAGCACGGTCAC C |||| |||||| || |||| ||
GTCGGC cggc tgcact gg cgaa GG /
- -- ca- cgcACAG- ACT

GAM2368 TGTCCTTACTGACATCTGCG 363 TGGATTCGGT 3433 --- C C T CT
TTTGTATCTGTGTGTGCGTG AACCAGGATA TGTCCT TACTGA ATCTG GT TGTAT G
CTGGATTCGGTAACCAGGAT |||||| |||||| ||||| || |||||
A atagga atggct taggt CG GCGTG T
cca - - T TG

GAM2369 ACATATCCGTCACCGGGAGG 358 TCCGTCACCG 3428 t ------- gt g tt TCAT
GTCGTTGTTCTCATATCGTG GGAGGGTCGT ACATA ccgtcacc gggagg c ttg C A
GTCGAGGGTCCTTCTGTTAG TGTT ||||| |||||||| |||||| | ||| |
GGGGTGACGGTGTGT TGTGT GGCAGTGG TCTTCC G AGC G /
- GGGATTG TG G TG TGCT

GAM2370 TTATTTTTTAAATATTAATT 359 TGAAATTTTA 3429 TAAATAT TT GACTA
TTTCATAGACTATTTACTAT TAAATAAAAA TTATTTTT TAA TTTCATA T
ATGAAATTTTATAAATAAAA TAA |||||||| ||| |||||||
ATAA aataaaaa att aaagtAT T
taaat-- tt ATCAT

GAM2371 TATCTTTTAATATGAATTAC 360 TCTTTTAATA 3430 aattac -- CTT CTGA

TTCACTTTATCTTTCTTACC TGAATTACTT TAtcttttaatatg ttcactTT ATCTTT AC T
TGATTATTGTTTAAAGATTA CACT |||||||||||||| |||||||| |||||| ||
AAAGTGAAATATATTGGAAG ATGGAAGGTTATAT AAGTGAAA TAGAAA TG /
GTA A----- AT TT- TTAT

GAM2372 TCTTCCGGAAAGACTTCAGA 369 CGGAAATAAA 3439 CA GATcg aaaag- aa---- T
AAA TGA
CAGATCGGAAATAAAAGACC AGACCGCATA GACTT GACA gaaat accgcat cagTGT G
TCAG A
GCATAACAGTGTTGAAATCA ACAG ||||| |||| ||||| ||||||| ||||||| | ||||
GTGAACTTCTGGGACATATT TTGAA TTGT CTTTG TGGTGTA GTTATA C GGTC
/
GGTAATAATGTGGTATACGA -- AAAA- AGCATA ATAATG - AG- TTC
GTTTCAAAATGTTAAGTTAA
TACGGTATGA
GAM2373 TTTATTATTATCCATAATAT 361 TATAATATAT 3431 TATCC A A ATA
ATAATATATAATATATAATA AATATATCTT TTTATTAT ATA TATATA TATATA T
TATAATATATAATATATCTT ATAA |||||||| ||| |||||| ||||||
ATAATAGG GGATaata tat atatat atatAT A
ttcta a a AAT

GAM2374 GGTAAGTACATGTTCATACA 370 TACATGTTCA 3440 AA- ta c ag-------- TCACT
AAGTTTTGACTCACTCTCTT TACAAAGTTT GGT G catgttcata aa ttttgac C
TGTTAGAAACCATTTCCGTT TGAC ||| | |||||||||| || |||||||
CTGTGGATATGCGCCAGACC CCA C GTATAGGTGT TT AAGATTG /
GAC GC C GCCTTTACCA TTTCT

GAM2375 TCACTTGGCACACTCTCGGA 374 AACTGGTTAA 3444 AC ACA CGGA A CA --- ACA
TTTAACAAGCATTGCTGGAC AAAAGAGCGC TC TTGGC CTCT TTTAAC AG TTGC TGG C
ACTTACCAACCGTAACTGGT CAAA || ||||| |||| |||||| || |||| |||
TAAAAAAGAGCGCCAAAGGG GG aaccg gaga aaattg tc aaTG ACC /
Ga c-- aa-- g -- CCA ATT

GAM2376 ATTTTTATCATAACACTACT 364 AACACTACTT 3434 CAT ct- tt-- ta AG
TTGGTTAGATGTTTTAGAAA TGGTTAGATG ATTTTTAT aaca ac tggt gatgtttt A
AAAAATATCGCCGTACCGTT TTTT |||||||| |||| || |||| ||||||||
CTTGTTTTTATAAAAAT TAAAAATA TTGT TG GCCG CTATAAAA A
TTT TCT CCAT -- AA

GAM2377 TGATTTTCTTTCTAATACTA 365 TGGGAATAAA 3435 T TC A C ATAT TC A A TC
TATATTTCTCTCGAAGAAGT ATACTACTGT TGATTT CTT TA TA TAT TTCTC GA GA GT T
TCTTGCACATCATCTGGGAA TGAG |||||| ||| || || ||| ||||| || || ||
TAAAATACTACTGTTGAGTA ACTAAA gag gt at ata aaggg CT CT CA T
AATCA T tt c c aaat t- A A CG

GAM2378 TTGATTTTCTTTCTAATACT 375 TGGGAATAAA 3445 T TC A C ATAT TC A A TT
ATATATTTCTCTCGAAGAAG ATACTACTGT TTGATTT CTT TA TA TAT TTCTC GA GA GT T
TTTTTGCACATCATCTGGGA TGAG ||||||| ||| || || ||| ||||| || || ||
ATAAAATACTACTGTTGAGT GACTAAA gag gt at ata aaggg CT CT CA T
AAATCAG T tt c c aaat t- A A CG

GAM2379 AGAAATTGGTCTGTGTTACA 371 TGTATTGGCT 3441 T T TACATA-- --- TC T
TATCTCTTCTATATTATTGT TAGAAAACTA AGAAA TGGTCTG GT TCT CT TATATTA T
TGATGTATTGGCTTAGAAAA TTAC ||||| ||||||| || ||| || |||||||
CTATTACTTAGACCATTTTC TCTTT ACCAGAT ca aga gg atgtAGT G
T T T ttatcaaa ttc tt T

GAM2380 CCTCGTGGCGCGCGTCCGCG 366 CTCCCGCCCG 3436 ---------- C T A CCC
C
CCGGGGTCGCGAGGTCCCGG CGACCCCGGC TCGTG GCG GCG
CCGCGCCGGGGTCGCG GGT GGAC G
ACCGAGGTCTCCCGCCCGCG GCGG ||||| ||| ||| |||||||||||||||| ||| ||||
ACCCCGGCGCGGCGCCGCGG AGCAC CGC CGC ggcgcggccccagcgc ccg tcTG
A
AAAAACAGACGACGACACGA AGCAGCAGACAAAAAGG - - - ccc G
GG

GAM2381 AAGACCACTGCAACAGCTTC 372 AAAAAGCACT 3442 A ----- C CTTC GTACGCT TT
TGCGTACGCTTGTATTTACA TTTGCCACAG AAGACC CT GCAA AG TGC TGTAT A
GTACATAAAAAAGCACTTTT AGCG |||||| || |||| || ||| |||||
GCCACAGAGCGGTCTT TTCTGg ga cgtt tc acg ACATG /
c gacac t ---- aaaaaAT AC

GAM2382 CCTTAGGGTGTTGAAAGGTG 367 TGTAGGAAAA 3437 TGAA - A CCGt gaa t----------
--- t
TCCAACGACCGTGTAGGAAA GAAGAGTTCG AGGTG TCCA CGA gtag aagaagag
tcg t
AGAAGAGTTCGTTCGCGACT TTCG ||||| |||| ||| |||| |||||||| |||
GGGCTTTGTCCCTGCCTCTT TCCAT AGGT GCT CATT TTCTTCTC AGC c
CTTCTGTTACCATTTCGTGG ATC- T - TTAC GTC CGTCCCTGTTTCGGGTC g
ATTACCTCTATCGCCTTAAG
G
GAM2383 GCGGTGTCTGTGTTTACCAC 376 TCTGTGTTTA 3446 - t cGT-- TT T T----------
TT
TCGTGACGACGTTCAGAACT CCACTCGTGA ccact cg gacga TCAGAAC CTG ACGG
TCTC C
TCTGTACGGTTCTCTTCGTG CGAC ||||| || ||||| ||||||| ||| |||| ||||
AGACTGAGCACGGCTCTGCC GGTGA GT CTGCT AGTTTTG GAC TGCC
AGAG /
CGTCAGTCGTTTTGACATTT T - TTTAC CT - CGTCTCGGCACGAGTC TG
TCGTCTGTAGTGGAGCGCGA

ATACCAGGGC
GAM2384 TATACACTAATGAGCCTCTT 368 TGGCAGAGCT 3438 T AT- CT --- - A
TGTTGTGTATTTTGCTTTAT GCTCTTATAG TA ACACTA GAGC CTTTGTT GTGT ATTTTGCTTT
T
TTAAAGCAAGATCACACCGT TGTT || |||||| |||| ||||||| |||| ||||||||||
GGCAGAGCTGCTCTTATAGT AT tgtgat ctcg gagacgg CACA TAGAACGAAA T
GTTTA t att tc tGC C T

GAM2385 CGCTTAGCAATGCGAAAGTT 373 TTAGTGCTGA 3443 T TGC A -- aag aca- T
AGTGCTGAAGTTTCACGACA AGTTTCACGA CGCT AGCAA GAA Gt tagtgctg tttcacg gg T
GGTTATCCAAGACGTGAAAG CAGG |||| ||||| ||| || |||||||| ||||||| ||
ATGGCACTGTTACCTTCAAC GCGA TCGTT CTT CA GTCACGGT AAAGTGC CC A
TTGCTAGCG - CAA C TT AG- AGAA T

GAM2386 GTGCCATTGCTGTATTGGTC 377 TGCTGTATTG 3447 Tt t ----- -- tataT - CT
TCAAGCATATATTTACGCAA GTCTCAAGCA GTGCCA gctgtat gg tct caagca TTAC GCAA T
CTTTGATTGCTGTAATTTTG TATA |||||| ||||||| || ||| |||||| |||| ||||
CTTGGAAGATTTTTCCATAC CACGGT CGACATA CC AGA GTTCGT AATG CGTT T
AGCTTGGCAC T- - TTTTT AG TTT-- T AG

GAM2387 ATACAATACTACACACGCCA 378 ACCATTGTGT 3448 T - C T C- T GCCT
TATATGCTGCTAGGCCTGTA TGTGTGTTAG ATACAA ACTA CACACG CATA ATG TGC AG G
AACTTGCAACCATTGTGTTG TTTT |||||| |||| |||||| |||| ||| ||| ||
TGTGTTAGTTTTGTGT TGTGtt tgat gtgtgt gtgt tac ACG TC /
t t t - ca T AAAT

GAM2388 GACATTTACCAGAGATACGT 379 TATTGTGTAC 3449 CA - -------- TG T T
GATACTCGGTCTACTGTGTA CTTGTAATCT GA TTTACC AGAGA TACG ATAC CGG C
TTGTGTACCTTGTAATCTCT CTAG || |||||| ||||| |||| |||| |||
AGGTAAACTTC CT AAATGg tctct atgt tatG GTC T
TC a aatgttcc gt T A

GAM2389 TACTGATCTCTTTGTTTTTT 381 GGGAAGGTTT 3451 T ----- TT--- G AT
TTTTTCTGTGTATTGTGATA GTAAGGACAA TACTGA CT CTTTGTTTTT TTTTCT TGT T
GGGAAGGTTTGTAAGGACAA AGGA |||||| || |||||||||| |||||| |||
AGGACAAAGTTCAGTA ATGACT GA gaaacaggaa ggaagg ATA G
T AACag tgttt g GT

GAM2390 GATTGCCATCGCGGACGCAC 380 TGCCGCAGAC 3450 C C-- A AC- A- ACC--
CCCCCG GC
GCGGGGACCCGCCAGAGACC CACCTCGCGG CG GGA GC CGCGGGGG CCGCC GAG
CTGC GCGCGGGCG G
CTGCCCCCCCGGCGCGGGCGG CGGC || ||| || ||||||| ||||| ||| |||| |||||||||
CGCCGCGCCCGCGTGCCGCA GC CCT CG GCGCCCC ggcgg ctc gacg
tGCGCCCGC C

GACCACCTCGCGGCGGCTCC - TTC - CTc cg cacca ccg--- GC
CCCGCGGCCTTTCCCGTGGC
CCTC
GAM2391 GGTTTTCTTCGAGGCCGTCG 389 TTCACGGGCC 3459 - A CGTC A --- A
CGAGGCCGAAAAATTTTTTT CGCGCCCGAG GGTTTTCT TCG GGC GCG GGCC GAAAA T
CACGGGCCCGCGCCCGAGAG AGAG |||||||| ||| ||| ||| |||| |||||
AGAGCC CCGAgaga agc ccg cgc ccgg cttTT T
g - ---- - gca T

GAM2392 GATCATATAGTTATGTATAT 382 TTAGTGACGA 3452 A A- Atta g -- gag gaaaAT
TAGTGACGAATCAAGAGATG ATCAAGAGAT GATC TATAGTT TGTAT gt acga atcaa at A
AAAATAATCCTGAATATATT GAAA |||| ||||||| ||||| || |||| ||||| ||
GATTTTCGTAACAGATACGG CTAG ATATCAG GCATA CA TGCT TAGTT TA A
AGACTATAGATC - AG GA-- A TT ATA AGTCCT

GAM2393 GAAATCAAGGGATGCGTTGA 390 TCAACGTCAT 3460 CAA- GG - A CTC
ATCTTCTCATAAAAAGACTC TTCGATTATT GAAAT G ATG CGTTGA TCTT A
AACGTCATTTCGATTATTTC TC ||||| | ||| |||||| ||||
cttta c tac gcaact AGAA T
ttag tt t C AAA

GAM2394 TGGGTCTCGCGATAGCTTTG 391 TTAACGGTGG 3461 T ----- TTTGT CG G - C
CCC G A
TGTTCGTCGATCGTCGACGC TTTGTACGAT GGTC CGC GATAGC GTT TC ATCGT CGA
GCCGCT AAC CG T
CGCTCCCAACGCGATCTCGG AGAA |||| ||| |||||| ||| || ||||| ||| |||||| ||| ||
TTAACGGTGGTTTGTACGAT CCAG GCG CTGTTG CGA ag tagca gtt tggtgg ttG GC C
AGAAAAGCCTGTTGTCAGAG - AGAGA TC--- Aa a t - caa - T
AGCGGACCCA

GAM2395 GATCCTGCTGTCTCTGCAAC 383 TCTCTGCAAC 3453 T C tc t ------ acA
ATCAATCCAGGCACAGAGCG ATCAATCCAG GA CCTG TG tc gcaacatcaatcca ggc G
CCGCAAGATGGATTGGTGTT GCAC || |||| || || |||||||||||||| |||
GTTGATCCAACAGGTTC CT GGAC AC AG TGTTGTGGTTAGGT CCG /
T A CT T AGAACG CGA

GAM2396 TAGAGCTTGTGAGTTGTTAT 392 TATTACGTTT 3462 CT T tatt tttgttgttt tCT TT
TACGTTTTGTTGTTTGAATC TGTTGTTTGA TAGAG TGTGAG TGT acgt gaatc GT T
TCTGTTTTGTTACTCTGATT ATCT ||||| |||||| ||| |||| ||||| ||
TCCTTCACGTTTGCACCTTA ATCTC ACATTC ACG TGCA TTTAG CA G
CACTCTCTA TC C TT-- CTTCC----- TCT TT

GAM2397 AGTGTGTGATAATGCCGGGG 384 TAAGAGCATA 3454 TG G TAAT C T - G C GC- G
CTTCACGCTACGCTCGCGCT GGTCGGTGCC AG T TGA GC GGGGC TC AC CTA GCTC
GCTC T

CGTAGAGCTAAGAGCATAGG CTCG || | ||| || ||||| || || ||| |||| ||||
TCGGTGCCCTCGTTGCTTCA TC G ACT Tg tcccg gg tg gat cgag CGAG /
GGTGCT GT G TCGT c t c - a aat A

GAM2398 GCACTTTTTTTTTCCGATTT 385 TAATGTAGCT 3455 A TT TTTG TCC- TACA
TGACTCCTCGTACATATATC ATTGGAGGAT GC CTTT TTTTCCGAT AC TCG T
GATAATGTAGCTATTGGAGG GGAG || |||| ||||||||| || |||
ATGGAGGC CG gagg aggaggtta tg AGC /
- t- tcga taat TATA

GAM2399 GCTCAACAGTATAGGATTTT 386 TGAGTTGTCT 3456 A GTATAGGATTTTAAGT G GA ATA G G TC
AAGTCTCCTTTGTAGAATCA GGTTAGGAGG GCTC ACA CTCCTTT TA ATCA AA TTA TGTG A
ATAAAGTTAGTGTGTCATTC GAGT |||| ||| ||||||| || |||| || ||| ||||
GTAGTGAGTTGTCTGGTTAG CGGG TGT gagggag at tggt tt agt ATGC /
GAGGGAGTGTGTCGGGC C Gt---------- g -- ctg g G TT

GAM2400 TGTCTAAATCTTGAAGAGGT 393 AGAGGTAATC 3463 AA TT -- aatc c t
AATCGAGCGGTTGGTTAACC GAGCGGTTGG TGTCT ATC GAaga ggt gag ggttgg t
GATCCTTACCGCCTGTCTTC TTAA ||||| ||| ||||| ||| ||| ||||||
TCGATAAGGCA ACGGA TAG CTTCT CCG TTC CTAGCC a
A- CT GT CCA- - a

GAM2401 CCCCGATGCGAAGGCCGAAA 394 TAGGACTAGC 3464 ----- GA G GAA- TAA
AGGGCTAACCATGCCCTTAG AAAAAATCGG CCCCGA TGC AG CC AAGGGC C
TAGGACTAGCAAAAAATCGG GG |||||| ||| || || ||||||
GG ggggct acg tc gg TTCCCG /
aaaaa a- a atGA TAC

GAM2402 GGAGCGGGGGGGGATCTCGAC 387 ACGGACAGAT 3457 G --- GA-- --------- C
GCGCGCGACGGACAGATCGA CGAGACGGAC GGAGC GGG GG TCTCGA CG G
GACGGACCAGGCCCGGCTTC CAGG ||||| ||| || |||||| ||
CTTCG CCC cc agagct GC C
G gga aggc agacaggca G

GAM2403 CAGCAATTTTACAGTTTTGT 388 TTACTCAGGC 3458 AC- TTTG --- A GC -- - CTC T
CTTGTCTGGAGACCGCTGCC GATTGTTG AGT TCTTG TCTGG GACCGCT CGGTC GC GCTAATCC AGG A
GGTCGCGCTAATCCCTCAGG ||| ||||| ||||| ||||||| ||||| || |||||||| |||
TAAGCTTAAAGGATTAGCTG tca AGGAT GGACC CTGGCGA GCCAG CG CGATTAGG TTC A
CTCGACCGAAAGCGGTCCCA gac ttA- GGT - AA CT T AAA G

GGTGGTAGGAATTACTCAGG
CGATTGTTG
GAM2404 ATCATAAAATCTTTAATTAT 395 TATCAAAGAA 3465 AA- A TATT TTA
TATTTATATTTTATTAGCGA CCTTATGAT ATCATAA TCTTT AT ATTTATATT T
TATAAATCTATCAAAGAACC ||||||| ||||| || |||||||||
TTATGAT tagtatt agaaa ta TAAATATAG T
cca c tC-- CGA

GAM2405 CCGCCGAAAGCGGTAGAAAG 396 AGCCAGAAGC 3466 C----- TA AAGa- ccctc-
agac
AGCCAGAAGCGGCCCTCGCA GGCCCTCGCA CCG CGAAAGCGG GA gccagaagcgg gc
g
GACGGTACGCATCCCCCTGT GACG ||| ||||||||| || |||||||||| ||
TTTTGGCCCCGCTCCCCCGC GGC GTTTTCGCC CT CGGTTTTTGTC CG /
TTTTGACATCACGG ACTACA CC CGCCC CCCCTA CATG

GAM2406 GTGGCGTAGGAGTGGCGAAC 402 GGAGTGGCGA 3472 GTA a a- catta
CGGCGTCATTATAATCAAAC ACCGGCGTCA GTGGC gg gtggcga ccggcgt t
GCCGGAGTCGCCGCCCGCCA TTAT ||||| || ||||||| |||||||
C CACCG CC CGCCGCT GGCCGCA A
--- - GA AACTA

GAM2407 ATTCCCTGACGACTACGAAC 397 TCCCTGACGA 3467 gac aa----- t GG
ACCTAAATGAAGCGGAAGGC CTACGAACAC ATtccctgac tacg cacc aaATGAAGC A
TTCATTTGGTGACCCCGACG CTAA |||||||||| |||| |||| |||||||||
TGATAGTTAGGGAAT TAAGGGATTG GTGC GTGG TTTACTTCG /
ATA AGCCCCA - GA

GAM2408 GGCGAAAAGCTGAGTGGCGT 403 TACCCTACCG 3473 AAAG G G - A------ ACT
CGGAGGGAGCTCTACTGCAG AGCACTCAGA GGCGA CTGAGTG C TCGG AGGG GCTCT
G
GGAGCCAACATACCCTACCG GAGT ||||| ||||||| | |||| |||| ||||
AGCACTCAGAGAGTCGTT TTGCt gactcac g agcc tccc CGAGG /
gaga - - a atACAAC GAC

GAM2409 GTTGATGGCCGGACCGTCGA 398 TCCCTAACGA 3468 GA G TCG g tg aa----- t
AG
TTCCCTAACGATTGCGAACA TTGCGAACAC TT TGGCCG ACCG ATtccctaac at cg cacc
gaATGAAGC A
CCTGAATGAAGCAGAAGGCT CTGA || |||||| |||| |||||||||| || || |||| |||||||||
TCATTTGGTGACCCCGACGT AG ACCGGC TGGT TAAGGGATTG TA GC GTGG
TTTACTTCG /
GATAGTTAGGGAATAGTGGT AC - GA- A GT AGCCCCA - GA
CGGCCACAGAC

GAM2410 TACAGTTCAAGGATAATTAC 404 TTCACTTGCT 3474 ATTACAT - CTTAAACCACCTCATAT
TCCC CA TACCT
ATCTGGGTAGTCTTAAACCA CTTTCACTAT CTGGG TAGT GAAAG AGT AAGCT
T
CCTCATATGAAAGTCCCAGT CCCA ||||| |||| ||||| ||| |||||
CAAAGCTTACCTTCATTACA Gaccc atca ctttc tca ttTGA C
GTTTCACTTGCTCTTTCACT ------- t ---------- tcgt c- CATTA
ATCCCAGTACCCTAAACCTG
TA
GAM2411 GACCGTTGAGTCCCTAACGA 405 GCGAACACCT 3475 AG Tg aa----- t gg
TTGCGAACACCTGAATGAAG GAATGAAGCG GACCGTTG TCCCTAACGAT cg cacc
gaatgaagc a
CGGAAGGCTTCATTTGGTGA GAAG |||||||| |||||||||| || |||| |||||||||
CCCCGACGTGATCGTTAGGG CTGGTGAT AGGGATTGCTA GC GTGG TTTACTTCG /
AATAGTGGTC A- GT AGCCCCA - ga

GAM2412 ACCACAAAATGTCACAATAA 399 TTAGTAGTTT 3469 - ATGTC TA TT T
TTATTTTTTTTAAAAAATTA GTCCCTTTGA ACCA CAAA ACAA ATTATT TTT A
GTAGTTTGTCCCTTTGATGG TGGT |||| |||| |||| |||||| |||
T tggt gttt tgtt tgatga AAA A
a ccc-- -- tt A

GAM2413 GGAACTTTAAATGTGACGCA 406 TGAGAGGAAC 3476 - AA GACGCA-- AGTGT--- G
TCTTTTCAGGTAGTGTTGGA CACAGAACAT GGA ACTTT ATGT TCTTTTCAGGT TG A
GACATAGATCAGATTTGAGA CAAA ||| ||||| |||| |||||||||| ||
GGAACCACAGAACATCAAAG CTT TGGaa taca aggagagtTTA AC G
GTATTC A ac agacacca GACTAGAT A

GAM2414 CTGAGTGACGTCGGAGGGAG 400 CGTCGGAGGG 3470 GAcg - gagc cac g
CTCCACGGCCGGGGGCCAAG AGCTCCACGG CTGAGT tcgg agg tc ggcc g
ATAACCTACCGAGAACTCAG CCGG |||||| |||| ||| || ||||
GACTCA AGCC TCC AG CCGG /
AG-- A AAT- AA- G

GAM2415 GACCGTCGATTCCCTGACGA 1882 TCCCTGACGA 4952 TCG c ag----- t AG
CTACGAGCACCTGAATGAAG CTACGAGCAC GACCG ATtccctgacga tacg cacc gaATGAAGC
A
CAGAAGGCTTCATTTGGTGA CTGA ||||| |||||||||||| |||| |||| |||||||||
CCCCGACGTGATCGTTAGGG CTGGT TAAGGGATTGCT GTGC GTGG TTTACTTCG /
AATAGTGGTC GA- A AGCCCCA - GA

GAM2416 GCAATTAGATTTGTAATGTT 401 TCGAATCTTG 3471 -- T TT--- ACC - G ------- A
AAC
TGATACCGCCAACGTCTCTG TCACGTTTAG AA TTAGATTTG AATGT GAT GC CAAC TCT
CTGA GA A

AAGAAACAAAAATCTCGGCT ATCT || ||||||||| ||||| ||| || |||| ||| |||| ||
GATATAGAAGTTGCGTCGAA TT AGtctagat ttgca cta tG GTTG AGA GGCT CT A
TCTTGTCACGTTTAGATCTG TA - ctgtt agc C A TATAGTC - AAA
AATTTGC

GAM2417 GTGGCTTGAACATCTACTTG 407 TTCAAAGTGT 3477 ----- TA TGAGA ---- TCGAA-GA
AGAAGATACTACGTTCGAAG CTACGTTAGA GTGGCTTGA ACATC CT AGATACT ACGT GC C
CGACCAGCGAGGTTACGTTC CGAT ||||||||| ||||| || ||||||| |||| ||
AAAGTGTCTACGTTAGACGA CATTGAACT TGtag ga tctgtga tGCA CG /
TGTTAAGATCAAGTTAC AGAAT ca ttgca aact TTGGAG AC

GAM2418 GATGTTAAGATCAAGTTACC 408 TATCGTAGCA 3478 A ---- CA AA- TT TAT TTC-AA GT
AATATTAAAAACATTTGTTA ACATTGGTTG GATCAA GTTAC ATATTAAA CA TGT AACA CCG GAAC T
TAACATTCCCGAAGAACGTT TAAC |||||| ||||| |||||||| || ||| |||| ||| ||||
GTGTTCGTGGTTACTGTTCC ttggtt cgatg tatAGTTT GT ACA TTGT GGT CTTG /
TACATTGGCATTTGATATCG g acaa c- ACG T- TCC CATT G- TG
TAGCAACATTGGTTGTAACA
TC
GAM2419 TGAAACAATTACGTATAAAG 409 TAAAGAACTA 3479 A G gaac caa t GA
AACTATGCAATATATTAGGT TGCAATATAT TGAA CAATTAC TAtaaa tatg tatat aggT T
GATAAGACCTATATAACTAT TAGG |||| ||||||| |||||| |||| ||||| ||||
ATTTGTGAGTAATTGCTTTA ATTT GTTAATG GTGTTT ATAT ATATA TCCA A
C A ---- CA- - GA

GAM2420 TAAAAACGATATACTGACTC 1888 CACTCGTAAT 4958 G --------- ACT ATT TA TT AA
GGATTTGATAGTTTATGCAA AGTATTTATT TAAAAAC AT ATACTG CGG TGA GT ATGC A
ATTAGCGTCCACCTCACTCG TTTC ||||||| || |||||| ||| ||| || ||||
TAATAGTATTTATTTTTCAT ATTTTTG TA tatgat gct acT CA TGCG T
GGTTTTTA G ctttttatt aat c-- C- CC AT

GAM2421 ACCTGAGTGTTCAAAAAAAT 1889 TCAATAGTAG 4959 GTTCAAAAAAAT AT TC CAA AACT G
CAATAAACCATCCCTCAATA GAGTGGTTTT ACCTGAGT CA AAACCA CCT TA TGT C
AACTTGTGCTGACATCAATA CTGT |||||||| || |||||| ||| || |||
GTAGGAGTGGTTTTCTGTAT TGGACTCG gt tttggt gga at ACA T
AAGTACTAGCTCAGGT ATCATGAATAt- ct ga tg- aact G

GAM2422 GCCCGACGTCAGTCAGTCAC 1883 AGGCGGTGAG 4953 A AGTCA ag g ga--- - aca- - ggg
CTGAGGCGGTGAGCCACACA CCACACAGCC GCCCG CGTC GTCACCTG gc gt gc cac gc cc G

GCCCGGGGTGAGGAGCGGAG CGGG ||||| |||| |||||||| || || || ||| || ||
GTGAGCGAGGGACGGCGTAG CGGGT GCAG CGGTGGAT CG CA CG GTG CG
GG /
GTGGCGACGGTGGGC G ----- G- G GGGAG A GAGG A AGT

GAM2423 GGAGAGGGACAGAGAGGACA 1890 GAGGACACAA 4960 GGGA caacgga ga gCC
CAACGGAGTCGAGGTTGCCA CGGAGTCGAG GGAGA CAGAgaggaca gtc ggtt A
AGGAACCGGGCGTTTTATTG GTTG ||||| |||||||||| ||| ||||
TCTTTTTTGCGTCTCC CCTCT GTTTTTTCTGT CGG CCAA /
GC-- TATTTTG G- GGA

GAM2424 AACTTATTATTGTTAGATGA 1884 TGACGAAATA 4954 ----- tg-- cctacTTTCG--- -
GA
CGAAATAACTGATAGACCTA ACTGATAGAC TGTTAG Atgacgaaataac ataga GATATA
TGT A
CTTTCGGATATATGTGAATC CTAC |||||| |||||||||||| ||||| |||||| |||
GACATTGTATCAGTAACTAT GCAATT TATTGTTTTATTG TATCT CTATGT ACA
T
AAATTCTATACCCGTTATTT ATTAA CCCA TAAATATCAATGA T GC
TGTTATAATTATTAACGAAC
ATTAGTT
GAM2425 GGGTTTAAGCAATCAGAGGC 1885 TCTGAAAGAT 4955 AAGCAA-- ----- CTCATTTT T
GTGTCTCATTTTGGTACGCC ATCAAGCCC GGGTTT TCAGA GGCGTGT GG A
ACACGCCGTACGTCTGAAAG |||||| ||||| ||||||| ||
ATATCAAGCCC cccgaa agtct CCGCACA CC C
ctatagaa GCATG -------- G

GAM2426 CACATTAGCATAAGATGTAC 1886 TGTAACAAAC 4956 - - TAAGA T t aa gtc cc A
TTGTAACAAACCGCGTCCTC CGCGTCCTCA CACATT AG CA TGTAC tg aaca ccgc ctca ta G
ACCTAAGCCTAATTGAGGCG CCTA |||||| || || ||||| || |||| |||| |||| ||
GCCTGTTCTATGTATAACCT GTGTAG TC GT ATATG AT TTGT GGCG GAGT AT C
TGACTAGATGTG A A TCCA- T C CC --- TA C

GAM2427 GGATAGCTCTGCGCAGCTAT 1891 TACCGCGCAG 4961 ---------- AGC CCCCACT
ACCCCACTTAATAAATTATA AGTATAAAAG GGATA GCTCTGCGC TATA T
CCGCGCAGAGTATAAAAGAT ATTA ||||| ||||||||| ||||
TATATTATCC CCTAT tgagacgcg atAT /
TATattagaaaata cc- TAAATAA

GAM2428 TATTTTGAAAGATATGAGTA 1887 TGAAAGATAT 4957 gata aa AT
AAATATTTAATGAAATAAGT GAGTAAAATA TATTTtgaaa tgagtaa tattta G
AACTTATTTAATAATTTCAA TTTA |||||||||| ||||||| ||||||
AATA ATAAAACTTT ATTTATT ATGAAT A
AATA CA AA

GAM2429 GTGGTGGGAGTGGGCGTGGT 1894 TTTAAATTGG 4964 G -- G- GTA G TT t tg
cca ga
ATGCGGGGGTTCTTTGTTTA GCCCAGGCGG GT GGGAGTG GCGTG TGCG GGGTTCT Gt
taaat ggc ggcg t
AATTGGGCCCAGGCGGATCA ATCA || ||||||| ||||| |||| ||||||| || ||||| ||| ||||
GTGCCAGTTTTGTTTGCATT TA TCCTCAC CGTAC GCGT TCCGGGG TA GTTTG TTG
CCGT c
GGGGGCCTGTGCGGCATGCG T AC AG G-- G GT C TT A-- Ga
ACACTCCTCAATTGC

GAM2430 ACGTCGAGCCCGCGTTGGGG 1901 CACCGGCACG 4971 --- C T C TCAC AC- CA
CATATCACGCTACTGTACAG TTCGACGT ACGTCGAGC CCG GT GGGG ATA GCT TGTA G
CTCTGCACTAAGCACTTTAT ||||||||| ||| || |||| ||| ||| ||||
ACTCTCACCGGCACGTTCGA tgcagcttg ggc ca TCTC TAT CGA ACGT C
CGT cac - c A TTCA ATC CT

GAM2431 ATTTGTTATTAAATGAATAA 1892 TAAATGAATA 4962 TT A ataaaatt tca
AATTAGATTCATCTATATCT AAATTAGATT AT GTT Ttaaatga agat t
TCTTCACTCATTTAAAAACT CATC || ||| |||||||| ||||
TAT TA CAA AATTTACT TCTA c
TT A CACTTCT- TAT

GAM2432 TAGTCACGACTGAAATAACC 1902 CGGCATGGTT 4972 ACT AA-- C -- TTT
GCGTGATTATTTTTTGGTAT TCTGTGACTA TAGTCACG GAAAT CCG GT GATTAT T
AATTCTACACGGCATGGTTT |||||||| ||||| ||| || ||||||
CTGTGACTA atcagtgt ctttg ggc CA TTAATA T
--- gtac A TC TGG

GAM2433 GAGAGAGAAAGAGACAGAGA 1903 ACCACGTTTT 4973 AGACA G C-- CC--- -
A CC
GACGCGAGACGAAAGAGACC TATCTTTTTT GAGAGAGAAAG GAGAGACGC AGA
GAAAGAGA ACG GG CG A
ACGGGACGCCACACGACCAC TATT |||||||||| ||||||||| ||| |||||||| ||| || ||
GTTTTTATCTTTTTTTATTC TTTTTTCTTTC TTTTTTGCG TCt ttttttct tgc cc GC /
TGCGTTTTTTATCCGCTTTC GCCTA - tat atttt a a AC
TTTTTT

GAM2434 AAATAAAATTCTGATTGGTC 1893 TGATTGGTCA 4963 A C -- gtcaat t
AATGTGAATGTATTCACTTA ATGTGAATGT AAATAAA TT tg attg gtgaa g
ACAGTTCCACAAATTTATTT ATTC ||||||| || || |||| |||||
TTTATTT AA AC TGAC CActt t
A C CT AATT-- a

GAM2435 CTACCAATCTTCAAATATCG 1895 TATCGCCCAT 4965 CAAT t c- aac ac
CCCATTTAACAGTACAAAAC TTAACAGTAC CTAC CTTCAAA atcgcc attt agt a

TAGGGGGTATGGCGGTTTTG AAAA |||| ||||||| |||||| |||| |||
AAGCTCGTAG GATG GAAGTTT TGGCGG TGGG TCa /
CTC- - TA GGA aa

GAM2436 AAATAAAATTCTGATTGGTC 1896 TGATTGGTCA 4966 A C -- gtcaat t
AATGTGAATGTATTCACTTA ATGTGAATGT AAATAAA TT tg attg gtgaa g
ACAATTCCACAAATTTATTT ATTC ||||||| || || |||| |||||
TTTATTT AA AC TAAC CActt t
A C CT AATT-- a

GAM2437 GATTATTTTTTGGTATAATT 1906 TATGAATTCT 4976 TTTTTG TAATTCTAC ---------- TC
CTACACGGCATAGTTTCTGT ACCCCCGTTA GATTAT GTA ACGG CATAGTT T
AACTATGAATTCTACCCCCG CATT |||||| ||| |||| |||||||
TTACATTTGTATAATC CTAATA cat tgcc gtatCAA /
TGTtta --------- cccatcttaa TG

GAM2438 GGCGCGCCAATAGGTAGGGA 1897 TACGTTCCCT 4967 C- - A GG- TGGATCT
GTCAATG CGT
TGGATCTACGTATGTCAATG AAAATGCTGT GGCG GC CA TA TAGGGA ACGTAT
GAGGC A
GAGGCCGTATAAAGCTTCAA GCTC |||| || || || |||||| |||||| |||||
TAATACGTTCCCTAAAATGC CCGC cg gt gt atccct tgcatA CTTCG T
TGTGCTCCGCC ct t c aaa ------- ATAA--- AAA

GAM2439 CATGGGATCCGGTTCGTAAT 1907 AAGGTTGTCG 4977 - CCG C - AT-- T
CGCGCTATCGTCTTCGTAAA TTACGAACAT CAT GGGAT GTTCGTAAT GCG CT CG C
GGTTGTCGTTACGAACATAT ATCC ||| ||||| |||||||||| ||| || ||
CCCGATG GTA Cccta caagcattg tgt gg GC T
G ta- c t aaAT T

GAM2440 GGGAATACAGACATCATTGG 1898 GACCTACAGC 4968 ATACA CATC --- G TGG
CAGGTGCAATGGCAGTTTTG CAGTTCATTA GGGA GA ATTGGC AGGT CAA C
GACCTACAGCCAGTTCATTA TCCC |||| || |||||| |||| |||
TCCC ccct ct tgaccg tcca GTT A
atta- ---- aca g TTG

GAM2441 GGCGCTACAGATGTAATTGA 1899 TATGATGGGA 4969 ----- GA- AATT AGAT
CGAAAGATCTGTATTTGTCT TGTGGTGGGT GGC GCTACA TGT GACGAA C
ATGATGGGATGTGGTGGGTT TGCC ||| |||||| ||| ||||||
GCC ccg tggtgt gta CTGTTT /
ttggg agg gtat ATGT

GAM2442 TTTGATAATGATAGACAGAA 1904 TGATAGACAG 4974 a c aatg gc t

TGCAATGCTGTACACAAATT AATGCAATGC TTTGATAAtg taga ag caat tg a
GGGACTTTTTATATTATCAA TGTA |||||||||| |||| || |||| ||
G GAACTATTAT ATTT TC GTTA AC C
- T AGG- A- A

GAM2443 ACAGAAAATCCGCAGGAGAT 1900 CAGGAGATTC 4970 AAAATCCGc - c------- a t
TCCAGCATTGTTCCAAGCTG CAGCATTGTT ACAG agga gatt cagc ttg t
TCTAACAAAATCTTCCTCAT CCAA |||| |||| |||| |||| |||
AATGAACTGT TGTC TCCT CTAA GTCG aac /
AAGTAATAC T AACAATCT - c

GAM2444 AGAAATTGCTTGCGCCAAAG 1905 TTACTGCATC 4975 T- C CAAAG G ATA--- gca gtg ca
AACGTTTGAAATATGTTACT AACGTGCTCA GAAAT GCTTG GC AAC TTTGAA TGttact tcaac ct g
GCATCAACGTGCTCAGAAAG GAAA ||||| ||||| || ||| |||||| ||||||| ||||| ||
AAGTTGAGAGTGACAAACCA TTTTG CGGAC CG TTG AAATTT ACAGTGA AGTTG Ga /
CTTTAAAGGTTAAGCCAGGC TT - AA--- G CACCAA G-- AA- aa
TTGTTTTT

GAM2445 GACGATTCACCTACCTGGCG 1908 TTGCAGCGTT 4978 - - T CT- tt---- -- a - a g
TTGCAGCGTTATTACGGATA ATTACGGATA GAC GATTC ACC AC GGCG gcagc gttatt cgg at cg a
CGGATCGGATACCGAATGGC CGGA ||| ||||| ||| || |||| ||||| |||||| ||| || ||
TAGCTGCCACCTCCGCCCTC CTG CTGAG TGG TG CCGC CGTCG CGGTAA GCC TA GC /
GTCGGTCGAGTCAGTC A C C CTC CTCCAC AT - A G T

GAM2446 CCCTTCCCGAGCGAGTGCGG 1909 TGAGAGGAAA 4979 - GA ---- GCGG CC--------- - AAAC
TTTCTCACATGCCGTGAGCA ACTTTATTGC CCCT TCCC GC GAGT TTTCTCACATG GTG AGC G
AACGAAAACGCTACACATAA AGGG |||| |||| || |||| |||||||||| ||| |||
TAAGACACGTGTGAGAGGAA GGGA Aggg cg ttca ggagagtGTGC CAC TCG A
AACTTTATTGCAGGGACAGG C a- ttat aaa- ACAGAATAATA A CAAA
G

GAM2447 ACGAAAAATGATGAAGGCAA 1910 TAAAAAGTGT 4980 GATGAAG A - AA ATAAAAAG AG TG GTG- - TG G
TCATTCCTCATAAGATGATA AGTGAGTGAG GCA TCATTC CTCAT GATG TA G T TGT G T T
AAAAGTAAGGTGTGTGTGTG AGTA ||| |||||| ||||| |||| || | | ||| | |
TGTGTGTGTGTGATAAAAAG TGT AGTGAG GAGTG TTat gt t g atA T G G
TGTAGTGAGTGAGAGTATTA GAGTG-- G T A- gagagtga ga gt aaaa G GT T
GTGAGTGAGTGAGTGTGTGA
GTGAGTGAGT

GAM2448 GTCGTTCTCGTTCAGAATCT 1913 TCGCAGCATA 4983 T GTTC A tcg - g g
TTCGCAGCATAAGTAGTATG AGTAGTATGT GTCGT CTC AGA TCTT cagc ataagta tat t
TCGATATACTTATCGTTGAA CGAT ||||| ||| ||| |||| |||| ||||||| |||
GACTCTTCCAGAGACGAT TAGCA GAG TCT AGAA GTTG TATTCAT Ata c
- ACCT C --- C - g

GAM2449 CCTACGCGAGGCTGAACCTC 1914 AAGAAGAGAA 4984 G TGAACCT AA CA- TC
G
CTGAATCACTGCATCTTTCT TAGTGGCCAG CCTAC CGAGGC CCTG TCACTG TCTT
TTGAG C
TGAGGCGTTTAAAGAAGAGA GGCC ||||| |||||| |||| |||||| |||| |||||
ATAGTGGCCAGGGCCTCGGT GGGTG GCTccg ggac ggtgat agaa aATTT /
GGG - ------- c- aag ga G

GAM2450 CTTGGTATAGAAACATGATG 1911 TGTGAAAAAT 4981 TG TAGAA GATGTA T- TG T
TATCACTTTGCCTTGGGGGG GTAATTACTG CT GTA ACAT TCAC T CCT G
TGATTGTGAAAAATGTAATT GG || ||| |||| |||| | |||
ACTGGG gg cat tgta agtg A GGG G
gt taa-- aaa--- tT GT G

GAM2451 CTGTACCTGCTCCTACAGTT 1915 CCTACAGTTT 4985 T c a gctgtac - CT T
TCTGCTGTACCAGTACCTGC CTGCTGTACC CTG ACCTGCTc tac gtttct cagt aC GCTGC C
TGCTCCTGTAGCTGTAGCTG AGTA ||| |||||||| ||| |||||| |||| || |||||
CTAAGAGACGTAGAGTAGGT GAT TGGATGAG ATG CAGAGA GTCG TG CGATG C
TAG - - - ATC---- A T- T

GAM2452 TGTGTTCTCCTCCCGCCGCT 1912 CTCGAGCTGA 4982 -------- CCGCC T ACCA
TGTGCAGCACCACCTCCCGC GGATCCGTGA TGTGTTC TCCTC GCTTG GCAGC C
TGCTCGAGCTGAGGATCCGT TGGA ||||||| ||||| ||||| |||||
GATGGACACA ACACagg aggag cgagc cGTCG C
tagtgcct t---- t CCCT

GAM2453 TCCAACAACTGTTTATGTAA 1920 TAAAGGAAAA 4990 AA CTGT TGt aaa--- ca ga
AGGAAAATAAAGACTCAGAG TAAAGACTCA TCC CAA TTA aaaggaaaat gact ga A
AAAATCCAAGTTCATATGAT GAGA ||| ||| ||| |||||||||| |||| ||
TTTTCTTTTATTGATTGGGG AGG GTT AGT TTTCTTTTTA TTGA CT /
GA GG ---- TAT GTATAC AC AA

GAM2454 GGATAAAACGAATCTTTAGT 1916 ATAGAAACAA 4986 AACGAA TA- GAG-- AGAA
ATGAGCTATTATAGAAGTAG TACAACGAGA GGATAA TCTT GTAT CTATTAT G
AATAATAGAAACAATACAAC AATA |||||| |||| |||| |||||||
GAGAAATAGATTGTCT TCTGTT agag cata gataATA /
AGataa caa acaaa AGAT

GAM2455 TATGTTCTTTTTTTATTGGG 1927 TACAATGCAA 4997 T TG- ---- G- - GG
AGGCGCGGGTAGGCGGGTAG AAGCCTTCGA TATGT CTTTTTTTAT GGAGGC GCG GTAG
GC G
CTTTACAATGCAAAAGCCTT CGTG ||||| |||||||||| |||||| ||| |||| ||
CGACGTGGAGGAAGGCGTG GTGCG GAAGGAGgtg cttccg cgt catT CG /
- cag aaaa aa T AT

GAM2456 GGTCCGTTTTGTCACGGGAA 1928 AGAGGAAACA 4998 C -- CAC--- --- a - --- g a
AGGAAAGAGGAAACAGGCCG GGCCGCGGAC GGT CGT TTTGT GGGAA AGGAAag ggaa
acagg cc cgg c
CGGACACCCGGGGGAGTTTG ACCC ||| ||| ||||| ||||| ||||||| |||| ||||| || |||
TGTTCCCTTTTCTTTCTTCC CCA GCG AAACA CCCTT TCTTTTC CCTT TGTTT GG
Gcc a
CACACACACAAAAGGCGTAC T GA CACACA CTT - G GAG G c
C

GAM2457 TTTCTTATTATATATCAATT 1921 AAGGATGTGC 4991 ATTATATATCAATTA AC TTAA
GCT AC CGCA
AATGACTATCTTAACTTTAT ATGAATAAAC TCTT ATG TATC CTTTATAGA TTCAT
TAT A
AGAGCTTTCATACTATCGCA CAAT |||| ||| |||| ||||||||| ||||| |||
ATTATATATCATGAATCATT AGAA tac gtag gaaATATTT AAGTA ATA /
TATAAAGGATGTGCATGAAT ATtaaccaaataag- gt ---- ACT CT TATT
AAACCAATTAAAGAAA

GAM2458 CTCCATATTTTACCATTGAC 1917 TATTTTACCA 4987 CAt gacaaa- c TC
AAACTCACATCTACTGTAAG TTGACAAACT CTC attttaccatt ct aca T
GTCAAAAGATGGTAAAATCA CACA ||| |||||||||| || |||
CGAG GAG TAAAATGGTAG GA TGT /
CAC AAAACTG A CA

GAM2459 GTGGTTTCTACTCAAAAGCT 1929 ACTCAAAAGC 4999 TTCTa a tc ca cctc AA
CGAACAACGCCTCGGGAAAG TCGAACAACG GTGGT ctcaaa gc gaa acg GGG A
ACCCACGTATTTACGCTTTG CCTC ||||| |||||| || ||| ||| |||
AGAAAATACCAC CACCA GAGTTT CG TTT TGC CCC /
TAAAA - CA A- A--- AG

GAM2460 CGATAGAGGGATTTAGAGAC 1922 AGAGGGATTT 4992 T gg tagaga t -- AGA
CTTTCTTCCACGTTAGAACG AGAGACCTTT CGA agag att cctttc tcC ACGTT A
ACGACGTAAGGACGAAAGGG CTTC ||| |||| ||| |||||| ||| |||||
AGGTTTCTTTTTCG GCT TTTC TGG GGAAAG AGG TGCAG C
T TT AG---- C AA CAG

GAM2461 GTATTATACATATATCTGTT 1918 TACATATATC 4988 t- - c attgTC
GATATGATTGTCACTTTACC TGTTGATATG GTATTA ac atatat tgttgatatg A

ATATCAACAATATATAGTTT ATTG |||||| || |||||| ||||||||||
TAATAT TATAAT TG TATATA ACAACTATAC /
TT A - CATTTC

GAM2462 TGAGCAAAGGGTACAAGGCC 1930 CAAGGCCCAA 5000 CA A ag -- at t CT
CAATCCAATCCGTTCGCCTT TCCAATCCGT TGAG AAGGGT ca gccc aatcca ccgt cgc T
GCGCGCGCGGCTGGATTTAG TCGC |||| |||||| || |||| |||||| |||| |||
GGTTGACCCTTACTCA ACTC TTCCCA GT TGGG TTAGGT GGCG GCG /
A- - -- AT C- C CG

GAM2463 GCGCCGCGAGGGTAGGTGGT 1919 TTCCTGATTC 4989 GC G - TG- ATA - TT
CGATAGCCCGTTTGACGGAG TGGTGTAGC GC CGC AGGGT AGG GTCG GC CCG T
TAGCGATATTCCTGATTCTG || ||| ||||| ||| |||| || |||
GTGTAGC cg gtg tctta tcc TAGC TG GGC /
at g g ttA GA- A AG

GAM2464 TTAGTGTTGGAATTATTAGT 1923 TACAACAATG 4993 AATTAT CTTC CA--- TG
ATTCTTCTTGTCATCTTGTT CTATACCTAA TTAGTGTTGG TAGTATT TTGT TCT T
CAGAAATATACAACAATGCT TACT |||||||||| ||||||| |||| |||
ATACCTAATACTAA AAtcataatc atcgtaa aaca AGA /
cat--- c--- tATAA CT

GAM2465 TAGGGTTCTGCTATTCAGAC 1931 TAGTAGGCCG 5001 G - TG TCA --- - AT
GTACGCACATTAAGTGTAGT TCATGTGGTG TAGG TT C CTAT GACG TAC GCAC T
AGGCCGTCATGTGGTGGTAA GTAA |||| || | |||| |||| ||| ||||
GCCTA ATCC aa g ggtg ctgc atg tGTG /
G t gt ta- cgg a AA

GAM2466 GTAGAATGTTTACATTATTA 1924 TGTGATCAAT 4994 ---- AA- T GAATC
ATACTGTGAATCAAACAAAC AAACACTGTG GTAGAATGTTTACA TTATT TAC GT A
TGTGATCAATAAACACTGTG AATA |||||||||||||| ||||| ||| ||
AATATTTTAC CATTTTataagtgt aataa gtg CA /
caca cta t AACAA

GAM2467 AGGTAAAGTGCTATCGCTTT 1263 TAAAGTGCTA 4333 aaa- tatcgc - aAAAAGAA
CGTGTGAAAAAGAACCATAG TCGCTTTCGT AGGt gtgc tttcgt gtg C
ACACCGCTACGAGAACTGCA GTGA |||| |||| |||||| |||
CCACCACCT TCCA CACG AGAGCA CGC C
CCAC TCA--- T CACAGATA

GAM2468 CATGGCCTGTGTAACTAGCC 1932 CATTTCACTA 5002 G T C GTTAC A
TTCTAGTGAAAGTTACCGAA GAACGCTGGT CATGGCCT TG AACTAGC TTCTAGTGAAA CG A
AACGCATTTCACTAGAACGC TCAG |||||||| || ||||||| |||||||||| ||

TGGTTCAGAGGCTATG GTATCGGA ac ttggtcg aagatcacttt GC A
g - c ac--- A

GAM2469 ATATGTTAATTGGAATATAC 1925 CATTCGAAAA 4995 TAATT A ACAC--- ATAG
ACTGCTATAGTTTACGGGCA TAATCCTAAC ATATGT GGA TAT TGCT T
TTCGAAAATAATCCTAACAC ACAT |||||| ||| ||| |||| ATAT TAtaca cct ata acGG T
caat- a aaagctt GCAT

GAM2470 GTAAGCTACCGTACATCTCT 1269 CTCACATAGA 4339 TA ACC ACA TTCACAAA C
TTCACAAACCCAGGGCTCAC GACAAGCACA G AGCT GT TCTCT CC A
ATAGAGACAAGCACAAGCTC AGCT | |||| || ||||| || GC C tcga cg agaga GG /
GC aca aac tacactc- G

GAM2471 GCGCGGCACTCAATCGTTAC 1926 TTACTGGTGG 4996 - CTCAATC t g tgctt- g ---------
A T
TGGTGGCTGCTTCTGGGACG CTGCTTCTGG GCGGCA Gt actg tggc ctg gacg AC
CAAGC C
ACACAAGCTCAGTTTGGTAT GACG |||||| || |||| |||| ||| |||| || |||||
GCAACTACGTCACAGCTCAT CGCCGT CA TGAC ACCG GAC CTGC TG
GTTTG /
CGCCAACAGTTACTGCCGCT T ------- T A CTACTC A ATCAACGTA - A
GC

GAM2472 AGTTGGATGAATAGTATGTC 1270 TTAGTGCACT 4340 GG A - TTAATAA A TT----
ATA
TTAATAATTGTTATTATTTC CTATAAAAAC AGTT ATGA TAGT ATGTC TTGTT TTAT
CACTAATTA T
ACTAATTAATATTTAGTAAT GAGA |||| |||| |||| ||||| ||||| |||| |||||||||
TAGTGCACTCTATAAAAACG TCAA TACT ATCA TACAG agcaa aata gtgattAAT T
AGAATGACATAACTAATCAT -- A A TAag--- a tctcac GAT
AACT

GAM2473 GTACGGCCCATGGGAGGGAA 1264 AGGGGGTGTT 4334 - A GG TT AC T
CATTTCCACGTGTTCCAATA CCTTAATAGG GTACGG CCC TG AGGGAACAT CC GTGT C
CAGGGGGTGTTCCTTAATAG GACT |||||| ||| || ||||||||| || |||| GGACTGTGC CGTGtc ggg at ttccttgtg gg CATA C
a - aa gg a- A

GAM2474 AATGAAGTTTAAAGAATATT 1271 CTTTAATTTT 4341 A ---- --- - AC
AAATTTGACGTACAGGCTTT ATTCTTATTT AATGA GTTTAA AGAATA TTAAA TTTG G
AATTTTATTCTTATTTTAAA TAAA ||||| |||||| |||||| ||||| |||| CCTTATT TTATT Caaatt tcttat aattt GGAC /
C ttat ttt c AT

GAM2475 ACCACCACAACCCCCCCAGA 1265 TATCGCAATA 4335 ------- ------- G
ACCCAAGCCCAATCCTATTG GGATTGGGCT CCCAGAACCCAAGCCCAATCCTATTGCGA
TGACCAC GACGCGC A
CGATGACCACGACGCGCGAA TGGG |||||||||||||||||||||||||||| ||||||| |||||||
GCGCGTCACTTCGTGTGGTC GGGTCTTgggttcgggttaggataacgct ACTGGTG
CTGCGCG /
ACTACGTATCGCAATAGGAT atGCATC TGCTTCA A
TGGGCTTGGGTTCTGGGGGG
GTTGTGGTGGT
GAM2476 GTCACAATGGCCTACGTGAC 1272 TACGTGAGAT 4342 A G A G - GTA A- TAAAAC
TTGGTATACGTGACCTAAAA AATGTAATGA GTCAC AT GCCT CGT AC TTG TACGTG CC A
CAACAAAGTGGCGTACGTGA GGTG ||||| || |||| ||| || ||| |||||| ||
GATAATGTAATGAGGTGGTG TAGTG TG tgga gta tg aat gtgcat GG A
GTGAT G g - a t aga GC TGAAAC

GAM2477 CAGACCCACCCCAGTCAGAC 1273 TGACATGGGT 4343 GA CA -------- A - GG--- GA
GA
CCAGTGGCGAGAGGCGAGCA GGGGATG CA CCCACCC GTC AG CC CAGT CGA
GGC G
GCTGTTGAAAAAATTGAGGA || ||||||| ||| || || |||| ||| |||
CTTGTTACATGACATGGGTG gt gggtggg cag TC GG GTTA GTT TCG /
GGGATG ag ta tACATTGT A A AAAAA G- AC

GAM2478 TGGCCCTCACCTGCCGCCTC 1266 AGAATGCACC 4336 CTCA - G GTTTCC CGGGA
C
CGTTTCCCGGTGCCGGGATT GTAGGAGGGG TGGCC CC TGCC CCTCC CGGTGC TTC
G
CCGAGGAAGAATGCACCGTA CATG ||||| || |||| ||||| |||||| |||
GGAGGGGCATGGCCGGCCA ACCGG Gg acgg ggagg gccacg aAG A
CC-- t - at---- taag- G

GAM2479 AGTTGCATGTGGAAAAATCA 1267 TCGCTTGGTC 4337 TGT AAAATCAAAATAAA CTG
CT
AAATAAAAAGTCTGGAGTCT CTGTAACT AGTTGCA GGA AAGT GAGT C
CACGCTCGCTTGGTCCTGTA ||||||| ||| |||| ||||
ACT tcaatgt cct ttcg ctCG /
--- gg---------- --- CA

GAM2480 GGAAAGGATCTCGTGCGCTA 1268 AAGGATCTCG 4338 Aaa t c- tat tc G
TAAGTCTAACGAAAGTTGAG TGCGCTATAA GG ggatc cgtg gc aag tAAC A
CTTGCAACATGGGTCTATGC GTCT || ||||| |||| || ||| ||||
C CC TCTGG GTAC CG TTC GTTG A
GTA - AA --- GA A

GAM2481 ATCAATGCTGGTGCCACGGT 1274 CTGGTGCCAC 4344 ct ca a ccct
TTCACCCCCTTCTTAAGGGA GGTTTCACCC ATCAATG ggtgc cggtttc cc t
GGCTGCTGCACCCACGTTGG CCTT ||||||| ||||| ||||||| ||
T TGGTTGC CCACG GTCGGAG GG C
AC TC - AATT

GAM2482 CCCTCTACGAAATGTTCAGT 1275 GGTGCATACT 4345 T AA T CGGAA A AA
CGGAAGCTGAGAACCTCCCG GACATTGTGA CCCTC ACGA TGT CAGT GCTG G C
GTGCATACTGACATTGTGAG GGG ||||| |||| ||| |||| |||| |
GG gggag tgtt aca gtca tggC C /
- -- - tacg- C TC

GAM2483 GGTAGGAAGTTGGCCAAAGG 1276 GTTACTGTCT 4346 TA - CCAAA TT ATATA
TTTCCGGATATAAGCCACCC AACTATCCCC GG GGA AGTTGG GGT CCGG A
GGTTACTGTCTAACTATCCC || ||| |||||| ||| ||||
C cc cct tcaatc tca gGCC /
-- a tg--- tt CACCG

GAM2484 AAGTTTAAGTAAGATACTTA 1277 TAAGATACTT 4347 A ta- tattttct - t AC
TTTTCTAGTAGCTAGTACGT ATTTTCTAGT AAGTTT AG agatact agt agc AGT G
TGCTTGCTCATTTTTCTAAT AGCT |||||| || ||||||| ||| ||| |||
AGTGTTTATTCTAAAACTT TTCAAA TC TTTGTGA TTA TCG TCG /
A TTA TAATCTTT C T TT

GAM2485 AACAAATAAACTTATAAACA 1282 TATAAACATA 4352 TAAAC tattttaa tt
TATTTTAAGCTTTACTGGTA TTTTAAGCTT AACAAA Ttataaaca gct a
TTGTTGTTTATAACCTTTTT TACT |||||| ||||||||| |||
GTT TTGTTT AATATTTGT TGG /
TTCC- TGTTA--- tc

GAM2486 ACAGTTTAAAATGTTAAACT 1283 TTTAAAATGT 4353 tt- ta ttt atTT A
TTTGTTATTTTTAATATGAT TAAACTTTTG ACAG taaaatgt aact gtt TTAATATG T
ATATGTTAACAGCTATAGTT TTAT |||| |||||||| |||| ||| ||||||||
GCATTTTATATTTGT TGTT ATTTTACG TTGA CGA AATTGTAT /
TAT -- TAT C--- A

GAM2487 GGCCGTCTCCTCTCGCGATC 1278 GACCTGCACG 4348 C CCTCTCG TCTG--- ACCCTCT
CTTAC CG
TGCGTGACCCTCTTCGACTT ACCCTCTTCG GG CGTCT CGA CGTG TCGA GGA C
ACGGACGCCCTCCTCGACCT ACTT || ||||| ||| |||| |||| |||
GCACGACCCTCTTCGACTTA CC GCAGG gct gcac agCT CCT /
CGGACGCCC C CAttca- tctccca gtcc--- ----- CC

GAM2488 GCACGACCCTCTTCGACTTA 1284 ACTTACGGAC 4354 CCTCTT ct - c ctcg c GACCCT
CGGACGCCCTCCTCGACCTG GCCCTCCTCG GCACGAC CGa tacgga cgcc tc ac tGCAC C
CACGACCCTCTTCTCGAGTG ACCT ||||||| ||| |||||| |||| || || |||||
CACGTAAAGACGGCGATTCG CGTGTTG GCT GTGCTT GCGG AG TG ACGTG T
TGCTCGTGTTGTGC T----- C- A C AAA- C AGCTCT

GAM2489 TATTAACAAGAATCATCCCA 1285 AGCAAATATA 4355 CAA CCCa aaata- a g
GCAAATATATTAGAGAAGCG TTAGAGAAGC TATTAA GAATCAT gc tattag gaagc c
CTCGTTTTATTAATACCAGT GCTC |||||| ||||||| || |||||| |||||
AGTAATAGTGATTCCATTGA ATAGTT CTTAGTG TG ATAATT TTTTG t
TA AC- ATAA ATGACC A c

GAM2490 CTAGATATGAACAACATGTA 1279 TGAACAACAT 4349 A a-- ---- taa a
ATTAGAATGCTAAGATTATG GTAATTAGAA CTAGAT tg aca acatg ttag a
TAATATGTACACAAGTTTGG TGCT |||||| || ||| ||||| ||||
GGTTTG AC TGT TGTAT AAtc t
A ACA ATAA TAG g

GAM2491 ACCACCACCACAACCCCCCG 1286 TTCCGGGGGG 4356 ACGAAGT ACGAAGT T
GAACACAGGCCCAAAATTTT TTGTGGTGGT CCCCCGGAACACAGGCCCAAAATTTTCGCT GACCAC GACGCGC T
CGCTACGAAGTGACCACACG GGT |||||||||||||||||||||||||||| |||||| |||||||
AAGTGACGCGCTTCGCGCGT gggggccttGTGTCCGGGTTTTAAAAGCGA CTGGTG CTGCGCG /
CGTGGTCAGCGAAAATTTTG ------- ------- C
GGCCTGTGTTCCGGGGGGTT
GTGGTGGTGGT
GAM2492 GGATTTTAGAATTTCCAAAT 1280 TCCAAATTCA 4350 T AATT aaa--- --- t
TCACCAGCGATTTATCGGTT CCAGCGATTT GGAT TTAG tcc ttcaccag cga t
TTGGTGAAATCCAAGGATTT ATCG |||| |||| ||| |||||||| |||
ATTAATGTCC CCTG AATT AGG AAGTGGTT Jct t
T ATTT AACCTA TTG a

GAM2493 GGATTTTAGAATTTCCAAAT 1281 TTGGTGAAAT 4351 T AATT AAA--- C TT
TCACCAGCGATTTATCTGTT CCAAGGATTT GGAT TTAG TCC TTCACCAG GAT A
TTGGTGAAATCCAAGGATTT ATTA |||| |||| ||| |||||||| |||
ATTAATGTCC CCTG Aatt agg aagtggtt TTG T
T attt aaccta - TC

GAM2494 GATGCGCTGCAAAGTTTCCT 1287 TCACCCAACA 4357 C- GCA TTCCTATTA TC CGC
ATTAGGGTTCCGCGCTTTAC TACTTGAAGC GATG GCT AAGT GGGT CG T
GTCACCCAACATACTTGAAG ACCA |||| ||| |||| |||| ||

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      CACCATC                          CTac  cga  ttca       ccca  GC  /
                                    ca  ag-   tacaa----   ct  ATT


GAM2495  ACAGGAAACATTAGAGTGAT 1288   TGTTATCGGA 4358       AACA-  AG   TAAA   TA
      TAAAACCATAAGCCTGGTGT       TTAAAAACCT       ACAGGA    TTAG  TGAT   ACCA  A
      TATCGGATTAAAAACCTCTT       CTTG          |||||||    ||||  ||||   ||||
      GT                              Tgttct    aatt  gcta    tGGT  G
                                       ccaaa    ag    ttg-    CC


GAM2496  AGGGCCACGTCGAGTGTACT 1289   TCTGTGACTG 4359        C  GAGT--  Ctc    ct   g--    a
      CTGTGACTGTCTGCTGCGGA       TCTGCTGCGG       AGGGCCA GTC     GTA  tgtga  gtct   ctgcgg c
      CACTGCGGAAAGGACCTTAC       ACAC          |||||||| |||     |||  |||||  ||||   ||||||
      ATTTGCTGTCAAGACTGGCT                  TCTCGGT CAG     CGT   ACATT  CAGG   GGCGTc /
      CT                              -  AACTGT   TT-    C-    AAA     a


GAM2497  ACCACCACCACAACCCCCCCG 1296   TCGCTGACCA 4366                          -------   -------   cg
      GAACACAGGCCCAAAATTTT       CGACGCGCGA       CCCCCGGAACACAGGCCCAAAATTTtcgct
gaccac     gacgcg  a
      CGCTGACCACGACGCGCGAA       AACG          ||||||||||||||||||||||||||||||    ||||||    ||||||
      ACGCGTCACTTCGTGTGGTC                  GGGGGGCCTTGTGTCCGGGTTTTAAAAGCGA     CTGGTG
   CTGCgc  /
      ACTTCGTAGCGAAAATTTTG                                  TGCTTCA     TGCTTCA     aa
      GGCCTGTGTTCCGGGGGGTT
      GTGGTGGTGGT
GAM2498  CTTGTAGAGCTATTCGCCAC 1303   CTTGGAAAGG 4373        AGCT   GCCA  TA   AGAAGA
      ATACCTAGAAGAATAAGACA       ATTTTGCTAT       CTTGTAG    ATTC    CA  CCT     A
      GGGCTTGGAAAGGATTTTGC       AAG           |||||||   ||||   ||  |||
      TATAAG                          gaatatc    tagg    gt  GGG     T
                                     gttt    aaag  tc   ACAGAA


GAM2499  CCTCGAGGACATTGTCCTAG 1297   AACCATTTCC 4367       -  GACA    CT   --   aac   ttc   --------
c
      ATTTGCAACCATTTCCACAA       ACAACCGCAA       CCTC GAG    TTGTC  AGAT  TTGC   cat   caca
accg a
      CCGCAACCGGTCGACCTTAT       CCGG          ||||  |||    |||||  ||||  ||||   |||   ||||       ||||
      GTGTTATGAGCAATTATCTG                  GGAG CTC    GACAG  TCTA  AACG   GTA   GTGT       Tggc a
      ACAGCTCAGAGG                        A  ----    --   TT    A--   TT-    ATTCCAGC    c


GAM2500  ACCACCACCACAACCCCCCCG 1298   TCGCTGACCA 4368                          -------   -------   g
      GAACACAGGCCCAAAATTTT       CGACGCGCGA       CCCCCGGAACACAGGCCCAAAATTTtcgct
gaccac     gacgcgc a
      CGCTGACCACGACGCGCGAA       AGCG          ||||||||||||||||||||||||||||||    ||||||    |||||||
      GCGCGTCACTTCGTGTGGTC                  GGGGGGCCTTGTGTCCGGGTTTTAAAAGCGA     CTGGTG
   CTGCgcg /
      ACTTCGTAGCGAAAATTTTG                                  TGCTTCA     TGCTTCA     a
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GGCCTGTGTTCCGGGGGGTT
GTGGTGGTGGT
GAM2501 CCCCAGCCTCTGCGCGTTTG 1299 GATGGCCCGG 4369 G G G TGT g gg gggtag tg - - CG
TTCGATGGCCCGGGTAGCTT GTAGCTTGTT CCA CCTCT CGC TT TC at ccc ct tttccc ACC CCCTAT G
GTTTCCCACCCCCTATCGGA TCCC ||| ||||| ||| || || || ||| || |||||| ||| |||||| GGTGGGGAGGTGGGGAGGTG GGT GGAGG GTG AG GG TG GGG GG GGAGGG TGG GGGGTG /
GGGAGGTGGGGAGGTGGGGA - G G --- G GA GTGGAG GT G A GA
GGTGGGGAGGTGGGG

GAM2502 CCTTATCCTTAGGGTTTAGT 1290 ATCCTTAGGG 4360 Ta tta----- ta---------- a
TTTGAAGCAGAGCGAGCGCA TTTAGTTTTG CCT tcc gggtt gttttg a
GCGAGCGTAAACAACCCGAA AAGC ||| ||| ||||| ||||||
TAAACGGACTAGG GGA AGG CCCAA CGAGAc /
TC CAAATAAG CAAATGCGAGCGACGCGAG g

GAM2503 TGTTTCTCTTTCTTTCCCCC 1291 TCCGTTGGTT 4361 - T T ATAAA-- T- -- ---- - TTCC
CCTCTCTCCGCAATAAACGC GGGTGGTTGG TTCCCC CCC CTC CCGCA CGCCT CC CGGA ACTGT GT C
CTTCCCGGAACTGTGTTTCC GGTG |||||| ||| ||| ||||| ||||| || |||| ||||| ||
CCCCCTACAACAGTGTTGTC AGGGGG GGG GGG GGCgt gtggg gg gcct TGACA CA C
CGTTGGTTGGGTGGTTGGGG C T - ggggttg tt tt GTTG A TCCC
TGCGGGGGTGGGCGGGGGAA
GCAAGAAAACG
GAM2504 GCTCTAATCTCTATCCTCCT 1300 TGGTGTGTGG 4370 CTAA AT C - TC TTTTT - - CCAC--- ACTTC
TCCCCTTTTTTCACTCCTCC GTGAGTGATG CT TCTCT C TC CT CCC TCA CTC CTC CGGCA C
CACCGGCAACTTCCCCTACT GCAG || ||||| | || || ||| ||| ||| ||| ||||| GCTGTTTTCCCGAGAGAGAT GA AGAga g ag ga ggg ggt GAG GAG GTCGT /
GGTGTGTGGGTGAGTGATGG CCG- cg t t gt tgtgt A A CCCTTTT CATCC
CAGAGAGCCAGC

GAM2505 GGCCCTTCCCTGTTGATTTA 1292 TTTGCGGAAC 4362 CCTTCC A --------- GCA C A
TGGCATCGCACACAACGGTG ACATTTTATT GGC CTGTTG TTTA TG TCGCA ACA C
TTTGCGGAACACATTTTATT TAAA ||| |||||| |||| || ||||| |||
TAAAACGACAGCGCC CCG GACAGC aaat ac ggcgt tGT G
C----- A ttattttac aa- t G

GAM2506 GACATGTGAGCAATAAGGAA 1293 TAAGGAACGT 4363 GCAAtaa t- ct taga
CGTGGGCTGCTAGATACAAC GGGCTGCTAG GACATGTGA ggaacg ggg gc t
GCCCCCTTCGTTCCTCACAT ATAC ||||||||| |||||| ||| ||
GTC CTGTACACT CCTTGC CCC CG a
------- TT C- CAAc

GAM2507 GTACACCGGAATTGCCAGGA 1294 CACCGGAATT 4364 a g tg ac-- c ---- TT
CGACCGGGTCCTTTCTTGGA GCCAGGACGA GTAc cc gaat ccagg ga cggG TCC T
TAAACCCGCTCAATGCCTGG CCGG |||| || |||| ||||| || |||| |||
AGATTTGGGCGTGC CGTG GG TTTA GGTCC CT GCCC AGG C
C G GA GTAA C AAAT TT

GAM2508 AGGATATTGAGTACATATAA 1295 TATTGAGTAC 4365 a--- a cat a ---- A
ATTAATTTTTTAAAACTGAA ATATAAATTA AGGAt ttg gta ataaatt att tTTTA A
AATATAATCAATTTATTACC ATTT ||||| ||| ||| ||||||| ||| |||||
GAGGGCGTCCT TCCTG AGC CAT TATTTAA TAA AAAGT A
CGGG - --- C TATA C

GAM2509 GATACAATTTTAGATGCTAT 1301 TAGATGCTAT 4371 A t at ga- agA- AAGA
TAATGATAATTTAGATTTTA TAATGATAAT GAT CAATTTtaga gct taat taattt TTTTA A
AAGAATTAATAAAAGACGAA TTAG ||| |||||||||| ||| |||| |||||| |||||
ATTAGTAATTAAGTTTTTAA CTA GTTGAAATTT TGA ATTA ATTAAA AAAAT /
AGTTGAATC A T -- ATG GCAG AATT

GAM2510 TACTAATAAAGTATGTTCAA 1302 TAAAGTATGT 4372 A-- --- at a
TGTTAATAAAAGTATTAACT TCAATGTTAA TACTA taaagtatgt tca gttaata a
CTGACAAATGTATTTTAATA TAAA ||||| |||||||||| ||| |||||||
TAGTA ATGAT ATTTTATGTA AGT CAATTAT A
ATA AAC CT G

GAM2511 ACTGTATTTGATTTTTTTAG 1310 AGATTGCAGA 4380 GTA AGGA TTGC G T AAC
CA AATT
GAAATTTTGCGTTGCAATCA TGTGTTGGAG TTTGATTTTTTT AATT GTT CAA CATATC
TGCA CTGA A
TATCAACTGCACACTGAAAT CTGA |||||||||||| |||| ||| ||| |||||| |||| ||||
TAAAGATCAGATTGCAGATG AAACTAAGGAAG TTag cga gtt gtgtag acgt gaCT /
TGTTGGAGCTGATTAGGAAG AA- GA-- t--- g - --- ta AGAA
GAATCAAAAAAGT

GAM2512 AGTGATGAAGATTAAGAAAA 2377 CATTTCTTAT 5447 T- T AA - - TA
ACCAGTCGGTATTTTCCAGA CTTCATCTTC AG GATGAAGAT AAGAAA CCA GTC GG T
CTTGGCATTTCTTATCTTCA T || ||||||||| |||||| ||| ||| ||
TCTTCT tc ctacttcta ttcttt GGT CAG CC T
tt - ac T A TT

GAM2513 GTGTCCGGGCAATCAGCCAT 1304 AGCCATTGCG 4374 -- AATCa a ggtat aa
TGCGGTATCCGGGCAATCTG GTATCCGGGC GTGT CCGGGC gcc ttgc ccgggc t
CCCGGTCTTGGCAAGGCGCC AATC |||| |||||| ||| |||| ||||||
CGGGAGCAC CACG GGCCCG CGG AACG GGCCCG /

AG ----- - GTTCT Tc

GAM2514 GGGCCCATGGTGGCGCGCGG 2378 TGATATGTTT 5448 --- -- CCAC C----- TCCC GT TG
T G
CCCCCACCGTCCCCATTTCC CAGTGACCCT GC GCG GCCC CGTCC CATT ACG T C
CATGGGCACC A
CACGGTTTGCTCATGGGCAC CGGA || ||| |||| ||||| |||| ||| | | ||||||||||
CGACGGTGCCCGTGGTGATA CG TGC CGGG GTagg gtga tgt a G
GTGCCCGTGG /
TGTTTCAGTGACCCTCGGAT TTT AG CCCA ctccca ctt- at gt - C
GACCCGGGCGACGTTTTGCG
CACCATGGTCC
GAM2515 TAATAAATTTCTTTTCACGA 1305 ATAAGTGGAC 4375 AA TC- GA- ------- GA CGT
TGCATCTTATTGAATGACGT ATATAGATGC TAATA TTTCTTT AC TGCATCT TATT ATGA
T
TTTCTCATAAGTGGACATAT AGAA ||||| ||||||| || ||||||| |||| ||||
AGATGCAGAAGTAATGAAGA ATTAT AAAGAAG TG acgtaga gtga taCT /
AAAGTATTA GA TAA aag tatacag a- CTT

GAM2516 ACTATCGTAATATATATTAT 1306 TCACTGAAAG 4376 G TATTAtca -- tt gcc AG-
T
CACTGAAAGACTTTTAGGCC ACTTTTAGGC ACTATC TAATATA ctgaa agact tag aagA
GAGATG A
AAGAAGGAGATGTAACATCT CAAG |||||| ||||||| ||||| ||||| ||| |||| ||||||
TAAGTCTTTTGTTAGTCTCT TGATAG ATTATAT GACTT TCTGA GTT TTCT
TTCTAC /
TTCAGAAGACTTTATATTAA A TTCAGAA- TC TT --- GAA A
GATAGT

GAM2517 GAGAATACTAAAATTCCTAA 1307 AGCTAGTTCT 4377 TT ACGATG Ca- -- tc c ca-
A- TT
CGATGATATGTTTTCAGCTA TCATAACGTC AA CCTA ATATGTTTT gc tagt ttcataa gtc ga
TG C
GTTCTTCATAACGTCCAGAA CAGA || |||| ||||||||| || |||| ||||||| ||| || ||
TGTTCACCAGCTCCATGACT TT GGAT TGTATAGGA CG ATCA AAGTATT CAG CT
AC /
TATGAATACTAATGCCTTAG T- AA---- TTC TA T- - TAC CG CA
GATATGTAATAGGTTTCTAA
TATTTACAAT
GAM2518 CGGGCCAAAGGATGGGGTGG 1308 TGATACGGTG 4378 GG G AAAA AAAGGG AG
CAA - AT
GGTGAGGGTAAAAGCACAAA CCAGCCCTGG GG TGGGGT AGGGT GCAC AGTACC
ACCGAAAA GGA CGG C
GGGAGTACCAGACCGAAAAC CCCC || |||||| ||||| |||| |||||| |||||||| ||| |||
AAGGACGGATCGGCCCGCTC CC Gccccg tcccg cgtg tCGTGG TGGCTTTT CCT
GCC G
CGTTTTTCGGTGGGGTGCTG AA g ac-- gcatag GG TG- C CG
ATACGGTGCCAGCCCTGGCC

CCGAACCCCCG
GAM2519 GTCCTCCACCTCCGCCACCG 1311 CCGCCGAGCC 4381 CC---- -- C CA- TTATC
CGATTTATCATCATCGTCGC GTTCCTCAGG GTCCT AC CTC GC CCGCGAT A
GGGCCGCCGAGCCGTTCCTC GAC ||||| || ||| || |||||||
AGGGAC caggg tg gag cg GGCGCTG /
actcct cc c ccG CTACT

GAM2520 GCCATCACCGTCGCCGATCG 1312 TTCACGTACG 4382 - T C TC - T - C-- C
ACCAGGACCGCCGCGCGGTC TTCTGGCCCG GC CA CA CG GCC GA CG AC AGGACCGC G
TTCACGTACGTTCTGGCCCG CTGC || || || || ||| || || || ||||||||
CTGCTGCGC CG GT gt gc cgg ct gc tg ttCTGGCG /
C c c c- t t a cac C

GAM2521 AACGGCTCTTGCGTATAATG 1309 TAATGCATGT 4379 - GC aa ttcc ta CGATC---
TC
CATGTTTCCGGTTATTTACT TTCCGGTTAT AACGG CTCTT GTAt tgcatgt ggt tttacT CG T
CGATCCGTCTTACGTAGTAC TTAC ||||| ||||| |||| ||||||| ||| |||||| ||
ATGGTAAACACCCATACATG TTGTC GGGAA TATG ATGTACA CCA AAATGG GC /
TAAGTATAAAAGGGACTGTT A AA A- TAC- C- TACATGAT AT

GAM2522 TCCCCCTCTGGACTTGTAAC 1313 TGGTAAGTGA 4383 CCCTCT TGTAACt agt ttg
AG- CT
TGGTAAGTGATAATCCTTGG TAATCCTTGG TCC GGACT ggta gataatcc gaagcT GTA C
AAGCTAGGTACTCGTTACGC AAGC ||| ||||| |||| |||||||| |||||| |||
AAGTTTTGGATTATCTTGTG AGG CTTGA CCGT CTATTAGG TTTTGA CAT /
CCCAACATTAGTTCTCGGA CT---- TTACAAC GTT --- ACG TG

GAM2523 GTCACGAGGGGAACGCAGTA 1314 TCTAAACCTT 4384 GA -- A T-- tctaa tt agtaa aAAG
CC G
CCTTTTCATCTAAACCTTTG TGCACGAGTA AC GCAGT CCTT TCA acct gcacg tt AT
GCTT A
CACGAGTAATTAAAGATCCG ATTA || ||||| |||| ||| |||| ||||| || || ||||
CTTGACGAGCCTATATGGAA TG TGTCA GGAA AGT TGGA CGTGC AA TA
CGAG /
GAGCGTGCCAGGTATTTGAC AA AT - TTC TTA-- C- GAG-- GGTA TC C
TTAAGGACTGTTAGTAACTG
AAGACCTGAC
GAM2524 GAACAATCGCCTTTGTGTAA 1315 TTGACATATC 4385 TCGC AA-- TT------ GA TTA
CAAATTAGC
ATGTTGCGGAGAATGTCATT CGTTGTTTCA ACAA CTTTGTGT ATG GCGGA ATGTCA
GG A
AGGCAAATTAGCAAACATAA CCAT |||| |||||||| ||| ||||| |||||| ||
AACCGGTTGACATATCCGTT TGTT GAAACACA tac tgcct tacagt CC /
GTTTCACCATGTTGACACAA TTTT GTTG cactttgt a- tGG AAAATACAA
AGTTTTTTGTTC

GAM2525 GTGATTTTGGCAATAGTCCG 1316 ACGAGCTGGT 4386 AT ---- TC AATCCAT
TGTAATCCATAATCCAGTAA GCTTGCTAGA GTG TTTGGCAA TAG CGTGT A
CACGAGCTGGTGCTTGCTAG CAC ||| |||||||| ||| |||||
ACAC cac agatcgtt gtc gcaCA A
-- cgtg ga ATGACCT

GAM2526 ATATGTGTTATTTTAGGATC 1317 TAGGATCATA 4387 ATTTtag c c acgGT
ATATTTACATATTTACGGTA TTTACATATT ATATGTGTT gat atattta atattt A
TATCAAAGATGTTAGATATA TACG ||||||||| ||| ||||||| ||||||
GTTAATAGGACACATAT TATACACAG TTG TATAGAT TGTAGA T
GATAA-- A - AACTA

GAM2527 TCTTTAAGAACCAAGTGTGA 2379 AAATATTTCA 5449 AG AA GA AG
GGTAGATAGAGCGGTTAAAT TATCGGTTAT TCTTTA AACC GTGTGAGGTA TAG C
ATTTCATATCGGTTATAAAG AAAG |||||| |||| |||||||||| |||
A Agaaat ttgg tatactttat aTT /
a- c- aa GG

GAM2528 TGGTAGTCTTGATAGCCTTT 2380 TACTAACTGC 5450 A CT CT ACA TTAAC
AACAAGCATTAACGCTGCTT TATTAACAAC TGGT GT TGATAGC TTA AGCA G
TGCTACTAACTGCTATTAAC CA |||| || ||||||| ||| ||||
AACCA acca ca attatcg aat tCGT C
a -- tc ca- TTCGT

GAM2529 TTCCTGGGTAGCTGGAGATA 2382 TAGCATTGAG 5452 - A-- T t at- - a ca
GCATTGAGCGTCTAGGCAGG CGTCTAGGCA TTC CTGGGT GC GGAGA agc tgagcgt ct gg g
TCCAGAATGCTCATTAGCTT GGTC ||| |||||| || ||||| ||| ||||||| || ||
TTCCTGCCTCACTCAGAGAA AAG GACTCA CG CCTTT TCG ACTCGTA GA Cc /
A CTC T - ATT A - tg

GAM2530 GTAGAAGTTGTATTTTTAGA 2381 AGTTGTATTT 5451 ag aga tcga GA
AGTCGAATCTGAGTCAAGAT TTAGAAGTCG GTAGA ttgtattttt ag atcT G
CTATAGAAAATATAAACTTT AATC ||||| |||||||||| || ||||
AT TATTT AATATAAAAG TC TAGA T
CA ATA ---- AC

GAM2531 AGGAGAGCGAGCAGAGAGGG 2383 CCACGCCCCA 5453 GAG G AGAG C GG GT --
T
GCCGGTGCGGGAGTTTGGAA TGCACGTGCC AG AGC AGC AGGGG C TGCGGGA TTGG
AAC C
CTCCGCGGTCATTCATCTCC C || ||| ||| ||||| | ||||||| |||| |||
CGCCACGCCCCATGCACGTG cc gca gta cccgc a GCCCTCT CTTA GGC C
CCC cgt c c--- - cc A- CT G

GAM2532 ACCATTAAAAATATTTTTAT 2384 TTAATAAATG 5454 TAAAAA TT- C T
CTGTTAGATTTAATTTAATA GCTCATGGAA ACCAT TAT TTAT TGTTAGAT T
AATGGCTCATGGAATGTGTG TGTG ||||| ||| |||| ||||||||
GT TGGTg gta ggta ataatKTA /
tgtaag ctc a A

GAM2533 CAGTGAGATATGGTCTAATT 2385 TAGCTGGCTG 5455 - C A TG - C C T- CCG-----
ACTT
GGAGACTATACGCTCCAGTT CATATATCTA AGTGA GATATGGT TA T G AGA TATA GC
CCAGTT CCGA A
CCGCCGAACTTATAATCTTG CTGA ||||| |||||||| || | | ||| |||| || |||||| ||||
GAAATTTTTAGCTGGCTGCA TTATT TTATACTA AT a c tct atat cg ggtcga GGTT T
TATATCTACTGAATAATCAT A - A gt a - a tc tTTTTAAA CTAA
ATTATTATTG

GAM2534 GTGTGTGTGTGTGCGTCCGT 2386 TCCCCGGGGT 5456 TCCG TTC CG GGT - AG
AAA C TT GTCA
TCGTTCGTTCGTCGGGGTGA TTTTTTACCG GTGCG TTCG GTT TCGG GAG GG GAAGAA
CG GGG C C
GGGAGGAAGAAAAACGCGGG CTTT ||||| |||| ||| |||| ||| || |||||| || ||| |
TTCGTCACACAAGGTCCCCG CATGC AAGC CAA AGTT ttc cc tttttt gc ccc G /
GGGTTTTTTTACCGCTTTAT TGTA --- AA At- g at ggg - tG AACA
TGAAAAACCGAAATGTCGTA
CACACATGTC
GAM2535 GCCTTCACGAGCACGGGCGA 2387 CACGAGCACG 5457 T a-- g a ga G- C
GCGAGCATATGGTGTCTATA GGCGAGCGAG GCCT cacg gcac ggcg gc gcataTG TGT T
CGAGCGTGTGTGGGCGTGTC CATA |||| |||| |||| |||| || ||||||| |||
GGTGTGTCCGTGTGGGT TGGG GTGC TGTG CTGT CG TGTGTGC GCA A
T CTG G G GG GA T

GAM2536 CCGACGGGCTGAACGTCCGG 2388 TGAAGAAACG 5458 A- G AA GG --- - G A
GCCTCTCGGTGACATCGGTG GGCGGGCGGG CCG CGG CTG CGTCCG CC TCT CG TG C
AAGAAACGGGCGGGCGGGCG CGGG ||| ||| ||| |||||| || ||| || ||
GGCTGACCGG GGC GTC ggc gcgggc gg aga gt GC A
CA g gg g- caa a G T

GAM2537 TTAGTGTTGGTATTATTAGT 2392 TACAGCAATG 5462 - TTAT - TCT CA TG
ATTCTTCTTGTCATCTTGTT CTATACCTAA TTAGTGTT GGTA TAGTATT CT TGT TCT T
CAGAAATATACAGCAATGCT TACT |||||||| |||| ||||||| || ||| |||
ATACCTAATACTAA AAtcataa ccat atcgtaa ga ATA AGA /
t ---- c cat A- CT

GAM2538 TTTTTTACCCATAAATAATA 2389 TACAATAATT 5459 CATAAATAATAA ttaatttctcgtaaaaG
AA
AATACAATAATTAATTTCTC AATTTCTCGT TTTTTTACC Atacaataa TAGAA T

GTAAAAGTAGAAAATATATT AAAA ||||||||| ||||||||| |||||
CTAATTTATTGTATGGTAAG AAGGAATGG TATGTTATT ATCTT A
GAA ---------- TA---------- AT

GAM2539 GGAGCATGCGGTGCTATATC 2393 TAATACGGAC 5463 T- ---- CT ---------- TT A
AGAGAAC
TTTTCCGTTTATTATACATG TTCATGATTT A GCGGT GCTATAT TT TCCGT ATTATAC
TG A
AGAGAACAATATATACGAGT AATA | ||||| ||||||| || ||||| ||||||| ||
ATAATACGGACTTCATGATT T TGCTA TGATGTA aa aggca taatATG GC /
TAATAATGTAGTAATTATCG TC TTAA at tttagtacttc -- A ATATATA
TCTTGTTCC

GAM2540 CTGTACTACTTTTATCATAA 2390 TTACTGGCAG 5460 ATAA-- CGTTTGA tt a gtggt-
T
TTAATAATCGTTTGAATATT ATAGGGGTGG ATC TTAATAAT ATA actggcag taggg
ataGCGAT C
ACTGGCAGATAGGGGTGGTA TATA ||| |||||||| ||| |||||||| ||||| ||||||||
TAGCGATTCCGTCGTTGTTA TAG AATTATTA TGT TGGCTGTC ATTCC
TGTTGCTG /
GTGACCTTAGCTGTCGGTTC ATTCTG ------- CT G AGTGAT C
TGTATTATTAAGTCTTAGAT
AAAAAGTGCCG
GAM2541 GTGACTGATCTATCGATTAG 2391 TGTCTGGATT 5461 - TC - GTGA T
GTGATGCTGTGATTCTGTCA TAGTTAC GTGACTGA TCTA GAT TAG TGCTGTGAT C
TAGCAGTGACTATGTCTGGA |||||||| |||| ||| ||| |||||||||
TTTAGTTAC cattgatt aggt ctg ATC ACGATACTG /
t -- t AGTG T

GAM2542 GACTCAAGCATATATACACG 2394 AAGCATATAT 5464 Ca - a cg ga AA
GCTCGGGGAGCAAGGTGTGA ACACGGCTCG GACT ag cat tatacacggct gg GC G
CTGTGGTCGTGTGTGGTGTC GGGA |||| || ||| |||||||||| || ||
TCTGGTC CTGG TC GTG GTGTGTGCTGG TC TG /
TC T - TG AG TG

GAM2543 ACAGAAGAAGTTCTATATCT 2403 TCTAAAAAAA 5473 A AA-- A CT-- C Ct aaaaaaaaa
a
AGGCACACTCTAAAAAAAAA AAAAAGCACA ACAG AG GTTCT TAT AGG ACA cta aagc c
AAAGCACACGCTTGCTGGCA CGCT |||| || ||||| ||| ||| ||| ||| |||| ||||
TGTCCCTCGTAATAAAGAAC TGTC TC CAAGA ATA TCC TGT GGT Ttcg a
AAAACTACTGT A AAAA A ATGC C AC CG------- c

GAM2544 TGGGGATGCGTGAGTGGCCC 2404 TCTAACCAAT 5474 AG------- T T CGG GGGAG T
A AA CAT
TCTGTGGGCGGTGGGGGAGA CCCCAGGGGC GCGTG TGGCCC CTG GGG TGG AG
CTTAT GG GTG A

GTCTTATAGGAAGTGCATAT CAAG ||||| |||||| ||| ||| ||| || ||||| || |||
AACCACAACCCATGGGTCTA CGCAC accggg gac ccc acc tc GGGTA CC CAC T
ACCAATCCCCAGGGGCCAAG AGACAAAga - - ta- aa--- t C AA CAA
AAACAGACACGCCCCA

GAM2545 TACATTAAGGCAGTGTTGAT 2397 AGGCAGTGTT 5467 A a agtg t ttca CC
TTTTTTTCATTGTACCCACT GATTTTTTTT TAC TTA ggc ttgattt tt ttGTA C
TACGAATAACGAATCAAAAG CATT ||| ||| ||| ||||||| || |||||
CCATGAAGTA ATG AGT CCG AACTAAG AA AGCAT A
A A AA-- C TA-- TC

GAM2546 TTATCAGCGTCTTATAATGT 2405 TTTTAAAAGT 5475 TC TAATGT GT TTTT TTC
GATGTCTTTTTTTTTATTTT AGTCTGTTAA TTA AGCGTCTTA GAT CTTTT TATT T
CTTGTCGGTATTTTAAAAGT GATG ||| ||||||||| ||| ||||| ||||
AGTCTGTTAAGATGTTTTTA AAT TTgtagaat ctg gaaaa ATGG T
A TT tgt--- at tttt CTG

GAM2547 CGCCCGCGCCCGACTCGCAG 2395 GCGGAGCGCG 5465 C GC ACT A A A G TC
CTCACGAGATGGCTGCTCTC CACGGCAGCG CGCC GC CCG CGC GCTC CG GATG CTGC T
GGCAGCGTCGCGGAGCGCGC GCG |||| || ||| ||| |||| || |||| ||||
ACGGCAGCGGCG gcgg cg ggc gcg cgag gc CTGC GACG /
- ac ac- - - g - GC

GAM2548 GCTCGCGGTGCAGCTGCCGC 2396 GTGCAGCTGC 5466 - ----- - ca ---- g
AGAGCCGCGAAAGCGTCGTG CGCAGAGCCG GCTCGCGgt gca gctgc cg gagc cgc a
CTCCACGCGCAGCTTCTCTG CGAA ||||||||| ||| ||||| || |||| |||
CGATCGCGGGC CGGGCGCTA CGT CGACG GC CTCG GCG a
G CTCTT C AC TGCT A

GAM2549 GTCGTGGTCGTCGTCGTGGC 2398 GGTTGAGGCT 5468 TG TG - ---- G T
CGTGGCCGTGTAGCGGGGCG GCTGCTGCGG GTCG GTCGTCGTCGTGGCCG GCCGT
GTAGCGG GGC CC G
CCTGCTGGGGTTGAGGCTGC CTGC |||| |||||||||||||| ||||| ||||||| ||| ||
TGCTGCGGCTGCGGCCGCGG CGGC CAGCAGCGGCGCCGGc cggcg cgtcgtc ttg GG C
CGACGACTGCGGC GT gt t ggag g T

GAM2550 TACCAATATTGGAATTATAA 2406 ATGCATCGGT 5476 AAT TATA- G ---- C - G
TATAGGTGTATTTGCGCACT AAATATAGCT TACC ATTGGAAT ATATAG TGTATTTGC GCA
TCG C A
CGCGACGGTTGATGCATCGG GTAT |||| |||||||| |||||| ||||||||| ||| ||| |
TAAATATAGCTGTATCTAAT ATGG TGATCTTG tatgtc atataaatg cgt aGT G C
GTTCTAGTCGGTA C-- TAATC g gcta - T G

GAM2551 CTTTTTCAAGATCCTGGTTT 2409 TGATTGATAA 5479 AAGA T Tt ---- aa ata aa- TC

GATTGATAAATGATATGCAA ATGATATGCA CTTTTTC TCC GGT gatt gata tg tgca atC T
AATCTCTGATGATCTCTGCA AAAT ||||||| ||| ||| |||| |||| || |||| |||
ATGCAAATGTCTCACAGTCT GAAAAAG AGG CCA CTGA CTGT AC ACGT TAG G
ACCGGAGAAAAAG ---- - T- CACT AA GTA CTC TA

GAM2552 CTTTGCTCTAATTTCAGGAA 2399 TTCACAGTTG 5469 AATT G CT AAA- TATCGC - AAAAGAA
CTGCTAACCAGGTAAAGTGC CTGACAACGG CT TCAG AACTG AACCAGGT GTGC TTTCG GGTGA C
TATCGCTTTCGGGTGAAAAA TGCT || |||| ||||| |||||||| |||| ||||| |||||
GAACCATAGACATCGCTACG gg agtc ttgac ttGGTCCA CACG AGAGC TCGCT C
AGAACTGCACCACCACCTGG caac g ac CCAC TCA--- A ACAGATA
TTCACAGTTGCTGACAACGG
TGCTGAAAG
GAM2553 TTTTTATTCTTGTTATTTAG 2400 TATACAGTTA 5470 A TGT -- A CA G
CTGAGTCATCGGTACCGAAT AGAGTATCTA TTTTT TTCT TAT TTAGCTG GT TCG T
ATACAGTTAAGAGTATCTAG GAGG ||||| |||| ||| ||||||| || |||
AGGGAGAA AAGAG gaga atg aattgac ta AGC A
g tct ag a tA C

GAM2554 CCTCTGGTACAGTTCTGACA 2401 TGAGGGCTGC 5471 ------- GACAA GA G
AAGAGGACTCTTGCAGAGAG GTGTTCTACT CCTCTGGTA CAGTTCT AGAG CTCTT C
GACTCTGAGGGCTGCGTGTT AGAG ||||||||| ||||||| |||| |||||
CTACTAGAGG Ggagatcat gtcggga tCTC GAGAG /
cttgtgc g---- AG A

GAM2555 TCCCAAGCTTTCGTTACCCT 2407 TGTAAATGTT 5477 G----- T AATGCAA g tagacttgg T
CTAGGGGTAACAAATGCAAT TAGACTTGGA CCCTCTA GGG AACA TGACt taaatgtt agtgtT A
GACTGTAAATGTTTAGACTT GTGT ||||||| ||| |||| ||||| |||||||| ||||||
GGAGTGTTTAAAACACTGAC GGGAGAT CTC TTGT ACTGG ATTTACAG TCACAA /
ATTTAGGTCAACGATGTTCT GAAAGA - AGCA--- - --------- A
CAGAAAGTAGAGGGTGGCCA
AACCGGA
GAM2556 TGTAGATACCATATAATGAA 2408 TGTTAAGATA 5478 ---- GAA----- T - G G- TTT TTAA A
TGTTTTATTAGGATAGTAGT GTAGTTCTGT ATAAT TGTTTTA TAGGAT A TA TTAATAG AG GAC G
TAATAGTTTAGTTAAGACAG TAAG ||||| ||||||| |||||| | || ||||||| || |||
TAGTTCTTTCTGTTAAGATA TATTG ATAgaat gtcttg t at aattgtC TC TTG T
GTAGTTCTGTTAAGATAGTA ATAG ATTTGATG t a g ag TT- ---- A
GTTTAGTTATGATAGTGGTT
TAGTTAAGACA
GAM2557 ATCTGCTCTGTTTTGTACAA 2402 TATGACACAC 5472 T A AAAAGT G T GATT A TG T AGT

AAAGTGGAAGTGTGTGTTTA AGTTCTGGAA TT GT CA GGAA TGTGTGTT ATAT CACAAA C
TAGTT AAC A
TATGATTCACAAAACTGTAG ACTG || || || |||| |||||||| |||| |||||| | ||||| |||
TTTAACAGTAAAAGTTAATT AA CA gt tctt acacacag tatG GTGTTT G GTTAA TTG /
GTGGTTTGTGGTATGACACA C - caaagg g - ---- - GT - AAA
CAGTTCTGGAAACTGACCAA
ACAGTGTTCTT
GAM2558 CATTTAGTACAACTTGGTCA 2410 TTCGTCCTAC 5480 TAGTACAA GG A GG GC - T-
AC- - A C
TGGGTGGCAGGAGATGGCAC AATCAGAGAA CATT CTT TC TG TG AGGA GA GGC
TGAGCGT CT GG A
TGAGCGTCTAGGCAGGCCCA GGGA |||| ||| || || || |||| || ||| ||||||| || ||
GAATGCTCATTAGCTTTTCG GTAG gga ag ac ac tcct ct TCG ACTCGTA GA CC G
TCCTACAATCAGAGAAGGGA TTTTag-- ag - ta a- g tT ATT A C G
TTTTGATG

GAM2559 GTAATTGAGTTTCCAAACTT 2411 TGTGGAAAAG 5481 GAG A TACA ATA
ACATTTGATACAGTACGAAA AAGTTGC GTAATT TTTCCA ACT TTTG C
ATGGTGTGGAAAAGAAGTTG |||||| |||||| ||| ||||
C cgttga aaaggt tGG AAGC A
aga g TAA- ATG

GAM2560 CAACAAACGTTGTGGAAATT 2412 TGTGGAAATT 5482 A t tt ttgt- CC---- C
CAAAATTGTTGTCCTAGGCC CAAAATTGTT CAAC AACGT gtggaaa caaaattg ccTAGG TGC
A
TGCCACGGCAATAAATCCTA GTCC |||| ||||| ||||||| |||||||| |||||| |||
GGCGTCTCAGTTTTGGTTTT GTTG TTGCA CGCTTTT GTTTTGAC GGATCC ACG C
TCGCTACGTTAGTTG A T TG TCTGC TAAATA G

GAM2561 CTATCTACCAGATTATTATG 2413 TAAGGTACTT 5483 TACC-- AT At--- gg tttt--
ataaa
TGTTATAAGGTACTTTTTCT TTTCTCATAA CTATC AGATT TATGTGTT aa tact ctcata
C
CATAATAAACTAGAGTATGA TAAA ||||| ||||| |||||||| || |||| ||||||
GTATGATAGTGTTTTTTCAA GGTAG TCTAA ATATACAA TT GTGA GAGTAT /
AACATATAAATCTAAAATTG TTAAAA -- AACTT TT TAGTAT GAGAT
ATGG

GAM2562 AATCTGATAACTTTAAACAT 2414 TAACTTTAAA 5484 At-- atgg t t
GGATTTTTGATGACATAGTG CATGGATTTT AATCTG aactttaaac at tt g
GTTTAAAGTTTAAACAGATT TGAT |||||| |||||||||| || ||
TTAGAC TTGAAATTTG TA AG a
AAAT GTGA C t

GAM2563 TCTCCAGACCCGGGTTTCAC 1203 GAAAGTGTGT 4273 -- GA G TT - GC GC C CTG
TT AAAG
CTTGCCCTCGCTCTCTCCGT GGTTGGGGGG CA CCC GGT CAC CTT CCTC TCTCTC
GTCTAT TAC AAG T

CTATCTGTACTTAAGAAAGT TGAC || ||| ||| ||| ||| |||| |||||| |||||| ||| |||
GATCCTTTTGTGTGTGGGCC gt ggg ttg gtg gaa gGGG AGAGAG CGGGTG GTG TTC
/
GAGAGAAGGGGAAAGTGTGT ca gg g gt t a- A- C T-- TT CTAG
GGTTGGGGGGTGACAGAGA

GAM2564 GGTTGACCTGTATTGTTATG 2415 TGAAGATGAT 5485 ACC-- A- TG GAACA C
AACAATTTGACACCTCAGAT GAAGACGATG GGTTG TGT T TTAT ATTTGA A
GAAGATGATGAAGACGATGA ACCA ||||| ||| | |||| ||||||
CCAACC CCAac gca a agta tAGACT C
cagta ga gt gaag- C

GAM2565 GTAAATTTAATAACTTTTGT 2416 ACTTTTGTAT 5486 A actt ---- - g----- TG TATT
AGA
ATCTATGGTGAATGTATGAA CTATGGTGAA TA TA ttgtatctat ggtg aat ta AATAT AATTT
T
TATTATTAATTTAGATAAAA TGTA || || |||||||||| |||| ||| || ||||| |||||
AATTTTGTATTTGTAATAAA AT AT AGCGTGGATA CCAC TTG AT TTATG TTAAA
/
GGTTACACCGGTAATAGGTG G AC-- ATGG A GAAATA GT TT-- AAA
CGACATAGTAAGTATAC

GAM2566 TTGCATACGTTCATCATTGG 1209 TTTTGCTGGC 4279 ACGTTCAT- T TC T TGTTT A
ATCCCATGTTGTTTCCAGAG TCCATTGTAT TTGCAT CA TGGA CCA GT CC G
GGTTTTGCTGGCTCCATTGT ATTA |||||| || |||| ||| || ||
ATATTAAGATGCAA AACGTA gt acct ggt cg GG A
GAattatat t c- - tttt- G

GAM2567 ACATCTCAATAAAAAAATGT 1204 AATGTAATAT 4274 - CAAT tataat ta---- T
AATATAATATTTATATCATT AATATTTATA ACAT CT AAAAAaatgtaa attta tcat T
TTGTGACATTATTGAATTAT TCAT |||| || |||||||||||| ||||| ||||
CATTTATATTTTTTTTAGCA TGTA GA TTTTTTTATATT TAAGT AGTG /
TGT C T--- TACTAT TATTAC T

GAM2568 CCGTCCCCCGCCCCGCCGCC 1205 TACCGAGGAG 4275 - - CCCC - CC - TCGCC C -
CT -- T
CTCCCCGTCGCCGCCTCCCC GCCGGGGACG C CC CCG GC CG CT CCCCG GC TCCCCG
CC CTC TACCTG C
GCCCTCTCTACCTGTCCGCG CCCC | || ||| || || || ||||| || |||||| || ||| ||||||
GGTACCGAGGAGGCCGGGGA G GG GGC CG GC GA GGGGC cg aggggc gg gag
atGGGC C
CGCCCCCGGGGAAGACCGAG A A AGC- A CA A ccc-- c c ag cc G
CCGACGGAGGAGACGG

GAM2569 CGTTTCACGTTTTTAATAGA 1215 CACCGCGTTC 4285 TC--- TTT- GA CAT
TGACCTCCATGCGCTGAGGA ATCAACG CGTT ACGT TAATAGAT CCTC G
TCTGTTACACCGCGTTCATC |||| |||| |||||||| ||||

AACG gcaa tgcg ATTGTCTA GGAG C
ctact ccac -- TCG

GAM2570 GCCACAGGGTGTCGCTCACG 1206 TCACGTAGTC 4276 A-- - T c t t ca a A T
TAGTCGCCGCGCGCCAGCAG GCCGCGCGCC GCC CAGG GTG CGCt acg ag cgccgcgcgc gc GC GCG T
CAGCGTTCCGCGGCGCGCGC AGCA ||| |||| ||| |||| ||| || |||||||||| || || |||
GTGGCGCCTCGTCGGCGCGC CGG GTCC CGC GCGG TGC TC GCGGTGCGCG CG CG CGC /
GCCTGCACGGC CAC G - C - C -- - G C

GAM2571 GATACATGGCAATGGACAAG 1207 CATGGCAATG 4277 Acat a a - a---------- ag
CATCAGAGTACCTGCGGAAA GACAAGCATC GAT ggca tgg caagc atc g T
TACTGCAAAGATGGCTTGCT AGAG ||| |||| ||| ||||| ||| |
ATGCTTAGGTC CTG TCGT ATC GTTCG TAG C /
GAT- - - G AAACGTCATAAAGGCGT CA

GAM2572 CAGGAGCGCGCCACCCTTTC 1208 TTCATGATTG 4278 - CGC -- TT C-- GTA
GTCGAACGTACAACGGTTCT GGCATGGTTC CAG GAG GCCA CCC TCGT GAAC C
TCATGATTGGGCATGGTTCA ACTC ||| ||| |||| ||| |||| ||||
CTCACTG GTC ctc tggt ggg agta CTTG A
A act ac tt ctt GCA

GAM2573 GAGGCACTGGCTCGGTTGGG 1216 CATTCGGCAT 4286 T CTCG- A ---- CGG
TAGCCAGCCTTTCGGGTAAT CTACCCGTGC GAGGCAC GG GTTGGGT GCCA GCCTTT G
AAAGGCTTGTTGGCATTCGG CTC ||||||| || ||||||| |||| ||||||
CATCTACCCGTGCCTC ctccgtg cc cggctta cGGT CGGAAA T
c atcta - TGTT TAA

GAM2574 ATGAAGTTAATGATACACAC 1223 TTAATGATAC 4293 t ata c ac gAATT
TACACTGTCGAATTTGATAG ACACTACACT ATGAAGt aatg ca actac tgtc T
GGACAAAGTAGTTGACACGT GTCG ||||||| |||| || ||||| ||||
TTATTTCAT TACTTTA TTGC GT TGATG ACAG G
T ACA - AA GGATA

GAM2575 TCGAACTAAACGAAATATTT 1210 GGACAAGCGT 4280 AAAC- ------- T A
GTCTTTCTATGAAATCATAG TGATTATTTC TCGAACT GAAATA TTTGTCTT CTATG A
AGGACAAGCGTTGATTATTT CATT ||||||| |||||| |||||||| |||||
CCATTCAGTTTGG GGTTTGA ctttat gaacaggA GATAC A
Cttac tagttgc - T

GAM2576 GGGTTAACGCCTGATGGTGC 1224 TACCTTATAG 4294 A CTGAT - TAAT A T
TAATGCACTGCCGCTTCGGC CGTAATCC GGGTTA CGC GGT GC GC CTGCCGC T

GGCGGGTCGCTACCTTATAG ||||||| ||| ||| || || |||||||
CGTAATCC cctaat gcg cca CG TG GGCGGCG C
- atatt t C--- - G

GAM2577 GCCGAATATTTTGTTTCGAA 1211 TATTTTGTTT 4281 Atattttgttt -- aaACGCCTACACCAA
A
CGGAGCAGAAACGCCTACAC CGAACGGAGC GCCGA cgaac ggagcag GAG C
CAAGAGACCACTCCTGTTCC AGAA ||||| ||||| ||||||| |||
CCGTTCGTCGGC CGGCT GCTTG CCTTGTC CTC C
---------- CC ---------- A

GAM2578 ATAGAGGGGTGTTTTTTAAA 1212 TACTATACGC 4282 G TT- A T - ATG
GTTACTGTATGCGTCACATG GAATACCCTC ATAGAGGG TGTTT TA AGT AC TGT C
TACTATACGCGAATACCCTC TAT |||||||| ||||| || ||| || |||
TAT tatctccc ataag at tca tG ACA /
- cgc a - T CTG

GAM2579 TTGGGAGGCAAAAAGAAAGA 1213 AGGCAAAAAG 4283 a aaaagaaagaaaacaccca A CGA
AAACACCCAGACGTAGGCCC AAAGAAAACA TTGGG ggca GACGT GGCC G
GAGGACCGGCCGGCGTCCTC CCCA ||||| |||| ||||| ||||
TGTCCCCGA AGCCC CTGT CTGCG CCGG G
- CTC---------- G CCA

GAM2580 TAGGTGTAGAATGGTCATAT 1214 TGTAGAATGG 4284 - agaa catat c ATG
GGCCAGTTTGATGATTTATA TCATATGGCC TAG Gtgt tggt ggc agttTG A
AACTGCTTTTTTACTAACAC AGTT ||| |||| |||| ||| ||||||
ACTA ATC CACA ATCA TCG TCAAAT T
A ---- TTTTT - ATT

GAM2581 TGTTGTACATGTGCAGAAAA 1217 CATGTGCAGA 4287 - -------- t - TATTTATCC CG
TGT
ATGTGTAAATACGTGTTATT AAAATGTGTA tgtgcagaa aaa gtgtaaata CGTGT CATG TCT
A
TATCCCATGCGTCTTGTACA AATA ||||||||| ||| ||||||||| ||||| |||| |||
TAGATATATGTTTTTATATA ATACGTTTT TTT CATATTTAT GCATA GTAT AGA /
CGCTATTTATACTTTATATA A CCTATATA - C TATTTTT-- AT TAC
TCCTTTTGCATAACCATAGA
CA
GAM2582 TCTTGTTTGTTCCCTGGAGT 1218 TCCCTGGAGT 4288 TT c -------- t- ga- ggT
ATGAGACTAGGGGGTGTTAA ATGAGACTAG TCTTG TGTt cc tggag atga ctaggg G
TCTTGGGAATTATTTTTCTA GGGG ||||| |||| || ||||| |||| ||||||
ACCTTGTTGGTAGCATTCAA AGAAC ACGA GG ATCTT TATT GGTTCT T
GA TT T TTGTTCCA TT AAG AAT

GAM2583 GGGGGTGCTAACACATTAAA 1225 TATAAAGCAT 4295 GG CACA- A GCAACA- A
ATGTTTTCGCAACAGGGCAA TTAGCACATC GG GTGCTAA TTA AATGTTTTC GGGC A
AGCTTAGATATAGAGGACAT T || ||||||| ||| ||||||||| ||||
TATAAAGCATTTAGCACATC tc cacgatt aat tTACAGGAG TTCG /
T ta tacga a ATATAGA A

GAM2584 AAGAGAGTTGTTTTTAAAAA 1219 CACTGGGTCA 4289 AAAACTATG- T ----- GAG
CTATGAAATTACCACCAGGA TTTAGATGAA AAGAGAGTTGTTTTTA AAAT ACC ACCAG
T
GTTGATTGGTCACTGGGTCA TTGT |||||||||||||||| |||| ||| |||||
TTTAGATGAATTGTGAAAAC TTTTTTCGACAAAAGt ttta tgg TGGTT /
AGCTTTTTT gttaagtaga c gtcac AGT

GAM2585 TTCGTGGACTCGACCGTACA 1226 TCGACCGTAC 4296 T Ctc c a --- ac-- ---- A
ATGC
CCTCGAGACGGTGGACGCAC ACCTCGAGAC TTCG GGA ga cgt cacc tcgag ggtgG ACGC
CTC G
TCATGCGTTACGAGGGCGTA GGTG |||| ||| || ||| |||| ||||| ||||| |||| |||
CAACCACCCCCGTTCGACCC AAGC CCT TT GCA GTGG AGCTT CCACC TGCG
GAG /
GGTGAACGATTCTTCCCGAA - TC- A A CCC GCCC AACA G CATT

GAM2586 TAAACATCCCTATAGTGAAA 1227 TCCCTATAGT 4297 At-- ta gaaa attag A
CTGATTAGTACAAGAGTAAA GAAACTGATT TAAAC cccta gt ctg taC A
CAGGAGCCCTGGGGTCTGGT AGTA ||||| ||||| || ||| |||
TTA ATTTG GGGGT CG GAC ATG G
GTCT CC AG-- AA--- A

GAM2587 TTTACAGTTCCATTCTCTCG 1220 AAGCGGTTCT 4290 AG CATTCT ACGCA T- C-
AAAAA ACAC
AACGCAATTATGAAATAAAC TTATTTCTTT TTTAC TTC CTCGA ATTA GAAATAAA AC
TAA T
ACAAAAATAAACACTATTCT AATA ||||| ||| ||||| |||| |||||||| || |||
TAAAGCGGTTCTTTATTTCT AAGTG AAG GAGCT taat ctttattt tg ATT /
TTAATAATCGAGCATGAAAG GA TAC--- Aa--- tt ct gcgaa CTTA
GTGAA

GAM2588 AGTACCGCGGCTTCTATAAT 1228 CCGCGGCTTC 4298 c- gc- taatcag-- C
CAGAGATGCTCGTATCTATC TATAATCAGA AGTA cgcg ttcta agatg T
TTCGTTTAGAACGACGCGAT GATG |||| |||| ||||| |||||
TACT TCAT GCGC AAGAT TCTAT C
TA AGC TTGCTTCTA G

GAM2589 CTGTATTAAGTTAGTTTCTG 1221 TAAGTAATTA 4291 T TT ta aat attt T G A- A
AATAAGTAATTAATAGATAG ATAGATAGAT TAG TCTGAA agtaatt agatag taGTT AT TAAAA
TGTTAAC T

ATTTTAGTTTATGTAAAAAT TTTA ||| |||||| ||||||| |||||| ||||| || ||||| |||||||
GTTAACATTTGTTAATAAGT ATT AGATTT TCATTGA TTTATC ATTAA TA ATTTT
ATAATTG T
TTTAGATAATTACTATTTTA - TT TA GAT ---- - G GA T
GAGTTACTATTTTAGATTTT
ACCATTTTAG
GAM2590 AATGTAAGTGTCCTTTTATA 1222 TAGAATATAT 4292 ATTGC - ---------- ----- AAAATCTT--
A
AGATTGCTCAGAGTGACTGA CAAACTGTTA AAG TC AGAGT GAC TGACA
TTCTATA C
CAAAAATCTTTTCTATAACT AAAA ||| || ||||| ||| ||||| |||||||
TATAGAATATATCAAACTGT TTC AG TCTCA CTG attgt aagatAT /
TAAAAATGTCTCCCTATTGT ATTA- T ATGTTATCCCT Taaaa caaactatat T
AACTCTTGAATTACTTATGG
CTATTATATT
GAM2591 GACTTATCCATCTGAATGAT 1229 TGAATGATGC 4299 TTAT TCt t tttat aC-- GG
GCGCGTTTATTGCACACGCG GCGTTTATTG GAC CCA gaa gatgcgcg tgcac GC C
GCGAAGCTCAAGTGCATGTG CACA ||| ||| ||| |||||||| ||||| ||
CATTTTCTTTTGGTTTGTT TTG GGT CTT TTACGTGT ACGTG CG G
TTT- TTT - ----- AACT AA

GAM2592 TACTCAAGTCCAGGCAAGTT 1230 TCCAGGCAAG 4300 CAA caa t---------- t
GAATTCCCTTGAGGGACACT TTGAATTCCC TACT Gtccagg gttgaa tccc t
CCCGTGGTTTGCGGTTTCAG TTGA |||| ||||||| |||||| ||||
CCCTGGGCAGTGGTA ATGG CGGGTCC CGACTT AGGG g
TGA --- TGGCGTTTGGTGCCCTCAC a

GAM2593 TGAATCTAATTGTTTAAAGT 1231 TGACAAACAC 4301 --- T AAAG- -- ATA
GTTTTAGATATAGGCTAAAT AGACATTTAT TGAATC TAA TGTTT TGTT TTAG T
GACAAACACAGACATTTATT TTGA |||||| ||| ||||| |||| ||||
TGATTTA ATTTag att acaga acag AATC /
ttt t cacaa tA GGA

GAM2594 CCTTGGCTGCTACACAGCAC 1232 CAGCACAATG 4302 GGCT- ACA c- taaa- g
AATGCTAAACAGGCTATTGA CTAAACAGGC CCTT GCT cag acaatgc cag c
AATTGTATTGTTTTTGGAGA TATT |||| ||| ||| ||||||| |||
GTTTACAGAGG GGAG TGA GTT TGTTATG Gtt t
ACATT GAG TT TTAAA a

GAM2595 AGTATTTTCAAAAAAAAAAA 1233 GGGCACCCTG 4303 AAAAAAA CCC
CCTACAAAACT TA-- G TT
AAAAAATAAACAGGGCACCC CGCACCCTGC AAAAAAAATAAACAGGGCA TGC GC
TGCC TA T
TGCCCTACAAAACTGCTATG CCTG |||||||||||||||||| ||| || |||| ||
CCGTATTTATTAGGGCACCC TTTTTTTTATTTgtcccgt acg cg acgg AT /
TGCGCACCCTGCCCTGTTTA ------- ccc ---------- tccc g TA

TTTTTTTTCTAAAATATT

GAM2596 GTACTTGGTCACTAGAGAAG 1239 GAGGTTAGTT 4309 TC A T TGTA T CAAC
TAGTGTATGTCTTCTCCAAC TCTCTTCCCT GTACTTGG ACTAG GAAG AG TG CTTCTC C
CTTAAGAGAGGTTAGTTTCT GGTT |||||||| ||||| |||| || || ||||||
CTTCCCTGGTTTAAGTAC CATGAATt tggtc cttc tc at ggagAG /
-- c - tttg t AATT

GAM2597 ATTAAGTAGAGAATAGTGTA 1240 TAAGTAGAGA 4310 t tagt---- --- --- T ACT
AGCCTGTAGTTACTGACAAG ATAGTGTAAG ATtaag agagaa gtaa gc ctg AGTT G
ACTTCAGACAGCCCTTTACT CCTG |||||| |||||| |||| || ||| ||||
CATAATTTTTTCTCTTAAT TAATTC TCTTTT CATT CG GAC TCAG A
- TTAATACT TCC ACA T AAC

GAM2598 GTTTCTAATAATATAACCCT 1247 AAAAAGCTCT 4317 A A C- A A- AA- GTGT
TAGAAGAATTAAAAGTAAGG TCAAAGTCGT GTTTCTA TAATAT AC CTT GAAGA TT AAGTAAG
G
TGTGAGAAATTTACTTAAAA CATA ||||||| |||||| || ||| ||||| || |||||||
AGCTCTTCAAAGTCGTCATA TAAAGAT GTTata tg gaa cttct aa TTCATTT A
TTGTAGAAAT - c ct a cg aaa AAAG

GAM2599 AGCAGCTGGCTTCACGCAAT 1234 TGCGTAGTAG 4304 - TC- TTTTTAGGTCA AA
TTTTAGGTCAAGGAAATTTC CATAGCTGTT AGCAGCTG GCT ACGCAA AGGA T
TCCTTTGCGTAGTAGCATAG |||||||| ||| |||||| ||||
CTGTT ttgtcgat cga tgcgtT TCCT T
a tga ---------- CT

GAM2600 ACGAGCGGGGCCTGTTTATG 1255 TATGGGCCGG 4325 G CT t --------- tcc at t T
GGCCGGGCGTCCCGATGAGT GCGTCCCGAT ACGAGCGGG C GTT atgggc cgggcg cg
gag AC G
ACTGTTGTTTCCGCCGCCCG GAGT ||||||||| | ||| |||||| |||||| || ||| ||
AACCCCCCCCGCCCATCAACC TGCTTGTCC G CAA TACCCG GCCCGC GC CTT TG
T
GCCTGTTCGT - C- C CCCCCCCAA C-- -- - T

GAM2601 GGATTGATTGTTCATAAATA 1256 AAGCCGGTTA 4326 GAT- - ATATTTTTAT- -- GACC
T
TTTTTATACTCTGACCAAGA TTTACGTTGT GGATT TGTTC ATAA ACT CT AAGAAA T
AATTATTTTTTTATTAAGCC TATG ||||| ||||| |||| ||| || ||||||
GGTTATTTACGTTGTTATGG CCTGG GCAAG tatt tgg ga TTTTTT A
AACGCGAAGGTCC AAGC g gttgcatttat cc aTTA T

GAM2602 ACTGTTTTTACCAGCGCTTC 1235 TAGGTTGTTT 4305 A- - - ------ - T
AAACTGTAGTTTTGACAAAT GGGGGAGAGC ACTGTTTTT CCAG CG CT TCAAA C G

AGGTTGTTTGGGGGAGAGCG GGT ||||||||| |||| || || ||||| |
GT tggcgagag ggtt gt gg AGTTT G T
gg t t atAAAC T A

GAM2603 TATCTTGGCTGCTGGATCTA 1241 TGCTGGATCT 4311 CT C aaa-- t aacAC T
AATATTTTAGAACACTGTTT AAATATTTTA TAT TGG tgctggatct tatt tag TG T
ACAACACCTATGATAATAAG GAAC ||| ||| |||||||||| |||| ||| ||
AGATCTAGTAACTAGAGTA ATG ATC ATGATCTAGA ATAG ATC AC T
AG A GAATA T CACA- A

GAM2604 GTGGCTCTTTGCGTAAAATC 1236 TAGCAGAAGT 4306 - G TAAAAT-- C-- T
TTCTCACATGATTGTAGCAG GAAAATTTGG GTGGC TCTTT CG CTTCT ACA G
AAGTGAAAATTTGGGAAGAG GAAG ||||| ||||| || ||||| |||
GCCAC CACCG Agaag gt gaaga tGT A
G g ttaaaagt cga T

GAM2605 GCTCCACCAATACTCGCCGC 1237 CAGTACTCTT 4307 AC--- ACT- ca- t ttt c acac
CAT
AGTACTCTTTTTCCTCACAC TTTCCTCACA GCTCC CAAT CGCCG gtac ct tc tc agc A
AGCCATATCTAGCTACCAGA CAGC ||||| |||| ||||| |||| || || || |||
CGATCCAGGTGCGTTCGGTG CGGGG GTTG GTGGC CGTG GA AG AG TCG T
CTTCGTTGTCCACGGGGC CACCT CTTC TTG - CCT C ACCA ATC

GAM2606 TGCCACACGTCGGTGATAAC 1248 CCACACGTCG 4318 cc a a a a CACTA
ATCCACTCACTACCCCACGG GTGATAACAT TG ac cgtcggtg taac tcc cT C
AGGAAGTTACATTGACGGTA CCAC || || |||||||| |||| ||| ||
CCA AC TG GCAGTTAC ATTG AGG GG /
CA - - A A CACCC

GAM2607 CTTTATGTCCGCTCGCCCTC 1238 AGAATGGTTC 4308 T CGCT C---- GA--- G
CCAGAGCGAAAGTGAGAATG CTGGGGCGTT CTT ATGTC CGCCCT CCA GC A
GTTCCTGGGGCGTTTTGGCG TTGG ||| ||||| |||||| ||| ||
TTGAG GAG TGCgg gcgggg ggt TG A
T tttt tcctt aagaG A

GAM2608 GTGGTTTCTTGTGCGACGCT 1257 CACCGGGGTG 4327 T T T AC
TCCTGTGTAACTGCATACAC TCGCCAGGAA GTGGTTTCTTG GCGACGCT CC GTGTA T
CGGGGTGTCGCCAGGAAACC ACCG |||||||||| |||||||| || |||||
GC Cgccaaaggac cgctgtgg gg cacAT G
- - c AC

GAM2609 GAAATTTTGTCCTTCCTTCC 2694 CTGCTGGAAG 5764 TG C TC C G
GGCCGCATGTTCATGCTGCT CTGGCGTGGA GAAATTT T CT CTTCCGGC GCAT T

GGAAGCTGGCGTGGAATTTC ATTT ||||||| | || |||||||| ||||
Ctttaag g gg gaaggtcg cGTA T
gt c tc t C

GAM2610 ATGATGCTGGTTATTACACA 1249 TATATGGGAG 4319 TG G TACAC ATA- T
TGTGTTTTAATATATATATATA TAAAGCATAT A AT CTGGTTAT ATGTGTTTTA TATATATATATA
A
TATATATATATATATATATG AACG | || |||||||| |||||||||| ||||||||||
GGAGTAAAGCATATAACGTA T TA GACCAATg tatacgaaat gtatatATATAT T
ACCAGAATTGT GT A caa-- gagg A

GAM2611 ATATAAATATACATTCATTT 1242 TATACATTCA 4312 ta c tg- -- T
ATTGTAAATAATTATATATA TTTATTGTAA ATATAAA tacatt atttat taaata aTTATA A
TATAATTTTGTTTGTTTGTA ATAA ||||||| |||||| |||||| |||||| ||||||
AATAATGTGCTTTTATAT TATATTT GTGTAA TAAATG GTTTGT TAATAT T
TC - TTT TT A

GAM2612 GAGATGCAGTCCTTGCATCG 1243 AGTCCTTGCA 4313 A a- c- at - CGC
GCGCGCCCGAGCCGCCCCCC TCGGCGCGCC GAG TGC gtc ttgc cggcgcg cccgagC C
GCTCGGGCCGCGCCGCGCAA CGAG ||| ||| ||| |||| ||||||| |||||||
ATGACGCGCGCTT TTC GCG CAG AACG GCCGCGC GGGCTCG C
- CG TA C- C CCC

GAM2613 CGGGTAGAAGAGGGATATTC 1244 AGAGGGATAT 4314 a tatt ca cAA
AGAGATCAGGGCAAGTCTCC TCAGAGATCA CGGGTAGA gaggga cagagat ggg G
CGAGTCTCTGCTCTCTCCTC GGGC |||||||| |||||| ||||||| |||
TACCTG GTCCATCT CTCTCT GTCTCTG CCC /
C C--- AG TCT

GAM2614 GTAAAAAGCGTTCAATAGTT 1258 AAGCGTTCAA 4328 AAAa tag - T C
GCCACGCTTTGACCGGTCAG TAGTTGCCAC GT agcgttcaa ttgc cacgctt GA C
GCGTGCGCAGTCTTGAATGC GCTT || ||||||||| |||| ||||||| ||
TCTGGAC CA TCGTAAGTT GACG GTGCGGA CT G
GGTC CT- C - G

GAM2615 ACGCGCGCCAGAGTTGGATC 1245 TCAAGGAAAT 4315 C ------- C- C G T- AACA
ACATCTCGTTGTTCTAACAC GTAAGTCTGC ACGCG GCCAGAGTTG GAT ACAT TC TTG
TCT C
GCTAAGGACTCAAGGAAATG CAAT ||||| |||||||||| ||| |||| || ||| |||
TAAGTCTGCCAATCGATTTT TGTGC CGGTTTTAGC ctg tgta ag aac AGG G
GGCTCGTGT T taaccgt aa a g tC AATC

GAM2616 GCAAAATACCAACCGCGCCC 1250 TGAGCCAAAT 4320 AA AACC--- GCC A A

GACACATAAAGGTGAGTTGT GAGGTGAGTT GCAA TACC GC CGAC CAT A
GAGCCAAATGAGGTGAGTTG GT |||| |||| || |||| |||
T tgtt gtgg cg GTTG GTG A
ga agtaaac agt A G

GAM2617 CTGAGGTTCAACCAGTTGAC 1246 AACCAGTTGA 4316 aa ag ga- -- gaagA AG
CTGTTTTGTGAAGAGGAGTT CCTGTTTTGT CTGAGGTTC cc tt cctgtt ttgt GG T
ACCGAACGAGCAGCAGGAGA GAAG ||||||||| || || |||||| |||| ||
GAGAGGAGGAGCCTCAG GACTCCGAG GG AG GGACGA AGCA CC /
GA AG AGA CG AG--- AT

GAM2618 GGGCTCTGGCCAACGGTGGA 1251 AACGGTGGAC 4321 TC CCa acctc tttttc TC
CCTCGTCTTTTTCCGTTCCC CTCGTCTTTT GGGC TGG acggtgg gtc cgT C
CCACGTTCCCGACACCACCA TCCG |||| ||| ||||||| ||| |||
CCGTCCCCACCGTCC CCTG ACC TGCCACC CAG GCA C
CC CC- ACCA- CCCTT- CC

GAM2619 CGCTCGACGGCGCGGCGGTG 1252 TCAAATAGTC 4322 T A-- ---------- - C G
ACCCCGTCCGCGGGTCGCGC GAGCCTCCGT CGC CG CGGCGCGGCGG TGAC
CCCGT CGCG G
GCGGGAGTCAAATAGTCGAG CGCG ||| || |||||||||| |||| ||||| ||||
CCTCCGTCGCGCCGCACCGG GCG GC GCCgcgctgcc actG GGGCG GCGC /
CG - CAC tccgagctgataa A C T

GAM2620 CGCACCGGCGAGTCGGGACG 1259 AGGCGGCCGA 4329 AC - GA GC GT CCT
CGCCCGTCCGGCCTCTCGTC CTCCGTCGAG CGC CGGCG AGTCGG CGC CC CCGG C
CGGGAGGAGGCGGCCGACTC GCG ||| ||||| |||||| ||| || ||||
CGTCGAGGCG gcg gctgc tcagcc gcg GG GGCC T
ga c g- ga AG TGC

GAM2621 TGGGGCACTTGCAGATTTGT 1253 ACGCGGGGGC 4323 A GC GTAA--- A- A- GGGG
AAGGCCACGCACGGCGGGGA TGCTCTAAAA TGGGGC CTT AGATTT GGCC CGC CGGC
A
GACAGGCCGACGCGGGGGCT ATTT |||||| ||| |||||| |||| ||| ||||
GCTCTAAAAATTTAAGGGCC ATCCCG GGA tttaaa tcgg gcg GCCG G
CTA - A- aatctcg gg ca GACA

GAM2622 GCTGCTCTAAAAATTTAAGG 1254 TTAAGGGCCC 4324 CTAAAAA ac---------- c
GCCCTACGGTCCACAGACCC TACGGTCCAC GCTGCT Tttaagggccct ggtc a
GCCTTCCCGGGGGGGCCCTT AGAC |||||| |||||||||||| ||||
GGAGCGACCGGCAGC CGACGG AGGTTCCCGGGG Ccag c
CCAGCG- GGGCCCTTCCGC a

GAM2623 GGAAGCGGAACCGATCGACC 1260 AAGCGGAACC 4330 g accg c ca----- C
GCCACCTGCTCCCAGGGACC GATCGACCGC GGaagc ga atcga cgc ccTG T
CTTGCGCTCGATGTCGTCGG CACC |||||| || ||||| ||| ||||
CTTCC CCTTCG CT TAGCT GCG GGAC C
G GCTG C TTCCCAG C

GAM2624 CAACTAAACGAAATTTTTGC 2699 ACGAAATTTT 5769 - c ----- -- T
TATGGCCGGCATCTTTGATG TGCTATGGCC CAACT AAa gaaatttt tgctatgg ccggcaTC T
CTGGAGTCGTAGTGTAATTG GGCA ||||| ||| |||||||| |||||||| ||||||||
AAATTTCATTTGGGTTG GTTGG TTT CTTTAAAG GTGATGCT GGTCGTAG /
G A TTAAT GA T

GAM2625 AGTTCAAGTGGTATATGTTG 1261 TTCAAGTGGT 4331 tc-- t ---------- ga G
AGAAAGGTGATAGCCTTATC ATATGTTGAG AGt aag ggtatatg ttga aagGT A
AAACAAACAGGATCATATGC AAAG ||| ||| |||||||| |||| |||||
CTCTTCATTACT TCA TTC CCGTATAC AACT TTCCG T
TTAC T TAGGACAAACA A- A

GAM2626 GTCGTGCGATTCAGAACACA 1262 GAACACACTT 4332 AT gaa---- - - ca t
CTTTTCTCAACCTTCTGGTA TTCTCAACCT GTCGTGCG TCA ca ca cttttct acc t
GAGAGGCTGCTGAAAATAAT TCTG |||||||| ||| || || ||||||| |||
GACGCGTACGAT TAGCATGC AGT GT GT GGAGAGA TGg c
GC AATAAAA C C -- t

GAM2627 GTCGTGAACGTTGCTGCTTA 2709 GAACGTTGCT 5779 - - ctgcttatacc T
TACCGTGGGTAATCTCACTA GCTTATACCG GTCGT ga acgttg gtggg A
CATCATCCAATGTATCGACG TGGG ||||| || |||||| |||||
AC CAGCA CT TGTAAC CACTC A
G A CTACTACAT-- T

GAM2628 GGAGCACGTGAACAGACCCA 2695 AGTGGCGTTT 5765 C ACAGACCCa g- t c- aca
GTGGCGTTTGCCGTGACAAG GCCGTGACAA GGAG ACGTGA gtggc tttgccg ga aag C
ACACTGTCCTTCCTCCGGCG GACA |||| |||||| ||||| ||||||| || |||
AAAAGCCGCTCGCGTCTTC CTTC TGCGCT CGCCG AAGCGGC CT TTC T
- --------- AA - CC CTG

GAM2630 GATATTTACTTTTTATATGC 2696 CACAGGTATT 5766 C TTAT ------- A
TTGCATTACAGAATGATATT ATTAAAATGA GATATTTA TTT ATGCTTG CATT C
CACAGGTATTATTAAAATGA GTAT |||||||| ||| ||||||| ||||
GTATC Ctatgagt aaa tatggac GTAA A
a ttat acTTATA G

GAM2631 TATAATCAATGATACGTGTA 2701 TCAATGATAC 5771 caa - a t TCC

TTAGAATACTTTCCGAATAA GTGTATTAGA TATAAt tgatacg tgt ttagaa acTT G
GTCTTCTAAATATTGTATTA ATAC |||||| ||||||| ||| |||||| ||||
ATTATG GTATTA ATTATGT ATA AATCTT TGAA /
--- T - C TAA

GAM2632 ATTTAAGTATTAATTGTCCT 2704 TTAATTGTCC 5774 tcctaat- tgc CTT---------- A
AA
AATCGTGAATGCATATCTCT TAATCGTGAA ttaattg cgtgaa aTATCT AAAA AATATATA
T
TAAAAAAATATATAAATCAT TGCA ||||||| |||||| |||||| |||| ||||||||
ATATATTATTTTCATAATCA AATTAAC GTATTT TATGGA TTTT TTATATAT /
TTTTCAGGTATAATTTTATG TTTTTAAT TAA CTTTTACTAATAC A AC
TAATTTTTCAATTAAACTAA
AT
GAM2633 GCCAGGCCTCCTGAAAATGT 2697 TGTGCTTATA 5767 CA - GAAA TCTTT C G
TCTTTGCCCGGGATGGTTAT TAGGAAGGCC GC GGCCT CCT ATGT GC CGGGAT G
TCTGTGCTTATATAGGAAGG GC || ||||| ||| |||| || ||||||
CCGC cg ccgga gga tata cg gtCTTA T
-- a ---- tt--- t T

GAM2634 AGAGAGGGGTTGCAACAACA 2698 TATGACACTC 5768 G--- CAACAACAG C CC
GGTCATCATTCCAAGGATAT ACACAACCTG AGAGA GGGTTG GTCAT ATT A
GACACTCACACAACCTGGAA GAAT ||||| |||||| ||||| |||
TCTCT TCTCt tccaac cagta tAG /
aagg acactca-- - GA

GAM2635 GAAGAATAGCGTGTGGAGCG 2702 TAGCGTGTGG 5772 - ggagcga -- TT
ATCCTTGGTGTTAATTCACC AGCGATCCTT GAAGA Atagcgtgt tcctt ggtg A
TTGAGGAGCACGTTATATCT GGTG ||||| ||||||||| ||||| ||||
TT TTTCT TATTGCACG AGGAG CCAC A
A ------- TT TT

GAM2636 CGTGCTGCTGCAAAAGCGAA 2703 AAACGCAAAA 5773 GC AAA AA AGA G T- GAAG-
A--- GG
GGGTAGAGACGCTCTTGTGA GACTTGGGGG TGCT TGC AGCG GGGT GAC CTCT GT
GCGTT GATAG C
AGGCGTTAGATAGGGCAATT GTCG |||| ||| |||| |||| ||| |||| || ||||| |||||
ATTGAAAAACGCAAAAGACT GCGA ACG TTGC CTCG ctg gggg ca cgcaa TTATT /
TGGGGGGTCGGCTCAACGTT A- C-- AA g-- g tt gaaaa aAAG AA
CGCAAAGCGCG

GAM2637 TCAGAATGGATGTCTTGCTG 2705 TAGCAGACTA 5775 AATGGAT TG--- AGATA
CTATAATAGATAGAGAAGGT TAGATTAATT TCAG GTCT CTGCTATAAT G
TATAGCAGACTATAGATTAA AGTT |||| |||| ||||||||||
TTAGTTGA AGtt taga gacgatATTG /
gattaat tatca GAAGA

GAM2638 CATGATATAGAAAAGAAATA 2706 ACTCCAAGAT 5776 a---------- ta
TTATTTCGTGATACGGATAC ACAGTTACTA AGAAATATTATTTCGTGATACGGATactccaagatac
gttac t
TCCAAGATACAGTTACTATT TTAG ||||||||||||||||||||||||||||||||||| |||||
AGTAACGATCTGTCAGATCT TCTTTATAATAAAGCACTATGCCTATGAGGTTCTATG
CAATg /
GTATCTTGGAGTATCCGTAT TCTAGACTGTCTAG at
CACGAAATAATATTTCTTTT
CTATATCATG
GAM2639 AAGGGTGGTGTTGGTTGGCG 2707 CTTCCGTTGA 5777 G TG -- G T
AGGGGGGGCTTCGGCCTTCC CCCAACTGAT AAG GTGGTGT GTTGG CGA GGGGGGC T
GTTGACCCAACTGATATCAC ATCA ||| ||||||| ||||| ||| |||||||
ACTT TTC Cactata caacc gtt ccttcCG C
A gt ca g G

GAM2640 ATATAATAATATTTATTGAT 2708 TATATTATAA 5778 T GA T - - taaa A
GATTGATATTATTAGAATAT TAAATGGATA TATTTAT GAT TTGATA TATTA GAAtat
attataataaatgga atTAT T
ATTATAATAAATGGATAAAA AAAT ||||||| ||| |||||| ||||| |||||| |||||||||||||| |||||
TTATATGGATAATAATTTTA GTAGATA TTA AATTAT ATAGT TTTATA TAATATTATTTATTT
TAATA G
TTTATTATAATAATATTTAT - AA T A A TAA- G
GATATTATTAAAAATTATAG
ATGTGTTATGT
GAM2641 ACGACGAGACCCCTATTAAA 2714 TATCAGGTGT 5784 G AG CC T---- GA TAA CAT
TAAAATGACTGTAAACGCAT TTTATTTTTT AC ACG AC CTAT AAATAAAAT CTG ACG A
ATAAACGTATCAGGTGTTTT CTAT || ||| || |||| ||||||||| ||| |||
ATTTTTTCTATAGTAGTGCG TG TGC TG GAta tttattttg gac tGC T
TGGT G G- AT tcttt tg ta- AAA

GAM2642 TCTAGACGATATAGTGGAAC 2710 AGTGGAACAA 5780 AC ATa g ata ga
AAAATATAGCGGATGAAAAA AATATAGCGG TCTAG GAT gtg aacaaaat gcggat A
TTTGTAGATTTTGTTATACA ATGA ||||| ||| ||| |||||||| ||||||
CGGTCTACTAGA AGATC CTG CAT TTGTTTTA TGTTTA /
AT GCA A GA- AA

GAM2643 CCTGTGAGGTCAACCTTCGT 2717 TGATACTGGC 5787 A AA---- TTC T- C
ATTTTTGTCAACGCAACTGA ATTAGGACCC CCTGTG GGTC CC GTATT TTGT A
TACTGGCATTAGGACCCTAC TACA |||||| |||| || ||||| ||||
AGG GGacat ccag gg catag AACG A
c gattac t-- tC C

GAM2644 GTCCGGCTGGTGGTGGAGTG 2711 TGGTGGTGGA 5781 t--- g -------- a g
TACAGGACCTGACATTCACG GTGTACAGGA GTCCGGC ggt gtg gagtgt cag a

ACCTACACGACCTACTGCTG CCTG ||||||| ||| ||| |||||| |||
GGC CGGGTCG CCA CAC CTTACA Jtc /
TCAT G ATCCAGCA - c

GAM2645 CCTTTCCGCGAATCTTGCGA 2712 CTAGGGCTAT 5782 - GC GA - GC- TT ATG
GATGCCTGCTGGTTTCTATG TGAGTAGGGT CCTTT CC GAATCTTGC GAT GCCT TGGT CT
G
GTGAAGGGGCCGCTAGGGCT TTGG ||||| || ||||||||| ||| |||| |||| ||
ATTGAGTAGGGTTTGGTAGA GGAGA gg tttgggatg tta cggg GCCG GA /
GG T -- ag t atc GG AGT

GAM2646 CTCCGTATCGAGCGAATTGC 2713 TTGGAGCTGG 5783 TA--- A - -- A CT C - C
CTT
TCCGGATCCCTGAGACGCCA TAGGCGAGTT CTCCG TCG GCGAATT GCT CCGG TCC
GAGA GC CATT TC C
TTCTCCTTCGGTGAAAATGA CGCC ||||| ||| ||||||| ||| |||| ||| |||| || |||| ||
GCCTCTTTTGGAGCTGGTAG GGGGC GGC cgcttga cgg ggtc agg TTCT CG GTAA AG /
GCGAGTTCGCCCGGATTTTC TTTTA c g at g tt C A A TGG
GGGG

GAM2647 GACGCGAATAAATATTTGAC 1824 TAAAATACCT 4894 C AA G ---------- AC AT
GTGCTCCGACGTAAATTTTA ATTCCCGTT GACG GAATA TATTT ACGTG CTCCG GTAA
T
TTATTCTGGAGAAGTAATGC |||| ||||| ||||| ||||| ||||| ||||
ATATGTAAAATACCTATTCC ttgc cttat ataaa tGTAT GAGGT TATT T
CGTT c cc a ACGTAATGAA CT AT

GAM2648 ATATTATCTTTATCTAACCG 1832 TTAACATAAA 4902 CT TAACCGAACAG---- - TT
AACAGATGTTGCTTTCTTAG TAGAAAAAAA ATATTAT TTATC ATGTTG CT C
TTAACATAAATAGAAAAAAA ACGA ||||||| ||||| |||||| ||
ACGATAACTATAATAT TATAATA AATag tacaat GA /
TC caaaaaaaagataaa t TT

GAM2649 CGCACACGGGCAGGCAGAAG 1825 TCGCAAGCAG 4895 ACA A C A - AGT GC
GCGCAGTCGATCTCGCACTG CCCTTTCCCA CGC CGGGC GG AGA GGC GC CGATCTC A
GGGTCGCAAGCAGCCCTTTC GCCC ||| ||||| || ||| ||| || |||||||
CCAGCCCGCGGCG GCG Gcccg cc ttt ccg cg gctGGGG /
GC- a c c a aac TC

GAM2650 GCAGATGTTATCGCAGTTGC 2715 TACAACAGCC 5785 - --- C A CG ----- CCATT
GCACCTGCCATTGCACGACA GTAGATTCAT GCAG ATG TTAT GC GTTG C ACCTG G
GGTCTCCAGTACAACAGCCG ACTG |||| ||| |||| || |||| | |||||
TAGATTCATACTGC Cgtc tac gatg cg caac G TGGAC /
a tta c a at ACCTC AGCAC

GAM2651 TTGTTTGGCTTTGTTCCAAC 2716 CACGTGGTGC 5786 TG TTT T AC TTTT AGTT TTT
TGTTTTTGGCCCGAGTTGGG GTCAGGTGA T TTTGGC GT CCA TGT GGCCCG GGG C
TTTCGTTTTCCCGGGTTTCA | |||||| || ||| ||| |||||| |||
CGTGGTGCGTCAGGTGA a ggactg cg ggt gca TTGGGC CCT G
gt --- t -- cT-- ---- TTT

GAM2652 GTAAATTATGATATGGCACA 1840 TATGGCACAT 4910 TT - aca c aga c
TGCGTTAGATGCTGCCAGAA GCGTTAGATG GTAAA ATG Atatggc tg gtt tg t
ACACACGGCTATATACATTT CTGC ||||| ||| ||||||| || ||| ||
TAT TATTT TAC TATATCG AC CAA AC g
-- A GC- A AG- c

GAM2653 CGGTGAAGACTGAGACGGTG 1833 GTGAAGACTG 4903 t - a--- -- aagactG - AAGAC - T GAAG
AAGACTGAGACGGTGAAGAC AGACGGTGAA gaaga ctg gacgg tg AG ACGGTG TG AGA GGT C
TGAGATGGTGAAGCCCCAGC GACT ||||| ||| ||||| || || |||||| || ||| |||
CTTCTGCAACCGCCGTACTA CTTCT GGC CTGCC AC TC TGCCGC AC TCT CCG /
ATGAAGCAGCCCGTCGCAAC - C AACG CG GAAGTAA A CA--- G T ACCC
GGCTCTTCCCG

GAM2654 CACCAAAGTCAACCGCGGGT 2718 TGAGACGGTG 5788 AA--- A-- CG-- AAA
TTTAAAAAATACATTAAGAC AAGACTGAGA CACC AGTC ACCG GGTTTTAA A
TGAGACGGTGAAGACTGAGA CGGT |||| |||| |||| ||||||||
CGGTG Gtgg tcag tggc tCAGAATT T
cagag aag agag ACA

GAM2655 GGACATTGTGTTACACCTGA 2719 TGAGGTGGAC 5789 ACATTG A GA -- CCCT AG C AA
GTCCTGACCCTGTAGGTCTA GAACAAGCC GG TGTT CACCT GTC CTGA GT GTCTA ATTGC T
CATTGCAATGAGCAATTAGA || |||| ||||| ||| |||| || ||||| |||||
CAGCTCAGAAGATGAGGTGG cc gcag gtgga tAG GACT CG CAGAT TAACG /
ACGAACAAGCC gaacaa - g- AA ---- A- - AG

GAM2656 CTCTGACTAAGCAAATATGA 2720 AGCAAATATG 5790 Aa----- tga- ------- cgata
GCCGCGCCCGATACATAAAG AGCCGCGCCC CTCTGACT gcaaata gcc gcgcc C
GTGCCAAATGAGGTGAGTTG GATA |||||||| ||||||| ||| |||||
TTTGCCAGAAGAGGTCAGAG GAGACTGG CGTTTGT TGG CGTGG /
AGAAGAC TGAG AGTAAAC AAATA

GAM2657 TATCAAATACTGTACGGAAT 1826 AACTCTGTTG 4896 AATAC AAT A TCTCTT
GGATTCATTCTCTTCTCTTT TATATCTACT TATCA TGTACGG GG TTCAT C

TTATGAAACTCTGTTGTATA GATA ||||| ||||||| || |||||
TCTACTGATA atagt atatgtt tc aAGTA T
catct gtc a TTTTTC

GAM2658 CAGATTGTTTAACTTTTACA 2721 TTTACTGTGA 5791 TT TA TTA TT A A
CAGTATTCAAGGAATGTCTG CTAAGTGTAA CAGA GTT ACTT CACAGTA CA GG A
TTTACTGTGACTAAGTGTAA CTCT |||| ||| |||| ||||||| || ||
CTCTG Gtct caa tgaa gtgtcat GT CT T
-- tg tca tt - G

GAM2659 ACGTTACATAATTCCTCTTT 2722 TATATGACAT 5792 ACA TCCTCTTTA cat
ATATATGACATAGGAGGGGC AGGAGGGGCC ACGTT TAAT tatatgacataggaggggc a
CATAATAGCCCCTCCTATGT ATAA ||||| |||| ||||||||||||||||||
CATATAGCATTAAAAACGT TGCAA ATTA ATATACTGTATCCTCCCCG /
AA- CG------- ATa

GAM2660 CTTCAATAGTTTTTGTATCA 2723 TCAATAGTTT 5793 tc t atcaaa - T TT
AATAGCGAAAATATTTTTTT TTGTATCAAA CT aatagttt tgt tag cGAAAA ATTTTTT C
TCTCAAAAAGTTTTTTGACT TAGC || |||||||| ||| ||| |||||| |||||||
GGTTAGCGTAAACTATTTTA GA TTATCAAA GCG GTC GTTTTT TGAAAAA /
G TT T ATTG-- A - CT

GAM2661 TTTAGAGAAGTTTAAAGATC 1846 AAAGATCCGC 4916 GA Taa ctac -- caacAA
CGCTACGACGAGCCAACAAT TACGACGAGC TTTAGA AGTT agatccg gacg agc T
GGAAGAGCTAACGTCTGGAT CAAC |||||| |||| ||||||| |||| |||
CTAGTGATTGTTTAAA AAATTT TTAG TCTAGGT CTGC TCG /
G- TGA ---- AA AGAAGG

GAM2662 TAGGAGTATCTATTTTAACA 1827 TATTTTAACA 4897 Ct tt-- agc tt c AT
AAGCATCGATTTGCTAATAT AAGCATCGAT TAGGAGTAT at taacaa atcga tg TAAT A
ACAATTATCATTTTGATTAA TTGC ||||||||| || |||||| ||||| || ||||
TTGTTATTTTATTCATATTC ATTCTTATA TA ATTGTT TAGTT AC ATTA /
TTA CT TTTT AAT TT T AC

GAM2663 GTAAAATATTTCCGGTAGGC 1834 TCTCTAAGTT 4904 CGG C TC TTTAATT-
TAGT ATA
GTGTATGTAGTGTTCTGTTA GATAAAC TAGG GTGTATGTAGTGT TGTTAT TGATATAT
ACAGCT T
TTTTAATTTGATATATTAGT |||| |||||||||||| |||||| |||||||| ||||||
ACAGCTATATAACAGTTGTG atct tATATACATCACA ACAATA ATTGTATG TGTTGA
/
TATGTTACACGCCATATAAC ga- c -- TACCGCAC ---- CAA
AACACTACATATATCTCTAA
GTTGATAAAC

GAM2664 TGCACAGTGCTGATCAATTG 1828 TGTTGACAGT 4898 C C----- ATC- G TAACt g ttaac t
ACTGGTATTAACTGTTGACA TTTAACTGTT TGCA AGTG TG AATTGACT GTAT gtt acagtt tgt c
GTTTTAACTGTTCATACAAA CATA |||| |||| || |||||||| |||| ||| |||||| |||
TTGTGACTATATATACAAGT ACGT TCAC AC TTGATTGA CATA CAG TGTTAA ACa a
TAGTTTCCCCAAAAAATCAC C TAAAAA CCCT A TATAT - ----- t
TCTGCA

GAM2665 GGGGAGGGGGGTGGCGGCTG 1829 TCCAACCGAT 4899 AGGG G GC GGAAAG AA A CCGAAA AGAGAAAA
GGGAAAGGGAAGGAACGCCC AAATCAAGCG GGGG GG TGGCG TGG GG GG ACGC CC G
GAAACCAGAGAAAAGGACCA CCGA |||| || ||||| ||| || || |||| ||
AAAGGGAAACGCGTCCAACC CCCC CC gccgc act cc cc tGCG GG /
GATAAATCAAGCGCCGACCA AAGA a ga aaatag aa - CAAAG- AAAACCAG
GAACCCC

GAM2666 ACCAGCACAGCAAGCATATA 1830 TTGTAGGTGT 4900 -------- G A G TG TAA
GGGTGGTAACAAGTTGTTGT TGCTGTACAG ACCAGC ACAGCAA CAT TA GG G C
AGGTGTTGCTGTACAGTAAG TAAG |||||| ||||||| ||| || || |
GCTGGT TGGTCG tgtcgtt gtg at tt T /
gaatgaca - g g GT GAA

GAM2667 GGACGGACAAGATTCACAAC 1831 TTGCTGTGGA 4901 GACAAGAT A TTTAA A-- CC
CTTTAAAACAACATTACCAA TGTGACAGCA GGACG TCACA CC AACA CATTA A
ATAGTGACCTGTTGCTGTGG ACGT ||||| ||||| || |||| |||||
ATGTGACAGCAACGTTC CTtgc agtgt gg ttGT GTGAT /
aacgac-- a tgtcg CCA AA

GAM2668 TAGGTATAATATAATTAATT 1835 TTAGTACTAC 4905 T ------ AT T- -- CA C
ATATGGTTTATTATCACAAT CCAATAATCA TAGGTATAATATAA TA ATTAT GGT TATTA TCACAATT AC A
TCAACCATGGTGATTGTGAA AATG |||||||||||||| || ||||| ||| ||||| |||||||| ||
TTAGTACTACCCAATAATCA ATCTATGTTATGTT GT taata cca atgat AGTGTTAG TG T
AATGTGCTTGTATTGTATCT C gtaaac ac tc tA -- G
A

GAM2669 TCAGCTTCAGATGAGCTCTA 1841 TGGAGAGACG 4911 CTT A- - ATTGA A
TTGAAGAGTCAAGAGGCTCT CTCAAACTGC TCAG CAG TGAGC TCT AGAGTC A
GGAGAGACGCTCAAACTGCC CTTG |||| ||| ||||| ||| ||||||
TTGA Agtt gtc actcg aga tCTCGG G
cc- aa c gagg- A

GAM2670 AAGCTAATTTTACGTGAGTT 1847 TTTTACGTGA 4917 ttt aa- tttaaa
AAAAGTTTAAAAAGATTTCT GTTAAAAGTT AAGCTAAt acgtgagtt aag A

TGGAAATTCACGTTATTAGT TAAA |||||||| ||||||||| |||
TT TTTGATTA TGCACTTAA TTC /
T-- AGG TTTAGA

GAM2671 TACGACTAACATTTTTATAG 1836 ACTAACATTT 4906 -- ca- a - ACA- A GT
TTATCATTACAATTTTTTAG TTATAGTTAT TAC Gactaa ttttt tagttat catt ATTTTTT GCA T
CAGTTAAATGCAAAAAAATA CATT ||| |||||| ||||| ||||||| |||| ||||||| |||
ACAGATGTATAATTGAAAGA ATG TTGATT AAGAA GTTAATA GTAG TAAAAAA CGT A
ACTTTTAGTTTTGTA TT TTC A T ACAA A AA

GAM2672 CATAATCATCATATTTTCTC 1842 TACCTCAGTT 4912 CATCA - C C TTAACC-- T TT
AACCTGATTAACCCTTCAAT AGATAAATAA CATAAT TATTT TCT AAC TGA CT CAA C
TCATCTTGTAGATTATACCT AAAT |||||| ||||| ||| ||| ||| || |||
CAGTTAGATAAATAAAAATT GTATta ataaa aga ttg act GA GTT A
ATG aaa-- t - - ccatATTA T CT

GAM2673 GCACCGTGGAGGTCGTTCTA 1837 TATCGCATGC 4907 AC GGTCG ta- gcg- cg t
CAACT
TCGCATGCGATTGTGCGAAT GATTGTGCGA GC CGTGGA TTC tcgcat attgtg aatg GC G
GTGCCAACTGCGAATGCCGT ATGT || |||||| ||| |||||| |||||| |||| ||
TATTACAATAAAAATGTGAC CG GCGCCT AAG AGTGTA TAACAT TTGC CG /
TTGAAAAATCCGCGAAGC AA AAA-- TTC AAAA TA - TAAGC

GAM2674 TTGTGGGATGTTCGTCGTAT 1838 CTTTGCACGT 4908 G GTC--- T - CA G --- C
CGGCAACATTGGCATCCGCT ACCAACCAGA TTGTG GATGTTC GTA CG GCAA TT GCA
TCCG T
GCGGATTATGTGGACTTTGC ACGT ||||| ||||||| ||| || |||| || ||| ||||
ACGTACCAACCAGAACGTTG AGCAC Ttgcaag cat gc cgtt AG TGT AGGC /
CACGA G accaac - a tc G ATT G

GAM2675 GATAAAAATATGTCGAGGGA 1839 TATGTCGAGG 4909 AAAAAta ga ga catt- A
TGACATTGATGAGACCCCTT GATGACATTG GAT tgtc gg tga gatgaG C
ATTCTCTCTCAAACTAAGAC ATGA ||| |||| || ||| ||||||
AGTAATCCATC CTA ACAG TC ACT TTATTC C
CCTAATG AA AA CTCTC C

GAM2676 GGGGGGAAGGAGGTTGACTG 1843 TGCAGCACTA 4913 G--- GT-- A AATT
CAACCTCAATTGATCAGAGG ACTCTTTACA GGGGG AAGGAG TG CTGCAACCTC G
TTGCAGCACTAACTCTTTAC ACCC ||||| |||||| || ||||||||||
AACCCCC CCccc tttctc ac gacgtTGGAG /
aaca aatc - ACTA

GAM2677 CATTCCCTAGCTATTATAAG 1844 TATCTGGCTA 4914 ---- T- TTAATT

GTTAATTGCAAAAACCCTTA AGATGGGAGT CATTCCC TAGCTA TATAAGG G
TATCTGGCTAAGATGGGAGT G ||||||| |||||| |||||||
G gtgaggg atcggt atATTCC C
taga ct CAAAAA

GAM2678 GGATGTAACGGTGGAGGTCC 1845 GGGCAAGAAT 4915 --------- G GGT--- G AG
GGCAGGAAGTGGGCAAGAAT TGACCGATTT GGATGTAA CGGT GA CC GC G
TGACCGATTTATCTATTGCA ATCT |||||||| |||| || || ||
TCC CCTACGTT gcca tt gg TG /
Atctattta g aagaac g AA

GAM2679 TTGTGGTCTAACTCAAGACT 1848 GTCGTGGTTG 4918 - T T A GCTGAA GC
AGCTGAATCGGTGCTATAAC ACACGCAG TTGTG GTC AAC CA GACTA TCGGT T
CGATAGTCGTGGTTGACACG ||||| ||| ||| || ||||| |||||
CAG gacgc cag ttg gt ctgAT AGCCA A
a - - g ------ AT

GAM2680 GTTTTAGAGCTGGATCCTCC 1853 TTAGACAGCT 4923 TAGA GG C CC AGGC C AA
TGACCCTGTAGGCCTACATT CAGAGGATGA GTTT GCT ATCCTC TGA CTGT CTA ATTGC
T
GCAATGAGCAATTAGACAGC GGTG |||| ||| |||||| ||| |||| ||| |||||
TCAGAGGATGAGGTGGATGA CAAG tgg taggag act gaca gat tAACG /
AC TAGg ag - c- ---- - AG

GAM2681 GTGCCTAAATCTGTTTCTGT 1854 CTAAGGGTGG 4924 AA-- TG TCTGTTAT ATT
TATTTTAGGGGCATTTGACG GTGTTGGGGT GTGCCT ATC TT TTTAGGGGC T
GTTCCTAAGGGTGGGTGTTG AT |||||| ||| || |||||||||
GGGTAT tatggg tgg gg gaatcCTTG G
gttg gt -------- GCA

GAM2682 GTCTGAAGGGGGGCCCTAAT 1860 TAAAGCTTCA 4930 --- GG- CC AA---- G
CAACTTAAGTGCTTAAGGTA AATTCATCTG GTC TGAA GGGGC TAATC CTTAA T
TAGGATTAAAGCTTCAAATT AC ||| |||| ||||| ||||| |||||
CATCTGAC cag actt cttcg atTAG GAATT G
tct aaa aa GATATG C

GAM2683 GTGCAGTGCACAGGAACAGA 1855 TTCACTGGAT 4925 G - AC- TC-- CATAC T
CATCCATCACCTACATACGC ATATTGTGTC GTGCA TGCACAGGA ACAG ATCCA ACCTA
GC T
TTCTGCTGGGTTCACTGGAT CTGT ||||| ||||||||| |||| ||||| ||||| ||
ATATTGTGTCCTGTGTGTGC CGCGT GTGtgtcct tgtt taggt tGGGT CG C
GC - g ata cact ----- T

```
GAM2684  AGGAGGAGGAGCACTATCCC 1849    GAGCAGGTGT 4919          G    C  TCCCTATACAATA        G
AAC
         TATACAATAGACACCTGTTG        TAGATTTACT        AGGAGGAG AGCA TA          GACACCTGTT CA   C
         CAAACCTTGTGGAGCAGGTG        ATTA              |||||||| |||| ||          ||||||||||  ||
         TTAGATTTACTATTATTGCT                    TCTTCCTC TCGT at          ttgtggacga GT   /
         ACTCCTTCT                          A    T  tatcatttaga--         g  GTT

GAM2685  TTTATTTGATGGGATGTAGA 1850    GGACCACACT 4920       TTT     A    A-   CAA   ACTA
         TGGCAACTAACTACCTCATA        ACACTCATTT        TTTA   GATGGG TGTAG  TGG   CTA    C
         GGACCACACTACACTCATTT        TTAA              ||||   |||||| |||||  |||   |||
         TTAAA                            Aaat   ttactc acatc  acc   gAT    /
                                     tt-     -     ac   ag-   ACTC

GAM2686  TGTACGTAATGGACATCATA 1851    TTTCTTGGTT 4921         TAAT   C    T---      GAT
         GGTACGATAGCAGTATCTTT        TCTTATTTGT        TGTACG    GGA ATCA    AGGTAC   A
         CTTGGTTTCTTATTTGTATA        ATA               ||||||    ||| ||||    ||||||
                                  atatgt    tct tggt    tCTATG   /
                                     ttat   t    tctt      ACG

GAM2687  CATTAGCAGTAACTGAATAT 1852    TATAATGCAA 4922       T  C  TA   GAAt      caaa  aa    ta-    T
         AATGCAAAACAAGCAATACA        AACAAGCAAT        CAT AG AG  ACT    ataatg    ac  gcaa   caaA A
         AATACATTTGACTTTGCAGT        ACAA              ||| || ||  |||    ||||||    ||  ||||   ||||
         CATTATTAAAGTCTCCTTAT                    GTA TC TC  TGA    TATTAC    TG  CGTT   GTTT C
         G                                T  C  --   AAT-      ----  A-    TCA    A

GAM2688  CGATACATAAAAGGTGAGTT 1856    TCAGGCAGCT 4926         ATAAAA      TATG    AAAT-------     A
         ATGTGCCAAATCAGATACAG        GCTCGCCAGA        CGATAC      GGTGAGT    TGCC         CAGAT C
         TCTGTGCCAAACTCAGGCAG        TGCG              ||||||      |||||||    ||||         |||||
         CTGCTCGCCAGATGCGTATC                    GCTATg      ccgctcg    acgg         GTCTG /
         G                                cgtaga      tcg-    actCAAACCGT     A

GAM2689  ATTACTGTTACCGCTGTAAT 1857    TAACAAAAGT 4927         -   CC     A    -------       -----   t    ttc
         AACAAAAGTATCTATAATTC        ATCTATAATT        ATTACT GTTA  GCTGT Ataa       caaaagt     atc ataa    c
         CCATTTATTGATAATTAACT        CCCA              |||||| ||||  ||||| ||||       |||||||     ||| ||||
         TTTGACAATATTTATAATAG                    TAATGA CAAT  TGATA TATT      GTTTTCA     TAG TATT   /
         TTTAACTAGTAAT                      T    T-     A    TATAACA      ATTAA   T    Tac

GAM2690  AAAGGAGAAATATCAGATTA 1858    TATTACACCA 4928         AA    C    T    C  -  C     GATAC
CAA
         TGACGGGTACTATTGGATAC        TCATTATTTT        AAAGGAG  ATAT AGAT ATGA GG GTA TATTG
CGACGAA  G
         CGACGAACAAGTAATTTGTT        ATGT              |||||||  |||| |||| |||| || ||| |||||     |||||||
         GATACGATATTACACCATCA                    TTTCTTC  tgta ttta tact cc cat atAGC     GTTGTTT   /
         TTATTTTATGTACTTCTTT                      A-   t    t    a  a   t     ATA--       AAT
```

GAM2691 ATATGACTAGACCGATGACC 1859 TCGATCATTC 4929 A- CC CCATTTAAAAA TCTCT-CT

ATTTAAAAAATACTCTCTAG TTTTAGCACA ATATG CTAGA GATGA ATAC AG T

CTTTAACTTAAACTGTATCG TGT ||||| ||||| ||||| |||| ||

ATCATTCTTTTAGCACATGT tgtac gattt ttact tATG TC T

ac tc agc-------- TCAAAT AA

GAM2692 GATTTTCAATTATGTATCAT 1867 TCCTCCTTGA 4937 TTTTCAATTATGT TTAT-- CAGT

TATAGCAACAGTAATTCTTG TTTTAGCATC GA ATCA AGCAA A

CTCCTCCTTGATTTTAGCAT CTCT || |||| |||||

CCTCTTC CT tagt tCGTT /

tctcctacgattt tcctcc CTTA

GAM2693 TATTTGTAAATGGATATCCT 1861 TATCCTATAA 4931 T GGAta -- t tagacACA

ATAAAATTTTTATTAGACAC AATTTTTATT TATTTG AAAT tccta taaaatt ttat G

AGGAGCAGATATAACAATTT AGAC ||||||| |||| ||||| ||||||| ||||

TAAATAGGAGAGATTTTCAA ATGAAC TTTA AGGAT ATTTTAA AATA /

GTA T GAG-- AA C TAGACGAG

GAM2694 GAACAAATTATATTAATGTA 1862 TAATGTACAT 4932 AA ATt tagaga ga G

CATTTAGAGATTAGAGATGA TTAGAGATTA GAACA TTAT aatgtacatt tta gaT A

AAATTATAAGACACAATGTA GAGA ||||| |||| |||||||||| ||| |||

TATTTGGTAATGTTT TTTGT AATG TTATATGTAA AAT TTA A

-- GT- CACAG- A- A

GAM2695 TGGGTGTTTTTGGGGTGTGG 1863 GGTCATTGGA 4933 T- G C A GG- gg t a-- - cagt

CGGACGCGGGGCGGTCATTG CGGGGTGCAG TGGGTG TTTTGGGGT TGG GG CGCG GC tcat gg cggg gtg t

GACGGGGTGCAGTTAAATAC TTAA |||||| |||||||| ||| || |||| || |||| || |||| |||

ATGCCCGGGACCCATGAAGC GCCCAC AAGACTCCG GCC TC GCGC CG AGTA CC GCCC TAC a

ATGCGCGACTTCCGGGCCTC CC G T A GTA A- C AGG G ATAa

AGAACCCACCCG

GAM2696 GACCTGCATTGCTACGAAGA 1868 GTAGTTCCGT 4938 T GAA - GAA GAG A----- C ATTC

GTTAAGTGAAGAAGAGACAG GTTGCTTTTG GCTAC GAGTT AAGT GAA ACAGAGG GGAGC ACGATTT C

AGGAGGAGCCACGATTTATT TGAT ||||| ||||| |||| ||| ||||||| ||||| |||||||

CCTTACAAGATTGTAGTTCC TGGTG TTCAG TTCG CTt tgttttc ccttg tgTTAGA T

GTGTTGCTTTTGTGATTCCA - ATA C AAC ag- gttgtg a ACAT

AGCTTCGACTTATAGTGGTT

GCAACTC

GAM2697 GCAAGACTTCGTTTATACGT 1869 ACTTCGTTTA 4939 cttc atac- ----- cA
GCTTGCTACAAATTTAGGAA TACGTGCTTG GCAAGa gttt gtgcttg cta A
TTCGAGCGCAACAGGAACTT CTAC |||||| |||| ||||||| |||
TTGC CGTTTT CAAG CGCGAGC GAT A
---- GACAA TTAAG TT

GAM2698 CTCATTGTGGTTTTCGCGCC 1864 CATTGTGGTT 4934 a- t cg c agag- AACC
TCAGAGTTGTTAACCACATT TTCGCGCCTC CTc ttgtgg tttcg c tc TTGTT A
CGGCAAAAGGGGAAGTATGA AGAG ||| |||||| ||||| | || |||||
AACCCACAAGGGAG GAG AACACC AAAGT G AG AACGG C
GG C AT A GGGAA CTTA

GAM2699 ACACTACATTTCTCAGAACC 1870 ACTACATTTC 4940 ac---- tc cca CTA
AAAAATTTCTAAATAAAGAT TCAGAACCAA ACact atttc agaa aaaatTT A
TTTTTCTATGAAATTCATAA AAAT ||||| ||||| |||| |||||||
AGTGT TGTGA TAAAG TCTT TTTTAGA A
AATACT TA --- AAT

GAM2700 TTTTTATTCTTCATTCGTTA 1865 AAAGGGCAAT 4935 ATT TC T ACTTTTAACACA GAA
A
CGACTTTTAACACACCCGAA ATTTTGCGTC TTTTT CTTCAT GT ACG CCC TGT T
TGTATCGACAAAGGGCAATA ATTT ||||| |||||| || ||| ||| |||
TTTTGCGTCATTTATGGAGT AAAAG GAGGTA ta tgc ggg aCA C
TAGAAAA ATT tt c gttttataac-- aa- G

GAM2701 GAGATAAGTTTCATAAGTTT 1871 TAAGTTTCAT 4941 t ttttatt-- TTTCA
ATTTTATTATCATTTCAAAT AAGTTTATTT GAGA aagtttcataagttta ATCA A
ATTTTGATTTCTTTTTCTAA TATT |||| |||||||||||||| ||||
ATTTGTGAAATTTTTTTC CTTT TTTAAAGTGTTTAAAT TAGT A
T CTTTTTCTT TTTAT

GAM2702 ATTATTACTATAGAAGATGT 1872 TAAGTAAAGC 4942 - AAGA TAGAAAAA TG G TTACAC
- A T
TAGAAAAAATGATGCTGGTT ATATAACGAC AT AG TGT A AT CTGGTTA ATGTGTTT AT
TATATA A
ATTACACATGTGTTTATATA TAAC || || ||| | || ||||||| |||||||| || ||||||
TATATATATATATAAGTAAA TA TC ATA T TA GACcaat tatacgaa tg atATAT T
GCATATAACGACTAACCAGA G ATGG TTAAAA-- GT A cagcaa a a A
ATTGTAAAATTATAGGTACT
GATAGAATAAT
GAM2703 ACAAAGCATTTCCACAACTG 1873 TACATGGGAA 4943 AA TTTCCACAAC GG A- GG
AA TTTC
CTGGGTTTACATGGGAAACA ACAAAGCATT AC AGCA TGCT GTTT CATG AAAC AGCA
C
AAGCATTTCCACAACTGCTG TCCA || |||| |||| |||| |||| |||| ||||

GGTTTACATGGGAAACAAAG TG TCGT acga caaa gtac tTTG TCGT A
CATTTCCACAACTGCTGGGT GG CAACaccttt aa gg a- GG CAAC

GAM2704 ACTGGCAGAACGAGCACAGC 1866 TGGCAGAACG 4936 ag ga --- g - TTAG-- G
AGGCCTTTAGGGTGGTAACT AGCACAGCAG ACtggc aac gcac agca gc ct GGT G
ACGTGTGGTGTGTGCTATCG GCCT ||||||| ||| |||| |||| || || ||| |||
TGCAGTTAGGTTAGT TGATTG TTG CGTG TCGT TG GG TCA T
GA A- CTA G T TGTGCA A

GAM2705 CCAACCTGCAAAACCAGCAC 1874 ACCAGCACAG 4944 AC TG Aacc a tg ta- gt A G TG
AGCTGGCCTATAGGGTGGTA CTGGCCTATA CCA C CAA agcac gc gccta gg GGT ACA AG T
ACAGAGTGTGGGTTGTGTAG GGGT ||| | ||| ||||| || ||||| || ||| ||| ||
CCGTCCAGTTAGGCTGGCGG GGT G GTT TCGTG CG CGGAT CC CCG TGT TT G
TGCTTTGTGGAGTGG GA GT ---- G GT TGA TG A G GG

GAM2706 GGCGGTGGCGATCAAAAGGC 1875 TAGAGTGTAA 4945 CGA AAAAG G- AA
GCGTATGAGAAACCGTTTAT TAGAATCACC GGCGGTGG TC GCGC TATGAG A
AGAGTGTAATAGAATCACCG GTC |||||||| || |||| ||||||
TC ctgccact ag tgtg atATTT C
a-- ataa- ag GC

GAM2707 GGTCGTCGGAAGTTACTGAT 1876 TCGGAAGTTA 4946 tc- ac --- aacaaca
GGAACAACAAGCGCCGCCCA CTGATGGAAC GGTCG ggaagtt tga tgg A
ACTTCAAATTTCCAGCCGAC AACA ||||| ||||||| ||| |||
C CCAGC CCTTTAA ACT ACC /
CGA -- TCA CGCCGCG

GAM2708 TGATGTGGTCTCTGGGATGA 1877 TAGTATGGCT 4947 TCT AATAT---- AGT
AATATTATTATATGTAGTAT TTTCTCGTTC TGATGTGG CTGGGATGA TATTATATGT A
GCAATATATAGTATGGCTTT CAGT |||||||| ||||||||| ||||||||||
TCTCGTTCCAGTCTTTATAT ATTATATT gaccttgct atgatATATA T
TA TCt cttttcggt ACG

GAM2709 TCTCTCAGAAAACGAGAGTG 2724 TAGGAGGTGA 5794 GAA- GA- GTGA CA
ACTTCTAGACACACTCTAGG TCGTAGTTGG TCTCTCA AAC GA CTTCTAGA C
AGGTGATCGTAGTTGGCATG CATG ||||||| ||| || ||||||||
AGAGA AGAGAgt ttg ct gaggatCT /
acgg atg agtg CA

GAM2710 CTGTTCTACGGAATTAACAA 1878 TAAGAAAATA 4948 - G TAAC- C AATATAAAG----- AAC

CTCGTGAATATAAAGATACA AGAAGCACAG CTGTT CTACG AAT AACT GTG ATAC A
ACATTCAGTATAAGAAAATA TTAT ||||| ||||| ||| |||| ||| ||||
AGAAGCACAGTTATATCATT GACAA GATGC TTA ttga cac tATG T
GCGTAGCAACAG C G CTAta - gaagaataaaagaa ACT

GAM2711 ATATGGGTGGGGCGGGCGTG 1879 TATGCAGATG 4949 GG- GG GGAG TA GG
TGTATGGGAGGGGG A
GGAGGGACCTAGTCTGTGGG TGGTCTGACA GC GCGTG GGACC GTCTGTG GTCA
CTGACCT C
GTCATGTATGGGAGGGGGCT CGTA || ||||| ||||| ||||||| |||| |||||||
GACCTACGAGGGTCAGGGTG TG tgcac tctgg tagacgt tAGT GACTGGG G
AGAGGAAGTTGATATGCAGA AGA Ga ag-- tg a- TGAAGGAGAGTGG- A
TGTGGTCTGACACGTAGGTA
GAGTCCTATAT
GAM2712 TGTTAATCATCAATCCGTTA 1880 TACGGAAACA 4950 CATC-- GTt aaatt t
CGGAAACAAATTATCATTTT AATTATCATT TGTTAAT AATCC acggaaac atcatttt a
TATAAAAATGGTTTGTGGTT TTTA ||||||| ||||| |||||||| |||||||
TCTGTTTAGGGTTACCTTTA ACAATTA TTGGG TGTCTTTG TGGTAAAA T
TTAACA TTTCCA ATT GTGTT A

GAM2713 ATCATTTTTAGAACTGACCA 1881 TCACATGGTT 4951 TC- A ---------- T
ACCATGTTCACGTAAGTGAC GGTCAGTTCT AGAACTGACCAACCATGT ACGTAAGTGACGTG
TGAC GCGCGC T
GTGATGACGCGCGCTTCGCG AAAA |||||||||||||||||| |||||||||||||| |||| ||||||
CGCTGCCTGCGGCAGTCACA tcttgactggttggtaca TGCATTCACTGCAC ACTG
CGCGCG /
CGTCACTTACGTCTCACATG ctC - ACGGCGTCCGT C
GTTGGTCAGTTCTAAAAATG
AT
GAM2714 GCACCCTGAAGATGGTTTGA 2725 TCTGCAGTCA 5795 A C A--- G ATGCT T -
ATTTGG
ATGCTCTGCAGTATGTCAAG GACAGTCTCA GC CC TG AGAT GTTTGA CTGCAG ATGTC
AAGA A
AATTTGGAACTTGCTCTTCG AACA || || || |||| |||||| |||||| ||||| ||||
GCGTCTGCAGTCAGACAGTC CG GG ac tctg cagact gacgtc tGCGG TTCT /
TCAAACATGGGC - T aaac a ----- - C CGTTCA

GAM2715 GGGTGTGTGTGTGGGGGTGG 2726 TCCCCGACTC 5796 G T TG T G C CC G AG
TGGGCGGCCGCGGGCGCGGA CTCTGTACTA GGGT TG GTG GGGG GGT GG GG GCGGGC
CGG G
GGGTCCGGCCCGTCCCCGAC GACT |||| || ||| |||| ||| || || |||||| |||
TCCTCTGTACTAGACTC Ctca at cat ctcc tca cc cc tGCCCG GCC /
g - gt - g - -- - TG

GAM2716 GGTATAGTTGCATATTTATT 2727 TGCATATTTA 5797 attttatgt a CTTT- T T ----------
T

TTATGTTCATTTTCTTTCTT TTTTATGTTC tc tttT CTTGCT GAG GT GTTAT T
GCTTGAGTGTGTTATTTCAA ATTT || |||| |||||| ||| || |||||
TAGCTCCTGTTTAGCAGGTC AG AAAA GAACGA TTC CA CGATA C
GAACCTTCAGCAAGTTCACA TTCCTTTT- A CACTT C - AGCTGGACGATTTGTCCT
A
AAAAGATTTTCCTTTTGTGT
GTTTCTTTTC
GAM2717 GGGGACCGTCCGTTCTCTCC 2731 TCCCTGTGCA 5801 GG C C- TCt tg ca- g cttgtTTG
G
CTGTGCAGGTGCGACTCTTG GGTGCGACTC G GAC GTC GTTC ccc tg ggtgc act TGCTG
T
TTTGTGCTGGTCGCGGCAGG TTGT | ||| ||| |||| ||| || ||||| ||| |||||
TGGCGCCCAACGTGGGGCTC C TTG CAG CGAG GGG GC CCGCG TGG ACGGC
C
GAGCTCGACAGTTTTC TT A CT CTC GT AAC G -------- G

GAM2718 GCTTGTTCAAATTTTATAAA 2728 TTTATAAAGA 5798 T TCAAATt gaatcatattc gG
GAATCATATTCATTAGGCAT ATCATATTCA GCT GT ttataaa atta C
ATAATAAAAAATATAATTTA TTAG ||| || ||||||| ||||
TAATACACTTACAGC CGA CA AATATTT TAAT A
- TTCACAT AATATAAAAAA AT

GAM2719 TAGTTCTTAACATCTATTAA 2729 TTGCTTTAAT 5799 CT CATCT TCATT TT
TCATTTATTCGCTTATTGCT TGTTTTTGTA TAGTT TAA ATTAA TA C
TTAATTGTTTTTGTAAACTA AACT ||||| ||| ||||| ||
Atcaa gtt taatt AT G
at tttgt tcgtt TC

GAM2720 CGTCCACTTAAGCTGGTGGT 2730 AGGCAGCTAC 5800 - -- - G T AGCT
GCGTTGTGGAGCTGAAGACC AGCAGCTTAT CGTCCACT TAAGCTG GTGG TGC TTG GG G
TAAGGCAGCTACAGCAGCTT GGTG |||||||| ||||||| |||| ||| ||| ||
ATGGTGGACG GCAGgtgg attcgac catc acg aAT CC /
t ga g g - AGAA

GAM2721 TGTAACAAGTGTAACAAACA 2732 TAACAAGTGT 5802 a c caca-- g G- AT --- T
TTAT
CAACTGTAATGATGATTATG AACAAACACA t acaagtgtaa aaa act TAAT ATG TATGTA ACTA
GCA G
TAACTATGCATTATGATACT ACTG | |||||||||| ||| ||| |||| ||| |||||| |||| |||
GCTGGTGATTATATATATAT A TGTTTATATT TTT TGA ATTA TAT ATATAT TGGT
CGT /
GAATTAGAGTAAAACTTTTT A T TCAAAA G AG AT TAG - CATA
TTATATTTGTAACA

GAM2722 GGTTTGTGGTTGTTATGTGC 2736 TGGTTGTTAT 5806 T g- ta cttta GG GGT
CTTTATTGTAGGGGTGTTGG GTGCCTTTAT GGT TGt gttgt tgtgc ttgtaG GTGTTGG T

GGTTATTATTAATGCACTAT TGTA ||| ||| ||||| ||||| |||||| |||||||
AGAGCTGTACAAGGCGATAA CCA ACA TAGCG ACATG GATATC CGTAATT A
ACACACC C AA GA TCGA- A- ATT

GAM2723 CTCACTCTGATATGTGCACC 2733 TGATATGTGC 5803 TCtg g - gtg t
GTGTGTGATTTTATCACGAA ACCGTGTGTG CTCAC atatgt ca cc tgtgat t
GGCTGGACATATGTTTGTGA ATTT ||||| |||||| || || ||||||
G GAGTG TATACA GT GG GCACTA /
TTTG G C AA- T

GAM2724 GAGCGACCGTTATTGGTTTG 2737 TGACAAGACC 5807 -- TTA GTTT ACGC
GAGTGACGCCCGGACATTCC GGATTCGTTC GAGCGA CCG TTG GGAGTG C
TGACAAGACCGGATTCGTTC |||||| ||| ||| ||||||
cttgct ggc aac CCTTAC /
ta cag agt- AGGC

GAM2725 TTTTTATAAACATGAAACCA 2734 TGTCTAAATG 5804 --- AAAC- Ct aaa taatta ttg T
CTGTCTAAATGTAATTATGA TAATTATGAT TTTTTATA AACATG CA gtct tg tgatc ATT A
TCTTGATTTATAGATGATGA CTTG |||||||| |||||| || |||| || ||||| |||
TCAGCCTTCAGAGGATTTTG AAAAGTAT TTGTAC GT TAGG AC ACTAG TAG T
ACCAGCATGTTTAATATGAA AAT GACCA TT AG- TTCCG- TAG A
AA

GAM2726 ATATGTACACATATTTTAAT 2735 TATTTTAATT 5805 -- a atatc- ttactTG
TATATCTGTTTTACTTGGAT ATATCTGTTT ATATGTACA CAt ttttaatt tgtt G
TTAATAACAATACTGAATTA TACT ||||||||| ||| |||||||| ||||
AAACATGATTGTATATAT TATATATGT GTA AAAATTAA ACAA /
TA C GTCATA TAATTTA

GAM2727 TTCCGTAATATCTGTTTTAT 2738 TCTGTTTTAT 5808 C Atc ata ga - a C
ATAGTGAGGGTTCACGCATG ATAGTGAGGG TTC GTAAT tgtttt tagt ggg ttc CG A
CGCGAGTCCCGACTAATGAG TTCA ||| ||||| |||||| |||| ||| ||| ||
GACAATTACTGAA AAG CATTA ACAGGA ATCA CCC GAG GC T
T --- GTA G- T C G

GAM2728 GTCTATTTCCCACGACATAC 2739 TCCGTGGGAA 5809 - ACGACATAC AATACCCA
TTCCGCGGAAAAATACCCAC GACGATGGGG GTC TATTTCCC TTCCGCGGAAA C
GCTCCTTAATTTCCGTGGGA GAAA ||| |||||||| ||||||||||
AGACGATGGGGGAAATGTGG CGG GTaaaggg agggtgcctTT G
C T ggtagcaga AATTCCTC

GAM2729 TTGTTAGTTGTTTTTAATGA 2417 TGTACATATA 5487 TAAT CCAC C ---- T-
AAATTAG- GC
TACCACACAACGAGATGTTT CATTTGGAAC GTTTT GATA ACAA GAG ATGTTTT ATG
TAACTTT C

TTATGAAATTAGTAACTTTG ATTA ||||| |||| |||| ||| ||||||| ||| |||||||
CCAAGAGGTTGTACATATAC CAAAA TTAT TGTT CTC tacaagg tac gtTGGAG /
ATTTGGAACATTAAACTCTT TGT- AA-- T AAat tt atatacat AA
TGTAATATTTGTAAAACAAA
ACAA

GAM2730 GGTGTGAAACTATGAGGAAC 2422 TGTGAAACTA 5492 - tatgaggaa- a AA
TGATGAGAAATGACTTACGG TGAGGAACTG GGtg tgaaac ctg tgaG A
CCATGATTTTGTTTCGTCGC ATGA |||| |||||| ||| ||||
T TCGC GCTTTG GGC ATTC T
T TTTTAGTACC - AG

GAM2731 TTTTTTTATAGCGTGAAGGA 2418 TAGCGTGAAG 5488 c---------- a- tat- a-- T
TATGATAAAAAATATAATTG GATATGATAA TTTTTTTTAtag gtga gga gataaa aaTA A
TTGTATTTATCCCATTCCAA AAAA |||||||||| |||| ||| |||||| ||||
TCACCTTATATGATTCTGTA AAAAAAATGTC CACT CCT CTATTT TTGT A
AAAAAA TTAGTATATTC AA TACC ATG T

GAM2732 ACGAATCATGATTTGATCTA 2423 TACATTCTCG 5493 AT- TTTG CT TTTCAG
CCATTTCAGCATTTATTGGT GGTTCGT ACGAATC GA AT ACCA C
TTATACATTCTCGGGTTCGT ||||||| || || ||||
tgcttgg ct tA TGGT /
gct taca TT TATTTA

GAM2733 GTGTACGGGTGCTTTATTAT 2434 TTGTATATAT 5504 TACG- T TATCAT -- AT
CATCAGCGTCATGCAGACTG AACGTACCAT GTG GGTGC TTAT CAGC GTC G
GTTGTATATATAACGTACCA GATC ||| ||||| |||| |||| |||
TGATCAC CAc ccatg aata gttG CAG /
tagta c tatat- GT AC

GAM2734 TCGATTGCGAAAATTTAATT 2427 CATTGGATAG 5497 GA GAAA- - T- A
CATTGTATGAAAATATTTCA GGGGCAAGGG TC TTGC ATTTAAT TCA TGTATGAAA T
TGTACTTGGCATTGGATAGG A || |||| ||||||| ||| |||||||||
GGGCAAGGGA ag aacg taggtta GGT ATGTACTTT /
gg gggga c TC A

GAM2735 CCCAAAACCAAGCCATCCAA 2424 ACCAAGCCAT 5494 Aa a aa- aaaaa TTGTCA
TTT T
ACATAAAAACAATAAATTGT CCAAACATAA CCCAA cca gccatcca cat cAATAAA GA TGT T
CAGATTTTGTTTAAGCATTC AAAC ||||| ||| |||||||| ||| ||||||| || |||
GTATCTTTATTGGAGTGGGG GGGTT GGT TGGTAGGT GTG GTTATTT CT ACG A
TGGATGGTGTGGGGTTGGG GG G GGG AG--- CTATG- T-- A

GAM2736 GTTTAAGTTCTAGATCAGGA 2419 GATCAGGAAA 5489 AA Aga- ag agagcat gt
AAAGAGCATAATGTCAAAAT AGAGCATAAT GTTT GTTCT tc gaaa aat c

TTATAATTTCGGAGAAAAGG GTCA |||| ||||| || |||| |||
ATAAAAAC CAAA TAGGA AG CTTT TTA a
AA AAAG G- AATAT-- AA

GAM2737 GTCCATTAACCGTTCTATGA 2420 TCATATGGTT 5490 C T TCT C C- C T
TCGACGCCGGTATTCTCGCA TATGCGC GT CAT AACCGT ATGAT GA GC GG A
CTCATCATATGGTTTATGCG || ||| |||||| ||||| || || ||
C cg gta ttggta tactA CT CG TC T
c t --- - CA C T

GAM2738 GCTTTCTTTCTAAAATTGTC 2421 TCTTTCTAAA 5491 tc- a catt TCGACAC T ATATT
ATTTATCATATCGACACGAA ATTGTCATTT GCTT tttctaaa ttgt tatcaTA GAA TGT T
TTGTATATTTAAATAGCATT ATCA |||| |||||||| |||| ||||||| ||| |||
TCTAACTTATGATATCATAA TGAA AAAGATTT AATA ATAGTAT CTT ACG /
TTTAGAAATACAAGT CAT - CT-- TCAAT-- T ATAAA

GAM2739 AGGTTTTTAGAGGAGGTACC 2425 TTTGTTGGGA 5495 TTT GTA TACC AT
GATACCCAGACATATGCAAG ACTTCTTTGG AGGT TAGAGGAG CCGA CAGACAT G
TGTTTGTTGGGAACTTCTTT CTT |||| |||||||| |||| |||||||
GGCTT ttcg gtttcttc ggtt gtttGTG C
--- aag ---- AA

GAM2740 ACACCGCACTTTGTTTGACT 2435 TAGATAATAG 5505 - GC T A- - G- A TG
GTATTAGTACCACATGGAGT CAGCACATGC AC ACC ACTTTGT TG CTGT ATTA TACC CA G
TGGGTAGATAATAGCAGCAC AGAG || ||| ||||||| || |||| |||| |||| ||
ATGCAGAGTAGGTAGT TG TGG Tgagacg ac gacg taat atGG GT A
A A- t ac a ag - TG

GAM2741 GTGGTAACACTGTGTCCAAA 2426 CGACTGGTGG 5496 AA G T A- - TC
GTGTAGTTCACCACTGCGAC TAGAGTGCAG GTGGT CACT TG CCA AGT GTAGT A
TGGTGGTAGAGTGCAGCCAC CCAC ||||| |||| || ||| ||| |||||
caccg gtga at ggt tca cGTCA /
ac g - gg g CC

GAM2742 CATTGCTCTGTTGTAAACTA 2428 TAAGTTAAAC 5498 ---- TTGTA- ATATAta aa- aaat agggA
TATATAAGTTAAACCAAAAT CAAAATTCGC CATTG CTCTG AACT agtt acca tcgc G
TCGCAGGGAGACAAGGTGAC AGGG ||||| ||||| |||| |||| |||| ||||
GGTGGTGAGAACTCAGTTGA GTGAC GAGAC TTGA TCAA TGGT AGTG /
GAGTCAGAGAATACAGTG ATAA TGAGAG C------ GAG GGC- GAACA

GAM2743 CTTGGTTGTGGTGATTTCAT 2429 TGTTGCTATA 5499 - TG T TTCT T--- -- TT TC
TCTCATTATTGTTGTTTTCT CACCGAG CTTGGT TGTGG AT TCA CA TATTGT TGTTTTC TCCG T

```
    TTCCGTCTTGCGGATGAAGA                  |||||| |||||  || |||   ||   ||||||  |||||||  ||||
    TGTTGCGATGCGGTTGTTGT                  gagcca atatc  tg GGT   GT   GTAGCG  GTAGAAG  AGGC /
    TGGTGTTGCTATACACCGAG                    c    gt  t   TGTT  TGGC    TT     T-   GT


GAM2744  AGATGATCTTTTTGTTCTTC 2430   TGTGCAGGGC 5500    TCTTT    ---     AT-    ATGAT   TG
TG---    CG
    TGGTTCATTTCCTATGATTG      ATGCGGGGAA      GA   TTGTTCT  TCTGGTTC  TTCCT   TGTT  GC
  CTGAC  A
    TTTGGCTGCTGACCGACGCG      TCAG          ||    |||||||  ||||||||  |||||    ||||  ||    |||||
    TCAGGATGTGCAGGGCATGC                  CT    AATAGGG   AGGCCAGg  aaggg    acgg  cg
GACTG  C
    GGGGAATCAGGACCGGACAC                   TT---     CAC      act    gcgt-   ga  tgtAG    CG
    GGGATAATTTCATCT

GAM2745  AGAACACGCGGTCCCCTGTG 2438   CCCCTGTGGT 5508    A    GG----      gg   tt   tt   TT
    GTGTTTTTGGTTATTTTTAT      GTTTTTGGTT      AGA CACGC    Tcccctgt  tgtt  tgg  attt  A
    TAAATCTCGTCGACAAACAG      ATTT          ||| |||||    ||||||||  ||||  |||  ||||
    GGGGAAAGGGGCGTGGTCT                   TCT GTGCG    GGGGGACA  ACAG  GCT  TAAA /
                              G    GGGAAA      A-   CT   C-   TT


GAM2746  GATTGATAACCTTGATGTAG 2445   TGTAGCAAGC 5515        A   T A   gc    a    - agag   AG
    CAAGCCAACCTTTGGAGAGT      CAACCTTTGG      GATTGATA CCT G tgta  aagcca  ccttt gg   TTTG  G
    TTGAGGTACAGGGACCCAAG      AGAG          |||||||| ||| | ||||  ||||||  |||||  ||    ||||
    AGGATGGTTTTATGCACCAG                  CTGATTAT GGA C ACGT  TTTGGT GGAGA CC   GGAC /
    GTATTAGTC                               -   - C   AT    A    A  CAG-   AT


GAM2747  CGCGACCGGCCAAAAGACCG 2439   TCACAGCGCT 5509    GA-    AAAA   C-   ----- C   G
    CGCGGCGCCCGTCGGGCCCT      CGTCGCGCGG      CGC   CCGGCC   GAC  GCGC    GG GCCC T
    CACAGCGCTCGTCGCGCGGC      CCGG          |||  ||||||   |||  ||||    || ||||
    CGGGCGGCG                               GCG   ggccgg   ctg  cgcg    CC CGGG /
                              GCG    cgcg   ct   acact -   C


GAM2748  TTGTTATATAGACCCACCAC 2431   TATATAGACC 5501     Tt     ccc    ca  g     T
    ATAGTGAGATTTTATCTCGG      CACCACATAG      TTG  atataga   acca  ta tgagAT T
    TGACTGGTTTTATGTTTCAA      TGAG          |||  |||||||  ||||  || ||||||
                            AAC  TGTATTT   TGGT  GT GCTCTA /
                             TT     ---    CA  G     T


GAM2749  TTTGTCGTGTGCTTTTCGTG 2440   GTGCTTTTCG 5510      -  gt-----  t      -  -    t  CGC
    TCTCGGGGCGGTTTCCGCGA      TGTCTCGGGG      TTTGT CGT     gct ttcgtgtct cgg ggcgg TTC   G
    CCGAACCCGTCGCCGCGGAC      CGGT          |||||  |||     |||  |||||||||  ||| |||||  |||
    GCGAGCAGCCGGATCAACGT                    GAACA GCA     CGA GAGCGCAGG GCC CTGCC AAG   /
    ACAAG                                   T   ACTAGGC   C      C   G    C   CCA
```

GAM2750 GTCCAATATTTTATATAAAA 2432 AGACGTTGTC 5502 - TTATATAAAAAC CTa gttgt
tc taaT
ACATTTTATTTCTAGACGTT AGAAAATCCT T CCAATATT ATTTTATTT gac cagaaaa ctg
A
GTCAGAAAATCCTGTAATAT GTAA | ||||||||| ||||||||| ||| ||||||| |||
TTTTAGTTTTTTTGGTTGTG A GGTTATAA TGAAATAAG TTG GTTTTTT GAT /
AATAAAGTATCGCCCTAATA T TAATCCCGCTA- TG- ----- T- TTTT
ATATTGGTAC

GAM2751 GAGTCTGCGCTGCGGCGGCG 2436 TCTGCGCTGC 5506 c -------- c - - ta
CTCTTTATACTGGGCGGACG GGCGGCGCTC GAGt tg cgctgcgg ggcg ct ctt T
CCCCCGCAGCGGCAAAACAC TTTA |||| || |||||||| |||| || |||
ACACTC CTCA AC GCGACGCC CCGC GG GGG A
C ACAAAACG C A C TC

GAM2752 TCGCTTTAAATACGGACTGA 2433 GAGTGCCAAA 5503 G TAAATAC GAAA AGGG T
AAGGAGGGCCTTCTACGGAA GTCTATGAGG TC CTT GGACT GG CCTTC A
GGAGTGCCAAAGTCTATGAG GA || ||| ||||| || |||||
GGA ag gag tctga cc gGAAG C
g ta----- aa-- gtga G

GAM2753 CACGCAGATATAAGGGCACT 2437 TAAGGGCACT 5507 ATAta - - aa- c- a
GGAACAGCTGCTACTAGGCA GGAACAGCTG CACGCAG agggcac tg g cag tgct c
CATTGAAGCTCGTGTGTCCT CTAC ||||||| ||||||| || | ||| ||||
CGCTGCGTG GTGCGTC TCCTGTG GC C GTT ACGG T
GC--- T T GAA AC A

GAM2754 GTGCAGTTTACTTTTAATCT 2441 TCTACATATT 5511 - TTT At- t- tt gt- ta
ACATATTTTACTGTGTTATT TTACTGTGTT GTG CAG ACTTTTA ctaca att act gt t
TATTTAAGTTTAATTTTGTA ATTT ||| ||| ||||||| ||||| ||| ||| ||
GTTGTAAAAGTTGTTTGCCA CAC GTT TGAAAAT GATGT TAA TGA TA /
C C TGT GTT TT TT ATT tt

GAM2755 GGAGGAGCCATTCCAACACC 2442 TCCAACACCG 5512 GC-- t aa -- g t cag TT
GGAGCTGCCAGCGTGGTTGT GAGCTGCCAG GGAGGA CAT cc cacc gga c gc cgtgG G
ACCATGAGTGCTGTCCGAGG CGTG |||||| ||| || |||| ||| | || |||||
TGCGGGTATGAATATTCTCT TCTCTT GTA GG GTGG CCT G CG GTACC /
ATAA T GC AG - T TGA AT

GAM2756 CATAGTTTTCTGTATTAGAT 2446 TATTAGATAG 5516 - ta g t tttcaattcC T TT
AGTACGCTTTCAATTCCAGT TACGCTTTCA CATAGTT TTCTG tta atag acgc AG GTGG A
GTGGTTATACCACCTTGTGT ATTC ||||||| ||||| ||| |||| |||| || ||||
CTATGTAAGTTAGAGTGGCT GTATCGG GAGAT AAT TATC TGTG TC CACC /
ATG T TG G - T--------- - AT

GAM2757 GCCTAGACATCAGACCGCGC 2447 CGTCACAGCC 5517 TA ATCA GCGCA T T T C
AGGCTGTTGTTGTGTTGCTT ATATAGGTTA GCC GAC GACC GGCTGT G TGTG TG T
GTACCACGTCACAGCCATAT CGTT ||| ||| |||| ||||||| | |||| ||
AGGTTACGTTCGGGT TGG ttg ttgg ccgaca c gcAC AT T
GC ca-- atata - t C G

GAM2758 TTTCCGTCGATCTGGAAGCT 2443 TCCTTCACCA 5513 C T CTG---- CT TA
TGTGTTCTAAATGAATATAT AATATCGCAG TTTC G CGAT GAAG TGTGTTC A
CCTTCACCAAATATCGCAGA AAG |||| | |||| |||| |||||||
AG gaag c gcta cttc ATATAAG /
a - taaacca ct TA

GAM2759 ATTTTCTTTGTTCTTTTATG 2452 TCTTTGTTCT 5522 c tt tatgt AAAA ACAAAC A
A
TTTATTTTGTTTGTCATTTA TTTATGTTTA TTt tttg cttt ttattttGTTTGTCATTTAA CA TTT TC
A
AAAAACAACAAACTTTATCA TTTT ||| |||| |||| |||||||||||||||||| || ||| ||
AATGACAAACAAATGACAAT GGA AGAT GAAG AATGAAACAAACAGTAAATT GT
AAA AG A
TAAATGACAAACAAAGTAAT A TT TGAT- AACA AAAC-- C T
AGTGAAGTTTAGAAAGGAT

GAM2760 TCTACGTATCTCGTCGTCCA 2444 TTTCTAGACG 5514 AC TCT GTCC TTTTATAT
ATATTTTATATAAAAACATT TTGCCAGA TCT GTA CGTC AATA A
TTATTTCTAGACGTTGCCAG ||| ||| |||| ||||
A aga cgt gcag ttAT A
c- t-- atct TTTACAAA

GAM2761 CCCGTCGGTCGGAAGCGAGT 2448 CTGCATGCCG 5518 - T AA- AGT TTCA- T
GCCCTTCAAGCGTGTCCGCT TCGGATGGG CCCGTC GG CGG GCG GCCC AGCG G
CCTCTGGGCTGCATGCCGTC |||||| || ||| ||| |||| ||||
GGATGGG gggtag ct gcc cgt cGGG TCGC T
g - gta --- TCTCC C

GAM2762 GGTTCTCACAAAAATATGCA 2449 TGCATGGAAG 5519 TCA AAAA TCT TG G
GATCTCTATGAGTGTTGTAG TGGTTGGGCC GGTTC CA TATGCAGA CTA A T
CTCTGCATGGAAGTGGTTGG ||||| || |||||||| ||| |
GCC ccggg gt gtacgtCT GAT T /
ttg gaag C-- GT G

GAM2763 GCTGCAAAGATCAGTGGCTT 2453 TTTACATTGG 5523 T C- - TTTCTAACT TAT
TTCTAACTGCAACTTATGGA CTTACTATAT GC GCAAAGAT AGTG GCT GCAACT G
ACAGTTGTTTACATTGGCTT CTTT || |||||||| |||| ||| ||||||
ACTATATCTTTGTGC CG TGtttcta tcat cgg tGTTGA G

- ta t ttacatt-- CAA

GAM2764 TAGTACATTACTTAATATCC 2454 TCCGTAAGTC 5524 ACTTA- c ta cttt t- ATCA AA
GTAAGTCTTTTTAGTTCATT TTTTTAGTTC TAGTACATT ATAt cg agt ttagt catttTTA ACT C
TTTAATCAACTAACCAAGTA ATTT ||||||||| |||| || ||| ||||| ||||||||| |||
ATAAAAATGTCATTAATGCT GTTATGTAA TATA GC TCG AATTA GTAAAAAT TGA /
CGCGTATATGAATGAAATGT AGTAAG T GC T--- CT AA-- AC
ATTG

GAM2765 CCCTTCGCCGACGCCGTGGC 2455 TGTGGGCTAT 5525 TTCG-- AC A T-- TTC
ACCTGGTTCACCCCCTGTGG GGCCGGAATA CCC CCG GCCGTGGC CC GG A
GCTATGGCCGGAATATTGGG TTGG ||| ||| |||||||| || ||
Ggg ggc cggtatcg gg CC /
ttataa -- - tgt CCC

GAM2766 TTATTATTTGCTATTCTTTC 2456 ATGATATTGA 5526 GC--- TCTT- AT A
AATATATTTAATATTAATGA TAAATATAAA TTATTATTT TAT TCAATAT TTA T
TATTGATAAATATAAAAAAA AAAA ||||||||| ||| ||||||| |||
AATGATAA AATAGTAAa ata agttata aAT A
aaaaa taaat gt T

GAM2767 CAGGTCAACAAAATAATTTG 2450 TGAAATGTTG 5520 ACAAAATAA tg at-- aaatcgctgt- - AA
AAATGTTGGAGAAATCGCTG GAGAAATCGC CAGGTCA TT aa gttggag aCTA CA A
TACTACAAAATATGCTAGTT TGTA ||||||| || || ||||||| |||| ||
TATTTTTATGCTTCAGCTCT GTTCGGT AG TT CGACTTC TGAT GT /
GTTTGGAAGTGGCTTG GA------- GT GTCT GTATTTTTATT C AT

GAM2768 GTGAGAAACAAAGACAAAGC 2457 TATAATATCA 5527 AAACAA - A GA GAC TCGTT A CAC
GAATACGACAAATTCGTTTA TTTAAGTATA GTGAG AGA C AAGC ATAC AAAT TATTA ACGT A
TTAAACGTCACATTTACGTA GTTT ||||| ||| | |||| |||| |||| ||||| ||||
TAATATCATTTAAGTATAGT CACTC TCT G tttg tatg ttta ataat tGCA /
TTCGTTCTGCCAACTCAC AACCG- T C a- aa- ct--- a TTT

GAM2769 CTGCTCGGATGGCGACCGTG 2451 GACCGTGCAC 5521 CTC -------- t actac cc
CACTACTCCCGCCGACCTGG TACTCCCGCC CTG GGATGGC gaccg gc tcccg g
GACCCCGCCGGTCACCCTCA GACC ||| ||||||| ||||| || |||||
CGTCGTCCCCCAG GAC CCTGCTG CTGGC CG AGGGT a
CC- CACTCCCA - CCCC- cc

GAM2770 CGCCAAGACCTTTTCACAGC 2458 GCAGTGCCGT 5528 - CTTTTCACA TTA CACATC
ACTTTATTGTCACATCATCA CATTGGTG CGCCAA GAC GCACT TTGT A
CACACAGCAGTGCCGTCATT ||||||| ||| ||||| |||| GGTG gtggtt ctg cgtga gACA / a c-------- c-- CACACT

GAM2771 ATGATACTTTTATTAATTCT 2459 TCTAATTGGA 5529 T AATTCTTCGTTCt- a - taacaa ct
TCGTTCTCTAATTGGATTTA TTTAACAACG ATGA ACTTTTATT cta ttg gatt cgat T
ACAACGATCTTTGGTCGCAA ATCT |||| ||||||||| ||| ||| |||| |||| TCACAACTAGCTTTTACTTG TATT TGAAAATAA GAT AAC CTAA GCTG /
TCTGAATAAAAGTTTAT - GTCTGTTCATTTTC C A C----- GT

GAM2772 TTAAATATTTAGTTTGATAT 2461 TTAATATTAT 5531 AA TT T TT TTGTA
TTTTGGTTTGTATAATTGTA ATTGTTTATC TT ATA TAGT TGATATT TGGT T
TTATTAATATTATATTGTTT AGG || ||| |||| ||||||| |||| ATCAGG gg tat gtta attataa ATTA A ac tt t tt TGTTA

GAM2773 TTAGAATTAGGACACCGGAA 2462 TAGGACACCG 5532 tagg ggaa aac AAGA
GTGGAACGCCTAAGAGAGCG GAAGTGGAAC TTAGAAT acacc gtgg gcct G
AGGCCCGCGGTGTAGGTTTT GCCT ||||||| ||||| |||| |||| GA AGTTTTG TGTGG CGCC CGGA /
GA-- ---- --- GCGA

GAM2774 GTTATAGCTGGGCACACTTG 2469 TAGCTGGGCA 5539 - gcacac - AC
CGGTTTCCGAACGCAGTCGG CACTTGCGGT GTTAt agctgg ttgcg gtttccGA G
AGATACGTAGTCAGCTAGTA TTCC ||||| |||||| ||||| |||||||| GC CGATG TCGACT GATGC TAGAGGCT C
A ------ A GA

GAM2775 GTAACGAATGCTCGTGTACT 2460 TACGTAGCGT 5530 CGA - CT AA T- CC T
TTATAATTGCATGCCCGATT GTTTTAC GTAA ATGCT CGTGTA TTAT TTGCA GC GAT A
ACAATCTGTTCTGTAAGAAT |||| ||||| |||||| |||| ||||| || ||| AATTATACGTAGCGTGTTTT catt tgcga gcatAT AATA AATGT TG CTA C
AC ttg t T- AG CT T- A

GAM2776 GTATAGAAGAGACGCAGTCA 2463 TAGAAGAGAC 5533 a act c CC TTGT CACACTAT T- CT A
ACTTGCCGGTGCCGTGAAAT GCAGTCAACT gtca tgc GGTG GTGAAA CTC GA GTTTTTA GTTAC A
TGTCTCCACACTATGATGTT TGCC |||| ||| |||| |||||| ||| || ||||||| ||||| TTTACTGTTACAAGGTAATT CAGT GTG TCAC CACTTT GAG CT CAGAAAT TAATG /

AAAGACCTTCGAGTTTTTCA - --- T CT TT-- -------- TC -- G
CTCCACTTGTGTGACGCTCC
TTCGATTAT
GAM2777 AAGTATTATATGTTTCCTAT 2464 TAGTGTAATA 5534 T- TTCC TG GAG C
GTGAGTGAGGCCATGCCTCG TATATTTACT AAGTA TATATGT TA T TGAGGC A
TTAGTGTAATATATATTTAC T ||||| ||||||| || | ||||||
TT ttcat atatata at g GCTCCG /
tt ---- gt atT T

GAM2778 AAAGTATTTACTATTCTGCA 2465 TCTGCAAGGG 5535 T Ttctgc agt c
AGGGAGTGAGGACGCATCCT AGTGAGGACG AAAGTAT TACTA aaggg gagga g
CCAACCTTTTAGTACGTACT CATC ||||||| ||||| ||||| |||||
TT TTTCATG ATGAT TTTCC CTCct c
C ------ AAC a

GAM2779 CGCCGACAAGACCTCAGCAT 2476 TTACTAGCCG 5546 CAAG - --- C - ATGG
GGCTCGGAGGCTATGGATCT TGACCTTGAC CGCCGA ACC TCAG CATGGCT GG AGGCT
A
TGAGCTTACTAGCCGTGACC GGTG |||||| ||| |||| ||||||| || |||||
TTGACGGTGGCTTTGGCG GCGGTT tgg agtt gtgccga tc ttCGA T
TCGg c cca - a GTTC

GAM2780 GCTAATATTCCAGTAAATAA 2477 TCCAGTAAAT 5547 T ---------- a ct - a- CTT
AACTTTTATGAACACTTGTA AAAACTTTTA GCTAATA tc cagtaaat aaa tttat ga CA G
ATGGCTCTGTAAATTTTTCA TGAA ||||||| || |||||||| ||| ||||| || ||
TTTACTGCACTTAAATTTGA TGGTTGT AG GTCATTTA TTT AAATG CT GT /
CTGTTGGT C TTTAAATTCAC C TT T CG AAT

GAM2781 TTATTGGTCGCTAAGTTTAT 2466 TTGGTCGCTA 5536 t --- a tatccctaa GT C
CCCTAATTGTCACGCGTGGT AGTTTATCCC TTA tggtc gcta gtt tT CA G
AAAAACAACAACATAGTCAA TAAT ||| ||||| |||| ||| || ||
GATCGTTAA AAT GCTAG TGAT CAA AA GT C
T AAC A CAACAAA-- TG G

GAM2782 GTGTCTAATGGTGGAAGCGT 2467 TCTAATGGTG 5537 gaa ---- - CC ---- G AG
CG AC
GGCACTGGCCGAAATGATAT GAAGCGTGGC gtg gcgtg gca ctgG GAAATGAT ATATT
CGTAT AG CG A
ATTGCGTATAGAGCGCGACA ACTG ||| ||||| ||| |||| |||||||| ||||| ||||| || ||
AACGAATTAGATGCGAATGT CAC CGTAT TGT GATT TTTTACTA TGTAA GCGTA TT
GC /
GAAGATCATTTTTATTAGAT ATC ACAA A AT GAAG - GA AA AA
GTAACATATGCCTACACCAA
TAGTAC
GAM2783 CCGTGACATTTGACAGACCT 2468 TTTGACAGAC 5538 TGA ttt g ---------- t

GGAATTGTTATTCTGATATA CTGGAATTGT CCG CA gaca acct ggaat g
TAGTGGGTGTGTCTGGCCGG TATT ||| || |||| |||| |||||
GGC GT CTGT TGGG TCtta t
CG- --- G TGATATATAG t

GAM2784 CAACATACATAATGTGCATG 2470 TAATGTGCAT 5540 C a-- c gaa a TCAG CTG
CGAAACCACTTTTTCAGTGT GCGAAACCAC CAACATA At atgtg atgc acc ctttt TGTACG A
ACGCTGACATTGTGCAACAC TTTT ||||||| || ||||| |||| ||| ||||| ||||||
GGAGGGGTAGCATCTACATA GTTGTAT TA TACAT TACG TGG GGAGG ACGTGT /
CAATATATGTTG A ACA C A-- - CACA TAC

GAM2785 CTAATAAGTGGAAGCCAATT 2471 TGGAAGCCAA 5541 ATAAG- aag attaag aagcca
AAGTAGAAGCCAATTAAACC TTAAGTAGAA CTA tgg cca tag A
TAATAAGTGGAAGCCAATTA GCCA ||| ||| ||| |||
AGTAG GAT ACC GGT ATC /
GAATTA GAA GAATA- CAAATT

GAM2786 GGCTTCTACTTAATTGGCTT 2478 TAATTGGCTT 5548 - --- CTT CTT Ttaatt tct--- t
ct
CCACTTATTAGGTTTAATTG CTACTTAATT ACTTAAT TGG CCA ATTAGGT ggct acttaat
gg T
GCTTCTACTTAATTGGCTTC GGCT ||||||| ||| ||| ||||||| |||| ||||||| ||
CACTTATTAGGTTTAATTGG TGGATTA ACC GGT TAATTCA TCGG TGGATTA
TC C
CTTCTACTTAATTGGCTTCC T TTC TTC --- TCT--- TTAATT T AC
ACTTATTAGGTTTAATTGGC
T
GAM2787 CCGTGCCTTATACATCACCC 2472 TATGTTCGTG 5542 T T TCACCCACCCC CT CAGT
ACCCCCGCTCATAATTCAGT ACGTCTTTGT CCG GCCT ATACA CG CATAATT C
CTTTAAATTATGTTCGTGAC ATCA ||| |||| ||||| || |||||||
GTCTTTGTATCAGGCTCGG GGC CGGa tatgt gc gtatTAA /
T c ttctgcagt-- tt ATTT

GAM2788 GGCCGTTCGTATTATAGCAT 2479 TAGCATTGGG 5549 T TATTA cat------ a -- - ac---- -
CATCTTC
TGGGACTCGCTGTTACTGCC ACTCGCTGTT TCG tag tggg ctc gc tgtt tg CCCT A
CTCATCTTCACATCCACAAG ACTG ||| ||| |||| ||| || |||| || ||||
GGACACATCTAGACACGTAG GGC ATC ACCC GAG TG ACAG AC GGGA C
GAGACCCATCACATTCTCTA - TTTCC TCTTACACT A GA C ATCTAC A
ACACCTA
CCTTTCGGCGGCC

GAM2789 GACGATAACTTGATTTCGAA 2480 TAACTTGATT 5550 cga tacc ---------- T
TAAATA
ATTACCCATGGAGATACTTT TCGAAATTAC tgattt aat catGGAGAT AC TTATTACTCCAT
A

ATTACTCCATTAAATAATTT CCAT |||||| ||| |||||||||| || ||||||||||||
ATCATGGAGTGATAATGTCC GCTAAA TTA GTACCTTTG TG AATAGTGAGGTA
/
TGTTTCATTTGTTTCCATGA ACA TACA TTTACTTTGTCC T CTATTT
CATATTACAAAATCGATTCC
GTC
GAM2790 CGGCGCTTTGTCTAGCCCTC 2481 TAGCCCTCTT 5551 TT Ct ctt g t
TTAGTGGGTATTGTTACCGG AGTGGGTATT CGGCGCT GT agccct agt ggta t
CTGGGGTTTTATTGGCGTTG GTTA ||||||| || |||||| ||| ||||
GTTGCGG TA TTGGGG TCG CCat g
T- TT --- G t

GAM2791 TTCAACTTATTAGGTTGTGA 2473 TACCGGAGTC 5543 A - - TTGT AA T
CTCCAATACCATTTTTATGG CTCCGTAATA TTC ACT TATTA GG GACTCC TACCAT T
TACCGGAGTCCTCCGTAATA TAGT ||| ||| ||||| || |||||| ||||||
TAGTCGAA AAG tga ataat cc ctgagg atGGTA T
C t g tc-- cc T

GAM2792 CTAGGCAGAGCCGGCGGGTA 2474 AGAGATCCGT 5544 CAGA C---- T - ------- C
CAG CAC
CATTTTTTCGTCAGACACGG TTTACAAAAT GCCGG GGGTACATTTT TCGT CA GA
ACGGGTC GC C
GTCCAGGCCACCTACAGCAG TGCA ||||| |||||||||| |||| || || ||||||| ||
AGATCCGTTTTACAAAATTG CGGCC TCTATGTAAGA GGCa gt tt tgcctag CG T
CACGGCAGAATGTATCTACG AAA- AAGCA C c taaaaca t aga ACA
AACCGGCAAAACTAG

GAM2793 CGAGGACGGCGAGGCGTCTG 2475 TTTCTCTGCT 5545 - TCT T TTAAA T - TGT G
TTAAAAA
CGTGTTAAACGGCTGTACGC GTCCGGTCGC GGCGAGG CG GCG G CGGCTG AC GCGGGG
GAT TGCTT A
GGGGTGTGATGTGCTTTTAA CTGC ||||||| || ||| | |||||| || |||||| ||| |||||
AAAACTGGCTCTAAGTAGTC CCGTTCC GC cgt c gctggc tg cgtctc CTG ATGAA C
TTTCTCTGCTGTCCGGTCGC A C-- c ----- c t ttt - TCTCGGT
CTGCCCGACCTTGCCGTCTT
CG
GAM2794 GGAATTTTTCTATTTTGATT 2482 TCTATTTTGA 5552 tct attta tatcca-- CT
TATGTCTATCCAGTAACTAC TTTATGTCTA GGAATTTT attttg tgtc GTAA A
CCTTACCGTATCGCGACACG TCCA |||||||| |||||| |||| ||||
AAATTTAGAGTTTC CTTTGAGA TAAAGC ACAG CATT C
TT- ----- CGCTATGC CC

GAM2795 CACACACTGGTGACAACCTG 2483 TACTCTGGTC 5553 AACCT TTCACTGCCATA--- A A TAT
AC A AA-- A
CATTCACTGCCATACGGAGG CCGGACCTAC C GCA CGG GGG AG TCCG GGA
CCA AGC T
GAAGTATTCCGACGGAACCA CCCT | ||| ||| ||| || |||| ||| ||| |||

AAAGCATTTGCTACTCTGGT G CGT Gtc ccc tc aggc cct ggt tCG T
CCCGGACCTACCCCTGACAT CGTC- CTACACATCCATACA - a c-- -- - ctca T
ACCTACACATCTGCCTGCGT
TGCTAGTTTTG

GAM2796 TGAGTGTTGTGTGTACCTAT 2484 TGGGAAAAAA 5554 GT G A-- - A AGGC
TTTCCACTGAGGGAGGCGCG AGGTGGGCAT TGAGT TGTGT TACCT TTTTCCAC TG GGG G
TATTCGCATGTGGGAAAAAA ACAA ||||| ||||| ||||| |||||||| || |||
AGGTGGGCATACAATTTA ATTTa atacg gtgga aaagggtG AC CTT /
ac g aaa T G ATGC

GAM2797 AATGTTTACAATCTAAACCT 2486 TGAGCTAAAT 5556 TTACAATCTAAAC- GAA A
CAGAATCATAAATGTGATGA TTACTAATAC AATGT CTCA TCAT A
GCTAAATTTACTAATACATT ATT ||||| |||| ||||
ttaca gagt AGTG A
taatcatttaaatc --- T

GAM2798 GGTTCTGTTTCTTCTTCCTT 2485 TCTAATGAAC 5555 T TCTTCTTCC TTT TTACGT
T
ATATATTTTTTTATTATTAC ATGTATAGTT GG TCTGTT TTATATAT TTTATTA ATTAT A
GTATTATTACATAATTATCT CCAT || |||||| |||||||| ||||||| |||||
CTAATGAACATGTATAGTTC CC AGACAA gatatgta aagtaat TAATA /
CATAATAACAGATCC T TAAtacctt c-- ctCTAT C

GAM2799 TTGGTTGGGGAGGAGTTCAC 2490 TCACAATATA 5560 G GAGTtc aa aa- ag - c G
GTT- TTG
AATATAAAAGTCAGAGTCTG AAAGTCAGAG TGGTTG GGAG ac tataa gtc a gt tg CGGTGA
ACT G
GCGGTGAGTTACTTTGGTCA TCTG |||||| |||| || ||||| ||| | || || |||||| |||
CGGTTCCGTTACCGGCGCGC ATCAGC TCTC TG ATATT CAG T CG GC GCCATT
TGG T
ATTCGACAAATTATACGGTC G ACCTAC GC AAA CT A C G GCCT CAC
ATCCACTCTGCGACTAA

GAM2800 GGCGTTGCCCCGGTTCGGTG 2491 TAACTCGAAC 5561 C TG CCC - GAT C GTCTTAT
ATCACCGGGTCTTATCTATA CCCCGTGACT GG GT C GGTTCG GT CAC GG C
TACACCGTGTAACTCGAACC CC || || | |||||| || ||| ||
CCCGTGACTCC cc ca g ccaagc ca GTG CC T
t gt ccc t at- - ACATATA

GAM2801 AAATTGGCCTCTTTATATGT 2487 TATGTTTTTT 5557 T - tt gctttc - TTTTTT G AAG
GTG
TTTTTGAGATGCTTTCCGTT GAGATGCTTT TTAta tgtttt gagat cgtTGGCG C GC GTT
TTGT A
GGCGCTTTTTTGCGGTTAAG CCGT ||||| |||||| ||||| |||||||| | || ||| ||||
TTGTGTGAAAGAACGAAGGA AGTGT GTAAAG CTCTA GTAATCGT G TG CAG
AGCA A

CGGTGTTGCTAATGCTTTAA T C GC ATTTC- T ------ G GA- AGA
TCTCCGGAAATGCTGTGATA
TGGCGCGATTT
GAM2802 ATAGCTTAGATAATATAGAT 2498 GATAATATAG 5568 - ga-------- tagattt tt
TTTGATTCACTCATAAACAT ATTTTGATTC ATAG CTTA taata tga c
TATTAAATTAGAAAATAAGA ACTC |||| |||| ||||| |||
CTAT TATC GAAT ATTAT Act /
A AAAAGATTAA TACAAAT ca

GAM2803 GCTGCTTGTGGCTTTTAACC 2492 TGTCAGAGAT 5562 TGT TAAC------ ACT T CACACA-- --- G AA
AGTCACTAGTCACGCCCACA TCAAGAGGTG GGCTTT CAGTC AG CACGCC
TGAC AGGA A
CATGACGAGGAAAAACTCCT TGTC |||||| ||||| || |||||| |||| ||||
GTCAGAGATTCAAGAGGTGT CCGAAA GTTAG Tc gtgtgg actg tCCT /
GTCTTAAGATTGCAGAAGAA CT- TCAAGAAGAC AAT t agaacttagag - CA
CTAAAGCCTCTCCAGC

GAM2804 TTCCACCAAAGATAATTATA 2488 TAATTTACAA 5558 A TAA ATT CCAT ta aaaag tt - A AG
ATAATTTACCCCATCATTAA AAAGTGTTTA ATTA TA TACC CAT atttaca tg taca gcT GCTTA T
TTTACAAAAAGTGTTTACAG CAGC |||| || |||| ||| ||||||| || |||| ||| |||||
CTAGCTTAAGTGGTAGGTAG TGAT AT ATGG GTA TGGATGT AT ATGT TGG TGGAT /
GTATGTAGGTATGTAGGTAT A TCG GT- AT-- -- ----- GG A A GG
GTAGGTATGTAGCTTAGTAG
TTTAGTGTAA
GAM2805 TTCAGGTGTAGACCCGTCAT 2502 GTGCATTTAT 5572 - AT TG ---------- ------ TG TT
TGTGACGCGTGGGTTGAGGT CTCAACAGTT CCC GTC TG ACGCGTGG GTTGAG G CCATGAAT G
GCCATGAATTTGTCATTCAT TTCC ||| ||| || |||||||| |||||| | ||||||||
GGTGCATTTATCTCAACAGT GGG CGG GC TGCGCGCC caactc c gGTACTTA /
TTTCCCTAACCGCGCGTTGC A C- GT AATCccttttga tattta gt CT
GCGGCAGGGTTTTTACTCTG
AG
GAM2806 CGCTGTTTTCGCGGTCCCGC 2489 TCCCGCTCGG 5559 TTTT t - g tgt c
TCGGGCTGTCGGCGTCCGTG GCTGTCGGCG CGCTG CGCGG cccgc tcg gc cgg g
CGCGGCGCGGGCCCGCGTTC TCCG ||||| ||||| ||||| ||| || |||
CGGCG GCGGC GCGCC GGGCG GGC CG gcc /
CTT- C C G T-- t

GAM2807 GGCACAGTCTCGCGTCAAGA 2493 AAGAGGCCGG 5563 C CAAGA C - GC---- AGCGCAC G A AGC
AGGGCCCGGAGCCCCTCCGA AGGGAGGAGA CTCG GT AGGGC CG GA CCCTCCG GCCT TT TCCC T
GCGCACGCCTGTTATCCCAG TCTT |||| || ||||| || || ||||||| |||| || ||||

CTCTCGGGGAAGAGGCCGGA GAGC CG TCCCG Gt ct gggaggc cgga aa GGGG
/
GGGAGGAGATCTTGAGCCCT T AGG-- A t agagga ------- g - CTC
GGAGCTCGAGACCTTGGCC

GAM2808 TGACGCCCTCTCTATTCTTT 2503 TATGATGATT 5573 A TTAt a at g ---------- A
AACGT
ATATGATGATTTAAGATTGA TAAGATTGAG TTCT atg tg ttaagattga tcca AC TTTTTCC
T
GTCCAACATTTTTCCAACGT TCCA |||| ||| || |||||||||| |||| || |||||||
TTTACAGGAAAAAGGTATTT AAGA TAT AC AATTCTAATT AGGT TG AAAAAGG
/
TTAACTATGGAATTAATCTT A TT-- C CC A ATCAATTTTTA G ACATT
AACCCACTATTTAGAAAAAA
ATAAAAGACA
GAM2809 TCCCTCATACCGCCTCGTGT 2499 TAAGTGGCTG 5569 C-- - C CG A---------- GT
GTCCAGTGTGTAAACTTCCA TGACCTGGA TCC TCATA CCGC T TGTGTCC GT G
GGTTCTAGTTTTGGGGATAT ||| ||||| |||| | ||||||| ||
ATAAGTGGCTGTGACCTGGA agg agtgt ggtg a ATATAGG CA T
tcc c - at GGTTTTGATCTTGGACCTT AA

GAM2810 CGGCCTGGGTGGGCGGAGGG 2504 TCCGTCCCCG 5574 - T--- ---------- AA
AACTAACCCAACGTATAAAT TTCCAAGGCC CGGCCT GGG GGGCGGA GGG C
CCGTCCCCGTTCCAAGGCCG G |||||| ||| ||||||| |||
gccgga cct cctgcct CCC T
a tgcc AAATATGCAA AA

GAM2811 CCTCATGCGGAACTCGTGCC 2494 TTCATATTTT 5564 C ACTC- GCCAAATTATAATC T
TG T- T T
AAATTATAATCTTGATGTGT AAAAACCCAA TG GGA GT TTGA GTGTG TAATATA
ATATT ATG A
GTGTAATATATATATTTATG CTCC || ||| || |||| ||||| ||||||| ||||| |||
TATTTATCAATGTTTTATAT AC cct ca aatt tatac GTTATAT TGTAA TAT T
TGTTCATATTTTAAAAACCC A caacc aa---------- t tt TT C T
AACTCCACATAGAAGG

GAM2812 GGACCCACCGGAACGGAGGG 2509 ACACAGCCGC 5579 A- A- AC A A ACC---- AAA--
CC
AGCGACCCGGCAAAGGCCCC ACAACCCGCC GG CCC CCGGA GG GGG GCG CGGC
GG C
ACCACACAGCCGCACAACCC CCCC || ||| ||||| || ||| ||| |||| ||
GCCCCCCTCCGGAAGGGAAC CC GGG GGCCT cc ccc cgc gccg CC /
C AA AA -- - - ccaacac acaca AC

GAM2813 ACCACCAGATACATTCTGTA 2495 GAGCAGGTGT 5565 A T AAA GTTT--- ---------
GG
AATAGTTTGCTGTGGTTGCT ATCTGGGGT ACC CCAGATACAT CTGT TA GCTGTGGT
TGCTTA G

TAGGGAATAGGCATAGAATA ||| |||||||||| |||| || |||||||| ||||||
CAACCATGGTTATAAGATAG tgg ggtctatgtg gacg AT TGGTACCA ACGGAT /
AGCAGGTGTATCTGGGGT - - ag- AGAATAT ACATAAGAT AA

GAM2814 CCGCTCGATAGATCGCGTCG 2496 AGGAAGTACC 5566 TCGA - ggaa aac accac
C
AGGAAGTACCAACCGTGACC AACCGTGACC CCGC TAGA TCGCGTCGa gtacc cgtg
tcCTC G
ACTCCTCCGGCGGGGATCCT ACTC |||| |||| ||||||||| ||||| |||| |||||
CCGCGACGGGTACATCGACG GGCG ATCT AGCGCAGCT CATGG GCGC AGGGG
G
CGATTCTACGCGG C--- T A--- GCA CTCCT C

GAM2815 GTGTCGTTTGTTGTGGGTGG 2500 TCGTTTGTTG 5570 c t tg- gg tataTACTATTTAAG AC
GATTATATACTATTTAAGGC TGGGTGGGAT GTGt gtt gttg ggtg at GC A
ACATTGTAAAATACGGACTT TATA |||| ||| |||| |||| || ||
TCATTTCACCAATCAACCAA CACA CAA CAAC CCAC TA TG /
CCACAC C C TAA TT CTTTCAGGCATAAAA TT

GAM2816 TGGCTACTTGGCAGTTACAA 2505 TACTTGGCAG 5575 ta---- tt agtt c TG
GTTCACCTCTGCCAGAAGTG TTACAAGTTC TGGC cttggcag aca cac tC C
TGTTTTTGCCAAGACATTTG ACCT |||| |||||||| ||| ||| ||
CCA ACCG GAACCGTT TGT GTG AG /
TTTACA TT ---- A AC

GAM2817 AATCTGAACTTCATCGAAAC 2510 TATAAACCAT 5580 AAC TCGAAACTCTCAT- c---- c
cat
TCTCATCTATAAACCATCTC CTCACTTACA AATCTG TTCA Ctataaac atct actta t
ACTTACATTATTTAAGTAGA TTAT |||||| |||| |||||||| |||| |||||
TTCCTAGTTTATAGTTATAT TTAGAC AAGT GATATTTG TAGA TGAAT /
AAAACAATTGAATACCAGAT CAT TAACAAAATATATT ATCCT - Tta
T

GAM2818 GCCGGCGCCGCGACGCGTCG 2497 CGTCGTCGGG 5567 - - G - AGAC
GCGCCAGACGAGCGGGCGCC CGATCGAGC GC CGG CGCC CGACG CGTCGGCGCC G
GGCGTCGTCGGGCGATCGAG || ||| |||| ||||| ||||||||||
C cg gct gcgg gctgc gcGGCCGCGG /
a a - t GCGA

GAM2819 TCTCTCCGCCCAGTCTCCGC 2501 CATCCGCAGG 5571 C- GCCCAGT - CTAA AA
CTAAGGGAAACCAGTCCCAT AGTCCCTCAG TCT TCC CTCC GC GGGA C
CCGCAGGAGTCCCTCAGGAC GACA ||| ||| |||| || ||||
AAGA AGA agg gagg cg cCCT C
ac actccct a ccta GA

GAM2820 GGTTTTAAAGTTTATGTATT 2506 TTTACATTAT 5576 G -- TG TT T- ATTAAA TG T - A CTT
ATTGTTTCTATATATTAAAA TCGTGATTGG A TTTA TGTATTAT T CTA AT AAT T GA AAT TAAATAT A
ATTGTTGAAATATAAATATC GACG | |||| |||||||| | ||| || ||| | || ||| |||||||
TTATGTAATGTTTACATTAT T GGAT ACGTGGTG G GAT TG tta g tt tta atttGTA T
TCGTGATTGGGACGGTCTTA G CA GA GG TC gcaggg gt c a c ATG
GGGGAGGTGGTGCAACTAGG
GTTTAAAGCC
GAM2821 TTTGCTACAGCTTATATAAA 2511 TACATTGCCT 5581 TG T-- - TTA- TT - A CT
TTTATGTGCGATACATCTTA GTCACGTGAA TT C ACAG C TATAAAT ATGTGCG AT CAT T
AGTGCATCCGTACGTTATTT || | |||| | ||||||| ||||||| || |||
ATACATTGCCTGTCACGTGA aa g tgtc g atATTTA TGCATGC TA GTG /
A gt cac c ttac T- C C AA

GAM2822 AATAAAAATTTCATAAATTC 2512 TAAAAATTTC 5582 t c ttcatat TT
ATATAAAGATTTTGTTTTTT ATAAATTCAT AAtaaaaa tt ataaa aaAGA T
TTTCTTTTTATTAATTTTTT ATAA |||||||| || ||||| |||||
ATT TTATTTTT AA TATTT TTTTT T
T T TTCTTT- TG

GAM2823 TATTTTTGTTTGAAGAAAGA 2515 TGTTTGAAGA 5585 tg- agaatgcc AATC
ATGCCATAATGACGTAATCA AAGAATGCCA TATTTT tttgaagaa ataatGACGT A
ATAAAATGTCATTATTTTTT TAAT |||||| ||||||||| ||||||||||
CAAAAATAAAATA ATAAAA AAACTTTTT TATTACTGTA A
TAA -------- AAAT

GAM2824 TACCTTCGTCCAATTGGTTA 2513 TAGCGCAGTT 5583 CTT A T --- T T--- TTGTC
ATCTGTGCTTCACTTGTCAC TATACACCTA TAC CGTCC AT GGT TAA CTGTGCT CAC A
CGGTTGTGTAATAGCGCAGT TAGG ||| ||||| || ||| ||| ||||||| |||
TTATACACCTATAGGGCGCC ATG GCGgg ta cca att gacgcga GTG C
TGTA TCC a t cat t tAAT TTGGC

GAM2825 TCCGCTTTAATAGCAGTACA 2514 AGCAGTACAT 5584 C TT - - tcagt tt
TTCAGTGAGGTTTTACCTCC TCAGTGAGGT TC GC TAATag c agtacat gagg t
ATATGTGCTAGTCTGTTATT TTTA || || |||||| | ||||||| ||||
GTCGA AG TG ATTGTC G TCGTGTA CTCC /
C TT T A TAC-- at

GAM2826 CTTAATGGTTCATTCGTTCG 2507 TAATGGTTCA 5577 t tcatt c- tat-- TT
TATATTCTTTTTCGATTTTT TTCGTTCGTA CTtaa ggt cgtt gta tC T
TATTCAACGCTAATACCTTA TATT ||||| ||| |||| ||| ||
AG GAATT CCA GCAA TAT AG T
- TAATC CT TTTTT CT

GAM2827 TTCTTTTATGACGGATAATG 2508 CGACAACAAG 5578 GATAATGTA C-- - -- CAGG- G
TC G A A
TAGCGGCCGATTCAGCGTCC TGCATGAAAT GCGGC GAT TCAGC GTC TC ATG
CTTGTTG TC AC A
AGGTCGATGTCCTTGTTGGT TAGA ||||| ||| ||||| ||| || ||| ||||||| || ||
CAACAAAGTCGACAACAAGT CGCTG CTA AGTTG Cag ag tac gaacaac ag TG /
GCATGAAATTAGACTCGTTG --------- CTC T CT attaa - gt - c A
ATATCCTCGTCGCTCATTTA
AGAA
GAM2828 GTGAGCCCGGCCGGCGGAGC 2516 CACCCGGAAA 5586 -- --- G AGC GAC TTTATA
T
CTCCGACCCTTTATAGCGTT GGAGAACCGC GTGAG CCC GGCCG CGG CTCC CC
GCGTT G
TGTGACGCACCCGGAAAGGA GGCC ||||| ||| ||||| ||| |||| || |||||
GAACCGCGGCCGCTGGGTCC CACTC GGG ccggc gcc gagg gg cGCAG /
TCAC CT TCG - aa- aaa ccca-- T

GAM2829 GCTTAATTTTTAGATATAGT 2521 AGTTGTAGAA 5591 TAGATA GA- ATAA
TGAATAATTGCAAATAATGT ACTACAGTTA GCTTAATTTT TAGTT ATAATTGCAA T
AGTTGCAGTTGTAGAAACTA AAAT |||||||||| ||||| ||||||||||
CAGTTAAAATTAAGC CGAATtaaaa atcaa tgttgaCGTT /
ttgac- aga GATG

GAM2830 CTTCGCCAGGGAAGGGATTC 2517 CACCCGGAGT 5587 C C A--- T c agtacttt a ac
ACCCGGAGTACTTTTGCATC ACTTTTGCAT CTT GC AGGGA GGGAT cac cgg tgc tc c
ACCCGCGAGCACTTTGAGGC CACC ||| || ||||| ||||| ||| ||| ||| ||
CGAGTGCATCCCCGACTCTC GAA CG TCTCT CCCTA GTG GCC ACG AG C
TGCAAG - - CAGC C A GGAGTTTC - CG

GAM2831 TTATTTTTTTTTTTTTATTA 2518 TACAATATAA 5588 TTTT--- A
TATTGTATTATTTAATACAA TAAAATATAT TTATTTTT TTTTATTATATTGTATT T
TATAATAAAATATATTTAAA TTAA |||||||| ||||||||||||||||
AATAA AATAAAaa aaaataatataacaKAA T
tttatat T

GAM2832 AGGAATGCCGTAGTCCTGTC 2528 TGCCGTAGTC 5598 AA --- t ct gga tAG C
GGAAGCTTTAGTGTGAGCCT CTGTCGGAAG AGG tgc cg agtc gtc agctt TGTGAG C
CTCACGGATAAGCTCGAGAT CTTT ||| ||| || |||| ||| ||||| ||||||
TAGACTCCGTTTGCAAGCCT TCC ACG GC TCAG TAG TCGAA GCACTC /
GA TTT C AT AGC TAG T

GAM2833 GGTGGCCGGCAAGGTGCAAT 2519 TCTAACATCT 5589 G -- ---- TGCA T TG T
GTTTAGTGAGTTACCTGTCT CCCCTTTAAA GGTG CC GGC AAGG ATGTT AG AG T

```
      AACATCTCCCCTTTAAAGCC       GCCA           |||| ||  |||   ||||   ||||| ||  ||
      AAGGCACC                     CCAC GG  ccg   ttcc   tacaa tc  TC A
                                 -  Aa   aaat   cctc   -  tG  C

GAM2834  GGAAATATGTAAGTTTGTTA 2522   TTAAAGCAGC 5592        GT-   TTGttaa   -  g    t
      AAGCAGCCAGTGTGACTTTG       CAGTGTGACT       GGAAATAT   AAGT      agcagc ca tgtgac t
      TCATGTGTGTTGTTGTTACT       TTGT           ||||||||  ||||     |||||| || ||||||
      TTCTGTATTTTC                 CTTTTATG   TTCA      TTGTTG GT GTACtg /
                                 TCT   TTG----     T  -     t

GAM2835  CTCTTTCCACCATCTTTTAG 2523   TAACTAAGAA 5593                                                AAAAAT
      TTGTATTCTTAGTTATCAAT       TACAACTAAA
CACCATCTTTTAGTTGTATTCTTAGTTATCAATAAAGGCGCGAAGCGCCATA     T
      AAAGGCGCGAAGCGCCATAA       AGAT           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      AAAATTATGTCATATGGCGC
GTGGtagaaaatcaacataagaatcaatAGTTATTTCCGCGCTTCGCGGTAT     /
      TTCGCGCCTTTATTGATAAC                                                    ACTGTA
      TAAGAATACAACTAAAAGAT
      GGTGGAAAGAG
GAM2836  CTGAGGGCTTTTCTAGTTTC 2520   TTCTAGTTTC 5590         Ttt    tt  gctg    tt
      CGCTGTGAGGTTTTACCTCG       CGCTGTGAGG       CTGAGGGCT   ctagt  cc   tgagg  t
      AAGGTTGCTAGTCTGGTTTT       TTTT           |||||||||  |||||  ||   |||||
      CAG                          GACTTTTGG   GATCG  GG   GCTCC  /
                                   TCT    TT  AA--    At

GAM2837  ATTAAATTTTTAAACATTCC 2524   TAAATTTTTA 5594        -   -     ttccttaaaaTC-     ATCTAAAC
AGTA
      TTAAAATCTATGTATCTAAA       AACATTCCTT       ATtaaa tttt taaaca          TATGT      GTGAC    A
      CGTGACAGTAAATCAGTCAT       AAAA           ||||||  |||| ||||||          |||||      |||||
      CCTGACATATTCTATTCCAT                    TAATTT AAAA ATTTGT          ATACA      TACTG    /
      TTTGTTTATAAAATTTTAAT                      T   T     TTTACCTTATCTT     GTCC----     ACTA

GAM2838  TTGACTTTGCATTTCTCTTA 2529   TACAGGGTCT 5599       CTTT   T    TTAA--       TTG   C
      ACTTGTGATTTGATTCTAGA       GTGGGAACTG       TTGA   GCA TTCTC     CTTGTGAT   ATT T
      GTACGTTACAGGGTCTGTGG       CTTT           ||||    ||| |||||     ||||||||   |||
      GAACTGCTTTTTCGA                    AGCT    cgt aaggg     ggacatTG   TGA A
                                 Tttt   c     tgtctg       CA-   G

GAM2839  GCGTTATTGGAGTTAACGGT 2535   TCGAACACCC 5605         TG  -   AC   TATGG     T
      TATGGTGAGACTTTGTCTCG       TAACTTTTGA       GCGTTAT  GA GTTA  GGT     TGAGAC T
      AACACCCTAACTTTTGATAA       TAAT           |||||||  || ||||  |||     ||||||
      TGC                          CGtaata  tt caat  cca     gctCTG /
                                     gt  t    c-   caa--      T
```

GAM2840 GTGGATAAATTCGCAAGGGT 2525 TCCGCCGTGA 5595 A AT AG T A G AA
ATCATGGCGGACGACCGGGG TCCATGCGGT GTGG TAA TCGCA GG ATCATGGCGGACG
CCGGG TTCG C
TTCGAACCCCGGATCCGGCC TACC |||| ||| ||||| || |||||||||||| ||||| ||||
GTCCGCCGTGATCCATGCGG CGcc att ggcgt cc tagtgccgcctGC GGCCT AGGC /
TTACCGC - -- a- - C - CC

GAM2841 TAGACGACCGGTTTATCATT 2536 ACCGGTTTAT 5606 ac atcattaattaatac GT
AATTAATACAATGTCTAAAT CATTAATTAA TAGACG cggttt aAT C
TCCATAACATATTACAAAAT TACA |||||| |||||| |||
CGCCGTCTA ATCTGC GCTAAA TTA T
C- ACATTATACAATACC AA

GAM2842 GCAGGTGTCACCGAGGTTGT 2530 AGGTTGTCGC 5600 --- A- Gag- cgc cat atg
CGCTGTCCCATCTTATGTGA TGTCCCATCT GCAGGT GTC CC gttgt tgtcc ctt T
AAAGTGGACGAATAACGAGA TATG |||||| ||| || ||||| ||||| |||
GGGAGACGAGATCTGC CGTCTA CAG GG CAATA GCAGG GAA /
GAG AG AGAG A-- T-- AAG

GAM2843 CACACCCAAGAACAACGATA 2526 TAATATCGTT 5596 CCC C- GGA ATCA
TGGATGATCACGACAACAAT TTTTCTTTGT CACA AAGAA AACGATAT TG C
AATATCGTTTTTTCTTTGTG G |||| ||||| |||||||| ||
gtgt ttctt ttgctata AC G
--- tt atA AACA

GAM2844 TTTGAAAAAGAGGGAGGGGG 2527 TACATTATCA 5597 G G G ATTT TTTAAG A-------
------- A
TGGTAATTTATGTGTTTTTT ACTCATCAAG GA GGG TGGTA ATGTGTTT GAAGTGGA
GAG C
AAGGAAGTGGAAGAGACTCT CTTA || ||| ||||| |||||||| |||||||| |||
CATATGTATACACAAGTTCA ct ctc actat tacatAGA TTTCACTT CTC /
CTTTATTTCAGATACATTAT a a a ---- CTTTA- GAACACATATGTATA T
CAACTCATCAAGCTTAAATT
CAAA
GAM2845 CCAACAATGTGATCTTGCTT 2531 AACAATGTGA 5601 tgatc g---------- A
GCGGAGGCAAAATTTGCACA TCTTGCTTGC CCaacaatg ttgcttgcgga GCAA A
GTATAAAATCTGCAAGTAGT GGAG ||||||||| |||||||||| ||||
GCTATTGTTGG GGTTGTTAT GATGAACGTCT CGTT /
CGT-- AAAATATGACA T

GAM2846 GCACGTGCCGTGCTGTCTCT 2532 TTCGCGCCGC 5602 A C - TC C CTTt c c- - cat
ac
CGCCCGACTTTTCGCGCCGC GGGCACATGG GC CGTGC GTGC TGTC TCGC CGA tcg gc
gcg ggca gg g
GGGCACATGGACGGCGCCTT ACGG || ||||| |||| |||| |||| ||| ||| || ||| |||| ||

TGCCACGCCAGCCCGACTTC CG GCGCG CGCG ACGG AGCG GCT AGC CG CGC CCGT CC g
TCGCGCGACTGGCACGCGCC - C C TC C CTTC C AC A TT- GC GCGCGGC

GAM2847 TCTTTACTTTTAAGAATGAA 2533 TTTAAGAATG 5603 Ttt- at t -- t
TGAGATGAGGGTGGCCCTCA AATGAGATGA TCTTTAC taaga gaa gaga tgaggg G
AATCTCTTCCTCTTATCGTG GGGT ||||||| ||||| ||| |||| ||||||
TGAAGA AGAAGTG ATTCT CTT CTCT ACTCCC /
TGCT C- - AA G

GAM2848 CTCATCTTTGGTGTGATTAG 2534 TTCACATTTG 5604 - TGGT ------- T
GTGTGGTGTAACTTTGTTAC ATTATGAGAT CTC ATCTT GTGATTAGGTGTGG TGTAAC T
GTATCCTTTCACATTTGATT AGAG ||| ||||| |||||||||||||| ||||||
ATGAGATAGAG gag tagag tattagtttacact GCATTG /
a ---- tTCCTAT T

GAM2849 CTGATACTTTGGAACTGTAT 2537 AACTGTATAC 5607 GAT TT a aa g CC---- TT
ACTAAGCCAAGTTTAGGCCC TAAGCCAAGT CT AC TGGaactgtat ct gccaa tttagG CG A
GTTATGCGATAAATCCTAGG TTAG || || |||||||||| || ||||| |||||| ||
TTGGTGGAGAATACGGTTTC GA TG GCTTTGGCATA GA TGGTT GGATCC GC /
GTTGTTGAAG AGT TT A GG - TAAATA GT

GAM2850 TAGCACCACCCGATCGTAAA 2538 TTTCATGGAG 5608 CC CGATCGTAA TATT ACCCAT GAAAACTCT
CTCCATGTATTGGTTACCCA TGGTTTGCTA TAGCA ACC ACTCCATG GGTT CTGCATC C
TCTGCATCGAAAACTCTCCG ||||| ||| |||||||| |||| |||||||
AACACTAGGTGCAGTAAGGC atcgt tgg tgaggtac tCGG GACGTGG /
TTTCATGGAGTGGTTTGCTA t- --------- tt-- AAT--- ATCACAAGC

GAM2851 ATTAGAATACAGAGTGGCTG 2539 TAGAATACAG 5609 - a t g ac TCTA
CGCCACCGCTTCTATTTTAC AGTGGCTGCG ATtagaa tac gag ggctgc cc CGCT T
AGTGAGGGTAGCCCTCCGTG CCAC ||||||| ||| ||| |||||| || ||||
CTTTTAGT TGATTTT GTG CTC CCGATG GG GTGA T
C C - - A- CATT

GAM2852 GTTCTGGTAGTCTGTCAGTT 2540 TAGTCTGTCA 5610 -- a t agt ag aaG
CGGAGAGTTAAGAAAAAACT GTTCGGAGAG GTTCT GGt gtctg c tcgg agtt A
ACCGGTTGTAGATGACCAAA TTAA ||||| ||| ||||| | |||| ||||
GGAC CAGGA CCA TAGAT G GGCC TCAA /
AA G - TT- A- AAA

GAM2853 GCTACTACGACGACTAAGCC 2541 TAGCGTGTCG 5611 TACT A TAA CCAAGA AACA G - - TG T

CAAGACGAACAACGTGCGCG ACGTCCATGC GC ACG CGAC GC CG AC TG CGC G CG
A
TGCGTACCGTGCGGCGACAG || ||| |||| || || || || ||| | ||
GTGACGATAGCGTGTCGACG cg tgc gctg cg GC TG AC GCG C GC /
TCCATGC tacc a tg- atA--- AG-- G A G GT C

GAM2854 GGCCATTCAAGTCTATTTTC 2542 TTAGTGCATT 5612 CATT CTATTTTCCCAA CTACC
ACCCA
CCAAGCACTACTACCACACC TGCAGCC GGC CAAGT GCACTA AC A
CAACAGCAGTCCTTTTAGTG ||| ||||| |||||| ||
CATTTGCAGCC ccg gttta cgtgat TG /
ac-- ---------- tTTCC ACGAC

GAM2855 GTGGGCGCCCTACGTCGGAC 2545 TCGCTGCGTG 5615 C CC- T ACTA TCT
TATGGGACCTCTGACGCGGT ATCGCCCCAC GTGGG GC TACG CGG TGGGACC G
CTCGCTGCGTGATCGCCCCA ||||| || |||| ||| |||||||
C caccc cg gtgc gtc gctCTGG A
- cta - ---- CGC

GAM2856 CGACGGTCTTTCTTTTCCGC 2543 TCCGCGTGTC 5613 CT Tt cg- g ----- t T A
GTGTCGGGTGACGTAGTTTT GGGTGACGTA CGACGGTCTTT T ccg tgtcgggt ac gtagtt
TCCTC TGT G
CCTCTTGTAGCAACGTGAGG GTTT |||||||||| | ||| |||||||| || |||||| ||||| |||
ACGACTACTCCGTGTGGCTC GTTGTCGGAAA G GGC GCAGCTCG TG CATCAG
AGGAG GCA C
GACGGTACGGTGGTCAAAGG CT GT ATG G TGCCT C T A
CTGTTG

GAM2857 TACTGTAGGAAAAAAAAGGA 2544 TGACGAGTTT 5614 -- AAAAAAGGATGG G T- TTC
C
TGGTTGTCGATGTATTGGTT CTACGAGGTA TACT GTAGGAA TTGTC ATG ATTGG
AGACGG T
CAGACGGCTTTCCGTCTATT |||| ||||||| ||||| ||| ||||| ||||||
CAATTTCATGACGAGTTTCT atgg catcttt agcag tAC TAACT TCTGCC T
ACGAGGTA ag g---------- - TT TA- T

GAM2858 ATAATTGTTCAGCAGAATGA 2550 TTGGATCATA 5620 TCAGCAGA TTT TT
TCCTTTACCCCTTTTGGGGG GTCATCATAA ATAATTGT ATGATCC ACCCC T
TTTGGATCATAGTCATCATA TTAT |||||||| ||||||| |||||
ATTAT tattaata tactagg TGGGG /
ctactga- tt- GT

GAM2859 TTTCACCTAATTATTTAATT 2551 TTTATCGATA 5621 CC T ATtt taat--- tc CC A
TTATCGATAATTTTTCTCCT ATTTTTCTCC TTTCA TAAT ATTTA tatcga ttttc ctttt AAAT T
TTTCCAAATATTATTTCTAA TTTT ||||| |||| ||||| |||||| ||||| ||||| ||||

AAGTTGAAAATATGAATTTG GAAGT ATTG TGAAT ATAGTT AAAAG GAAAA TTTA /
ATATACTAAGTGTTATGAAG -- - CAT- TAAGTAT TT TC T

GAM2860 GGGAAGCCGGGGAGTCACCA 1933 AGTCACCAAC 5003 AA-- G Gag a aaccca aa
ACCCACCCTGAATCGACAGG CCACCCTGAA GGG GCC GG tc cc ccctg t
GCAAAAAGGGAAGCCGGGCA TCGA ||| ||| || || || |||||
CCGCCC CCC CGG CC AG GG GGGAC c
GCCA G GA- - AAAAAC ag

GAM2861 TTGGCCATAGCTTCGCTATA 2546 TCCATGGTGT 5616 G -- AT T
CCCCACCACAACCACCACCA GGTGGTGGTG
CATAGCTTCGCTATACCCCACCACAACCACCACCACCAC ACC GGACAC GGCC T
CCACGACCGGACACATGGCC GTTG ||||||||||||||||||||||||||||||||||||||||| ||| |||||| ||||
TTTGGCCGTGTCCATGGTGT GTATCGAAGCGATATGGGGTGGTgttggtggtggtggtg tgg
cctGTG CCGG /
GGTGGTGGTGGTTGTGGTGG - ta -- T
GGTATAGCGAAGCTATGGCC
AA
GAM2862 GAGCGGACACGGTTATCGTT 2547 TAAACGCGAG 5617 AC TTATC C- G GA A
CCTGGCGGATATAAGTATAT TTAGCCTTTC GAGCGGAC GG GTT CT GCG TATA G
AAACGCGAGTTAGCCTTTCC CCGT |||||||| || ||| || ||| ||||
CGTCCGTTT TTTGCCtg cc cga ga cgc atAT T
c- tttc- tt g aa A

GAM2863 GGCGTCCGCGTGTCTAAACC 2552 GTTTGCTTCC 5622 G C AACC T T
GCGTGCTCGCTGACGCGGGT TATATAGTGG GGCGTCCGC TGT TA GCG GCTCGC G
TTGCTTCCTATATAGTGGAC ACGT ||||||||| ||| || ||| ||||||
GTC Ctgcaggtg ata at cgt tgGGCG A
- t cctt t C

GAM2864 GAAACAAGCAATATATTCTT 1934 TCTTAAGTTA 5004 A AA tctta tatag- tcaaacCACATCA
TAT
AAGTTATAGGTACGTCAAAC TAGGTACGTC GA AC GCAATATAT agt gtacg AGG A
CACATCAAGGTATATCCCCT AAAC || || ||||||||| ||| ||||| |||
CTCTTTATAAACTGTACAAT CT TG TGTTATATA TCA CATGT TCC /
CATACTCATATATTGTAGGT A GA C---- TACTAA CAAATATTTCTC- CCT
ATC

GAM2865 ATAGTAAAACCTCCCGAATC 1935 TGCCTCGGGA 5005 AAA CC ATCTCA T A
TTCTG
TCAGTCTCTCGAAGCGTGGT GCTCGAAGGG ATAGT ACCT CGA G CTCTCGA GCGTGG
C
TCTGCCAGCGTCCATGCCTC TGCT ||||| |||| ||| | ||||||| ||||||
GGGAGCTCGAAGGGTGCTAT TAtcg tggg gct c gagggct cgtACC C
--- aa ------ - c TGCGA

GAM2866 CTGTTGACAGGTAGAGATCC 2548 GACAGGTAGA 5618 Tga tccc taA TA C
CGGGAGGTAAAGGTGCATAG GATCCCGGGA CTGT caggtagaga gggagg AGGTGCA GG A
GCACACCTGCGCCTGACTCT GGTA |||| |||||||||| |||||| ||||||| ||
CCTTTTCTACCTGACCGCAG GACG GTCCATCTTT TCCTCT TCCGCGT CC C
CCA ---- CAG -- A

GAM2867 TTAAATTTTTATCACTCTAT 2553 TGAAAAATGA 5623 AT ACTCTATA ACC AAT
ATTTTCAACCTTTAGAAATA AAAAAATTAA TTAA TTTTATC TTTTCA TTTAGA A
GTATCTGAAAAATGAAAAAA AGAT |||| ||||||| |||||| ||||||
ATTAAAGATAGAATTAA AATT AAGAtag aaaagt aagtCT /
-- aaattaaa aaa ATG

GAM2868 GATAATTTTTCTCACTTTCC 2549 TTGAAATTAG 5619 TTT- CA - CT---- TT
AAATATTAATTCTAATTTTT TATTATGGAA GATAATT CT CTTTCCA AATATTAATT AATT T
AATGATTTCTTGAAATTAGT AGAA ||||||| || ||||||| |||||||||| ||||
ATTATGGAAAGAAGTTTTGA CTATTAG Ga gaaaggt ttatgattaa TTAG A
TTATC TTTT a- a agttCT TA

GAM2869 GATACGGGCGCGGTTAGAAG 1936 GAAGTTACTC 5006 C TTAg tac t- g c T
TTACTCATTCGGTGCTTGTT ATTCGGTGCT GATACGGGCG GG aagt tcat cg tg ttgttG T
GTTGCCAACAATCAGCGTTA TGTT |||||||||| || |||| |||| || || ||||||
TGAACTTGTTTCTGCCTGTA CTATGTCCGT CT TTCA AGTA GC AC AACAAC G
TC - TTG- --- TT G T C

GAM2870 GTGTTATACATATATATATA 1941 TATTATATAT 5011 A A-- - T
TATATATATATATATATATA ATACACGTAG GTGTT TAC TATATATATA TATATATATATA A
TATATATATTATATATATAC ACAC ||||| ||| |||||||||| ||||||||||
ACGTAGACAC cacag atg atatatatat atATATATATAT T
- cac t A

GAM2871 GTGATTAATATATATATATA 1942 TAATATATAT 5012 - a A
TATATATATATATATATATA ATATATATAT GTG ATt atatatatatatatatatatAT T
TATATATATATATATATATA ATAT ||| ||| ||||||||||||||||||||||
GATACAT TAC TAG TATATATATATATATATATATATA A
A A T

GAM2872 ACATTTGTTGGCAAGAAAAG 1937 TGACCGTAGG 5007 T G ------ A A GATA A CTT
AGCACCGATAACGGTAAGAA CGTTCATTTA ACA TTGTTG CAAG AAA GAGC CC ACGGT
AGAA T
CTTTTATTTTTTGACCGTAG CTAA ||| |||||| |||| ||| |||| || ||||| ||||
GCGTTCATTTACTAACCTTG TGT AACAAC GTTC ttt cttg gg tgcca tTTT T
GCAACAATTGT T G Caatca a c a--- g TTA

GAM2873 TGCTATATTCAAGTTTTTGC 1938 TATCATGTGA 5008 TCAAGTT-- TG C TAT T
CTGTATCGTTTTCGTATCAT ATAATATACT TGCTATAT TT C TG CG T
GTGAATAATATACTGTATAG GTAT |||||||| || | || ||
TA ATGAtatg aa g ac GC T
tcatataat gt t tat T

GAM2874 GCGGTCACATTATACTTAGT 1943 TTGAAACAGA 5013 C - - TAG TCTCTTGTG T
CATCTCTTGTGGTTGTTAAC TATACATGTA GCGGT ACAT TATA CT TCA GTTG T
AACAATCTTGAAACAGATAT ACCG ||||| |||| |||| || ||| ||||
ACATGTAACCGC Cgcca tgta atat ga agt CAAC A
a c a caa tCTAA---- A

GAM2875 ACGTAGGTGGTTATTTGATC 1944 AGGTGGTTAT 5014 T t tc - ggat-- GGT
GTTGGGATGATTGTGGTTAA TTGATCGTTG ACG aggtggttat tga gt tg GATTGT T
CAACAATCTACATACACATT GGAT ||| |||||||||| ||| || || ||||||
TTCATATGACCGCCTTCGT TGC TCCGCCAGTA ACT TA AC CTAACA A
T T TT C ATACAT ACA

GAM2876 GTAATACTATCTATAAACAT 1945 TCTATAAACA 5015 A t acata at-- TA
AAGTATATAATAAATACTTT TAAGTATATA GTA TACTA ctataa agtat aataaA C
TTATTTACGGTACTCTTGTA ATAA ||| ||||| |||||| ||||| ||||||
GTGGTGATAC CAT GTGGT GATGTT TCATG TTATTT /
A - C---- GCAT TT

GAM2877 GCAATTTGCCTAACATGGAG 1946 TAACATGGAG 5016 TT Ct t- -- ac
GATTGAGGACCCACCTTTTA GATTGAGGAC GCAA TGC aaca ggaggatt gagg c
ATTCTCTTCTGTTTGCATTG CCAC |||| ||| |||| |||||||| ||||
C CGTT ACG TTGT TCTCTTAA TTCc /
-- T- CT TT ac

GAM2878 TGTCCTTACTCCGTCTTGGT 1947 CGTCCCATCT 5017 A- CTTG TG TG GT
GGGTGGGTGGCTGTGTATGG GTGCGGGGAG TGTCCTT CTCCGT G GGTGGG GCT G
CGTCCCATCTGTGCGGGGAG GGGG ||||||| |||||| | |||||| |||
GGGGGCA ACGgggg ggggcg t ctaccc cGG T
ga ---- gt tg TA

GAM2879 TTAAAGTAACCTAACACCAT 1939 AAAGTAACCT 5009 cc ccata ctTTA
AACACTTTACTTTCCTTGTA AACACCATAA TTaaagtaa taaca aca C
CTTATGTTACTTTACTTTAG CACT ||||||||| ||||| |||
GATTTCATT ATTGT TGT T
TC ATTCA TCCTT

GAM2880 TGACCAGTGAACAATTTGTT 1948 TTGGTTGCAA 5018 ---------- CA -- TAGTTT
TAATGTTAGTTTATTCAATG ATATTCATTA TGACC AGTGAA ATTTGT TTAATGT A
CATTGGTTGCAAATATTCAT CTTC ||||| |||||| |||||| |||||||
TACTTCTCCAATCCCAGGTC ACTGG ttactt taaacg ggttACG /
A ACCCTAACCTcttca a- tt TAACTT

GAM2881 GAAGTTAATGGAAATAGGGC 1940 TTAATGGAAA 5010 G - aaata g ---------- GG - GAA
GTTTGTTAGGGGTTGTGAAA TAGGGCGTTT GAA ttaa tgg gggc ttt gttaG GTT GT A
TAAACGAACAACTGGCTTCA GTTA ||| |||| ||| |||| ||| ||||| ||| ||
GTGATTAGAGAGCTCAAACC CTT AATT ACC CTCG GAG CGGTC CAA CA /
AGTTAAGTTC G G AAA-- A ATTAGTGACTT AA G AAT

GAM2882 GATCTTTCCCACGTTGTATG 1949 TCTTTCCCAC 5019 - catctTC -------- CC A CAGC---
-- T
CCATCTTCCAGCAGAGCCGC GTTGTATGCC ttgt atgc CAGC AGAG GCGGAGT GA
AACC C
GGAGTAGACAGCAACCTCAA ATCT |||| |||| |||| |||| ||||||| || ||||
GGTTAAAAACAGATCACTTC AACA TATG GTCG TCTC CGCTTCA CT TTGG
A
GCTCTCTCACCAAAAGCTGC C TTC---- AAAACCAC T- - AGACAAAAA A
TTGTATCACAACCAGGAATC
TC
GAM2883 GATCGTCTTTTTGGCTGTGA 1953 TGAACTCATT 5023 C TTTTT T AG C CAATA
AGTCCCTCAATAAATACTAG GCCTCCGGCT GAT GTC GGC GTGA TC CT A
TGAACTCATTGCCTCCGGCT GTC ||| ||| ||| |||| || ||
GTC ctg cgg ccg tact ag GA /
t cct-- t ca t TCATA

GAM2884 GTCGTACACCCGGCTGACGA 1950 TTCCCGAACG 5020 A CG GAGAAACA C T G
GAAACACGCTTCGGGGGTGG AGGACATAGT GTCGT CACC GCTGAC CG TTCGGGGG
GGACCA G
ACCAGGGCTGGTTCTTCCCG CAGC ||||| |||| |||||| || |||||||| ||||||
AACGAGGACATAGTCAGCGG CAGTA GTGG cgactg gc aagccctt CTTGGT G
TGATGAC - -- atacagga - - C

GAM2885 ATTCAACTTGTTAAATTAAT 1951 TTAGTAGTAA 5021 A- GGATAG A G- G G
GA GTT
AATGGATAGTTTAAAATAGT TAAGATAGTT CTTGTTA ATTAATAAT TTTAAA TA TTATTA TA
TAATAA TA T
TATTAGTAGTAATAAGATAG TAAA ||||||| ||||||||| |||||| || |||||| || |||||| ||
TTTAAAATAGTTATTAGTAG GAATAAT TGATTATTG aaattt at aataat at attATT AT A
TAATAAGATAGTTTAAAATA GA ATA--- g ag g g G- AAA
GTTATTAGTAGTAATAAGAT
AGTTTAAAAT
GAM2886 GTCGAGGAACACGCCCCCGG 1952 AGGCCGGCGG 5022 AACA - A CC Aa - c ----
gacttcTT

ACCCCGTATAAGGCCGGCGG GCGCCTCGGA AGG CGCCC CCGG CC GTAT gg ccgg gggcg cctcg C
GCGCCTCGGACTTCTTCTTT CTTC ||| ||||| |||| || |||| || |||| ||||| |||||
TTTGGCGAGGAACACGCCCC TCC GTGGG GGCC GG TATG CC GGCC CCCGC GGAGC /
CGGACCCCGTATAAGGCCGG ---- C - AA CC A - ACAA GGTTTTTT
CGGGTGCCTCGGAC

GAM2887 GCTGGCACGGCCGGCGCCGC 1958 GCGCGGGGCA 5028 T G G G GATGACGA
GCAAGATGACGACGGGAGAG GGCAGTGCCG GC GGCAC GCC GC CCGCGCAA C
GTTGCGCGGGGCAGGCAGTG C || ||||| ||| || ||||||||
CCGC cg ccgtg cgg cg ggcgcgTT /
- a a g GGAGAGGG

GAM2888 ATGCAATATTACTAATATTT 1954 GCAATATTAC 5024 ctaatattttc- c TTATATA T
TCACACGCTTATATACCTAT TAATATTTTC ATgcaatatta aca GC CC A
TGGACAATGTTGTATATCCC ACAC |||||||||| ||| || ||
ACCCCTAATATTGCAT TACGTTATAAT TGT TG GG T
CCCCACCCTATA - TAACA-- T

GAM2889 ATCGCAGAATGTATAAAGAA 1959 AAGAATATAA 5029 CAGAA a aatactaaac t
TATAATACTAAACTTTGCTC TACTAAACTT ATCG TGTATAa gaatat tttgc C
TAGTAGACATACTGATATTC TGCT |||| ||||||| |||||| ||||| ATTATACACGAT TAGC ACATATT CTTATA AGATG T
----- A GTCATAC--- A

GAM2890 AGTTCTATTACATTGCTAGC 1955 TATAGAATTT 5025 TACATTG- GC-- G GA
TACTTGTAGGAATGCTAAAG AGTATAGAAC AGTTCTAT CTA TACTT TAG A
TACTTATAGAATTTAGTATA T |||||||| ||| ||||| ||| GAACT tcaagata gat ATGAA ATC /
tgatttaa atTC - GT

GAM2891 CTTAGAGACTACTTTGTCTT 1956 TACTTTGTCT 5026 C- ttt- c a actaCTC C ---- CTG
TCAAATATGACTACTCCCTC TTCAAATATG AGAGA tac gtcttt aaat tg CCT TCATC CATTGGT T
TCATCCATTGGTCTGTTAAA ACTA ||||| ||| |||||| |||| || ||| ||||| ||||||| CCAATGTGGTGATGATAGGT TCTCT ATG CGGAAA TTTA AC GGA AGTAG GTAACCA /
AAGATGCAAATTTAAAGGCT AT TATT - A GTAGAAT T TGGT AAT
TATGTATATCTCTAAG

GAM2892 TTGACGATAAACCTATAGAG 1960 TAGCATTAAT 5030 ATAAACCTA GA T- at aa a
TTGCTTTAGCATTAATAAAT AAATGTAAAA TTGACG TA GTTGC Ttagc taataaatgta act t
GTAAAACTATATAGTATATA CTAT |||||| || ||||| ||||| |||||||||| |||

TTTATTACCGTTGATTGTAA AACTGC AT TAATG AGTTG ATTATTTATAT TGA A
TAATACGTCAA --------- AA TT CC A- T

GAM2893 GCAAGTTACACAAACAAAGC 1961 TAAGATCATT 5031 T ACAAAC C T-- CA---------- T
AAAGTAAGCCAACAGTTTTC TCAGTTTCGT GCAAGT AC AAAG AAAG AAGC ACAG T
TGTAAGATCATTTCAGTTTC CTTT |||||| || |||| |||| ||||

ATATAATTTCCGGGATTATT TATT |||||||||| |||| ||||||||
ttattagggc taat tgatATAT T
ctt ata AA

GAM2900 TGGAAGAGATTTTCTAACGC 1962 TAACGTGCGT 5032 GATTTTCTA C AC AG GTG
CGCGACTAAAGAGCTGTGGT GCCGTCTTCT TGGAAGA ACGC GCG TAAAG CT G
AAAAGACTTTAACGTGCGTG A ||||||| |||| ||| ||||| ||
CCGTCTTCTA atcttct tgcg tgc atTTC GA T
gccg----- - a- A- AAA

GAM2901 CTTTTATCACCGGCTGCACT 1963 AGACCAGACA 5033 TC TGCA AAAAG GATA CAA AA
GATCAAAAGTGGTTGGATAC ATCAAAGATC CTTTTA ACCGGC CTGATC TGGTTG CTG TCA C
TGCAATCAAACACCTGAGAC AGGT |||||| |||||| |||||| |||||| ||| |||
CAGACAATCAAAGATCAGGT GAAGAT TGGTtg gactag actaac gac aGT A
TGGTTTAGAAG T- ---- aa--- a--- cag CC

GAM2902 GATATAATTTTATGTATGTG 1964 TGTGGAGTGG 5034 TTTA- g t aa a gt AT C GA AGA GG
GAGTGGAAGCGGAGCGTGAT AAGCGGAGCG TGTAt tggag gg gcgg gc gat ATTG GATGT AGC GGC A
ATATTGCGATGTGAAGCAGA TGAT ||||| ||||| || |||| || ||| |||| ||||| ||| |||
GGCGGATGAGCCGGGTTGGA GTATA ATTTT CC TGTC TG TTA TAAC CTATA TTG CCG T
TATCCAATCAATTGAGTACT TAAGG A - GG A AG AC - GG GG- AG
GTGGCCTTTTAAATATGGGA
ATGTTATGTC
GAM2903 ACTTGAAACCTCATTCACAT 1970 TTATTTGAGT 5040 C TT G TTT GG CTC
AGCTTAGGTTTTTAGGCACT GTGTGTGAGC ACTTGAAA CTCA CACATA CTTAGGT TA CA C
CCAATTTGAATATTATTTGA TTTC |||||||| |||| |||||| ||||||| || ||
GTGTGTGTGAGCTTTCAAGT TGAActtt gagt gtgtgt gagttta AT GT A
c -- - tt- AA TTA

GAM2904 TTAGTATTAATTGCTACCGT 1965 TTAATTGCTA 5035 tt-- ccg cat- a G ATA
TACATTGTACAAATGGAGAT CCGTTACATT TTAGTA aattgcta tta tgt cAAATG AG T
ATTCCCTGTATTTGGCATTT GTAC |||||| |||||||| ||| ||| |||||| ||
CTAAAATTAGCAATTTTATT AATCGT TTAACGAT AAT ACG GTTTAT TC /
GCTAA TATT TAA CTTT - G CCT

GAM2905 GTGACTAAACCGCATAGGTC 1974 CACCTGGTGC 5044 CT C - - GCCAAC------ C
ATTGCCAACAACCGCACCCG GATTTTATCA GTGA AAA CGCAT AGGT CATT AACCG A
GTTAATCAGATATAAAATGC C |||| ||| ||||| |||| |||| |||||
ACCTGGTGCGATTTTATCAC cact ttt gcgtg tcca GTAA TTGGC C
at a g c AATATAGACTAA C

GAM2906 GCCAAAAGTTGCGTGTCTGA 1971 AAGTTGCGTG 5041 Aaa - gagt tgG-- TT
GTGGACGTGGGTTTTTATAG TCTGAGTGGA GCCA gttgcgtgt ct ggacg G T
AGTCGTCCTAAGCGCGTGCG CGTG |||| ||||||||| || ||||| |
GCGGGTGGC CGGT CGGCGTGCG GA CCTGC T T
GGG C AT-- TGAGA AT

GAM2907 CTTTTAAGCTTATTGTAATA 1972 TTTAAGCTTA 5042 tt - t t t ATA CA TG T
TATATGAATAGCTATTCACA TTGTAATATA CT taag c tattg aatatata gA GCTATTCA G GGAC T
GTGGGACTTGGTCTTGTGTT TATG || |||| | ||||| |||||||| || |||||||| | ||||
GAATAGTATCTTATATATTT GA ATTC G ATAAT TTATATAT CT TGATAAGT T TCTG /
TAATATGTCTTATTAG TT T T T T A-- TG GT G

GAM2908 TTGGATTATTCATTTTTATG 1981 TATTGTGCAG 5051 GA TCATT T ATT A-- CGA
AACTATGTTATTTACAAAGC ACGTGGTTCT TTG TTAT TTTA GAACTATGTT TACAA GCTT
A
TTCGAAAGTGAGTATATTGT TGGG ||| |||| |||| |||||||||| ||||| ||||
GCAGACGTGGTTCTTGGGTT AGC AATG gggt cttggtgcag gtgtt TGAG /
GTTGTAAACGA A- TTGTT t ac- atA TGA

GAM2909 TAACGTGTAGTTTTGATGAT 1975 ATGATGGTGA 5045 T TT t tg c t t TGG
GGTGACACATGGTTGTTGTT CACATGGTTG TAACG GTAG TTGa gatgg aca atgg tg tgtTA C
ATGGCTTTTAGCATCACTTA TTGT ||||| |||| |||| ||||| ||| |||| || |||||
TTGTTGCTATTTTAGGGTTA ATTGT CATT GATT TTATC TGT TATT AC ACGAT /
CTGTTA - GG - GT - C T TTT

GAM2910 ATGATATTATCGATAGTTGT 1982 TCGATAGTTG 5052 c a tg - tgctct
GATAATGTGCTCTTTTATTT TGATAATGTG ATGATATTAt gat gttg at aatg T
TATTAATTGCGATGATTATA CTCT |||||||||| ||| |||| || ||||
ATATTAT TATTATAATA TTA TAGC TA TTAT /
- G GT A TTTATT

GAM2911 TAGGAAATTGGTTTATAATG 1983 TGAAAATAAA 5053 ATTG--- AATGTATA T TTTT
TTC
TATAATTTTTTTAGTTTTTA TACAAAGGTT TAGGAA GTTTAT ATTTTTT AGT ATAGA T
TAGATTCTTTATTCTATACT CCTG |||||| |||||| ||||||| ||| |||||
TAAAAAATGAAAATAAATAC gtcctt taaata tAAAAAA TCA TATCT T
AAAGGTTCCTG ggaaaca aaag---- T ---- TAT

GAM2912 TGTTCAGTCTAAAAATAATG 1976 TTACTTGGAA 5046 TC CTAAA - - A A T C CC
TTGGGTATTTATAATTACCG ACACCCATAC TGT AGT AATA ATGT TGGGT TTT TAA TA CG C
CCCCCGTGTTACTTGGAAAC ATAT ||| ||| |||| |||| ||||| ||| ||| || ||
ACCCATACATATGTTCCACT ACA TCA TTGt taca accca aaa gtt at GT C

CTACA TC CC--- a t c g c t GC

GAM2913 TGCTAAGTTTCAGTTTAAAT 1984 TAAGTTTCAG 5054 aa tc t ca TTGCAA- T
CATTTCCTTGCAATTCTCTA TTTAAATCAT TGCt gtt agtt aaat tttcc TTC C
GAACAATATTGGAAACCATT TTCC |||| ||| |||| |||| ||||| |||
TCAACTCAACAAGCA ACGA CAA TCAA TTTA AAAGG AAG T
A- C- C CC TTATAAC A

GAM2914 TTAAGTCTATTGTTCATGGC 1985 TATTGTTCAT 5055 tat t ---- c- t tA
TTAAGTCTATTACTCATAGC GGCTTAAGTC TTAAGTC tg tca tgg ttaag ctat C
TTAACTCCATTACTGATCAT TATT ||||||| || ||| ||| ||||| ||||
GACTTAA AATTCAG AC AGT ACC AATTC GATA /
T-- T CATT TC - CT

GAM2915 TCGCAACACAACATGGTTAC 1977 TTAAGGCTTG 5047 G T ACCCATAG GAAATTT
CCATAGATTGAGGAAATTTC TTGTGTTGGA TC CAACACAACA GGTT ATTGAG C
CAATAAACTCAGTATTAAGG || |||||||||| |||| ||||||
CTTGTTGTGTTGGA ag gttgtgttgt tcgg TGACTC /
- - aattA--- AAATAAC

GAM2916 TTGTTTACCGACGCGTTCAA 1986 ACGCGTTCAA 5056 TT ac---- ttc c tg tt AA
TAAAACGAATGGTTAAAAGT TAAAACGAAT TTG TACCG gcg aataaaa gaa g AA G
TGTTTTTTGTTTTTTTTATT GGTT ||| ||||| ||| ||||||| ||| | ||
TTCGTATAAAATGGTATTTA GAT ATGGT TGC TTATTTT TTT T TT T
G TT AAAATA TT- T GT TT GT

GAM2917 GTAGCACTCGAAATTTCAAA 1978 TAGCGGCTGG 5048 AG C ATTTCAAA A AAATAC -
A
CGGCATGTAAATACGAATGT TGTTCGATGT GT CA TCGAA CGGC TGT GAATGTC CTT
G
CCTTAGAAAGCGACGTTTAG CAC || || ||||| |||| ||| ||||||| |||
CGGCTGGTGTTCGATGTCAC ca gt agctt gtcg gcg tTTGCAG GAA /
ct - gtg----- - a----- C A

GAM2918 GCTGCCATGTATTTCCTGGA 2625 AGCAAGTAGA 5695 C TTTCCTG a gat ag ca
GAGCAAGTAGATGATGAGGA TGATGAGGAA GCTGC ATGTA GAG gcaagta gatg gaac g
ACCAGATAGTTTATATCCAT CCAG ||||| ||||| ||| ||||||| |||| ||||
ACTTGCACTTAAAGTCTACA TGATG TACAT TTC CGTTCAT CTAT TTTG A
TTGTAGT T CTGAAA- A AC- A- AT

GAM2919 TCAGACTGAGGGGCCCTTAG 2626 TTCTTCGCGG 5696 AG TT- TT G
GTTTATATGAAATATATTCT GTTTAACAGT TCAGACTG GGGCCC AGG TATAT A
TCGCGGGTTTAACAGTTTGG TTGG |||||||| |||||| ||| |||||

ggtttgac tttggg ttc ATATA /
aa cgc tt A

GAM2920 ATCACTCAAGATTACTTACT 1979 TCAAGATTAC 5049 Ctca t act-- ttt
TCTATTTTAATGTATAGATT TTACTTCTAT ATCA agat actt tctat a
AAAAGGTTATTTCGTATGAT TTTA |||| |||| |||| |||||
TAGT TTTA TGGA AGATA A
ATGC T AAATT TGT

GAM2921 TGAAGACCCGAGAGAAGAGC 1980 ACAAAAATTT 5050 ---------- CTTTACAAAAA AAAAA a
ttc acaa
TTTACAAAAAACACAAAAAA CAATAAAAAC AAGAG ACACA acaaa at aataaaa t
ACAAAAATTTCAATAAAAAC AATT ||||| ||||| ||||| || |||||||
AATTTAAATTTTATTTATCT TTCTC TGTGT TGTTT TA TTATTTT t
TTGTATGTGTGTCTCTTGCA ACCCCCAACG ---------- GTA-- C T-- AAAT
ACCCCCACCCCTTATAGATC
TTCA
GAM2922 TGTTAAAATATCAAATGTTA 2632 TATCAAATGT 5702 atca - gttt TCTTC
CAATAGTTTTTTTGTTATCT TACAATAGTT TGTTAAAAt aatgt tacaata tttTGTTA T
TCTTTTATTAATAAAGCCAT TTTT ||||||||| ||||| ||||||| ||||||||
ATTGTGTATATTAATTTTAA ACAATTTTA TTATA GTGTTAT GAAATAAT /
CA A--- T ACC- TATTT

GAM2923 CTGTATACAAGACAAACCAA 2627 TACAAGACAA 5697 acaaaccaa- caatA
AAATACAATAAACGCGATAT ACCAAAAATA CTGTAtacaag aaata A
TTAAACATTTTATTTGTGTA CAAT |||||||||| |||||
CAG GACATGTGTTT TTTAT A
ATTTTACAAA AGCGC

GAM2924 GCCGAGCACGCCGCCGCGAT 2628 TCCGTGGACG 5698 A A - A-- AGA AGAT
CGGAGACCCAGATCTGCAGG GCGGCCGGC GCCG GC CGCCG CCGCG TCGG CCC C
GCCGAGTCCGTGGACGGCGG |||| || ||||| ||||| |||| |||
CCGGC cggc cg gcggc ggtgc AGCC GGG /
- - a ctG --- ACGT

GAM2925 CGGGTCGCCCCTCGACGACG 2629 TACTGCGCGA 5699 CGCCCCT C C - ACC---- CC
CCGTCGCCGACCCGATCCAA CCGCCTCGTC CGGGT CGACGA GC GTCGC CG CGAT A
AATCGTAAATACTGCGCGAC GTTC ||||| |||||| || ||||| || ||||
CGCCTCGTCGTTCCCCACCC GCCCA gctgct cg cagcg gt GCTA /
G CCCctt- c c c catAAAT AA

GAM2926 GAGTACTTATTAAGAATGAC 2630 TGACAAATGA 5700 TA ATT GAATGACAAAT A a
caaatgacaaat GATT
AAATAACAAATGACAAATGA CAAATGACAA AG CTT AA AACAA tg caaatga gaC
C

CAAATGACAAATGACGATTC ATGA || ||| || ||||| || ||||||| |||
TAAAAGTCTATATAAGCATT TC GAA TT TTGTT AC GTTTATT CTG T
ATTTGCCAATTGTTTTTCAC TC AT- AAAATCACTTT A C ACGAATATAT-- AAAA
TAAAATTTAAAGCTCTC

GAM2927 GGCGTCGTCGTCGGGCCGGG 2633 CTCGCACTCC 5703 GT- C---- -- GC GT TC---
TT AA
TGCGTCGCCGTTCGGGCCGG GGCGCCGTGT CGG GCGT GCCG TTCGG CGGACG
CGGTGTC GCG TCT A
ACGGTCGGTGTCTCGCGTTT TCGC ||| |||| |||| ||||| |||||| ||||||| ||| |||
CTAAAAGAGGGCTCGCACTC GCC TGTA CGGC GAGTC gcttgt gccgcgg cgc GGG
A
CGGCGCCGTGTTCGCACTGA GCT TTTTA CA Ac -- cctca tc AG
GACCGGCATTTTATGTTCGC
CGGCCCCACCC
GAM2928 GAGTTGGCTACACCGAGATC 2634 CACCGAGATC 5704 - Aca- g - at----- a- tt AC
CGGCATCATACCTTACGTGA CGGCATCATA GAG TTGGCT cc agat ccggc cat cc ACGTGA
T
ACTGCTTACGTTTGGGGATG CCTT ||| |||||| || |||| ||||| ||| || ||||||
TTTTTGCGTCGGTGTTTGGG TTC AACTGA GG TTTG GGCTG GTA GG TGCATT /
GAGGAGTCAATCTT T GGAG G T CGTTTTT GG TT CG

GAM2929 TTTGTAGTTTTAAGATTGAG 2631 TAAGCTTTTT 5701 A TT T------- TTTTTT C A CTA
GTTTTTTGACGCTAGCCCTA CCTCATAAAT TTTGT GTT AAGA TGAGG GA GCT GCC T
TAGTAGGTAAGCTTTTTCCT ATTT ||||| ||| |||| ||||| || ||| |||
CATAAATATTTCTTTGGCAC AGACA CGG TTCt actcc tt cga tGG A
AGA - T- ttataaat tt---- t a ATG

GAM2930 GCTGTGGGTTATATGTTTGC 2635 TGGTCGGAGA 5705 GT- TA-- CG ACAA CAATA
GATTTTCCACAAAGAACAAT GTTATAAGCA GCT GGGT TATGTTTG ATTTTCC AGAA A
AATAACTCTTCTGGTCGGAG TACC ||| |||| |||||||| ||||||| ||||
AGTTATAAGCATACCGTGCC TGA CCCG atacgaat tgagagg tCTT T
CCAAAGT AAC TGcc at ctgg CTCAA

GAM2931 GACTTTTATCACGTTATCTC 2638 TAGTATAGCA 5708 TATCAC- - CA- TAA
ATGTATAAAATATTACAAAT TAAACTAAAG GACTTT GTTAT CT TGTA A
AGTATAGCATAAACTAAAGT TC |||||| ||||| || ||||
C ctgaaa cgata ga ACAT A
tcaaata t tAA TAT

GAM2932 TTGCATATTATATTTTATAT 2636 TATTATATTT 5706 C - a atttTAT
TTTATATTTTATATTTTGTA TATATTTTAT TTG Atatta tattttat ttttat A
ATAAGAATAGAATGCTAATG ATTT ||| |||||| |||||||| ||||||
TCAA AAC TGTAAT GTAAGATA AGAATA /
- C - ATGTTTT

GAM2933 TTTATTTTTTTCTTTTTAAT 2639 TCAGAGAGAT 5709 - A AATTTA CTTTTTCT CT
CTATCAAT
TTTAATTTATTAATTTTCTT AAAAAGATAG TCTTTTT ATTTT TTAATTTT ATATTTAG AATT
A
TTTCTATATTTAGCTAATTC A ||||||| ||||| |||||||| |||||||| ||||
TATCAATAATTTTTCTCAAT agagaga tAAAA AATTGAAA TATAAATC TTAA A
TTCTAAATATTATTTCTAAA t c ------ ATCTTTAT T- CTCTTTTT
AGTTAAAAAATCAGAGAGAT
AAAAAGATAGA
GAM2934 GTCGGAGAGTTATAAACATA 2637 AAGGGGTTTT 5707 A ATAA CCATGC- AAAG TC
CCATGCACCAAAGGGTCAGT ACTTTATGTG GTCGG GAGTT ACATA ACC GG A
TTTAAGGGGTTTTACTTTAT AATT ||||| ||||| ||||| ||| ||
GTGAATTCACCGAC CAGCC Cttaa tgtat tgg TT G
A g--- ttcattt ggaa TT

GAM2935 TGTTGATCGCATATTGCTAT 2640 TCGCATATTG 5710 T c ata - tcaaCCCAA TT - TA
TTCTGCTCAACCCAAAGTGT CTATTTCTGC TGT GAt gc ttgctattt ctgc AGTG AG C C
TAGCTACGTTGTCTCTCACT TCAA ||| ||| || ||||||||| |||| |||| || |
CAGAACCTGTAGTAAATAGT ACA TTG TG AATGATAAA GATG TCAC TC G G
AAAGTTGTTTACA T T A-- T TCCAAGAC- TC T TT

GAM2936 ATCAATTTTTAGTTTTAAAT 2641 TATAGCCAAT 5711 TT TTTAAATA ACCTAGG AAA
ATATTGGTACCTAGGACAAA AATTATTCCA ATCAATT TAGT TATTGGT AC G
GAAAGTATATATAGCCAATA CTAA ||||||| |||| ||||||| ||
ATTATTCCACTAAATTGAT TAGTTAa atca ataaccg TG /
-- ccttatta atatATA AAA

GAM2937 TTACGTAATAATGACCGGAT 2642 ATCCCGTTCC 5712 ATA GAC TGTAAT AACAAATC
GTAATTCGAACAAATCATAA GAAAATATAC TTACGTA AT CGGA TCG A
AACACCGATCCCGTTCCGAA GTGA ||||||| || |||| |||
AATATACGTGA agtgcat ta gcct aGC /
a-- aaa tgccct CACAAAAT

GAM2938 TACTACTCTTAAAACACATG 2643 TGTATAAGCT 5713 ---- AAAC TATT AGG
TGTATTGTGTTAGGTTAAAG TTAGTAGTA TACTACT CTTA ACATGTG GTGTT T
CATCCTTTATATGTATAAGC ||||||| |||| ||||||| |||||
TTTAGTAGTA atgatga gaat tgtATAT TACGA /
tttc a--- TTCC AAT

GAM2939 CCTCTTTCGATTTCTACACG 2646 TCAGTTAGAC 5716 TTTC - C GA AAA TAT
AGAAAAGTTATAAAATACAT GATCATTGAG CCTC GATT TCTA AC GA GT A
CAGTTAGACGATCATTGAGG G |||| |||| |||| || || ||
ggag ctag agat tg ct CA A
tta- c - a- A-- TAA

GAM2940 TCGGAACGCGTGAGGAGGCG 2644 AGGCACCGCC 5714 AAC A A- CAC A- CGCG
GCACTGCTAGCGACGCGGAC CGCCCGCGCT TCGG GCGTG GG GGCGG TGCT GCGA G
ACATTGCGAGGCACCGCCCG CGA |||| ||||| || ||||| |||| ||||
CCCGCGCTCGA agct cgcgc cc ccgcc acgg CGTT A
--- - gc --- aG ACAC

GAM2941 GCGAGCCGCGTCGTTCGCGG 2645 CACGCTGTTC 5715 AG C T TT -- G - GCCACA
ACGCGGCGGTGGGTCCGGCC GTCCGCGCTC GCG C GCG CG CGCGGACG CGGCG
TGGGTC CG G
ACAGAGCGACACGCGGCCCA GTCG ||| | ||| || |||||||| ||||| |||||| ||
CGCTGTTCGTCCGCGCTCGT CGC G Cgc gc gcgcctgc gtcgc acCCGG GC A
CGCAGTCCGC CT A t tc tt - C ACAGCG

GAM2942 TTTGAGCCCCAAGCGGTACG 2647 TACACTGAAC 5717 A CC -- AC CTACATAT
GACTACATATTTTCCATAAA TTGAGCACAA TTTG GC CAAG CGGT GGA T
TCTACACTGAACTTGAGCAC A |||| || |||| |||| |||
AAA aaac cg gttc gtca tCT T
a a- aa ca AAATACCT

GAM2943 TAAAGCTTTCTCTATCTTTT 2654 TCTATCTTTT 5724 GC c----- -- tctttaa CC C ATT
TATCTCTTTAATTTTTCAAC TATCTCTTTA TAAA TTTCt tatct ttttatc tttTTCAA TT TGA A
CTTCTGAATTAATATCATAA ATTT |||| ||||| ||||| ||||||| |||||||| || |||
ACTTGAGAAAAATTATTGAT ATTT AAAGG ATAGA AAAATAG AAAGAGTT AA ACT
/
AAAATTAGATAATTTATGGA A- TATTTA TT TTATTAA CA T ATA
AAATTTA

GAM2944 GAAAGCACACGATACACATG 2648 AAGCACACGA 5718 a c t catgt a- G ATG A A
TATCCAGTATGCTATATGAT TACACATGTA GAaagc ca ga aca atcc GTAT CTAT ATTA
CATAATT T
TAACATAATTATAAAATTAT TCCA |||||| || || ||| |||| |||| |||| |||| |||||||
GATGATAAATGGGGTATAGG TTTTCG GT CT TGT TAGG TATG GGTA TAGT
GTATTAA A
GATTGTTCTGAGCTTTT A - - ----- GA G AA- A A

GAM2945 GAGGCATCTCAGTGTTTGAA 2649 CACTGATTGA 5719 C------- TGA- GGAAG
TTGGAAGAATGTGTGGTGAA CATTGTGCCT GAGGCAT TCAGTGTT ATT A
TGGCACTGATTGACATTGTG C ||||||| |||||||| |||
CCTC ctccgtg agtcacGG TGG A
ttacagtt TAAG TGTGT

GAM2946 ATTCTTGAGGCATCTCAGTG 2655 TGGAAGAATG 5725 ----- AG-- T AA aa tgt at----
TGATT

TTTGAATTGGAAGAATGTGT TGTGGTGAAT CATCTC TG TTG Ttgg gaatg ggtga ggcaC
G
GGTGAATGGCACTGATTGAC GGCA |||||| || ||| |||| ||||| ||||| |||||
ATTGTGCCTCTAAGTCACCT GTGGGG GC AGC GATT CTTAT CCACT CCGTG
/
ATTCAATTAGGGCGACCGTG TTAGA GTGT C GG AA --- GAATCT TTACA
TGGGGGTGAGATTTAATTGG
CGAGAACCAT
GAM2947 TATGTTATAAAACAGTGTAG 2650 TATAAAACAG 5720 c a A
CGTTGAATTTTAAAAAAATC TGTAGCGTTG TATGTtataaaacagtgtag gttg attTT A
CAACATTATACTGTTTTATA AATT |||||||||||||||||| |||| |||||
ATATA ATATAATATTTTGTCATATT CAAC TAAAA /
A C A

GAM2948 CCGTGGCGTAAATATAGGAC 2651 TAGGACATAG 5721 C AA acata taca ac
ATAGATCGGTACAGATACAC ATCGGTACAG CCGTGG GTA TAtagg gatcgg gat A
CGTCACCTGATCACCCCCTA ATAC |||||| ||| |||||| |||||| |||
TACTATCTATGG GGTATC TAT ATATCC CTAGTC CTG /
- C- CCCA- CA-- CC

GAM2949 ACACTTTCCCGCGTGTCGCG 2652 TGCCTGGCGC 5722 TTT C-- TC- GT T T
TGTGGTTCATGTGTGTGCCT CCCCACCCTC ACAC CCCG GTG GCGT GGT CA G
GGCGCCCCCACCCTCGGGTT GGGT |||| |||| ||| |||| ||| ||
CGTGT TGTG gggc cac cgcg ccg GT T
CTt tcc ccc gt t G

GAM2950 TGCGTGTGTGGTTAACGCCT 2653 TTGCATGGCG 5723 TAA CT T GAA GA AA-
AAGG-- TG A T
TTGTTTGCTGAATGAGTTGA TGTTAAATGG CGC TTGT TGCT TGAGTT TGT GTTTAATA
G AG TAA G
TGTAAGTTTAATAAAGGGTG GGCG ||| |||| |||| |||||| ||| |||||||| | || |||
AGATAATGTTTAACTTGCAT GCG AATA ATGG ATTCGG gcg taaattgt c tC ATT /
GGCGTGTTAAATGGGGCGGG --- T- T GAA G- ggg gcggta gt A T
GCTTAAAGGGTATATAATGC
GCCGTGGGCTA
GAM2951 GGCGCACATGAGGAATATAA 2656 TGAGGAATAT 5726 CACAtga ataatatagcaaca - C
A G
TATAGCAACAGTCGGCTCGG AATATAGCAA GGCG ggaat gtCGGCTC GGG CGACG
CGGGC C
GCCGACGACGGGCGCTCGCT CAGT |||| ||||| |||||||| ||| ||||| |||||
CGGCGTCGACTCGGAGCCGG CTGC TCTTA CGGCCGAG CTC GCTGC
GCTCG T
CCGATTCTCGTC ------- GC---------- G A G C

GAM2952 GTCTAGGGGAAGGACATGGG 2659 TAGGGGAAGG 5729 a aaggacat c T ACC
GCAGGGGGATGGAGACCAGG ACATGGGGCA GTCt gggg gggg aggggGA GGAG A

ACCTCCTCCTCCTCCCCCTC GGGG |||| |||| |||| ||||||| ||||
CAGGAC CAGG CCTC CCCC TCCTCCT CCTC G
A -------- - - CAG

GAM2953 CCGTCGTCACAGCTGGAAGG 2663 GAGCTTCCAG 5733 GT CA GAAGG C--- TTAAT - G AT
ACACCGTTAATCTGGAGCGT TTGTTCGTAA CC CGTCA GCTG ACA CG CTGGA GC TTGAA A
TGAAATAGTCTTCAGAGCTT ATGT || ||||| |||| ||| || ||||| || |||||
CCAGTTGTTCGTAAATGTAT GG GCAGT CGAT tgt gc gacct cg gACTT G
GTGTAGCGCTGACGCAGG AC CG GTGTA aaat ttgtt t a CT

GAM2954 GGTGTCTGAAAGCTCGCCAA 2657 TGAAAGCTCG 5727 -- a c caag c gcg
GGTCTCGCGTAAAAGAACAG CCAAGGTCTC GGT GTCtgaa g tcgc gt tc t
ATGTGAACTTCAGATGTACC GCGT ||| ||||||| | |||| || ||
CCA TAGACTT C AGTG CA AG A
TG - A TAGA - AAA

GAM2955 TCTTAAGTATTAACTTTAAA 2658 TATAAAGATT 5728 T T T AT-- AA --- tgtgt aac
TATAATTATAAAGATTGTGT GTGTATTCTT TC TAAG AT AACTTTAA AT Ttataa agat attcttc G
ATTCTTCAACGACAGAGGAG CAAC || |||| || |||||||| || |||||| |||| |||||||
TTCTCTATCTACTTTATAAC AG GTTC TG TTGAAATT TG AATATT TCTA TGAGGAG /
AGTTTTATTAAAGTTTGTTC C T T ATTT AC TCA TCTCT ACA
TTGCGA

GAM2956 CGAGTGCTCACCCCCGAGGA 2660 TTGCCACTCG 5730 -- - CCC --- CGCACCCATCTCC AGT
GCTCGCCGCACCCATCTCCG CGAGCAGATT CGAGT GCT CA CCGAGGA GCTCGC GCAGCT A
CAGCTAGTAACAAGGTTGCC CTCG ||||| ||| || ||||||| |||||| ||||||
ACTCGCGAGCAGATTCTCGG GTTCA CGA GT Ggctctt cgagcg cgttGG A
CATTGTAGCGGACTTG GG T TAC aga ctcac-------- AAC

GAM2957 CACCCACAAAGGAGTTTGTA 2661 AGGAGTTTGT 5731 C ag gtaaaa- atc
AAATAAAATCTCTGTTTAGA AAAATAAAAT CAC CACAA gagttt taaa t
CCTTAAAATTTGTTGTGTGT CTCT ||| ||||| |||||| ||||
G GTG GTGTT TTTAAA ATTT /
T G- ATTCCAG Gtc

GAM2958 GTGAGTTTGTGGACCCAAAG 2664 GTGGACCCAA 5734 ---------- Tg a caaa-- c- agaga
CCCTCAGAGACAACGCGACA AGCCCTCAGA GTGAGT T tgg cc gcc tc c
GGCCAGTATGGACCGTGATA GACA |||||| | ||| || ||| ||
CTTTTATTTATTAACTCAC CACTCA A GCC GG CGG AG /

ATTATTTATTTTCAT GT A TATGAC AC CGCAa

GAM2959 TGACGTGGATACTAGTAAAA 2665 TGACGTGGAT 5735 GGA--- AAAAAAGT AA- TC
AAAGTGCGTCAAAGCTCTTA ACTAGTAAAA TGACGT TACTAGTA GCGTCA GC T
GCGTGTGACGTGGATACTAG GGGA |||||| ||||||||| |||||| ||
TAAAAGGGACGTCA ACTGCa atgatcat tgcagt CG /
gggaaa agg----- GTG AT

GAM2960 TACCCCAGATTTACCCGTTA 2662 CCTAAAATTC 5732 CAG - - G Cc -- c c-- tc C C
AG
CCCTAAAATTCCCTCCCCTT CCTCCCCTTT ATTTA C CC TTA ctaaa attc ct ccctt tctT ACTCG
CG G
TCTCTTCACTCGCCGAGGCC CTCT ||||| | || ||| ||||| |||| || ||||| |||| ||||| ||
ACGCCGAGTAGGACCGAGGG TAGAT G GG AAT GATTT TGAG GA GGGAG AGGA
TGAGC GC C
TACAGCGAGTCTTTTAGTTT ATG T T - TT TC C CAT CC - C AC
AAGGTGTTAGATGTAAGGTA

GAM2961 GCCGTAGGGCTGGCAGGGAC 2666 GGGCTGGCAG 5736 ----- ca a acccagcA TTTT
GGCACCCAGCAGCTATTTTC GGACGGCACC GCCGTAgg gctgg ggg cggc GCTA C
ATCTCTAGCGCCGCCTACTA CAGC |||||||| ||||| ||| |||| ||||
GCGGAAATCTGCGGT TGGCGTCT CGATC TCC GCCG CGAT A
AAAGG A- - -------- CTCT

GAM2962 TTCTAGGGTTCTATTATCAT 2667 TAGGGTTCTA 5737 -- at tt AT G T
CAATTCCATAGTGAGTCTTT TTATCATCAA TTCtag ggttctatt catcaa cc AGT AG C
GACTTCGGTTTGGTGGCAGT TTCC |||||| ||||||||| |||||| || ||| ||
AGGGCTTTCTGGAG GAGGTC TCGGGATGA GTGGTT GG TCA TT /
TT CG T- CT G T

GAM2963 TCTGAACACTTTCTTGAAAG 2673 TTGAAAGTTG 5743 AACA --- a- t ct cca gt
TTGCGGCTGACCACCGTACA CGGCTGACCA TCTG CTTT Cttga agt gcgg ga cc A
GGAATTCTCTCGCACTAGTC CCGT |||| |||| ||||| ||| |||| || ||
GGGTTTGAAGCGCGGG GGGC GAAG GGGCT TCA CGCT CT GG /
GC-- TTT GA - CT TAA AC

GAM2964 TGTTATCAAATGTACTGTTT 2668 ACGCAAATGG 5738 TATC G ATac----- a tt c ttt
AATACGCAAATGGATTTACT ATTTACTACG TGT AAAT TACTGTTTA gca atgga ta tacg t
ACGTTTTAATTGTATGTCTT TTTT ||| |||| ||||||||| ||| ||||| || ||||
CATGTGCAGGCTCTAGTGGA ACA TTTA ATGATAGGT CGT TACTT GT ATGT /
TAGTAATTTTCTCACA CTCT - GATCTCGGA G CT - TAA

GAM2965 CTATGCATACTATGTGCCCC 2669 TAGCAGAGTA 5739 AT - G- CC C G
GCGATGGCGGCTGTCGTCCT CGTTCGCATG CTATGC AC TAT TGC CG GATGGC G

GTAGCAGAGTACGTTCGCAT G |||||| || ||| ||| || ||||||
GG ggtacg tg atg acg GT CTGCTG C
ct c ag at C T

GAM2966 GTAGTGGATGTCCTGGACCA 2674 TGTCATGGAC 5744 G-- - - A-- -- TG T
TCGTGGCTACGGCTGCGTAG CATCGTGGCT GTAGT GATG TCC TGG CCAT CG GC A
TGGATGTCATGGACCATCGT AC ||||| |||| ||| ||| |||| || ||
GGCTAC catcg ctac agg act GGTG GC CG C
gtg c t gtA AT GT G

GAM2967 GCGAGTGGTCGTTGACGTTG 2681 TATCAAGTAC 5751 -- TCG - GTT ---- G
TGGTTGTTTTACGAAGTAAA AGTTCTACTT GC GAGTGG TTG AC GTGGT TGTTTTAC A
ATATATAGCTATCAAGTACA TTGC || |||||| ||| || ||||| ||||||||
GTTCTACTTTTGC cg ttcatc gac tg tatCG ATAAAATG /
tt tt- a aac ATAT A

GAM2968 GGCGACAGGAAGTCTGTCCA 2675 TGAGGGAAGG 5745 A A-- TCCA - A - AA
AAGT CTA
ACCTCATTACCCTTTCCAAA CGTGAGAGCG GGCGAC GG AGTCTG AC CTC TTAC CCTTTCC
AGC CGG C
GCAAGTCGGCTACCATACCG TCAG |||||| || |||||| || ||| |||| ||||||| ||| |||
TAAGCTGAGGGAAGGCGTGA CCGCTG CC TCAgac tg gag agtg ggaaggg tCG GCC
C
GAGCGTCAGACTACACCGTC - ACA ---- c - c ag AAT- ATA
GCC

GAM2969 CTTTTTTTTTGTGAGGCTTT 2682 TATAAAATTG 5752 T GAG --- TT
GTATAAATTGTTTTTTATAT TAAATAAAAA CT TTTTTTTGT GC TTTGTATAAA G
AAAATTGTAAATAAAAAAAC AACA || ||||||||| || ||||||||||
AG Ga aaaaaaata tg aaatatATTT T
c aa- tta TT

GAM2970 TAATACTTGACTGACTTAAA 2670 TACTTGACTG 5740 c ct aa--- - tAATTAATA TTC
ACTTGATAATTAATAATATA ACTTAAAACT TAAta ttgactga ta ac ttga ATATAA G
ATTCGTTTTTATATGTGACT TGAT ||||| |||||||| || || |||| ||||||
ATTTTAACGTCTAAATGTAT ATTAT AATTGATT GT TG AATT TATATT /
TAGTTAAATATTA A AT AAATC C TTATCAGTG TTT

GAM2971 TAGCTACTGAAGATAAAGAA 2683 TATTTCAAAA 5753 A ATAAAGAA ---- AA
GAAGTAAGAAAATCTGAAGT AGCTTTAGAA TAGCT CTGAAG GAAGTA AG A
ATTTCAAAAAGCTTTAGAAG GTTG ||||| |||||| |||||| ||
TTG gttga gatttc ctttat TC /
a gaaaaa-- GAAG TA

GAM2972 TAGCCTCCCACTTTTATGGA 2671 ATGAGTCATG 5741 CCC----- - AAATCTG CT
AATCTGGTAGCTCCTCCTAC AAATGTCCCT TAGCCT AC TTTTATGG GTAG C
ATGAGTCATGAAATGTCCCT TCAA |||||| || |||||||| ||||
TCAAAGGCTG GTCGGA tg aaagtact CATC C
aacttccc t gagta-- CT

GAM2973 CGTCTAGGCCACGTACAGTC 2672 TACAGTGTTA 5742 - ------ G T- --- TC- CCTCT
TATTGTCCTCGGACCCTCTG CTGTTGTGTG CGTCTA GG CCAC TACAG CTATT GTCC
GGAC G
CCTATAGGTTAATAGGAATA TATC |||||| || |||| ||||| ||||| |||| ||||
CAGTGTTACTGTTGTGTGTA GGATCT Gc tgtt gtcat tgaca GGAT TGGA /
TCGCTCTAGG C tatgtg - tg tAA AAT TATCC

GAM2974 AGTGCGGTGGCGATTGTATG 2687 TAAGCCGGTT 5757 GC A- TATGTAT T- - AA
TATCCTCTTATTTCGGGAAT CGAGGCGCCA AGT GGTGGCG TTG CC CTTAT TTCGGG T
GGACCCGAGTGTAAGCCGGT CTAA ||| ||||||| ||| || ||||| ||||||
TCGAGGCGCCACTAAACT TCA tcaccgc agc gg gaatG GAGCCC G
aa gg tt----- cc T AG

GAM2975 TTTTTTTAATGGTGTTGTGG 2676 TGAGGAATGA 5746 AA- -- TG - g- -- a ag
ATGAGGAATGAGGAATGAGA GGAATGAGAG TTTTTTT TGGTG T TG GAtgag aatga gga tgag
t
GTGTCTTATCTAGTCATTGG TGTC ||||||| ||||| | || |||||| ||||| ||| ||||
TTTATTACATGGATCATCAG AAAGAGG ACTAC G AC TTATTT TTACT TCT ATTc /
AGGGAGAAA GAG TA GT A GG GA - tg

GAM2976 TGTGTTGTTTTTAAAAAAAG 2677 TAAAAAAAGA 5747 G Tt catt
AAAAAAAAAGGCATTATTTT AAAAAAAAGG TGTGTT TTT aaaaaaagaaaaaaaaagg A
TTCTTTTTTTTTCTTTTTTT CATT |||||| ||| ||||||||||||||||||
TTAAAAATATA ATATAA AAA TTTTTTTCTTTTTTTTTCT T
- TT TTTT

GAM2977 TTATAATTTATTTATCTAAT 2678 TAATATTAAA 5748 TTTATT Cta gt- TA
ATTAAAATATATATAGTTTA ATATATATAG TTATAA TAT atattaaaatatatata ttaAT A
ATTAATCATTAATAATGTAT TTTA |||||| ||| |||||||||||||||| |||||
GTATTTTAATATGTAATATT AATATT ATA TATAATTTTATGTATGT AATTA /
ATTTATAA TATT-- ATG AAT CT

GAM2978 GTTTGTATCGCATCTTTCCT 2679 TCGCATCTTT 5749 T Atcg tt ag TTA T CCT--
CTA
GTGTGTAGTTGTTTATGTTG CCTGTGTGTA GT TGT catct cctgtgtgt ttgT TGT GGATG
GTGGGT T
GATGCCTGTGGGTCTATCAC GTTG || ||| ||||| ||||||||| |||| ||| ||||| ||||||
ACCCGCCCCTCCATCCCACA CG ACA GTAGG GGGCACACA AACA ACA CCTAC
CGCCCA /

AACACAAAACACACGGGTTG C AAA- TT A- CAA C CTCCC CAC
GATGAAAACACGC

GAM2979 GGCGCCTACGCACTTTGTAT 2684 TATAAGACTG 5754 TAC - ----- g ga- aaatactagG
AACTA
ATAAGACTGATTGTAAATAC ATTGTAAATA CC GCACTTTG TA tataa act ttgt TGGAGT
G
TAGGTGGAGTAACTAGGAAA CTAG || |||||||| || ||||| ||| |||| ||||||
AACTCTAACAAAAAGGTGTT GG TGTGAAAT AT GTGTT TGG AACA ATCTCA
/
GTGCTGTTTATTAAAGTGTA CA- T TTGTC G AAA ---------- AAAAG
CGGAGCC

GAM2980 TTGGATAAATTAGGTTGACA 2680 TTGACATTAG 5750 TAAAT---------- g t aca a
TTAGTAACAGAAAGTATTCA TAACAGAAAG TTGGA TAGGtt acat agta gaa g
ATATTATGTAGACCTATAAA TATT ||||| |||||| |||| |||| |||
AAATGAGACCCTCCAA AACCT ATCCAG TGTA TTAT Ctt t
CCCAGAGTAAAAAAT A - AA- a

GAM2981 CCTGTTTCACCTATCTCTAA 2685 TAAGTAGGAT 5755 TTTCAC TC AAA- AA TGACAT--
ATCT T
AAATCAAAAATTCTATGACA TAATATTTGG G CTATC TAA TC AAATTCTA TTTTAT
TTATTT T
TTTTTATATCTTTATTTTTT AATT | ||||| ||| || |||||||| |||||| ||||||
GGAATAAGTAGGATTAATAT T GATAG ATT AG Tttaaggt aggatg aatAAG T
TTGGAATTTGAGAAAAATTA TAA--- CT AAAA AG ttataatt ---- G
TCGATAGAATTAGG

GAM2982 TTTTTATAAATTTTTATGAG 2686 TAAAGTGTAT 5756 TTT ----- - A
TATTTTTACAAAAATGTATA GTCTTATGTA TTTTTATAAAT TATGAG TATTTT TACA A
AAGTGTATGTCTTATGTATA TATT |||||||||| |||||| |||||| ||||
TTTATAAAAA AAAAATATtta gtattc gtgaaa ATGT A
tat tgtat t A

GAM2983 CCTTTAAAATTGATGCATTA 2688 ATGCATTATA 5758 a c tagt
TAAGATCGTGTAGTAAATCC AGATCGTGTA CCTTTAAAATTGatgcattata gat gtg a
ACTATCCTGTAATGCATTAA GTAA |||||||||||||||||||| ||| |||
TTTTAAAGG GGAAATTTTAATTACGTAATGT CTA CAC /
C T CTAa

GAM2984 TCTGTGGGGGAGTGGGGTGT 2691 TGGTTTGAAC 5761 GG - G GG ATTAG G TAG
TGTGGATATTAGAGGGTAGA GTCTCCATTA TCTGTGGG AGTGGGG TGTT T AT AG G A
GGGTGCTGGTTTGAACGTCT ACCC |||||||| ||||||| |||| | || || |
CCATTAACCCACGGG GGGCAccc ttacctc gcaa g tg tC T /
aa t - tt g---- G GGG

GAM2985 AGCTTTTATGTGTGTGAAGA 2689 TGTGTGAAGA 5759 TTTTAT- t agt g ta
AGTGATGTTTAGGGTAAGGT AGTGATGTTT AGC Gtgtg gaaga gat tt g
CTGTCTTTTTGCATTGGATT AGGG ||| ||||| ||||| ||| ||
TGCT TCG TACGT TTTCT CTG AA g
TTTAGGT T GT- G Tg

GAM2986 GAGAGTTGAAACCTTCGCTA 2690 TCGCTACTCA 5760 A Ttc---- tactcaag ag
CTCAAGTTAGTAAGAAACTA AGTTAGTAAG GAGAGTTG AACC gc ttagta a
CTAGAATTCATGCACAATTT AAAC |||||||| |||| || ||||||
GGTTGCAACTCTT TTCTCAAC TTGG CG GATCAT a
G TTTAACA TACTTAA- ca

GAM2987 TTGTGTCCATATGTGTACCC 1145 TACCTCAACA 4215 CATATGTGTACCCGAGAAA AA AA
T CCTAA C AATAA
GAGAAAGTAATTTAATGTTG TTCTCAACAG TC GT TTT TGTTG AGAA GAG TATT
A
TAGAACCTAAGAGCTATTAA AAAA || || ||| ||||| |||| ||| ||||
TAAAAACCCAATACCTCAAC GG CA aaa acaac tctt ctc atAA /
ATTCTCAACAGAAAACCACG ---------- CC ag - acaa- c CCCAA
GCACAG

GAM2988 TACATTTCTAAATATAAATT 1153 CATTTCTAAA 4223 a ct ataaattaaattt A T- AG
AAATTTGTTATGATCTGATA TATAAATTAA TAc ttt aaat GTT TGATC GATA C
AGCGAGTATCTTGATCAAAT ATTT ||| ||| |||| ||| ||||| ||||
TGTCGTGCTAAAATTTTTAA ATG AAA TTTA TAA ACTAG CTAT G
ACGTA C TT AAATCGTGCTGT- - TT GA

GAM2989 CGTGTTTATTCAAGGGAGTG 1154 AGGGAGTGGG 4224 - CAag a gga g c
GGATAGGGTTCGACGGTTCG ATAGGGTTCG CGTGTTT ATT gg gtg tagg ttcga g
AAACTTAACACACCAAATAA ACGG ||||||| ||| || ||| |||| |||||
TCGAGCGCG GCGCGAG TAA CC CAC ATTC AAGCT g
C TAAA A A-- A T

GAM2990 CCCCCCTCACCGGTGTTAAT 1155 TTTGCCGTTT 4225 - AC G AATA CAC - A T C
GCTCGCA
ACGCACGACAATAAATGAGC ATTTGTTTAT CCCC CCTC CG TGTT CG GACAA TAAATG GC
GACA AC C
TGACACACGCTCGCACATAC TGGG |||| |||| || |||| || ||||| |||||| || |||| ||
ACAGTTTGTTTGCCGTTTAT GGGG GGGG GC ACAG gt ttgtt atttgc cg ttGT TG /
TTGTTTATTGGGGACAGCGA C CA G gg-- tat t - t T ACACATA
CGGGGCGGGG

GAM2991 TTTTTAAAAATTTGAATTTA 1156 TGACAAAGTA 4226 AAAA--- C--------- ---- C
TGTTCGTCATTTGACCCAGG AGGTAATATA TTTTTA TTTGAATTTATGTT GTCATTTG
AC C
TAAGATAAATGACAAAGTAA AATT |||||| |||||||||||||| |||||||| ||

GGTAATATAAATTTAAGGTC AAAAAT GAATttaaatataa cagtAAAT TG A
AATCTAAAAA CTAACTG tggaatgaaa AGAA G

GAM2992 GGCTCCGAAGGTCCGCTGCT 2692 TGAGAAGTAG 5762 T AA- - CGG- C T--- C C TC
CGGCTCCGCTCACCGCTCCG CGTGTGGACT GGC CCG GGTCCGC TGCT CTC GC CAC GCT CGG T
GTCTGGCTGCAGCAGTGCTT GAAC ||| ||| ||||||| |||| ||| || ||| ||| |||
CGCTGAGAAGTAGCGTGTGG TTG GGc tcaggtg gcga gag CG GTG CGA GTC /
ACTGAACGGTGTT T aag t tgaa t CTTC A C GG

GAM2993 TCTGTCTGTCGCGAAACGTA 2693 ATAATGCCTA 5763 CTGTCG- AAC -- C T -- A
CAGCTCTAATTACATTGTTT ATTGATCTAA TCTGT CGA GTAC AG TC AATTA CATTGTTT A
AAGGAGATAATGCCTAATTG GTAC ||||| ||| |||| || || ||||| ||||||||
ATCTAAGTACATGTTGACCA AGACG GTT catg tc ag ttaat gtaataGA G
AACGCAGA CAAACCA GTA aa t - cc G

GAM2994 CTTCGAGAAAAGCGCTCTTC 1146 TGTTGCGTCT 4216 AGAAA-- - TCTT---------- TA
GAGTACTCCCTCGGCAGACT CCCATAGTGA CTTCG AG CGC CGAG C
ATTCTGTTGCGTCTCCCATA AG ||||| || ||| ||||
GTGAAG gaagt tc gcg GCTC T
gataccc t ttgtCTTATCAGACG CC

GAM2995 CGGGTTGACAAAATCGAACG 1147 TGAGCTCCGC 4217 G AAA GAA- T AA TT
GTGTTTAAGCTTTGACCGGT GAAGACTCTG CGGGTT ACA TC CGG GTTT GCT G
GAGCTCCGCGAAGACTCTGT TAAG |||||| ||| || ||| |||| |||
AAGCCTG GTCCga tgt ag gcc cgag tGG A
a ctc aagc t -- CC

GAM2996 CGTGAGAGGCTGACAGCTTA 1148 ACCCCGTATA 4218 CT C T- CAAAAT-- A AAATACAC AGCACC AT
CGAAGCAAAATCACAAAGAA TCACAAGTCT GA AGCT ACGAAG CACA AGA ATGC TAGAT C
AATACACATGCAGCACCTAG CTGT || |||| |||||| |||| ||| |||| |||||
ATATCCAGTTTAACCCCGTA TT TTGA TGTTTT Gtgt tct tatg ATTTG /
TATCACAAGTCTCTGTGTCA TT T TC TTATAACT c gaacacta cccca- AC
ATATTTTTTGTCTAGTTTTT
TTTTCCTCCTG
GAM2997 CCCGGACAGCGTGCAAGTCT 1149 TAGAGAGCAC 4219 ACAG CAA - GA AG GGG GA
CGACTAAGGAGCGGGCGCGA ACACGACGAC CCCGG CGTG GT CTC CTA GAGC CGC G
GCGAGCGAAAGTTTTATAGA CGGG ||||| |||| || ||| ||| |||| |||
GAGCACACACGACGACCGGG gggcc gcac ca gag gat TTTG GCG C
agca a-- c a- AT AAA AG

GAM2998 GTTGTCAAGGGCTGTGAACA 1150 TCAAGGGCTG 4220 c g ac a aA
CATTGGCAATCTCGCCGACG TGAACACATT GTTGt aag gctgtga ac ttggc T
TCATTACGGCACTTAATAAC GGCA ||||| ||| ||||||| || |||||
CAATA TTC CGGCATT TG AGCCG C
A A AC C CT

GAM2999 CCGCTCGATCTCGGCTCTGT 1157 ATCGCGGTCC 4227 GATCT CT T CGT
CGGTCGCCGTCCTTCGCGAT GTTCGGGAGC CCGCTC CGG CTG CGGTCGC C
CGCGGTCCGTTCGGGAGCGG GG |||||| ||| ||| |||||||
ggcgag gcc ggc gctaGCG C
ggctt t- - CTT

GAM3000 TCGTGTTGATATGATAAATG 1158 TCAAAAGATT 4228 ATGATAAAT CAAA G
ACAAATGATACGCTGTATCA AATACGA TCGTGTTGAT GA TGATAC C
ACATCTCAAAAGATTAATAC |||||||||| || ||||||
GA agcataatta CT ACTATG /
gaaaact-- ACA- T

GAM3001 AACTAATTAATTATTTAATG 1151 TTTAATGTGT 4221 TT T - gttttata - A- TT
TGTTTTATATTATATTTTTA TTTATATTAT AACTAA AA TAttta atgt ttatatttTTATA TATTTT
ATGA A
TATATTTTAATGATTAATTC ATTT |||||| || |||||| |||| |||||||||||| |||||| ||||
ATAAAAAATGTTATAGAGAT TTGATT TT ATAAGT TGCG AATATAGAGATAT GTAAAA
TACT /
ATAAGCGTATGAATATTTTT TT T A -------- T AA TA
TTAGTT

GAM3002 GGTTGTAGCGAAATGTCCCC 1152 CATGCCGCCG 4222 --------- TA AA T A A GC
AACCCC
AACAGCGGCCAGTCAACCCC CTCAAACTTA GGTT G GCG ATG CCCCA C GCG CAGTC
C
CTTAAGCGACTGATGCGTGG AACC |||| | ||| ||| ||||| | ||| |||||
GGCATGCCGCCGCTCAAACT ccaa c cgc tac GGGGT G CGT GTCAG /
TAAACC attcaaact gc cg - - - A- CGAATT

GAM3003 TACCCGTAAATAAGCACGCT 1160 GTATGGCTGT 4230 GTAAATA ACGCTTTAAAT A AA
TTAAATCAAACAACAACAGG AAAGGGTA TACCC AGC CA ACAAC C
TTGTATGGCTGTAAAGGGTA ||||| ||| || |||||
atggg tcg gt tgTTG /
aaatg-- ---------- a GA

GAM3004 GTGTTTACAAACAAGCAATC 1167 ATCACTTTGT 4237 C C TCTATA C CAGCATC
TATAATTCGCACAGCATCAA TTATTTTAGA GTGTTTA AAA AAGCAA ATT GCA A
GAATTTCTGCAATCACTTTG CAC ||||||| ||| |||||| ||| |||
TTTATTTTAGACAC cacagat ttt tttgtt taA CGT A

- a tcac-- - CTTTAAG

GAM3005 GAAATATCCTTAGAAGCATG 1159 TGAGTATATT 4229 ---------- GA T T TTC GAGCCAT - A-- AA
TCTTTCGGCAGAGCCATTAC ATATGCCTTA CTTA AGCA G CT GGCA TAC CGGT GC A
CGGTAGCAAAAAAGCAACAT GCCT |||| |||| | || |||| ||| |||| ||
TGAGTATATTATATGCCTTA GAAT TCGt c ga ccgt atg gtTA CG A
GCCTGCTCATAAGCGTCCTT CTTTTTTTTCCTGC AC c - tt- atattat a CAA AA
TTTTTTCATGGTATTTT

GAM3006 GCGACGGGCCGTTACGTTTC 1168 CACCGTGTTG 4238 AC C GT a tgc--- tcc---------- ca
ACCGTGTTGCGTCTCCGACA CGTCTCCGAC GCG GGGC GTTAC TTc ccgtgt gtc ga c
CTGATCAAGCTGTTCACGGC ACTG ||| |||| ||||| ||| |||||| ||| ||
AATGACATTCTTATACGGGA CGC CCCG CGATG AAG GGCATA CAG CT t
ACAGTAGCGCCCACGC A- - AC - TTCTTA TAACGGCACTTGTCGAA Ag

GAM3007 CTCCATAGTTCAAATGGAGC 1161 TTCAAATGGA 4231 AG a--- gag-- gaaaa taG
CTGAAAATTATAGTAATTTA GCCTGAAAAT CTCCAT ttca atg cct tta T
AAATTAAGGAGAGACATAAG TATA |||||| |||| ||| ||| |||
ATGAAAGATGGGG GGGGTA AAGT TAC GGA AAT A
GA AGAA AGAGA ATTAA TTA

GAM3008 TAACATGCAAAAAAAATATG 1169 TTTAAACTTA 4239 AA- TA cttattt agcacT
TTTAAACTTATTTTAAGCTA TTTTAAGCTA TAACATGCAA AAAA TGtttaaa taagct T
GCACTTATTTAAAAGCTTGT GCAC |||||||||| |||| |||||||| ||||||
TTTAAACACGTTTTAAATTG ATTGTATGTT TTTT ACAAATTT GTTCGA A
TATGTTA AAA GC T------ AAATTT

GAM3009 CATTAAATTATCATTTTTGA 1170 TAAATTATCA 4240 ca aat t A C ATC
ATGTATTTATACCAGATCAA TTTTTGAATG CATtaaattat tttttg gta tT TAC AG A
AAACTTGTACAATTATTAAT TATT |||||||||| |||||| ||| || ||| ||
AAAAAATAATTTAGTG GTGATTTAATA AAAAAT TAT AA ATG TC A
-- AAT T C T AAA

GAM3010 TTGATTTTCTTTCTAATACT 1162 TGGGAATAAA 4232 T TC A C ATAT TC A A TC
ATATATTTCTCTCGAAGAAG ATACTACTGT TTGATTT CTT TA TA TAT TTCTC GA GA GT T
TTCTTGCACATCATCTGGGA TGAG |||||| ||| || || ||| ||||| || || ||
ATAAAATACTACTGTTGAGT GACTAAA gag gt at ata aaggg CT CT CA T
AAATCAG T tt c c aaat t- A A CG

GAM3011 TCTCCGGTCTCCATAACTCG 1163 TGAGCACCTC 4233 C C CATAAC C CG A----- TTA T

CTCTCGCCTGGAGCTTTTAT CCCAGGGAAG TCT CGGT TC TCG TCT CCTGG GCTT TATAC A

ATACTAACGTGTGATGAGCA ATGA ||| |||| || ||| ||| ||||| |||| ||||| CCTCCCCAGGGAAGATGATG AGA GCCG AG agt aga ggacc cgag GTGTG A ACGCCGAGA - C T----- - ag cctcca tA- C

GAM3012 GGCGGCGGGGCAGCGGCGCG 1164 TCCGCGCTCG 4234 C AG - GA GA GAGA

GGCGACGGGAGCGAGAGGGC GGCCCCCCGC GGCGG GGGGC CG GCGCGGGC CGG GC G

GAGCGACCGGTCCGCGCTCG C ||||| ||||| || |||||||| ||| || GGCCCCCCGCC ccgcc ccccg gc cgcgcctG GCC CG G - g- t -- AG AGCG

GAM3013 GGGTTGTAAGTTTTAATCAG 1165 TCCTGGGTGT 4235 G AATCAGTAGG- - AAA - AAG

TAGGTGTACCCAAAAAGGCC CAGGATTTTT GG TTGTAAGTTTT TG TACCCA AGG CC A AAGAGTGCGGATCTCCTGGG ATAG || |||||||||| || |||||| ||| || TGTCAGGATTTTTATAGAGA CC AACATTCAGAg ac gtgggt tCT GG G CTTACAAGCC G atatttttagg t cc- A CGT

GAM3014 CTTTTGGCCCCTCTGGGTCG 1166 CCTCTGGGTC 4236 T c gt gaagt g

CGAGGAAGTGGCGGACGCCT GCGAGGAAGT CT TTGGCCc tctgg cgcgag ggc G TAAGCTCGTGCCGGACGGGC GGCG || ||||||| ||||| |||||| ||| CGACGG GG AGCCGGG AGGCC GTGCTC CCG A C C -- GAATT C

GAM3015 GGAAACGCGCCAGACTCCGG 1174 TGAAGGATTT 4244 A-- - CCAGAC GGAAC aa tttatca t

AACTATGAAGGATTTATCAC ATCACTGTAT GGA ACG CG TCC TAtg gga ctg a TGTATACAGACTCCGACGTA ACAG ||| ||| || ||| |||| ||| ||| CGAAGGATAATCACGACGTA CCT TGC GC AGG ATGC CCT gac t ACTCC CAA A ACTAAT AAGC- AG CA----- a

GAM3016 GCTTAAGTACGGGCCGCGGC 1171 CTGCCGCAAG 4241 T GGC C - A- C AT G TT TC C

GATCGCGGGCGTCGATCGCG CGCGATCCCG TTAAG ACG CG GG CG TCGCGGG GTCG CGC TGCGGC GGAG CGG T

TGCGGCTTGGAGTCCGGCTG CGAC ||||| ||| || || || ||||||| |||| ||| |||||| |||| ||| CCGTTTCTGCCGCAAGCGCG GGTTC TGC GC CC GC agcgccc tagc gcg acgccg tcTT GCC /

ATCCCGCGACACGACCCGAC T A-- - A Ac - -- a -- T- G GTTCTTGGGC

GAM3017 GGCGACGGCCGCGCTTACGC 1172 TCAGCCACCA 4242 A-- C TTA C C- - CC

GGCGCTGGGTCCGCCCACAT CGCCCGCGCG GGCG CGG CGCGC CG GG GCTGG GT G

CAGCCACCACGCCCGCGCGC CCCG |||| ||| ||||| || || ||||| ||
CCGCCCCGCC CCGC gcc gcgcg gc cc cgact CA C
CCC c ccc a ac A CC

GAM3018 TTGGTCAATCGGTACTCAGA 1173 TCAGATGCTT 4243 TCAATCGG c tctctccaatatatc ATA
TGCTTCTCTCCAATATATCG CTCTCCAATA TTGG TACt agatgct GGTACTCA T
GTACTCAATATATAGTGAGT TATC |||| |||| ||||||| ||||||||
ACCAAATGGCATTTTGGTAA AACC ATGG TTTACGG CCATGAGT A
AAATCCCAA CTAAAA-- T TAAA---------- GAT

GAM3019 TCGTTTTTTTTAACCCAGTT 1175 TAAATGGTTA 4245 TTT-- CAG T T - - ACA- TG A AA
TTACGTATAATATGATAACA AATATACAAT T TTTAACC TT TACG ATAA TA TGATA TTTGT ATATA TG A
TTTGTTGATATAATGAAATG GA | ||||||| || |||| |||| || ||||| ||||| ||||| ||
ACGTATATACAAACTTATAT a aaattgg aa ATGT TATT GT ACTAT AAACA TATAT GC T
CAATGCTTATTGTATAAATG catat ta- t - C A ATTC -- - AG
GTTAAATATACAATGA

GAM3020 TCTGACAACGAACAAAACGA 1176 ACGAACAAAA 4246 ACAac- aaaac- caa acC
ACTCAAAGCACCCACAAGCT CGAACTCAAA TCTG gaac gaact agc C
CTAGTTCAACAAAGTTCATC GCAC |||| |||| ||||| |||
ACGCAGA AGAC CTTG CTTGA TCG A
GCACTA AAACAA TC- AAC

GAM3021 GGTCTGTACATAATAAGAAA 1177 TAGCTTTCAC 4247 ATAATAAGAAAA AG ---- TG
AACTTAGGGTGAAAGTTAGG CTCAAGTAAG GGTCTGTAC ACTT GGTGAAAGTTA GGT C
TTGCTCACCACTATAGCTTT TACA ||||||||| |||| |||||||||| |||
CACCTCAAGTAAGTACAGAT CTAGacatg tgaa ccactttcgat CCA /
C aa---------- ct ATCA CT

GAM3022 GAGAGAAAAGAAAAAAACCG 1178 ATAGAACCGC 4248 A AAA- AAA- C GG C C TCTAAAA C CA A
CGGGTGCCGGTGCTGTCTAA TGTCGCCGCC GA GA AAAC GCG TG CGGTG TG GGC GTTTT ATAAA A
AAGGCCGTTTTCAATAAAAA GTCG || || |||| ||| || ||||| || ||| ||||| |||||
TTTTTATAGAACCGCTGTCG CT CT TTTG CGT gc gccgc gc tcg caaga taTTT T
CCGCCGTCGTTTGCCGTTTG - GCTG GCTG C TT t c tg----- c -- T
TCGTCGTCGTCGTC

GAM3023 TTTGTTTATTTTTATGATGT 1179 TTTATGATGT 4249 TTATTtt--- aacatat- a T AG CA
AACATATATTAATGTTTACA AACATATATT TTTGT tatgatgt att atg TTACACAG CG A
CAGAGCGCAATAACGTCCTG AATG ||||| |||||||| ||| ||| |||||||| ||

TGTAATTATAAATTCTCATT AAACA ATACTACA TAA TAT AATGTGTC GC T
GACATCATATTTTTCTATTA TTATCTTTTT GTTACTCT A T CT AA
CAAA

GAM3024 TCTAGTCAAGTGCTTTTATT 1180 TGACCACAGA 4250 AGTC ----- --- CATATG
CCACAG CTAC
TTGTCATATGCTGCCACAGG GACCAACAAA TCT AAGTGCT TTTATTT TGT CTG
GTGGG C
TGGGCTACCTCAACCCATGA TAAA ||| ||||||| ||||||| ||| ||| |||||
CCACAGAGACCAACAAATAA AGA TTCACGG AAGTaaa aca gac tACCC /
ATGAATCGCCGGCACTTTAA AAT- CCGCT taa accaga accag- AACT
AGA

GAM3025 CGTCGCCTCCTGGAACTCCC 1181 TGGAACTCCC 4251 - Ct aactcc t a t C- ATCT
GGATATACCTCGCCCCGTAG GGATATACCT CGTCGC CTC gg cgga at cc cgccC GTAG T
ATCTTATATGTTACCTGGGT CGCC |||||| ||| || |||| || || ||||| ||||
GGGATTTCCGCGCCTCGAGC GCAGTG GAG CC GCCT TA GG GTGGG CATT A
GTGACG C CT GC---- T - - TC GTAT

GAM3026 GGGGGGCAGTGATAAGTCAT 1182 TAAGTCATGA 4252 - GCAG t c ac- agat
GACAATTTTAGATGAGGTAG CAATTTTAGA GG GGG TGA aagt atg aatttt g
AAATTTTGCATATTTTCAGA TGAG || ||| ||| |||| ||| ||||||
CCCACC CC CCC ACT TTTA TAC TTAAAG a
A AG-- - - GTT ATGg

GAM3027 ATTCCACGTTCTCATAAAAA 1188 TCCACGTTCT 4258 - c aaacag- TAAAAA AC
CAGGCACTTAAAAAGAGCAC CATAAAAACA ATtcc acgttct ataa gcaCT GAGC C
CAGGTTTAGTGTAGTCTTAT GGCA ||||| ||||||| |||| ||||| ||||
TATAGAATGTAGGAAT TAAGG TGTAAGA TATT TGTGA TTTG /
A - ATTCTGA ------ GA

GAM3028 CGGATTATCTATGTGCATGG 1183 TGCATGGAGT 4253 - TATGt--- ----- a tatc AA
AGTGTCCTACATATCAAAAT GTCCTACATA CGGATT ATC gcatgga gtgtcct ca aaAAT A
AAATGGTTTTACTGAAGGAT TCAA |||||| ||| ||||||| ||||||| || |||||
ACAATTGTTCATGTTGTTTC GTTTAA TGG TGTACTT CATAGGA GT TTTTG /
TTGGTAAATTTG A TTCTTTGT GTTAA A CA-- GT

GAM3029 TCCTCTCGATCGGATCGCAA 1189 TCTCGATCGG 4259 tct a t caa tt- AA
CGCTTTACCCTAGAAGCCAC ATCGCAACGC TCC cg tcgga cg cgc taCCCTAG G
TAGGGTGTACGCGGCCGTTC TTTA ||| || ||||| || ||| ||||||||
TGACGTTGGA AGG GC AGTCT GC GCG GTGGGATC C
TT- - T CG- CAT AC

GAM3030 AGGCAAGATTCACTCTGCAA 1184 TGCAAGACGT 4254 CAA TCt------- cg t- gaa- T
GACGTGTGAAGTAGCGAACG GTGAAGTAGC AGG GATTCAC gcaaga tg gaagtagc cGC
C

CTCACGCGAAGAGCTATTTT GAAC ||| ||||||| |||||| || |||||||| |||
TTCAGTTTTTGTTCTTTCTC TCC CTAGGTG TGTTTT AC TTTTATCG GCG A
TCGTGGATCGCTCCT TCG CTCTCTTTCT TG TT AGAA C

GAM3031 ATGCATTATATATTTTATAT 1190 TATATGAATT 4260 TTT attatag aagag
GAATTATAGTTGCAAGAGTT ATAGTTGCAA ATGCATTATATA tatatga ttgc t
ACACGTAAAACAACTCATAT GAGT |||||||||||| ||||||| ||||
ACATTATATAATGTAT TATGTAATATAT ATATACT AATG /
TAC CAACAA- CACAT

GAM3032 ACAGATTTGGGGTGGAGACG 1185 TGGGGTGGAG 4255 ATTt--- - ag-- ------- gatACT---
A
GCGTGGGCGATACTGTATAA ACGGCGTGGG ACAG gg ggtgg acggcg tgggc GTATA
A
AGTTGTACTACTTACCAGCC CGAT |||| || ||||| |||||| ||||| |||||
CAGTCAGTGTGCTGTAGTGC TGTC CC CCACC TGTCGT ACCCG CATGT G
CACCACCTGTAAAGCTGT GAAATGT A GTGA GTGACTG ACCATTCAT T

GAM3033 TTATTGATAAGGATTAATGA 1186 TAAGGATTAA 4256 g- ta- c
TTATTTAACAAATTAAATAA TGATTATTTA TTATTGAtaag at atgattatttaa a
TTATATTATAGCTTATCAAT ACAA |||||||||| || ||||||||||
AA AATAACTATTC TA TATTAATAAATT a
GA TTA A

GAM3034 TCGGGGGGAGGAGAGGAAAC 1187 AGAGGAAACC 4257 G Ga aaa--- a cac
CGGGGACTCACCGGCGGCCT GGGGACTCAC TCGG GGGAG gagg ccgggg ct c
CGGACCGAGCCTCGCTCCCG CGGC |||| ||||| |||| |||||| ||
CCGG GGCC CCCTC CTCC GGCTCC GG /
G G- GAGCCA - cgg

GAM3035 AGGCTGTCCGGAAATCTAAG 1191 TAAGTTAATG 4261 CT AAA t ataaa gatg
TTAATGAATAAAGTAGATGG AATAAAGTAG AGG GTCCGG TCtaagt aatga gta g
TTAATACTCATTGCTTAGAA ATGG ||| |||||| ||||||| ||||| |||
TTGGACTACTT TTC CAGGTT AGATTCG TTACT CAT /
AT A-- - ----- AATT

GAM3036 TAAATAGTATTTTAGGGTTA 1192 TTTTAGGGTT 4262 TAG- t - aat-- taAA
AAGTAATACTTTAAAGGGAC AAAGTAATAC TAAA TAt ttagggttaaa gt actt G
AAGTCACAGACATTTGATCT TTTA |||| ||| |||||||||| || |||
TAGTATAAATTTTTA ATTT ATA GATTCTAGTTT CA TGAA /
TTAA T A GACAC CAGG

GAM3037 CTGATGTCCCGTCCGGTTTT 1196 ACGACATTAA 4266 GA GT GG --- CACG C G

TAACACGGTCCCGGGCCCGT ATAGGAAGGG CT T CCCGTCC TT TTTAA GTC CG G
GACGACATTAAATAGGAAGG ACGG || | ||||||| || ||||| ||| ||
GACGGGGTGGGGG GG G Gggcagg ag aaatt caG GC C
GG TG ga gat acag T C

GAM3038 AATCTTACCACTGTGTGTGT 1193 TCGTGCTGTC 4263 T - ---------- TG - TG TG C TG
GCGTGTGTGTGTCGAGTC CGCACATATT T AC CACTGT GTGTGTGCG T G TG TCGAGT GTGT T
GTGTTGTCCGCACATTTGAG TTAT | || |||||| |||||||| | | || |||||| |||| TCGTGCTGTCCGCACATATT A TG GTGACA tatacacgc g c gc AGTTTA CACG / TTATCTTTTGGGTACAGTGT T T TGGGTTTTCtattt ct t gt tG - CC GTTAGATT

GAM3039 TAGTATTGAAAAGGTGTTTG 1194 TTTGATGCAT 4264 A AAAG - TT - TG TTCT- - T
TATTTATGTATATTTGGTTT ATTGAATATC TAGT TTGA GTGTT TGTA TATGT ATATT GT TCAAGTAGC CC A
CTTCAAGTAGCCCTATAGGC ACAT |||| |||| ||||| |||| ||||| ||||| || ||||||||| || GCTATTTGATGCATATTGAA GTCA AACT TACGA ACGT Ataca tataa ta agtttATCG GG T
TATCACATATTTGCACAGCA - ---- C TT c gt tacgt C A TTCAAACTG

GAM3040 TTTTGTTCATACGTATAGTC 1195 TCGAAACGAT 4265 CATACG---- T C TT--- T TA T CTA
TTCTTAAGTTTTTAATATTT GTTATTTTTA TT TA AGT TTCTTAAGTT TAATATT GTT TCGA ACG A
GTTTATCGATACGCTAACAC ATTT || || ||| |||||||||| ||||||| ||| |||| ||| CCGTCTCGAAACGATGTTAT AA AT TCA AAGAAtttaa attgtag caa agct TGC C TTTTAATTTAAGAAACTTTA TAAAAATAAA T - ttttt - -- C CCA AAATAAAAATAACAAAA

GAM3041 GACTGTTTGTGCATGTGTTT 1197 TGGAAGGATG 4267 - TGT - T tg atgtt aactg a
TGGAAGGATGTTGGAAACTG TTGGAAACTG GA CTGTT GCATG TGT T gaagg gga tc c
TCACGTGAGCTCTCCCCTAG TCAC || ||||| ||||| ||| | ||||| ||| || CCTTTTGACATACCGTGTTG CT GGCGG TGTGC ATA A TTTCC CCT AG G TGGCGGCTC C TGT C C GT GATCC CTCG- T

GAM3042 CGATAAGTCGCGTGTAGGCG 1198 AACCGGATAT 4268 -- TCGCGTGT - AC- - CATCaa atct gatttaa
ACTGGCTACATCAACCGGAT CTGCGGGGAT T AAG AGG CG TGG CTA ccggat gcggg A
ATCTGCGGGGATTTAAAAAG TTAA | ||| ||| || ||| ||| |||||| ||||| ACGACCCGTTGTCATCCGGC G TTC TCC GC ACC GAT GGCCTA TGCCC / TTAGACCAAACCGTCCTTTT CC TACTATTT T CAA A TC---- CTGT AGCAGAA ATCATCTTCCGTCG

GAM3043 TATATGGTGCACTATGTAAA 1199 TATGGTGCAC 4269 -- ---------- a - TATG
GCT
CGACATTATGGGCGTGCTTT TATGTAAACG TAtatgg tgcacta tgt aac gacat GGCGT T
TAAATGCCGTGTCTGTTCAC ACAT ||||||| ||||||| ||| ||| ||||| |||||
ACTTCATTAAAATATTTGGT ATGTACT GCGTGGT ACA TTG CTGTG CCGTA T
GCGTTTCATGTA TT TTATAAAATTACTTC C T ---- AAT

GAM3044 CCCCATGGGCTCTCTTCTAG 1200 CACTTGGTGA 4270 ATGGG TT GAAACGAAAAT
CGAAAC
AAACGAAAATGGTGCTCGAA GAGAAAGGGG CCCC CTCTC CTA GGTGCT A
ACAAAAACTAGGCACTTGGT |||| ||||| ||| ||||||
GAGAGAAAGGGG gggg gagag ggt tcacGG A
aaa-- t- ---------- ATCAAA

GAM3045 AGTTTGTATATTTAAGAATG 1201 TTTAAGAATG 4271 T t aaataaa tt C G GATT
AAAATAAAATATTTTCGAAG AAAATAAAAT AGTT GTATAt taagaatga ata tT GAA C A
CGATTATAAAGTTCAATTTG ATTT |||| |||||| ||||||||| ||| || ||| |
TCATTTGTCATTTTTGTGTA TCAA TATATG GTTTTTACT TGT AA CTT G /
TATCAACT C T GTTTAC- TT - - AAAT

GAM3046 AATCGTTCTCACACGTTCGA 2554 CACACGTTCG 5624 CT- - c ga ta ca
ATTACCGACACACATCTGTC AATTACCGAC AATCGTT ca ca gttc at ccgaca c
GGCTATAGGACTTGCTGCAC ACAC ||||||| || || |||| || ||||||
AACGGTT TTGGCAA GT GT CAGG TA GGCTGT A
CAC C T A- TC CT

GAM3047 TGCATCGGTGCCGTAACCTT 2555 TCGGTGCCGT 5625 Atc cc cct--- t- AC
CGCTGCTTTACTTAAAAAGC AACCTTCGCT TGC ggtg gtaa tcgc gcttT T
CTGTGATTTCATTTACCACC GCTT ||| |||| |||| |||| |||||
CCAGCA ACG CCAC CATT AGTG CGAAA T
ACC -- TACTTT TC AA

GAM3048 TACAATAAAGATATATCTTA 1202 TATCTTAACC 4272 ATAAAGATAtat aacc a
ACCTTTATCTTTGAGCCCAA TTTATCTTTG TACA ctt tttatctttg g
GGATAGACAAAAAGTAAGAA AGCC |||| ||| ||||||||||
AAACATGTA ATGT GAA AGATAGGAAC c
ACAAAAAGAAT- AAAC c

GAM3049 AGGAGTAAAGTTGTTGCTTC 2559 AAGAATGTTT 5629 AAA TT Ca--- tttc- - a T
AAGAATGTTTCATACAACTG CATACAACTG AGGAGT GTTG GCTT agaatg ata caactg agaG
G
AAGAGTGGTTCTGTAGTTGC AAGA |||||| |||| |||| |||||| ||| |||||| ||||
TATTTATGTATTCTAAGAAA TCTTCA CAAC TGAA TCTTAT TAT GTTGAT TCTT /
AGTCCAACCCACTTCT CC- C- AAGAA GTATT C G G

GAM3050 TTTTAGAACTGACCAACCAT 2556 GAACTGACCA 5626 tc- A -------- TG
GTTCACGTAAGTGACGTGAT ACCATGTTCA TTAgaactgaccaaccatgt acgtaAGTGACGTG TGAC
GCGCGC C
GACGCGCGCTGCGCGCGCGC CGTA |||||||||||||||||| |||||||||||| |||| ||||||
CTTCGGACGTCACACGTCAC AATCTTGACTGGTTGGTACA TGCATTCACTGCAC ACTG
CGCGCG /
TTACGTTTCACATGGTTGGT CTT - CAGGCTTC CG
CAGTTCTAAAA

GAM3051 TGGATCTTTACAAATAGAAG 2557 TCCATTGTAA 5627 T ATA TCTATTTT
GATCTATTTTTGTTACATTT AGCTTCA TGGA CTTTACAA GAAGGA T
TCTTTCCATTGTAAAGCTTC |||| |||||||| ||||||
A actt gaaatgtt ctTTCT G
c ac- TTTACATT

GAM3052 GTCAACATAACTATTTTGTT 2563 TAACTATTTT 5633 aa---- ttc tgaaac
CAGTTTGAAACCATGATTAG GTTCAGTTTG GTCAACAt ctattttg agtt C
CTTTTGAAATAGATACTGAT AAAC |||||||| |||||||| ||||
GTTGAT TAGTTGTA GATAAAGT TCGA /
GTCATA TT- TTAGTA

GAM3053 AAAATCGATTCCGTCCAAGA 2564 TCGATTCCGT 5634 c ccaag aaaaACA
TGATAAAAACATTTACCGGC CCAAGATGAT AAAAt gattccgt atgat T
ATCATAAACACGGAGTTTAT AAAA ||||| |||||||| |||||
TTT TTTTA TTGAGGCA TACTA T
T CAAA- CGGCCAT

GAM3054 GGCATTAAATCGTATCTATC 2558 TCTATCGGAT 5628 TTAAA TAtctat - - ttta AT
GGATTACCAAAAATTTAGCA TACCAAAAAT GGCA TCG cggatt acc aaaaa gC G
TGTCGCCGTTTTTTTAGGTC TTAG |||| ||| |||||| ||| ||||| ||
GATCCGCCGTCGGCTGCC CCGT GGC GCCTAG TGG TTTTT CG /
C---- TGCC--- C A TTGC CT

GAM3055 CGGGGGGAACAATGACGCAA 2565 CGGCGCCTAC 5635 G AACAATGA AAAA C CGCTG
AAGGGCCCCGGGCGCTGAGT TCGCGCCGCC CGGG GG CGC GGGC CCGGG A
TAAATCCGGCGCCTACTCGC CG |||| || ||| |||| |||||
GCCGCCCG gccc cc gcg tccg ggcCT G
g -------- ctca c AAATT

GAM3056 TTTATAATTAGATTTAAATT 2566 TACAGGTTTA 5636 T A - TT TT AAAAGAT
AAAAA
GGCTTCAATTAGACTTAAAA ATTGGCTTTT TTTA AATT GATT TAAA GGC CAATTAGACTT
TGAATG A

GATTGAATGAAAAAAGTATC TTAT |||| |||| |||| |||| ||| |||||||||||| ||||||
CATTTACAGGTTTAATTGGC AAAT TTAG TTAA attt tcg gttaatttgga atTTAC /
TTTTTTATAATTAGATTTAA - A t tt -- c------ CTATG
A

GAM3057 GGCGAGCGGCGAGGGCGACA 2560 TCCCGCGGTC 5630 C C -- AC T-- G A- G
CTGCTGGCGCGAGGGGACCC CGCCCGGTCC GG GAGCGG GA GGGCG ACTGC GGC CG
GG G
GCCGGGCTCCCGCGGTCCGC CCGC || |||||| || ||||| ||||| ||| || ||
CCGGTCCCCGCTCCCC CC CTcgcc ct cccgc tggcg tCG GC CC A
C c gg c- ccc G CG C

GAM3058 GCAAGACCGCGATGGCGTGT 2561 TGCCTTAGTC 5631 AA- - C --- TGT G AGA AG
GTTCCTCCCGAGTCTCAGAC ACGGATCGGG GC GA CCG GAT GGCG GTTCCTCCCGA
TCTC CC T
CAGTTTTGGGTAGGGGTCGG GT || || ||| ||| |||| |||||||||||| |||| ||
GAGGAATTGCCTTAGTCACG tg ct ggc ctg ccgt TAAGGAGGGCT GGGG GG T
GATCGGGGT ggg a a att --- - ATG TT

GAM3059 TATAATATAATTTTAATTTT 2562 TTTATATATT 5632 AA ttta - ttt
ATATATTTAATAATTTTTCA TAATAATTTT TATAATAT TTTTAAT tatattta ataat t
ATATTATATAAATATACATT TCAA |||||||| ||||||| |||||||| |||||
AAAAATATTATA ATATTATA AAAATTA ATATAAAT TATTA c
-- C--- A Taa

GAM3060 TAGATATAACGTATATATTC 2570 TATAACGTAT 5640 tat- t att at- ATA
ATTATATTTCCCATCTAATA ATATTCATTA TAGA aacg atat catt attTCCCATCTA A
AATTATGGGTGGGAAATCTG TATT |||| |||| |||| |||| ||||||||||||
AATGCGAGTGTTCGTTTTTT ATTT TTGC TGTG GTAA TAAAGGGTGGGT A
TTTA TTTT T AGC GTC ATT

GAM3061 ACTGTCTCTATGCCGCCTAC 2575 TGCCTGGTGG 5645 G GC - A Ttg tg aaagaa g
cTTG
TGTTGCCTGGTGGGAAAGAA GAAAGAACGG ACT TCTCTAT CGC CT CTG cc gtggg cg ggc
A
CGGGGCCTTGAGTAAGCCGC GGCC ||| ||||||| ||| || ||| || ||||| || |||
GCCCATTGGGGTCGGGGAGT TGG AGAGATA GTG GG GGC GG TACCC GC CCG
/
GATAGAGAAGGT A -- A - TG- GT ------ G AATG

GAM3062 GCGCCCCCCCCCCCGCGCGC 2576 AAGCACCCGC 5646 C C---------- CC CT CG TG
TGTGCCGTCTGACGGAAAGC GTGTAGGGCT GCGC CC CCC CGCGCG GTGC TC A
ACCCGCGTGTAGGGCTGCAT GCAT |||| || ||| |||||| |||| ||
ATAAATGGAGCGC CGCG GG ggg gtgcgc cacg AG /
A TAAATAtacgtc at c- aa GC

GAM3063 GTATTTTCATACAATAATTT 2577 TAGTTTATTT 5647 --- A A T T TAtagtt c tat
TTTAATGTTTATAGTTTATT CAATCGATTA GTATTTT CATAC ATA TTT TTAA GTT tatttcaat
gat c
TCAATCGATTATCAGTATCA TCAG ||||||| ||||| ||| ||| |||| ||| ||||||||| |||
TTGAAATATTAACTTAACAA CATAAGA GTATG TAT AAA AATT CAA ATAAAGTTA CTA
/
AATATGTATGTATAGAATAC TAT - A C - TT----- - Tga

GAM3064 TTCGAAGACATTAATACTGG 2567 TAGAGGACGC 5637 GACAT TAC - ----- GT GAC
TTTTCTTTCTCGTTATGACG AAAGAGAGAC TTCGAA TAA TGGTTT TCT TTCTC TAT G
ATCAATATAGAGGACGCAAA CAAT |||||| ||| |||||| ||| ||||| |||
GAGAGACCAATTTAGATTCG GAGCTT ATT accaga aga aggag ATA A
AG AG--- ta- g aacgc at ACT

GAM3065 GCCGCCAACCCGAGCGCCGG 2580 AGAAGGAGGA 5650 CCAACC --- C - ----------
aaacaagaa at
AGAAGGAGGAGAAACAAGAA GAAACAAGAA CG CGAG CG CGGag aaggag gag
ga C
GAATCACTCGAGACACGGCT GAAT || |||| || ||||| |||||| ||| ||
CAGAACCCAGCGACTCTTTA GC GCTC GC GCCTT TTTCTC CTC CT /
TTCCGCGTCCCTCGCACCCG CCAC-- CCT - A AGCGACCCAAGA GGCACAGAG
CA
GC

GAM3066 GGTTGGATTGTTTGTGTACA 2568 TACATTTATT 5638 TG ---------- TTATTT
TTTATTTTCATTTTGTGTAC TTCATTAAAG GGT GATTGTTT GTGTACAT T
ATTTATTTTCATTAAAGCGA CGAT ||| |||||||| ||||||||
TCTGACC CCA Ctagcgaa tacatGTG /
GT attacttttatt TTTTAC

GAM3067 TACTGTTAAAGGCTCCAGGG 2569 TTAAAGGCTC 5639 taa gaaactgaat G TAGAGT T
AAACTGAATTAGAGCCTAGA CAGGGAAACT TACTGt aggctccagg TAGA CC ACG T
GTACGTTGACGTTAGAATGG GAAT |||||| |||||||||| |||| || |||
TCTACTTGGGGTTTCTACAG GTGACA TTTGGGGTTC ATCT GG TGC G
TG TC- ---------- - TAAGAT A

GAM3068 GCGCGTATTTTTTCTTCACT 2581 GCGTATTTTT 5651 ttc t- t---- - C TA G
GTTGTCGGCGTCCTCTAGCG TCTTCACTGT GCgcgtatttttttc ac gttg cGGCG TC TC GC A
AGCGCACGAAGATTGCCGCC TGTC |||||||||||||| || |||| ||||| || || ||
CACCGACCTGTTCGAAAGAG CGCGCGTGAGAAAG TG CAGC GCCGT AG AG CG G
TGCGCGC CT- TC CACCC T A CA C

GAM3069 TTTGCCCCCCCCCCGACGCG 2571 CATTTCTCCT 5641 CCCCC ACGC GAC TCA ----
TTACA

AGAAAGACCTTGTCAGTGGG CCGGGGCGCA TTTGC CCCCG GAGAAA CTTG GTG
GGCG G
CGTTACAGCACCTTGCCTCT AG ||||| ||||| |||||| |||| ||| ||||
TCACGATCAAGACATTTCTC gaacg ggggc ctcttt GAAC CAC CCGT /
CTCCGGGGCGCAAG c---- ctc- acA TAG TTCT TCCAC

GAM3070 GGCTACTACTATAAGGCCTT 2572 TATAAGGCCT 5642 ACT- tat- ct a gatcttGG ATACTT
T
TAGCTTCGATCTTGGTGTAT TTAGCTTCGA GGCT AC aaggc tt gcttc TGT GCGTG A
ACTTGCGTGTAGGCGCGCTA TCTT |||| || ||||| || ||||| ||| |||||
ACAAAAAAGGGGCAGCAGTC TCGG TG TTCTG GA CGGGG ACA CGCGC G
TTTAATGTCACGGGCT GCAC TAAT AC - AAAAA--- AT---- G

GAM3071 GGTAAAGTTATACATTTACC 2584 AAAGTTATAC 5654 - t accgtt cAA- A
GTTGGACAAGGTAAGATTAC ATTTACCGTT GGTaaa gttataca tt gga GGTA G
CGACATCCTAATAGAATTGT GGAC |||||| |||||||| || ||| ||||
ATAACTTTTGCT TCGTTT CAATATGT AA CCT CCAT A
T T GATAAT ACAG T

GAM3072 ATATAATATTTCGTCGATAC 2573 TAATATTTCG 5643 a t c gtgatttCTC TT
GTGATTTCTCGTGTTTTTTC TCGATACGTG ATAt atatt cgt gatac GTG T
ATATAAAAAAGTATTATGAA ATTT |||| ||||| ||| ||||| |||
TATAATAT TATA TATAA GTA TTATG TAC T
A - - AAAAAATA-- TT

GAM3073 TGATCTCACGTCACAGTTTT 2574 TCTCACGTCA 5644 c c agttttttt TCTCGCGT
TTTTTTCATATGTCTCGCGT CAGTTTTTTT TGAt tca gtcac tttcATATG T
TGATACATCCCGTATGAAAT TTTC |||| ||| ||||| |||||||||
ATTTAAGGTGGTTGAAATCA ACTA AGT TGGTG AAAGTATGC G
A - GAATTTAT- CCTACATA

GAM3074 GGCGGCAAGCGAGATCCCTC 2588 AGGCAAAGCG 5658 AA AGATCC AGAC -- TCG
CGAGACGTCTGGCTCGTACT GGGCGCGCGC GGCGGC GCG CTCCG GTCTG GC T
GCTGCAGGCAAAGCGGGGCG CGCT |||||| ||| ||||| ||||| ||
CGCGCCGCT tcgccg cgc ggggc cggaC CG /
cg ------ gaaa GT TCA

GAM3075 TGACTTTCTGGAAATGGATT 2578 TGGAAATGGA 5648 TTTCtg a tttctgcaaatag T
TCTGCAAATAGAAGGATCTA TTTCTGCAAA TGAC gaa tgga aAGGA C
TCTTTACAACATCATTTTTC TAGA |||| ||| |||| |||||
CAATTTAATGTGTCA ACTG TTT ACCT TTTCT T
TGTAA- A TTTTACTACAACA A

GAM3076 GTTCATCTGCGTGAGCTTCC 2589 AAGGATCATT 5659 T- -------- G- TCTCA
GATCTCAGTATTGTTTGGAA GATTAACGCG GTTCA CTGCGT GA CTTCCGA G
GGATCATTGATTAACGCGGT GTTT ||||| |||||| || |||||||
TTGAAC CAAGt ggcgca ct gaaGGTT T
tt attagtta ag TGTTA

GAM3077 TATGTAATATTGTGGGACAT 2579 TGTAATATTG 5649 t tg gg c g T GTCATA
GTGTTGTGTGTCATATAAGA TGGGACATGT TAtgtaa at t ga at tgttg GT T
AAAACCAACAGATTTAAGTG GTTG ||||||| || | || || ||||| ||
ATTTTATATA ATATATT TA G TT TA ACAAC CA A
T GT AA - G - AAAAGA

GAM3078 GTCAAAAGAGGCCGCCAGCT 2585 TTTGTGCGAC 5655 AAAA- C C CT--
ACCCCAGAAAAGAA AG
AGACACCCCAGAAAAGAAGC ACGTTTTATT GTC GAGG CGC AG AGAC
GCAGAGAA A
AGAGAAAGAGACTTCTTTGT CTGC ||| |||| ||| || |||| ||||||||
GCGACACGTTTTATTCTGCG CAG CTCC Gcg tc tttg tgtttCTT G
TCCTCCGCTCGAC CTCGC T - ttat cacagcg------- CA

GAM3079 TTTGGTCGATGTAAAATTTT 2590 TGTAAAATTT 5660 CGA aaattttt - AAA
TGTCGATAAAAATTAAAAAA TTGTCGATAA TTTGGT tgta gtcgataa aaatTAA A
TAACTTAATTTATTATTGAT AAAT |||||| |||| |||||||| |||||||
CTCGTGTGTACAACCGAA AAGCCA ACAT TAGTTATT TTTAATT T
--- GTGTGCTC A CAA

GAM3080 TAAATTTCTGCGAGAGCACA 2582 GCGCATGGAA 5652 TTT G - CACCGCAC TTA GC
GAT
CCGCACCCTTACGCTGGCTC TTGTTGCTGG TAAA CTGC AG AGCA CC CGCTG TCG A
GGATAGCTACGAATAGCGCA CAGC |||| |||| || |||| || ||||| |||
TGGAATTGTTGCTGGCAGCT ATTT gacg tc ttgt gg gcgAT AGC G
TTTTA TTc g g taa----- tac A- ATC

GAM3081 GCCGCTCGGGGACTGCGCGA 2583 GACTGCGCGA 5653 C T a- - gaga- aaagaga gG
GACAAAAGAGAGGGGACGCC GACAAAAGAG GC GC CGGGg ct gcgc ca gg A
GGAGGGGTGGGAGGGCGCAA AGGG || || ||||| || |||| || ||
GGACCCCGCGCGC CG CG GCCCC GA CGCG GT CC /
- C AG A GGAGG GGGGAGG GC

GAM3082 TATTTTAATGGAACTGGATC 1144 TGGAACTGGA 4214 TTAAt- tca -------- c
ATTAGGACCTCTCCCGCCCA TCATTAGGAC TATT ggaactgga tta gga c
TTTAAATTTTTAGTTTCTAC CTCT |||| ||||||||| ||| |||
AATAATA ATAA CTTTGATTT AAT CCt t
TAACAT TTA TTACCCGC c

GAM3083 GTTTAGTGTAATAAATTTAA 2586 TTAGTGTAAT 5656 t ataaatttaataaa A AA
TAAAATATTGACAAAATAGT AAATTTAATA GT tagtgta at TTGAC A
TAAATGAATATATGAAAGTA AAAT || ||||||| || |||||
CATTATAC CA ATTACAT TA AATTG A
T GAAAGTATATAAG- - AT

GAM3084 GGCGGCGGGTCCCTCTTGTC 2587 TCCCTCTTGT 5657 G c tcttgtctcg g - TCACG
TCGGAGACGGCGGGTCACGG CTCGGAGACG GGCG CGGGt cc gagacg cg gG G
GTATTTCACGACGTCTCACG GCGG |||| ||||| || |||||| || ||
GTACTCGACGCC CCGC GCTCA GG CTCTGC GC CT /
A T CA-------- A A TTATG

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GENE    TARGET   UTR SEQUENCE            SEQID   BINDING-SITE
======== ========= === ======================= ======= ==========================
GAM15   KCNK4    3'  CAATATTGAGTGATGACATT   37825        TAAATA
                                TAATATTG     ATGACATT
                                ||||||||     ||||||||
                                GTTATAAC     TACTGTAA
                                    TCAC__
GAM15   PCDHB9   3'  AGCCATTAAAAATTTAA     33319           A
                                AGCCATTAAAAA TTTAA
                                |||||||||||| |||||
                                TCGGTAATTTTT AAATT
                                           _
GAM15   SDC2     3'  GCCATTAAGGATTTAAA     42567        AAA
                                GCCATTAA   ATTTAAA
                                ||||||||   |||||||
                                CGGTAATT   TAAATTT
                                    CC_
GAM16   CBFB     3'  ACTGCCTAAGGTTGA       12036     A   GGCC
                                ACT CCTG    AGGTTGA
                                ||| ||||    |||||||
                                TGA GGAT    TCCAACT
                                  C   ____
GAM16   DUOX1    3'  ATGGCCACCTGGAACAAGGTTG 32652     A       GC  _
                                ATG CTACCTGG  CA GGTTG
                                ||| ||||||||  || |||||
                                TAC GGTGGACC  GT CCAAC
                                  C       TT  T
GAM16   EPHA8    3'  TGGCTGCCTGGGCCCTGCTG   33906    A  A      AG
                                TG CT CCTGGGCC  GTTG
                                || || ||||||||  ||||
                                AC GA GGACCCGG  CGAC
                                 C  C       GA
GAM16   HOXC5    5'  TGACTCTTTGAAGTTGA     33249      ACC   GCCA
                                TGACT   TGG    GGTTGA
                                |||||   |||    ||||||
                                ACTGA   ACT    TCAACT
                                   GAA  ____
GAM16   UBE2H    3'  ATGCTATGCACCTCAGGTTGAG 17803     A   CC  G   __
                                ATG CTA  TG GCC  AGGTTGAG
                                ||| |||  || |||  ||||||||
                                TAC GAT  AC TGG  TCCAACTC
                                  _  __  G   AG
GAM16   ABCC1    3'  CAGGGGCAGGGTGTGCGTG   33398      C     C  _
                                CAGG GCAGGG GTG GTG
                                |||| |||||| ||| |||
                                GTCC CGTCCC CAC CAC
                                  C     A   G
GAM16   ARCN1    3'  CAGGCGTGGTGGCGTGCACCTG 11650       CAG_    G TG AG
           TA                    CAGGCG    GGCGT G  C  GTA
                                ||||||    ||||| |  |  |||
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                                GTCCGC   CCGCA C  G  CAT
                                   ACCA    _ GT GA
GAM16   B4GALT5  3'  CAGGTGGGGGTGTGAGCAG   21936     CGCA  C   T
                                CAGG   GGG GTGG GCAG
                                ||||   ||| |||| ||||
                                GTCC   CCC CACT CGTC
                                  ACC_  A   _
GAM16   CCND1    3'  GGCTGCAGGGCCGTTGGGTA  38213    _     G  G  CA
                                GGC GCAGGGC TG TG  GGTA
                                ||| ||||||| || ||  ||||
                                CCG CGTCCCG GC AC  CCAT
                                  A      _ A __
GAM16   CDH4     3'  GGTGCAGGGCGCTGTGGGGGT  12179    C       G   CA
                                GG GCAGGGCGT GTG  GGT
                                || |||||||| |||  |||
                                CC CGTCCCGCG CAC  CCA
                                 A        A  CC
GAM16   CISH     5'  GGCGCGGAGCGCGTGCTGGGTA 40360      A      G  A_
                                GGCGC GGGCGTG TGC  GGTA
                                ||||| ||||||| |||  ||||
                                CCGCG CTCGCGC ACG  CCAT
                                   C      _  AC
GAM16   CSF1R    5'  CAGGTGCAGGGCTGCAAGGT   23309     C      GTGG   _
                                CAGG GCAGGGC    TGCA GGT
                                |||| |||||||    |||| |||
                                GTCC CGTCCCG    ACGT CCA
                                  A      _____    T
GAM16   CSNK2A2  5'  GGCGCGGGGCGCAGAGGGT    12487      A    TG TGCA
                                GGCGC GGGCG  G    GGT
                                ||||| |||||  |    |||
                                CCGCG CCCGC  C    CCA
                                   C    GT TC__
GAM16   CYP1A2   3'  CAGGCGTGGTGGTGTGTGCCTG 8913       CA  GC   _   AG
           TA                    CAGGCG  GG  GTG GTGC  GTA
                                ||||||  ||  ||| ||||  |||
                                GTCCGC  CC  CAC CACG  CAT
                                   A_  AC   A   GA
GAM16   ERBB2    5'  GGCGCGGGGCGCGGGGT     20821      A      TGCA
                                GGCGC GGGCGTGG    GGT
                                ||||| ||||||||    |||
                                CCGCG CCCGCGCC    CCA
                                   C       _____
GAM16   F2R      5'  CAGAGCGCAGGGTGCCCACGGG 12791     _      C  GGT  A
           TA                    CAG GCGCAGGG GT   GC GGTA
                                ||| ||||||| ||   || ||||
                                GTC CGCGTCCC CG   TG CCAT
                                  T       A  GG_  C
GAM16   FBP1     5'  AGAGCGCGGGGCTGCAGGT   7997     _   A   GTGG
                                AG GCGC GGGC    TGCAGGT
                                || |||| ||||    |||||||
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                                TC CGCG CCCG    ACGTCCA
                                 T   C   ____
GAM16   HMGA1    3'  CAGGTGCAGGGTGCGGCTAAGT 44161      C     C    GC
                                CAGG GCAGGG GTGGT  AGGT
                                |||| |||||| |||||  ||||
                                GTCC CGTCCC CGCCG  TTCA
                                  A     A    A_
GAM16   ITGA6    3'  AGTGCAGGTGAGTGTAGGT   6827     C    GCGT   C
                                GG GCAGG    GGTG AGGT
                                || |||||    |||| ||||
                                TC CGTCC    TCAC TCCA
                                 A    AC__    A
GAM16   ITGB1    5'  GGGTGTCGGGCGCGGCGGGT   38052    CGCA_        CA
                                GG    GGGCGTGGTG  GGT
                                ||    ||||||||||  |||
                                CC    CCCGCGCCGC  CCA
                                 CACAG         __
GAM16   ITGB4    5'  GGCGCGGGGGGGTTGGGGGGT   6846       A   CG_   TGCA
                                GGCGC GGG   TGG    GGT
                                ||||| |||   |||    |||
                                CCGCG CCC   ACC    CCA
                                  C   CCA   CC__
GAM16   KLF4     5'  GGCGCGGGCCACGGGCGGGT   20156      A  G    T  A
                                GGCGC GG CGTGG GC GGT
                                ||||| || ||||| || |||
                                CCGCG CC GTGCC CG CCA
                                  C  G    _  C
GAM16   LAIR1    3'  CAGGTGCAGAGGCCAGGTGGGT 14052      C    _   GT    CA
           A                     CAGG GCAG GGC  GGTG  GGTA
                                |||| |||| |||  ||||  ||||
                                GTCC CGTC CCG  CCAC  CCAT
                                  A   T   GT   __
GAM16   LMO6     3'  AGGGGCGGGGCGTGGGGGT   26040     C  A       TGCA
                                AGG GC GGGCGTGG    GGT
                                ||| || ||||||||    |||
                                TCC CG CCCGCACC    CCA
                                 C  C       C___
GAM16   MAPK8IP1 3'  CAGGGGCAGGGCGGGCACTTGC 24152      C       T   ____
           AGGT                   CAGG GCAGGGCG GGT    GCAGGT
                                |||| |||||||| |||    ||||||
                                GTCC CGTCCCGC CCG    CGTCCA
                                  C       _   TGAA
GAM16   MGAT5    3'  GGTGCAGGGCTGAGCAGGTA   14475    C      G   T
                                GG GCAGGGC TGG GCAGGTA
                                || ||||||| ||| |||||||
                                CC CGTCCCG ACT CGTCCAT
                                 A      _  _
GAM16   MUC3B    3'  GGGGCAGGGCGGAGGGGGT    45342    C       TG TGCA
                                GG GCAGGGCG  G    GGT
                                || ||||||||  |    |||
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                                CC CGTCCCGC  C    CCA
                                 C       CT CC__
GAM16   OCLN     5'  GACGCGGGAGTGTAGGT     14904      A   CGT    C
                                GGCGC GGG   GGTG AGGT
                                |||||| |||   |||| ||||
                                CTGCG CCC   TCAC TCCA
                                  _  ____   A
GAM16   PRKAR1A  5'  GGCGCGAGGCTGCGGGT     15609      AG   GTGG   A
                                GGCGC  GGC    TGC GGT
                                |||||  |||    ||| |||
                                CCGCG  CCG    ACG CCA
                                   CT   _____  C
GAM16   UBQLN1    5'  GGCGCAGGGCCACCGTAGCGGG 30279          _____     CA
            T                    GGCGCAGGGC    GTGGTG  GGT
                                ||||||||||    ||||||  |||
                                CCGCGTCCCG    CATCGC  CCA
                                      GTGG     __
GAM17   CNR1     3'  GCTGTCAGCCCCATTGTCCCTT 37692    A__  C       C
                                GC   CA TTTTATTG CCCTT
                                ||   || |||||||| |||||
                                CG   GT GGGGTAAC GGGAA
                                 ACA  C       A
GAM17   EXTL1    3'  CCGCACCCCTCTGCTCCTT   20865       A    AT   C
                                CCGCAC CTTTT  TGC CCTT
                                |||||| |||||  ||| ||||
                                GGCGTG GGGAG  ACG GGAA
                                   _    __  A
GAM17   TMEPAI   3'  CGCTCACATGCCCCTT      33601     A   TTTTAT
                                CGC CAC     TGCCCCTT
                                ||| |||     ||||||||
                                GCG GTG     ACGGGGAA
                                  A  T_____
GAM17   ITGA5    3'  GGTGATTGGTGGTGCAGTTG   41502         C  AGAG
                                GGTGATTGG GG    GGTTG
                                ||||||||| ||    |||||
                                CCACTAACC CC    TCAAC
                                      A  ACG_
GAM18   DIAPH2   3'  TGTTACCCTTTTTGATTTTTCT 28689         C    TAACTC
            A                    TGTTACCC TTTT     TCTA
                                ||||||| ||||     ||||
                                ACAATGGG AAAA     AGAT
                                     A    CTAAAA
GAM18   EPHB2    3'  TGTATCCCTTTTACTCT     32683     TAC      TA
                                TGT   CCCTTTT  ACTCT
                                |||   |||||||  |||||
                                ACA   GGGAAAA  TGAGA
                                  TA_      __
GAM18   LYN      3'  GTTACTTTTCCTCTCTA     14287      CCCTT   AA
                                GTTAC    TTT  CTCTCTA
                                |||||    |||  |||||||
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                                CAATG    AAA  GAGAGAT
                                  _____  AG
GAM18   NRIP1    3'  TGTATGCCCTTTCTCACTGTTC 40990     TAC      A  C_
            T                    TGT   CCCTTTTT ACT  TCT
                                 |||   |||||||| |||  |||
                                 ACA   GGGAAAGA TGA  AGA
                                   TAC       G   CA
GAM18   PCTP     3'  TGTTATCCCTTCTACATTTCTA 34537      C      TAACTC
            A                    TGTTA CCCTTTT     TCTAA
                                 ||||| |||||||     |||||
                                 ACAAT GGGAAGA     AGATT
                                   A      TGTAA_
GAM18   SMAP     3'  TGCTACTCCAACTCTCTA    27455       C  TTTTT
                                 TGTTAC CC     AACTCTCTA
                                 ||||||  ||    |||||||||
                                 ACGATG GG     TTGAGAGAT
                                   A  _____
GAM18   SORCS1   3'  TGTTTCCCTCTTTCTCT     38106      AC      TAAC
                                 TGTT  CCCTTTT    TCTCT
                                 ||||  |||||||    |||||
                                 ACAA  GGGAGAA    AGAGA
                                   A_      ____
GAM18   TIMP3    5'  TGCTACCCCTCCAGTTTCTCT  7471           TTAAC
                                 TGTTACCCCTTT     TCTCT
                                 ||||||||||||     |||||
                                 ACGATGGGGAGG     AGAGA
                                        TCAA_
GAM18   TRPC5    5'  TGTTCTCCCAGCTCTCTA    29773      AC   TTTTTAA
                                 TGTT  CCC      CTCTCTA
                                 ||||  |||      |||||||
                                 ACAA  GGG      GAGAGAT
                                   GA   TC_____
GAM18   TRPS1    3'  TGCTACCCTTTTTTTCCT    30475        C    AA
                                 TGTTACCC TTTTT  CT
                                 |||||||| |||||  ||
                                 ACGATGGG AAAAA  GA
                                      A    AG
GAM18   ATP6V1C1 5'  CCAGGAAGGTGTCAAACGAGG  11784        ATAT   TTTG
                                 CCAGGAAG    TCA    GAGG
                                 ||||||||    |||    ||||
                                 GGTCCTTC    AGT    CTCC
                                      CAC_   TTG_
GAM18   BACE     3'  CCAGAGGAAGATTTGGG     39954    C_      ATTCAT    A
                                 CC  AGGAAGAT     TTGG G
                                 ||  ||||||||     |||| |
                                 GG  TCCTTCTA     AACC C
                                   TC       _______   _
GAM18   BCRP2    3'  CAGGAAGATATGTATCCG    41650          TC
                                 CAGGAAGATAT  ATTTG
                                 ||||||||||  |||||
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                                GTCCTTCTATA  TAGGC
                                      CA
GAM18   BIN3    3'  CCCAGGATGGGTCTTTTGGAGG 33076       AGATAT  A
                                CCCAGGA     TC TTTGGAGG
                                |||||||     || ||||||||
                                GGGTCCT     AG AAACCTCC
                                    ACCC__  A
GAM18   DGUOK   3'  CCTGGGGAGAAGCCTGGAG   38960    CA  A   TATTCA
                                CC  GG AGA     TTTGGAG
                                ||  || |||     |||||||
                                GG  CC TCT     GGACCTC
                                 AC  C   TC____
GAM18   EBAG9   5'  CCTGAGGAAGGCGGCTTTGGAG 20115    C_     ATATTCA
            G                    CC  AGGAAG      TTTGGAGG
                                ||  ||||||      ||||||||
                                GG  TCCTTC      AAACCTCC
                                 AC     CGCCG__
GAM18   ELMO1   3'  CAGGAAGATGTTTGG       39048         ATTCA
                                CAGGAAGAT    TTTGG
                                |||||||||    |||||
                                GTCCTTCTA    AAACC
                                     C____
GAM18   HAS3    3'  AGAAAGGACATTTGGAGG    39766       ATATT
                                AGGAAG    CATTTGGAGG
                                ||||||    ||||||||||
                                TCTTTC    GTAAACCTCC
                                   CT___
GAM18   IREB2   3'  CCAGGAAGGTTATTCATATAAG 42452        A_      TTG
                                CCAGGAAG  TATTCAT   GAG
                                ||||||||  |||||||   |||
                                GGTCCTTC  ATAAGTA   TTC
                                     CA      TA_
GAM18   LUZP1   3'  CCCAGGCAGATATTCAAGG   37958       A       TTT
                                CCCAGG AGATATTCA   GG
                                |||||| |||||||||   ||
                                GGGTCC TCTATAAGT   CC
                                   G        T__
GAM18   LZTR1   3'  CCAGGAGGGATTTGGAG     27634       A_   ATTCAT
                                CCAGGA  GAT     TTGGAG
                                ||||||  |||     ||||||
                                GGTCCT  CTA     AACCTC
                                   CC  _______
GAM18   NESH    5'  CCAGGGGCCCATTTGGG     32337      AAGATA       A
                                CCAGG     TTCATTTGG G
                                |||||     ||||||||| |
                                GGTCC     GGGTAAACC C
                                  CC_____       _
GAM18   RCE1    3'  CCCAGGAAGTTGGGGGG      23067         ATATTCAT    A
                                CCCAGGAAG       TTGG GG
                                |||||||||       |||| ||
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                                GGGTCCTTC       AACC CC
                                         _________   C
GAM18   SMOH    3' CCTTGGGAACATGTTTGGAGG 24812    CA_   G  ATTCA
                                CC   GGAA AT    TTTGGAGG
                                ||   |||| ||    ||||||||
                                GG   CCTT TA    AAACCTCC
                                  AAC    G  C____
GAM19   DLG5    3' AGGTCCTACCCCAACGACACTT 44444    A    A     CTAT
                                AG TCCTA CCCAAT    CTT
                                || ||||| ||||||    |||
                                TC AGGAT GGGTTG    GAA
                                 C    G     CTGT
GAM19   IFNAR2  3' GATCCTAAAGTCTGTCT     9318         CCCAA   A
                                GATCCTAA     TCT TCT
                                ||||||||     ||| |||
                                CTAGGATT     AGA AGA
                                     TC___   C
GAM19   RBBP9   3' AATCCTATAGGTCTATCTT   43134       ACCCAA
                                GATCCTA     TCTATCTT
                                |||||||     ||||||||
                                TTAGGAT     AGATAGAA
                                    ATCC__
GAM19   BAPX1   3' ACAAGACAGGTGGGA       10155         AT  AGCAA
                                ACAAGACAG  TG    GGA
                                |||||||||  ||    |||
                                TGTTCTGTC  AC    CCT
                                     C_  ______
GAM19   CDC42   3' CAAAACAGAAATAAGGGGAT   12156         T_   CAA
                                CAAGACAGA  TGAG   GGAT
                                |||||||||  ||||   ||||
                                GTTTTGTCT  ATTC   CCTA
                                     TT    C__
GAM19   FRZB    5' CAAGTGGACACAAGGAT     11152      ACA   TGA
                                CAAG   GAT   GCAAGGAT
                                ||||   |||   ||||||||
                                GTTC   CTG   TGTTCCTA
                                  AC_   ___
GAM19   HIP1    3' CACGAGATAGGTAACAAGGAT  23750     A   C  ATTG
                                CAC AGA AG    AGCAAGGAT
                                ||| ||| ||    |||||||||
                                GTG TCT TC    TTGTTCCTA
                                  C   A  CA__
GAM19   IL12RB2 5' CATAAGACGGAGCAAGG     11424    C     AGATT
                                CA AAGAC     GAGCAAGG
                                || |||||     ||||||||
                                GT TTCTG     CTCGTTCC
                                 A    C____
GAM19   MGA     3' TGAAGACAGAACAGGG      41729    C       TTGA   A
                                A AAGACAGA    GCA GG
                                | ||||||||    ||| ||
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                                A TTCTGTCT   TGT CC
                                 C      ____  C
GAM19   PHKA2   3' CACGTGACAGATTGAGAGTGTG 7117     AA       CAAG_
            ATC                  CAC  GACAGATTGAG    GATC
                                 |||  ||||||||||    ||||
                                 GTG  CTGTCTAACTC    CTAG
                                   CA         TCACA
GAM19   PTGS1   3' ACAGTGATGGGCCCAAGGATC  38725     AT_  A  __
                                 ACAG   TG GC  AAGGATC
                                 ||||   || ||  |||||||
                                 TGTC   AC CG  TTCCTAG
                                   ACT  C  GG
GAM19   RBL2    3' CACAAAACAGGTAGGA     24704         ATTGAGCA
                                 CACAAGACAG       AGGA
                                 ||||||||||       ||||
                                 GTGTTTTGTC       TCCT
                                       CA_______
GAM20   FZD7    3' AAAGCAACAAGTCATCAC    18628            C
                                 AAAGTAACAAGTCA CGC
                                 |||||||||||||| |||
                                 TTTCGTTGTTCAGT GTG
                                          A
GAM20   MMP19   5' AAAGAACAAGTCACCTCT    35573     T        GC
                                 AAAG AACAAGTCACC  CT
                                 |||| ||||||||||  ||
                                 TTTC TTGTTCAGTGG  GA
                                   _         A_
GAM20   MSL3L1  3' AAAGTAACAAGTGTCGTGTC  38574          CAC  CC
                                 AAAGTAACAAGT   CG  TC
                                 ||||||||||||   ||  ||
                                 TTTCATTGTTCA   GC  AG
                                       CA_  AC
GAM20   RAD51C  3' GTAACAAGTCCACTTGTACAC  38484         _  CGCCT
                                 GTAACAAGTC AC     CAT
                                 |||||||||| ||     |||
                                 CATTGTTCAG TG     GTG
                                       G  AACAT
GAM20   CBFA2T3 3' TGCTTTTTTAAAAAAACT    23272
                                 TGCTTTTTTAAAAAAATT
                                 ||||||||||||||||||
                                 ACGAAAAAATTTTTTTGA

GAM21   ACTA1   5' GGCGCTGTCCGCTGCG      40435    A    GGGCG
                                 GG GCTGT    TCGCTGCG
                                 || |||||    ||||||||
                                 CC CGACA    GGCGACGC
                                  G    ______
GAM21   EXTL1   5' GGGCTGTGGCCCCTGTGG    20871    A     GCG  G   C
                                 GG GCTGTGG   TC CTG GG
                                 || |||||||   || ||| ||
```

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                                CC CGACACC   GG GAC CC
                                 _     ___ G   A
GAM21   FMNL     3' TCGGGGCTGGGGCTTGCG    25314     A   T   GTCGC
                                TCGG GCTG GGGC    TGCG
                                |||| |||| ||||    ||||
                                AGCC CGAC CCCG    ACGC
                                  C   _   A____
GAM21   PHKA2    5' TCGGGGCTGTGGCCTCCAAGCG 7118      A     G G  GCT
           G                     TCGG GCTGTGG C TC   GCGG
                                |||| ||||||| | ||   ||||
                                AGCC CGACACC G AG   CGCC
                                  C      _ G  GTT
GAM21   PPGB     3' GGAGCTGGTTGCTGG      7174        TGGGC  C   C
                                GGAGCTG    GT GCTG G
                                |||||||    || |||| |
                                CCTCGAC    CA CGAC C
                                   _____ A   A
GAM21   PTK2     3' GGAGCTGTGAGTGCTG     24690          CGTC
                                GGAGCTGTGGG   GCTG
                                ||||||||||   ||||
                                CCTCGACACTC   CGAC
                                      A___
GAM21   ADD1     3' GGGCCTCAGTGGGGCTTGGGGG 30511     G_  A___
                                GGGC  TAG   GCTTGGGGG
                                ||||  |||   |||||||||
                                CCCG  GTC   CGAACCCCC
                                  GA  ACCC
GAM21   CA12     5' GCGCGGGCTGTGCCGGGGG   10246     A   GTAGA  T
                                GCGC GGGC    GCT GGGGG
                                |||| ||||    ||| |||||
                                CGCG CCCG    CGG CCCCC
                                  _   ACA__  _
GAM21   CDH4     3' GCAGGGCGCTGTGGGGG     12176        AGAGCT
                                GCAGGGCGT    TGGGGG
                                |||||||||    ||||||
                                CGTCCCGCG    ACCCCC
                                     AC____
GAM21   COLQ     3' GCAGGGCGTGGAGTCGA     38701        A  C
                                GCAGGGCGT GAG TTGG
                                ||||||||| ||| ||||
                                CGTCCCGCA CTC AGCT
                                     C  _
GAM21   CSNK2A2  5' GCGCGGGGCGCAGAGGG    12486     A      GCTT
                                GCGC GGGCGTAGA   GGG
                                |||| |||||||||   |||
                                CGCG CCCGCGTCT   CCC
                                  C      ____
GAM21   CTGF     5' GCGCGGGGCCTGGAGCGCTGG 12501     A   GTA  _
                                GCGC GGGC  GAGC TTGG
                                |||| ||||  |||| ||||
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                                CGCG CCCG   CTCG GACC
                                  C    GAC    C
GAM21   DIA1    3'  GCGTGGGGTGCGCGGGGG    28788     CA   C  AGA  T
                                GCG  GGG GT   GC TGGGGG
                                |||  ||| ||   || ||||||
                                CGC  CCC CA   CG GCCCCC
                                  A_   _ ___  C
GAM21   EGFR    3'  GCGTAAGGAGGGGGTTTGGGGG 23397     C    CGTAGAGC
          C                      GCG AGGG       TTGGGGGC
                                |||  ||||       ||||||||
                                CGC TTCC       AACCCCCG
                                  A   TCCCCCA_
GAM21   FLNA    3'  GCGGGGCAGGCTTGGGGGC   11135    A  C   A
                                GC GGG GTAG GCTTGGGGGC
                                ||  ||| |||| ||||||||||
                                CG CCC CGTC CGAACCCCCG
                                 _  _   _
GAM21   HPD     3'  GGGCGGAGCCTTGGGGGC    41157      TA   _
                                GGGCG  GAGC TTGGGGGC
                                |||||  |||| ||||||||
                                CCCGC  CTCG AACCCCCG
                                   __    G
GAM21   HRMT1L2  3'  GCAGGGCGGGAGAGCCGGGC   11359       T_     TGG
                                GCAGGGCG  AGAGCT   GGGC
                                ||||||||  ||||||   ||||
                                CGTCCCGC  TCTCGG   CCCG
                                     CC     ___
GAM21   ITPR3    5'  GCCCAGGGCGTGGGGG     13690    G      AGAGCTT
                                GC CAGGGCGT      GGGG
                                ||  ||||||||      ||||
                                CG GTCCCGCA      CCCC
                                 G       C_______
GAM21   MBD4     5'  GCCCAGGGTGTGGGGC     19413    G    C  AGAGCTTG
                                GC CAGGG GT      GGGGC
                                ||  ||||| ||       |||||
                                CG GTCCC CA      CCCCG
                                 G    A _________
GAM21   MIC2     5'  GCAGGGCGTGGGCGAAGGC   14504         AGA  TT
                                GCAGGGCGT   GC  GGGGGC
                                |||||||||   ||  ||||||
                                CGTCCCGCA   CG  CTTCCG
                                     CC_  __
GAM21   MLPH     5'  GCGCGGGGCGCAGAGCGG    35867     A        TTGGG
                                GCGC GGGCGTAGAGC    GG
                                ||||  ||||||||||    ||
                                CGCG CCCGCGTCTCG    CC
                                  C         ______
GAM21   NRGN     5'  GCGCAGGGCGGGGATGGGG   26127          TA  GCT
                                GCGCAGGGCG  GA   TGGGG
                                |||||||||  ||   |||||
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                                CGCGTCCCGC  CT   ACCCC
                                      CC  ___
GAM21   PIM2     5'  CGCAGGGCGTGGACGCCCGGGG 41022          A  _
                                CGCAGGGCGT GA GCTTGGGG
                                |||||||||| || ||||||||
                                GCGTCCCGCA CT CGGGCCCC
                                      C  G
GAM21   ST14     5'  GCGCGGGGCGCGGGGC      35064      A     AGAGCTTG
                                GCGC GGGCGT       GGGGC
                                |||| ||||||       |||||
                                CGCG CCCGCG       CCCCG
                                  C     _________
GAM21   TESK1    5'  GCGCAGGGCCTGGGCTTGGG   26614          GTAGA
                                GCGCAGGGC    GCTTGGG
                                |||||||||    |||||||
                                CGCGTCCCG    CGAACCC
                                      GACC_
GAM21   WDR3     3'  GCGGGGCGTAGGGGTGGG    27689    A       AGCT
                                GC GGGCGTAG    TGGG
                                || ||||||||    ||||
                                CG CCCGCATC    ACCC
                                 C       CCC_
GAM22   HOXC6    3'  GGAATCAAAACACATC      21075          TGT  G
                                GGAATCAA   CG CATC
                                ||||||||   || ||||
                                CCTTAGTT   GT GTAG
                                      TT_  _
GAM22   MAP3K14  3'  TCCCACGGAGTCTCGGC     19544          A  AATG
                                TTCCACGGA TC    TCGGC
                                |||||||||  ||    |||||
                                AGGGTGCCT AG    AGCCG
                                      C  _____
GAM22   AQP6     5'  GCCCTGGGCCTTGGAGCCTGAA 38246      _  TGA  C   A
            AG                    GCCC GG   CT GGA CCTGAAAG
                                ||||  ||   ||  ||| ||||||||
                                CGGG CC   GA CCT GGACTTTC
                                  A  CG_  A   C
GAM22   ATP11A   3'  GGTGCTTTCCTGAAAG      44178      A  CGGAA
                                GGTG CT    CCTGAAAG
                                ||||  ||    ||||||||
                                CCAC GA    GGACTTTC
                                  _  AA___
GAM22   DMRT2    3'  GCCTGATGACCCTGAA       27262     C     TCGGAA
                                GCC GGTGAC     CCTGAA
                                |||  ||||||     ||||||
                                CGG CTACTG     GGACTT
                                  A     _______
GAM22   KIF5A    5'  GCCCGGCGAAGCCTG       22548          CTC  AA
                                GCCCGGTGA   GG  CCTG
                                |||||||||   ||  ||||
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                              CGGGCCGCT  TC  GGAC
                                         ___  __
GAM22  LTA     3'  CCGGTGACTTGATCAGGGAA  8238         C  AACCT
                              CCGGTGACT GG    GAA
                              |||||||||  ||    |||
                              GGCCACTGA CT    CTT
                                    A  AGTCC
GAM22  P3      5'  GCTCGGGCCGTCTCGGAGTCTG 33383    C   __  A    AC
                              GC CGG  TG CTCGGA  CTG
                              || |||  || ||||||  |||
                              CG GCC  GC GAGCCT  GAC
                               A  CG  A    CA
GAM22  PLCB2   3'  GCCTGATGGGGCCTGGAA   21320    C   ACTC  AA   A
                              GCC GGTG   GG  CCTG AA
                              ||| ||||   ||  |||| ||
                              CGG CTAC   CC  GGAC TT
                                A   _____ C_   C
GAM22  RAB36   3'  GCCCGGTGGTGTGGGGCTCCCA 22243        ACTC__  AA
                              GCCCGGTG    GG  CCTG
                              ||||||||    ||  ||||
                              CGGGCCAC    CC  GGGT
                                   CACACC  GA
GAM22  SOD3    3'  GCCTAGGAGGAACCTGAA   16956    CG T  CTC
                              GCC  G GA  GGAACCTGAA
                              |||  | ||  ||||||||||
                              CGG  C CT  CCTTGGACTT
                                AT _  ___
GAM23  ATP11A  3'  AACTTGTTGTCAGAG      44167        CC   CTAA
                              AACTTGTTG  TCAG   AG
                              |||||||||  ||||   ||
                              TTGAACAAC  AGTC   TC
                                         __   ____
GAM23  BCL2L2  3'  GCTCCTCTTGGCTAAAGGT   19745    G   A__
                              GTT CCTC   GCTAAAGGT
                              ||| ||||   |||||||||
                              CGA GGAG   CGATTTCCA
                                _   AAC
GAM23  CLNS1A  3'  CAACTTGTTGTCTCAGTATAG  10524         C    C  A
                              TAACTTGTTG CTCAG TA AG
                              |||||||||| ||||| || ||
                              GTTGAACAAC GAGTC AT TC
                                    A    _ A
GAM23  DMD     3'  TAATTTGTTACCTTAGAGCTTT 19691    C       C__   AAA
          GGGT                    TAA TTGTTGCCT   AGCT   GGT
                              ||| |||||||||   ||||   |||
                              ATT AACAATGGA   TCGA   CCA
                                A       ATC   AAC
GAM23  KRT2A   3'  TAACTTGCTGCCAGTTAGAGGT 7686           TC  C  A
                              TAACTTGTTGCC  AG TA AGGT
                              ||||||||||||  || || ||||
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                                ATTGAACGACGG  TC AT TCCA
                                      __ A  C
GAM23   PAIP2    3'  TAACTTGTAGCCTCAGTAA   32406       T     C
                                TAACTTGT GCCTCAG TAA
                                |||||||| ||||||| |||
                                ATTGAACA CGGAGTC ATT
                                     T     _
GAM23   PREP     3'  TAACTTGTTGCAGAAAGG    15554         CTC  CT
                                TAACTTGTTGC  AG  AAAGG
                                ||||||||||  ||  |||||
                                ATTGAACAACG  TC  TTTCC
                                      ___ __
GAM23   WASF3    3'  TAACTTGTTGATTCAGCT    27389         CC
                                TAACTTGTTG  TCAGCT
                                ||||||||||  ||||||
                                ATTGAACAAC  AGTCGA
                                      TA
GAM23   BUB3     3'  ACCCTTCTCTGTATCAAA    21801      CG   ACCATC
                                ACCCT  CTC    TATCAAA
                                |||||  |||    |||||||
                                TGGGA  GAG    ATAGTTT
                                   A_  AC____
GAM23   CYP4F3   3'  ACCCCGCCTCTATCAA     9451      T   CACCA
                                ACCC CGCT    TCTATCAA
                                |||| ||||    ||||||||
                                TGGG GCGG    AGATAGTT
                                     _   _____
GAM23   MS4A1    3'  ACCCTTTTTATCATTCTATCAA 6596      CGC__   CCA
                                ACCCT    TCA   TCTATCAA
                                |||||    |||   ||||||||
                                TGGGA    AGT   AGATAGTT
                                   AAAAT   A__
GAM23   NOS1     3'  CTCTGCTCACTGGTATCAAAA  8374     _     CATC
                                CTC GCTCAC    TATCAAAA
                                ||| ||||||    ||||||||
                                GAG CGAGTG    ATAGTTTT
                                  A     ACC_
GAM23   PDE1A    5'  CCTCTCTTATCTATCAAAA   22708     G  CACC
                                CCTC CT    ATCTATCAAAA
                                |||| ||    ||||||||||
                                GGAG GA    TAGATAGTTTT
                                   A  A___
GAM23   SERPINB9 3'  ACTCAGCATTATCTATCAAA   19994      C  ___
                                GCTCA CA   TCTATCAAA
                                ||||| ||   |||||||||
                                TGAGT GT   AGATAGTTT
                                   C  AAT
GAM23   SLC13A4  5'  ACCCTCGCTGTTTCTACAA   29723        CACCA   T
                                ACCCTCGCT    TCTA CAA
                                |||||||||    |||| |||
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                                TGGGAGCGA    AGAT GTT
                                     CAA__   _
GAM23   SNX6    5' CCCGCTCACTAAGAGCATCA  34559        CATC__
                                CTCGCTCAC    TATCA
                                |||||||||    |||||
                                GGGCGAGTG    GTAGT
                                     ATTCTC
GAM24   PDGFRA  3' AAATTATATATCATTTATT   26284
                                AAATTATATATCATTTGTT
                                |||||||||||||||||||
                                TTTAATATATAGTAAATAA

GAM24   FOS     3' AAATAAAAATATAAATAT    23515
                                AAATAAAAATATAAATGT
                                |||||||||||||||||||
                                TTTATTTTTATATTTATA

GAM25   CYP1B1  3' TTAAAGCTTGGCTGGCTTTTTT 6457       CC  AAT
           TT                    TTAAAGC  GG   GTTTTTTTTT
                                |||||||  ||   ||||||||||
                                AATTTCG  CC   CGAAAAAAAA
                                     AA  GAC
GAM25   GPD2    3' TTAAAGTTTTGGAATGTTTT  7629       CCC_
                                TTAAAG   GGAATGTTTT
                                ||||||   ||||||||||
                                AATTTC   CCTTACAAAA
                                     AAAA
GAM25   SON     3' TCAAAGCCTGGAGATGTTTTT 38461       C  _
                                TTAAAGCC GGA ATGTTTTT
                                |||||||| ||| ||||||||
                                AGTTTCGG CCT TACAAAAA
                                      A  C
GAM25   NAPB    3' TAATTGACACAACAAAAT    43176    C
                                TAA TGACACAACAAAAT
                                ||| ||||||||||||||
                                ATT ACTGTGTTGTTTTA
                                  A
GAM25   NCOA6   5' TGAGCTGACACAACACATCTCT 30441    TAA        AAA_
           G                     TG  CTGACACAACA   TCTG
                                ||   ||||||||||   ||||
                                AC   GACTGTGTTGT   AGAC
                                 TC_         GTAG
GAM25   PPP2R5C 3' TGACGGAAACGAAATCTG    15526     AC_  A
                                TGAC   AAC AAATCTG
                                ||||   ||| |||||||
                                ACTG   TTG TTTAGAC
                                  CCT   C
GAM25   RELN    3' TGTAACTGATATTACAAC    45359        C___
                                TGTAACTGA   ACAAC
                                |||||||||   |||||
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                                ACATTGACT   TGTTG
                                     ATAA
GAM26   NOV     3'  TGGTGGGTGGCGCAGCAGCT  14815      A    GCTC
                                TGGTG GTGGC   GCAGCAGCT
                                ||||| |||||   |||||||||
                                ACCAC CACCG   CGTCGTCGA
                                   C   ____
GAM26   SMOH    3'  GGTGAGTGTGTGCAGCAGCT  24816        GCGCTC
                                GGTGAGTG    GCAGCAGCT
                                ||||||||    |||||||||
                                CCACTCAC    CGTCGTCGA
                                     ACA___
GAM26   ACTN1   5'  CTGAGCAACGGCTGCTGCCC  9931         ACTCC
                                CTGAGCAAC   CTGCCC
                                |||||||||   ||||||
                                GACTCGTTG   GACGGG
                                     CCGAC
GAM26   CCND2   3'  TGCTGAGCAAAGCTGGCT   12052         CA  CC
                                TGCTGAGCAA  CT  CT
                                ||||||||||  ||  ||
                                ACGACTCGTT  GA  GA
                                      TC  CC
GAM26   FLRT1   5'  GCTCACATTCCCTGCCCC   40599    A_  C
                                GC  ACA TCCCTGCCCC
                                ||  ||| ||||||||||
                                CG  TGT AGGGACGGGG
                                 AG   A
GAM26   GFAP    3'  CTGGGCAGGTGACTGCCCCA  13121    A   ACACTCC
                                CTG GCA     CTGCCCCA
                                ||| |||     ||||||||
                                GAC CGT     GACGGGGT
                                  C   CCACT__
GAM26   GPR61   5'  TGCTGAGCAGTCCCGGCTCCCA 44267        ACAC    T  _
                                TGCTGAGCA   TCCC GC CCCA
                                |||||||||   |||| || ||||
                                ACGACTCGT   AGGG CG GGGT
                                     C___   C  A
GAM26   H1F0    5'  GCTGAGCAAAGCCTGCC    23701        CACTC
                                GCTGAGCAA   CCTGCC
                                |||||||||   ||||||
                                CGACTCGTT   GGACGG
                                     TC___
GAM26   HIP1    3'  TGTTGAGTGGCCCTGCCCC   23762    C   CAACACT
                                TG TGAG     CCCTGCCCC
                                || ||||     |||||||||
                                AC ACTC     GGGACGGGG
                                 A   ACC____
GAM26   HSF2BP  3'  TGCTGAGCAGCAAGAAGCTGCC 28149        A  CTCC_
            C                    TGCTGAGCA CA    CTGCCC
                                |||||||||  ||    ||||||
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                                ACGACTCGT GT    GACGGG
                                     C  TCTTC
GAM26   MEN1    5'  CTGGGCCCACCCCTGCCCC   39250    A  AA   T
                                CTG GC  CAC CCCTGCCCC
                                ||| ||  ||| |||||||||
                                GAC CG  GTG GGGACGGGG
                                  C  G_  _
GAM26   MME     5'  TGCTGAGCCGACACATCCC   28606       A_   _
                                TGCTGAGC  ACAC TCCC
                                ||||||||  |||| ||||
                                ACGACTCG  TGTG AGGG
                                     GC    T
GAM26   NPR1    5'  TGCGTGAGCGCCTGCCCC    44589    _    AACACTC
                                TGC TGAGC      CCTGCCCC
                                ||| |||||      ||||||||
                                ACG ACTCG      GGACGGGG
                                  C    C_______
GAM26   OFD1    5'  TGCTGAACGTTCTCTGCC    18814       AACAC  C
                                TGCTGAGC    TC CTGCC
                                ||||||||    || |||||
                                ACGACTTG    AG GACGG
                                     CA___  A
GAM26   PKD1    3'  TACTGAGCGGTGTCCACTCC   7141        AA____
                                TGCTGAGC     CACTCC
                                ||||||||     ||||||
                                ATGACTCG     GTGAGG
                                     CCACAG
GAM26   RAGE    3'  TACAAAGTATTTCCTGCCCCA  30604    T   CAACACTC
                                TGC GAG       CCTGCCCCA
                                ||| |||       |||||||||
                                ATG TTC       GGACGGGGT
                                  T   ATAAA___
GAM26   TGM3    3'  TGGTGAGCTCTCCCTGCTCC   17506    C    AACA      C
                                TG TGAGC    CTCCCTGC CC
                                || |||||    |||||||| ||
                                AC ACTCG    GAGGGACG GG
                                 C    A___       A
GAM26   TNS     3'  TGCTGAGCCACATGCC      35482        A  CTCCC
                                TGCTGAGC ACA     TGCC
                                |||||||| |||     ||||
                                ACGACTCG TGT     ACGG
                                     G  _____
GAM26   ZNF161  3'  TGCTGAGCAATATTTACATCTC 28364        _______  _
            C                    TGCTGAGCA     ACA CTCC
                                ||||||||||     ||| ||||
                                ACGACTCGT      TGT GAGG
                                     TATAAA   A
GAM27   CENPC1  5'  TCTCAGGCGACTGCCGCG    12237    C       ACCTC
                                TC CAGGCGACT     CTGCG
                                || |||||||||     |||||
```

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                                AG GTCCGCTGA    GGCGC
                                 A       C____
GAM27   EDNRA    5'  TCCTGGGCACTGCTTCTCCCGG 42000    CA  G  AC__    C
                G                TCC  GGC ACT   CTCCTG GG
                                 |||  ||| |||   |||||| ||
                                 AGG  CCG TGA   GAGGGC CC
                                  AC  _  CGAA    _
GAM27   GPC1     3'  TCCAAGGTGGGCCCTGCGG   13258    C  CGACTACC
                                 TCC AGG      TCCTGCGG
                                 ||| |||      ||||||||
                                 AGG TCC      GGGACGCC
                                  T  ACCC____
GAM27   KCNF1    5'  AGCTCGGCCTCCTGCGGG    13824    GACTA
                                 GGC    CCTCCTGCGGG
                                 |||    ||||||||||
                                 TCG    GGAGGACGCCC
                                  AGCC_
GAM27   PLAU     3'  TCCCAGGCACTGTCACGTGGG  42880       G  ACC  C  C
                                 TCCCAGGC ACT   TC TG GGG
                                 |||||||| |||   || || |||
                                 AGGGTCCG TGA   AG GC CCC
                                      _  C__  T  A
GAM27   SCN2A2   3'  GGCATAGACCTCCTGTGGG   34243     ACT      C
                                 GGCG   ACCTCCTG GGG
                                 ||||   |||||||| |||
                                 CCGT   TGGAGGAC CCC
                                   ATC       A
GAM27   FGFR1    3'  GTAGTTGCCCTTGTCAGA    31948          CG_
                                 GTAGTTGCCCT   CAGA
                                 ||||||||||   ||||
                                 CATCAACGGGA   GTCT
                                       ACA
GAM27   SLC7A8   5'  CGGTGTTGCTCTAGATCTG   29286     A    CC  GC
                                 CGGT GTTGC  TC  AGATCTG
                                 |||| |||||  ||  |||||||
                                 GCCA CAACG  AG  TCTAGAC
                                   _    __  A_
GAM27   TCTA     3'  CGGCAGTTGTCCCTGAGGTCTG 35280        _   CGC  A
                G                CGGTAGTTG CCCT   AG TCTGG
                                 |||||||| ||||   || |||||
                                 GCCGTCAAC GGGA   TC AGACC
                                      A   C__  C
GAM27   THY1     3'  GGTGGTGCCCTCACATCTGG   26630     A  T       GA
                                 GGT GT GCCCTCGCA  TCTGG
                                 ||| || |||||||||  |||||
                                 CCA CA CGGGAGTGT  AGACC
                                  C  _        __
GAM28   NEDD4    3'  TTTACAGTTCTCACAGG     43106         _  TAAC
                                 TTTATAGT CTC    CAGG
                                 ||||||||| |||    ||||
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                                AAATGTCA GAG    GTCC
                                    A  T___
GAM28   PATE     3'  TAGCAACCTGCAGGATATA   39644      CT  AAC
                                TAGT  CT   CAGGATATA
                                ||||  ||   |||||||||
                                ATCG  GG   GTCCTATAT
                                  TT  AC_
GAM28   ADRBK2   3'  GGGGAGTCTAAGATGTGTTT   23132    TA _    T
                                GG  AG CTAGG GTGTGTTT
                                ||  || ||||| ||||||||
                                CC  TC GATTC TACACAAA
                                 CC  A    _
GAM28   DPYSL2   3'  AGGGGGCCATGTGTTTAA    10743     TAA   AGGT
                                AGG   GCT    GTGTGTTTAA
                                |||   |||    ||||||||||
                                TCC   CGG    TACACAAATT
                                  CC_   ____
GAM28   TNFRSF14 3'  AGGAGGGCTGGGTGTGTG    19231     TAA   A
                                AGG   GCT GGTGTGTG
                                |||   ||| ||||||||
                                TCC   CGA CCACACAC
                                  TCC   C
GAM29   IL1R1    3'  AAAATTATTATTCCAAATA    9347        TA
                                AAAGTT  ATTATTCCAAATA
                                ||||||  ||||||||||||
                                TTTTAA  TAATAAGGTTTAT
                                        __
GAM29   CALU     3'  GTGAATTTTAATTGTAGTGAAA 10260            TTTTA_
            CCA                   GTGAATTTTGATT     AAACCA
                                ||||||||||||      ||||||
                                CACTTAAAATTAA     TTTGGT
                                       CATCAC
GAM29   HGD      3'  GTGAATTTTCATTTTAACC    6781          G    TTAA
                                GTGAATTTT ATTTT    AACC
                                ||||||||| |||||    ||||
                                CACTTAAAA TAAAA    TTGG
                                     G    ____
GAM29   IL7      3'  GTCAATTTTGAATCTTTGAAAC 9400     G       T    A
            CA                    GT AATTTTGA TTTTT AAACCA
                                || ||||||||| ||||| ||||||
                                CA TTAAAACT AGAAA TTTGGT
                                 G       T    C
GAM29   ROBO1    3'  GTGATTGTGCTTTTAAAACCA  39486     ATT   AT
                                GTGA   TTG  TTTTTAAAACCA
                                ||||   |||  ||||||||||||
                                CACT   AAC  GAAAATTTTGGT
                                  ___   AC
GAM30   NEF3     3'  AGGGAGCACCCTGAGCTTGCAT 23924    A       A    AT
                                AG GAGCACCTT AGCT  CAT
                                || ||||||||| ||||  |||
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                                TC CTCGTGGGA TCGA  GTA
                                 C        C    AC
GAM30   TYR     3'  AAGAGCACTTTAATTCACATAC 7497          C    GCTAT
                                GAGAGCAC TTAA     CATAC
                                |||||||| ||||     |||||
                                TTCTCGTG AATT     GTATG
                                    A    AAGT_
GAM30   DAZ     3'  CAGCTTCCAATCTCAGTT    19847       AAGATA
                                TAGCTT     CAATCTCAGTT
                                ||||||     ||||||||||||
                                GTCGAA     GTTAGAGTCAA
                                   G_____
GAM30   OXR1    5'  GCTTGAGATACAAACGTTT   32836      A       TCTCA
                                GCTT AGATACAA     GTTT
                                |||| ||||||||     ||||
                                CGAA TCTATGTT     CAAA
                                  C       TG___
GAM30   SNAI2   3'  TAGCTATAGACAACATCTCAGT 16884       TA     CA
            TT                   TAGCT  AGATA  ATCTCAGTTT
                                |||||  |||||  ||||||||||
                                ATCGA  TCTGT  TAGAGTCAAA
                                   TA     TG
GAM31   FGF2    3'  TTTATACTGCAGTTGAAAAAT  12850      A       _
                                TTTA ACTGCAGTT AAAAGT
                                |||| ||||||||| ||||||
                                AAAT TGACGTCAA TTTTTA
                                  A        C
GAM31   RYR3    3'  TTAGACTGCAGTTATTATCTT  9776      A        AAA
                                TTA ACTGCAGTTA   GTTTT
                                ||| ||||||||||   |||||
                                AAT TGACGTCAAT   TAGAA
                                  C        AA_
GAM31   ZIC3    3'  TTTAAACTCGCAGTTAAA    18256        _
                                TTTAAACT GCAGTTAAA
                                |||||||| |||||||||
                                AAATTTGA CGTCAATTT
                                     G
GAM32   CDC25A  3'  TGGAGGGAAGCTTGGGCTG   12152      A       CGAT
                                TGGAG GAAGCTTGG    GCTG
                                ||||| |||||||||    ||||
                                ACCTC CTTCGAACC    CGAC
                                  C        ____
GAM32   CSNK1A1 3'  TGGGGAGAAACAAATGCTG   12465     A      TTGGC
                                TGG GAGAAGC     GATGCTG
                                ||| |||||||     |||||||
                                ACC CTCTTTG     TTACGAC
                                  C      T_____
GAM32   DPH2L2  3'  TGGGCAGAGGCCAGGGATGCTG 10737     AG   A   T  C
            C                    TGG  AGA GCT GG GATGCTGC
                                |||  ||| ||| || ||||||||
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                                ACC  TCT CGG CC CTACGACG
                                  CG   C   T  _
GAM32   EGFL5    5'  TGGGGAGGACGCTGCTG     44543     A   AAGCTT    A
                                TGG GAG     GGCG TGCTG
                                ||| |||     |||| |||||
                                ACC CTC     CTGC ACGAC
                                  C  _______    G
GAM32   MAT1A    3'  TGGGGAGAAGGTAGAGATGCTG 44908     A     CT   C
           C                     TGG GAGAAG  TGG GATGCTGC
                                ||| ||||||  ||| ||||||||
                                ACC CTCTTC  ATC CTACGACG
                                  C     C_   T
GAM32   PIP5K1A  3'  TGGAGTGGAGGGGATGCTG    18662      AGA  CTT  C
                                TGGAG   AG   GG GATGCTG
                                |||||   ||   || |||||||
                                ACCTC   TC   CC CTACGAC
                                   ACC  ___  _
GAM32   PTK7     3'  TGGGGAGGACTCACTTGCTG   15863     A   AA    G GA
                                TGG GAG  GCTTG C  TGCTG
                                ||| |||  ||||| |  |||||
                                ACC CTC  TGAGT G  ACGAC
                                  C   C_    _ A_
GAM32   RELA     3'  TGGAGAGAGCCAGTGCTG    35037        A   TGGCGA
                                TGGAGAGA GCT     TGCTG
                                |||||||| |||     |||||
                                ACCTCTCT CGG     ACGAC
                                     _   TC_____
GAM32   RTN4     5'  TGGAGGGTGGAGATGATGCTGC 42494       AGAAGCTT GC
                                TGGAG       G  GATGCTGC
                                |||||       |  ||||||||
                                ACCTC       C  CTACGACG
                                   CCACCT__ TA
GAM32   SCA1     3'  GGGGAGAAGGAGGGATGCTGC  7283     A     CTT  C
                                GG GAGAAG   GG GATGCTGC
                                || ||||||   || ||||||||
                                CC CTCTTC   CC CTACGACG
                                 C     CT_  _
GAM32   TCF3     3'  TGGAGAGAGGCCTGGGTGC    43332        A     CGA
                                TGGAGAGA GCTTGG   TGC
                                |||||||| ||||||   |||
                                ACCTCTCT CGGACC   ACG
                                     C     C__
GAM32   TCP1     3'  TGGGCAGAAGTCGTGGTGTTGC 36245     AG    CT_   CGA
                                TGG  AGAAG   TGG   TGC
                                |||  |||||   |||   |||
                                ACC  TCTTC   ACC   ACG
                                  CG    AGC   ACA
GAM32   BTG2     3'  TTGGTTTCTTTTCCTCCT    27625         GTCCCGG  GG
                                TTGGTTTCT      TC  CCT
                                |||||||||      ||  |||
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                                AACCAAAGA      AG  GGA
                                    AA_____  GA
GAM32   CD22     3'  TTCGTTTCTGTCCTTTTCTGGG 12106    G        CGG  __
              C                   TT GTTTCTGTCC   TC  GGC
                                  || ||||||||||   ||  |||
                                  AA CAAAGACAGG   AG  CCG
                                   G         AAA  AC
GAM32   MMP19    3'  GGTTTCTGTTTGGCCT      35590          CCCGGTC
                                  GGTTTCTGT      GGCCT
                                  |||||||||      |||||
                                  CCAAAGACA      CCGGA
                                      AA_____
GAM32   SPON1    3'  TTGTTTTCTGTCTCGGTAAC   41673     G       C    C
                                  TTG TTTCTGTC CGGT GGC
                                  ||| |||||||| ||||| |||
                                  AAC AAAGACAG GCCA TTG
                                    A       A   _
GAM32   ZNF268   3'  TGGTTTCTGTCCTGAATGA   41765           C  TC
                                  TGGTTTCTGTCC GG  GG
                                  |||||||||||| ||  ||
                                  ACCAAAGACAGG CT  CT
                                        A  TA
GAM33   MMP20    3'  ATGAAAAAAATTGGAAGTATT  21924    T          A
                                  AT AAAAAAATTGGAA TATT
                                  || |||||||||||| ||||
                                  TA TTTTTTTAACCTT ATAA
                                   C           C
GAM33   PIK3CD   3'  TTAAAAAAATAGAAAATATT   22738          T
                                  TTAAAAAAAT GGAAATATT
                                  |||||||||| |||||||||
                                  AATTTTTTTA CTTTTATAA
                                        T
GAM33   CCNT2    3'  ACATAGCATTTCAAATTCAAT  38488      _    AC
                                  ACATA CATT  CAAATTCAAT
                                  ||||| ||||  ||||||||||
                                  TGTAT GTAA  GTTTAAGTTA
                                     C    A_
GAM33   COL19A1  3'  CATACAAGATACAAATTCAAT  12373       TTAC_
                                  CATACA     CAAATTCAAT
                                  ||||||     ||||||||||
                                  GTATGT     GTTTAAGTTA
                                      TCTAT
GAM33   CREM     3'  GGAACAACATTCCCAATTCAAT 12437   A    T    A  A
                                  A AACA ACATT CC AATTCAAT
                                  | |||| ||||| || ||||||||
                                  C TTGT TGTAA GG TTAAGTTA
                                   C    _     _  G
GAM33   FOLH1    3'  ACATACCACACAAATTCAAT   20987       AT   _
                                  ACATAC  TAC CAAATTCAAT
                                  ||||||  ||| ||||||||||
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                                TGTATG  GTG GTTTAAGTTA
                                  __  T
GAM33   SNCAIP   3'  AAAACATACATTTTCCCAA   45501          A__
                                AAAACATACATT  CCAA
                                ||||||||||||  ||||
                                TTTTGTATGTAA  GGTT
                                      AAG
GAM33   ZNF136   3'  AAAACATCTGTTCAAATTCAAT 40875       ACATTAC
                                AAAACAT     CAAATTCAAT
                                |||||||     ||||||||||
                                TTTTGTA     GTTTAAGTTA
                                   GACAA__
GAM34   ATP1A1   5'  CGGTGCTCAGTGCCCGGCGCC  8694         ACA  G  _
                                TGGTGCTCA  TGC TG CGCC
                                |||||||||  ||| || ||||
                                GCCACGAGT  ACG GC GCGG
                                     C__  G  C
GAM34   EDNRA    5'  TGGAGCTCGGCGTGCGC    42004    T   AACAT
                                TGG GCTC    GCGTGCGC
                                ||| ||||    ||||||||
                                ACC CGAG    CGCACGCG
                                  T   C____
GAM34   GSTZ1    3'  TGGTGTTACGGTGAGCACGCCA 11324      CTCA  A_  C TG
                                TGGTG   AC  TG G  CGCCA
                                |||||   ||  || |  |||||
                                ACCAC   TG  AC C  GCGGT
                                  AA__  CC  T GT
GAM34   ICMT     3'  TGGTGCTCTGGCCCCGCGCC  29661       AACAT  G_
                                TGGTGCTC    GC  TGCGCC
                                ||||||||    ||  ||||||
                                ACCACGAG    CG  GCGCGG
                                     AC___  GG
GAM34   IL12RB2  5'  GTGCTCAGCGTACACAGCCA  11434       ACAT    ___
                                GTGCTCA   GCGTGC   GCCA
                                |||||||   ||||||   ||||
                                CACGAGT   CGCATG   CGGT
                                    ____     TGT
GAM34   LOXL2    3'  ATGGTGCTCAGTGAGCGCCC  14192        ACA  C   G
                                ATGGTGCTCA  TG GTGC CC
                                ||||||||||  || |||| ||
                                TACCACGAGT  AC CGCG GG
                                     C__  T   _
GAM34   PPARA    5'  ATGGTGCTGGTTGTGCGCC   22765       CAACATGC
                                ATGGTGCT      GTGCGCC
                                ||||||||      |||||||
                                TACCACGA      CACGCGG
                                    CCAA____
GAM34   ZNF2     3'  GGTGCTCAGTAAGTGC     34382        ACA  C
                                GGTGCTCA  TG GTGC
                                ||||||||  || ||||
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                                CCACGAGT   AT CACG
                                    C__  T
GAM34   BGN     3'  TTTTCACGTTGCACGGT    11825        CATAC     T
                                TTTTCACG    TTGCAC GT
                                ||||||||    |||||| ||
                                AAAAGTGC    AACGTG CA
                                   _____    C
GAM35   COG3    3'  TTCTGTAAAGTTCTTTGC    36421     A        AA
                                TTC TGTAAAGTTTT  GC
                                ||| ||||||||||  ||
                                AAG ACATTTCAAGA  CG
                                  _         AA
GAM35   EVA1    3'  TTCTGTATCTTAAGCTT     40348     A   AAA
                                TTC TGT   GTTTTAAGCTT
                                ||| |||   ||||||||||
                                AAG ACA   TAGAATTCGAA
                                  _  ___
GAM35   ADAM28  3'  TACAGATTTTAACT        34741          AATTAGG
                                TACAGATTTTA      GCT
                                ||||||||||       |||
                                ATGTCTAAAAT      TGA
                                      _______
GAM35   ARSB    3'  CAGATTTTATCAGCTT      6249          AATTAG
                                CAGATTTTA     GGCTT
                                |||||||||     |||||
                                GTCTAAAAT     TCGAA
                                    AG____
GAM35   AXL     3'  CAGATTCTAGAGCTT       34882        TAAAT
                                CAGATTT    TAGGGCTT
                                |||||||    ||||||||
                                GTCTAAG    ATCTCGAA
                                   _____
GAM35   BPAG1   3'  TACAAATTTTAAATCTCAACTT 33783             AG
                                TACAGATTTTAAATT  GGCTT
                                ||||||||||||||  |||||
                                ATGTTTAAAATTTAG  TTGAA
                                      AG
GAM35   CAPN2   3'  TACAGATTTAAAGCT       11969        TTAAAT
                                TACAGATT     TAGGGCT
                                ||||||||     |||||||
                                ATGTCTAA     ATTTCGA
                                   _______
GAM35   DCK     3'  TACAGATTTGAAATTAAG    8981          T
                                TACAGATTT AAATTAGG
                                ||||||||| ||||||||
                                ATGTCTAAA TTTAATTC
                                    C
GAM35   ERBB3   3'  CACAGATTTTAAGCT       12752          AATTAG
                                TACAGATTTTA     GGCT
                                ||||||||||      ||||
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                                GTGTCTAAAAT     TCGA
                                       _______
GAM35   GRINL1A  3'  TACAAATTTTAAATGTAGCCC  43002            TAG
                                TACAGATTTTAAAT   GGCTT
                                ||||||||||||||  |||||
                                ATGTTTAAAATTTA   TCGGG
                                       CA_
GAM35   HMG20A   3'  TACAATAAACTTAGGGCTT   32871      ATTT    _
                                TACAG   TAAATT AGGGCTT
                                |||||   |||||| |||||||
                                ATGTT   ATTTGA TCCCGAA
                                   _____    A
GAM35   HTR2A    3'  AGATTTACTTAGGGCTTC    8385       TAAA
                                AGATTT   TTAGGGCTTC
                                ||||||   ||||||||||
                                TCTAAA   AATCCCGAAG
                                    TG__
GAM35   TMEPAI   3'  CAGATCTTTAAACAAAGG    33590       _   T
                                CAGATTTT AAAT AGGG
                                |||||||| |||| ||||
                                GTCTAGAA TTTG TTCC
                                     A   T
GAM36   AP1M1    3'  GTGGGTGACACGTGGCCCCGC  37173      GC  _  A
                                GTGGGT  GAC CGT GCCCCGC
                                ||||||  ||| ||| |||||||
                                CACCCA  CTG GCA CGGGGCG
                                   __  T  C
GAM36   CASP10   3'  GGTGGGTGGACTGTGAC     37390       C   C  AG
                                GGTGGGTG GAC GT  C
                                |||||||| ||| ||  |
                                CCACCCAC CTG CA  G
                                     _  A  CT
GAM36   CLECSF11 5'  AGGTGGGTGCAGAAGC      39041         ACCGT
                                AGGTGGGTGCG    AGC
                                ||||||||||    |||
                                TCCACCCACGT    TCG
                                       CT___
GAM36   DNLC2A   3'  AGCTGGGTGCGGGCTTCCTGC  30506    G      ACC  AG  CC
                                AG TGGGTGCG   GT  CC  GC
                                || ||||||||   ||  ||  ||
                                TC ACCCACGC   CG  GG  CG
                                 G      C__  AA  A_
GAM36   F2RL3    3'  GGTGGGTGTGGTCTGTCCCG   19528       CGACC  AGC_
                                GGTGGGTG    GT   CCCG
                                ||||||||    ||   ||||
                                CCACCCAC    CA   GGGC
                                     AC___  GACA
GAM36   MGST3    5'  GTGGGTGCGGCGCCCTCGC    21188        ACC  A   _
                                GTGGGTGCG   GT GCCC CGC
                                |||||||||   || |||| |||
```

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                                CACCCACGC   CG CGGG GCG
                                    ___ _    A
GAM36   RAB38    3' AGTGCCGACTGTGGCCCG    41263      _  C  A   C
                                GGTGC GAC GT GCCC G
                                ||||| ||| || |||| |
                                TCACG CTG CA CGGG C
                                   G   A  C   A
GAM36   RYR2     3' GGTGAGTGTGGCTGCCACG   9768        CGACC  A   C
                                GGTGGGTG    GT GCC CG
                                ||||||||    || ||| ||
                                CCACTCAC    CG CGG GC
                                    AC___  A   T
GAM36   SEPX1    3' GGTGGGTGTGGGCTGCCCGC  32269       CGACC  A   C
                                GGTGGGTG    GT GCCC GC
                                ||||||||    || |||| ||
                                CCACCCAC    CG CGGG CG
                                    ACC__  A   _
GAM36   SNL      5' AGGTGGGTGGCGGGTCCCTGC 16935        _ ACCGTAG   C
                                AGGTGGGTG CG      CCC GC
                                ||||||||| ||      ||| ||
                                TCCACCCAC GC      GGG CG
                                    C  CCA____   A
GAM36   TMEPAI   3' GTGGGTGCGCGCCCCG     33618        ACCGTA
                                GTGGGTGCG     GCCCCG
                                |||||||||     ||||||
                                CACCCACGC     CGGGGC
                                    G_____
GAM36   TNFRSF6B 5' GGGGGTGGCCATAGCCCTGC  32362    T    CGA      C
                                GG GGGTG   CCGTAGCCC GC
                                || |||||   ||||||||| ||
                                CC CCCAC   GGTATCGGG CG
                                 _    C__       A
GAM36   ADD1     3' TCGGCCCATCATGCCCAG    30527       ACCA  C
                                TCGGCC    CG GCTCGG
                                ||||||    || ||||||
                                AGCCGG    GT CGGGTC
                                   GTA_  A
GAM36   AOC3     3' TCGGCCACGGCTCCAGGCTGGG 19021        CAC  G  C   CA
                                TCGGCCAC   GC CT GGC  GG
                                ||||||||   || || |||  ||
                                AGCCGGTG   CG GG CCG  CC
                                    C__  A  T   AC
GAM36   BACE2    5' TCGGCCGGCGCGCGGGGCTGCG 39997      ACCA    TC   CA_
          G                      TCGGCC   CGCGC  GGC   GG
                                ||||||   |||||  |||   ||
                                AGCCGG   GCGCG  CCG   CC
                                   CC__    CC   ACG
GAM36   CAPN2    5' TCCGCGCTGCGCTCGGCTGGG  11971    G  CACCAC       CA
                                TC GC     GCGCTCGGC  GG
                                || ||     |||||||||  ||
```

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                                AG CG     CGCGAGCCG  CC
                                 G  CGA___        AC
GAM36   GNB1     5'  TCGGCCGCCGCTCGGCAG    13212        A  ACGC      C
                                TCGGCC CC    GCTCGGC AG
                                |||||| ||    ||||||| ||
                                AGCCGG GG    CGAGCCG TC
                                   C _____      _
GAM36   ID3      3'  TCGGCCACTGCGGGAGGGCAGG 44275         CAC   CTC  C
                                TCGGCCAC   GCG   GG CAGG
                                ||||||||   |||   || ||||
                                AGCCGGTG   CGC   CC GTCC
                                     A__   CCT  C
GAM36   ITPR2    5'  TCGGCCGTCACAGCGCCGGC   13680        AC  _    T
                                TCGGCC  CAC GCGC CGGC
                                ||||||  ||| |||| ||||
                                AGCCGG  GTG CGCG GCCG
                                   CA   T   _
GAM36   KLHL2    5'  CGGCCATGGCCCGCTCGGCCGG 28529        CCACG        A
           G                     CGGCCA     CGCTCGGCC GG
                                ||||||     ||||||||| ||
                                GCCGGT     GCGAGCCGG CC
                                   ACCGG        C
GAM36   KLK5     5'  TCGGCACTGCGCTGAGACCCAG 29683       C  CAC     C __
           G                     TCGGC AC   GCGCT GG  CCAGG
                                ||||| ||   ||||| ||  |||||
                                AGCCG TG   CGCGA TC  GGTCC
                                  _ A__     C  TG
GAM36   LAMC3    5'  CCGGCCCCGCTCGGCTAGG    25862        A  ACGC      C
                                TCGGCC CC    GCTCGGC AGG
                                |||||| ||    ||||||| |||
                                GGCCGG GG    CGAGCCG TCC
                                   _ _____       A
GAM36   NOS1     5'  TCGGCCGCTGCTCGCTGCCCGG 8379         ACCAC  _    __   A
                                TCGGCC    GC GCTCG  GCC GG
                                ||||||    || |||||  ||| ||
                                AGCCGG    CG CGAGC  CGG CC
                                   ______ A    GA   G
GAM36   PDGFB    5'  GCCCGCTGCGCGCTCGGCTGGG 15178     ACCA_        CA
                                GCC    CGCGCTCGGC  GG
                                |||    ||||||||||  ||
                                CGG    GCGCGAGCCG  CC
                                  GCGAC         AC
GAM36   PER2     3'  GGCTGCTCTCGGCCAG      35618     CACCAC  G
                                GGC     GC CTCGGCCAG
                                |||     || |||||||||
                                CCG     CG GAGCCGGTC
                                  A_____  A
GAM36   RPE      5'  TCGGCCCCTAAATTGGCCAGG  41642        A  ACGCGCTC
                                TCGGCC CC       GGCCAGG
                                |||||| ||       |||||||
```

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                                AGCCGG GG       CCGGTCC
                                   _ ATTTAA__
GAM36   RPS6KA2  5' CCGGCCACCGCGGCCGG     34457         A  C  T
                                TCGGCCACC CG GC CGG
                                ||||||||| || || |||
                                GGCCGGTGG GC CG GCC
                                    C  _  _
GAM36   SLC1A1   5' TCGGCCGTGCGCGCGTGGGCTG 20036       ACCA    TC_  CA
           GG                    TCGGCC   CGCGC   GGC  GG
                                ||||||   |||||  |||  ||
                                AGCCGG   GCGCG   CCG  CC
                                   CAC_    CAC   AC
GAM36   TRPM2    3' TCGGCCAGTGCTCAGTGGCCAG 17696       CCACGC   ___
           G                    TCGGCCA     GCTC   GGCCAGG
                                |||||||     ||||   |||||||
                                AGCCGGT     CGAG   CCGGTCC
                                   CA____    TCA
GAM37   ADCY6    3' TCCTCATGCCTGTCTTTGTAC  34179    A      A  ACACTC
                                TC CTCATGCC GT     GC
                                || ||||||| ||     ||
                                AG GAGTACGG CA     TG
                                 _       A  GAAACA
GAM37   BCL7A    5' TCACTCGCGCACAGACACTCGC 34219       A  _  T
           AC                    TCACTC TGC CAG ACACTCGCAC
                                |||||| ||| ||| ||||||||||
                                AGTGAG GCG GTC TGTGAGCGTG
                                   C   T  _
GAM37   DLG5     5' TCACTCATGATGAGCTTGTAC  44465        _____  CA
                                TCACTCAT    GC  GTAC
                                ||||||||    ||  ||||
                                AGTGAGTA    CG  CATG
                                    CTACT  AA
GAM37   HNRPM    5' CTCTCGAGATACACTCGC    25568     A  CCA
                                CTC TG   GTACACTCGC
                                ||| ||   ||||||||||
                                GAG GC   TATGTGAGCG
                                  A  TC_
GAM37   MLH1     3' CACTTATGTTGGTACACT    6997      C   CCA
                                CACT ATG   GTACACT
                                ||||  |||   |||||||
                                GTGA TAC   CATGTGA
                                   A   AAC
GAM37   SLC6A8   3' TCACGCACGCGTGCACTCGCAC 24785     T    CA  A
                                TCAC CATGC  GT CACTCGCAC
                                |||| |||||  || |||||||||
                                AGTG GTGCG  CA GTGAGCGTG
                                   C     __  C
GAM37   ANKTM1   3' TACTAGATGGAATACAG     28807        AT    A
                                TACTGGAT  GAGTG CAG
                                ||||||||  ||||| |||
```

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                                ATGATCTA  CTTAT GTC
                                    C_    _
GAM37   DDX6    3'  TACTAGATGAGACA      20555       TA  GT
                                TACTGGA  TGA  GACA
                                |||||||  |||  ||||
                                ATGATCT  ACT  CTGT
                                    __   __
GAM37   DPH2L2  3'  TACTGGACAGTGCA      10735       ATG   A
                                TACTGGAT   AGTG CA
                                ||||||||   |||| ||
                                ATGACCTG   TCAC GT
                                    ___    _
GAM37   GYPA    3'  TACTACAAATGAGTGACAG   44625     GAT
                                TACTG   ATGAGTGACAG
                                |||||   ||||||||||
                                ATGAT   TACTCACTGTC
                                   GTT
GAM37   MAP3K5  3'  TACTGGATTTAAAGTGCAG   25444       AT_   A
                                TACTGGAT   GAGTG CAG
                                ||||||||   ||||| |||
                                ATGACCTA   TTCAC GTC
                                    AAT    _
GAM37   MOX2    3'  CACTGGATAGACACAG     42514        T  GTG
                                TACTGGATA GA   ACAG
                                |||||||| ||   ||||
                                GTGACCTAT CT   TGTC
                                    _ G__
GAM37   MS4A3   3'  TACAGGTAATAAGTGACAG   26009    T  AT
                                TAC GG  ATGAGTGACAG
                                ||| ||  ||||||||||
                                ATG CC  TATTCACTGTC
                                  T  AT
GAM37   NLGN1   3'  TACTGGTAAACAACAG     31387      ATA   TG
                                TACTGG   TGAG  ACAG
                                ||||||   ||||  ||||
                                ATGACC   ATTT  TGTC
                                   ___    GT
GAM37   OAS3    3'  TGGATATGTGTGTGGCAG    26184       A  A__
                                TGGATATG GTG   CAG
                                |||||||| |||   |||
                                ACCTATAC CAC   GTC
                                    A   ACC
GAM37   OPCML   3'  TACTGGATAGTTTTCAAACAG  14953        TGAGT__
                                TACTGGATA      GACAG
                                |||||||||      |||||
                                ATGACCTAT      TTGTC
                                     CAAAAGT
GAM37   PGAM1   3'  CACTGGACCCATGTGGCAG   44055       ATGA  A
                                TACTGGAT    GTG CAG
                                ||||||||    ||| |||
```

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                                GTGACCTG   CAC GTC
                                    GGTA   C
GAM37   PYGM     5'  TACTGGTTTAATGACAG     24699       ATATG
                                TACTGG    AGTGACAG
                                ||||||    ||||||||
                                ATGACC    TTACTGTC
                                   AAA__
GAM37   SLC25A12 3'  ACTGGATACATTACAG      18978         AGTG
                                ACTGGATATG   ACAG
                                ||||||||||   ||||
                                TGACCTATGT   TGTC
                                     AA__
GAM37   SOX10    3'  TACTGAGATAAATAACAG     28014       AT
                                TACTGG  ATGAGTGACAG
                                ||||||  ||||||||||
                                ATGACT  TATTTATTGTC
                                   C_
GAM37   TEM6     3'  TACTGGATATATTCTTTACAG  35559          AGTG__
                                TACTGGATATG     ACAG
                                ||||||||||      ||||
                                ATGACCTATAT     TGTC
                                     AAGAAA
GAM37   ZNF10    5'  TACTTCCTTGAGTGACAG     31742     GGATA
                                TACT    TGAGTGACAG
                                ||||    ||||||||||
                                ATGA    ACTCACTGTC
                                  AGGA_
GAM38   BAALC    3'  CCATGGGCAGTGGGTTG      36036          CGCA
                                CCATGGGCAGTG   TG
                                ||||||||||||   ||
                                GGTACCCGTCAC   AC
                                     CCA_
GAM38   CELSR1   3'  CAAGGGCAGTGGCCCC      30649    T      C  ATG
                                CA GGGCAGTG GC   CC
                                || ||||||| ||   ||
                                GT CCCGTCAC CG   GG
                                 T      _  G__
GAM38   LARS2    5'  CCATGGGCGCCGCCATG     31675        AG   G
                                CCATGGGC  TGC CATG
                                ||||||||  ||| ||||
                                GGTACCCG  GCG GTAC
                                     CG   _
GAM38   NDUFS2   5'  TCCTATCTGTGCATGCC     21240     A  GGCAG  C
                                TCC TG    TG GCATGCC
                                ||| ||    || |||||||
                                AGG AT    AC CGTACGG
                                  _  AG___  A
GAM38   NRAP     3'  TCCATGGGCAGATGGAAC     40199          _  C_
                                TCCATGGGCAG TG  GC
                                |||||||||| ||  ||
```

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                                AGGTACCCGTC AC  TG
                                      T  CT
GAM38   PTPRO    5'  TCCTGGCGAGCGCATGC    36225    ATG   AGT
                                TCC   GGC   GCGCATGC
                                |||   |||   ||||||||
                                AGG   CCG   CGCGTACG
                                  A__   CT_
GAM38   SARDH    5'  TCCAGGGCAGTGGC      28252     T      CGCAT
                                TCCA GGGCAGTG    GC
                                |||| ||||||||    ||
                                AGGT CCCGTCAC    CG
                                  _      _____
GAM38   SCNN1G   3'  TCTGTGAGCAGTTGGCTTG   9794     CA      _ C  A
                                TC  TGGGCAGT G GC TG
                                ||  |||||||| | || ||
                                AG  ACTCGTCA C CG AC
                                 AC       A _  A
GAM38   TNFRSF13C 3'  TCCATGGGGGCTGAATGC    38121        CAGT  GC_
                                TCCATGGG   GC   ATGC
                                ||||||||   ||   ||||
                                AGGTACCC   CG   TACG
                                     C___  ACT
GAM38   XT3      3'  TCCATGGGGTACATGC     33667        CA  GC
                                TCCATGGG  GT  GCATGC
                                ||||||||  ||  ||||||
                                AGGTACCC  CA  TGTACG
                                    __  __
GAM38   ALDH1B1  3'  GCCTAGTATGTATATTTCATA  8671     CT    CCTCAA
                                GCC  GTATG     GTTTCATA
                                |||  |||||     ||||||||
                                CGG  CATAC     TAAAGTAT
                                  AT    ATA___
GAM38   IGFBP4   3'  GCCCTCTGTGCTTCAAGTC   11400      GTA   C
                                GCCCT   TGC TCAAGTT
                                |||||   ||| |||||||
                                CGGGA   ACG AGTTCAG
                                   GAC   A
GAM38   NCOA6IP  3'  CCTGTAAGTTTCCATTTCATA  36049       TGCC  AA
                                CCTGTA    TC  GTTTCATA
                                ||||||    ||  ||||||||
                                GGACAT    AG  TAAAGTAT
                                   TCAA  G_
GAM38   PIM1     3'  GCCCTGTAGCCTCTTCCAT   44966        T    AAG
                                GCCCTGTA GCCTC   TTTCAT
                                |||||||| |||||   ||||||
                                CGGGACAT CGGAG   AAGGTA
                                  _    ___
GAM38   POP2     3'  ACCCTGTGAGGTGGGTTTCATA 35255        ATGCCTCAA
                                GCCCTGT       GTTTCATA
                                |||||||       ||||||||
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                                TGGGACA       CAAAGTAT
                                   CTCCACC__
GAM38   XPR1     3'  CTGTATGGTTAAGTTTCATA  21850       CCTC
                                CTGTATG    AAGTTTCATA
                                |||||||    ||||||||||
                                GACATAC    TTCAAAGTAT
                                   CAA_
GAM39   ARHGAP6  3'  CGCTCACTGGAGATCCTGCAG  25963        TCT   A_
                                CGCTCACTG   GTCT  CAG
                                |||||||||   ||||  |||
                                GCGAGTGAC   TAGG  GTC
                                     CTC    AC
GAM39   CARKL    3'  GCTCTCTGTCTACAG      29996     ACTG
                                GCTC    TCTGTCTACAG
                                ||||    ||||||||||
                                CGAG    AGACAGATGTC
                                  _____
GAM39   CCR9     3'  GCTCACTGTATTCCTCAG    36297        CTG   A
                                GCTCACTGT   TCT CAG
                                |||||||||   ||| |||
                                CGAGTGACA   AGG GTC
                                     TA_   A
GAM39   CD164    3'  CCTTTCACTGTCTTCTA     25681    GC       G
                                CC  TCACTGTCT TCTA
                                ||  ||||||||| ||||
                                GG  AGTGACAGA AGAT
                                 AA       _
GAM39   EPHA3    3'  CCAGAATTATTGTCTGTCTGCA 23439     CTCAC__       A
           G                     CCG      TGTCTGTCT CAG
                                |||      ||||||||| |||
                                GGT      ACAGACAGA GTC
                                  CTTAATA       C
GAM39   EXTL3    3'  CCCCTCAGAGCCTGTCTGCAG  11030     G   CT      A
                                CCC CTCA  GTCTGTCT CAG
                                ||| ||||  |||||||| |||
                                GGG GAGT  CGGACAGA GTC
                                  _   CT      C
GAM39   GTF2H1   3'  GCTTGTCTGTCAGGCCAG    23691     CAC      TA__
                                GCT   TGTCTGTC    CAG
                                |||   ||||||||    |||
                                CGA   ACAGACAG    GTC
                                  ___       TCCG
GAM39   HLF      3'  CTCTTGCTGTTATCTACAG   13390     A__   C
                                CTC   CTGT TGTCTACAG
                                |||   |||| |||||||||
                                GAG   GACA ATAGATGTC
                                  AAC   _
GAM39   NPDC1    3'  CACCCGTTCCTGCGCTCTAC  31725       C  A   CTG
                                CACCCG TC CTGT   TCTAC
                                |||||| || ||||   |||||
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                                GTGGGC AG GACG   AGATG
                                   A  _   CG_
GAM39   NR2F6    3'  CCCTTGAGGTCTGTCTGCAG  23448     GCTCACT       A
                                CCC      GTCTGTCT CAG
                                |||      |||||||| |||
                                GGG      CAGACAGA GTC
                                  AACTC__       C
GAM39   PRKY     3'  CACCCTCTTCAGATGTCTACAG 15686       G  _  CTGTC
                                CACCC CT CA    TGTCTACAG
                                ||||| || ||    |||||||||
                                GTGGG GA GT    ACAGATGTC
                                   A  A  CT___
GAM39   PRPS1    3'  CCTGCTCCTGCCTTACA     15726    C    A     GTC
                                CC GCTC CTGTCT   TACA
                                || |||| ||||||   ||||
                                GG CGAG GACGGA   ATGT
                                 A   _    ___
GAM39   RAF1     3'  CCACTTGCGCATCTACAG    44331       CAC   C
                                CCGCT   TGT TGTCTACAG
                                |||||   ||| |||||||||
                                GGTGA   ACG GTAGATGTC
                                   ___   C
GAM39   SRP14    3'  GCTCTTCACAGAGATGTCTACA 17116    ___    TGTC_
           G                     GC   TCAC    TGTCTACAG
                                ||   ||||    |||||||||
                                CG   AGTG    ACAGATGTC
                                 AGA    TCTCT
GAM39   STK11    3'  CACCCGCCAGCTGGTCTGC    7829          CA   _
                                CACCCGCT  CTG TCTGT
                                ||||||||  ||| |||||
                                GTGGGCGG  GAC AGACG
                                     TC   C
GAM39   ABAT     5'  TGAGGGACAGGGACACCCTTTG 40778     CA       GTGGA_
           CG                     TGA  GACAGGGA     TTGCG
                                |||  ||||||||     |||||
                                ACT  CTGTCCCT     AACGC
                                  CC       GTGGGA
GAM39   HAO1     3'  ACAGATGGGAAAATATTGTGC  32757       CA    TGG    C
                                ACAGA  GGGAG   ATTG GC
                                |||||  |||||   |||| ||
                                TGTCT  CCCTT   TAAC CG
                                   A_    TTA    A
GAM39   LZTR1    3'  GACAGGGAGGGGGTCTGC    27637          T_  A
                                GACAGGGAG  GG TTGC
                                |||||||||  || ||||
                                CTGTCCCTC  CC GACG
                                      CC  A
GAM39   PKHD1    3'  TGACAGATCAGGGAGCAGGGTG 39809         _       TG AT
                                TGACAGA CAGGGAG  G  TG
                                ||||||| |||||||  |  ||
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                                ACTGTCT GTCCCTC  C  AC
                                    A      GT CC
GAM39   PPIL1    3'  TGATAAACAGGGGCATTTGTGC 32001     C      A  GA  C
                                TGA AGACAGGG GTG  TTG GC
                                ||| |||||||| |||  ||| ||
                                ACT TTTGTCCC CGT  AAC CG
                                  A       _  A_  A
GAM39   WISP2    3'  AGGCAGGGAGTGGGC       19307    A        ATT
                                AG CAGGGAGTGG   GC
                                || ||||||||||   ||
                                TC GTCCCTCACC   CG
                                 C        ___
GAM40   PDGFRA   3'  AAATTATATATCATTTATT   26284
                                AAATTATATATCATTTGTT
                                ||||||||||||||||||
                                TTTAATATATAGTAAATAA

GAM41   ADAMTS4  3'  CCGGGCGTGGTGGTAGGTGCC  23002    A  AACC       C
                                CC GG    GGTGGTAGG GCC
                                || ||    ||||||||| |||
                                GG CC    CCACCATCC CGG
                                 C  GCA_        A
GAM41   APOL1    3'  GGGCATGGTGGTAGGCGCC   18938    AACC
                                GG    GGTGGTAGGCGCC
                                ||    ||||||||||||
                                CC    CCACCATCCGCGG
                                 CGTA
GAM41   CYP8B1   3'  GGGCAAGGTGGTAGGTGCC   20507    AACC       C
                                GG    GGTGGTAGG GCC
                                ||    ||||||||| |||
                                CC    CCACCATCC CGG
                                 CGTT        A
GAM41   DFFB     3'  GGCCCTGGTGGTAGGTGCC   44601    AA  _       C
                                GG  CC GGTGGTAGG GCC
                                ||  || ||||||||| |||
                                CC  GG CCACCATCC CGG
                                 G_  A        A
GAM41   DNM2     3'  CCTGGGGATGTAGGCGCC    22380    A  AACC  TG
                                CC GG    GG  GTAGGCGCC
                                || ||    ||  |||||||||
                                GG CC    CC  CATCCGCGG
                                 A  _____  TA
GAM41   FMNL     5'  GGACGCCTGGAGGCGCCC    25300     A_  GG   T
                                GGA  CC  TGG AGGCGCCC
                                |||  ||  ||| ||||||||
                                CCT  GG  ACC TCCGCGGG
                                  GC  __   _
GAM41   GAS11    5'  TCCGGGACCAGGGCGC      11220     A   A    TGGTA
                                TCC GGA CCGG    GGCGC
                                ||| ||| ||||    |||||
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                                AGG CCT GGTC    CCGCG
                                  C  _  _____
GAM41   GNAI2    3'  TCCAGGAATGGTGGCG     42652       ACCG    A
                                TCCAGGA   GTGGT GGCG
                                |||||||   ||||| ||||
                                AGGTCCT   TACCA CCGC
                                    ____   _
GAM41   GPR30    5'  GGAACCGATGGCCGCCC    11313          AGG
                                GGAACCGGTGGT  CGCCC
                                ||||||||||||  |||||
                                CCTTGGCTACCG  GCGGG
                                     ___
GAM41   HR       5'  CCCAGGGGCTGGAGAGGCGCCC 32913       AACC  _  T_
                                TCCAGG   GG TGG  AGGCGCCC
                                ||||||   || |||  ||||||||
                                GGGTCC   CC ACC  TCCGCGGG
                                   ____ G  TC
GAM41   IGF1     3'  CCGGGCATAGTGGTGGGTGCC  8337    A  AACC    A  C
                                CC GG   GGTGGT GG GCC
                                || ||   |||||| || |||
                                GG CC   TCACCA CC CGG
                                 C  GTA_    C  A
GAM41   MTMR1    5'  CCGGGAGCCGGCGGTGGCGCCC 43153    A  A      A
                                CC GGA CCGGTGGT GGCGCCC
                                || ||| |||||||| |||||||
                                GG CCT GGCCGCCA CCGCGGG
                                 C  C      _
GAM41   P53AIP1  3'  TCCAGGGAGGTGTAGGCGC   35239      AACC   G
                                TCCAGG   GGTG TAGGCGC
                                ||||||   |||| |||||||
                                AGGTCC   CCAC ATCCGCG
                                   CT__   _
GAM41   RORA     5'  TCCAGAAACTGGGGCTGTGC  39517        C  T  AG_
                                TCCAGGAAC GG GGT  GC
                                ||||||||| || |||  ||
                                AGGTCTTTG CC CCG  CG
                                     A  _  ACA
GAM41   RTN2     3'  GGCTGGGGGCAGGCGTCC   24726   AACC  T     _
                                GG   GG GGTAGGCG CC
                                ||   || |||||||| ||
                                CC   CC CCGTCCGC GG
                                 GAC_ _      A
GAM41   SCN4A    3'  TCTGGGAACGCAGGCGC    7329    CA   CGGTG
                                TC  GGAAC   GTAGGCGC
                                ||  |||||   ||||||||
                                AG  CCTTG   CGTCCGCG
                                 AC   _____
GAM41   TMEFF2   5'  TCCAGGGACTGGGCTCAGCCC  32107      A  C_  GGTA  G
                                TCCAGG AC  GGT   GGC CC
                                |||||| ||  |||   ||| ||
```

```
                                AGGTCC TG  CCG    TCG GG
                                   C  AC   AG__  _
GAM41   DGKE    5'  CCAGCAGGCCTTGGCCGCC   18889       C  A  AG   A  A
                                CCAGCA GG CC  TTG CC CC
                                |||||| || ||  ||| || ||
                                GGTCGT CC GG  AAC GG GG
                                   _ _ __  C  C
GAM41   EGR3    3'  CAGAGCGGATGGAAGACCACCT 40542     CA    CCAGTT
                                CAG  CGGA     GACCACCT
                                |||  ||||     ||||||||
                                GTC  GCCT     CTGGTGGA
                                  TC    ACCTT_
GAM41   FBXL11   3'  CCACATGGACCAACCCTCACCT 29427     G  C     GT GAC
                                CCA CA GGACCA  T   CACCT
                                ||| || ||||||  |   |||||
                                GGT GT CCTGGT  G   GTGGA
                                  _ A     TG GA_
GAM41   FGFR1    5'  CAGCACGGGTACCGTCGCC   31931         __  A    A
                                CAGCACGG  ACC GTTG CC
                                ||||||||  ||| |||| ||
                                GTCGTGCC  TGG CAGC GG
                                     CA  _   _
GAM41   FMOD    3'  CCAGCACAGGCAAGATTTGGCT 12928         AC ________   A
           GCC                    CCAGCACGG  CA      GTTG CC
                                |||||||||  ||      |||| ||
                                GGTCGTGTC  GT      CGAC GG
                                     C_  TCTAAAC   _
GAM41   HSF2BP   3'  CCAGCACAGACATGGACCAC   28143          CA  T
                                CCAGCACGGAC  GT GACCAC
                                ||||||||||  || ||||||
                                GGTCGTGTCTG  TA CTGGTG
                                      __  C
GAM41   MAPRE2   5'  CCGCACGGACCGTGCCTGCCGC 30690    A       A_   GA  A
           CT                     CC GCACGGACC  GTT  CC CCT
                                || |||||||||  |||  || |||
                                GG CGTGCCTGG  CGG  GG GGA
                                 _       CA   AC  C
GAM41   PPFIA3   3'  CCAGCACGGTCCTCAC      41415          A  AGTTGAC
                                CCAGCACGG CC      CAC
                                |||||||||  ||      |||
                                GGTCGTGCC GG      GTG
                                     A  A_______
GAM41   PRX     3'  CCAGCGTGACCAGCTCCACCT  34108       ACG       GA
                                CCAGC   GACCAGTT  CCACCT
                                |||||   ||||||||  ||||||
                                GGTCG   CTGGTCGA  GGTGGA
                                  CA_       __
GAM41   SAS     3'  CCAACGCGGGTGGATCACC   33216       A   ACCA  T  C
                                CCAGC CGG    GT GA CACC
                                ||||| |||    || || ||||
```

```
                                GGTTG GCC   CA CT GTGG
                                  C  ____  C  A
GAM41   TNFRSF11A 3'  CCAGCATGGATAAATTAACCAC 19270      C  CC
          CT                    CCAGCA GGA  AGTTGACCACCT
                                |||||| |||  ||||||||||||
                                GGTCGT CCT  TTAATTGGTGGA
                                  A  AT
GAM41   VDR     3'  CCAGCTGGGCTGGGCTCGACC  7516      AC  ACCA  _
                                CCAGC  GG   GTT GACC
                                |||||  ||   ||| ||||
                                GGTCG  CC   CGA CTGG
                                  AC  GACC  G
GAM42   BCL2    3'  TCTCTTGCGGAGTATTTGTGCA 8526       TA   GCC  A
                                TCTCTTGC  GGTA  TGT CA
                                ||||||||  ||||  ||| ||
                                AGAGAACG  TCAT  ACA GT
                                    CC   AA_  C
GAM42   CASP2   3'  TCTCTTGCATTTCCTGTGCA  37402      TAGGTAG   A
                                TCTCTTGC     CCTGT CA
                                ||||||||     ||||| ||
                                AGAGAACG     GGACA GT
                                    TAAA___    C
GAM42   CDKN2D  3'  TCTTTTAAAACGCTGTACAA  38614     GCTAGGT  _
                                TCTT     AGC CTGTACAA
                                ||||     ||| ||||||||
                                AGAA     TTG GACATGTT
                                  AATT___  C
GAM42   IL16    3'  CCTTTTGCTGGGTGGCGTCCTA 21096    C   A  AG___
                                TCT TTGCT GGT    CCTG
                                ||| ||||| |||    ||||
                                GGA AACGA CCA    GGAT
                                  A   C  CCGCA
GAM42   MMP15   3'  TTGCCGGCTGTACAA      14565      A  TAGC
                                TTGCT GG   CTGTACAA
                                |||||  ||  ||||||||
                                AACGG CC   GACATGTT
                                  _  ____
GAM42   PIM1    3'  TCTCTTTTATTCCCCTGTACA  44972      GC  GGTAG
                                TCTCTT  TA   CCTGTACA
                                ||||||  ||   ||||||||
                                AGAGAA  AT   GGACATGT
                                  A_  AAGG_
GAM42   ACATN   3'  AACAATGTCAGACTAG     21839       TTTGTC
                                AACAGTGT    CAGACTAG
                                ||||||||    ||||||||
                                TTGTTACA    GTCTGATC
                                  ______
GAM42   ADAT1   3'  ACAGGGTTTCACCAGGTTGGCC 28991     T    T   ACTA
                                ACAG GTTTTG CCAG   GCC
                                |||| |||||| ||||   |||
```

```
                                TGTC CAAAGT GGTC   CGG
                                  C    _   CAAC
GAM42   ALDH3A2  3'  CACTGTGTTGTCCAGGCT   42913   G  T     A
                                CA TGT TTGTCCAG CT
                                || ||| |||||||| ||
                                GT ACA AACAGGTC GA
                                 G  C      C
GAM42   DRD2     3'  GTGAGGTGGGTCCGGACTAGCC 9020     TTTT__   A
                                GTG    GTCC GACTAGCC
                                |||    |||| ||||||||
                                CAC    CAGG CTGATCGG
                                  TCCACC   C
GAM42   ITGAL    3'  GTTTCGCCAGGCTGGCC    13620      T   A  A
                                GTTTTG CCAG CT GCC
                                |||||| |||| || |||
                                CAAAGC GGTC GA CGG
                                   _   C  C
GAM42   LUZP1    3'  CACTATATTGTCCAGGCT   37957   G  T     A
                                CA TGT TTGTCCAG CT
                                || ||| |||||||| ||
                                GT ATA AACAGGTC GA
                                 G  T      C
GAM42   MAFF     3'  ACCATGTTGTCCAGGCT    29508   A   TT    A
                                AC GTGT  TGTCCAG CT
                                || ||||  ||||||| ||
                                TG TACA  ACAGGTC GA
                                 G  __     C
GAM42   MYO1B    3'  ACAGGGTTTTGCCATGTTGGCC 29224     T    T  GACTA
                                ACAG GTTTTG CCA    GCC
                                |||| |||||| |||    |||
                                TGTC CAAAAC GGT    CGG
                                  C    _  ACAAC
GAM42   NPR2L    3'  GTGTTTTGGATGCACTGGCC  27251       TCCAG  A
                                GTGTTTTG    ACT GCC
                                ||||||||    ||| |||
                                CACAAAAC    TGA CGG
                                     CTACG  C
GAM42   PSMD5    3'  ACAGGGTTTTGCCATATTGGCC 22776     T    T  GACTA
                                ACAG GTTTTG CCA    GCC
                                |||| |||||| |||    |||
                                TGTC CAAAAC GGT    CGG
                                  C    _  ATAAC
GAM42   SWAP70   3'  ACAGGGTTTCACCAGGTTGGCC 43420     T    T  ACTA
                                ACAG GTTTTG CCAG   GCC
                                |||| |||||| ||||   |||
                                TGTC CAAAGT GGTC   CGG
                                  C    _   CAAC
GAM42   TNFSF14  3'  GTTTTGCCATGTTAGCC    19184      T  GAC
                                GTTTTG CCA  TAGCC
                                |||||| |||  |||||
```

```
                                CAAAAC GGT   ATCGG
                                   _  ACA
GAM42   UBE3A    3'  AACAGTGTTCTAAAGGCTGGCC 39274          TCC  A  A
                                AACAGTGTTTTG   AG CT GCC
                                |||||||||||   || || |||
                                TTGTCACAAGAT   TC GA CGG
                                      T__  C  C
GAM42   ZNF264   3'  ACAGGGTTTTGCCATGTTGGCC 18264     T     T  GACTA
                                ACAG GTTTTG CCA    GCC
                                |||| |||||| |||    |||
                                TGTC CAAAAC GGT    CGG
                                  C     _  ACAAC
GAM42   ZNF74    3'  ACCATGTTGTCCAGGCT    18298    A   TT     A
                                AC GTGT  TGTCCAG CT
                                || ||||  ||||||| ||
                                TG TACA  ACAGGTC GA
                                 G   __      C
GAM43   FXYD1    5'  TCACGCAAAAGCTGCCGGGGTG 34866        CA_      AC
           AGG                    TCGCGCAG   CTGCCGGG  GAGG
                                |||||||||  ||||||||  ||||
                                AGTGCGTT   GACGGCCC  CTCC
                                     TTC       CA
GAM43   ADAMTS8  5'  CCCCGGCCCGCGTGCGCCCG   28160      T    C  TGA
                                CCCCGG CCCGCG GC   CCG
                                |||||| |||||| ||   |||
                                GGGGCC GGGCGC CG   GGC
                                   _     A  CG_
GAM43   ADRA2A   5'  CCCGGGTCCCGCGAACTG    8630     C       C
                                CCC GGTCCCGCG GCTG
                                ||| ||||||||| ||||
                                GGG CCAGGGCGC TGAC
                                  C        T
GAM43   AP2S1    5'  CCCCGGTCCCGCGGCGAC    34644          C  T
                                CCCCGGTCCCGCG GC GAC
                                |||||||||||| || |||
                                GGGGCCAGGGCGC CG CTG
                                          _ _
GAM43   AQP5     5'  CCTCGGTGCCGTGCGCCCCG   11628    _   C  C    GA
                                CC CGGT CCG GCGCT  CCG
                                || |||| ||| |||||  |||
                                GG GCCA GGC CGCGG  GGC
                                 A   C  A    __
GAM43   DDX38    3'  CCCCGCTCCCGCCATGCCG   30411      G     G  C  A
                                CCCCG TCCCGC CG TG CCG
                                ||||| |||||| || || |||
                                GGGGC AGGGCG GT AC GGC
                                   G     _ _ _
GAM43   EZH2     5'  GTCCCGCGCGCCGACTCGCG  20878             _
                                GTCCCGCGCGCTGAC CGCG
                                |||||||||||||| ||||
```

```
                                CAGGGCGCGCGGCTG GCGC
                                       A
GAM43   FGD1    5'  CCCCGGCCCCGCGCGGGGA   20900            CT
                                CCCCGGTCCCGCGCG  GA
                                |||||||||||||||  ||
                                GGGGCCGGGGCGCGC  CT
                                       CC
GAM43   GNA11   3'  CCCCGGCCTGCGTGCTGGGCG  13161      T  C   C   ACC
                                CCCCGG CC GCG GCTG   GCG
                                |||||| || ||| ||||   |||
                                GGGGCC GG CGC CGAC   CGC
                                   _ A  A   C__
GAM43   HIC1    5'  CAGTGCGTGTTGACCGC    44563     CCC   CGC
                                CGGT   GCG   TGACCGC
                                ||||   |||   |||||||
                                GTCA   CGC   ACTGGCG
                                  ___   ACA
GAM43   IL6R    5'  CCTCGGCCCCGCGCCG     8172     _        GCTGAC
                                CC CGGTCCCGCGC     CG
                                || ||||||||||      ||
                                GG GCCGGGGCGCG     GC
                                 A         _______
GAM43   INSR    5'  CCCCGGTGCCCATGGCTG    43377        _   CGC
                                CCCCGGT CCCG   GCTG
                                ||||||| ||||   ||||
                                GGGGCCA GGGT   CGAC
                                    C    AC_
GAM43   LMO4    5'  CCTCGGCCCGCGCGGCGC    27651    _  T      CTGAC
                                CC CGG CCCGCGCG    CGC
                                || ||| ||||||||    |||
                                GG GCC GGGCGCGC    GCG
                                 A  _       C____
GAM43   MDFI    5'  CCCCGGACTCGTGCGAGCCG   24614       __  CC   C
                                CCCCGG  TC  GCG GCTG
                                ||||||  ||  ||| ||||
                                GGGGCC  AG  CGC CGGC
                                    TG  CA   T
GAM43   MMP2    5'  CCCTGGCCCCGCGCGTCG    21194     C         C
                                CCC GGTCCCGCGCG TG
                                ||| ||||||||||| ||
                                GGG CCGGGGCGCGC GC
                                  A         A
GAM43   MSF     5'  CCAGCTGCGCGTTGACCGC   44720      CCC    C
                                CCGGT   GCGCG TGACCGC
                                |||||   ||||| |||||||
                                GGTCG   CGCGC ACTGGCG
                                  A__    A
GAM43   MYBL2   5'  CCCCGGCCCGGACCG      14702       T   CGCGCT
                                CCCCGG CCCG     GACCG
                                |||||| ||||     |||||
```

```
                                GGGGCC GGGC     CTGGC
                                  _  ______
GAM43   SLC20A2  5' CCTCGGTCCCGTGCGGTCCCCG 27571   _      C  CTGA
                                CC CGGTCCCG GCG   CCG
                                || |||||||| |||   |||
                                GG GCCAGGGC CGC   GGC
                                 A       A  CAGG
GAM43   SMARCD2  5' CCCGTCCCGCGGTGCCGC   16912     G     CGC  A
                                CCCG TCCCGCG   TG CCGC
                                |||| |||||||   || ||||
                                GGGC AGGGCGC   AC GGCG
                                  _      C__  _
GAM43   STXBP1   5' CCTCGTCCCGCGACGCCTGCG  17203   G_      _   GACC
                                CC  GTCCCGCG CGCT   GCG
                                ||  |||||||| ||||   |||
                                GG  CAGGGCGC GCGG   CGC
                                 AG       T   A___
GAM43   WASF3    5' GGTCCCGCCGCGCCGCG    27387       G   T A
                                GGTCCCGC CGC G CCGCG
                                |||||||| ||| | |||||
                                CCAGGGCG GCG C GGCGC
                                  _  _ _
GAM44   AQP6     5' CCAGGTAGCCATTGACCAGGGC 38237          __ ATAA
           TT                    CCAGGTAGCCGT  GC   GCTT
                                ||||||||||||  ||   ||||
                                GGTCCATCGGTA  TG   CGAA
                                      AC  GTCC
GAM44   SLA      3' ACCAGTAGCACGATGAGCTTA  27563      G   _ _  CATA
                                ACCAG TAGC CG TG   AGCTTA
                                ||||| |||| || ||   ||||||
                                TGGTC ATCG GC AC   TCGAAT
                                  _   T  T  _____
GAM44   SYT1     3' ACCAAGTATGTGGTGTAAG   24850       GCC_  CA
                                ACCAGGTA   GTG  TAAG
                                ||||||||   |||  ||||
                                TGGTTCAT   CAC  ATTC
                                     ACAC  __
GAM44   TAP2     3' CCAGGTAGCAGATATAAAGCTT 8080         CGTGCAT
           A                     CCAGGTAGC      AAGCTTA
                                |||||||||      |||||||
                                GGTCCATCG      TTCGAAT
                                     TCTATAT
GAM44   WASF3    3' CAGTGTAGCCAAGCTT     27376    _     TGCATA
                                CAG GTAGCCG     AGCTT
                                ||| |||||||     |||||
                                GTC CATCGGT     TCGAA
                                  A     _______
GAM44   CRMP1    5' TGCGGGGCTGTCTGACTGG   10601     ACAA  C      A
                                TGC   GC GTCTGATT GG
                                |||   || |||||||| ||
```

```
                                ACG   CG CAGACTGA CC
                                  CCC_ A      _
GAM44   GPR4     5'  TGCAGGGCAATTAGGA     40893     CAA  CGTCT
                                TGCA  GC    GATTAGGA
                                ||||  ||    ||||||||
                                ACGT  CG    TTAATCCT
                                  CC_ _____
GAM44   NINJ1    3'  TGCAGGGTCCCTGGGTTAGGAA 19986     CAAG  GT   A_
           G                     TGCA   CC  CTG  TTAGGAAG
                                ||||   ||  |||  ||||||||
                                ACGT   GG  GAC  AATCCTTC
                                  CCCA __   CC
GAM45   ACPT     3'  CTGGTAGTGGAAGACCGTGGGC 38890         _   C   CCA
           T                     TTGGTAGTG AAG CTG   GGCT
                                |||||||||| ||| |||   ||||
                                GACCATCAC TTC GGC   CCGA
                                     C   T   AC_
GAM45   CACNA1D  3'  TGGTACTCTGCCAGGCT     8770      AGTGAA  _
                                TGGT     GC CTGCCAGGCT
                                ||||     || ||||||||||
                                ACCA     TG GACGGTCCGA
                                  _______ A
GAM45   COG5     3'  TGGTGTCTGTCAGGC      26815     A  GAAGC   C
                                TGGT GT     CTG CAGGC
                                |||| ||     ||| |||||
                                ACCA CA     GAC GTCCG
                                  _ _____   A
GAM45   IRAK4    3'  TTAGTAGTGGAGTCAGCTGGGC 41463         A  CCT  CA
           T                     TTGGTAGTG AG   GC  GGCT
                                |||||||||| ||   ||  ||||
                                AATCATCAC TC   CG  CCGA
                                     C  AGT  AC
GAM46   BCL7A    5'  GAAAGAGTTGGGCATCGCGCAT 34207          ATT  A_   C
           CT                    GAAAGAGTTGG   TC  GCA CT
                                ||||||||||   ||  ||| ||
                                CTTTCTCAACC   AG  CGT GA
                                      CGT  CG   A
GAM46   C1orf6   3'  AAGGGGTTGGAGCCCATGCCT  33522     A_     T    GCA
                                AAG  GTTGGA TTCA   CCT
                                |||  |||||| ||||   |||
                                TTC  CAACCT GGGT   GGA
                                  CC     C    AC_
GAM46   CCNT2    3'  TGAAGGCAAAATTTCAGTGCCT 38496      A A  TG       CA
                                TGAA G GT  GATTTCAG  CCT
                                |||| | ||  ||||||||  |||
                                ACTT C CG  TTAAAGTC  GGA
                                  _ _ TT       AC
GAM46   CNTNAP2  3'  TGAGAGGATTGGATCTCA    30495     A  AG
                                TGA AG  TTGGATTTCA
                                ||| ||  ||||||||||
```

```
                                ACT TC  AACCTAGAGT
                                  C  CT
GAM46   COL18A1  3'  GAGATGAAGTCAGCACCT    39054     TTG  TT
                                GAG   GA  TCAGCACCT
                                |||   ||  |||||||||
                                CTC   CT  AGTCGTGGA
                                  TA_  TC
GAM46   FACL4    3'  GAAAGGCAATTTTCAGCA    35679       A  TGGA
                                GAAAG GT    TTTCAGCA
                                |||||  ||    ||||||||
                                CTTTC CG    AAAGTCGT
                                   _  TTA_
GAM46   GP2      3'  AGAGACGGAGTTTCAGCA    11302      T   _
                                AGAG TGGA TTTCAGCA
                                ||||  ||||  ||||||||
                                TCTC GCCT AAAGTCGT
                                  T    C
GAM46   HTR4     5'  TGAGTGAGTTGGATTTCAA    9305      AA
                                TGA  GAGTTGGATTTCAG
                                |||  ||||||||||||||
                                ACT  CTCAACCTAAAGTT
                                  CA
GAM46   VSNL1    3'  TGAAAAGTTGGAAAGTTGC    18039      A       TTTCA
                                TGAA GAGTTGGA     GC
                                ||||  ||||||||     ||
                                ACTT TTCAACCT     CG
                                   _       TTCAA
GAM46   POLG     3'  GGGGCTTCTGCTTCATTTTT   15449    T    CTGG
                                G GGCT    TCTGCTTCATTTTT
                                |  ||||    ||||||||||||||
                                C CCGA    AGACGAAGTAAAAA
                                 C   _____
GAM46   PSMD7    3'  GTGGCTTCTCTTCATTTT     15838       CTGG   G
                                GTGGCT    TCT CTTCATTTT
                                ||||||    |||  |||||||||
                                CACCGA    AGA GAAGTAAAA
                                     _____   _
GAM47   ADAT1    3'  TAGCTTGCTCTAAGTTCC     28997      C       CACATA
                                TAGC TGCTTTAA      TCC
                                ||||  ||||||||      |||
                                ATCG ACGAGATT      AGG
                                   A       CA_____
GAM47   C14orf1  3'  GCCTGCTCCATATC        28414          TAACA
                                GCCTGCTT     CATATC
                                ||||||||     ||||||
                                CGGACGAG     GTATAG
                                     ______
GAM47   CTNNB1   3'  TACCCTACCCATACATATCCCA 12520     G       TAAC
                                TA CCTGCTT    ACATATCCCA
                                ||  |||||||   ||||||||||
```

```
                                AT GGATGGG    TGTATAGGGT
                                 G      TA__
GAM47   NEURL    3'  TAGCCAGGCCACATGTCC    20101      T_  TTTAA    A
                                TAGCC  GC    CACAT TCC
                                |||||  ||    ||||| |||
                                ATCGG  CG    GTGTA AGG
                                   TC  _____    C
GAM47   SGPL1    3'  GCCTGTTCCATATCCC      45040      C   AACA
                                GCCTG TTT    CATATCCC
                                ||||| |||    ||||||||
                                CGGAC AAG    GTATAGGG
                                  _  _____
GAM47   UNC119   3'  TAGTCTGCTTTATTGTGCATC  23112     C       ACACA
                                TAG CTGCTTTA     TATC
                                ||| ||||||||     ||||
                                ATC GACGAAAT     GTAG
                                  A       AACAC
GAM47   ENTPD3   3'  AGGCAGCCACTTCACCTGCATT 10349       G     G
                                AGGCAG CCACTT CACTTGCATT
                                |||||| |||||| ||||||||||
                                TCCGTC GGTGAA GTGGACGTAA
                                  _     _
GAM48   BCR      5'  CGGCGAGGCGCGGGCGCTGCTC 20247    A  C  A   A      C
           T                     CG CG GG TGC GGCGCTGC CT
                                 || || || ||| |||||||| ||
                                 GC GC CC GCG CCGCGACG GA
                                  C  T  _   C       A
GAM48   CYP1B1   5'  GGACACCTGCTGCCCT      6450        AGGC
                                GGATGC    GCTGCCCT
                                ||||||    ||||||||
                                CCTGTG    CGACGGGA
                                   GA__
GAM48   GSTT2    5'  CGACGCGGTGTGGGCAGCAGC  9211          A  CA   _  T
                                CGACGCGG TG  GGC GC GC
                                |||||||| ||  ||| || ||
                                GCTGCGCC AC  CCG CG CG
                                     _  AC   T  T
GAM48   NPAS2    5'  GCGGCGGGAGGCGCTGCTCT   14821      ATGC       C
                                GCGG    AGGCGCTGC CT
                                ||||    ||||||||| ||
                                CGCC    TCCGCGACG GA
                                  GCCC        A
GAM48   APOD     3'  GCAGCCTCCCTGTAGAACC    11607           GC__
                                GCGGCCTCCCTG    GCC
                                ||||||||||||    |||
                                CGTCGGAGGGAC    TGG
                                       ATCT
GAM48   ASL      5'  TGAGCGCGCGCCACGGTGCTCG 43534         _   TCCC   C  C
                                TGAGCGCG GCC    TGG GC CG
                                |||||||| |||    ||| || ||
```

```
                                ACTCGCGC CGG   GCC CG GC
                                     G  T___   A A
GAM48   BAG1    5'  TGAGCGCGGCGTCTCACAACCC 45410        CTCC  G  _
                                TGAGCGCGGC   CT GCG CCC
                                ||||||||||   || ||| |||
                                ACTCGCGCCG   GA TGT GGG
                                      CA__  G  T
GAM48   EMX2    3'  TGGCGCGGCCTCGG      44701    A       CCT
                                TG GCGCGGCCTC  GG
                                || ||||||||||  ||
                                AC CGCGCCGGAG  CC
                                 _       ___
GAM48   FHL1    3'  TGATGACAGCCCTGGCGCC   11098    GC    TCC
                                TGA  GCGGCC  CTGGCGCC
                                |||  ||||||  ||||||||
                                ACT  TGTCGG  GACCGCGG
                                  AC    ___
GAM48   FLNA    5'  TGACCGCGGGGTGGCGCCC   11138    G   CCTCCC
                                TGA CGCGG    TGGCGCCC
                                ||| |||||    ||||||||
                                ACT GCGCC    ACCGCGGG
                                  G   CC____
GAM48   HIC1    5'  TGACCGCGGCCTCTGGGCCCG  44569    G      CC  C
                                TGA CGCGGCCTC  TGG GCCCG
                                ||| |||||||||  ||| |||||
                                ACT GCGCCGGAG  ACC CGGGC
                                  G       __  _
GAM48   MADH6   3'  CGCGGCCTCCCACCC      24596          TGGC
                                CGCGGCCTCCC   GCCC
                                ||||||||||   ||||
                                GCGCCGGAGGG   TGGG
                                      ____
GAM48   TCEB3   5'  TGGCGCGGCCTCCTCGCC    17316    A       CTGG
                                TG GCGCGGCCTCC   CGCC
                                || ||||||||||   ||||
                                AC CGCGCCGGAGG   GCGG
                                 _        A___
GAM48   TIF1    5'  GAGCGCGGTCTCCGCCC    41272        C   CTGGC
                                GAGCGCGG CTCC    GCCC
                                |||||||| ||||    ||||
                                CTCGCGCC GAGG    CGGG
                                    A   _____
GAM49   CACNA2D3 5' ACCGGAGTACTTAGCAGCAAT 32899    A        AA
                                ACC GAGTACTTGGCA  GAT
                                ||| ||||||||||||  |||
                                TGG CTCATGAATCGT  TTA
                                  C         CG
GAM49   EGR3    3'  ACCAAGTACCTTAGAGAT    40535     G     GGCAA
                                ACCA AGTACTT    AGAT
                                |||| |||||||    ||||
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                                TGGT TCATGGA    TCTA
                                  _     ATC__
GAM49   IL2RB   3'  CAGAGTAACAAAGAT      9378        CTTG
                                CAGAGTA   GCAAAGAT
                                |||||||   ||||||||
                                GTCTCAT   TGTTTCTA
                                   ____
GAM49   WW45    3'  ACCAGAGTACTTGTTTGCAA  34814          ___
                                ACCAGAGTACTTG  GCAA
                                ||||||||||||  ||||
                                TGGTCTCATGAAC  CGTT
                                      AAA
GAM49   AARS    3'  GAGCTCTTGGCTGGACG    11487       A  ACGA
                                GAGCTCTT GC   GATG
                                |||||||| ||   ||||
                                CTCGAGAA CG   CTGC
                                    C  AC__
GAM49   ADAMTS4 3'  GAGTCTTAGCATGAGGC    23007    C      C   ATGA
                                GAG TCTTAGCA GAG   GC
                                ||| |||||||| |||   ||
                                CTC AGAATCGT CTC   CG
                                  _      A  ____
GAM49   BRCA1   3'  GAGCTCCTCTTGAGATG    28634       AGCAC
                                GAGCTCTT   GAGATG
                                ||||||||   ||||||
                                CTCGAGGA   CTCTAC
                                    GAA__
GAM49   CA14    5'  GAGCTCCTGGCGTGAGTG    29058       A  AC   A
                                GAGCTCTT GC  GAG TG
                                |||||||| ||  ||| ||
                                CTCGAGGA CG  CTC AC
                                    C  CA  _
GAM49   FGFR1   3'  GAGCATCTTACCCGATG     31940    _    G ACGA
                                GAGC TCTTA C   GATG
                                |||| ||||| |   ||||
                                CTCG AGAAT G   CTAC
                                  T    _ GG__
GAM49   GABRR2  3'  GCTTCTCTGAGAGATGAG    13043    _  AGCAC
                                GCT CTT    GAGATGAG
                                ||| |||    ||||||||
                                CGA GAG    CTCTACTC
                                  A  ACT__
GAM49   LAMB2   3'  GAGCTCTTCAGTGCATAGGCA  14073       A___  CG  ATGA
                                GAGCTCTT   GCA  AG   GCA
                                ||||||||   |||  ||   |||
                                CTCGAGAA   CGT  TC   CGT
                                    GTCA  A_  ____
GAM49   LAMB3   3'  GAGCTCTTAGTTTCAATGGCA  6906         CACGA   A
                                GAGCTCTTAG    GATG GCA
                                ||||||||||    |||| |||
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                                CTCGAGAATC    TTAC CGT
                                      AAAG_   _
GAM49   MEN1    3'  GAGCTCCTGGCATGTGGC    39182        A   CGAGA  A
                                GAGCTCTT GCA    TG GC
                                |||||||| |||    || ||
                                CTCGAGGA CGT    AC CG
                                     C   AC___  _
GAM49   PCOLN3  3'  GGGCTGCACGGGGTGGGCA   15753   A   CTTA    AGA  A
                                G GCT   GCACG   TG GCA
                                | |||   |||||   || |||
                                C CGA   CGTGC   AC CGT
                                 C  _____    CCC  C
GAM49   SLC16A2 3'  GGCTCAGCCTGAGATGAG    27150   A   TT   AC
                                G GCTC  AGC  GAGATGAG
                                | ||||  |||  ||||||||
                                C CGAG  TCG  CTCTACTC
                                _   __  GA
GAM49   TEM8    3'  GAGTTCTCAGATGAG      38181     C   AGCACG
                                GAG TCTT     AGATGAG
                                ||| ||||     |||||||
                                CTC AGAG     TCTACTC
                                  A   _______
GAM50   ALX3    3'  TGAGCCAAGTAAGCTGTCT   27070   A   TGT       A
                                A GGCC   GAGTAAGCT TCT
                                | ||||   ||||||||| |||
                                A TCGG   TTCATTCGA AGA
                                 C   ___        C
GAM50   MTNR1B  3'  GGCCTGTGAGCATCT      25553          AAGCT
                                GGCCTGTGAGT    ATCT
                                ||||||||||    ||||
                                CCGGACACTCG    TAGA
                                      _____
GAM50   OCA2    3'  GGAATCTTGAGTAAGTTATCTC 41191    CCTG_      C
                                GG    TGAGTAAG TATCTC
                                ||    |||||||| ||||||
                                CC    ACTCATTC ATAGAG
                                 TTAGA       A
GAM50   PPP2R4  3'  GGCTTGGGAGGCTGTCT    41330    C  T   TAA   A
                                GGC TG GAG   GCT TCT
                                ||| || |||   ||| |||
                                CCG AC CTC   CGA AGA
                                  A  C   ___   C
GAM50   SLC12A7 3'  GGCCCTTGAAAGCTATCTC   27331      G   GT
                                GGCCT TGA  AAGCTATCTC
                                ||||| |||  ||||||||||
                                CCGGG ACT  TTCGATAGAG
                                  A   __
GAM50   VWF     5'  AGGGCTGCGGCTATCT      8126      C    AGTAA
                                AGG CTGTG    GCTATCT
                                ||| |||||    |||||||
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                                TCC GACGC    CGATAGA
                                  C   _____
GAM50   XT3     3'  AGGCCATATCTCAGGCTGTCTC 33659      TGTGAG  A   A
                                AGGCC     TA GCT TCTC
                                |||||     || ||| ||||
                                TCCGG     GT CGA AGAG
                                   TATAGA  C   C
GAM51   AQP6    3'  GTCAGGACTCCTAC       38255     GCC   G
                                GTCA   GGA CTCCTAC
                                ||||   ||| |||||||
                                CAGT   CCT GAGGATG
                                  ___   _
GAM51   CDH11   3'  TGGGCGCTGGCCGGAGCCC   38038    AA   CA
                                TG  CGT  GCCGGAGCTC
                                ||  |||  ||||||||||
                                AC  GCG  CGGCCTCGGG
                                 CC   AC
GAM52   AGTR1   3'  TAGAAAAGTCGGTTCAG     28919     T    A  A
                                TAG AAAA TC GTTCAG
                                ||| |||| || ||||||
                                ATC TTTT AG CAAGTC
                                  _    C  C
GAM52   CDH6    3'  GCCAGAAGGATTAGTTCAGT   22327    A   T  AA  C
                                GC TAG AA  AT AGTTCAGT
                                || ||| ||  || ||||||||
                                CG GTC TT  TA TCAAGTCA
                                 _  _ CC  A
GAM52   CRADD   3'  TAGTAAAGTCCACAGTTCAGT  19178       AAT__
                                TAGTAAA    CAGTTCAGT
                                |||||||    |||||||||
                                ATCATTT    GTCAAGTCA
                                    CAGGT
GAM52   ID4     3'  TAGCTATAGTGAAAATCA    11387     _    A
                                TAGC ATAGT AAAATCA
                                |||| ||||| |||||||
                                ATCG TATCA TTTTAGT
                                  A    C
GAM52   OTC     5'  ATAGTAAAAATATCTCAGT   8043          CAG
                                ATAGTAAAAAT   TTCAGT
                                ||||||||||   ||||||
                                TATCATTTTTA   GAGTCA
                                      TA_
GAM52   UGP2    3'  TAACATAGTAAAGTACCTTTTA 27593          A_  AG  C
           GT                    TAGCATAGTAAA  ATC  TT AGT
                                ||||||||||||  |||  || |||
                                ATTGTATCATTT  TGG  AA TCA
                                       CA   AA  _
GAM52   AR      3'  TCTAAACTTCCCGTGGCATAAG 6246         A_    A  C
           A                     TCTAAACT  TCGTG CA AAGA
                                ||||||||  ||||| || ||||
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                                AGATTTGA  GGCAC GT TTCT
                                     AG    C  A
GAM52   ILF1    3'  TCTGAACTTGAACAAGAC    21119     A   ATCG   C
                                TCT AACT    TGA ACAAGAC
                                ||| ||||    ||| |||||||
                                AGA TTGA    ACT TGTTCTG
                                  C   ____  _
GAM52   OPA1    3'  AACTACAGACACAAGACA    39266      T  T
                                AACTA CG GACACAAGACA
                                ||||| || ||||||||||
                                TTGAT GT CTGTGTTCTGT
                                  _ _
GAM52   PIK3R3  3'  AACTGTCCCATCACAAGACA  41430     A  G  A
                                AACT TC TG CACAAGACA
                                |||| || || |||||||||
                                TTGA AG GT GTGTTCTGT
                                  C  G  A
GAM52   RNF4    3'  TCTGGGCATCGTGACAC     16359     AAAC
                                TCT    TATCGTGACAC
                                |||    ||||||||||
                                AGA    GTAGCACTGTG
                                  CCC_
GAM53   DYT1    3'  CAGAAACACTTGGAATTAA    6474        TATA    A
                                TAGAAAC    ACTT GAATTAA
                                |||||||    |||| |||||||
                                GTCTTTG    TGAA CTTAATT
                                     ____    C
GAM53   CEACAM5  3'  TTATACAAAGAGCAGATTTTTA 20380         TATA
           T                     TTATATAAA    TAGATTTTTAT
                                |||||||||    ||||||||||
                                AATATGTTT    GTCTAAAAATA
                                     CTC_
GAM53   DRIL1   3'  CTATATAGATATATAGAT    23368        A
                                TTATATA ATATATAGAT
                                ||||||| ||||||||||
                                GATATAT TATATATCTA
                                     C
GAM53   WNT5B   3'  TTATATAATATAGACCTTT   37213        AAT
                                TTATATA   ATATAGATTTTT
                                |||||||   ||||||||||||
                                AATATAT   TATATCTGGAAA
                                     ___
GAM54   DAAM1   3'  TTTAAATCTATGTTTTTCCAAC 31432       ACA  GC_
           AA                     TTTGAA   TA   TTTTCCAACAA
                                ||||||   ||   ||||||||||||
                                AAATTT   AT   AAAAGGTTGTT
                                   AG_  ACA
GAM54   MAGEA12  3'  TTTGAACAATTCCAAC     23853      AACATA  TT
                                TTTGA     GC  TTCCAAC
                                |||||     ||  |||||||
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                                AAACT     TG  AAGGTTG
                                  _______ TT
GAM54   MAGEA2   3'  TTTGAACAATTCCAAC     41310      AACATA  TT
                                TTTGA     GC  TTCCAAC
                                |||||     ||  |||||||
                                AAACT     TG  AAGGTTG
                                  _______ TT
GAM54   NPY1R    3'  TTTAAAATATAGTTTCTCCAA  9485        C    C
                                TTTGAAA ATAG TTTTCCAA
                                ||||||| |||| ||||||||
                                AAATTTT TATC AAGAGGTT
                                    A   A
GAM54   PCDH8    3'  GAAATAGCTTCCAACA      15115     AC     TT
                                GAA  ATAGCT  TCCAACA
                                |||  ||||||  |||||||
                                CTT  TATCGA  AGGTTGT
                                  __     __
GAM54   PPP1CC   3'  TTGAAACAGATTTCTTTTTTAA 43920        TAG__    CC
          CA                      TTGAAACA    CTTTT  AACA
                                ||||||||    |||||  ||||
                                AACTTTGT    GAAAA  TTGT
                                    CTAAA     AA
GAM55   ACADVL   3'  GAACACTAGGCCCCTTCGG   6158         A   ACA_
                                GGACACTAG CCC    GG
                                ||||||||| |||    ||
                                CTTGTGATC GGG    CC
                                    C   GAAG
GAM55   ADAM19   3'  AAGGTTGGGCCACAGGAAA   37760     ACACTAGAC
                                AAGG       CCACAGGAAA
                                ||||       ||||||||||
                                TTCC       GGTGTCCTTT
                                  AACCC____
GAM55   ADCY6    3'  AAGACAGAGGCCCACAGGA   34160      CT  A
                                AGGACA  AG CCCACAGGA
                                ||||||  || |||||||||
                                TTCTGT  TC GGGTGTCCT
                                   C_  C
GAM55   AGA      3'  AGGAACACTAGATGATGAGA   6183      _     CCCACA
                                AGGA CACTAGA     GGA
                                |||| |||||||     |||
                                TCCT GTGATCT     TCT
                                  T      ACTAC_
GAM55   AMACR    3'  AGCCCAGAGACCCACGGGGAAA 42856    GA  CT      A_
                                AG  CA  AGACCCAC  GGAAA
                                ||  ||  ||||||||  |||||
                                TC  GT  TCTGGGTG  CCTTT
                                 GG  C_      CC
GAM55   ARHGEF7  3'  AAGATACTGGATCCACAGAAA  19356     C   A  C
                                AGGA ACT GA CCACAGGAA
                                |||| ||| || |||||||||
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                                TTCT TGA CT GGTGTCTTT
                                  A  C  A
GAM55   ATP1B2   3'  AGGAGCATCCACAGGA      11737      _  CTAGAC
                                AGGA CA     CCACAGGA
                                |||| ||     ||||||||
                                TCCT GT     GGTGTCCT
                                  C  A_____
GAM55   CDH10    3'  AGACATCCTACAGGAAA     27485       CTAGA  C
                                GGACA    CC ACAGGAAA
                                ||||||    || ||||||||
                                TCTGT    GG TGTCCTTT
                                  A____  A
GAM55   CYLN2    3'  GGAGGCCTCACAGGAAAA    18056      CACTA A  _
                                GGA    G CC CACAGGAAAA
                                |||    | || ||||||||||
                                CCT    C GG GTGTCCTTTT
                                 _____ C  A
GAM55   DRD1     5'  AAGGGCACTAGACCCCGGCTAA 9004       A        AC____
            GG                    AAGG CACTAGACCC     AGG
                                |||| ||||||||||     |||
                                TTCC GTGATCTGGG     TCC
                                  C        GCCGAT
GAM55   EGF      5'  AAGGGAAGCCACAGGAAA    12648      ACACT  AC
                                AAGG    AG  CCACAGGAAA
                                ||||    ||  ||||||||||
                                TTCC    TC  GGTGTCCTTT
                                  CT___  __
GAM55   EN2      5'  GGACACGCACAGGAA       10958       TAGACC
                                GGACAC     CACAGGAA
                                ||||||     ||||||||
                                CCTGTG     GTGTCCTT
                                   C_____
GAM55   ESPN     3'  AGGGGGCTGAGCCCCGCAGGAA 36439     ACA  _  A   A
            AA                    AGG   CT AG CCC CAGGAAAA
                                |||   || || ||| ||||||||
                                TCC   GA TC GGG GTCCTTTT
                                  CCC  C  G   C
GAM55   FMR2     3'  AAGAACACTAGCAGGAAA    12945          ACCCA
                                AAGGACACTAG    CAGGAAA
                                ||||||||||    |||||||
                                TTCTTGTGATC    GTCCTTT
                                       _____
GAM55   GJB3     5'  AGGACACTAGATCCAGGGAA  35834          C   CA
                                AGGACACTAGA CCA  GGAA
                                |||||||||| |||  ||||
                                TCCTGTGATCT GGT  CCTT
                                       A  C_
GAM55   GRM3     3'  GGCACTAGACTCAGCCTAGAA  9151     A       C  CA__
                                GG CACTAGAC CA    GGAA
                                || |||||||| ||    ||||
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                                CC GTGATCTG GT    TCTT
                                 _      A  CGGA
GAM55   HBE1     3'  AGGGTGTCAGGGTCACAGGAA  23724     ACAC   ACC
                                AGG    TAG   CACAGGAA
                                |||    |||   ||||||||
                                TCC    GTC   GTGTCCTT
                                  CACA   CCA
GAM55   HDAC4    3'  AAGGTCCAAGGACCCACAGG   25737      A_  CTA
                                AAGG  CA   GACCCACAGG
                                ||||  ||   ||||||||||
                                TTCC  GT   CTGGGTGTCC
                                  AG  TC_
GAM55   HNRPF    3'  AAGGGCCTAGCAGGAA      22452      ACA    ACCCA
                                AAGG   CTAG    CAGGAA
                                ||||   ||||    ||||||
                                TTCC   GATC    GTCCTT
                                  CG_   _____
GAM55   IRAK1    3'  AGGACACTCGGTTACATGAAA  11469        AGACCC   G
                                AGGACACT     ACA GAAA
                                ||||||||     ||| ||||
                                TCCTGTGA     TGT CTTT
                                     GCCAA_   A
GAM55   IVD      3'  AAGGCCACTAGGTGCAGGAAAA 13694      A     ACCCA
                                AAGG CACTAG    CAGGAAAA
                                |||| ||||||    ||||||||
                                TTCC GTGATC    GTCCTTTT
                                  G     CAC__
GAM55   KCNJ15   3'  GGATACGGGACCCACACAGA   13877     C  TA      _
                                GGA AC  GACCCACA GGA
                                ||| ||  |||||||| |||
                                CCT TG  CTGGGTGT TCT
                                  A  CC       G
GAM55   LZTFL1   5'  AGGGTAGTTGGACCACAGAAAA 33768     ACACTA_   C
                                AGG      GACC ACAGGAAA
                                |||      |||| ||||||||
                                TCC      CTGG TGTCTTTT
                                  CATCAAC   _
GAM55   LZTS1    3'  AAGAACACCCACAGGAA     34259       ACTAG
                                AAGGAC    ACCCACAGGAA
                                ||||||    ||||||||||
                                TTCTTG    TGGGTGTCCTT
                                          _____
GAM55   MEN1     3'  AGGACACTGTGCTCAGAGAA   39146       AGACCCA  _
                                AGGACACT      CAG GAA
                                ||||||||      ||| |||
                                TCCTGTGA      GTC CTT
                                     CACGA__   T
GAM55   MPP2     3'  AAGGACACTGACTAAGGGAAA  40787        A   CCACA
                                AAGGACACT GAC    GGAAA
                                ||||||||| |||    |||||
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                                TTCCTGTGA CTG    CCTTT
                                     _  ATTC_
GAM55   NR4A1   5' GGAGCAGTCCCACAGGA    13418    CAC  A
                                GGA  TAG CCCACAGGA
                                |||  ||| |||||||||
                                CCT  GTC GGGTGTCCT
                                  C__  A
GAM55   PAM     3' AAGAATGCTGAACAGGAAA   39881      CA  A  CCC
                                AAGGA  CT GA  ACAGGAAA
                                |||||  || ||  ||||||||
                                TTCTT  GA CT  TGTCCTTT
                                   AC  _  ___
GAM55   PHEMX   3' GGCAAACCACAGGAA      40021    A  CTA   C
                                GG CA  GACC ACAGGAA
                                || ||  |||| |||||||
                                CC GT  TTGG TGTCCTT
                                 _  ___   _
GAM55   PML     3' GGACACTAGAGCTTAGGAA   37730         CCCAC
                                GGACACTAGA    AGGAA
                                ||||||||||    |||||
                                CCTGTGATCT    TCCTT
                                     CGAA_
GAM55   PMP2    3' AAGGACACTGATTGGGAA    15417         A  CCCACA
                                AAGGACACT GA    GGAA
                                |||||||| ||    ||||
                                TTCCTGTGA CT    CCTT
                                     _  AAC___
GAM55   PON1    3' AAGAACACTGGGTCCTCGGAA  7776          AGAC  ACA
                                AAGGACACT   CC  GGAA
                                |||||||||   ||  ||||
                                TTCTTGTGA   GG  CCTT
                                     CCCA  AG_
GAM55   PPP3CA  3' GGAGAAATATCCACAGGAAAA  9614      CACTAGAC
                                GGA       CCACAGGAAAA
                                |||       |||||||||||
                                CCT       GGTGTCCTTTT
                                  CTTTATA_
GAM55   PRKACA  3' AGGGGCCTAGACCCTCGCAGGA 15575     ACA      A__
                                AGG  CTAGACCC  CAGGA
                                |||  ||||||||  |||||
                                TCC  GATCTGGG  GTCCT
                                  CCG       AGC
GAM55   QDPR    3' AGGGGCAACCACACAGGAAAA  7236     ACACTA  _
                                AGG     GACC CACAGGAAAA
                                |||     |||| ||||||||||
                                TCC     TTGG GTGTCCTTTT
                                  CCG___    T
GAM55   RAB5B   3' AGGAACACTAGGGAGGAGGA  16087     _     ACCCAC
                                AGGA CACTAG     AGGA
                                |||| ||||||     ||||
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                                TCCT GTGATC     TCCT
                                  T     CCTCC_
GAM55   RAP1B    3'  AAGGGTACCACCACAGGAAA  31820     AC   GAC
                                AAGG  ACTA   CCACAGGAAA
                                ||||  ||||   ||||||||||
                                TTCC  TGGT   GGTGTCCTTT
                                  CA   ___
GAM55   RARB     3'  AAGGACACTAGAGTTACATGG  32056          CCC  _
                                AAGGACACTAGA   ACA GG
                                ||||||||||||   ||| ||
                                TTCCTGTGATCT   TGT CC
                                       CAA   A
GAM55   SCA1     3'  AAGGACACAGACCCCGAGGA   7269         T     AC
                                AAGGACAC AGACCC  AGGA
                                ||||||||| ||||||  ||||
                                TTCCTGTG TCTGGG  TCCT
                                    _     GC
GAM55   SHANK2   3'  GGATGCAAACCACAGGA     29462     CAC     C
                                GGA   TAGACC ACAGGA
                                |||   |||||| ||||||
                                CCT   GTTTGG TGTCCT
                                  AC_     _
GAM55   SLC1A3   3'  AGGACACTGAGGCCTAGA     20039        _  A  CACA
                                AGGACACT AG CC    GGA
                                |||||||| || ||    |||
                                TCCTGTGA TC GG    TCT
                                     C  C  A___
GAM55   SOLH     3'  GGAGACCCTGAGCCCACAGG   24830    A    A  A  _
                                A GGAC CT GA CCCACAGG
                                | |||| || || ||||||||
                                C TCTG GG CT GGGTGTCC
                                 C    _  A  C
GAM55   SOX10    3'  GGCTGCAGAACAGGAAAA    28007    ACAC    CCC
                                GG    TAGA   ACAGGAAAA
                                ||    ||||   |||||||||
                                CC    GTCT   TGTCCTTTT
                                  GAC_   ____
GAM55   SOX11    3'  GGACACAGGCCGGTCAGGAAAA 17025       T  A  CA_
                                GGACAC AG CC   CAGGAAAA
                                |||||| || ||   ||||||||
                                CCTGTG TC GG   GTCCTTTT
                                   _  C  CCA
GAM55   STK6     5'  AAGGACACTCAGGGACGGAGGA 18772         A___   CCAC
                                AAGGACACT    GAC    AGGA
                                |||||||||    |||    ||||
                                TTCCTGTGA    CTG    TCCT
                                     GTCC   CC__
GAM55   TIMP3    3'  AAGACACTGATGTCCACTTGTG 7437         A  C__    A_____
            GGA                    AGGACACT GA   CCAC     GGA
                                ||||||||| ||   ||||     |||
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                                TTCTGTGA CT   GGTG    CCT
                                    _ ACA    AACAC
GAM55   TK2     3'  AAGGACACAGACAGTACGGGA  21444        T   CC_  A
                                AAGGACAC AGAC   AC GGA
                                |||||||| ||||   || |||
                                TTCCTGTG TCTG   TG CCT
                                    _    TCA  C
GAM55   TNNT3   3'  AAGGACACAGACGCGGGGGA  27592        T   CCACA
                                AAGGACAC AGAC    GGA
                                |||||||| ||||    |||
                                TTCCTGTG TCTG    CCT
                                    _    CGCCC
GAM55   VANGL2  3'  GGAGACAACTTCCCACAGG   43460   A    _ AGA
                                A GGACA CT   CCCACAGG
                                | ||||| ||   ||||||||
                                C TCTGT GA   GGGTGTCC
                                 C    T  A__
GAM55   WARS    3'  GGAACTCACAGGAA       42623    C   AGACC
                                GGA ACT    CACAGGAA
                                ||| |||    ||||||||
                                CCT TGA    GTGTCCTT
                                  _  _____
GAM55   WNT3A   3'  GGAGACACTAGCTCCAGGGA  37546   A       AC   CA
                                A GGACACTAG  CCA  GGA
                                | |||||||||  |||  |||
                                C TCTGTGATC  GGT  CCT
                                 C       GA   C_
GAM55   WNT3A   3'  AGAAGCCCCACCCACAGGAA  37533     CA  AG
                                AGGA  CT  ACCCACAGGAA
                                ||||  ||  ||||||||||||
                                TCTT  GG  TGGGTGTCCTT
                                  CG  G_
GAM55   ZNF144  3'  AAGGCCACACACACAGGAAAA  28332     ACA   G  C
                                AAGG   CTA AC CACAGGAAAA
                                ||||   ||| || ||||||||||
                                TTCC   GGT TG GTGTCCTTTT
                                  ___   G  T
GAM55   ZNF179  3'  AAGGACACAGACCCAAGAGA   28371        T      CA
                                AAGGACAC AGACCCA  GGA
                                |||||||| |||||||  |||
                                TTCCTGTG TCTGGGT  TCT
                                    _      TC
GAM56   ADD1    3'  CCTCCTCCTTCTCTAACATTGG 30516       GTAG  __   C
                                TCTCTT   CC  CTC AACATTGG
                                ||||||   ||  ||| ||||||||
                                GGAGGA   GG  GAG TTGTAACC
                                   _____ AA  A
GAM56   B3GALT2 5'  TCTCTTGTAGTCATTCTCCTTG 19113         CC___   AACA
            G                    TCTCTTGTAG    CTCC    TTGG
                                ||||||||||    ||||   ||||
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```
                                AGAGAACATC    GAGG   AACC
                                     AGTAA   ____
GAM56   DPP6    3'  TCTTGTAGCCCCTCACCAT   39135         TC  A
                                TCTTGTAGCCC  CA CAT
                                ||||||||||  || |||
                                AGAACATCGGG  GT GTA
                                      GA  G
GAM56   FCAR    3'  TCTCTTGTGTCCTTCAA    39342       AGC   C
                                TCTCTTGT   CCT CAA
                                ||||||||   ||| |||
                                AGAGAACA   GGA GTT
                                    CA_   A
GAM56   HLF     3'  TCTCTGTACAACATT      13396      T   GCCCTC
                                TCTCT GTA     CAACATT
                                ||||| |||     |||||||
                                AGAGA CAT     GTTGTAA
                                  _  _______
GAM56   ROBO1   3'  TCTTGTAGGTTTCGACATTGG  39489        CCC  CA
                                TCTTGTAG   TC  ACATTGG
                                ||||||||   ||  |||||||
                                AGAACATC   AG  TGTAACC
                                    CAA  C_
GAM56   THY1    3'  TCCTTTGTAGCCCTCTCCACTG 26633    TC        CAA
                                TC  TTGTAGCCCTC   CATTG
                                ||  ||||||||||   |||||
                                AG  AACATCGGGAG   GTGAC
                                 GA         AG_
GAM57   HNRPF   3'  GCTGGGGCCGTGTGTCTATT   22457    TGTC    __
                                GCT   GGGCT  GTGTCTATT
                                |||   |||||  |||||||||
                                CGA   CCCGG  CACAGATAA
                                  C___    CA
GAM58   ABP1    3'  CTCTGGATGCCAGGGAGGGG   41789         __
                                CTTTGGATG  GGGGAGGGGG
                                |||||||||  |||||||||
                                GAGACCTAC  TCCCTCCCC
                                     GG
GAM58   AK3     5'  CTTCGCGAGGAGGGG      30182      GATG
                                CTTTG   GGGGAGGGG
                                |||||   |||||||||
                                GAAGC   CTCCTCCCC
                                  G___
GAM58   ARHGDIA 3'  CTTTGGTATGGGGAGGGG    20205      ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAAACC   CCCCTCCCC
                                   ATA
GAM58   ASGR2   5'  CCTTGGCCAAGGAGGGG     38950      ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
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                                GGAACC  TTCCTCCCC
                                   GG_
GAM58   BAZ2A   3' CTCTGAAGGGAGGGG     30306      ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GAGACT  TCCCTCCCC
                                  ___
GAM58   BCL3    3' CCGAAGATGGGGGGGGG    23205   TT      A
                                CT  GGATGGGGG GGGG
                                ||  ||||||||| ||||
                                GG  TCTACCCCC CCCC
                                 CT       _
GAM58   CENTD2  5' CTGTGGCTGGGGAGGGG    31593   T   ATG
                                CT TGG  GGGGAGGGG
                                || |||  |||||||||
                                GA ACC  CCCCTCCCC
                                 C  GA_
GAM58   COMT    5' CTCTGGCTGCGGGAGGGG    8892       A  G
                                CTTTGG TG GGGAGGGG
                                |||||| || ||||||||
                                GAGACC AC CCCTCCCC
                                   G  G
GAM58   DGKG    5' CTCTCGGGGGAGGGG      10654     GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GAGA  GCCCCCTCCCC
                                  ___
GAM58   DLG4    5' CTTTACTAAGGGAGGGG     10706     GA
                                CTTTG  TGGGGGAGGGG
                                |||||  ||||||||||
                                GAAAT  ATTCCCTCCCC
                                  G_
GAM58   DUSP4   5' CTTTGGGGAGAAGGGAGGGG  38418      AT__
                                CTTTGG   GGGGGAGGGG
                                ||||||   ||||||||||
                                GAAACC   TTCCCTCCCC
                                   CCTC
GAM58   EPM2A   3' CTTAGGGAAATCAGGAGGGG  24969    T_  TGG_
                                CTT  GGA   GGGAGGGG
                                |||  |||   ||||||||
                                GAA  CCT   TCCTCCCC
                                 TC  TTAG
GAM58   EVX1    5' CTCCGGTGGGGGAGGGG     12770      A
                                CTTTGG TGGGGGAGGGG
                                |||||| ||||||||||
                                GAGGCC ACCCCCTCCCC
                                  _
GAM58   FE65L2  3' TTTGAGCAGGGGGAGGGG    39325      AT_
                                TTTGG  GGGGGAGGGG
                                |||||  ||||||||||
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                                AAACT   CCCCCTCCCC
                                   CGT
GAM58   FGFR1    3'  CTGTGGCAGGGAGGGG     31939    T   ATG
                                CT TGG   GGGGAGGGG
                                || |||   |||||||||
                                GA ACC   TCCCTCCCC
                                 C   G__
GAM58   FGFR3    3'  CTTTGGGTGTGGGAGGGG    6615       A  G
                                CTTTGG TG GGGAGGGG
                                |||||| || ||||||||
                                GAAACC AC CCCTCCCC
                                   C  A
GAM58   FMNL     5'  CTTCCTGCGGGGAGGGG     25299     GGA  _
                                CTTT   TG GGGGAGGGG
                                ||||   || |||||||||
                                GAAG   AC CCCCTCCCC
                                  G__  G
GAM58   GLTSCR1  3'  CTTCGGGAGGAGGGG      31836      ATG
                                CTTTGG   GGGGAGGGG
                                ||||||   |||||||||
                                GAAGCC   CTCCTCCCC
                                   ___
GAM58   GPRK7    3'  CTATGGATGGGAATCAGG    40179    T       A_
                                CT TGGATGGGGG  GGG
                                || ||||||||||  |||
                                GA ACCTACCCTT  TCC
                                 T        AG
GAM58   HD       3'  TCTGGGTGTCTGGAGGGG    13363      A  GG_
                                TTTGG TG   GGAGGGG
                                ||||| ||   |||||||
                                AGACC AC   CCTCCCC
                                   C  AGA
GAM58   HOXB2    5'  CAATGGTGGGGGAGGGG     13431    TT   A
                                C  TGG TGGGGGAGGGG
                                |  ||| ||||||||||
                                G  ACC ACCCCCTCCCC
                                 TT  _
GAM58   HPCA     3'  CCCCTTTGGGGGAGGGG     13422     GGA
                                CTTT   TGGGGGAGGGG
                                ||||   ||||||||||
                                GGGG   ACCCCCTCCCC
                                  AA_
GAM58   IGF1     3'  CTTTGCAAGGGAGGGG      8338       GAT
                                CTTTG   GGGGGAGGGG
                                |||||   ||||||||||
                                GAAAC   TTCCCTCCCC
                                   G__
GAM58   IL2RB    3'  CTGTGGACGGGGAGGGG     9382     T       G
                                CT TGGATGGGG AGGGG
                                || ||||||||| |||||
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                                GA ACCTGCCCC TCCCC
                                 C       _
GAM58   KCNJ10   5' CCTTGGATGGGCCGCGGGG  13867          GGA_
                                CTTTGGATGGG  GGGG
                                ||||||||||  ||||
                                GGAACCTACCC  CCCC
                                      GGCG
GAM58   KPNA1    3' TTTGTGTGGGGGGAGGGG  44321    GA    _
                                TTTG  TGGGGG AGGGG
                                ||||  |||||| |||||
                                AAAC  ACCCCC TCCCC
                                  AC     C
GAM58   LENG4    5' CTCTGATGACAGGAGGGG  35884    G   _
                                CTTTG ATGG GGGAGGGG
                                ||||| |||| ||||||||
                                GAGAC TACT TCCTCCCC
                                  _   G
GAM58   LPIN2    3' CCTTGCTGTGGGGAGGGG  31207    GA  _
                                CTTTG  TG GGGGAGGGG
                                |||||  || |||||||||
                                GGAAC  AC CCCCTCCCC
                                  G_  A
GAM58   MAPK3    3' CTTTGACAGGGAGGGG    43841     ATG
                                CTTTGG  GGGGAGGGG
                                ||||||  |||||||||
                                GAAACT  TCCCTCCCC
                                   G__
GAM58   MAT1A    3' CAACGGTGGGGGAGGGG   44901   TT  A
                                C  TGG TGGGGGAGGGG
                                |  ||| ||||||||||
                                G  GCC ACCCCCTCCCC
                                 TT  _
GAM58   MGA      3' CCTTGGGTAAGAGGGG    41722     ATGG
                                CTTTGG  GGGAGGGG
                                ||||||  ||||||||
                                GGAACC  TTCTCCCC
                                   CA__
GAM58   MID2     3' CTTAGGTGTAGGAGGGG   38057    T  A  GG
                                CTT GG TG  GGAGGGG
                                ||| || ||  |||||||
                                GAA CC AC  CCTCCCC
                                  T  _  AT
GAM58   MSF      3' CTCTGAGGGGAGGGG     44727     GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAGAC  TCCCCTCCCC
                                    ____
GAM58   MVK      3' CTCTGGGAGGGAGGGG    41341      AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
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                              GAGACC  CTCCCTCCCC
                                   __
GAM58   NAGA    3'  CTTTGGAAAAGGAGGGG    7037       T
                              CTTTGGA GGGGGAGGGG
                              ||||||| ||||||||||
                              GAAACCT TTTCCTCCCC
                                   _
GAM58   OCLN    5'  CTTCGGATGGAACCTTGGGG  14903          GA__
                              CTTTGGATGGGG   GGGG
                              ||||||||||||   ||||
                              GAAGCCTACCTT   CCCC
                                    GGAA
GAM58   PAX2    3'  CTGTGTCGGGGGAGGGG    19606   T  GA
                              CT TG  TGGGGGAGGGG
                              || ||  ||||||||||
                              GA AC  GCCCCCTCCCC
                               C  A_
GAM58   PCDH9   5'  CTTTGGAGGGGAGGGG     44398      TG
                              CTTTGGA  GGGGAGGGG
                              |||||||  |||||||||
                              GAAACCT  CCCCTCCCC
                                   __
GAM58   PCTK1   3'  CTTAGGGTGGAGGAAGGG   37471    T  A
                              CTT GG TGGGGGAGGGG
                              ||| || ||||||||||
                              GAA CC ACCTCCTTCCC
                                T  C
GAM58   PFKM    5'  CTTGGGAAAGGGGGGAGGGG  41178    T  T__
                              CTT GGA   GGGGGAGGGG
                              ||| |||   ||||||||||
                              GAA CCT   CCCCCTCCCC
                                C   TTC
GAM58   PODXL   3'  CTTTGCTGGGGAGGGG     23973     GATG
                              CTTTG   GGGGAGGGG
                              |||||   |||||||||
                              GAAAC   CCCCTCCCC
                                 GA__
GAM58   POLR2C  3'  CTGTGTATGTGGGAGGGG   15452   T  G  G
                              CT TG ATG GGGAGGGG
                              || || ||| ||||||||
                              GA AC TAC CCCTCCCC
                               C  A   A
GAM58   PSD     3'  CCTTGGGGAGGAAGGAGGGG  15782     AT_  _
                              CTTTGG   GGG GGAGGGG
                              ||||||   ||| |||||||
                              GGAACC   CCT CCTCCCC
                                 CCT   T
GAM58   PTPN6   5'  CTCTGTAGGGAGGGG     38704     GATG
                              CTTTG   GGGGAGGGG
                              |||||   |||||||||
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                                GAGAC   TCCCTCCCC
                                  A___
GAM58   PTPRA    5' CTTTAGGAGAAGGGG      38911      GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GAAAT  CCTCTTCCCC
                                  ___
GAM58   RABL2A   3' TCTGCCTGGGGGGAGGGG    30198     GA    _
                                TTTG  TGGGGG AGGGG
                                ||||  |||||| |||||
                                AGAC  ACCCCC TCCCC
                                  GG     C
GAM58   RABL2B   3' TCTGCCTGCGGGGAGGGG    28205     GA  _
                                TTTG  TG GGGGAGGGG
                                ||||  || |||||||||
                                AGAC  AC CCCCTCCCC
                                  GG  G
GAM58   RALB     3' TTTGGGAGGGAAGAAGGGG   16149      AT  __
                                TTTGG  GGG  GGAGGGG
                                |||||  |||  |||||||
                                AAACC  CCC  CTTCCCC
                                  CT   TT
GAM58   RB1      3' CTTTAGGTGTAGGGGAGGGG  44933       A__
                                CTTTGG  TGGGGGAGGGG
                                ||||||  ||||||||||
                                GAAATC  ATCCCCTCCCC
                                   CAC
GAM58   REQ      3' CTCTGGAGACCAGAGGGG    26542       TGGG
                                CTTTGGA   GGAGGGG
                                |||||||   |||||||
                                GAGACCT   TCTCCCC
                                   CTGG
GAM58   RXRA     3' CTTTGGAAAAAGGGG       16424       TGG
                                CTTTGGA  GGGAGGGG
                                |||||||  ||||||||
                                GAAACCT  TTTTCCCC
                                  ___
GAM58   RXRG     3' TTTGGGGACAGGAAGGGG    27945      ATG_
                                TTTGG   GGGGAGGGG
                                |||||   |||||||||
                                AAACC   TCCTTCCCC
                                  CCTG
GAM58   RYR1     3' CCTTAGGGGGAGGGG       8066       GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GGAAT  CCCCCTCCCC
                                  ___
GAM58   SDHC     3' CTGTGGGCAAAAAAGGGG    42978    T  AT
                                CT TGG  GGGGGAGGGG
                                || |||  ||||||||||
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                                GA ACC  TTTTTTCCCC
                                 C  CG
GAM58   SF1     5' CTCCCGGGGGGAGGGG     21562     GGAT
                                CTTT   GGGGGAGGGG
                                ||||   ||||||||||
                                GAGG   CCCCCTCCCC
                                  GC__
GAM58   SORCS2  3' CTCTGGAGTGGGGAGGGG   34054       TG
                                CTTTGGA  GGGGAGGGG
                                |||||||  |||||||||
                                GAGACCT  CCCCTCCCC
                                    CA
GAM58   SPOCK   5' CCTTGGATGGGTCCAGGG   41733         GGA
                                CTTTGGATGGG  GGGG
                                ||||||||||  ||||
                                GGAACCTACCC  TCCC
                                      AGG
GAM58   STC1    3' CTTTGGAAGTTTAAGGGG   17177       T  GG_
                                CTTTGGA GG  GAGGGG
                                ||||||| ||  ||||||
                                GAAACCT TC  TTCCCC
                                   _ AAA
GAM58   STXBP1  3' TTTGGTCCGAGGGAGGGG   17213      A_
                                TTTGG  TGGGGGAGGGG
                                |||||  ||||||||||
                                AAACC  GCTCCCTCCCC
                                  AG
GAM58   SURF4   3' CTTTACCAAGGGAGGGG    37653     GA
                                CTTTG  TGGGGGAGGGG
                                |||||  ||||||||||
                                GAAAT  GTTCCCTCCCC
                                  G_
GAM58   TBXA2R  3' CTCTGGATGGGAAAAAGGGG  9851          __
                                CTTTGGATGGGG  GAGGGG
                                ||||||||||  ||||||
                                GAGACCTACCCT  TTCCCC
                                      TT
GAM58   TCF7    3' CTGTGAATGGGGAGGGG    17321   T      G
                                CT TGGATGGGG AGGGG
                                || |||||||| |||||
                                GA ACTTACCCC TCCCC
                                 C       _
GAM58   TDGF1   3' CTTTGGGAAAAAAAGGGG   17361      AT
                                CTTTGG  GGGGGAGGGG
                                ||||||  ||||||||||
                                GAAACC  TTTTTTCCCC
                                  CT
GAM58   TNFSF12 3' CTCTAGAGGGAGGGG      19186      TGG
                                CTTTGGA  GGGAGGGG
                                |||||||  ||||||||
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                                GAGATCT  CCCTCCCC
                                   ___
GAM58   TYRO3   3' CTTTGGAAGAGGGG      26652      TGGG
                                CTTTGGA  GGAGGGG
                                |||||||  |||||||
                                GAAACCT  TCTCCCC
                                   _____
GAM58   ZNF148  5' CCTTGAGAGGAGGGG     35023     GAT
                                CTTTG  GGGGGAGGGG
                                |||||  ||||||||||
                                GGAAC  TCTCCTCCCC
                                   ___
GAM58   ZNF289  3' CCTCTGGGGGAGGGG     42254     GGA
                                CTTT  TGGGGGAGGGG
                                ||||  ||||||||||
                                GGAG  ACCCCCTCCCC
                                   ___
GAM59   GABRR1  3' TGTCGTATTTCCTGCAGCACCT 13042     ATG  C  AA
                                TGTC  AT TT  TGTAGCACCT
                                ||||  || ||  ||||||||||
                                ACAG  TA AA  ACGTCGTGGA
                                  CA_ _  GG
GAM59   MHC2TA  3' TGTCACGATTTTCATTTAGC  6992        C  AATG
                                TGTCATGAT TT   TAGC
                                |||||||| ||   ||||
                                ACAGTGCTA AA   ATCG
                                     A  GTAA
GAM59   MYEOV   3' TATCATGATTTTCCCAGCACCT 39878       C  AATG
                                TGTCATGAT TT   TAGCACCT
                                |||||||| ||   ||||||||
                                ATAGTACTA AA   GTCGTGGA
                                     A  GG__
GAM59   STAU2   3' TGTTGTATCTTAATGGTGTACC 30808    CATG      TAGC
           T                     TGT   ATCTTAATG   ACCT
                                |||   |||||||||   ||||
                                ACA   TAGAATTAC   TGGA
                                  ACA_       CACA
GAM60   FLRT2   3' AGATGTTGTCCTCCCTGGT   29836       _  G
                                AGATGTTG CC CTCTGGT
                                |||||||| || |||||||
                                TCTACAAC GG GGGACCA
                                     A  A
GAM60   SPOCK   3' GATGTTACTGTACAGCGTGG  41735       CGCTCT  T  C
                                GATGTTGC     GG CG GG
                                ||||||||     || || ||
                                CTACAATG     TC GC CC
                                     ACATG_ _  A
GAM60   ADH5    5' AGCGAGGGGGGCGGGGC    8576        AA    C
                                AGCGGGGG  GCGGG GT
                                ||||||||  ||||| ||
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                                TCGCTCCC  CGCCC CG
                                    CC    _
GAM60   AMMECR1  5' GCGGGGGCGAGCACGCTGCGGC 31698       A_   G G  A
                                GCGGGGG  AGCG GC TGC GC
                                |||||||  |||| || ||| ||
                                CGCCCCC  TCGT CG ACG CG
                                    GC   G _  C
GAM60   AQP5     5' GCGGAGGAGGTGGATGCGGC  11633       A CG  C   A
                                GCGGGGGA G  GG GTGC GC
                                ||||||||  |  || |||| ||
                                CGCCTCCT C  CC TACG CG
                                    _ CA _   C
GAM60   AXL      5' CAGCGGGGGAGGGGGCAGGGC  34883        A C    T_
                                CAGCGGGGGA G GGGCG  GC
                                ||||||||||  | |||||  ||
                                GTCGCCCCCT C CCCGT  CG
                                      _ C    CC
GAM60   BACH2    5' GCGGCGGGAGTGGGCAGGC   34793     _   A C    T
                                GCGG GGGA G GGGCG GC
                                |||| |||| | ||||| ||
                                CGCC CCCT C CCCGT CG
                                  G   _ A    C
GAM60   CAPON    5' GCGGCGGGAGCGGGCTGCGCGG 41922     _   A    _   A
          C                      GCGG GGGA GCGGGC GTGC GC
                                ||||  |||| ||||||  |||| ||
                                CGCC CCCT CGCCCG CGCG CG
                                  G   _    A   C
GAM60   COL6A2   3' GCAGGTGGAGCGGGTGTGTGGC 38441      _  A    C   CA
                                GCGGG GGA GCGGG GTG  GC
                                |||||  |||  |||||  |||  ||
                                CGTCC CCT CGCCC CAC  CG
                                  A   _    A  AC
GAM60   CTF1     3' CAGCGGGAGGAGGCGGGGC   10625       _  A    C
                                CAGCGGG GGA GCGGG GT
                                |||||||  |||  |||||  ||
                                GTCGCCC CCT CGCCC CG
                                    T   C    _
GAM60   DISC1    3' GCGGGGGAGGGAAGAGCAGC  33043       AGC   CGT_
                                GCGGGGGA   GGG   GCAGC
                                ||||||||   |||   |||||
                                CGCCCCCT   CCC   CGTCG
                                     ___   TTCT
GAM60   DNASE1   5' CAGTGGTGGGGGGCCTGCAG   23353    C  G  AAGC   G
                                CAG GG GG   GGGC TGCAG
                                |||  ||  ||   ||||  |||||
                                GTC CC CC   CCCG ACGTC
                                  A  A ____   G
GAM60   DPP6     5' CGGTGGGGAGGCAGCA      39129    _  AAGC    T
                                CGG GGG   GGGCG GCA
                                |||  |||   |||||  |||
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                                GCC CCC    TCCGT CGT
                                  A   C___    _
GAM60   ENG     3'  CAGCGGGGAGGTGCTGTTGGC  6491         AA_  G___
                                CAGCGGGGG   GC    GGC
                                |||||||||   ||    |||
                                GTCGCCCCT   CG    CCG
                                     CCA  ACAA
GAM60   EPO     3'  GCGGGGGAGGGTGTGGC     9032         AGC   C  _
                                GCGGGGGA   GGG GTG C
                                ||||||||   ||| ||| |
                                CGCCCCCT   CCC CAC G
                                     ___   A   C
GAM60   F2RL3   3'  CAGCGGGGAGGGGCGTGGC   19512        GA  C      _
                                CAGCGGGG  AG GGGCGTG C
                                ||||||||  || ||||||| |
                                GTCGCCCC  TC CCCGCAC G
                                     __  _      C
GAM60   FKBP1A  3'  GCTGGGGGAAGGGTGCAG    38280    _     AGC   C
                                GC GGGGGA   GGG GTGCAG
                                || ||||||   ||| ||||||
                                CG CCCCCT   TCC CACGTC
                                 A     ___   _
GAM60   FKBP2   5'  CAGCGGGGGGGAGGGGGT    38390         A  C   C
                                CAGCGGGGG AG GGG GT
                                ||||||||| || ||| ||
                                GTCGCCCCC TC CCC CA
                                     C  _   _
GAM60   FUT5    3'  CAGCAGGGGAGGCTCCTGGCAG 13019          A  GGGCGT
                                CAGCGGGGGA GC     GCAG
                                |||||||||| ||     ||||
                                GTCGTCCCCT CG     CGTC
                                     C  AGGAC_
GAM60   GRB14   5'  GCGGGGGAGGGGAGGGGGC   21044         _____  C
                                GCGGGGGA    AG GGGC
                                ||||||||    || ||||
                                CGCCCCCT    TC CCCG
                                     CCCC  C
GAM60   HD      3'  GCGGGGGAGGCGGGAGGC    13353         A    CGT
                                GCGGGGGA GCGGG   GC
                                |||||||| |||||   ||
                                CGCCCCCT CGCCC   CG
                                     C    TC_
GAM60   HHIP    5'  GCGGGGCAGGCGGAGGC     35411       GGAA      T__
                                GCGGG   GCGGGCG   GC
                                |||||   |||||||   ||
                                CGCCC   CGTCCGC   CG
                                   _____     CTC
GAM60   HMGA2   5'  GCGGGGCGAGCGCGAGCTGGC  18523        _  A_     GT
                                GCGGGG GA  GCGGGC  GC
                                |||||| ||  ||||||  ||
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                                CGCCCC CT  CGCTCG  CG
                                   G  CG     AC
GAM60   HRMT1L1  3'  CAGCGGGGGTGGCCACGGCAGC 42180         AA  GG   T
                                CAGCGGGGG  GC  GCG GCAGC
                                |||||||||  ||  ||| |||||
                                GTCGCCCCC  CG  TGC CGTCG
                                     AC  G_  _
GAM60   KCNK5    3'  CAGCGGGCAGGGTGTGCAG   19030       GGAAGC   C
                                CAGCGGG     GGG GTGCAG
                                |||||||     ||| ||||||
                                GTCGCCC     CCC CACGTC
                                   GT_____  A
GAM60   LEF1     5'  CAGCGGGCGGAAGCGGGGC   32202       _       C
                                CAGCGGG GGAAGCGGG GT
                                ||||||| ||||||||| ||
                                GTCGCCC CCTTCGCCC CG
                                   G       _
GAM60   LFNG     3'  CAGCGGGGAGGTGGCAGC    45216       GA  CG    T
                                CAGCGGGG  AG  GGCG GC
                                ||||||||  ||  |||| ||
                                GTCGCCCC  TC  CCGT CG
                                    __  CA   _
GAM60   MX2      3'  GCGGGGGAGTGGAGAGGC    14696       A C   CGT
                                GCGGGGGA G GGG   GC
                                |||||||| | |||   ||
                                CGCCCCCT C CCT   CG
                                    _ A   CTC
GAM60   NLGN2    3'  CAGCGGGGGGGACGAGGCGGC  44746        AA  _    T
                                CAGCGGGGG  GCG GGCG GC
                                |||||||||  ||| |||| ||
                                GTCGCCCCC  TGC CCGC CG
                                     C_   T   _
GAM60   PAFAH1B1 3'  CAGCGGGGAGGCGGGGC     7700         AA    C
                                CAGCGGGGG  GCGGG GT
                                |||||||||  ||||| ||
                                GTCGCCCCT  CGCCC CG
                                     C_    _
GAM60   PDGFB    5'  CAGCGGGGGAGGCTGCGGG   15170         A___
                                CAGCGGGGGA   GCGGG
                                ||||||||||   |||||
                                GTCGCCCCCT   CGCCC
                                      CCGA
GAM60   PLXNB3   3'  GCAGGGGAGGTGGCAGGC    23947        A___
                                GCGGGGGA   GCGGGC
                                ||||||||   ||||||
                                CGTCCCCT   CGTCCG
                                     CCAC
GAM60   PPFIA3   3'  GCGGGGCGGAGCTGAGTGGC  41423       GA_  _  CGT
                                GCGGGG  AGC GGG  GC
                                ||||||  ||| |||  ||
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                                CGCCCC  TCG CTC  CG
                                   GCC  A  AC_
GAM60  PPP1CB  5' GCGGCGGAGGCTGCGGC    15503     G  A  GG  T
                                GCGG GGA GC  GCG GC
                                |||| ||| ||  ||| ||
                                CGCC CCT CG  CGC CG
                                  G  C  A_  _
GAM60  PRPS2   5' GCGGAGGAGGTGGCGGAGGC  15732       A CG   T__
                                GCGGGGGA G  GGCG  GC
                                |||||||| |  ||||  ||
                                CGCCTCCT C  CCGC  CG
                                    _ CA   CTC
GAM60  PRPSAP1 5' GCGGGGGAACGGGGAGAGC  15735       G   CGT_
                                GCGGGGGAA CGGG   GC
                                ||||||||| ||||   ||
                                CGCCCCCTT GCCC   CG
                                     _   CTCT
GAM60  PTGER3  5' CAGCGGGAGGGGGCAGACGCGG 9643       _ AA      _
          C                      CAGCGGG GG  GCGGGCGTG C
                                |||||||  ||  ||||||||| |
                                GTCGCCC CC  CGTCTGCGC G
                                    T  CC       C
GAM60  PTMA    5' GCGGAGGAGGCGCGCGGC    15869       A  G  T
                                GCGGGGGA GCG GCG GC
                                |||||||| ||| ||| ||
                                CGCCTCCT CGC CGC CG
                                    C  G  _
GAM60  RNPEPL1 5' CAGCGGGGGCGGCGGCGCGGGC 32876        AA  _  T
                                CAGCGGGGG  GCGG GCG GC
                                |||||||||  |||| ||| ||
                                GTCGCCCCC  CGCC CGC CG
                                     GC   G  C
GAM60  SCN8A   5' GCGAGGGAGGCAGCGGC    30533       A   G  T
                                GCGGGGGA GCGG CG GC
                                |||||||| |||| || ||
                                CGCTCCCT CGTC GC CG
                                    C  _ _
GAM60  SMARCD2 5' AGCGGGGGCAGCGGGAACCCGC 16910       A    __ G
                                AGCGGGGG AGCGGG  C TGC
                                |||||||| ||||||  | |||
                                TCGCCCCC TCGCCC  G GCG
                                    G     TT G
GAM60  TMEFF2  5' GCGGGGAAGCAGCAGC     32105      G    G  T
                                GCGGGG AAGCGG CG GC
                                |||||| |||||| || ||
                                CGCCCC TTCGTC GT CG
                                   _    _ _
GAM60  TMEPAI  5' GCGGGGGAGGCGCGC      33612       AGCG
                                GCGGGGGA   GGCGTGC
                                ||||||||   |||||||
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                                CGCCCCCT   CCGCGCG
                                    ____
GAM60   TNFRSF8  5' AGCGGGGGAAGCGCGCGGC   10307          G  T
                                AGCGGGGGAAGCG GCG GC
                                ||||||||||||| ||| ||
                                TCGCCCCCTTCGC CGC CG
                                      G  _
GAM60   TPM1     5' GCGGGGCGAGCGCGC      7487       GGAA
                                GCGGG   GCGGGCGTGC
                                |||||   ||||||||||
                                CGCCC   CGCTCGCGCG
                                   _____
GAM60   YY1      5' GCGGGGGAAGGGGCGGGC    18174         C    T
                                GCGGGGGAAG GGGCG GC
                                |||||||||| ||||| ||
                                CGCCCCCTTC CCCGC CG
                                      _    C
GAM61   GCLM     3' TCATATTGAAGGAAATTACAGG 13135        AAA     _
                                TTATATTGA  AGGAAGT ACAGG
                                |||||||||  ||||||| |||||
                                AGTATAACT  TCCTTTA TGTCC
                                     ___     A
GAM61   NRIP1    3' TATATTGAAAAGGATCAGG   40985          A  AGTA
                                TATATTGAAAA GGA   CAGG
                                |||||||||| |||   ||||
                                ATATAACTTTT CCT   GTCC
                                      _  A___
GAM61   PXF      3' TTATTTTGAGAAAGGAAA    16014     A   A
                                TTAT TTGA AAAGGAAG
                                |||| |||| ||||||||
                                AATA AACT TTTCCTTT
                                  A   C
GAM61   RHD      3' TATTCAAAAAGGGAAGTATAGG 32043     G     _    C
                                TATT AAAAAGG AAGTA AGG
                                |||| ||||||| ||||| |||
                                ATAA TTTTTCC TTCAT TCC
                                  G     C    A
GAM61   SRD5A1   3' TTATATTGATAACAGGTACAGG 9834         A  A  AA
                                TTATATTGA AA GG  GTACAGG
                                ||||||||| || ||  |||||||
                                AATATAACT TT TC  CATGTCC
                                     A  G  __
GAM61   B3GALT2  5' TACCCTCCTTGTTCATAT    19112         ATA
                                TACCCTCCTT   TATAT
                                ||||||||||   |||||
                                ATGGGAGGAA   GTATA
                                      CAA
GAM62   OCRL     3' TTACACAACACTGGATAT    7090         A  _
                                TTACACGG GC GGATAT
                                |||||||| || ||||||
```

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                                AATGTGTT TG CCTATA
                                     G  A
GAM63   BACH2    3'  TGAGTCATTGCTGGGAAC    34811        C  CCGA
                                TGAGTCAT GC    GGAC
                                |||||||| ||    ||||
                                ACTCAGTA CG    CTTG
                                     A  ACC_
GAM63   GFAP     3'  TGAGTCATCGCTCAGGA     13127          C G
                                TGAGTCATCGC C AGGA
                                |||||||||||| | ||||
                                ACTCAGTAGCG G TCCT
                                      A _
GAM64   COL1A1   3'  GGTTTTTGGTCATGTTCG    6380     CC_        C
                                GG   TTGGTCATGT CG
                                ||   |||||||||| ||
                                CC   AACCAGTACA GC
                                 AAA         A
GAM64   ADCY8    5'  GGAGGAGGAGGGGGGTCACGGT  10009     AA   C  A  C  ACT
                                GGA  AGG AG GG GT   TGGT
                                |||  ||| || || ||   ||||
                                CCT  TCC TC CC CA   GCCA
                                  CC   _  C  _  GT_
GAM64   ALDH3B2  3'  GGATGGGGCAGAGGTGG     8683      AAA       CGTACT
                                GGA   GGCAGAGG     TGG
                                |||   ||||||||     |||
                                CCT   CCGTCTCC     ACC
                                  ACC       _______
GAM64   B4GALT1  3'  AGAAAAGGTAGAGTTTGG     11274         C    GCGTAC
                                GGAAAAGG AGAG     TTGG
                                |||||||| ||||     ||||
                                TCTTTTCC TCTC     AACC
                                     A   A_____
GAM64   FGF1     5'  GGAAGCAGAATCCACTTGGT   37571     AAA      GCG
                                GGA   GGCAGAG   TACTTGGT
                                |||   |||||||   ||||||||
                                CCT   TCGTCTT   GTGAACCA
                                  ___      AG_
GAM64   HPRT1    5'  GGAGGAGGCGGAGGCGCA    6798      AA   A
                                GGA  AGGC GAGGCGTA
                                |||  |||| ||||||||
                                CCT  TCCG CTCCGCGT
                                  CC    C
GAM64   IRF1     5'  GAAGAAGGCAGAGGTTGCCGGG 42042     A        CGTA  T
           T                     GGA AAGGCAGAGG    CT GGT
                                ||| ||||||||||    || |||
                                CTT TTCCGTCTCC    GG CCA
                                  C         AAC_  C
GAM64   MAP3K14  5'  GAGAAAGGCAGGGGCAAAGGGT 19539    GA       A    TACTT
                                G  AAAGGCAG GGCG     GGT
                                |  |||||||| ||||     |||
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                                C  TTTCCGTC CCGT    CCA
                                 TC      C   TTC__
GAM64   MAP3K4   3'  GGAGGAGACAGAGGCGATGGT  25430    AA        TACT
                                GGA  AGGCAGAGGCG   TGGT
                                |||  ||||||||||   ||||
                                CCT  TCTGTCTCCGC   ACCA
                                  CC        T___
GAM64   MAPT     3'  GGCAGAGGGCGGGGGCCGGGT  32590       _  TA__  T
                                GGCAGAGG CG   CT GGT
                                |||||||| ||   || |||
                                CCGTCTCC GC   GG CCA
                                     C  CCCC  C
GAM64   PGD      3'  GGCAAGGGCAGAGGGCATGGT  44243    AAAA      C   CT
                                GG   GGCAGAGG GTA  TGGT
                                ||   |||||||| |||  ||||
                                CC   CCGTCTCC CGT  ACCA
                                 GTTC      _  __
GAM64   SALL2    5'  GGAGGGGCAACGCTCACTTGGT 41899    AAA    AG  G
                                GGA   GGCAG  GC TACTTGGT
                                |||   |||||  || ||||||||
                                CCT   CCGTT  CG GTGAACCA
                                  CC_    G_  A
GAM64   SCAP1    3'  GGAAAAGGCAGATGTG      19006          GGCGTACT
                                GGAAAAGGCAGA       TG
                                ||||||||||||       ||
                                CCTTTTCCGTCT       AC
                                       AC_______
GAM65   CSPG3    3'  TCTTTGTCTCCCTGAGAGAT   20492     _     __
                                TCTT GTTTTC  GAGAGAT
                                |||| ||||||  |||||||
                                AGAA CAGAGG  CTCTCTA
                                  A     GA
GAM65   GNE      5'  TGCTTGTTTCGTTTTGAGAG   24215     CTTATC      C
                                TGC     TTGTTTT GAGAG
                                |||     ||||||| |||||
                                ACG     AGCAAAA CTCTC
                                  AACAA_      _
GAM65   IGF1     3'  TGTCTTATCTGTGAGAG     8359     C      T  TTTC
                                TG CTTATCT GT    GAGAG
                                || ||||||| ||    |||||
                                AC GAATAGA CA    CTCTC
                                 A      _ _____
GAM65   PPP2R5E  3'  CCTTATTTTGTTTTTTATCTCT 26467       C     T________  GAGA
           G                     CCTTAT TTGTT       TC    G
                                 ||||||| |||||       ||    |
                                 GGAATA AACAA       AG    C
                                    A     AAAAIIIT  AGAG
GAM66   ADAMTS8  5'  GGATGCATCTTCCGAAGAGGCT 28165    A    _  C     CG
           C                     A ATGC TC TCCGA  AGAGGCTC
                                 | |||| || |||||  ||||||||
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                                C TACG AG AGGCT  TCTCCGAG
                                 C   T A    __
GAM66   B4GALT3  3'  AAATGCCCAGGGAGGGGCT   19104      T  TCCGAC   A
                                AAATGC CC     GAG GGCT
                                ||||||  ||     ||| ||||
                                TTTACG GG     CTC CCGA
                                   _  TCC___   C
GAM66   GRLF1    3'  GGACGCTCCTCTGTGGCT    44229   A      CGACGAGA
                                A ATGCTCCTC       GGCT
                                | |||||||||       ||||
                                C TGCGAGGAG       CCGA
                                 C        ACA_____
GAM66   ITCH     3'  AAATGCCTCTTACCAAGAGGCT 36451      TC  CCGA
                                AAATGC  CT    CGAGAGGCT
                                ||||||  ||    |||||||||
                                TTTACG  GA    GTTCTCCGA
                                   GA  ATG_
GAM66   MGAT5    5'  ATGCTTCCTGAGAGGCT     14470      _  CCGAC
                                ATGCT CCT     GAGAGGCT
                                |||||  |||     ||||||||
                                TACGA GGA     CTCTCCGA
                                  A  _____
GAM66   MRPS12   5'  AAATGCTCCCCGATCCGCT   37890        T   CGAGAG
                                AAATGCTCC CCGA     GCT
                                |||||||||  ||||     |||
                                TTTACGAGG GGCT     CGA
                                    _   AGG___
GAM66   MUC12    3'  GCTCCCGGATGGAGAGGCT   45331      CCGAC
                                GCTCCT    GAGAGGCT
                                ||||||    ||||||||
                                CGAGGG    CTCTCCGA
                                   CCTAC
GAM66   PIAS3    3'  TGCCCCTTCCCCAAGAGGCTC  25913       _  GA
                                TGCTCCT CC  CGAGAGGCTC
                                |||||||  ||  ||||||||||
                                ACGGGGA GG  GTTCTCCGAG
                                    A  G_
GAM66   RNMT     3'  AAATGCTCTCTGACCAA     19142        C  C   G
                                AAATGCTC TC GAC AG
                                ||||||||  || ||| ||
                                TTTACGAG AG CTG TT
                                    _  A   G
GAM66   WHSC1L1  3'  TGCTGTACTGAGAGGCT     35718     CCTCCG  _
                                TGCT     AC GAGAGGCT
                                ||||     ||  ||||||||
                                ACGA     TG CTCTCCGA
                                  CA____  A
GAM67   ANKH     3'  TATTCCTACTCCAGTGACC    38326      GTAC     ___
                                TATTCC    TGCTCC   GACC
                                ||||||    ||||||   ||||
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                                ATAAGG   ATGAGG   CTGG
                                   ____     TCA
GAM67   CXADR    3'  TATTCCGTACAGTTCCTGA   10641        TGC  _
                                TATTCCGTAC   TCC GA
                                ||||||||||   ||| ||
                                ATAAGGCATG   AGG CT
                                     TCA   A
GAM67   MTMR3    3'  TACTCCTGGCTCTGACC    34397      GTACT   C
                                TATTCC    GCTC GACC
                                ||||||    |||| ||||
                                ATGAGG    CGAG CTGG
                                   AC___   A
GAM67   MTNR1A   3'  CATTCTGTACTTCTCTTGAC  25548     C    G  C_
                                TATTC GTACT CTC  GAC
                                ||||| ||||| |||  |||
                                GTAAG CATGA GAG  CTG
                                   A    A  AA
GAM67   MX1      5'  TTCCTGTAGCCTCCGACC    14692     _  CTG
                                TTCC GTA   CTCCGACC
                                |||| |||   ||||||||
                                AAGG CAT   GAGGCTGG
                                  A  CG_
GAM67   POMZP3   5'  TATTCCGCAGGTCCTGGCC   29246       CTGC   GA_
                                TATTCCGTA   TCC   CC
                                |||||||||   |||   ||
                                ATAAGGCGT   AGG   GG
                                     CC__   ACC
GAM67   SCA1     3'  TTCCTATTGCTCCAAACC    7300      G  C      _
                                TTCC TA TGCTCCGA CC
                                |||| || |||||||| ||
                                AAGG AT ACGAGGTT GG
                                  _ A       T
GAM68   ANK1     3'  GCCACAGCTCCTTCTCCTGCAG 33863     TTTC        C
                                GCT   TTCCTTCTCC GCAG
                                |||   |||||||||| ||||
                                CGG   GAGGAAGAGG CGTC
                                  TGTC        A
GAM68   EIF4EBP2 3'  GCTTTTCTTCTAATCCTTGCAG 19893         C TC   C_
                                GCTTTTCTTC T  TCC  GCAG
                                |||||||||| |  |||  ||||
                                CGAAAAGAAG A  AGG  CGTC
                                     _ TT   AA
GAM68   GAD1     5'  ACGCTTTTTTTTTTTCCTT   30286       C____
                                ACGCTTTT    TTCCTT
                                ||||||||    ||||||
                                TGCGAAAA    AAGGAA
                                     AAAAA
GAM68   KTN1     3'  GCTTTTTTTTTCCTTCTTTAAA 22555      C__      CCCG__
           TCAG                  GCTTTT   TTCCTTCT    CAG
                                ||||||  ||||||||    |||
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                                CGAAAA  AAGGAAGA    GTC
                                   AAA      AATTTA
GAM68   MYBL1   3' CGCTCTTTCCTTCTCTCG   41977      CT     C
                                CGCTTTT  TCCTTCTC CG
                                |||||||  |||||||| ||
                                GCGAGAA  AGGAAGAG GC
                                   __      A
GAM68   NORE1   3' ACTTTTTTTTTCCTTCTC   36426      C__
                                GCTTTT  TTCCTTCTC
                                ||||||  |||||||||
                                TGAAAA  AAGGAAGAG
                                   AAA
GAM68   PODXL   3' CGCTTTCCAGGCCCTCTTTTCC 23968       TT_    C__
                                CGCTTTTC  CCTTCT  CC
                                ||||||||  ||||||  ||
                                GCGAAAGG  GGGAGA  GG
                                     TCC    AAA
GAM68   POV1    3' TTTTCCTCCTTTTTGCAG   18846        CTCCC
                                TTTTCTTCCTT   GCAG
                                ||||||||||    ||||
                                AAAAGGAGGAA   CGTC
                                     AAA__
GAM68   SET     3' TTTTCTTTTTTCCCACAG   16564      CC  C
                                TTTTCTT  TT TCCCGCAG
                                |||||||  || ||||||||
                                AAAAGAA  AA AGGGTGTC
                                   __ A
GAM68   ADAM29  5' GCTCCTTCTTCTGAGTTG   44621       C  CGC
                                GCTCCTTCT CT  GTTG
                                |||||||| ||  ||||
                                CGAGGAAGA GA  CAAC
                                     A  CT_
GAM68   ADCY1   3' TGCTCCTCCTCCACCCTG   45223         TC  G
                                TGCTCCTTCTCC  GC TTG
                                ||||||||||  || |||
                                ACGAGGAGGAGG  TG GAC
                                     __ G
GAM68   ADD1    3' CTCCTTCTCTAACATTG    30518       CTC
                                CTCCTTCTC  GCGTTG
                                |||||||||  ||||||
                                GAGGAAGAG  TGTAAC
                                     AT_
GAM68   ADD2    3' TGCTCCTCCTCCCTCCCGTTG 32734         _ G
                                TGCTCCTTCTCC TC CGTTG
                                |||||||||||| || |||||
                                ACGAGGAGGAGG AG GCAAC
                                     G  G
GAM68   ARF4L   3' TGCTCCTCTCTCCTTCATTG  43075      _    CG
                                TGCTCCT TCTCCT  CGTTG
                                ||||||| ||||||  |||||
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                                ACGAGGA AGAGGA  GTAAC
                                    G     A_
GAM68   COL9A3   3'  TGCTTCCTCACGTT       12346      CCTTC
                                TGCT    TCCTCGCGTT
                                ||||    ||||||||||
                                ACGA    AGGAGTGCAA
                                  _____
GAM68   EGFR     3'  TGCTCCTTGCTCACAGTTG   23399        CTC    _
                                TGCTCCTT   CTCGC GTTG
                                ||||||||   ||||| ||||
                                ACGAGGAA   GAGTG CAAC
                                    C__     T
GAM68   IRTA2    3'  GCTCCTTCTCTTCCGTTG    36341         C  G
                                GCTCCTTCTC TC CGTTG
                                |||||||||| || |||||
                                CGAGGAAGAG AG GCAAC
                                     A  _
GAM68   MLPH     3'  TGCTCCTTCTTGTTTCTCATTG 35869         CC__  G
                                TGCTCCTTCT    TC CGTTG
                                ||||||||||    || |||||
                                ACGAGGAAGA    AG GTAAC
                                     ACAA  A
GAM68   PGF      3'  CTCTTTCTCTCACGTTG     15250     C     C
                                CTC TTCTC TCGCGTTG
                                ||| ||||| ||||||||
                                GAG AAGAG AGTGCAAC
                                  A    _
GAM68   PLA2G2A  5'  TGCTCCCTCTGGGAGGTTG   7155          CCTCGC
                                TGCTCCTTCT     GTTG
                                ||||||||||     ||||
                                ACGAGGGAGA     CAAC
                                     CCCTC_
GAM68   SNL      5'  TGCTCCTTTGTTCGGCTG    16950        CTCC   C
                                TGCTCCTT    TCG GTTG
                                ||||||||    ||| ||||
                                ACGAGGAA    AGC CGAC
                                    ACA_   _
GAM68   TLE1     5'  TGCTCTTCTCCTCCTCGT    22922       C       G_
                                TGCTC TTCTCCTC  CGT
                                ||||| ||||||||  |||
                                ACGAG AAGAGGAG  GCA
                                   _       GA
GAM68   TPSB1    5'  TGTTCCTTCTACCCAGT     17660    C      C   C
                                TG TCCTTCT CTCG GT
                                || ||||||| |||| ||
                                AC AGGAAGA GGGT CA
                                 A      T   _
GAM69   ADAM19   3'  TCAGGGTTCCATGGTCATG   37776     AA   AAGCT
                                TCA  GTT    TGGTCATG
                                |||  |||    ||||||||
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                                AGT  CAA    ACCAGTAC
                                  CC   GGT__
GAM69   CYFIP2   5'  GTCAAAGTTAGCCTGGTACATG 43913          A     _
              A                   GTCAAAGTTA GCTTGGT CATGA
                                  |||||||||| ||||||| |||||
                                  CAGTTTCAAT CGGACCA GTACT
                                        _      T
GAM69   DDEF1    3'  CGTTCAAAAACTTGGTTATGA  40567    _    TTAA     C
                                  CGT CAAAG   GCTTGGT ATGA
                                  ||| |||||   ||||||| ||||
                                  GCA GTTTT   TGAACCA TACT
                                    A    ____      A
GAM69   FACL5    3'  ATTAAGGTTGGAAATCATGA   42010       C   ___
                                  GTTAAG TTGG   TCATGA
                                  |||||| ||||   ||||||
                                  TAATTC AACC   AGTACT
                                     C    TTT
GAM69   MAP1A    3'  GTAGGAGTTAAGCTGTGG    14346    CAA       _
                                  GT   AGTTAAGCT TGG
                                  ||   ||||||||| |||
                                  CA   TCAATTCGA ACC
                                   TCC        C
GAM69   MPV17    3'  GTAAAGTTGATAAGGTCATGA  43263    C     AAGCTT
                                  GT AAAGTT     GGTCATGA
                                  || ||||||     ||||||||
                                  CA TTTCAA     CCAGTACT
                                   _     CTATT_
GAM69   PPFIA3   5'  GCCAGGATGGGCTTGGTCGTG  41420     AA  TAA      A
                                  GTCA  GT   GCTTGGTC TG
                                  ||||  ||   |||||||| ||
                                  CGGT  TA   CGAACCAG AC
                                    CC  CC_       C
GAM69   ZNF146   3'  GTTAAAGTTAACCTCATTCGTG 28355    C       G   GG  A
                                  GT AAAGTTAA CTT  TC TG
                                  || |||||||| |||  || ||
                                  CA TTTCAATT GAG  AG AC
                                   A       G   TA  C
GAM69   CHD2     3'  GGGATCCCTGATACCTAG    10447     CTTTA
                                  GGGA    TCTGATACCTAG
                                  ||||    ||||||||||||
                                  CCCT    GGACTATGGATC
                                    AG___
GAM69   PRKCG    3'  GGGACGTTGGGGACACCTAG   15629      TTTATCT
                                  GGGAC      GATACCTAG
                                  |||||      |||||||||
                                  CCCTG      CTGTGGATC
                                     CAACCC_
GAM70   B3GALT2  5'  TGACAAAAATGTTTTCTTCTCC 19114          A_   CCA_
              T                    TGACAAAGAT  TTTC    CCT
                                  ||||||||||  ||||    |||
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                                ACTGTTTTTA AAAG  GGA
                                     CA  AAGA
GAM70  BAZ2A   3' ACAAGGAATGCTCCACCTCA 30298    A TATTTC
                                ACAA GA    CCACCTCA
                                |||| ||    ||||||||
                                TGTT CT    GGTGGAGT
                                  C TACGA_
GAM70  CDH1    3' TGAGGTAGACCCACCTCA   20369    CAA  TATTT
                                TGA  AGA   CCCACCTCA
                                |||  |||   |||||||||
                                ACT  TCT   GGGTGGAGT
                                  CCA  _____
GAM70  DDX11   3' ACAGAGAATGCGACCCACCTC 36164    A  TATTT_
                                ACA AGA    CCCACCTC
                                ||| |||    ||||||||
                                TGT TCT    GGGTGGAG
                                  C  TACGCT
GAM70  FGF2    3' GATCAACCCTCCCACCTCA  12838    AT___
                                GAT    TTCCCACCTCA
                                |||    ||||||||||
                                CTA    GAGGGTGGAGT
                                  GTTGG
GAM70  MYH1    3' TGACAAAGATTTTCACA    25561        A  C
                                TGACAAAGAT TTTC CA
                                |||||||||| |||| ||
                                ACTGTTTCTA AAAG GT
                                      _   T
GAM70  PCSK1   3' TGACAAAACAACCACTTC   7755       ATATTTC  C
                                TGACAAAG     CCAC TC
                                ||||||||     |||| ||
                                ACTGTTTT     GGTG AG
                                     GTT____   A
GAM70  VDR     3' ACAAAGACCCACCT      7508       TATTT
                                ACAAAGA    CCCACCT
                                |||||||    |||||||
                                TGTTTCT    GGGTGGA
                                      _____
GAM70  VDR     3' TGATGGGAAGAAAACCCACCTC 7530    CA__   TATTT
          A                      TGA   AAGA   CCCACCTCA
                                |||   ||||   |||||||||
                                ACT   TTCT   GGGTGGAGT
                                  ACCC   TTT__
GAM70  GNAO1   3' AACCGGATTCTACAGCAT   44936       CC  TCCC
                                AACCGGAT  CTG   TAGCAT
                                ||||||||  |||   ||||||
                                TTGGCCTA  GAT   GTCGTA
                                     A_  ____
GAM70  ITSN1   3' AACCAGATGATCTCCTGGCAT 16650       CCCT  _  A
                                AACCGGAT   GTC CCT GCAT
                                ||||||||   ||| ||| ||||
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                                TTGGTCTA   TAG GGA CGTA
                                    C___   A   C
GAM70   NHP2L1   3'  AACCAGATCTCTGTCCTGGCTC 22676        C     ___  AG
            CATC                    AACCGGATC CTGTCC   CT  CATC
                                ||||||||| ||||||   ||  ||||
                                TTGGTCTAG GACAGG   GA  GTAG
                                    A     ACC  G_
GAM71   AOC3     3'  CCCTCCTGGCTGGGTGGC    19015   G   GGG   AGCC   C
                                C CTCC   GGC    GGG GGC
                                | ||||   |||    ||| |||
                                G GAGG   CCG    CCC CCG
                                 G   A__   A___   A
GAM71   APBA2    3'  TCCTCTGGGCCCGGGCGGC   24282    GG_   AG
                                TCC   GGGC  CCGGGCGGC
                                |||   ||||  |||||||||
                                AGG   CCCG  GGCCCGCCG
                                  AGA   __
GAM71   AXIN1    3'  GCTCTGGGCCCTGCGGGTGGCC 41381     CGG   AGC_   C
                                GCTC   GGGC    CGGG GGCC
                                ||||   ||||    |||| ||||
                                CGAG   CCCG    GCCC CCGG
                                  A__    GGAC    A
GAM71   CA12     5'  CCGGGGGCTCCCGGTGGCC   10242        AG   GC
                                CCGGGGGC  CCGG  GGCC
                                ||||||||  ||||  ||||
                                GGCCCCCG  GGCC  CCGG
                                    AG   A_
GAM71   CAPN10   3'  GCCCCGGGGGGTGGTGTTCTTGG 35772          CAGCCGGGC_
            CC                    GCTCCGGGGG        GGCC
                                ||||||||||        ||||
                                CGGGGCCCCC        CCGG
                                     ACCACAAGAA
GAM71   CDK10    3'  TCTGGGGGCAGCAGTGGG    38153    C       C__
                                TC GGGGGCAGC   GGG
                                || |||||||||   |||
                                AG CCCCCGTCG   CCC
                                 A        TCA
GAM71   DBN1     5'  CGGGGGGAGGGCGGCC      38931       CAGCC
                                CGGGGG    GGGCGGCC
                                ||||||    ||||||||
                                GCCCCC    CCCGCCGG
                                   CT___
GAM71   DDB1     3'  GCTCTGGGGGCAGCTGGC    12559      C       CG
                                GCTC GGGGGCAGC  GGC
                                |||| |||||||||  |||
                                CGAG CCCCCGTCG  CCG
                                  A        A_
GAM71   EP300    5'  CGCTCCGGCGGCGGGCGCAGGC 10979        G   A_  _
            GGCC                    CGCTCCGG GGC  GC CGGGCGGCC
                                ||||||||  |||  ||  |||||||||
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                                GCGAGGCC CCG  CG GTCCGCCGG
                                    G  CC  C
GAM71   FBXL3A   5' GCTCCGGGGACGGCGGCGGC  29128          A  CG
                                GCTCCGGGGGC GC  GGCGGC
                                |||||||||| ||  ||||||
                                CGAGGCCCCTG CG  CCGCCG
                                      C  __
GAM71   FGF18    5' CGCTCCGGGGTCGGGGCGCGCG 38004         GCAGC_  G
           GC                    CGCTCCGGGG     CG GCGGC
                                |||||||||     || |||||
                                GCGAGGCCCC     GC CGCCG
                                     AGCCCC  G
GAM71   FUT5     3' CGCCCGGGGGCAGGGC      13021     T       GCC
                                CGC CCGGGGGCA   GGGC
                                ||| |||||||||   ||||
                                GCG GGCCCCCGT   CCCG
                                 _       ____
GAM71   GALGT    5' GCCCGGGGGCGGTTGG      11183    T      AGCC  GC
                                GC CCGGGGGC   GG  GG
                                || ||||||||   ||  ||
                                CG GGCCCCCG   CC  CC
                                 _      _____ AA
GAM71   GLS      5' GCTCCGGGCGTGGGCGGCC   31377        GGCAGCC
                                GCTCCGGG      GGGCGGCC
                                ||||||||      ||||||||
                                CGAGGCCC      CCCGCCGG
                                    GCA____
GAM71   HRB      5' GCGCCGGGGGCCCGCGG     21088    T      AG  GG
                                GC CCGGGGGC  CC  GCGG
                                || ||||||||  ||  ||||
                                CG GGCCCCCG  GG  CGCC
                                 C      __  __
GAM71   LPIN2    3' GCTCGGGGGGGCAGTCTGC    31213     C      CCGG
                                GCTC GGGGGCAG   GC
                                |||| ||||||||   ||
                                CGAG CCCCCGTC   CG
                                  C      AGA_
GAM71   MAPK4    3' GCTCTGTGGGGCCTGGAGCGGC 15661     CG_    AGCC
           C                     GCTC  GGGGC   GGGCGGCC
                                |||| |||||  ||||||||
                                CGAG  CCCCG   CTCGCCGG
                                  ACA   GAC_
GAM71   MATK     5' GCTCCGGGGACCGCGGC     40311          AGCCGG
                                GCTCCGGGGGC     GCGGC
                                ||||||||||     |||||
                                CGAGGCCCCTG     CGCCG
                                      G_____
GAM71   MFI2     3' GCTCTGGGGCGGGGCGGC    25466     CG    AGCC
                                GCTC  GGGGC   GGGCGGC
                                ||||  |||||   |||||||
```

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                                CGAG  CCCCG   CCCGCCG
                                  A_    C___
GAM71   MSI1    3'  CTTTTGGGGAGGGGGCGG   14640   CCG   C  CC
                                CT   GGGG AG  GGGCGG
                                ||   |||| ||  ||||||
                                GA   CCCC TC  CCCGCC
                                 AAA   _  C_
GAM71   ODF2    3'  GCTTGGGGGGCAAGTGGC    14930    CC     GCCG  C
                                GCT  GGGGGCA   GG GGC
                                |||  |||||||   || |||
                                CGA  CCCCCGT   TC CCG
                                  A_     _____ A
GAM71   PGF     5'  CTCCCGTAGCTGGGCGGCC   15249    GGG   AGCC
                                CTCC   GGC   GGGCGGCC
                                ||||   |||   ||||||||
                                GAGG   TCG   CCCGCCGG
                                  GCA   A___
GAM71   SLC1A2  5'  GCTCCGGGGGCTCCGAGGGTGG 41597         AG  __   C
            C                    GCTCCGGGGGC  CC  GGG GGC
                                ||||||||||  ||  ||| |||
                                CGAGGCCCCCG  GG  CCC CCG
                                      A_  CT   A
GAM71   SLC1A4  5'  CGCCCCGGGGGTCTCGCGGCC  16745         CAGCCGG
                                CGCTCCGGGGG     GCGGCC
                                ||||||||||     ||||||
                                GCGGGGCCCCC     CGCCGG
                                      AGAG___
GAM71   SP3     5'  CGCTCCGGCGGCGGCGGGGGCC 44375       G   A  C   C
                                CGCTCCGG GGC GC GGG GGCC
                                |||||||| ||| || ||| ||||
                                GCGAGGCC CCG CG CCC CCGG
                                    G   C  _   _
GAM71   STK31   5'  CCCTCTGGGGTGGCGGGCGGC  37276   G   C   GCA  C
                                C CTC GGGG   GC GGGCGGC
                                | ||| ||||   || |||||||
                                G GAG CCCC   CG CCCGCCG
                                 G   A   AC_  _
GAM71   VEGF    5'  CTCCGGGGGCGGGCTCCGGCC  17951         AGCC   ___
                                CTCCGGGGGC   GGGC   GGCC
                                ||||||||||   ||||   ||||
                                GAGGCCCCCG   CCCG   CCGG
                                      _____   AGG
GAM71   BMP1    3'  GCAGGTCCTGGGGCCTGGG   25980    C        AGCC
                                GC AGGTCCTGGGGC   GGG
                                || ||||||||||||   |||
                                CG TCCAGGACCCCG   CCC
                                 _         GA__
GAM71   CAPN5   5'  CCGCGGGTCCAGCCG      44927     CA    TGGGGC
                                CCGC  GGTCC     AGCCG
                                ||||  |||||     |||||
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                                GGCG  CCAGG     TCGGC
                                  C_    _______
GAM71   CKTSF1B1  3'  GCCAGGAGGCAGCTGG      30087       TCCTG      C
                                GCCAGG    GGGCAGC GG
                                ||||||    ||||||| ||
                                CGGTCC    TCCGTCG CC
                                   _____      A
GAM71   COL18A1   3'  GCCAGGTCCTGGGGCCAGGG  36131             AGCC
                                GCCAGGTCCTGGGGC   GGG
                                ||||||||||||||   |||
                                CGGTCCAGGACCCCG   CCC
                                        GT__
GAM71   CRAT      3'  CCAGGTCCTGGGAGTTTGGG  19661           CAGCC
                                CCAGGTCCTGGGG    GGG
                                ||||||||||||    |||
                                GGTCCAGGACCCT    CCC
                                        CAAA_
GAM71   CREBBP    5'  CCCCGGGCACGGGCGGCCGGG  20429    G  A   CCTG    A
                                CC CC GGT    GGGC GCCGGG
                                || || |||    |||| ||||||
                                GG GG CCG    CCCG CGGCCC
                                 _ C   TG__    C
GAM71   EFNB1     5'  CGCCGAGTCCTGGCTCCCGGG  20713     AG    GG   AG
                                CGCC  GTCCT  GGC  CCGGG
                                ||||  |||||  |||  |||||
                                GCGG  CAGGA  CCG  GGCCC
                                  CT    __   AG
GAM71   HR        5'  GCTAGGGCGGGGCGGCTGGG   32924    C   TCC     A  C
                                GC AGG   TGGGGC GC GGG
                                || |||   |||||| || |||
                                CG TCC   GCCCCG CG CCC
                                 A  C__     C  A
GAM71   MAG       3'  GCTGGCAGGGAGGGGCAGCTGG 14322    ___    TCCT       C
           G                     GC   CAGG    GGGGCAGC GGG
                                ||   ||||    |||||||| |||
                                CG   GTCC    CCCCGTCG CCC
                                 ACC    CT__       A
GAM71   NF2       3'  GCAGGTCCTGGGGTGGCTGGG  7067     C         CA  C
                                GC AGGTCCTGGGG  GC GGG
                                || ||||||||||  || |||
                                CG TCCAGGACCCC  CG CCC
                                 _          AC  A
GAM71   NKX2H     5'  CGCCATGCGCTGGCAGCCGGG  30757      G  C  GG
                                CGCCA GT CT  GGCAGCCGGG
                                ||||| || ||  ||||||||||
                                GCGGT CG GA  CCGTCGGCCC
                                   A  C  __
GAM71   P3        5'  GCCAGGCCCGGCCG        33380        T   GGGCA
                                GCCAGG CCTG    GCCG
                                |||||| ||||    ||||
```

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                                CGGTCC GGGC    CGGC
                                  _  _____
GAM71   PFKFB4   3'  CACCAGGTCCATGCTGGGCAGC 21285          TG___     C
            TGGG                  CGCCAGGTCC    GGGCAGC GGG
                                  ||||||||||    ||||||| |||
                                  GTGGTCCAGG    CCCGTCG CCC
                                     TACGA      A
GAM71   PGF      5'  CCAGGTCCTCCCGTAGCTGGG  15246         GGGGC   C
                                  CCAGGTCCT    AGC GGG
                                  |||||||||    ||| |||
                                  GGTCCAGGA    TCG CCC
                                     GGGCA   A
GAM71   PRX      3'  CGCCGGCGGGCAGGGGCAGCCG 34114      A   CCT__
            GG                    CGCC GGT    GGGGCAGCCGGG
                                  |||| |||    ||||||||||||
                                  GCGG CCG    CCCCGTCGGCCC
                                    _  CCCGT
GAM71   REST     5'  CCGCCAGGGTCTGGGGCCCCGG 24707        TC      AG
            G                     CCGCCAGG  CTGGGGC  CCGGG
                                  ||||||||  |||||||  |||||
                                  GGCGGTCC  GACCCCG  GGCCC
                                     CA      G_
GAM71   RPS6KA1  5'  CCGGGTCCTGGGGTCCCTGG  40380    A        CAG  _
                                  CC GGTCCTGGGG   CC GG
                                  || ||||||||||   || ||
                                  GG CCAGGACCCC   GG CC
                                   C         AG_  A
GAM71   RUNX3    3'  CCTCAGGAGGCAGCTGG     20320    GC    TCCTG     C
                                  CC  CAGG    GGGCAGC GG
                                  ||  ||||    ||||||| ||
                                  GG  GTCC    TCCGTCG CC
                                   A_   _____      A
GAM71   RXRA     3'  CCGCCAGGGGCAGCTGG     16420       GGTCCT      C
                                  CCGCCA     GGGGCAGC GG
                                  ||||||     |||||||| ||
                                  GGCGGT     CCCCGTCG CC
                                     _______       A
GAM71   SCN1A    5'  CAGGTCCTGGTGGTACAAG   44813          _  CA  C
                                  CAGGTCCTGG GG  GC GG
                                  |||||||||| ||  || ||
                                  GTCCAGGACC CC  TG TC
                                     A  A_  T
GAM71   SOX10    3'  CAGGTCCTGGGATAGAGGG   27998          GC  CC
                                  CAGGTCCTGGG  AG  GGG
                                  ||||||||||  ||  |||
                                  GTCCAGGACCC  TC  CCC
                                     TA  T_
GAM71   SPHK2    3'  CCAGGTCCTGTCATTGG     33503          GGG  GCC
                                  CCAGGTCCTG   CA   GG
                                  |||||||||   ||   ||
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                                GGTCCAGGAC  GT  CC
                                    A__  AA_
GAM71  SPTBN4  3'  CAGGTCCTGGGGGTGGG    36085         CAGCC
                                CAGGTCCTGGGG   GGG
                                ||||||||||||   |||
                                GTCCAGGACCCC   CCC
                                    CA___
GAM71  TRPV4   3'  GCCAGGTTCCAGCTGG     41347      _  TGGGGC  C
                                GCCAGG TCC    AGC GG
                                |||||| |||    ||| ||
                                CGGTCC AGG    TCG CC
                                  A  ______  A
GAM71  WNT7A   5'  CCGCCGGGGCCGCGGGCCGGG  21524     A  TC  G  CA
                                CCGCC GG  CTG GG  GCCGGG
                                ||||| ||  ||| ||  ||||||
                                GGCGG CC  GGC CC  CGGCCC
                                  _ CC  G __
GAM72  CYP21A2  3'  TTAAGCCTCAATCCTCTGCAGC 7986         C  A    A
          G                      TTAAGCTTCA GTC TCTGCA CG
                                 ||||||||| ||| |||||| ||
                                 AATTCGGAGT TAG AGACGT GC
                                      _  G    C
GAM72  BAZ2B   3'  GGCAGGCACTACCAAGATTAAG 30323     AGAC  CT
                                GGCA   CAC  TCGAGATTAAG
                                ||||   |||  ||||||||||
                                CCGT   GTG  GGTTCTAATTC
                                  CC__  AT
GAM72  CDKN1A  3'  GGTGAGGCCCCTTCAAA    38512   CA  A  A
                                GG  AG CC CCTTCGAG
                                ||  || || ||||||||
                                CC  TC GG GGAAGTTT
                                 AC  C  _
GAM72  EGLN2   5'  GGCAAGACCTCCCCAATTA   38829       A   CGA
                                GGCAAGACC CCTT   GATTA
                                ||||||||| ||||   |||||
                                CCGTTCTGG GGGG   TTAAT
                                     A  ___
GAM72  UGT1A1  3'  GGGACCACCTTTGAA      7866    CAA      C
                                GG   GACCACCTT GAG
                                ||   ||||||||| |||
                                CC   CTGGTGGAA CTT
                                ___       A
GAM72  UGT1A4  3'  GGGACCACCTTTGAA      28295   CAA      C
                                GG   GACCACCTT GAG
                                ||   ||||||||| |||
                                CC   CTGGTGGAA CTT
                                ___       A
GAM72  UGT1A9  3'  GGGACCACCTTTGAA      34289   CAA      C
                                GG   GACCACCTT GAG
                                ||   ||||||||| |||
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                                CC   CTGGTGGAA CTT
                                 ___        A
GAM73   ATP1A2   3'  CCTCATTATCTCTCCCCAAATG 8704     CT  GGG   C
            T                    CC  GT   CTC CCCCAAATGT
                                 ||  ||   ||| ||||||||||
                                 GG  TA   GAG GGGGTTTACA
                                  AG  ATA   A
GAM73   CRKL     3'  CCGCTGTGTGCATTCCAAATGT 23306    _    G  TCCCC
                                 CC CTGTG GC     CCAAATGT
                                 || ||||| ||     ||||||||
                                 GG GACAC CG     GGTTTACA
                                  C     A  TAA__
GAM73   EDAR     3'  ACCCTGGGGTGTTTTCTAAATG 35299       T   CTCCCCCC
            T                    ACCCTG GGG       AAATGT
                                 |||||| |||       ||||||
                                 TGGGAC CCC       TTTACA
                                    _   ACAAAAGA
GAM73   GYPC     3'  CCTGCTGTTCCCCCCAAATGT  32542      GGGC
                                 CCTGT    TCCCCCCAAATGT
                                 |||||    ||||||||||||
                                 GGACG    AGGGGGGTTTACA
                                    ACA_
GAM73   GYPC     3'  CCTGCTGTTCCCCCCAAATGT  13324      GGGC
                                 CCTGT    TCCCCCCAAATGT
                                 |||||    ||||||||||||
                                 GGACG    AGGGGGGTTTACA
                                    ACA_
GAM73   HNRPK    3'  CCCTGTCCCACCCCCCAAATGT 36314       GGGCT
                                 CCCTGT     CCCCCCAAATGT
                                 ||||||     ||||||||||||
                                 GGGACA     GGGGGGTTTACA
                                     GGGT_
GAM73   HNRPK    3'  CCCTGGCCCACCCCCCAAATGT 36313      GT  G  _
                                 CCCT  GG CT CCCCCCAAATGT
                                 ||||  || || ||||||||||||
                                 GGGA  CC GG GGGGGGTTTACA
                                    __  G  T
GAM73   MKI67    3'  CCCTGTGAAGCCCTCAGATGT  14515         CTC   C  A
                                 CCCTGTGGG   CCC CA ATGT
                                 |||||||||   ||| || ||||
                                 GGGACACTT   GGG GT TACA
                                       C__   A  C
GAM73   MUCDHL   3'  CCCGGGGACCCCCCGGGTGT   34931      T   CT     AAA
                                 CCTG GGG  CCCCCC   TGT
                                 |||| |||  ||||||   |||
                                 GGGC CCC  GGGGGG   ACA
                                    _   T_     CCC
GAM73   MUCDHL   3'  CCCGGGGACCCCCCCGGGTGT   34931      T   CT     AAA
                                 CCTG GGG  CCCCCC   TGT
                                 |||| |||  ||||||   |||
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                                GGGC CCC  GGGGGG  ACA
                                  _  T_    CCC
GAM73   NPR1    3'  TGTGGGCCAGCCCCAGATGT  44593       CC    A
                                TGTGGGCT  CCCCA ATGT
                                |||||||| |||||| ||||
                                ACACCCGG  GGGGT TACA
                                    TC    C
GAM73   NRIP1   5'  CTGTGTTTCTCCCAAATGT   40962     GGC  CC
                                CTGTG  TC  CCCAAATGT
                                |||||  ||  |||||||||
                                GACAC  AG  GGGTTTACA
                                  AA_  A_
GAM73   SIRPB2  3'  CCTGTGGGCAGGCAGATGT   38896       TCCCCC  A
                                CCTGTGGGC    CA ATGT
                                |||||||||    || ||||
                                GGACACCCG    GT TACA
                                     TCC___  C
GAM73   SIRPB2  3'  CCTGTGGGCAGGCAGATGT   32996       TCCCCC  A
                                CCTGTGGGC    CA ATGT
                                |||||||||    || ||||
                                GGACACCCG    GT TACA
                                     TCC___  C
GAM73   TPSB1   5'  ACCCAGTGGGCTCTCCCC   17657     T      C
                                ACCC GTGGGCTC CCCC
                                |||| |||||||| ||||
                                TGGG CACCCGAG GGGG
                                  T      A
GAM74   CA14    3'  TCCAGGGGAAGGAGG     29060    G  A  GCTAGC
                                TC CAG GGA    AGGAGG
                                || ||| |||    ||||||
                                AG GTC CCT    TCCTCC
                                 _  C  _______
GAM74   CLASP1  5'  GCAGGGCTTTCTGGTAGGAGGA 42241     A  AG__  AGC
          C                      GCAG GG   CT  AGGAGGAC
                                |||| ||   ||  ||||||||
                                CGTC CC   GA  TCCTCCTG
                                  _ GAAA  CCA
GAM74   CLECSF11 5' TCGCGGCCTGAGGCAGGAGG  39042    AGAG_  CTA
                                TCGC   GAG  GCAGGAGG
                                ||||   |||  ||||||||
                                AGCG   CTC  CGTCCTCC
                                  CCGGA  ___
GAM74   CYP24   5'  CGCGGGAAGGCAGGAGGA   8943    AGA   CTA
                                CGC  GGAG  GCAGGAGGA
                                |||  ||||  |||||||||
                                GCG  CCTT  CGTCCTCCT
                                 C__   C__
GAM74   FABP2   3'  GAGAGGCTGAGGCAGGAGGA  6586    GA  A__
                                GAG  GCT  GCAGGAGGA
                                |||  |||  |||||||||
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                                CTC  CGA   CGTCCTCCT
                                  TC   CTC
GAM74   GPR4     3'  GGAGGCCAAGGCAGGAGGA   40887     _   __
                                GGAG CTA  GCAGGAGGA
                                |||| |||  |||||||||
                                CCTC GGT  CGTCCTCCT
                                  C   TC
GAM74   INPP5B   3'  GCAGAGGAACTGGTGAA     45472          AGCA  A
                                GCAGAGGAGCT   GG GGA
                                ||||||||||    || |||
                                CGTCTCCTTGA   CC CTT
                                      ____ A
GAM74   ISLR     3'  GCAGAGGAGCAGACAACAGA  24435          TA   G
                                GCAGAGGAGC  GCAG AGG
                                ||||||||||  |||| |||
                                CGTCTCCTCG  TGTT TCT
                                      TC   G
GAM74   JPH3     5'  CCGGAGGAGAGGAGGA     34015     CA     CTAGC
                                TCG  GAGGAG    AGGAGGA
                                |||  ||||||    |||||||
                                GGC  CTCCTC    TCCTCCT
                                 __    _____
GAM74   KRTHA8   5'  CAGTGGTGTAGCAGGAGGAC  27668     A  AGC
                                CAG GG   TAGCAGGAGGAC
                                ||| ||   ||||||||||||
                                GTC CC   ATCGTCCTCCTG
                                  A  AC_
GAM74   LIMD1    3'  TCCCAGAGGGGACAGGAGGA  30636    G     AGCTA
                                TC CAGAGG    GCAGGAGGA
                                || ||||||    |||||||||
                                AG GTCTCC    TGTCCTCCT
                                 G     CC___
GAM74   LPIN1    3'  CGCAGAGGAGTTAGTTAAGG  42636          C   CAG
                                CGCAGAGGAG TAG   GAGG
                                |||||||||| |||   ||||
                                GCGTCTCCTC ATC   TTCC
                                      A   AA_
GAM74   MAP2K2   3'  CCGCAGGGGTGAGGCAGGAGG  36207       A  AGCTA
                                TCGCAG GG    GCAGGAGG
                                |||||| ||    ||||||||
                                GGCGTC CC    CGTCCTCC
                                   _  CACTC
GAM74   NOTCH2   3'  GCAGGAAGTAGGGGGA     35908     A   C   CA  A
                                GCAG GGAG TAG  GG GGA
                                |||| |||| |||  || |||
                                CGTC CTTC ATC  CC CCT
                                  _   _   __  _
GAM74   NRXN2    5'  TCGCGAGGAGCTAGGGG     39833     A        CA
                                TCGC GAGGAGCTAG  GG
                                |||| ||||||||||  ||
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                                AGCG CTCCTCGATC  CC
                                  _        C_
GAM74   PACSIN3  3' GCAGAAGGGCTGTCAGGA    32142        A   AG
                                GCAGAGG GCT  CAGGA
                                ||||||| |||  |||||
                                CGTCTTC CGA  GTCCT
                                    C   CA
GAM74   RB1      3' GCAGAAGAGTTCAGGA      44935         CTAG
                                GCAGAGGAG   CAGGA
                                |||||||||   |||||
                                CGTCTTCTC   GTCCT
                                     AA__
GAM74   SAS      3' GGAGACTGAGGCAGGAGGA   25588      _ A__
                                GGAG CT   GCAGGAGGA
                                |||| ||   |||||||||
                                CCTC GA   CGTCCTCCT
                                  T  CTC
GAM74   SLC22A1LS 5' TCGCAGAGAGTGGGGG     28257        GAGCT  CA  A
                                TCGCAGAG    AG  GG GG
                                ||||||||    ||  || ||
                                AGCGTCTC    TC  CC CC
                                     _____  AC  _
GAM74   SOX4     5' TCGCAGAGGAGTTATAG     16992          C  GC
                                TCGCAGAGGAG TA  AG
                                |||||||||| ||  ||
                                AGCGTCTCCTC AT  TC
                                      A  A_
GAM74   UMPS     3' GAGAGACTGAGGCAGGAGGA  7502      GA   A__
                                GAG  GCT   GCAGGAGGA
                                |||  |||   |||||||||
                                CTC  TGA   CGTCCTCCT
                                  TC   CTC
GAM74   VAV2     3' TCACAGAGGAGCTAGAGA    17921            C
                                TCGCAGAGGAGCTAG AGG
                                |||||||||||||| |||
                                AGTGTCTCCTCGATC TCT
                                          _
GAM74   ZNF142   5' CCGGGGGGAGCCAAGGAGGAC  22927     CAGA      GC
                                TCG   GGAGCTA  AGGAGGAC
                                |||   |||||||  ||||||||
                                GGC   CCTCGGT  TCCTCCTG
                                  CCC_      __
GAM74   ACTG2    3' GAGTAGTCTCGAGGGGATC    11517      TC      A
                                GAGTA  CTCGAGG GGATT
                                |||||  ||||||| |||||
                                CTCAT  GAGCTCC CCTAG
                                   CA      _
GAM74   APBA1    3' GAGGTCCTTGTGGATTCTT    43088     TA   CGAGGA
                                GAG  TCCT     GGATTCTT
                                |||  ||||     ||||||||
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                                CTC  AGGA     CCTAAGAA
                                  C_   ACA___
GAM75   BRCA1    3'  GAAACAGAACTACCCTGAT   28633       AA   GG
                                GAGACA  AAT  TCCTGAT
                                ||||||  |||  |||||||
                                CTTTGT  TTG  GGGACTA
                                   C_   AT
GAM75   BRCA1    5'  GAAACAGAACTACCCTGAT   28633       AA   GG
                                GAGACA  AAT  TCCTGAT
                                ||||||  |||  |||||||
                                CTTTGT  TTG  GGGACTA
                                   C_   AT
GAM75   CLC      3'  CGAGGCAAGGTCCTGAT     29896      A   AAAT
                                CGAG CAA    GGTCCTGAT
                                ||||  |||    |||||||||
                                GCTC GTT    CCAGGACTA
                                  C  _____
GAM75   CNGA3    3'  GAGACAAAAAGTCCCA      10536         AT
                                GAGACAAAA  GGTCCTG
                                |||||||||  |||||||
                                CTCTGTTTT  TCAGGGT
                                      __
GAM75   FANCF    3'  GACAAAAATATCTTGAT     35534         G  C
                                GACAAAAATG TC TGAT
                                |||||||||| || ||||
                                CTGTTTTTAT AG ACTA
                                      _  A
GAM75   GSTA4    3'  GACAAAAAAGGTTGAT      11323        T   CC
                                GACAAAAA GGT  TGAT
                                |||||||| |||  ||||
                                CTGTTTTT CCA  ACTA
                                     T  __
GAM75   KIF5C    3'  GAGAACATGGTCCTGAT     21152      CAAAA
                                GAGA    ATGGTCCTGAT
                                ||||    ||||||||||
                                CTCT    TACCAGGACTA
                                  TG___
GAM75   MID1     3'  GAGACAAAAGGAAAATTGAT   37784         AT  TCC__
                                GAGACAAAA  GG    TGAT
                                |||||||||  ||    ||||
                                CTCTGTTTT  CC    ACTA
                                      __  TTTTA
GAM75   MYCL2    3'  GAGGTAATGGTCCACGTTGAT  23901     ACAAA      ____
                                GAG    AATGGTCC    TGAT
                                |||    ||||||||    ||||
                                CTC    TTACCAGG    ACTA
                                  CA___       TGCA
GAM75   NINJ1    3'  GAGACAGAGGCTGGCCCTG    19984       AAAA_
                                GAGACA    TGGTCCTG
                                ||||||    ||||||||
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                                CTCTGT    ACCGGGAC
                                   CTCCG
GAM75   RAD17   3' GAAACAAAAATGAAGCTG   39410          TC
                                GAGACAAAAATGG CTG
                                |||||||||||| |||
                                CTTTGTTTTTACT GAC
                                      TC
GAM75   RORB    3' AAAACAAAATCCTGAT    27918       AATG
                                GAGACAAA   GTCCTGAT
                                ||||||||   ||||||||
                                TTTTGTTT   TAGGACTA
                                    ____
GAM75   SCA7    5' GAGACACGATCCTG      7308       AAAA
                                GAGACA   TGGTCCTG
                                ||||||   ||||||||
                                CTCTGT   GCTAGGAC
                                    ____
GAM75   TCP10   3' CAAGGCAGAAATGGCCCC   21426     A A
                                CGAG CA AAATGGTCCT
                                |||| || ||||||||||
                                GTTC GT TTTACCGGGG
                                  C C
GAM75   TCTA    3' AAGACAAAAGAACTGAT    35275       AAT TC
                                GAGACAAA GG CTGAT
                                |||||||| || |||||
                                TTCTGTTT TC GACTA
                                   ___ TT
GAM75   TGM4    3' GAGACAATGGTGGCCCTGAT 17464       AAA
                                GAGACAA TGGTCCTGAT
                                ||||||| ||||||||||
                                CTCTGTT ACCGGGACTA
                                    ACC
GAM75   TMOD2   3' GATAAAATGGTCCTGAT    30968   CA
                                GA AAAATGGTCCTGAT
                                || ||||||||||||||
                                CT TTTTACCAGGACTA
                                 A_
GAM75   BMP7    3' GGCCCCAAAGGGTCTGAATTC 11874       _   CA
                                GGTCTCAA GGGTC AATTC
                                |||||||| ||||| |||||
                                CCGGGGTT CCCAG TTAAG
                                     T   AC
GAM75   DUSP4   5' TGACGGTCTAAAGGGTCAAATT 38428       C     C
                                TGACGGTCT AAGGGTC AAATT
                                ||||||||| ||||||| |||||
                                ACTGCCAGA TTCCCAG TTTAA
                                      T     _
GAM76   BHLHB3  3' AGGATATATCAGTTTGGACTTG 36257     GCTC_  C
           T                     AGGA    CAG TTGGACTTGT
                                ||||    ||| ||||||||||
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                                TCCT    GTC AACCTGAACA
                                  ATATA  A
GAM77   AOAH    3'  GGGCCTGTGACGTGGTCCCTCG 45021        G  A_______  TGAG
                                GGGCCTGTG AC      CC   G
                                ||||||||| ||      ||   |
                                CCCGGACAC TG      GG   C
                                     _ CACCIIIA  GAGT
GAM77   ARF3    3'  GGGCATGTGGACATGATCCCTC 11675     C     A_______  TGAG
          G                      GGGC TGTGGAC      CC   G
                                |||| |||||||      ||   |
                                CCCG ACACCTG      GG   C
                                  T     TACTIIIA  GAGT
GAM77   ARF5    3'  AGGCCTGTGGCTATGGGGGA  11681        ACACC  A
                                GGGCCTGTGG    TG GGGA
                                ||||||||||    || ||||
                                TCCGGACACC    AC CCCT
                                     GAT__  C
GAM77   ARHGDIA 3'  GGGCCTGTGGGTGGGGG    20210        ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACC    AC CCC
                                     C____  C
GAM77   ATRN    3'  GGGCCTGTGGGAATTAAGGG  40276        ACACC
                                GGGCCTGTGG    TGAGGG
                                ||||||||||    ||||||
                                CCCGGACACC    ATTCCC
                                     CTTA_
GAM77   BCLG    3'  GGGCTTTTGGACACCTTGGGG  39823    CTG       GA
                                GGGC  TGGACACCT  GGG
                                ||||  |||||||||  |||
                                CCCG  ACCTGTGGA  CCC
                                  AAA       AC
GAM77   BMP1    3'  GGGCCTGTAGGGAGGAGTGGGG 25986        ACACC__  A
          GA                    GGGCCTGTGG     TG GGGA
                                ||||||||||     || ||||
                                CCCGGACATC     AC CCCT
                                     CCTCCTC  C
GAM77   CDH5    5'  GCCTGTGGGGCTGAGGGA    12187       ACAC
                                GCCTGTGG   CTGAGGGA
                                ||||||||   ||||||||
                                CGGACACC   GACTCCCT
                                    CC__
GAM77   COL18A1 3'  GGCCTGTGGGCACCCCGGG   39058       A   GA
                                GGCCTGTGG CACCT  GGG
                                ||||||||| |||||  |||
                                CCGGACACC GTGGG  CCC
                                     C    G_
GAM77   CRYAA   3'  GGGTCTGGGACACCCTGA    7565     C  T    _
                                GGG CTG GGACACC TGA
                                ||| ||| ||||||| |||
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                                CCC GAC CCTGTGG ACT
                                  A  _     G
GAM77   DVL1    3'  GGGCCTGTGCACCGCAGGG   40413        GA   TG
                                GGGCCTGTG  CACC  AGGG
                                |||||||||  ||||  ||||
                                CCCGGACAC  GTGG  TCCC
                                     __    CG
GAM77   ENG     3'  GGTTCTGTGGGGTGGAGGGA  6504     GC     ACACCT
                                GG  CTGTGG     GAGGGA
                                ||  ||||||     ||||||
                                CC  GACACC     CTCCCT
                                 AA     CCAC__
GAM77   EPHB3   3'  AGGTCTGGGCCCTGAGGG    20784     C   T  ACA
                                GGG CTG GG   CCTGAGGG
                                ||| ||| ||   ||||||||
                                TCC GAC CC   GGACTCCC
                                  A  _ G__
GAM77   FBXL7   3'  GGGCCTGTGTGCGAGGG     29410        GACACC
                                GGGCCTGTG     TGAGGG
                                |||||||||     ||||||
                                CCCGGACAC     GCTCCC
                                     AC_____
GAM77   FGFR1   3'  GCCTGTGGCAGGGAGGG     31942        A  CCT
                                GCCTGTGG CA   GAGGG
                                |||||||| ||   |||||
                                CGGACACC GT   CTCCC
                                     _  CC_
GAM77   GAMT    5'  GGGCTTGTGGGCCGGGG     6683       C    ACAC   A
                                GGGC TGTGG    CTG GGG
                                |||| |||||    ||| |||
                                CCCG ACACC    GGC CCC
                                  A    C___   _
GAM77   GPR4    5'  GGTCTGTGGACGGCAGGA    40890    C       ACCTGA
                                GG CTGTGGAC     GGGA
                                || ||||||||     ||||
                                CC GACACCTG     TCCT
                                 A       CCG___
GAM77   GRB7    3'  GGGCTGTTTTCTATCTGAGGGA 23642      C   GGACAC_
                                GGGC TGT      CTGAGGGA
                                |||| |||      ||||||||
                                CCCG ACA      GACTCCCT
                                  _   AAAGATA
GAM77   GZMM    3'  GGTCCTGTGGAGACAGCGAGGG 23696    G       C  C_
                                GG CCTGTGGA AC  TGAGGG
                                || |||||||| ||  ||||||
                                CC GGACACCT TG  GCTCCC
                                 A       C  TC
GAM77   IARS    5'  GGGCGTACCTGAGGG       30201      CT  GGAC
                                GGGC  GT    ACCTGAGGG
                                ||||  ||    |||||||||
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                                CCCG  CA    TGGACTCCC
                                  __  _____
GAM77   IDH3B    3'  GGGCCTATGGGTGGG       27902          ACACC  A
                                GGGCCTGTGG     TG GG
                                ||||||||||     || ||
                                CCCGGATACC     AC CC
                                     C_____  _
GAM77   KIF5B    5'  GGGCTTGTGGTCGCGAGGG   21139      C    ACACC
                                GGGC TGTGG     TGAGGG
                                |||| |||||     ||||||
                                CCCG ACACC     GCTCCC
                                  A     AGC__
GAM77   KLK4     3'  GGGCCTGAGGGAGGAGGG    41750        T_   CACCT
                                GGGCCTG  GGA    GAGGG
                                |||||||  |||    |||||
                                CCCGGAC  CCT    CTCCC
                                    TC   C_____
GAM77   KLK4     3'  GGGTCTGAGGGAGGAGGG    41753     C   T_   CACCT
                                GGG CTG  GGA    GAGGG
                                |||  |||  |||    |||||
                                CCC GAC  CCT    CTCCC
                                  A   TC   C_____
GAM77   KRT6A    3'  GGGCCTGAGGACTGTGGGA   24476        T    ACC  A
                                GGGCCTG GGAC   TG GGGA
                                ||||||| ||||   || ||||
                                CCCGGAC CCTG   AC CCCT
                                    T    ____ A
GAM77   L1CAM    3'  GGGCCTGCTGGAGAGGG     35804         _    CACCT
                                GGGCCTG TGGA    GAGGG
                                ||||||| ||||    |||||
                                CCCGGAC ACCT    CTCCC
                                    G    ______
GAM77   LARS2    3'  AGGCAACATCTGGGGG      31671      CTGTG   C   A
                                GGGC    GACA CTG GGG
                                ||||    |||| ||| |||
                                TCCG    TTGT GAC CCC
                                  ______   A   C
GAM77   LPO      3'  GGCCCTGTGGACCAAAGGGA  42741    G       ACCT
                                GG CCTGTGGAC    GAGGGA
                                || |||||||||    ||||||
                                CC GGACACCTG    TTCCCT
                                  G       GT__
GAM77   MMP19    3'  GCCCGTACCTGAGGGA      35587       GGAC
                                GCCTGT    ACCTGAGGGA
                                ||||||    ||||||||||
                                CGGGCA    TGGACTCCCT
                                     ____
GAM77   MMP2     3'  GGGCCTGTGGGAGCCAGGG   21200          ACA  TG
                                GGGCCTGTGG   CC  AGGG
                                ||||||||||   ||  ||||
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                                CCCGGACACC  GG  TCCC
                                     CTC  __
GAM77  NAGA    3'  AGGTTTGTGGACACATCTGGGG 7034     CC       __  A
          A                   GGG  TGTGGACAC  CTG GGGA
                              |||  |||||||||  ||| ||||
                              TCC  ACACCTGTG  GAC CCCT
                                AA       TA  _
GAM77  NYX     5'  GGACCCCTACCTGAGGG    35444       G GGAC
                              GGGCCT T   ACCTGAGGG
                              |||||| |   |||||||||
                              CCTGGG A   TGGACTCCC
                                 G ____
GAM77  PODXL   5'  AGGCCTGTGGGTGGCTCCGGA  23956         ACAC  GA
                              GGGCCTGTGG   CT  GGG
                              ||||||||||   ||  |||
                              TCCGGACACC   GA  CCT
                                    CACC  GG
GAM77  POLR2E  3'  GGGCTGTGTGGATGGAGGA   40923     C_    CACCT
                              GGGC  TGTGGA    GAGGG
                              ||||  ||||||    |||||
                              CCCG  ACACCT    CTCCT
                                AC    AC___
GAM77  PRKACA  3'  GGGCCTGTGGTTGGGTGGGA  15584         ACACCTGA
                              GGGCCTGTGG      GGGA
                              ||||||||||      ||||
                              CCCGGACACC      CCCT
                                    AACCCA__
GAM77  PSCD4   3'  GGGCCTGTGTGAGG       30128         GACACC
                              GGGCCTGTG    TGAGG
                              |||||||||    |||||
                              CCCGGACAC    ACTCC
                                   _______
GAM77  RAP1GA1 5'  AGGTCTAGTGCCTGAGGGA   16159    C  _  GACA
                              GGG CT GTG   CCTGAGGGA
                              ||| || |||   |||||||||
                              TCC GA CAC   GGACTCCCT
                                A  T  ____
GAM77  RFNG    3'  GGCCGTGGCACCTGAGGGA   44774     T   A
                              GGCC GTGG CACCTGAGGGA
                              |||| |||| ||||||||||
                              CCGG CACC GTGGACTCCCT
                                  _   _
GAM77  SCRT1   5'  GGGCCTGCGGAGCCGGGG   36368          CAC  A
                              GGGCCTGTGGA  CTG GGG
                              ||||||||||  ||| |||
                              CCCGGACGCCT  GGC CCC
                                    C__  _
GAM77  SLC21A3 3'  GGGCCTGTTGTGGGGTGGGGGA 22906        GGACACC  A
                              GGGCCTGT     TG GGGA
                              ||||||||     || ||||
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                                CCCGGACA      AC CCCT
                                    ACACCCC  C
GAM77   SLC30A3  3'  GGGCCATGTGGGGAGGG     18431      _    ACACCT
                                GGGCC TGTGG     GAGGG
                                ||||| |||||     |||||
                                CCCGG ACACC     CTCCC
                                   T    C_____
GAM77   SLC7A5   5'  GGGCCTGGGACACCCGGGA   18553       T       A
                                GGGCCTG GGACACCTG GGG
                                ||||||| ||||||||| |||
                                CCCGGAC CCTGTGGGC CCT
                                    _       _
GAM77   SMARCD1  3'  GGTCCTGCTGCTACCTGAGGG  40087    G    GGAC
                                GG CCTGT    ACCTGAGGG
                                || |||||    |||||||||
                                CC GGACG    TGGACTCCC
                                 A    ACGA
GAM77   TAZ      3'  GGGCCTGTGGTGGGGG      31770          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACC    AC CCC
                                    _____  C
GAM77   TCF7     3'  GGGCCTGTGGGGGCCCTGGGG  17323          ACA_   A
                                GGGCCTGTGG    CCTG GGG
                                ||||||||||    |||| |||
                                CCCGGACACC    GGAC CCC
                                    CCCG   _
GAM77   TIMP4    5'  GAGCCTGTGAGGTCTGGGGGA  17530          ACAC   A
                                GGGCCTGTGG    CTG GGGA
                                ||||||||||    ||| ||||
                                CTCGGACACT    GAC CCCT
                                    CCA_   C
GAM77   TP73     3'  GGGCCTGTGAGGTGCCTGGGGA 24069          ACA_   A
                                GGGCCTGTGG    CCTG GGGA
                                ||||||||||    |||| ||||
                                CCCGGACACT    GGAC CCCT
                                    CCAC    _
GAM77   TRH      3'  AGGCCTGTGGTGGGGG      28288          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                TCCGGACACC    AC CCC
                                    _____  C
GAM77   WFDC1    5'  GGGCCTGTGAGTGGGG       34524          ACACC  A
                                GGGCCTGTGG    TG GGG
                                ||||||||||    || |||
                                CCCGGACACT    AC CCC
                                    C____  _
GAM77   WNT3A    3'  GGGCTGTGGACAGGCGGA    37549      C       CCTGA
                                GGGC TGTGGACA    GGG
                                |||| ||||||||    |||
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                                CCCG ACACCTGT    CCT
                                  _      CCG__
GAM77   ZNF261   3' GGGCCTGTCACCCTGAGGGA  22991       GG  A
                                GGGCCTGT  AC CCTGAGGGA
                                ||||||||  || |||||||||
                                CCCGGACA  TG GGACTCCCT
                                    G_  _
GAM77   ARCN1    3' ATGTTTGTGCCATTTCC    11649       CCA   T
                                GTGTTTG   GCT ATTTCC
                                |||||||   ||| ||||||
                                TACAAAC   CGG TAAAGG
                                   A__   _
GAM77   ASGR2    3' TCAGTGTTTCTTCCTTTCC   38957       GCCAG   A_
                                TCAGTGTTT    CTT  TTTCC
                                |||||||||    |||  |||||
                                AGTCACAAA    GAA  AAAGG
                                     _____  GG
GAM77   BST1     5' TCGCTGTTTGCCGTTTCC    20267    AG      AGCTTA
                                TC  TGTTTGCC     TTTCC
                                ||  ||||||||     |||||
                                AG  ACAAACGG     AAAGG
                                 CG       C_____
GAM77   CYP1B1   3' TCAGTGTTTCTCTCTTTTC   6454         GCCAG   A
                                TCAGTGTTT    CTT TTTC
                                |||||||||    ||| ||||
                                AGTCACAAA    GAG AAAG
                                     GA___   A
GAM77   EIF4G2   3' TCAGTGTTGCTATTCAGTTTTC 10878       T ____   CTTA
                                TCAGTGTT GC    CAG    TTTC
                                |||||||| ||    |||    ||||
                                AGTCACAA CG    GTC    AAAG
                                    _  ATAA   A___
GAM77   IL13RA1  3' TCAATGTTTGTTGGGAATTTC  11445        CCAGCTT
                                TCAGTGTTTG      ATTTC
                                ||||||||||      |||||
                                AGTTACAAAC      TAAAG
                                     AACCCT_
GAM77   KCNJ3    3' TCAGTGTTTGTTCAGAGCTCAT 13851        CC___
           CT                    TCAGTGTTTG    AGCTTATTT
                                 ||||||||||    |||||||||
                                 AGTCACAAAC    TCGAGTAGA
                                      AAGTC
GAM78   ABCA2    3' CGGGCAGGAGAAAGGCCA    45523    A  A
                                TGG CA GAGAAAGGCCA
                                ||| || ||||||||||
                                GCC GT CTCTTTCCGGT
                                  C  C
GAM78   ARSB     3' GAGCAAGAGAAGGGCCAA    6251    GA      A
                                G  CAAGAGAA GGCCAA
                                |  |||||||| ||||||
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                                C  GTTCTCTT CCGGTT
                                 TC       C
GAM78   CYP8B1   3'  GATCATGGAAACCAAGGGAGG  20505          CAA_   AA
                                GATCATGGA    GAG  AGG
                                |||||||||    |||  |||
                                CTAGTACCT    TTC  TCC
                                     TTGG   CC
GAM78   FGF5     3'  TCAGGACTATCAAGAGGCCA   37592     T    AA__    AA
                                TCA GGAC    GAGA  GGCCA
                                ||| ||||    ||||  |||||
                                AGT CCTG    TTCT  CCGGT
                                  _    ATAG    __
GAM78   FXYD7    3'  GACATGGACACTGAGGGGCCA  35128    T       A_   AAA
                                GA CATGGACA  GAG   GGCCA
                                || ||||||||  |||   |||||
                                CT GTACCTGT  CTC   CCGGT
                                 _       GA   C__
GAM78   GYS1     3'  GATCATGGGAAAGG        44787          ACAAGA
                                GATCATGG     GAAAGG
                                ||||||||     ||||||
                                CTAGTACC     CTTTCC
                                     _______
GAM78   MUCDHL   3'  TGGACAAGGACGGCGAGGCCAA 34947          A  A____
                                TGGACAAG GA     AGGCCAA
                                |||||||| ||     |||||||
                                ACCTGTTC CT     TCCGGTT
                                     _ GCCGC
GAM78   MUCDHL   3'  TGGACAAGGACGCGAGGCCAA  34946          A  A___
                                TGGACAAG GA    AGGCCAA
                                |||||||| ||    |||||||
                                ACCTGTTC CT    TCCGGTT
                                     _ GCGC
GAM78   PIK3CG   3'  GACCAGCAGAGGAAGGTCA    15304       TGGACA    A    C
                                GATCA      AGAG AAGG CA
                                |||||      |||| |||| ||
                                CTGGT      TCTC TTCC GT
                                   CG____    C    A
GAM78   RUNX1    3'  CATAAACAGGAGAAAGGC     12013          A
                                CATGGACA GAGAAAGGC
                                |||||||| |||||||||
                                GTATTTGT CTCTTTCCG
                                     C
GAM78   SERPIND1 3'  ATCATGGATTTGAAAGGTCA   6772           CAAGA     C
                                ATCATGGA     GAAAGG CA
                                ||||||||     |||||| ||
                                TAGTACCT     CTTTCC GT
                                     AAA__      A
GAM78   TYK2     3'  GATCATGGTTAGGCTCACGGCC 40859          ACAAGAGAAA
            AA                    GATCATGG         GGCCAA
                                ||||||||         ||||||
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                                CTAGTACC        CCGGTT
                                    AATCCGAGTG
GAM78   CALU    3'  TAAAAAGTTTGTAGTAACAGTC 10261           CCTTTAT
                                TGAAAAGTTTGTAG      GTC
                                |||||||||||||      |||
                                ATTTTTCAAACATC      CAG
                                      ATTGT__
GAM78   LAMC1   3'  TGAAAAATGTAATCTTTGTGTC 14094       TT   GC   A
                                TGAAAAG  TGTA  CTTT TGTC
                                |||||||  ||||  |||| ||||
                                ACTTTTT  ACAT  GAAA ACAG
                                    __   TA   C
GAM78   PLAG1   3'  TGAAGAGTTGTAGCCCAAGT   15359     A   T     TTAT
                                TGAA AGTT GTAGCCT   GT
                                |||| |||| |||||||   ||
                                ACTT TCAA CATCGGG   CA
                                  C   _     TT__
GAM78   TES     3'  GCTTGGCTTTTATGTC     43540      TA  C
                                GTTTG  GC TTTATGTC
                                |||||  || ||||||||
                                CGAAC  CG AAATACAG
                                   __  A
GAM79   ABCC11  3'  CTTAGATGGTTCTGGGGTTC   37615     CC        C
                                CTTG  TGGTTCTGGGG TC
                                ||||  |||||||||| ||
                                GAAT  ACCAAGACCCC AG
                                  CT         A
GAM79   ADORA2A 3'  TGCTCCAGCCTGGGGCTCC   8607     _ TG  T
                                TGC C  GT CTGGGGCTCC
                                ||| |  || ||||||||||
                                ACG G  CG GACCCCGAGG
                                 A GT  _
GAM79   AGXT    3'  TGCCTGGTTCTGCCTCC     6191          GGG
                                TGCCTGGTTCTG   CTCC
                                ||||||||||||   ||||
                                ACGGACCAAGAC   GAGG
                                       G__
GAM79   ANKRD3  3'  CTTCCACGCCTGGGGCT     33965     G  TG  T
                                CTT CC  GT CTGGGGCT
                                ||| ||  || ||||||||
                                GAA GG  CG GACCCCGA
                                  _  TG  _
GAM79   BDKRB2  3'  CCTGCCGGGTTCTGGAGCC   8401       T    T___  GGCT
                                CTTGCC GGTTC    GG    C
                                |||||| |||||    ||    |
                                GGACGG CCAAG    CC    G
                                   C    AIII  TCGG
GAM79   CARKL   3'  CCTGCCTGAGCCTGGGCTCC   29991        TT    G
                                CTTGCCTGG  CTGGG CTCC
                                |||||||||  ||||| ||||
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                                GGACGGACT  GACCC GAGG
                                     CG    _
GAM79   CD5     3'  TGCTTGTTTTGGGGCTC    30548    CTG   C
                                TGC   GTT TGGGGCTC
                                |||   ||| ||||||||
                                ACG   CAA ACCCCGAG
                                  AA_   A
GAM79   CD72    3'  TGCCTGGCTGGCTC       12142        CTGG
                                TGCCTGGTT   GGCTC
                                |||||||||   |||||
                                ACGGACCGA   CCGAG
                                     _____
GAM79   CKTSF1B1 3'  TTGCTGGTTCTGAATGTC    30097     C       GC
                                TTGC TGGTTCTGGG  TC
                                |||| ||||||||||  ||
                                AACG ACCAAGACTT  AG
                                  _        AC
GAM79   CNR1    3'  TGCCTGGTGAGCTC       32004        TCTG
                                TGCCTGGT   GGGCTC
                                ||||||||   ||||||
                                ACGGACCA   CTCGAG
                                     _____
GAM79   DAP3    5'  TGCCTGGGGCCGGCTCC    21574       TT  GG
                                TGCCTGG  CT  GGCTCC
                                |||||||  ||  ||||||
                                ACGGACC  GG  CCGAGG
                                    CC  __
GAM79   DLEC1   3'  CTTGCAGTCCCTGGGGCT   28845     CT    _
                                CTTGC  GGTTC TGGGGCT
                                |||||  ||||| |||||||
                                GAACG  TCAGG ACCCCGA
                                  __    G
GAM79   DUOX2   3'  CTGCCTGGGACTGATGGGG   30444        TT ___
                                TTGCCTGG  CT   GGGG
                                ||||||||  ||   ||||
                                GACGGACC  GA   CCCC
                                     CT  CTA
GAM79   EGFL6   5'  GCCTGGCCGAGGCTCC     31776       TT
                                GCCTGG  CTGGGGCTCC
                                ||||||  ||||||||||
                                CGGACC  GGCTCCGAGG
                                     __
GAM79   ENTPD5  3'  CTTTTTGGCTCACAGGGCTC  10352    GCC    _
                                CTT   TGGTTC TGGGGCTC
                                |||   |||||| ||||||||
                                GAA   ACCGAG GTCCCGAG
                                  AA_     T
GAM79   EPHA2   3'  CTTGGCCGATGGGGCTCC    20736     C   TTC
                                CTTG CTGG   TGGGGCTCC
                                |||| ||||   |||||||||
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                                GAAC GGCT   ACCCCGAGG
                                  C   ___
GAM79   ESRRA    5'  CTGGTCACCTGGGGCTCC    20828       __
                                CTGGTT  CTGGGGCTCC
                                ||||||  ||||||||||
                                GACCAG  GACCCCGAGG
                                   TG
GAM79   F9       3'  CTTGCTTGGCTCTGAACACT   6574       C       _
                                CTTGC TGGTTCTGGG GCT
                                ||||| |||||||||| |||
                                GAACG ACCGAGACTT TGA
                                  A         G
GAM79   GAB2     3'  TGCCTGTCCCAGGGTTCC    38686       G   TG   C
                                TGCCTG TTC  GGG TCC
                                |||||| |||  ||| |||
                                ACGGAC AGG  CCC AGG
                                   _  GT   A
GAM79   GALNT2   3'  TTGTTTGGTTCTGACCC     21012     CC      GG
                                TTG  TGGTTCTG  GCTC
                                |||  ||||||||  ||||
                                AAC  ACCAAGAC  TGGG
                                  AA      __
GAM79   GPC1     3'  CTTGCCTGTGTTGGGGGCTCC  13244         _  CT
                                CTTGCCTG GTT  GGGGCTCC
                                |||||||| |||  ||||||||
                                GAACGGAC CAA  CCCCGAGG
                                     A   C_
GAM79   GRLF1    3'  CTTCCTGTGCATGGGGGCTCC  44227     G   _  TCT
                                CTT CCTG GT   GGGGCTCC
                                |||  |||| ||   ||||||||
                                GAA GGAC CG   CCCCGAGG
                                  _   A  TAC
GAM79   HD       3'  CTTGCCTGGCTCGCC       13349           TGGG
                                CTTGCCTGGTTC    GCT
                                ||||||||||||    |||
                                GAACGGACCGAG    CGG
                                          _____
GAM79   HMGB2    5'  CTTCCCTCACGGGGCTCC    13407     G   G TTC
                                CTT CCT G   TGGGGCTCC
                                |||  ||| |   |||||||||
                                GAA GGA T   GCCCCGAGG
                                  G   G ___
GAM79   HR       5'  CCTGCCCTCATGGGGCTC    32914       GGT  _
                                CTTGCCT   TC TGGGGCTC
                                |||||||   || ||||||||
                                GGACGGG   AG ACCCCGAG
                                     ___  T
GAM79   IL11RA   3'  CCTGCCTGGTTTCTATCC    21091          _  GGGC
                                CTTGCCTGGTT CTG    TCC
                                |||||||||| |||    |||
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                                GGACGGACCAA GAT    AGG
                                      A  ____
GAM79   IRAK1    3'  CTGCCTTCCAGGGGCT     11472       GG   T
                                TTGCCT  TTC GGGGCT
                                ||||||  ||| ||||||
                                GACGGA  AGG CCCCGA
                                   __   T
GAM79   ITGAL    3'  TGCTTGGCACTGGGGCTCC   13626     C    T
                                TGC TGGT CTGGGGCTCC
                                ||| |||| ||||||||||
                                ACG ACCG GACCCCGAGG
                                  A    T
GAM79   ITPKB    3'  CTTCCTAGGGGGCTC      13644     G    TTCT
                                CTT CCTGG    GGGGCTC
                                ||| |||||    |||||||
                                GAA GGATC    CCCCGAG
                                  _    _____
GAM79   JRK      5'  TGCTCCCCTTCTGGGGCTCC  44504     _  GG
                                TGC CT  TTCTGGGGCTCC
                                ||| ||  ||||||||||||
                                ACG GG  AAGACCCCGAGG
                                  A  GG
GAM79   KCNA7    3'  TTGTTGAGACGGGGGCTCC   36663     CC   TTCT
                                TTG  TGG    GGGGCTCC
                                |||  |||    ||||||||
                                AAC  ACT    CCCCGAGG
                                  A_   CTGC
GAM79   KEL      5'  CTTCCTGGTTCCACTC      7679      G       GGG
                                CTT CCTGGTTCT   GCTC
                                ||| |||||||||   ||||
                                GAA GGACCAAGG   TGAG
                                  _       ____
GAM79   LAD1     3'  CTTGGTTGGTTCTAGATTC   24489      CC        GC
                                CTTG  TGGTTCTGGG  TC
                                ||||  ||||||||||  ||
                                GAAC  ACCAAGATCT  AG
                                   CA         A_
GAM79   LDHB     5'  CTTGCCTGGTGGGCTCC     14119          TCTG
                                CTTGCCTGGT    GGGCTCC
                                ||||||||||    |||||||
                                GAACGGACCA    CCCGAGG
                                      _____
GAM79   LOH11CR2A 5'  CTGGCTACTCATGGGGCTC   31189       ____ _
                                CTGGT   TC TGGGGCTC
                                |||||   || ||||||||
                                GACCG   AG ACCCCGAG
                                   ATG  T
GAM79   LZTS1    3'  TCGTCCTGCTTGGGGCTC    34275     _   G TC
                                TTG CCTG T  TGGGGCTC
                                ||| |||| |  ||||||||
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                                AGC GGAC A  ACCCCGAG
                                  A   G __
GAM79   MAN2B1   5' CTTCCTCCTGGGGTTC     8032     G  GGT     C
                                CTT CCT   TCTGGGG TC
                                ||| |||   ||||||| ||
                                GAA GGA   GGACCCC AG
                                  _  ___      A
GAM79   MAP1B    5' TTGTGTGGTCGGGGGCTCC   25401    CC    CT
                                TTG  TGGTT  GGGGCTCC
                                |||  |||||  ||||||||
                                AAC  ACCAG  CCCCGAGG
                                  AC    C_
GAM79   MAPK10   5' TGTTTGGTTCTGAAAGGGTC  39984    CC      ___  C
                                TG  TGGTTCTG   GGG TC
                                ||  ||||||||   ||| ||
                                AC  ACCAAGAC   CCC AG
                                 AA       TTT  _
GAM79   MAPK7    5' TTGCTTGGTCCCAGGAGCTC  40046     C     TG  _
                                TTGC TGGTTC  GG GCTC
                                |||| ||||||  || ||||
                                AACG ACCAGG  CC CGAG
                                  A     GT  T
GAM79   MAT1A    3' TGCCTGGCCTGGGTGGGGCT  44907         C___
                                TGCCTGGTT    TGGGGCT
                                |||||||||    |||||||
                                ACGGACCGG    ACCCCGA
                                     ACCC
GAM79   MSI1     3' CCTGCGGCCTGGGGCT     14638      CT   T
                                CTTGC  GGT CTGGGGCT
                                |||||  ||| ||||||||
                                GGACG  CCG GACCCCGA
                                  __  _
GAM79   MYCL1    3' CTTGTCCCCTGGGGCTCC    23888     _  GGTT
                                CTTG CCT    CTGGGGCTCC
                                |||| |||    ||||||||||
                                GAAC GGG    GACCCCGAGG
                                  A  ____
GAM79   NR1D1    5' TTCCCTGGGACAGAGGGCTC  34708    G    TTCT_
                                TT CCTGG    GGGGCTC
                                || |||||    |||||||
                                AA GGACC    TCCCGAG
                                 G    CTGTC
GAM79   NRCAM    3' CTTGCCTGATTTCTTAGATTC 22691          _  G  GC
                                CTTGCCTGGTT CT GG  TC
                                |||||||||| || ||  ||
                                GAACGGACTAA GA TC  AG
                                     A  A  TA
GAM79   NUCB1    3' CTGGTCTTCAGGGGCTCC    26154       CT__
                                CTGGTT    GGGGCTCC
                                ||||||    ||||||||
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                              GACCAG   CCCCGAGG
                                 AAGT
GAM79   NUP98    3' TGCCATTACCTGGGGCTCC   32236    TGGT
                              TGCC   TCTGGGGCTCC
                              ||||   ||||||||||
                              ACGG   GGACCCCGAGG
                                TAAT
GAM79   PAX2     5' TGCCTTCCCCGTGGGGCTCC  19641     GG  _
                              TGCCT  TTC TGGGGCTCC
                              |||||  ||| |||||||||
                              ACGGA  GGG ACCCCGAGG
                                 AG   C
GAM79   PCDHGA1  3' CTTCCTGCTGGGGCTC     36730    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA10 3' CTTCCTGCTGGGGCTC     36872    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA11 3' CTTCCTGCTGGGGCTC     36882    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA12 3' CTTCCTGCTGGGGCTC     36891    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA2  3' CTTCCTGCTGGGGCTC     36737    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA3  3' CTTCCTGCTGGGGCTC     33160    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA4  3' CTTCCTGCTGGGGCTC     36821    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
                              GAA GGAC   GACCCCGAG
                                _   ___
GAM79   PCDHGA5  3' CTTCCTGCTGGGGCTC     36830    G   GTT
                              CTT CCTG   CTGGGGCTC
                              ||| ||||   |||||||||
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                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGA6  3' CTTCCTGCTGGGGCTC    36837   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGA7  3' CTTCCTGCTGGGGCTC    36846   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGA8  3' CTTCCTGCTGGGGCTC    36856   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGA9  3' CTTCCTGCTGGGGCTC    36863   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGB1  3' CTTCCTGCTGGGGCTC    36899   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGB2  3' CTTCCTGCTGGGGCTC    36908   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGB3  3' CTTCCTGCTGGGGCTC    36917   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGB4  3' CTTCCTGCTGGGGCTC    36926   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGB5  3' CTTCCTGCTGGGGCTC    36935   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
                                GAA GGAC  GACCCCGAG
                                  _  ___
GAM79  PCDHGB6  3' CTTCCTGCTGGGGCTC    36941   G  GTT
                                CTT CCTG  CTGGGGCTC
                                ||| ||||  |||||||||
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                              GAA GGAC  GACCCCGAG
                                _  ___
GAM79  PCDHGB7  3' CTTCCTGCTGGGGCTC    36949   G  GTT
                              CTT CCTG  CTGGGGCTC
                              ||| ||||  |||||||||
                              GAA GGAC  GACCCCGAG
                                _  ___
GAM79  PCDHGC3  3' CTTCCTGCTGGGGCTC    37056   G  GTT
                              CTT CCTG  CTGGGGCTC
                              ||| ||||  |||||||||
                              GAA GGAC  GACCCCGAG
                                _  ___
GAM79  PCDHGC4  3' CTTCCTGCTGGGGCTC    37071   G  GTT
                              CTT CCTG  CTGGGGCTC
                              ||| ||||  |||||||||
                              GAA GGAC  GACCCCGAG
                                _  ___
GAM79  PCDHGC5  3' CTTCCTGCTGGGGCTC    37079   G  GTT
                              CTT CCTG  CTGGGGCTC
                              ||| ||||  |||||||||
                              GAA GGAC  GACCCCGAG
                                _  ___
GAM79  PFKFB4   3' CTGCTGTGGTTGGGGCTC  21289    C_  TC
                              TTGC  TGGT  TGGGGCTC
                              ||||  ||||  ||||||||
                              GACG  ACCA  ACCCCGAG
                                AC  __
GAM79  PK428    5' CTTGCCCGGAGGCGGCT   18803      TTCT _
                              CTTGCCTGG   GG GGCT
                              |||||||||   || ||||
                              GAACGGGCC   CC CCGA
                                   T___  G
GAM79  PKD2L1   3' CTTGCCTGATTCCCTTCGGAGC 32019        T_______ GGCT
          C                    CTTGCCTGGTTC     GG  C
                              ||||||||||||     ||  |
                              GAACGGACTAAG     CC  G
                                    GGAAGIII  TCGG
GAM79  PLXNA1   3' CTTGCCCGGCTACGGGCT  43621       CTG
                              CTTGCCTGGTT  GGGCT
                              ||||||||||  |||||
                              GAACGGGCCGA  CCCGA
                                    TG_
GAM79  PNUTL1   3' TGTCTGGAGGGCTCC     15436   C  TTCT
                              TG CTGG   GGGGCTCC
                              || ||||   ||||||||
                              AC GACC   TCCCGAGG
                               A  _____
GAM79  RAD9     3' CTGCCACTGGCTGGGGCT  21372     __  TT
                              TTGCC  TGG  CTGGGGCT
                              |||||  |||  ||||||||
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                              GACGG  ACC  GACCCCGA
                                TG  __
GAM79   RAP1    3'  CTTGACTGAGAAGGGCTCC   33268     C   TTCT
                              CTTG CTGG   GGGGCTCC
                              |||| ||||   ||||||||
                              GAAC GACT   TCCCGAGG
                                T   CT__
GAM79   RBP3    3'  CTGTCTGCCCTGGGGCTC    16186     C  G
                              TTG CTG TTCTGGGGCTC
                              ||| ||| ||||||||||
                              GAC GAC GGGACCCCGAG
                                A  _
GAM79   REN     5'  CTTCCCTCAGTCTGGGGCTC  8048      G  _  T
                              CTT CCT GGT CTGGGGCTC
                              ||| ||| ||| |||||||||
                              GAA GGA TCA GACCCCGAG
                                G  G  _
GAM79   RLBP1   3'  CTTGCCTGTTTTCACAGACTC  7257        G_  TG
                              CTTGCCTG  TTC  GGGCTC
                              ||||||||  |||  ||||||
                              GAACGGAC  AAG  TCTGAG
                                   AA   TG
GAM79   RNF18   3'  CTTCCTGGGATAAAGGGGTTCC 33777     G    TTCT__   C
                              CTT CCTGG     GGGG TCC
                              ||| |||||     |||| |||
                              GAA GGACC     CCCC AGG
                                _    CTATTT   A
GAM79   SFTPC   3'  CTTTCCCGTTGGGGCT     44672     G   GTTC
                              CTT CCTG   TGGGGCT
                              ||| ||||   |||||||
                              GAA GGGC   ACCCCGA
                                A   A___
GAM79   SHOX    3'  TGCCTGGGAGGCTC       27832       TTCT
                              TGCCTGG   GGGGCTC
                              |||||||   |||||||
                              ACGGACC   CTCCGAG
                                  ____
GAM79   SIGLEC11 3' CTGCCTGGTTTCCTGTGCT   38085        __   GG
                              TTGCCTGGT  TCTG  GCT
                              |||||||||  ||||  |||
                              GACGGACCA  GGAC  CGA
                                   AA   A_
GAM79   SLC22A11 3' TTGACTAAAGGGGCTCC    32967     C   TTCT
                              TTG CTGG   GGGGCTCC
                              ||| ||||   ||||||||
                              AAC GATT   CCCCGAGG
                                T   T___
GAM79   SLC28A1  3' CTTCCCTGAAGAGGGCTC    20112     G   TTCT
                              CTT CCTGG   GGGGCTC
                              ||| |||||   |||||||
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                                GAA GGACT    TCCCGAG
                                  G    TC__
GAM79   SMARCB1   3'  GCCCTGCCTGGGGCTCC     42311      G  T
                                GCCT GT CTGGGGCTCC
                                |||| || ||||||||||
                                CGGG CG GACCCCGAGG
                                  A  _
GAM79   SNK       3'  GCCTGGTTCTGGGTTCC     27362            GC
                                GCCTGGTTCTGGG  TCC
                                ||||||||||||  |||
                                CGGACCAAGACCC  AGG
                                       A_
GAM79   SPTA1     5'  CTTGCTTGGTCCTAGAATCC   17096      C         C
                                CTTGC TGGTTCTGGGG TCC
                                ||||| |||||||||| |||
                                GAACG ACCAGGATCTT AGG
                                   A          _
GAM79   TGFBR2    3'  CTGCTTGGTTCTGGAGTTC    17473      C         C
                                TTGC TGGTTCTGGGG TC
                                |||| |||||||||| ||
                                GACG ACCAAGACCTC AG
                                  A          A
GAM79   TSGA10    5'  TTGTCTGCTTCCAAAGTC     36113     C   G   TG   C
                                TTG CTG TTC  GGG TC
                                ||| ||| |||  ||| ||
                                AAC GAC AAG  TTC AG
                                  A   G   GT   _
GAM79   UBE2L3    3'  CTTTTTGGTTTTGGAGC      17826     GCC     C
                                CTT   TGGTT TGGGGC
                                |||   ||||| ||||||
                                GAA   ACCAA ACCTCG
                                  AA_    A
GAM79   XRCC5     3'  CTTGTTTTGTTAGAACTCC    34490      CCTG  TC
                                CTTG    GT  TGGGGCTCC
                                ||||    ||  |||||||||
                                GAAC    CA  ATCTTGAGG
                                  AAAA  __
GAM79   ABCB11    3'  CCCAGCAATCCCTC         19043        CCCGCC
                                CCCAGC     GATCCCTC
                                ||||||     ||||||||
                                GGGTCG     TTAGGGAG
                                  _______
GAM79   ABCC11    5'  AGCCTGTGCTTGATCCCTC    37614      CC_  C_
                                AGCC   GC  GATCCCTC
                                ||||   ||  ||||||||
                                TCGG   CG  CTAGGGAG
                                  ACA  AA
GAM79   ABL1      5'  CCCCCGCCCCGCCGCCGCCT   28704      A        A  _
                                CCCC GCCCCGCCG TC CCT
                                |||| ||||||||| || |||
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                                GGGG CGGGGCGGC GG GGA
                                  G       _ C
GAM79   ABL2    5' ACCCCTGGTCACATTCCTCC  28721     AGCCC  CG  C
                                ACCCC    CGC  AT CCTCC
                                |||||    |||  || |||||
                                TGGGG    GTG  TA GGAGG
                                   ACCA_  __  A
GAM79   ACVR1B  3' ACCTCGGTTCCTCCGGCCCCTC 33756    CCAGCC  G   AT
           CC                    ACC     CC CCG  CCCTCCC
                                |||     || |||  |||||||
                                TGG     GG GGC  GGGAGGG
                                  AGCCAA  A   CG
GAM79   ADAMTS1  3' CCTCCAGCCTTCTTGCTTTCCC 28111   _     CC___  CGA
                                CC CCAGCC    GC   TCCC
                                || ||||||    ||   ||||
                                GG GGTCGG    CG   AGGG
                                 A     AAGAA  AA_
GAM79   ADCY6   5' CCCCCGCCCCGCCGCCC    34168     A       AT
                                CCCC GCCCCGCCG  CCC
                                |||| |||||||||  |||
                                GGGG CGGGGCGGC  GGG
                                  G       __
GAM79   ADCY6   3' CCCCAGCCCTGGCCGGCC    34166        C_   AT
                                CCCCAGCCC  GCCG  C
                                |||||||||  ||||  |
                                GGGGTCGGG  CGGC  G
                                     AC    CG
GAM79   ADCY8   5' CCAGAAGCATCCCTCCC     9997      CCCC  CG
                                CCAG   GC  ATCCCTCCC
                                ||||   ||  |||||||||
                                GGTC   CG  TAGGGAGGG
                                  TT__  __
GAM79   ADD2    5' CCCAGCCCTGTCCAAGGCTCC  32726        CG_   TCC
                                CCCAGCCC   CCGA   CTCC
                                ||||||||   ||||   ||||
                                GGGTCGGG   GGTT   GAGG
                                     ACA    CC_
GAM79   ADSS    5' CCCCCGCCCCGCCGGGCC    43476     A       AT
                                CCCC GCCCCGCCG  CC
                                |||| |||||||||  ||
                                GGGG CGGGGCGGC  GG
                                  G       CC
GAM79   AP1B1   3' AGCCCCGCCTGGTCCCTCC   10033        GA_
                                AGCCCCGCC   TCCCTCC
                                |||||||||   |||||||
                                TCGGGGCGG   AGGGAGG
                                     ACC
GAM79   ASB2    5' ACCCCACCCCCCGGTCCCCCTC 32049      G   G   A__
           CC                    ACCCCA CCCC CCG   TCCCTCCC
                                |||||| |||| |||   ||||||||
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                                TGGGGT GGGG GGC   GGGGAGGG
                                  _   _  CAG
GAM79   ATSV     3'  CCCGACCCCGCTCCCTCC    20223     A      CGA
                                CCC GCCCCGC   TCCCTCC
                                ||| |||||||   |||||||
                                GGG TGGGGCG   AGGGAGG
                                  C      ___
GAM79   BCAR1    3'  ACTCCAGCCCCGTCTGGTGACC 41940    C       CC____
           C                     AC CCAGCCCCG     GATCC
                                || |||||||||     |||||
                                TG GGTCGGGGC     CTGGG
                                 A        AGACCA
GAM79   BMP4     5'  GCTCCGCGCTCCTTCCCTCCC  10193    _ _  CGA_
                                GC CC CGC    TCCCTCCC
                                || || |||    ||||||||
                                CG GG GCG    AGGGAGGG
                                 A  C   AGGA
GAM79   BTG2     3'  ACCTCCAGTTCCCTCCTCCC   27614     _   C_  G  GA
                                ACC CCAG  CCC CC  TCCC
                                ||| ||||  ||| ||  ||||
                                TGG GGTC  GGG GG  AGGG
                                  A   AA  A __
GAM79   C18orf1  3'  CCCCAGCCTCGAAGACCTTTC  41218        C  CC    CC
                                CCCCAGCC CG  GATC  TC
                                |||||||| ||  ||||  ||
                                GGGGTCGG GC  CTGG  AG
                                     A  TT    AA
GAM79   CALM3    3'  CCCCATCCCTCCTTCCC     23229      GC   G  GA
                                CCCCA  CCC CC  TCCC
                                |||||  ||| ||  ||||
                                GGGGT  GGG GG  AGGG
                                   A_   A  A_
GAM79   CAPN1    3'  CCCAGCCCCGGGGCCTCCC   23249         CCGATC
                                CCCAGCCCCG     CCTCCC
                                ||||||||||     ||||||
                                GGGTCGGGGC     GGAGGG
                                     CCC___
GAM79   CCNDBP1  5'  CCCTGCCCTGCCTCCTCC    29100     A   C   GATC
                                CCC GCCC GCC    CCTCC
                                ||| |||| |||    |||||
                                GGG CGGG CGG    GGAGG
                                  A   A   A___
GAM79   CCT3     3'  CCCCAACCTGATCCCT      42865        CCGCC
                                CCCCAGCC    GATCCCT
                                ||||||||    |||||||
                                GGGGTTGG    CTAGGGA
                                     A_____
GAM79   CDC25A   5'  CCCCGCCCCGCCGACACC    12146      A        TC
                                CCCC GCCCCGCCGA  CC
                                |||| ||||||||||  ||
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                                GGGG CGGGGCGGCT  GG
                                  _       GT
GAM79   CDK3    5'  ACCCCAGCCCAGCGCTCCC   10377        C  CGA
                                ACCCCAGCCC GC   TCCC
                                |||||||||| ||   ||||
                                TGGGGTCGGG CG   AGGG
                                     T  CG_
GAM79   CDKN1B  3'  GCCCCACCCTGCCCTCCC    19801       GAT
                                GCCCCGCC   CCCTCCC
                                ||||||||   |||||||
                                CGGGGTGG   GGGAGGG
                                    GAC
GAM79   CDKN2C  5'  CCGCAGCCCCGCCGAGCC    38559    C        T
                                CC CAGCCCCGCCGA CC
                                || ||||||||||| ||
                                GG GTCGGGGCGGCT GG
                                 C          C
GAM79   CDKN2C  5'  CCGGCCCCGCCAGGTCCC    38560    A       A_
                                CC GCCCCGCCG  TCCC
                                || |||||||||  ||||
                                GG CGGGGCGGT  AGGG
                                 C        CC
GAM79   CDKN2D  5'  ACCCCGGCCCTCCCGGCGGGCT 38608      A   CG   ATCC_
          CC                      ACCCC GCCC  CCG    CTCC
                                |||||  ||||  |||    ||||
                                TGGGG CGGG  GGC    GAGG
                                  C   AG   CGCCC
GAM79   CDX2    5'  GCCTCCGAGGCGGTCCCTCCC  10406    _  C__  A
                                GCC CCG   CG TCCCTCCC
                                ||| |||   || ||||||||
                                CGG GGC   GC AGGGAGGG
                                  A   TCC  C
GAM79   CEBPA   3'  CAGCCCCAAGAATTCTCCC   20385       CC  TCC
                                CAGCCCCG  GA   CTCCC
                                ||||||||  ||   |||||
                                GTCGGGGT  CT   GAGGG
                                     T_  TAA
GAM79   CEBPD   5'  CCCAGCCCCGCCGCCT     45513          ATC
                                CCCAGCCCCGCCG   CCT
                                ||||||||||||   |||
                                GGGTCGGGGCGGC   GGA
                                                ___
GAM79   CGB     5'  CCCCAGCCCTCTCCTCTC    8825         CGCCGA  _
                                CCCCAGCCC     TCC CTC
                                |||||||||     ||| |||
                                GGGGTCGGG     AGG GAG
                                     AG____   A
GAM79   CHRNA4  3'  CCTGGCCCCGCCCCTC     8849     CA      GATC
                                CC  GCCCCGCC   CCTC
                                ||  ||||||||   ||||
```

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                                GG  CGGGGCGG   GGAG
                                 AC      _____
GAM79   CRHR1    3'  CCTCCAGCCCCCATCTTCTC  20439    _      GCCG   C_
                                CC CCAGCCCC   ATC  CTC
                                || ||||||||   |||  |||
                                GG GGTCGGGG   TAG  GAG
                                 A      G___   AA
GAM79   CRYBB3   3'  CCCCAACCCTGGAGCCTCC   19837        CGCC  TC
                                CCCCAGCCC   GA  CCTCC
                                |||||||||   ||  |||||
                                GGGGTTGGG   CT  GGAGG
                                      AC__  C_
GAM79   CSNK1G2  3'  CCCCACCCCTGCCTTCCC    10608      G   C   GA
                                CCCCA CCC GCC  TCCC
                                ||||| ||| |||  ||||
                                GGGGT GGG CGG  AGGG
                                   G   A   A_
GAM79   CSRP1    3'  CCCAGCCCTTTCCCCTTCC   19839        CGCCGA    _
                                CCCAGCCC     TCCCT CC
                                ||||||||     ||||| ||
                                GGGTCGGG     GGGGA GG
                                     AAA___     A
GAM79   CUL5     3'  ACCCCACCCTCACCCTTCC   18491       G   _   GA
                                ACCCCA CCC CGCC  TCC
                                |||||| ||| ||||  |||
                                TGGGGT GGG GTGG  AGG
                                   _  A   GA
GAM79   CYP11A   3'  CCCCACCCCTGGGCCTTCCTCC 8939       G   ____   GATC
           C                     CCCCA CCCC   GCC    CCTCCC
                                ||||| ||||   |||    ||||||
                                GGGGT GGGG   CGG    GGAGGG
                                   _    ACC   AA__
GAM79   CYP21A2  5'  AGCCCCAGCCATCCCTCC    7980        _  G
                                AGCCCC GCC ATCCCTCC
                                |||||| ||| ||||||||
                                TCGGGG CGG TAGGGAGG
                                   T   _
GAM79   DEDD     3'  CCCAGCCCCATTCTCCC     37426          CCGA
                                CCCAGCCCCG    TCCC
                                |||||||||    ||||
                                GGGTCGGGGT    AGGG
                                     AAG_
GAM79   DLG4     3'  ACCCCTGCCCCACCCTCCC   10698      A       GA
                                ACCCC GCCCCGCC  TCCC
                                ||||| ||||||||  ||||
                                TGGGG CGGGGTGG  AGGG
                                   A       G_
GAM79   DMPK     3'  CCCGGCCCCTCCCTCC      20609     A    GCCGA
                                CCC GCCCC    TCCCTCC
                                ||| |||||    |||||||
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                                GGG CGGGG    AGGGAGG
                                  C   _____
GAM79   DNAJB1   3'  CCAACTCCCCTTCCCTCCC   26029      C  G  GA
                                CCAGC CC CC  TCCCTCCC
                                |||||| || ||  ||||||||
                                GGTTG GG GG  AGGGAGGG
                                  A  _  A_
GAM79   DPYSL3   3'  ACCCCAGCCCCTCTGCACCC  10759          GCCGAT
                                ACCCCAGCCCC     CCC
                                ||||||||||     |||
                                TGGGGTCGGGG     GGG
                                      AGACGT
GAM79   DSCR3    5'  CCCCGCCCCTTTCCCTC     25822      A    GCCGA
                                CCCC GCCCC    TCCCTC
                                |||| |||||    ||||||
                                GGGG CGGGG    AGGGAG
                                  _    AA___
GAM79   DVL1     3'  ACCCTGCGGGCCATGGTCCCTC 40404     CA  CCC   A__
            CC                    ACCC  GC   GCCG   TCCCTCCC
                                |||| ||  ||||  ||||||||
                                TGGG  CG   CGGT   AGGGAGGG
                                  A_  CC_   ACC
GAM79   EDAR     5'  AGCCCCGCTTCCTTTCC     35300        CGA   C_
                                AGCCCCGC   TCC  TCC
                                ||||||||   |||  |||
                                TCGGGGCG   AGG  AGG
                                    A__   AA
GAM79   EEF2     3'  CCCATCCCGCCTCCC      45411      GC     GA
                                CCCA  CCCGCC  TCCC
                                ||||  ||||||  ||||
                                GGGT  GGGCGG  AGGG
                                  A_     __
GAM79   EFNA3    3'  GCCCCGCCCCATCTCTCC    22399        _ G   C
                                GCCCCGC C ATC CTCC
                                ||||||| | ||| ||||
                                CGGGGCG G TAG GAGG
                                    G G   A
GAM79   EFNB2    3'  CCCCAGCCCCACTCCCT     19879           CGA
                                CCCCAGCCCCGC   TCCCT
                                ||||||||||||   |||||
                                GGGGTCGGGGTG   AGGGA
                                      ____
GAM79   EGLN2    5'  ACCCCAGCCCTGCTATGTTTCC 38810          C  CGATC__
            TCC                   ACCCCAGCCC GC      CCTCC
                                ||||||||||  ||      |||||
                                TGGGGTCGGG CG      GGAGG
                                    A  ATACAAA
GAM79   EIF4A1   3'  CCCTTGGCTCCCTTCCCTCCC  10867     CA_  _   GCCGA
                                CCC   GC CCC    TCCCTCCC
                                |||   || |||    ||||||||
```

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                                GGG  CG GGG    AGGGAGGG
                                  AAC  A  A____
GAM79   EMP3    5'  GCCCCGCCCTTCTCCTCC   10903       GA  _
                                GCCCCGCC  TC CCTCC
                                ||||||||  || |||||
                                CGGGGCGG  AG GGAGG
                                    GA  A
GAM79   EPB41L2  3'  ACCACAGCCCCCTCCCCCTC  11003    C     G_  GAT
                                ACC CAGCCCC  CC  CCCTC
                                ||| |||||||  ||  |||||
                                TGG GTCGGGG  GG  GGGAG
                                  T     GA  ___
GAM79   EPB49   3'  ACCCCACCTCCTGCCCCTCCC  12720      GCC  G  GA
                                ACCCCA  CC CC  TCCCTCCC
                                ||||||  || ||  ||||||||
                                TGGGGT  GG GG  GGGGAGGG
                                   ___  A  AC
GAM79   ESR2    5'  CAGCTCGGGTGGTCCCTCCC  11011     CC  CCGA_
                                CAGC  CG    TCCCTCCC
                                ||||  ||    ||||||||
                                GTCG  GC    AGGGAGGG
                                  A_  CCACC
GAM79   F2RL3   3'  CCCCAGCTCCAGCCCCATCTC  19514       _  C  GAT  __
                                CCCCAGC CC GCC  CC  CTC
                                ||||||| || |||  ||  |||
                                GGGGTCG GG CGG  GG  GAG
                                    A  T  ___  TA
GAM79   FADD    3'  ACCCCAGCCATGCCTCTCCC  19241       CC  GA
                                ACCCCAGCC  GCC  TCCC
                                |||||||||  |||  ||||
                                TGGGGTCGG  CGG  AGGG
                                     TA  AG
GAM79   FCAR    5'  CCTCAGCCCCGTTGCTCTCC  39341    C     CCGATCC
                                CC CAGCCCCG     CTCC
                                || ||||||||     ||||
                                GG GTCGGGGC     GAGG
                                 A      AACGA__
GAM79   FDXR    3'  CCCAGCCCTTCCCCTCC    35928       CGCCGA
                                CCCAGCCC    TCCCTCC
                                ||||||||    |||||||
                                GGGTCGGG    GGGGAGG
                                    AA____
GAM79   FKBP1B   5'  CCCCAGCCCCGCCGTCGCTC  38332          A  C
                                CCCCAGCCCCGCCG TC CTC
                                |||||||||||||| || |||
                                GGGGTCGGGGCGGC AG GAG
                                       _  C
GAM79   FOLR1   5'  ACCCCAGCCCTCACTCCACC  32502        _  CGA  CT
                                ACCCCAGCCC CGC  TCC  CC
                                |||||||||| |||  |||  ||
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                                TGGGGTCGGG GTG   AGG  GG
                                     A  ___   T_
GAM79   FOXE1    3'  CCTCGCCCCACCTCCTCC    20940    CA      GATC
                                CC  GCCCCGCC   CCTCC
                                ||  ||||||||   |||||
                                GG  CGGGGTGG   GGAGG
                                 AG       A___
GAM79   FUS1     3'  ACCCCAGCCTGCACTCTCTC   28581         CC  CGA  C
                                ACCCCAGCC  GC   TC CTC
                                |||||||||  ||   || |||
                                TGGGGTCGG  CG   AG GAG
                                     A_  TG_  A
GAM79   GAC1     3'  GCTCTAGCCAAAGTCCCTCCC  26794    CCC_    __
                                GC   GCCGA  TCCCTCCC
                                ||   |||||  ||||||||
                                CG   CGGTT  AGGGAGGG
                                 AGAT    TC
GAM79   GADD45B  3'  CCCCAGCTCCCAAGTCCC    31827        _   CCGA
                                CCCCAGC CCCG    TCCC
                                ||||||| ||||    ||||
                                GGGGTCG GGGT    AGGG
                                    A   TC__
GAM79   GPR48    5'  CCCCAGCCCCCGCCGTGGCTC  32982          _   ATCC
                                CCCCAGCCCC GCCG    CTC
                                |||||||||| ||||    |||
                                GGGGTCGGGG CGGC    GAG
                                     G   ACC_
GAM79   HCFC1    3'  CCTCAGCTCCGCCTTCCCTCCC 43388    C   C    GA
                                CC CAGC CCGCC  TCCCTCCC
                                || |||| |||||  ||||||||
                                GG GTCG GGCGG  AGGGAGGG
                                 A   A    A_
GAM79   HCFC1    3'  CCCCAGCCCTCCCTCAAGCTCC 43386         CG  GATCC
           C                     CCCCAGCCC  CC    CTCCC
                                |||||||||  ||    |||||
                                GGGGTCGGG  GG    GAGGG
                                     AG  AGTTC
GAM79   HIP12    3'  AGCCTGGTCCCACCCCTCC   42391     CCG_  G
                                AGCC    CC ATCCCTCC
                                ||||    || ||||||||
                                TCGG    GG TGGGGAGG
                                  ACCA  G
GAM79   HMGA2    3'  ACCCCACCCCCCCCCTC      18502       G   GCCGAT
                                ACCCCA CCCC     CCCTC
                                |||||| ||||     |||||
                                TGGGGT GGGG     GGGAG
                                   G   _______
GAM79   HMX1     3'  CCCCAGCCTGCCTGCTCC    33207        CC   GATCC
                                CCCCAGCC  GCC    CTCC
                                ||||||||  |||    ||||
```

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                                GGGGTCGG  CGG    GAGG
                                    A_  AC___
GAM79  HS3ST3A1  5'  CCCCGGCCCCGAGAGACTTCTC 25802     A    CC_  CC
                                CCCC GCCCCG  GAT  CTC
                                |||| ||||||  |||  |||
                                GGGG CGGGGC  CTG  GAG
                                  C     TCT  AA
GAM79  HSD17B3  3'  ACCCCAGCCCCCTCCATC    6808          G_  G
                                ACCCCAGCCCC  CC ATC
                                ||||||||||  || |||
                                TGGGGTCGGGG  GG TAG
                                      GA  _
GAM79  HUNK    5'  CCCAGCCCCGCCTGGGTCTC  31059          GATCC
                                CCCAGCCCCGCC    CTC
                                ||||||||||||    |||
                                GGGTCGGGGCGG    GAG
                                      ACCCA
GAM79  ID3     5'  CCCTGCCCCCGCCGGCCC    44269    A   _   AT
                                CCC GCCCC GCCG  CC
                                ||| ||||| ||||  ||
                                GGG CGGGG CGGC  GG
                                  A    G   CG
GAM79  IGFBP2   3'  ACCCCAGCTCCCCGACC     8252        C  G
                                ACCCCAGC CC CCGATC
                                |||||||| || ||||||
                                TGGGGTCG GG GGCTGG
                                    A  _
GAM79  IMPA2    5'  CCCCGACCCCCGCCGGCCC    45457     A       AT
                                CCCC GCCCCCGCCG  CC
                                |||| |||||||||  ||
                                GGGG TGGGGCGGC  GG
                                  C       CG
GAM79  ISGF3G   5'  CCCCAGCCTCGCCGCCC     25882       C    AT
                                CCCCAGCC CGCCG  CCC
                                |||||||| |||||  |||
                                GGGGTCGG GCGGC  GGG
                                    A   __
GAM79  ITGAL    3'  CCCAGCCCCGGCCCTC      13616         CCGAT
                                CCCAGCCCCG    CCCTC
                                ||||||||||    |||||
                                GGGTCGGGGC    GGGAG
                                      C____
GAM79  ITGB3    3'  AGCCCCAAATCCCTCCC     6838        CC
                                AGCCCCG  GATCCCTCCC
                                |||||||  ||||||||||
                                TCGGGGT  TTAGGGAGGG
                                        __
GAM79  KRAS2    5'  CCTCTGGCCCCGCCGCCGCCT  37886    CCA_       A  _
                                CC   GCCCCGCCG TC CCT
                                ||   ||||||||| || |||
```

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                                GG   CGGGGCGGC GG GGA
                                 AGAC       _ C
GAM79   LAMB2   5' ACCCCAACCCTACCCCTTCC  14069        CG  GAT  C
                                ACCCCAGCCC  CC   CC TCC
                                ||||||||||  ||   || |||
                                TGGGGTTGGG  GG   GG AGG
                                     AT  ___  A
GAM79   LAMC1   5' CCCCGCCTCCGCGCTTCCC   14081     A  _   CGA
                                CCCC GCC CCGC   TCCC
                                |||| ||| ||||   ||||
                                GGGG CGG GGCG   AGGG
                                  _  A   CGA
GAM79   LIMD1   3' ACCCCGGCTCCTCATCCC    30626      A  C  GC G
                                ACCCC GC CC  C ATCCC
                                ||||| || ||  | |||||
                                TGGGG CG GG  G TAGGG
                                   C  A  A_ _
GAM79   LMO4    3' CCCCAGCTCCCTCCCCCTCCC  27648       _  G  GAT
                                CCCCAGC CCC CC   CCCTCCC
                                ||||||| ||| ||   |||||||
                                GGGGTCG GGG GG   GGGAGGG
                                    A   A  ___
GAM79   LPIN2   3' CCCCAGGCCCAGTTCCTCCC  31205       C   CCGATC
                                CCCCAG CCCG     CCTCCC
                                |||||| ||||     ||||||
                                GGGGTC GGGT     GGAGGG
                                   C   CAA___
GAM79   LRP4    3' CCCAGCCCCTGTTGTTCTCTC  42059        GCCGA_  C
                                CCCAGCCCC     TC CTC
                                |||||||||     || |||
                                GGGTCGGGG     AG GAG
                                     ACAACA  A
GAM79   LY64    3' CCCTGCCCAGTCCCTCC    24567    A   CGCCGA
                                CCC GCCC     TCCCTCC
                                ||| ||||     |||||||
                                GGG CGGG     AGGGAGG
                                  A   TC____
GAM79   M6A     5' CCCAGCCCTGACACCTC    33388       CGCC  TC
                                CCCAGCCC   GA  CCTC
                                ||||||||   ||  ||||
                                GGGTCGGG   CT  GGAG
                                    A___  GT
GAM79   MAGEA4  3' CCCAGCCCTGCCCCTTCC    14323       C  GAT  C
                                CCCAGCCC GCC   CC TCC
                                |||||||| |||   || |||
                                GGGTCGGG CGG   GG AGG
                                    A   ___  A
GAM79   MAP1B   3' ACCCCACCCTGCTCTCTC    25388      G  C  CGA  C
                                ACCCCA CCC GC   TC CTC
                                |||||| ||| ||   || |||
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                                TGGGGT GGG CG   AG GAG
                                   _  A ___  A
GAM79   MAP3K11  5' CCGACCCCGCTCCCT      14532    A     CGA
                                CC GCCCCGC   TCCCT
                                || |||||||  |||||
                                GG TGGGGCG   AGGGA
                                 C     ___
GAM79   MAPT     3' CCTCGGCCTCCCCCGTGGCCTC 32589    CCA  _  G   ATC
            CC                   CC   GCC CC CCG   CCTCCC
                                ||  ||| || |||  ||||||
                                GG  CGG GG GGC   GGAGGG
                                 AGC   A  G   ACC
GAM79   MB       3' ACCCCAGCCCCAGCCCCTCAGC 23854          _  GA  C_
            TCC                   ACCCCAGCCCC GCC  TC  CTCC
                                |||||||||| |||  ||  ||||
                                TGGGGTCGGGG CGG  AG  GAGG
                                      T   GG  TC
GAM79   MB       3' CCCCAGCCCCTCAGCTCCTCC  23857         GC  ATC
                                CCCCAGCCCC  CG   CCTCC
                                ||||||||||  ||   |||||
                                GGGGTCGGGG  GT   GGAGG
                                     A_  CGA
GAM79   MBTPS1   5' CCTCAGCTCCGCCGACCC    19131    C    C
                                CC CAGC CCGCCGATCC
                                || |||| ||||||||||
                                GG GTCG GGCGGCTGGG
                                 A    A
GAM79   MECP2    3' CCCAGCCCCATTCTCCC     22582         CCGA
                                CCCAGCCCCG    TCCC
                                ||||||||||    ||||
                                GGGTCGGGGT    AGGG
                                     AAG_
GAM79   MECP2    3' CAGTCACCATCCCCCTCCC   22579     CCC    A_
                                CAG   CGCCG  TCCCTCCC
                                |||   |||||  ||||||||
                                GTC   GTGGT  GGGGAGGG
                                  A__     AG
GAM79   MGAT3    5' CCCGGCCCCGATCCCCTCCC  14457     A     CCGA
                                CCC GCCCCG    TCCCTCCC
                                ||| ||||||    ||||||||
                                GGG CGGGGC    GGGGAGGG
                                  C     TA__
GAM79   MGEA5    5' CCTCCGGCTCCTTCCCCTCCC  29214    _  A  C  GCCGA
                                CC CC GC CC    TCCCTCCC
                                || || || ||    ||||||||
                                GG GG CG GG    GGGGAGGG
                                 A  C  A  AA___
GAM79   MIC2     5' CCCCGCCCCGGCCTCCC     14501      A     _  GA
                                CCCC GCCCCG CC  TCCC
                                |||| |||||| ||  ||||
```

```
                                GGGG CGGGGC GG  AGGG
                                  _     C  __
GAM79   MMP14    3'  CCCCACCCCCCCGACATCCCTC 22634      G   G   __
                                CCCCA CCCC CCGA  TCCCTC
                                ||||| |||| ||||  ||||||
                                GGGGT GGGG GGCT  AGGGAG
                                   G   _   GT
GAM79   MNT      3'  CCTCAGCTCTGTCCCCTCCC  33708    C   CCCGCCGA
                                CC CAGC       TCCCTCCC
                                || ||||       ||||||||
                                GG GTCG       GGGGAGGG
                                 A   AGACA___
GAM79   MPDU1    3'  CCCCATCTCCACTCCCTTCC  22175      GCC   CGA    _
                                CCCCA  CCGC  TCCCT CC
                                |||||  ||||  ||||| ||
                                GGGGT  GGTG  AGGGA GG
                                   AGA   ___    A
GAM79   MSF      5'  CCCCCGCCCCGCCCCCGCCTCC 44721      A      GA  _
            C                    CCCC GCCCCGCC  TC CCTCCC
                                ||||  ||||||||  || ||||||
                                GGGG CGGGGCGG  GG GGAGGG
                                  G       G_  C
GAM79   MYC      5'  CAGCGCGATCCCTCCC      14706      CCC  C
                                CAGC   GC GATCCCTCCC
                                ||||   || ||||||||||
                                GTCG   CG CTAGGGAGGG
                                  ___  _
GAM79   MYO1D    3'  ACCCCGCCCTTGCTGTTTCTC  43484      A   C_  CGATCC
                                ACCCC GCCC  GC     CTC
                                ||||| ||||  ||     |||
                                TGGGG CGGG  CG     GAG
                                  _    AA  ACAAA_
GAM79   MYOG     3'  CCCCAACCCCTTTTCCC     40420          GCCGA
                                CCCCAGCCCC    TCCC
                                ||||||||||    ||||
                                GGGGTTGGGG    AGGG
                                     AAA__
GAM79   NCOR2    3'  CCCCGGCCCCTTCCCCTCCC  26728     A    GCCGA
                                CCCC GCCCC    TCCCTCCC
                                |||| |||||    ||||||||
                                GGGG CGGGG    GGGGAGGG
                                  C    AA___
GAM79   NDRG2    3'  CCCAAGCTTAGCTCCCTCCC  32192     C  CCC  CGA
                                CCC AGC   GC   TCCCTCCC
                                ||| |||   ||   ||||||||
                                GGG TCG   CG   AGGGAGGG
                                  T   AAT  ___
GAM79   NDRG2    3'  CCCCAGCCCCAAATCCCCTCCC 32194          CCGA
                                CCCCAGCCCCG    TCCCTCCC
                                ||||||||||    ||||||||
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```
                                GGGGTCGGGGT   GGGGAGGG
                                      TTA_
GAM79   NDRG2    3'  CCCCAGCACCAATCCTTCCC  32193       CCC      C
                                CCCCAGC  GCCGATCC TCCC
                                |||||||  |||||||| ||||
                                GGGGTCG  TGGTTAGG AGGG
                                   ___      A
GAM79   NEO1     5'  GCCCTTGCCTCCTTCCCTCCC  14753     C_  GA__
                                GCCC  GCC   TCCCTCCC
                                ||||  |||   ||||||||
                                CGGG  CGG   AGGGAGGG
                                  AA  AGGA
GAM79   NGB      3'  CCCAGCCCTGCCCCATCACCTC 34581       C _ G  _
                                CCCAGCCC GC C ATC CCTC
                                |||||||| || | ||| ||||
                                GGGTCGGG CG G TAG GGAG
                                     A  G G  T
GAM79   NHLH1    3'  ACCCCAGCCTTCCTCCC    24647        CCG  GA
                                ACCCCAGCC  CC  TCCC
                                |||||||||  ||  ||||
                                TGGGGTCGG  GG  AGGG
                                     AA_ __
GAM79   NPDC1    3'  CCAGGCCCTGCCCCTCCC   31726    _  C  GATC
                                CCAG CCC GCC   CCTCCC
                                |||| ||| |||   ||||||
                                GGTC GGG CGG   GGAGGG
                                  C  A  _____
GAM79   NRXN2    3'  CCCCAGCCTTCCTTCCC    31474       CCG  GA
                                CCCCAGCC  CC  TCCC
                                ||||||||  ||  ||||
                                GGGGTCGG  GG  AGGG
                                     AA_  A_
GAM79   NRXN2    5'  CCCCGGCCCCGCCCGGCCC  31475     A      GAT
                                CCCC GCCCCGCC  CCC
                                |||| ||||||||  |||
                                GGGG CGGGGCGG  GGG
                                  C      GCC
GAM79   P4HB     3'  CCGGCTCCGTCCCTCC     9544    A  C  CCGA
                                CC GC CCG   TCCCTCC
                                || || |||   |||||||
                                GG CG GGC   AGGGAGG
                                 C  A  _____
GAM79   P53AIP1  3'  ACCCCAGCCTTCCCTCC    35229        CCGCCGA
                                ACCCCAGCC     TCCCTCC
                                |||||||||     |||||||
                                TGGGGTCGG     AGGGAGG
                                     A_______
GAM79   PABPN1   5'  ACCCCAGCTTCCCCTCATTTCC 21604        ___  GCCGA
           C                     ACCCCAGC  CCC   TCCC
                                |||||||  |||   ||||
```

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                              TGGGGTCG  GGG   AGGG
                                 AAG  AGTAA
GAM79  PAPOLA  5' GCCCTGGGTCCAACCCCTC  37205    CG___
                              GCCC   CCGATCCCTC
                              ||||   ||||||||||
                              CGGG   GGTTGGGGAG
                                ACCCA
GAM79  PAX9    5' CCCCAGTTCCGCACTCCC   26201     CC  CGA
                              CCCCAG CCGC  TCCC
                              |||||| ||||  ||||
                              GGGGTC GGCG  AGGG
                                 AA  TG_
GAM79  PHF1    3' ACCCCACCTCGGACTCCTCCC 15267       ___ TC
                              GCCCCGCC  GA CCTCCC
                              |||||||| || ||||||
                              TGGGGTGG  CT GGAGGG
                                 AGC GA
GAM79  PML     5' ACCCCAGCTTAGTTTCGATTCT 37750      CCCGC__  CC
          C                   ACCCCAGC    CGAT CTC
                              ||||||||    |||| |||
                              TGGGGTCG    GCTA GAG
                                 AATCAAA  A_
GAM79  POU3F2  3' GCCCCGCGCTCTGCCCCTCCC 24670      CGA___
                              GCCCCGC    TCCCTCCC
                              |||||||    ||||||||
                              CGGGGCG    GGGGAGGG
                                 CGAGAC
GAM79  POU5F1  3' CCCTAGCTCCTCCCCTCC   15470   C  C GCCGA
                              CCC AGC CC   TCCCTCC
                              ||| ||| ||   |||||||
                              GGG TCG GG   GGGGAGG
                                A  A A____
GAM79  PPOX    5' CCCCAGCCTTTTCGGTCTCTCC 7178       CCGC A C
                              CCCCAGCC   CG TC CTCC
                              ||||||||   || || ||||
                              GGGGTCGG   GC AG GAGG
                                 AAAA C A
GAM79  PPP2R5D 3' AGCCCCAGGGTGGTCCCTTCC 26453      CCGA__   _
                              AGCCCCG    TCCCT CC
                              |||||||    ||||| ||
                              TCGGGGT    AGGGA GG
                                 CCCACC   A
GAM79  PPP5C   3' CCCCAGCTGCTCCACCTCCTTC 26486      C___   GA  C
          C                   CCCCAGC   CCGCC TCC TCC
                              |||||||   ||||| ||| |||
                              GGGGTCG   GGTGG AGG AGG
                                 ACGA   __  A
GAM79  PRKACA  3' ACCCCAGCGCCTCCCT     15572       CCC  GA
                              ACCCCAGC  GCC TCCCT
                              ||||||||  ||| |||||
```

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                                TGGGGTCG  CGG  AGGGA
                                   ___  __
GAM79   PRKACA   3'  ACCCCAGGCCTGAGAACTCCTC 15573       C  CGCC  TC
            C                    ACCCCAG CC   GA  CCTCC
                                 ||||||| ||   ||  |||||
                                 TGGGGTC GG   TT  GGAGG
                                    C  ACTC  GA
GAM79   PRSS8    3'  CCCCAGCCTCCCGCAGAGTCC  15758        __   C  _
                                 CCCCAGCC  CCGC GA TCC
                                 ||||||||  |||| || |||
                                 GGGGTCGG  GGCG CT AGG
                                     AG   T  C
GAM79   PTGS1    5'  CCAGCCCATCCCCTCC      38731        CGCCGA
                                 CCAGCCC     TCCCTCC
                                 |||||||     |||||||
                                 GGTCGGG     GGGGAGG
                                     TA____
GAM79   PTPRH    3'  CCAGCCCCCTCCTCC       15948        GCCGAT _
                                 CCAGCCCC     C CCTCC
                                 ||||||||     | |||||
                                 GGTCGGGG     G GGAGG
                                      _______ A
GAM79   PXF      3'  CCCCAGCCCAGGCTGTTTCTCC 16008         C_  CGATCC
            C                    CCCCAGCCC  GC     CTCCC
                                 |||||||||  ||     |||||
                                 GGGGTCGGG  CG     GAGGG
                                     TC  ACAAA_
GAM79   RAB26    3'  CCAGCCCCAGCCCTCC      30745         CCGAT
                                 CCAGCCCCG    CCCTCC
                                 |||||||||    ||||||
                                 GGTCGGGGT    GGGAGG
                                     C____
GAM79   RAB27A   3'  CCCCACCCCAATCCCCTTCC  21361      G   GCC    __
                                 CCCCA CCCC   GATCCC  TCC
                                 ||||| ||||   ||||||  |||
                                 GGGGT GGGG   TTAGGG  AGG
                                   _   ___      GA
GAM79   RAD54L   5'  ACCCCAGCACCTCTCTCTC   18713        CCC   GA  C
                                 ACCCCAGC   GCC  TC CTC
                                 ||||||||   |||  || |||
                                 TGGGGTCG   TGG  AG GAG
                                     ___   AG  A
GAM79   RAMP3    3'  CCCCAGCCCCTCCCT       25199         GCCGA
                                 CCCCAGCCCC    TCCCT
                                 ||||||||||    |||||
                                 GGGGTCGGGG    AGGGA
                                      _____
GAM79   RCN1     3'  ACCCCGCTCCGTTTGGCTTCCC 16197       A  C   CCGA___
                                 ACCCC GC CCG      TCCC
                                 ||||| || |||      ||||
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                                TGGGG CG GGC      AGGG
                                  _ A  AAACCGA
GAM79   RENBP    5' ACCCTTGCCCCGCCCTCC    16241     CA      GA
                                ACCC  GCCCCGCC  TCC
                                ||||  ||||||||  |||
                                TGGG  CGGGGCGG  AGG
                                  AA       G_
GAM79   RFX2     3' GCCCAGCTGGGTCCCTCCC   8451      C  CGA_
                                GCCC GC    TCCCTCCC
                                |||| ||    ||||||||
                                CGGG CG    AGGGAGGG
                                  T  ACCC
GAM79   RNMT     3' CCCCAGTTCCGTCATTCCC   19149       CC   C  A
                                CCCCAG  CCG CG TCCC
                                ||||||  ||| || ||||
                                GGGGTC  GGC GT AGGG
                                   AA   A  A
GAM79   RRM2B    5' CCCGGCCCCGCCTCCC      42714     A       GA
                                CCC GCCCCGCC  TCCC
                                ||| ||||||||  ||||
                                GGG CGGGGCGG  AGGG
                                  C       __
GAM79   S100A10  5' CCCCAGCCCTGTCTCCTCCC   40388         CGCCGA  _
                                CCCCAGCCC     TC CCTCCC
                                |||||||||     || ||||||
                                GGGGTCGGG     AG GGAGGG
                                     AC____  A
GAM79   SCO1     3' CCTCGCCCCGCCATGTCCTTCC 21379    CA       A_  C
                                CC  GCCCCGCCG  TCC TCC
                                ||  |||||||||  ||| |||
                                GG  CGGGGCGGT  AGG AGG
                                 AG        AC   A
GAM79   SDC2     5' CCTCTGGCTCCCTCCCTCC   42562    CCA_ _   GCCGA
                                CC    GC CCC     TCCCTCC
                                ||    || |||     |||||||
                                GG    CG GGG     AGGGAGG
                                 AGAC  A  _____
GAM79   SDS      3' ACTCCAGCCCCTCCAGGGGTCT 27766    C       G   ATCC_
            C                    AC CCAGCCCC CCG     CTC
                                || ||||||| |||     |||
                                TG GGTCGGGG GGT     GAG
                                 A       A   CCCCA
GAM79   SFN      3' CCTCAGCTCTGCCAGTCCCTC  43966    C    CCC    A
                                CC CAGC   GCCG TCCCTC
                                || ||||   |||| ||||||
                                GG GTCG   CGGT AGGGAG
                                 A   AGA   C
GAM79   SFRP1    3' ACCCCACCCGAGGCTCCCTCCC 16566       GC    CCGA
                                ACCCCA  CCCG    TCCCTCCC
                                ||||||  ||||    ||||||||
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                                TGGGGT  GGGC    AGGGAGGG
                                   __   TCCG
GAM79   SGCA     3'  ACCCCACCCCACCCCCTC    6170        G      GAT
                                ACCCCA CCCCGCC   CCCTC
                                |||||| |||||||   |||||
                                TGGGGT GGGGTGG   GGGAG
                                   _     ____
GAM79   SGCA     3'  ACCCCACCCCCTCTCCC     6171        G    GCCGA
                                ACCCCA CCCC    TCCC
                                |||||| ||||    ||||
                                TGGGGT GGGG    AGGG
                                   G   AG___
GAM79   SIRT3    5'  CCCCGGCCCCGCCTCCGCCTCC 29258      A       GA  _
            C                    CCCC GCCCCGCC  TC CCTCCC
                                |||| ||||||||  || ||||||
                                GGGG CGGGGCGG  GG GGAGGG
                                  C       A_  C
GAM79   SLC26A4  5'  CCTACCCCTCCTGCATTCTTCC 7760     A    G  GA___  CC
            C                    CC GCCCC CC    TC  TCCC
                                || ||||| ||    ||  ||||
                                GG TGGGG GG    AG  AGGG
                                 A    A  ACGTA  A_
GAM79   SLC6A6   3'  ACCCCAGCTCCTGCCGGGAGAG 16780        _  C    ATCCCT
            CC                   ACCCCAGC CC GCCG     CC
                                |||||||| || ||||     ||
                                TGGGGTCG GG CGGC     GG
                                    A  A    CCTCTC
GAM79   SLC9A1   3'  CCTCAGCTCCCTCCCTTCC   43232    C   _  GCCGA    _
                                CC CAGC CCC    TCCCT CC
                                || |||| |||    ||||| ||
                                GG GTCG GGG    AGGGA GG
                                 A   A  ______    A
GAM79   SLN      5'  CCAACTCCTTCTCCCTCCC   16877      C  GCCGA
                                CCAGC CC    TCCCTCCC
                                ||||| ||    ||||||||
                                GGTTG GG    AGGGAGGG
                                   A  AAG__
GAM79   SMARCC2  5'  GCCCCGCCGCCGCCC      40074        ATC  T
                                GCCCCGCCG   CC CCC
                                |||||||||   || |||
                                CGGGGCGGC   GG GGG
                                      ___  C
GAM79   SMT3H1   5'  GCCCCGCCGCTCTCCC     40995        ATCC
                                GCCCCGCCG   CTCCC
                                |||||||||   |||||
                                CGGGGCGGC   GAGGG
                                     GA__
GAM79   SOX15    5'  ACTCCGCCCCTGTCCCTCC   28018    C  A    GCCGA
                                AC CC GCCCC    TCCCTCC
                                || || |||||    |||||||
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                                TG GG CGGGG    AGGGAGG
                                 A  _    AC___
GAM79   SRC     3'  CCCCAGCCCTTCTCCTGGTTCC 24033        CG__  GATC_
            TC                   CCCCAGCCC   CC    CCTC
                                 |||||||||   ||    ||||
                                 GGGGTCGGG   GG    GGAG
                                      AAGA  ACCAA
GAM79   SRGAP2  3'  CCCCACCCCACCTCTCTTCC  43976     G     GA  CC
                                 CCCCA CCCCGCC  TC  TCC
                                 ||||| |||||||  ||  |||
                                 GGGGT GGGGTGG  AG  AGG
                                   _      AG  A_
GAM79   STAT5B  5'  CCGGCCGCCGACTCTCC    29717    A  CC    CC
                                 CC GCC  GCCGAT  CTCC
                                 || |||  ||||||  ||||
                                 GG CGG  CGGCTG  GAGG
                                  C  __     A_
GAM79   STAT6   5'  CCCCAGCCCGCTGTTTCC    17152        C  CGA_
                                 CCCCAGCCC GC    TCC
                                 ||||||||| ||    |||
                                 GGGGTCGGG CG    AGG
                                      _ ACAA
GAM79   STC1    3'  CCTACCCCTCCTCCCTC    17172    A    G  GA
                                 CC GCCCC CC  TCCCTC
                                 || ||||| ||  ||||||
                                 GG TGGGG GG  AGGGAG
                                  A    A  __
GAM79   TACSTD2  5'  CCCAGCCCCAGCCCTCC     14292         CCGAT
                                 CCCAGCCCCG    CCCTCC
                                 ||||||||||    ||||||
                                 GGGTCGGGGT    GGGAGG
                                      C_____
GAM79   TACSTD2  5'  CCCCAGCCCTCCCTTGATTTCT 14293        CG  __  CC
            C                    CCCCAGCCC  CC  GAT  CTC
                                 |||||||||  ||  |||  |||
                                 GGGGTCGGG  GG  CTA  GAG
                                      AG  AA   AA
GAM79   TCF2    3'  CCCCAGCCCTCAGGCCTTTC  27022        _ __  GA
                                 CCCCAGCCC C  GCC  TC
                                 ||||||||| |  |||  ||
                                 GGGGTCGGG G  CGG  AG
                                      A TC   AA
GAM79   TCF20   3'  CCCACCCCTCCCCCCTCCC   42533     G   G  GA
                                 CCCA CCCC CC  TCCCTCCC
                                 |||| |||| ||  ||||||||
                                 GGGT GGGG GG  GGGGAGGG
                                   _   A  __
GAM79   TEM5    3'  CCCGGTTCCCACTCCCCTCCC 37230    CAGC    CGA
                                 CCC   CCCGC   TCCCTCCC
                                 |||   |||||   ||||||||
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                                GGG   GGGTG  GGGGAGGG
                                  CCAA    A__
GAM79   TGT     3'  CCAGCCCCTCCCTCC      36302        GCCGA
                                CCAGCCCC    TCCCTCC
                                ||||||||    |||||||
                                GGTCGGGG    AGGGAGG
                                     _____
GAM79   TLX1    5'  CCCTGGCCCCACCGGGGGGCCC 24331    CA       AT___
                                CCC  GCCCCGCCG    CCC
                                |||  |||||||||    |||
                                GGG  CGGGGTGGC    GGG
                                  AC       CCCCC
GAM79   TMEM2   3'  ACCCTTGGCCATCCCTCC    30150     C__   G
                                GCCC   GCC ATCCCTCC
                                ||||   ||| ||||||||
                                TGGG   CGG TAGGGAGG
                                  AAC   _
GAM79   TMEPAI  3'  CCCCACCCCTCATGCTCTCC   33594      G   GC  ATCC
                                CCCCA CCCC  CG    CTCC
                                ||||| ||||  ||    ||||
                                GGGGT GGGG  GT    GAGG
                                   _    A_  ACGA
GAM79   TNFRSF6B 3'  ACCCCAGCCCTCCGGGGCCT   37279         CG   ATC
                                ACCCCAGCCC  CCG   CCT
                                ||||||||||  |||   |||
                                TGGGGTCGGG  GGC   GGA
                                     A_   CCC
GAM79   TRPM6   3'  CCCAGCCCCACATCTCTCC   32788          CG   C
                                CCCAGCCCCGC  ATC CTCC
                                ||||||||||  ||| ||||
                                GGGTCGGGGTG  TAG GAGG
                                     __   A
GAM79   WHSC1   3'  ACCCCACCCCGTCTTGTTCCC  39348       G    CCGA__
                                ACCCCA CCCCG     TCCC
                                ||||||| |||||     ||||
                                TGGGGT GGGGC     AGGG
                                   _    AGAACA
GAM79   WNT7A   5'  CCTCCAGCCCCCGCCCCTCCC  21525    _      GC  A
                                CC CCAGCCCC  CG TCCCTCCC
                                || ||||||||  || ||||||||
                                GG GGTCGGGG  GC GGGGAGGG
                                 A      __ _
GAM79   YWHAG   3'  ACCCTGCCCCCCCCCTCC    29784     CA    G  GAT
                                ACCC  GCCCC CC   CCCTCC
                                ||||  ||||| ||   ||||||
                                TGGG  CGGGG GG   GGGAGG
                                  A_    _ ____
GAM79   ZIC1    3'  CCGGTCCCTCCCCCCTCCC   18230    AGC   G  GA
                                CC   CCC CC  TCCCTCCC
                                ||   ||| ||  ||||||||
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                                GG   GGG GG  GGGGAGGG
                                 CCA  A  __
GAM79   ZIC3     5'  CCTGTCCCGGGCACCCCTCC   18246    AGC   CCG
                                CC   CCCG   ATCCCTCC
                                ||   ||||   ||||||||
                                GG   GGGC   TGGGGAGG
                                 ACA    CCG
GAM79   ZNF219   5'  CCCGGCCCCCGCCCCCTCCC   32317     A    _   GAT
                                CCC GCCCC GCC   CCCTCCC
                                ||| ||||| |||   |||||||
                                GGG CGGGG CGG   GGGAGGG
                                  C    G   ___
GAM79   ZNF8     3'  CCCCAGCCCCTCCTTCC     41964          G  GA
                                CCCCAGCCCC CC  TCC
                                |||||||||| ||  |||
                                GGGGTCGGGG GG  AGG
                                      A  A_
GAM80   CARD4    3'  AAGCCCACCATGGTGG      25889          CAACACGA
                                AAGCCTACTGT       TGG
                                ||||||||||        |||
                                TTCGGGTGGTA       ACC
                                      CC_______
GAM80   DDAH2    5'  AGCTCATATACTACGATGGG   30353     C  C   CA  _
                                AGC TA TGT  AC ACGATGGG
                                ||| || |||  || ||||||||
                                TCG GT ATA  TG TGCTACCC
                                  A  _   __  A
GAM80   JMJ      3'  AAGTTTACTGTCAAAAAGAGGG 22482     CC        CAC  T
            A                    AAG  TACTGTCAA   GA GGGA
                                ||| |||||||||   || ||||
                                TTC  ATGACAGTT   CT CCCT
                                  AA        TTT  _
GAM80   MKLN1    3'  AGCTTTACTGTCAGTCAGTGGA 43083     C_       ACA  A
                                AGC  TACTGTCA   CG TGGG
                                |||  ||||||||   || ||||
                                TCG  ATGACAGT   GT ACCT
                                  AA       CA_  C
GAM80   PTGFRN   3'  AAGGCTACTGTCAATGCA    42579     C         CA
                                AAG CTACTGTCAA  CG
                                ||| ||||||||||  ||
                                TTC GATGACAGTT  GT
                                  C         AC
GAM80   PTPRC    3'  TACTGTCAAGTTTGGGA     38969          CACGA
                                TACTGTCAA    TGGGA
                                |||||||||    |||||
                                ATGACAGTT    ACCCT
                                      CAA__
GAM80   PTPRZ1   3'  AAGTTACTGTCAGGTGATGGGA 15984     CC        ACAC
                                AAG  TACTGTCA    GATGGGA
                                |||  ||||||||    |||||||
```

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                                TTC  ATGACAGT    CTACCCT
                                  A_       CCA_
GAM80   SNCB     3'  AGCCACTGTCGGGGATCGGG   16928      T     AACAC  _
                                AGCC ACTGTC     GAT GGG
                                |||| ||||||     ||| |||
                                TCGG TGACAG     CTA CCC
                                  _     CCC__   G
GAM80   TEM8     3'  AGCTGGCTGTCAACAGA     38173     CTA       C
                                AGC   CTGTCAACA GA
                                |||   ||||||||| ||
                                TCG   GACAGTTGT CT
                                  ACC       _
GAM80   ALDH3A1  3'  GGAGAGCCAGTGAGGGTGG   8665        G     CC   C
                                GGAGAGC CAGTGA  GGG TGG
                                ||||||| ||||||  ||| |||
                                CCTCTCG GTCACT  CCC ACC
                                   _     __   _
GAM80   ASGR2    5'  GGAGAGTGGAGGAGGGGCTGGT 10140       CGC  T  CC
                                GGAGAG   AG GA  GGGCTGGT
                                ||||||   || ||  ||||||||
                                CCTCTC   TC CT  CCCGACCA
                                   ACC  _  C_
GAM80   ATP7B    5'  GGAGAGCGTGGTGTTAAAG   6277         CA   ACC
                                GGAGAGCG  GTG   GGG
                                ||||||||  |||   |||
                                CCTCTCGC  CAC   TTC
                                     AC   AAT
GAM80   B4GALT1  3'  GGAGGTGCAAAGGGCTGGT   11284     AGC    TGACC
                                GGAG   GCAG    GGGCTGGT
                                ||||   ||||    ||||||||
                                CCTC   CGTT    CCCGACCA
                                  CA_    T____
GAM80   CCND3    5'  GGAGAGCGCGGGGCGCGG    12063        AGTGACC   _
                                GGAGAGCGC      GGGC TGG
                                |||||||||      |||| |||
                                CCTCTCGCG      CCCG GCC
                                     C_______   C
GAM80   COX10    5'  GGAGAGCGTGGTGTCTGGAGGT 10552        CA   ACCG  CT
                                GGAGAGCG  GTG   GG  GGT
                                ||||||||  |||   ||  |||
                                CCTCTCGC  CAC   CC  CCA
                                     AC   AGA_  T_
GAM80   DRD2     3'  GGGGGCCCAGCCCCAGGGCTGG 9019     AGA  G   GA  _
           T                     GG   GC CAGT  CC GGGCTGGT
                                ||   || ||||  || ||||||||
                                CC   CG GTCG  GG CCCGACCA
                                 CC_  G   G_  T
GAM80   EFNA1    3'  GGATGGCACTGTCGGGCTGGT  20704     GA   A  GAC
                                GGA  GCGC GT   CGGGCTGGT
                                |||  |||| ||   |||||||||
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                                CCT  CGTG CA   GCCCGACCA
                                  AC    A ___
GAM80   GABRA2   5'  AGAGAGCGTGGAGCGATGGGCT 9041         C__    CC
            GGT                   GGAGAGCG   AGTGA  GGGCTGGT
                                |||||||||  |||||  |||||||||
                                TCTCTCGC   TCGCT  CCCGACCA
                                    ACC    A_
GAM80   PFKL     3'  GGAGGGCCTGGCAGGCTGG    15237     A  GCAG  AC
                                GGAG GC    TG  CGGGCTGG
                                |||| ||    ||  ||||||||
                                CCTC CG    AC  GTCCGACC
                                  C  G___  C_
GAM80   PHKG2    3'  GGAGAGAGGTACCGGGCTGGT  7130        CGC  TG
                                GGAGAG   AG  ACCGGGCTGGT
                                ||||||   ||  ||||||||||
                                CCTCTC   TC  TGGCCCGACCA
                                   ___  CA
GAM80   PTMS     3'  GGAGGGCGCAGTGTCTGG     15890      A       ACCGGG
                                GGAG GCGCAGTG     CTGG
                                |||| |||||||||      ||||
                                CCTC CGCGTCAC     GACC
                                  C       A_____
GAM80   RAB5A    3'  GGAAGTCATACTGGGCTGG    20010      AG GCAGTG  C
                                GGAG  C     AC GGGCTGG
                                ||||  |     || |||||||
                                CCTT  G     TG CCCGACC
                                  CA TA____  A
GAM80   SLC2A1   3'  GGGAGCAGGCCGGGCTGG    27141    A    CAGTGA
                                GG GAGCG     CCGGGCTGG
                                || |||||     |||||||||
                                CC CTCGT     GGCCCGACC
                                 _    CC____
GAM80   TFAP2A   3'  GGTGGGCGCGCGGGGGGCTGGT 17401    AGA    A   ACC
                                GG   GCGC GTG   GGGCTGGT
                                ||   |||| |||   ||||||||
                                CC   CGCG CGC   CCCGACCA
                                 ACC    _  CC_
GAM80   TGFB1    5'  GAGAGCGCGAACAGGGCTGGT  8540         AGT   C
                                GAGAGCGC   GAC GGGCTGGT
                                ||||||||   ||| ||||||||
                                CTCTCGCG   TTG CCCGACCA
                                    C__   T
GAM80   TNC      3'  GACCGATGGTTGGGCTGGT   13466    G  CA   ACC
                                GA CG  GTG   GGGCTGGT
                                || ||  |||   ||||||||
                                CT GC  TAC   CCCGACCA
                                 G  __   CAA
GAM81   AKAP2    3'  CCCTGTGTCTGCTTTGGGAACG 28493       ACG_  ACCA
            CC                    CCCTGT   GC   GGAACGCC
                                ||||||   ||   ||||||||
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                                GGGACA   CG   CCTTGCGG
                                   CAGA  AAAC
GAM81   ARNTL    5' CCGTGGCTCGCCGGGAGCGCC  10134     AC  A__  A  A
                                CTGT  GGC   CC GGA CGCC
                                ||||  |||   || ||| ||||
                                GGCA  CCG   GG CCT GCGG
                                  __  AGC  C   C
GAM81   HPS1     3' CCTGTGCTGCAGTGGACGC   6801      ACG   CCA   A
                                CCTGT   GCA   GGA CGC
                                |||||   |||   ||| |||
                                GGACA   CGT   CCT GCG
                                  CGA   CA_  _
GAM81   IL5RA    3' ACCCTGTACGGCATGGG    8161           CCA
                                ACCCTGTACGGCA   GG
                                ||||||||||||   ||
                                TGGGACATGCCGT   CC
                                       AC_
GAM81   MTMR3    3' ACTCTGTACAGGTGGTTCCACG 34389    C       CACCAGGA
            C                    AC CTGTACGG       ACGC
                                || ||||||||       ||||
                                TG GACATGTC       TGCG
                                 A       CACCAAGG
GAM81   MUCDHL   3' CCTTGTGGTCAGGGAGGAACGC 34935    C   AC  _  CC_
            C                    CC TGT  GG CA   AGGAACGCC
                                || |||  || ||   |||||||||
                                GG ACA  CC GT   TCCTTGCGG
                                 A  __  A  CCC
GAM81   ST5      3' CCCTGTACCGCATCGTGGCC  24044        G   CCAGGAAC
                                CCCTGTAC GCA       GCC
                                |||||||| |||       |||
                                GGGACATG CGT       CGG
                                    G   AGCAC___
GAM81   TMPRSS2  3' CCTGCACCAGGAGTGC     24932     GTACG       AC
                                CCT    GCACCAGGA  GC
                                |||    |||||||||  ||
                                GGA    CGTGGTCCT  CG
                                  _____        CA
GAM81   GPRK6    3' GTCCCAGGGATGGCCCAG    13272    A      CGTC  A_
                                GT CCCAGGGA   GG  CGG
                                || ||||||||   ||  |||
                                CA GGGTCCCT   CC  GTC
                                 _       A___  GG
GAM81   TG737    5' TTCGGGCCCAGGGACGACGCAG 27203     TA        T  GA_
            CGG                    TTCG  CCCAGGGACG CG   CGG
                                ||||  |||||||||| ||   |||
                                AAGC  GGGTCCCTGC GC   GCC
                                  CC        T  GTC
GAM82   ABCB4    5' TATTTTACCTGACAAATTC   7771         G     TT
                                TATTTTAC CTGACA  TTT
                                |||||||| ||||||  |||
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                                ATAAAATG GACTGT  AAG
                                    _     TT
GAM82   M17S2    5'  TATCTTACGCTGATATTC    36590            C
                                TATTTTACGCTGA ATTT
                                |||||||||||| ||||
                                ATAGAATGCGACT TAAG
                                      A
GAM82   C18orf1  3'  TAAATATTTTCAACATTAAGAT 41225         _ T
           A                     TAAATATTT C ATATTAAGATA
                                 ||||||||| | ||||||||||
                                 ATTTATAAA G TGTAATTCTAT
                                       A T
GAM82   PEX3     3'  TCTAAAAAAATATATTAAGAT  18853       TATTTC
                                 TCTAAA     TATATTAAGAT
                                 ||||||     ||||||||||
                                 AGATTT     ATATAATTCTA
                                    TTTT__
GAM82   ZNF265   3'  TCAAAATATTTCTACATAAGAT 24150    T          T
           A                     TC AAATATTTCTATAT AAGATA
                                 || ||||||||||||| ||||||
                                 AG TTTATAAAGATGTA TTCTAT
                                  T          _
GAM83   CKAP1    5'  CGCGTCGCCATGGAGCCCGACG 43880            A   ___
           GGAC                    CGCGTCGCCATGGAG CCGA   GAC
                                 |||||||||||||| ||||   |||
                                 GCGCAGCGGTACCTC GGCT   CTG
                                       G    GCC
GAM83   TEC      3'  TCGTGGCGCTCACGTGACCGAG 17391     CGT  _   GA
           A                     TCG   CGC CATG  GACCGAGA
                                 |||   ||| ||||  ||||||||
                                 AGC   GCG GTGC  CTGGCTCT
                                   ACC   A   A_
GAM84   CIT      3'  TTCAATTTCCTCTTTTTTTTT  43065      CA  A
                                 TTCAA  TC TCTTTTTTTTT
                                 |||||  || ||||||||||
                                 AAGTT  AG AGAAAAAAAAA
                                    AA  G
GAM84   GAD1     5'  CTCAACACGCTTTTTTTTT    30289        CAT
                                 TTCAACAT   CTTTTTTTTT
                                 ||||||||   ||||||||||
                                 GAGTTGTG   GAAAAAAAAA
                                      C__
GAM84   LPIN2    5'  TTCAGCATCACCTGCCACTTCT 31228      A      TTTTT
           T                     TTCA CATCATCT     TTTCTT
                                 |||| ||||||||     ||||||
                                 AAGT GTAGTGGA     GAAGAA
                                   C       CGGT_
GAM84   MME      3'  TTCAACATCTTCTTTTCCCTT  28616         A
                                 TTCAACATC TCTTTTTTTTT
                                 ||||||||| ||||||||||
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```
                                AAGTTGTAG AGAAAAGGGAA
                                      A
GAM84   SELE    3'  TTCAACATCTGTCATTTTTTT  7807          A_  T
                                TTCAACATC  TC TTTTTTT
                                |||||||||  || |||||||
                                AAGTTGTAG  AG AAAAAAA
                                      AC  T
GAM84   SMPX    3'  TTCACATCAATCCTTTTTTCT  30729      A    _
                                TTCA CATCA TCTTTTTTTTT
                                |||| ||||| ||||||||||
                                AAGT GTAGT AGGAAAAAAGA
                                   _    T
GAM85   AQP1    3'  CATTTTCCTTTATTTTCTTAA  7547      CA     T
                                CAT  TCTTTT TTTTCTTAA
                                |||  |||||| |||||||||
                                GTA  AGGAAA AAAAGAATT
                                  AA     T
GAM85   CACNA1C  5'  CATCATTATTTTTTTTCC    8747        CT
                                CATCAT  TTTTTTTTCT
                                ||||||  ||||||||||
                                GTAGTA  AAAAAAAAGG
                                    AT
GAM85   DSPG3   3'  AACTCATCTGGTGTTTTCTTAA 41172     A     TTTT
                                AAC TCATCT    TTTTCTTAA
                                ||| ||||||    |||||||||
                                TTG AGTAGA    AAAAGAATT
                                  _     CCAC
GAM85   F8      3'  CATCATCATTTTCTTTCTT   6563         T
                                CATCATC TTTTTTTTCTT
                                |||||||  ||||||||||
                                GTAGTAG AAAAGAAAGAA
                                     T
GAM85   MME     3'  CAACATCTTCTTTTCCCTT   28596    T        TT
                                CA CATCTTTTTTT  CTT
                                ||  ||||||||||  |||
                                GT GTAGAAGAAAA  GAA
                                  T         GG
GAM85   MME     3'  CAACATCTTCTTTTCCCTT   28596    T        TT
                                CA CATCTTTTTTT  CTT
                                ||  ||||||||||  |||
                                GT GTAGAAGAAAA  GAA
                                  T         GG
GAM85   MME     3'  CAACATCTTCTTTTCCCTT   28610    T        TT
                                CA CATCTTTTTTT  CTT
                                ||  ||||||||||  |||
                                GT GTAGAAGAAAA  GAA
                                  T         GG
GAM85   MME     3'  CAACATCTTCTTTTCCCTT   28596    T        TT
                                CA CATCTTTTTTT  CTT
                                ||  ||||||||||  |||
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```
                                GT GTAGAAGAAAA  GAA
                                 T          GG
GAM85   NR2F2    3'  AACATCCTTTTATATCCTTTCT 34229        ATCTTT__
             TAA                    AACATC       TTTTTTCTTAA
                                    ||||||       ||||||||||
                                    TTGTAG       AGGAAAGAATT
                                       GAAAATAT
GAM85   PPP3CA   3'  ACAGCCATTTTTTTTTTTCTTAA 9608      _    C
                                    ACA TCAT TTTTTTTTTCTTAA
                                    ||| |||| ||||||||||||||
                                    TGT GGTA AAAAAAAAAGAATT
                                      C   _
GAM85   TFAP2C   3'  CAGCATCCTCTTAATTCTTAA  17403    T        TT
                                    CA CATCTTTTT  TTCTTAA
                                    || |||||||||  |||||||
                                    GT GTAGGAGAA  AAGAATT
                                     C         TT
GAM85   UGT1A1   3'  CATCATTCTTTTTCCCCAA    7865        CT
                                    CATCAT  TTTTTTTTCTTAA
                                    ||||||  ||||||||||||
                                    GTAGTA  AGAAAAAGGGGTT
                                       __
GAM85   UGT1A4   3'  CATCATTCTTTTTCCCCAA    28294       CT
                                    CATCAT  TTTTTTTTCTTAA
                                    ||||||  ||||||||||||
                                    GTAGTA  AGAAAAAGGGGTT
                                       __
GAM85   UGT1A9   3'  CATCATTCTTTTTCCCCAA    34288       CT
                                    CATCAT  TTTTTTTTCTTAA
                                    ||||||  ||||||||||||
                                    GTAGTA  AGAAAAAGGGGTT
                                       __
GAM86   LAMC1    3'  GGATCATCAAGAACTAAGTTAC 14086          _    TTT
                                    GGATCATTAA AATTA   TTAC
                                    |||||||||| |||||   ||||
                                    CCTAGTAGTT TTGAT   AATG
                                          C    TC_
GAM86   NCALD    3'  AGGAAGACTAGGATTATTTTTA 36760      TC    AA
             C                       AGGA  ATTA  ATTATTTTTAC
                                     ||||  ||||  ||||||||||||
                                     TCCT  TGAT  TAATAAAAATG
                                       TC    CC
GAM87   ATP2C1   3'  CAGGTTTTGCCTTTTT      30784    C    CCTAAG
                                    CA GGTT     GCCTTTTT
                                    || ||||     ||||||||
                                    GT CCAA     CGGAAAAA
                                     _    AA____
GAM87   CDH10    5'  CATGTTTCCCAAAGCTTTTTTA 27486    CGG        C
                                    CA   TTCCTAAGGC TTTTTA
                                    ||   |||||||||| ||||||
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                                GT   AAGGGTTTCG AAAAAT
                                 ACA        A
GAM87   CSPG3    3'  TCCACGGTGCTTTTT      20491        TCCTAAG  C
                                TCCACGGT      GC TTTT
                                ||||||||      || ||||
                                AGGTGCCA      CG AAAA
                                    ________ A
GAM87   EGLN2    5'  TCTGCGGTCCCTAAGGGCTT  38837    CA         C
                                TC  CGGTTCCTAAGG CTT
                                ||  ||||||||||||| |||
                                AG  GCCAGGGATTCC GAA
                                 AC          C
GAM87   ELAVL3   3'  CACGGTTCGCTTTTTT     10882        CTAAG  C
                                CACGGTTC    GC TTTTT
                                ||||||||    || |||||
                                GTGCCAAG    CG AAAAA
                                    ______ A
GAM87   FREB     3'  AGCTCTCTGGGGCCTTTTTA  37221      _  AA
                                GGTTC CT  GGCCTTTTTA
                                ||||| ||  ||||||||||
                                TCGAG GA  CCGGAAAAAT
                                   A  CC
GAM87   SLC1A4   3'  CACGGTTCCTGGTCCCTTTT  16742         AA  _
                                CACGGTTCCT  GG CCTTTTT
                                ||||||||||  || |||||||
                                GTGCCAAGGA  CC GGGAAAA
                                     __ A
GAM88   MBNL     5'  TCGCTGTGCAGCCTCTTATC  34323    ATATAC TG
                                TCG     G  GTTTCTTATC
                                |||     |  ||||||||||
                                AGC     C  CGGAGAATAG
                                  GACA__ GT
GAM88   RGS5     3'  CATTGATATCATAGTCT    18832    C    A
                                CAT GATAT CGTGGTTT
                                ||| ||||| ||||||||
                                GTA CTATA GTATCAGA
                                  A    _
GAM88   ULBP2    3'  CATTAATATAAATTTTTTCTTA 36096    CG    C  GG
          T                      CAT  ATATA GT  TTTCTTAT
                                 |||  ||||| ||  ||||||||
                                 GTA  TATAT TA  AAAGAATA
                                   AT    T  AA
GAM89   ATP1B1   3'  TGAAAGAGCCAAAAAAC    11735     AT
                                TGAA  AGAGCTAAAAAAC
                                ||||  ||||||||||||
                                ACTT  TCTCGGTTTTTTG
                                    __
GAM89   CCNF     3'  TGGGACAGAGCTCTAAAAC   12081    AA       AA
                                TG  ATAGAGCT  AAAAC
                                ||  ||||||||  |||||
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                                AC  TGTCTCGA  TTTTG
                                 CC       GA
GAM89   EGR1    3'  TAAAATAGAACCACAAAA    12666           A
                                TGAAATAGAGCTA AAAA
                                ||||||||||||| ||||
                                ATTTTATCTTGGT TTTT
                                       G
GAM89   NRG1    3'  TGAAAAGAGCAAAAAAC     30349      T    T
                                TGAAA AGAGC AAAAAAC
                                ||||| ||||| |||||||
                                ACTTT TCTCG TTTTTTG
                                  _    _
GAM89   OLR1    3'  GAAATAGAAGCCTAAAAA    14939        _  A
                                GAAATAGA GCT AAAAA
                                |||||||| ||| |||||
                                CTTTATCT CGG TTTTT
                                      T   A
GAM89   RNMT    3'  TGGCACTAAGCTAAAAAAC   19158    AA  A
                                TG  AT GAGCTAAAAAAC
                                ||  || ||||||||||||
                                AC  TG TTCGATTTTTTG
                                 CG  A
GAM89   SCA1    3'  TGAAATAGAACCACAAAA    7294           A
                                TGAAATAGAGCTA AAAA
                                ||||||||||||| ||||
                                ACTTTATCTTGGT TTTT
                                       G
GAM89   TRPS1   3'  TGAAACAGTACTGAAAAAC   30469        A  A
                                TGAAATAG GCT AAAAAC
                                |||||||| ||| ||||||
                                ACTTTGTC TGA TTTTTG
                                      A   C
GAM89   FGF23   3'  TTGGCTTTGCCATAAA      33960       CTAA  A
                                TTGGCT    TT GTCATAAA
                                ||||||    || ||||||||
                                AACCGA    AA CGGTATTT
                                   ____  _
GAM89   NRXN1   3'  GCTCTGATGTCATAAAA     39843      A  TA
                                GCTCT AT  GTCATAAAA
                                ||||| ||  |||||||||
                                CGAGA TA  CAGTATTTT
                                   C  __
GAM89   PRKAR2B 3'  TATTGGCTGCTGATCAAT    15622        _  A
                                TATTGGCT CT ATTAGT
                                |||||||| || ||||||
                                ATAACCGA GA TAGTTA
                                      C  C
GAM89   SLC4A7  3'  CATTGGCTTTAAAAGAGCATAA 18822        C   TT_  T
                                TATTGGCT TAA   AG CATAA
                                |||||||| |||   || |||||
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                                GTAACCGA ATT   TC GTATT
                                    A   TTC  _
GAM90   F3      5'  GAGTGCGAGGGGGTGCGG    42550    A    T  CTGTTA
                                GA TGCGA GG     GTGCGG
                                || ||||| ||     ||||||
                                CT ACGCT CC     CACGCC
                                 C    C  C_____
GAM90   ITGA4   5'  ATGCGACGGTTGGCCAACGGG  9418          C  TTAGT
                                ATGCGATGG TG    GCGGG
                                ||||||||| ||    |||||
                                TACGCTGCC AC    TGCCC
                                    A  CGGT_
GAM90   L1CAM   3'  GAGTGCGATGCTGGGAGTGGG  35801    A      G   TT    C
                                GA TGCGATG CTG  AGTG GG
                                || ||||||| |||  |||| ||
                                CT ACGCTAC GAC  TCAC CC
                                 C      _   CC   _
GAM90   RDS     3'  TGTGATGGCCACCTGTGTGGG  7247     C     TG TA   C
                                TG GATGGC  T  GTG GGG
                                || ||||||  |  ||| |||
                                AC CTACCG  G  CAC CCC
                                 A     GT GA   A
GAM90   MFI2    3'  TTCCTGTTTTTCGGCGGCTGC  25473      GC_    A   A  A
                                TTCC   TTTTC GCG GC TGT
                                ||||   ||||| ||| || |||
                                AAGG   AAAAG CGC CG ACG
                                  ACA    C  _ _
GAM90   PAH     3'  GCTTTTCAATAATGTA      7093          CG GCA
                                GCTTTTCAG  A   TGTA
                                |||||||||  |   ||||
                                CGAAAAGTT  T   ACAT
                                    AT ___
GAM90   SSX1    3'  TTCTGCTTCTCATCAAGGGCAT 24836     C      G   __
            GT                    TTC GCTTTTCA CGA  GCATGT
                                ||| |||||||| |||  ||||||
                                AAG CGAAGAGT GTT  CGTACA
                                  A       A   CC
GAM90   SSX2    3'  TTCTGCTTCTCATCATGGGCAT 45535     C      G  A__
            GT                    TTC GCTTTTCA CG   GCATGT
                                ||| |||||||| ||   ||||||
                                AAG CGAAGAGT GT   CGTACA
                                  A       A  ACC
GAM90   SSX3    3'  TTCTGCTTCTCATCATGGGCAT 34253     C      G  A__
            GT                    TTC GCTTTTCA CG   GCATGT
                                ||| |||||||| ||   ||||||
                                AAG CGAAGAGT GT   CGTACA
                                  A       A  ACC
GAM90   SSX4    3'  TTCTGCTTCTCATCATGGGCAT 45416     C      G  A__
            GT                    TTC GCTTTTCA CG   GCATGT
                                ||| |||||||| ||   ||||||
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                                AAG CGAAGAGT GT   CGTACA
                                  A       A  ACC
GAM90   STAR    3'  TTCTGCTTTGTGCACATGTAC  7392      C     TCA  GA
                                TTC GCTTT   GC  GCATGTAC
                                ||| |||||   ||  |||||||||
                                AAG CGAAA   CG  TGTACATG
                                  A    CA_  __
GAM90   THPO    3'  TTCCCTTTTCAGTCCTGTGTA  7855       G       CGAGCA
                                TTCC CTTTTCAG     TGTA
                                |||| ||||||||     ||||
                                AAGG GAAAAGTC     ACAT
                                  _       AGGAC_
GAM90   TPK1    3'  GCTTTCTTAGCATGTA      35355        CAGCG
                                GCTTTT    AGCATGTA
                                ||||||    ||||||||
                                CGAAAG    TCGTACAT
                                   AA___
GAM91   ACTB    3'  AAAAACCAAAACAAAACAA    9921             CTGT
                                AAAAACTAAAAC    AGAACAA
                                ||||||||||||    |||||||
                                TTTTTGGTTTTG    TTTTGTT
                                          _____
GAM91   ADAM17  3'  AAAAACTAAAACCTGAAA     17251              T
                                AAAAACTAAAACCTG AGA
                                |||||||||||||| |||
                                TTTTTGATTTTGGAC TTT
                                          _
GAM91   BACH2   3'  AAAAACAAAAACCCAGAGGCAG 34765        T      _____
                                AAAAAC AAAACCT    GTAG
                                |||||| |||||||    ||||
                                TTTTTG TTTTGGG    CGTC
                                   T      TCTC
GAM91   BCL6    3'  AAACTGAAAACTAGAACAAA   39902       _    CTG
                                AAACT AAAAC   TAGAACAAA
                                ||||| |||||   |||||||||
                                TTTGA TTTTG   ATCTTGTTT
                                  C    ___
GAM91   CDKN1B  5'  AAAAACAAAACCGAACAA     19793        T     TGTA
                                AAAAAC AAAACC    GAACAA
                                |||||| ||||||    ||||||
                                TTTTTG TTTTGG    CTTGTT
                                          _    _____
GAM91   CDYL    3'  AAAACCAAAACTGTCTATAAA  22086           ___
                                AAAACTAAAAC   CTGTAGA
                                ||||||||||   |||||||
                                TTTTGGTTTTG   GATATTT
                                       ACA
GAM91   CXCL13  3'  AAAACTAAAATCCAGAGCAG   26950          _ T__
                                AAAACTAAAA CC   GTAG
                                |||||||||| ||   ||||
```

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                                TTTTGATTTT GG   CGTC
                                      A  TCT
GAM91   DDX3    3'  AAAACTGCACTGTAGAGCA   35808       AAAAC      A
                                AAAACT    CTGTAGA CA
                                ||||||    ||||||| ||
                                TTTTGA    GACATCT GT
                                   CGT__      C
GAM91   DSG1    3'  AAAAACAAAACCTGAAA     12598       T      T
                                AAAAAC AAAACCTG AGA
                                |||||| |||||||| |||
                                TTTTTG TTTTGGAC TTT
                                  _      _
GAM91   ELAVL2  5'  AAAAACAAACCAAGGAACAAA 20743       TA    TGTA
                                AAAAAC  AAACC   GAACAAA
                                ||||||  |||||   |||||||
                                TTTTTG  TTTGG   CTTGTTT
                                   __    TTC_
GAM91   FZD10   3'  AAAACCAAAACAAAACAA    28446         CTGT
                                AAAACTAAAAC   AGAACAA
                                ||||||||||    |||||||
                                TTTTGGTTTTG   TTTTGTT
                                      ____
GAM91   IGF1    3'  AAAAACAAAACCAAGAAACAAA 8331        T     TGTA
                                AAAAAC AAAACC   GAACAAA
                                |||||| ||||||   |||||||
                                TTTTTG TTTTGG   TTTGTTT
                                   _     TTC_
GAM91   LTB4R   5'  AAAAACTAAAAATTCCTGGCAG 8875          ___   _
                                AAAAACTAAAA   CCTG TAG
                                ||||||||||   |||| |||
                                TTTTTGATTTT   GGAC GTC
                                      TAA   C
GAM91   MAK     3'  AAAACTAAAACACTCTAAA   25377         _  G
                                AAAACTAAAAC CT TAGA
                                |||||||||| || ||||
                                TTTTGATTTTG GA ATTT
                                      T  G
GAM91   MTR     3'  AAAAACCAAAACAAAACAA   7011          CTGT
                                AAAAACTAAAAC   AGAACAA
                                ||||||||||    |||||||
                                TTTTTGGTTTTG   TTTTGTT
                                      ____
GAM91   NAV2    3'  AAAAACCAAAACTGAGCAG   41138         CT_
                                AAAAACTAAAAC   GTAG
                                ||||||||||   ||||
                                TTTTTGGTTTTG   CGTC
                                      ACT
GAM91   SEDL    3'  AAAAACAAAAACCCACAAA   31003       T     TG
                                AAAAAC AAAACC  TAGA
                                |||||| ||||||  ||||
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                                TTTTTG TTTTGG  GTTT
                                   T     GT
GAM91   SHANK2   3'  AAAGACTGTGGAATGTAGAACA 29445     A   AAAACC
            A                   AAA ACT     TGTAGAACAA
                                ||| |||     ||||||||||
                                TTT TGA     ACATCTTGTT
                                  C   CACCTT
GAM91   SLC19A2  3'  ACTAAACCAGAACAAA      42883       A  TGT
                                ACTAAA CC   AGAACAAA
                                |||||| ||   ||||||||
                                TGATTT GG   TCTTGTTT
                                   _ ___
GAM91   SMARCA1  3'  AAAAGCTAAAACCTCAGCACAA 40048      A       G   A
                                AAAA CTAAAACCT TAG ACAA
                                |||| ||||||||| ||| ||||
                                TTTT GATTTTGGA GTC TGTT
                                  C       _  G
GAM91   SMS      3'  AAAAACAAAAGCCCACAGA    21395       T   A  TG
                                AAAAAC AAA CC  TAGA
                                |||||| ||| ||  ||||
                                TTTTTG TTT GG  GTCT
                                   T   C  GT
GAM91   SRRM1    3'  AAAATCAAAACCAAAAAAACAA 25186      C      TGT
            A                   AAAA TAAAACC   AGAACAAA
                                |||| |||||||   ||||||||
                                TTTT GTTTTGG   TTTTGTTT
                                  A      TTT
GAM91   TRHDE    3'  GAAAAATATGTAGAACAA    30107    T    CC
                                C AAAA  TGTAGAACAA
                                | ||||  ||||||||||
                                C TTTT  ACATCTTGTT
                                 T    AT
GAM91   WHSC1    3'  GGAAACCAAAACTACCTCCGAA 39370    A       __  GTA
            CAAA                    A AAACTAAAAC  CT   GAACAAA
                                | ||||||||||  ||   |||||||
                                C TTTGGTTTTG  GG   CTTGTTT
                                 C        AT  AGG
GAM91   ADAR     3'  CAACCCTAGAAAGATCA     31902       C     A
                                CAGCCC TAGAAA ATCA
                                |||||| |||||| ||||
                                GTTGGG ATCTTT TAGT
                                   _     C
GAM91   ADRBK1   3'  CAGCCCCTGAAGTCA       11525        A   AAA
                                CAGCCCCT GAA   TCA
                                |||||||| |||   |||
                                GTCGGGGA CTT   AGT
                                     _  C__
GAM91   ATRN     3'  TACACCCCATTAAATCAAA   40279      G   TAGAA
                                TACA CCCC    AAATCAAA
                                |||| ||||    ||||||||
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                                ATGT GGGG    TTTAGTTT
                                  _   TAA__
GAM91   BCL9    3'  AATAAAGCCCAAATCA     20233     C    CTAGAA
                                AATA AGCCC     AAATCA
                                |||| |||||     ||||||
                                TTAT TCGGG     TTTAGT
                                  T   _______
GAM91   EGLN1   5'  ATACAGCCTCTATTTCAA    35160       C   GAAAAA
                                ATACAGCC CTA     TCAA
                                |||||||| |||     ||||
                                TATGTCGG GAT     AGTT
                                    A   AA____
GAM91   GPR85   5'  ATACAGCCTCAGTCA      33259       CC   AAAAA
                                ATACAGCC  TAG    TCA
                                ||||||||  |||    |||
                                TATGTCGG  GTC    AGT
                                    A_  _____
GAM91   PCDHGA11 3'  GCCCCTTTGAAATCAAA    36883      AGAA
                                GCCCCT   AAATCAAA
                                ||||||   ||||||||
                                CGGGGA   TTTAGTTT
                                   AAC_
GAM91   PPIF    3'  AACACACAGAAAAATCAA    25056      GCCCC
                                AATACA    TAGAAAAATCAA
                                ||||||    ||||||||||||
                                TTGTGT    GTCTTTTTAGTT
                                   _____
GAM91   PPP2R4  3'  ACAGCCCCTGCTCTCAAA    41322       AGAAAAA
                                ACAGCCCCT     TCAAA
                                |||||||||     |||||
                                TGTCGGGGA     AGTTT
                                    CGAG___
GAM91   RABGGTB 3'  ATACATGGGGGAAAAATCAA  21366     GCCCCTA
                                ATACA     GAAAAATCAA
                                |||||     ||||||||||
                                TATGT     CTTTTTAGTT
                                  ACCCC__
GAM91   SCO1    3'  AACCCCTAGAGAAATCAAA   21377        A
                                AGCCCCTAGA AAATCAAA
                                |||||||||| ||||||||
                                TTGGGGATCT TTTAGTTT
                                    C
GAM91   SHANK2  3'  AATACAGCATGGATTAGAAATC 29446       CCC___    AA
           AAA                   AATACAGC    TAGAA  ATCAAA
                                |||||||     |||||  ||||||
                                TTATGTCG    ATCTT  TAGTTT
                                    TACCTA   __
GAM92   ATP8B2  5'  GGATCAACTGCAGAAT     42208        AA   A
                                GGATCGATT  GCA AAT
                                |||||||||  ||| |||
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```
                                CCTAGTTGA  CGT TTA
                                     __  C
GAM92   CNTNAP2  3' AGAGATTTAAAGCAAAATAA  30481      ATCGATT
                                AGAGG      AAGCAAAATAA
                                |||||      ||||||||||
                                TCTCT      TTCGTTTTATT
                                  AAAT___
GAM92   DLL3     3' AGAGGGATGCAAAATA      32623      ATC   TAA
                                AGAGG   GAT   GCAAAATA
                                |||||   |||   ||||||||
                                TCTCC   CTA   CGTTTTAT
                                  ___   ___
GAM92   ETF1     3' AAGGATTGACCCAAGCAAAATA 21827       C   _
            AA                    GAGGAT GATT AAGCAAAATAAA
                                |||||| |||| ||||||||||||
                                TTCCTA CTGG TTCGTTTTATTT
                                   A   G
GAM92   F8A      3' GAGGGCGCCGTGCAAAATAAA  29109      AT  ATTAA
                                GAGG  CG    GCAAAATAAA
                                ||||  ||    ||||||||||
                                CTCC  GC    CGTTTTATTT
                                  C_  GGCA_
GAM92   LBR      3' AGGAGAAAAGCAAAATAA    40426      TC  TT
                                AGGA  GA  AAGCAAAATAA
                                ||||  ||  ||||||||||
                                TCCT  CT  TTCGTTTTATT
                                  __  T_
GAM92   PCDHA9   3' AGGAGACCTATTAGGCAAAATA 36538    AG   G   A
                                AG  GATC ATTA GCAAAATA
                                ||  |||| |||| ||||||||
                                TC  CTGG TAAT CGTTTTAT
                                 CT   A   C
GAM92   PTGS1    3' AGAGGATTCTCAAGCAAAGTAA 38727       CGA       A
                                AGAGGAT   TTAAGCAAA TAA
                                |||||||   ||||||||| |||
                                TCTCCTA   AGTTCGTTT ATT
                                    AG_       C
GAM92   SEL1L    3' AGAGAAAGACAAAGCAAAATAA 22843       TC   T
            A                    AGAGGA  GAT AAGCAAAATAAA
                                ||||||  ||| ||||||||||||
                                TCTCTT  CTG TTCGTTTTATTT
                                   T_   T
GAM92   SHANK2   3' AGAGGTAGCAAAATA      39327      ATCGATTA
                                AGAGG       AGCAAAATA
                                |||||       |||||||||
                                TCTCC       TCGTTTTAT
                                  A_______
GAM92   SLC25A17 3' AAAGGATTGATTCAAAATAAA 26821       C   AAG
                                AGAGGAT GATT   CAAAATAAA
                                ||||||| ||||   |||||||||
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                                TTTCCTA CTAA   GTTTTATTT
                                    A   ___
GAM93   RFXAP    3'  TTTAAAGTTTTAAAGTTTTC   8060          AATT
                                TTTAAAGTTTTA   GAGTTTTC
                                ||||||||||||   ||||||||
                                AAATTTCAAAAT   TTCAAAAG
                                     _____
GAM94   ITGA1    3'  TTCGCTGTCACTTGTTGCACTT 41863      C        A_
                                TTCGT GTCACTTGTT  ACTT
                                ||||| ||||||||||  ||||
                                AAGCG CAGTGAACAA  TGAA
                                   A         CG
GAM95   ENAM     5'  TGAAATATATTCTTAATGGTC  36678       TTA   AAC
                                TGAAATAT   TCT   AATGGTC
                                ||||||||   |||   |||||||
                                ACTTTATA   AGA   TTACCAG
                                     TA_   A__
GAM95   FDX1     3'  TGAAATATTTATTTATAAGGTC 41269          C  ACAAT
                                TGAAATATTTAT TA    GGTC
                                ||||||||||||  ||    ||||
                                ACTTTATAAATA AT    CCAG
                                      A  ATT__
GAM95   PRKACB   3'  TATTTATCTAAACCAATG    15596          __
                                TATTTATCTAA  CAATG
                                ||||||||||  |||||
                                ATAAATAGATT  GTTAC
                                      TG
GAM95   RAD54B   3'  TGAAATATTTAACTAGGC    39584          T   ACAAT
                                TGAAATATTTA CTA    GGT
                                ||||||||||| |||    |||
                                ACTTTATAAAT GAT    CCG
                                      T  _____
GAM95   SLC6A8   3'  TGAAATATTTGCCTTGGT    24788         AT  AACAA
                                TGAAATATTT  CT    TGGT
                                ||||||||||  ||    ||||
                                ACTTTATAAA  GA    ACCA
                                      CG  _____
GAM95   UGT2B4   3'  TGAAATATTTCTAATGGT    43535         TA    ACA
                                TGAAATATT  TCTA   ATGGT
                                |||||||||  ||||   |||||
                                ACTTTATAA  AGAT   TACCA
                                     __   ___
GAM95   AASS     3'  TATCACACACATGTTCAGAGGT 25097          A___   T
                                TATCACACACA   TAGA GT
                                ||||||||||    |||| ||
                                ATAGTGTGTGT    GTCT CA
                                      ACAA   C
GAM95   ANXA5    3'  TATCATGGTTACAAATGTAATA 10103       CACACA
           T                    TATCA     ATAGATGTAATAT
                                |||||     ||||||||||||
```

```
                                ATAGT     TGTTTACATTATA
                                  ACCAA_
GAM95   BCKDHB   3'  TATCACACACATAATAT     6291          ATA
                                TATCACACACA   GATGT
                                ||||||||||   |||||
                                ATAGTGTGTGT   TTATA
                                      A__
GAM95   CYP3A43  3'  TATCACAAATGGAACATGTAAT 38400       CACAATAG
           AT                    TATCACA       ATGTAATAT
                                |||||||       |||||||||
                                ATAGTGT       TACATTATA
                                    TTACCTTG
GAM95   DR1      3'  TATAGCACACAATAGATG    40443     CA
                                TAT  CACACAATAGATG
                                |||  ||||||||||||
                                ATA  GTGTGTTATCTAC
                                  TC
GAM95   HIVEP2   3'  TATTACATACAACAGACAT    27554     C   C
                                TAT ACA ACAATAGATGT
                                ||| ||| ||||||||||
                                ATA TGT TGTTGTCTGTA
                                  A   A
GAM95   IL1F9    3'  TATTACACACAATGAGGTA    33350     C       A  T
                                TAT ACACACAAT GA GTA
                                ||| ||||||||| || |||
                                ATA TGTGTGTTA CT CAT
                                  A       _  C
GAM95   KCNN4    5'  TCACACACAATGGTCTGT     13929          AGA_
                                TCACACACAAT    TGT
                                ||||||||||    |||
                                AGTGTGTGTTA    ACA
                                      CCAG
GAM95   LRP8     3'  TCACACACATACACATAT     37799         _  G
                                TCACACACA ATA ATGT
                                ||||||||| ||| ||||
                                AGTGTGTGT TGT TATA
                                     A   G
GAM95   ZIC1     5'  ATCATGCACAATATATGT     18225      CA      G
                                ATCA  CACAATA ATGT
                                ||||  ||||||| ||||
                                TAGT  GTGTTAT TACA
                                  AC      A
GAM95   ZNF36    3'  TATCACACACGTAGAAGT     45296          AA    T
                                TATCACACAC  TAGA GT
                                ||||||||||  |||| ||
                                ATAGTGTGTG  ATCT CA
                                      C_    T
GAM96   ACTN2    3'  TAAACTGACTTCCACGTGTCCT 9951           _ G  T__
           T                     TAAACTGATT C AT   TCCTT
                                ||||||||||| | ||   |||||
```

```
                                ATTTGACTGA G TG   AGGAA
                                     A G  CAC
GAM96   ERBB4    3'  AACTGAACAAATTTCCTT    23453       TTC
                                AACTGA   GATTTCCTT
                                ||||||   |||||||||
                                TTGACT   TTAAAGGAA
                                   TGT
GAM96   MCL1     3'  TAAATTCGATACTTCCTT    35000    T      __
                                C GATTCGAT  TTCCTT
                                | ||||||||  ||||||
                                A TTAAGCTA  AAGGAA
                                 T       TG
GAM96   MOX2     3'  TAAACTGACTTCCTC       42519         TCGAT
                                TAAACTGAT    TTCCTT
                                |||||||||    ||||||
                                ATTTGACTG    AAGGAG
                                     _____
GAM96   PIGN     3'  CAAACTGATTTCTGACTC    29546          _ _
                                TAAACTGATT C GATTT
                                |||||||||| | |||||
                                GTTTGACTAA G CTGAG
                                     A A
GAM96   RNF12    5'  ACTGATCACCACTTCCTT    32032        CG_
                                ACTGATT   ATTTCCTT
                                |||||||   ||||||||
                                TGACTAG   TGAAGGAA
                                   TGG
GAM96   SH3BP4   3'  TAAACTATGACTTCCTT     30963        ATTC
                                TAAACTG    GATTTCCTT
                                |||||||    |||||||||
                                ATTTGAT    CTGAAGGAA
                                   A___
GAM96   ZNF265   3'  AACTGTTGATTTCCTT      24146       A  C
                                AACTG TT GATTTCCTT
                                ||||| || |||||||||
                                TTGAC AA CTAAAGGAA
                                   _ _
GAM97   CYP8B1   3'  TATGTTGGATGACACTG     20508       AGAC
                                TATGT    GATGACACTG
                                |||||    ||||||||||
                                ATACA    CTACTGTGAC
                                   AC__
GAM97   ENTPD6   3'  TATGCAGACACACAGACACTG  10341          AT__
                                TATGTAGACG    GACACTG
                                ||||||||||    |||||||
                                ATACGTCTGT    CTGTGAC
                                     GTGT
GAM97   FUT6     5'  ATGCCCGTGACACTG       6648       AGA  A
                                ATGT   CG TGACACTG
                                ||||   || ||||||||
```

```
                                TACG   GC ACTGTGAC
                                  G__  _
GAM97   IFNAR2   3'  TATGTAAACAATGCACTG    9323          A
                                TATGTAGACGATG CACTG
                                |||||||||||| |||||
                                ATACATTTGTTAC GTGAC
                                          _
GAM97   PDLIM1   3'  TGCTGACAAGGTGACACTG   34196    A    __
                                TGT GACGA  TGACACTG
                                ||| |||||  ||||||||
                                ACG CTGTT  ACTGTGAC
                                  A    CC
GAM97   RAD52    3'  ATGTAGACAATTGCTG     39554         GACA
                                ATGTAGACGAT    CTG
                                ||||||||||    |||
                                TACATCTGTTA    GAC
                                      AC__
GAM97   RAP1     3'  TATGTAGACCAACTCCTG    33269        GAT   A_
                                TATGTAGAC   GAC  CTG
                                |||||||||   |||  |||
                                ATACATCTG   TTG  GAC
                                     G__   AG
GAM97   SULT2B1  5'  TGTAAAGTGGTGACACTG    21419       CGA_
                                TGTAGA    TGACACTG
                                ||||||    ||||||||
                                ACATTT    ACTGTGAC
                                   CACC
GAM97   ZNF264   3'  TATGTGCACAATAACCACTG   18274      AG      _
                                TATGT  ACGATGAC ACTG
                                |||||  |||||||| ||||
                                ATACA  TGTTATTG TGAC
                                   CG       G
GAM97   FACL3    3'  TACATATAGTCAACGAAA    20882       A   GT
                                TACATG TAG  GACGAAA
                                |||||| |||  |||||||
                                ATGTAT ATC  TTGCTTT
                                   _   AG
GAM97   PEX10    3'  TACATGACAAAAAACTGA    15223          T   _
                                TACATGATAGG GAC GA
                                |||||||||||| ||| ||
                                ATGTACTGTTT TTG CT
                                      T   A
GAM97   SPAP1    3'  TGATAGGTAAAAGAAGATATT  39867         C_   A
                                TGATAGGTGA  GAA ATATT
                                ||||||||||  ||| |||||
                                ACTATCCATT  CTT TATAA
                                      TT   C
GAM98   FOSB     3'  GCAACAGTGCAGAACCA     27540        AA
                                GCAACAGT  CAGAACCA
                                ||||||||  ||||||||
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```
                                CGTTGTCA  GTCTTGGT
                                    C_
GAM98   GPR63    3'  TTATTCTTGGTAACAGAAC   36267     GCAACA
                                TTAT     GTAACAGAAC
                                ||||     ||||||||||
                                AATA     CATTGTCTTG
                                  AGAAC_
GAM98   SCEL     3'  TTATGCAATAACAGAA     40718       ACA
                                TTATGCA   GTAACAGAA
                                |||||||   |||||||||
                                AATACGT   TATTGTCTT
                                    ___
GAM98   WNT5A    3'  CATTATGCAATAAATTAAGAGC 18116         C  TAAC   A
            CA                    TATTATGCAA AG    AGA CCA
                                ||||||||||  ||    ||| |||
                                GTAATACGTT TT    TCT GGT
                                      A  TAAT   C
GAM98   WNT5A    3'  CATTATGCAATAAATTAAAGAG 18115         CAG__   C   A
            CCA                   TATTATGCAA    TAA AGA CCA
                                ||||||||||    ||| ||| |||
                                GTAATACGTT    ATT TCT GGT
                                      ATTTA  _  C
GAM98   GALNT7   3'  TACTGTCTTAGTAAATGTTTAA 38360       CTA  CAC
                                TACTGTC   AG   AATGTTTAA
                                |||||||   ||   |||||||||
                                ATGACAG   TC   TTACAAATT
                                    AA_  AT_
GAM98   GPM6B    3'  TACTGCTCTCTAATGTTTA   42542      TC  AAGCAC
                                TACTG  CT     AATGTTTA
                                |||||  ||     ||||||||
                                ATGAC  GA     TTACAAAT
                                   GA  GA____
GAM98   JAK2     3'  TGTTAACAGACAATGTTTAA   22480     CCTA  C
                                TGT    AG ACAATGTTTAA
                                |||    || ||||||||||
                                ACA    TC TGTTACAAATT
                                  ATTG  _
GAM99   CAPZA1   5'  TCCAGAATAGGCGC       43721          GAAGTC
                                TCCAGAATAGG     CGC
                                ||||||||||     |||
                                AGGTCTTATCC     GCG
                                    _______
GAM99   CBS      3'  GTCCAGAACAGGGAAAACC   6307              T
                                GTCCAGAATAGGGAAG CC
                                |||||||||||||||| ||
                                CAGGTCTTGTCCCTTT GG
                                          T
GAM99   CD79B    3'  GTCCAGGAAAGGGGTTGGGCCA 8423        AAT    AAGTCC
            T                    GTCCAG   AGGG     GCCAT
                                ||||||   ||||     |||||
```

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                                CAGGTC  TCCC    CGGTA
                                   CTT   CAACC_
GAM99   NRIP1   3' GTCCAGAAATGGAATACTGTC 40968       TAG   ____
                                GTCCAGAA  GGAA   GTC
                                ||||||||  ||||   |||
                                CAGGTCTT  CCTT   CAG
                                    TA_   ATGA
GAM99   RFX2    3' GTCCAGAATAAGGAACCCA  8458          G
                                GTCCAGAATAGGGAA TCCG
                                |||||||||||||| ||||
                                CAGGTCTTATTCCTT GGGT
                                                _
GAM99   TGFB1   5' GTCTTGAATAGGGGATC    8551    CA     AA
                                GTC  GAATAGGG  GTC
                                |||  ||||||||  |||
                                CAG  CTTATCCC  TAG
                                  AA      C_
GAM99   CD81    3' TCCCTGTGGCCAGAGCTG   20348    CAT      A
                                TCCC  TGGCCAGAG TG
                                ||||  ||||||||| ||
                                AGGG  ACCGGTCTC AC
                                  AC_      G
GAM99   FLRT2   3' ATTGGCCAGTGAGCATG    29838       AGA  _
                                ATTGGCCAG  TGA CGTG
                                |||||||||  ||| ||||
                                TAACCGGTC  ACT GTAC
                                     ___  C
GAM99   SOX11   3' TCCCCACTGGCTAGGCTGCCGT 17039         C  AGA  A
          G                      TCCCCATTGGC AG  TG CGTG
                                ||||||||||| ||  || ||||
                                AGGGGTGACCG TC  AC GCAC
                                      A  CG_  G
GAM99   SPTBN2  5' TCCTTGTGGCCAGAGGCTG  28075    CCAT      A_
                                TCC   TGGCCAGAG  TG
                                |||   |||||||||  ||
                                AGG   ACCGGTCTC  AC
                                  AAC_      CG
GAM100  SLC7A5  5' CGCACCGGCCGGGCC      18544     ATAG G
                                CGCA   T GGCCGGGCC
                                ||||   | |||||||||
                                GCGT   G CCGGCCCGG
                                  ____ G
GAM100  CLCN4   3' TCAAAATAAGGATGTGTCCCTT 12291   C      TCA  CGC
                                TC AAATAAGG  GT  CCCTT
                                || ||||||||  ||  |||||
                                AG TTTATTCC  CA  GGGAA
                                 T      TA_  CA_
GAM100  PER2    3' TCCACAGTTTTAAGTCGCCCCT 19348     AATAAGGTC
            T                   TCCA       AGTCGCCCCTT
                                ||||       ||||||||||
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                                AGGT       TCAGCGGGGAA
                                  GTCAAAAT_
GAM100  TCF8    3'  CCAGGTAAGGGCCGCCCCTT  36235    AA    TCA
                                CCA  TAAGG   GTCGCCCCTT
                                |||  |||||   ||||||||||
                                GGT  ATTCC   CGGCGGGGAA
                                  CC    ___
GAM101  ACCN2   3'  GGACAGTCACTGGGC      33449      CCCC
                                GGACAG    CATTGGGC
                                ||||||    ||||||||
                                CCTGTC    GTGACCCG
                                   A___
GAM101  ARHGDIB  3'  TAGGGACTCATTGGGC     10128    T   AGCCCC
                                TAG GGAC     CATTGGGC
                                ||| ||||     ||||||||
                                ATC CCTG     GTAACCCG
                                  _   A_____
GAM101  BACE    3'  AGTGGACAGTCTCCAGTCTTCC 39951        CCC   TTGGG
                                AGTGGACAG   CCA    CC
                                |||||||||   |||    ||
                                TCACCTGTC   GGT    GG
                                     AGA   CAGAA
GAM101  BMP1    3'  ATGGACAGTCTCACCAGGCCA  25972       CCCC   TG
                                GTGGACAG    CAT  GGCCA
                                ||||||||    |||  |||||
                                TACCTGTC    GTG  CCGGT
                                     AGA_   GT
GAM101  CEACAM5  3'  GTGGACAGTTTCATGAAGC   20376       CCCC   TG
                                GTGGACAG    CAT  GGC
                                ||||||||    |||  |||
                                CACCTGTC    GTA  TCG
                                     AAA_   CT
GAM101  ERBB4    3'  TGGATTCCCTCATTGGGCC   23458     CAG   C
                                TGGA   CCC CATTGGGCC
                                ||||   ||| |||||||||
                                ACCT   GGG GTAACCCGG
                                  AA_   A
GAM101  MECP2    3'  ATGGAGCCCCTGTTGGGCCA  22574     CA    CA
                                GTGGA  GCCCC  TTGGGCCA
                                |||||  |||||  ||||||||
                                TACCT  CGGGG  AACCCGGT
                                   __     AC
GAM101  PAX2     3'  AGTGGGCAGCCCCCCACTTCCA 19604      A      ATTGGG
                                AGTGG CAGCCCCC     CCA
                                ||||| ||||||||     |||
                                TCACC GTCGGGGG     GGT
                                   C       GTGAA_
GAM101  PCOLN3   3'  GTGGACAGGCTCCCTGTCG   15754        _ _   CA
                                GTGGACAG C CCC  TTG
                                |||||||| | |||  |||
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                                CACCTGTC G GGG  AGC
                                    C A   AC
GAM101  TXNRD2   3'  GTGGACAGTCCCCTGAGCCA  26978       C   AT
                                GTGGACAG CCCC  TGGGCCA
                                |||||||| ||||  |||||||
                                CACCTGTC GGGG  ACTCGGT
                                    A   __
GAM101  AP2B1    3'  TGCCCTAATGTTAGCACAGGT  10496       ____
                                TGCCCTAAT   GCATAGGT
                                |||||||||   ||||||||
                                ACGGGATTA   CGTGTCCA
                                     CAAT
GAM101  C18orf1  3'  CCTAATGCATCCAG       41220         AGGTA
                                CCTAATGCAT    TCAG
                                ||||||||||    ||||
                                GGATTACGTA    GGTC
                                      _____
GAM101  ITGA1    3'  TGTCCTGGTGTTATAGGCACTG 41860    C   AA  C_      CA
           TC                     TG CCT  TG  ATAGGTAT  GTC
                                || |||  ||  ||||||||  |||
                                AC GGA  AC  TATCCGTG  CAG
                                 A  CC  AA      A_
GAM101  LAMC1    3'  TGCCCTAAGTGCTCAG      14095        _  ATAGGTA
                                TGCCCTAA TGC      TCAG
                                |||||||| |||      ||||
                                ACGGGATT ACG      AGTC
                                    C  ________
GAM101  MPP5     3'  TGCCCAGTGCATAGAAGCACAG 35399      TAA      TAT_
           TC                     TGCCC   TGCATAGG    CAGTC
                                |||||   ||||||||    |||||
                                ACGGG   ACGTATCT    GTCAG
                                   TC_       TCGT
GAM101  SYT1     3'  TGTCCTATGCATAGCTTTTCAG 24856    C   A     GTA_
           T                     TG CCTA TGCATAG    TCAGT
                                || |||| |||||||    |||||
                                AC GGAT ACGTATC    AGTCA
                                 A   _      GAAA
GAM101  ZFP93    3'  TGTCCTAATTATAGGTAT    20148    C     GC
                                TG CCTAAT  ATAGGTAT
                                || ||||||  ||||||||
                                AC GGATTA  TATCCATA
                                 A     A_
GAM102  CEP1     3'  ACTATGTACAAGTGATTTATAA 28137        AA   TC_
           A                      ACTATGTA  GAGT   TTATAAA
                                ||||||||  ||||  |||||||
                                TGATACAT  TTCA   AATATTT
                                    G_    CTA
GAM102  COL6A2   3'  ATGACCAGGGTTCTTATAAA   38435     TAA  A
                                ATG   AG GTTCTTATAAA
                                |||   || ||||||||||
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```
                                TAC   TC CAAGAATATTT
                                  TGG  C
GAM102  SLC20A2  5'  GCCAAGAGTTCTTGTAAA    27574    A        A
                                GT AAGAGTTCTT TAAA
                                || |||||||||| ||||
                                CG TTCTCAAGAA ATTT
                                 G         C
GAM102  TSG      3'  ACTATGTAAGAGTTCTCA    33998         A
                                ACTATGTAA GAGTTCTTA
                                ||||||||| |||||||||
                                TGATACATT CTCAAGAGT
                                      _
GAM103  B3GALT5  3'  AGTGGCTGGTCCCCATTGA   37676      GTAGC
                                AGTGG    CCCCATTGG
                                |||||    |||||||||
                                TCACC    GGGGTAACT
                                   GACCA
GAM103  COL18A1  3'  GTGGGGGCTTCCTCCGAGCCGC 39059      TA  CC  A
                                GTGGG  GC  CC TTGGGCCGC
                                |||||  ||  || |||||||||
                                CACCC  CG  GG GGCTCGGCG
                                   C_  AA  A
GAM103  DSC3     3'  AGTGGGTGTTTCAGTAGCCG   35941       AGCCCC  TTG
                                AGTGGGT     CA   GGCCG
                                |||||||     ||   |||||
                                TCACCCA     GT   TCGGC
                                    CAAA__  CA_
GAM103  KCNJ16   3'  AGTGGTAGCCCTCATAATTGC  33014      G     C   TGG_
                                AGTGG TAGCCC CAT    GC
                                ||||| |||||| |||    ||
                                TCACC ATCGGG GTA    CG
                                   _     A   TTAA
GAM103  MFAP2    3'  AGTGGGGAGCCCCCATCG    32705       T
                                AGTGGG AGCCCCCATTG
                                |||||| ||||||||||
                                TCACCC TCGGGGGTAGC
                                   C
GAM103  PEA15    3'  AGTGGGTAGATGGTGGGTTGC  19076         CCCCCAT   CC
                                AGTGGGTAG      TGGG  GC
                                |||||||||      ||||  ||
                                TCACCCATC      ACCC  CG
                                     TACC____   AA
GAM103  ZNF261   3'  AGTGGGTACCCCCTTTG     22988        G    A
                                AGTGGGTA CCCCC TTG
                                |||||||| ||||| |||
                                TCACCCAT GGGGG AAC
                                     _    A
GAM103  DFFB     3'  CAGTGGCTCACACCTGTCAT   44596    A        ATA
                                CA TGGCTCATAC   GTCAT
                                || ||||||||||   |||||
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```
                                GT ACCGAGTGTG   CAGTA
                                 C         GA_
GAM103  MAGP2    3'  TAAGCCATATAGTCATCA    18498   T  T   CA
                                A GGC CATA  TAGTCATCA
                                | ||| ||||  |||||||||
                                A TCG GTAT  ATCAGTAGT
                                 T  _   __
GAM103  PODXL    3'  GGCTTCCTAGTCATCAT     23979      CATACA
                                GGCT     TAGTCATCAT
                                ||||     ||||||||||
                                CCGA     ATCAGTAGTA
                                  AGG___
GAM103  TPMT     3'  CAATGGCTCATACCTGT     7493             ATA
                                CAATGGCTCATAC   GT
                                ||||||||||||   ||
                                GTTACCGAGTATG   CA
                                        GA_
GAM104  NDUFA2   3'  TCAGTGGTTGCACCATTAAGGG 14739        GAG    C
                                TCAGTGG   GTACC ATTAAGGG
                                |||||||   ||||| ||||||||
                                AGTCACC   CGTGG TAATTCCC
                                    AA_    _
GAM104  RAB5B    3'  AGGGGAAACACCATTAGGGG   16088    T   GG   C   A
                                AG GGGA  TACC ATTA GGG
                                || ||||  |||| |||| |||
                                TC CCCT  GTGG TAAT CCC
                                 _   TT   _   C
GAM104  ADCY6    3'  ACCTCCTGACTCCTCTACCAAC 31611     C       CC_  TG
           T                     GCC CCTGACTCC   AT  GCT
                                ||| |||||||||   ||  |||
                                TGG GGACTGAGG   TG  TGA
                                  A        AGA  GT
GAM104  ARMET    5'  GCCCTCCCTCATTGGCT     25666      CCTGAC   _
                                GCCC     TCCC CATTGGCT
                                ||||     |||| ||||||||
                                CGGG     AGGG GTAACCGA
                                  _______   A
GAM104  ASC      5'  CCCGACTCCCCGCC        29939          ATTG
                                CCTGACTCCCC    GCT
                                ||||||||||    |||
                                GGGCTGAGGGG    CGG
                                       ____
GAM104  BCL7A    3'  GCCCCCTGGCTCGAAGCT    34210        A   CCCATT
                                GCCCCCTG CTC     GGCT
                                |||||||| |||     ||||
                                CGGGGGAC GAG     TCGA
                                    C   CT____
GAM104  C1QB     3'  GCCCTACTGTGTCCATTGGCT  7945      C_   ACTCC
                                GCCC  CTG    CCATTGGCT
                                ||||  |||    |||||||||
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                                CGGG  GAC    GGTAACCGA
                                  AT   ACA__
GAM104  COL18A1  3'  CCCTTGAATCTCCCAGCTTGG  39053     C   __    CA_
                                CCC TGA  CTCCC   TTGG
                                ||| |||  |||||   ||||
                                GGG ACT  GAGGG   AACC
                                  A   TA    TCG
GAM104  DISC1    3'  TGACTCCCTAACCAA      33051        CAT
                                TGACTCCC   TGGCTAA
                                ||||||||   |||||||
                                ACTGAGGG   ATTGGTT
                                     ___
GAM104  ELK3     5'  GCCCCCGACTTTCCATGCT   23420       T   CC   TG
                                GCCCCC GACT  CCAT  GCT
                                |||||| ||||  ||||  |||
                                CGGGGG CTGA  GGTA  CGA
                                   _   AA   __
GAM104  ESR1     3'  GCTACCTGGGTCATTGGCTAA  6529     CC   ACTCCC
                                GC  CCTG     CATTGGCTAA
                                ||  ||||     ||||||||||
                                CG  GGAC     GTAACCGATT
                                 AT   CCA___
GAM104  EVX1     5'  GCTCCCTGGGTCTCCAGCGG   12771    C    AC  C   T
                                GC CCCTG  TC CCA TGG
                                || |||||  || ||| |||
                                CG GGGAC  AG GGT GCC
                                 A    CC  A   C
GAM104  FUT7     3'  GCTTCCTGACCTCTGTGCCCA  20993    CC    _ ____
                                GC  CCTGAC TC    CCCA
                                ||  |||||| ||    ||||
                                CG  GGACTG AG    GGGT
                                 AA     G  ACAC
GAM104  GAB2     3'  CCTTGACTCCCTGGGTTGG   38678    C      CA__
                                CC TGACTCCC    TTGG
                                || ||||||||    ||||
                                GG ACTGAGGG    AACC
                                 A       ACCC
GAM104  GNAZ     3'  GCCCCCTGTTTTCTGCCCCTGG 13182        A___ _   AT
                                GCCCCCTG   CT CCCC  TGG
                                ||||||||   || ||||  |||
                                CGGGGGAC   GA GGGG  ACC
                                    AAAA  C   __
GAM104  GNGT2    5'  GCCTCCTAGTTCTTCATCAGCT 36484    C   AC  CC   TG
                                GCC CCTG  TC  CAT  GCT
                                ||| ||||  ||  |||  |||
                                CGG GGAT  AG  GTA  CGA
                                  A   CA  AA   GT
GAM104  GPR65    5'  GCTCCTGGCAATTGGCTA    40735    CC   ACTCCCC
                                GC  CCTG     ATTGGCTA
                                ||  ||||     ||||||||
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```
                              CG  GGAC      TAACCGAT
                               A_    CGT____
GAM104  GSTM3    3'  CCCAACTCTATTGGCTA     42761    TG   CCC
                              CC  ACTC   ATTGGCTA
                              ||  ||||   ||||||||
                              GG  TGAG   TAACCGAT
                               GT    A__
GAM104  HBE1     5'  GCCCCCTGTTCTCCATGG    23726        AC  C    T
                              GCCCCCTG  TC CCAT GG
                              ||||||||  || |||| ||
                              CGGGGGAC  AG GGTA CC
                                   A_ A    _
GAM104  HEM1     5'  GCCCCCTGGTTTCTTCGG    23739        AC_  CCCA
                              GCCCCCTG   TC    TTGG
                              ||||||||   ||    ||||
                              CGGGGGAC   AG    AGCC
                                   CAA  A___
GAM104  HLA-DMB  5'  CCCTTGACCCCCCAAATGA   13381     C        T_
                              CCC TGACTCCCCA  TGG
                              ||| ||||||||||  |||
                              GGG ACTGGGGGGT  ACT
                                A         TT
GAM104  HOXD3    3'  GCTTCCTGACTCTACCCAT   27898    CC       __
                              GC  CCTGACTC  CCCAT
                              ||  ||||||||  |||||
                              CG  GGACTGAG  GGGTA
                               AA       AT
GAM104  HSF2BP   5'  GCCCTCTGACCCCTCACGCCA 28146     C       C   TG
                              GCCC CTGACTCC CAT  GCTA
                              |||| |||||||| |||  ||||
                              CGGG GACTGGGG GTG  CGGT
                                A       A  __
GAM104  IFIT4    3'  GCCCCCTGTCTTCCTATCG   43368        A  C  C
                              GCCCCCTG CT CC ATTG
                              |||||||| || || ||||
                              CGGGGGAC GA GG TAGC
                                   A  A  A
GAM104  ITPKB    3'  GCCCCCTGGGCTCTCCGGTGG  13647        A_   C  AT
                              GCCCCCTG  CTC CC  TGG
                              ||||||||  ||| ||  |||
                              CGGGGGAC  GAG GG  ACC
                                   CC   A  CC
GAM104  KCNK6    3'  CCTCCCTGACTTTCCAGGCT   22079    _      CC   TT
                              CC CCCTGACT  CCA  GGCT
                              || ||||||||  |||  ||||
                              GG GGGACTGA  GGT  CCGA
                               A       AA  __
GAM104  MSF      5'  GCCCCCTGGCTCAGCT      44730        A   CCCATT
                              GCCCCCTG CTC     GGCT
                              |||||||| |||     ||||
```

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                                CGGGGGAC GAG     TCGA
                                    C  _______
GAM104  NEDD4L   3'  CCCCTGACTGCCCCGAC    31617        _   ATT
                                CCCCTGACT CCCC   GGC
                                ||||||||| ||||   |||
                                GGGGACTGA GGGG   CTG
                                    C   ___
GAM104  Nrap     3'  CCTGACTCCCTAAGTGTTGG  40191        CA____
                                CCTGACTCCC     TTGG
                                ||||||||||     ||||
                                GGACTGAGGG     AACC
                                     ATTCAC
GAM104  P2RY6    3'  CCTGACTCCTTGGACT      19989        CCA   _
                                CCTGACTCC   TTGG CT
                                |||||||||   |||| ||
                                GGACTGAGG   AACC GA
                                    ___    T
GAM104  PIK3R2   5'  GCCCCACTGGCCCCATTGG   22748      _  ACT
                                GCCCC CTG   CCCCATTGG
                                ||||| |||   |||||||||
                                CGGGG GAC   GGGGTAACC
                                   T  C__
GAM104  PTBP1    3'  GCCCCCTGCCTCTCTCTGG   36720       A  CCCA
                                GCCCCCTG CTC    TTGG
                                |||||||| |||    ||||
                                CGGGGGAC GAG    GACC
                                    G   AGA_
GAM104  TAL1     3'  CCTGACCCTCCGGCC       17282       C  ATT
                                CCTGACTC CC   GGCT
                                |||||||| ||   ||||
                                GGACTGGG GG   CCGG
                                    A  ___
GAM104  TEAD3    3'  GCTCACTGACTCCCTTGG    17375    CCC       CA
                                GC   CTGACTCCC  TTGG
                                ||   |||||||||  ||||
                                CG   GACTGAGGG  AACC
                                 AGT        __
GAM104  TEM8     3'  GCCCCCTGGCTTTCCCATTCTC 38183       A  C_     GG
            C                    GCCCCCTG CT  CCCATT  CT
                                ||||||||  ||  ||||||  ||
                                CGGGGGAC GA  GGGTAA  GG
                                    C  AA     GA
GAM105  CBFB     3'  TGTGATGTCTATTACTGC    35636         CACCAA  C
                                TGTGATGTCT     GC GC
                                ||||||||||     || ||
                                ACACTACAGA     TG CG
                                     TAA___  A
GAM105  COL4A4   3'  TGTGATGTGTTTATGCTAACGT 6411         CTCACCAA  ___  C
            CGC                    TGTGATGT       GC   CG CGC
                                ||||||||       ||   || |||
```

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                                ACACTACA      CG  GC GCG
                                    CAAATA__  ATT  A
GAM105  DNCI1   5'  TGTGCTGTCTCACGCTGC   44996     A      CAA  C
                                TGTG TGTCTCAC  GC GC
                                |||| ||||||||  || ||
                                ACAC ACAGAGTG  CG CG
                                  G      ___  A
GAM105  GARS    5'  GTGACGCGGCGCCGGGTCGCCG 13061       CTCA  AAGC
          C                      GTGATGT   CC   CGCCGC
                                |||||||   ||   ||||||
                                CACTGCG   GG   GCGGCG
                                    CCGC  CCCA
GAM105  MYD88   3'  TGTGATGTCCAGCTGCG    14724         CACCA  C  C
                                TGTGATGTCT    AGC GC G
                                ||||||||||    ||| || |
                                ACACTACAGG    TCG CG C
                                      _____   A  A
GAM105  SLC20A2 5'  TGTGATGTCTCCTCCTGC   27580          A_  AA
                                TGTGATGTCTC  CC  GC
                                ||||||||||  ||  ||
                                ACACTACAGAG  GG  CG
                                      GA  A_
GAM106  PPP2R5E 3'  TCCTAATTTTAAAACTAAAGG  26478          CT    A
                                TCCTAATTTTAA  CTAAA GG
                                ||||||||||||  ||||| ||
                                AGGATTAAAATT  GATTT CC
                                      TT    _
GAM106  TZFP    5'  CCTAACTCAGAGGCTCTAAGAG 30787        TAA__     A
          G                     CCTAATTT    CTCTAA AGG
                                ||||||||    |||||| |||
                                GGATTGAG    GAGATT TCC
                                    TCTCC     C
GAM106  APPL    3'  TGTAAAATTATTAAAGTCTTAG 29015          T    A
          TG                      TGTAAAATTATT AAGTT TGGTG
                                ||||||||||| ||||| |||||
                                ACATTTTAATAA TTCAG ATCAC
                                      T     A
GAM106  CNTN3   3'  TGTAAAATAGTGCTTTATGGTG 42488        TATTTAAG
                                TGTAAAAT       TTATGGTG
                                ||||||||       ||||||||
                                ACATTTTA       AATACCAC
                                    TCACGA__
GAM106  UGDH    3'  TGTAAAATATTTAAGTT     17887         T
                                TGTAAAAT ATTTAAGTT
                                |||||||| |||||||||
                                ACATTTTA TAAATTCAA
                                      _
GAM107  ARHGAP6 5'  AAAGTGAAAGCTGCCGGATGG  30204          C_    _
                                AAAGTGAAAGT  CTGGA GG
                                ||||||||||  ||||| ||
```

```
                                TTTCACTTTCG  GGCCT CC
                                      AC    A
GAM107  ATF5    5'  AAAGTGGAAGACTCCATGG   28934       A  __  _
                                AAAGTG AAG  TCC TGG
                                |||||| |||  ||| |||
                                TTTCAC TTC  AGG ACC
                                   C   TG   T
GAM107  ATP7A   3'  AAACTGAAAGCATGGAGGATGG 6257     G     CC      A
            C                    AAA TGAAAGT  TGGAGGAT GC
                                ||| |||||||  |||||||| ||
                                TTT ACTTTCG  ACCTCCTA CG
                                  G      T_      C
GAM107  C18orf1 3'  GGATGGAAGATAGAGGATGGC  41222   A  A  TCC      A
                                A GTG AAG   TGGAGGAT GC
                                | ||| |||   |||||||| ||
                                C TAC TTC   ATCTCCTA CG
                                 C  C  T__       C
GAM107  COG2    3'  AGTGGGAGTGGAGGATGGC   28878     AA  CCT     A
                                AGTG  AGT   GGAGGAT GC
                                ||||  |||   ||||||| ||
                                TCAC  TCA   CCTCCTA CG
                                  CC  ___      C
GAM107  DDX11   3'  AAGAGAAAGTCGTTGATGG   36162     T     CTG  _
                                AAG GAAAGTC   GA GG
                                ||| |||||||   || ||
                                TTC CTTTCAG   CT CC
                                  T      CAA  A
GAM107  GPR4    5'  GGAGGGAAGTCTGGAGGAT   40888   A  T   A   C
                                A AG GAA GTC TGGAGGAT
                                | || ||| ||| ||||||||
                                C TC CTT CAG ACCTCCTA
                                 C  C  _  _
GAM107  PDE7A   3'  GGAGTGAAAGCTTGGCGG   42287   A       CC  A
                                A AGTGAAAGT  TGG GG
                                | |||||||||  ||| ||
                                C TCACTTTCG  ACC CC
                                 C       A_  G
GAM107  PIK3R3  3'  GGAGTGAAAGTGTTGGGAGG  41445   A       CCT_
                                A AGTGAAAGT   GGAGG
                                | |||||||||   |||||
                                C TCACTTTCA   CCTCC
                                 C       CAAC
GAM107  SEL1L   3'  AAAGTGAAAGTTGGTAG     22841          CC  _
                                AAAGTGAAAGT  TGG AG
                                ||||||||||  ||| ||
                                TTTCACTTTCA  ACC TC
                                      __  A
GAM107  SLC17A7 3'  GGAATGGAGGTCCTGGAAACTG 33695   A   AAA       ATA
            C                    A AGTG  GTCCTGGAGG  GC
                                | ||||  ||||||||||  ||
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                                C TTAC   CAGGACCTTT   CG
                                 C    CTC        GA_
GAM107  TIMP3    3'  GTGGGGCCAGGAGGATAG    7465      AAA   CT
                                GTG   GTC  GGAGGATAG
                                |||   |||  |||||||||
                                CAC   CGG  CCTCCTATC
                                  CC_   T_
GAM108  ABCA4    3'  GCTGCTAGTGGGATGGCCCGGG 42556    CAC    CCAGCCA
            G                    GC   CTAG      GCCCGGGG
                                ||   ||||      ||||||||
                                CG   GATC      CGGGCCCC
                                 AC_    ACCCTAC
GAM108  ACK1     3'  CACCCAGGGCAGGGCCTGGGG  25106        C_   CCA   C
                                CACCTAG  CAG   GCC GGGG
                                |||||||  |||   ||| ||||
                                GTGGGTC  GTC   CGG CCCC
                                    CC   C__   A
GAM108  ADAM12   5'  CTGTCCGAGTTGGCCCGGGG   18470    AG  _  CCA
                                CT  CC AG   GCCCGGGG
                                ||  || ||   ||||||||
                                GA  GG TC   CGGGCCCC
                                 CA  C  AAC
GAM108  ADD1     3'  GCACACACTGGGTCAGCCCGGG 30521    _   _  AGCCAGC
            G                    GC CAC CT      CAGCCCGGGG
                                || ||| ||      ||||||||||
                                CG GTG GA      GTCGGGCCCC
                                 T   T  CCCA___
GAM108  B4GALT7  3'  GCCACCTACGCCAGCTGCATGG 28545         _     CA  CCG
                                GCCACCTA GCCAGC  GC   GG
                                |||||||| ||||||  ||   ||
                                CGGTGGAT CGGTCG  CG   CC
                                    G     A_  TA_
GAM108  DIA1     3'  GCCAACCCCCCAGCTCGGGG   28786      CCTA   AG    C
                                GCCA   GCC  CCAGC CGGGG
                                ||||   |||  ||||| |||||
                                CGGT   TGG  GGTCG GCCCC
                                  _____  GG    A
GAM108  DSCAM    5'  GCCGCTCGGCACCTGCCCGGGG 10803     AC  AGCCA   A
                                GCC  CT    GCC GCCCGGGG
                                |||  ||    ||| ||||||||
                                CGG  GA    TGG CGGGCCCC
                                  C_  GCCG_   A
GAM108  EN2      5'  GCCGCCTGGGCCGCCCGGG    10955     A   AGCCA   A
                                GCC CCT    GCC GCCCGGG
                                ||| |||    ||| |||||||
                                CGG GGA    CGG CGGGCCC
                                  C   CC___   _
GAM108  F2RL3    5'  GCCGCTTGCCAGCCAGCCCG   19520     AC  A
                                GCC  CT GCCAGCCAGCCCG
                                |||  || ||||||||||||
```

```
                                CGG  GA CGGTCGGTCGGGC
                                  C_  A
GAM108  GLUL     5'  CAGACAGCGGCCGGCCCGGGG  13153    CC   CA  A
                                CA  TAGC  GCC GCCCGGGG
                                ||  ||||  ||| ||||||||
                                GT  GTCG  CGG CGGGCCCC
                                 CT   C_  C
GAM108  HSPG2    3'  GCCACCCAGCTCTATCTGGGG  24362         CAGCCAGCCC
                                GCCACCTAGC        GGGG
                                ||||||||||        ||||
                                CGGTGGGTCG        CCCC
                                      AGATAGA___
GAM108  IL15     5'  GCCACCCAGTTCCCTCCCGGGG 8226          CCAG  AG
                                GCCACCTAG   CC  CCCGGGG
                                |||||||||   ||  |||||||
                                CGGTGGGTC   GG  GGGCCCC
                                      AA__  GA
GAM108  JUND     5'  CCCGCCGCGCCGGCCCGGG   23797     A  A_  A
                                CCT GCC  GCC GCCCGGG
                                ||| |||  ||| |||||||
                                GGG CGG  CGG CGGGCCC
                                  _  CG  C
GAM108  KCNF1    5'  GCCGCCGGCCTCGCCCGGG   13834     ACCTA  A  A_
                                GCC    GCC GCC  GCCCGGG
                                |||    ||| |||  |||||||
                                CGG    CGG CGG  CGGGCCC
                                  _____  C  AG
GAM108  LIMK1    5'  CCACCGCCGCCGGCCCGGGG  14167      TA  A  A
                                CCACC  GCC GCC GCCCGGGG
                                |||||  ||| ||| ||||||||
                                GGTGG  CGG CGG CGGGCCCC
                                   __  _  C
GAM108  MAP3K5   5'  ACCGCCTGGCCAGCCACAGCTC 25432     A  A      __  C
           GGGG                  GCC CCT GCCAGCCA  GC CGGGG
                                ||| ||| ||||||||  || |||||
                                TGG GGA CGGTCGGT  CG GCCCC
                                  C  C       GT  A
GAM108  NCOR2    3'  GCACAGGGCCAGCCCGGGG   26732    _ __
                                GC CA  GCCAGCCCGGGG
                                || ||  ||||||||||||
                                CG GT  CGGTCGGGCCCC
                                 T  CC
GAM108  NF2      5'  GCCGGCTGGCCGGCCCGGG   7068      ACCTA  CA  A
                                GCC    GC  GCC GCCCGGG
                                |||    ||  ||| |||||||
                                CGG    CG  CGG CGGGCCC
                                  C____  AC  C
GAM108  OVOL1    5'  GCCACCACACAGCCCGGG    21274       TAGCCA  _
                                GCCACC     GC CAGCCCGGG
                                ||||||     || |||||||||
```

```
                                CGGTGG     TG GTCGGGCCC
                                   _______ T
GAM108  RFC2    3'  CCTGGCCAGCCACTGGAG    16279     A       G CC
                                CCT GCCAGCCA C  GGGG
                                ||| |||||||| |  ||||
                                GGA CGGTCGGT G  CCTC
                                  C       _ A_
GAM108  RFX1    3'  CCACCTGCGCCGGCCCGGGG   16290       A  CA   A
                                CCACCT GC  GCC GCCCGGGG
                                |||||| ||  ||| ||||||||
                                GGTGGA CG  CGG CGGGCCCC
                                   _ __   C
GAM108  RXRG    5'  GCTTCCTAGCAGCCCGGG    27942    CA     CAGCC
                                GC  CCTAGC    AGCCCGGG
                                ||  ||||||    ||||||||
                                CG  GGATCG    TCGGGCCC
                                 AA     ______
GAM108  WW45    5'  GCCGCCTGTCCGGAGCCCGGGG 34821     A   AG  AGCC
                                GCC CCT  CC    AGCCCGGGG
                                ||| |||  ||    |||||||||
                                CGG GGA  GG    TCGGGCCCC
                                  C   CA  CC__
GAM108  EFNA1   5'  CCTGGCCAGGCCGAGCGGGGAC 20697     A    _ _   CC
          G                      CCT GCCAG CC AGC  GGGGACG
                                ||| ||||| || |||  |||||||
                                GGA CGGTC GG TCG  CCCCTGC
                                  C    C  C   __
GAM109  IL24    3'  TGAGGATCTGCTTTGTGCT   27790    T      T   CTAC
                                TG GGATTTG CTT    GCT
                                || ||||||| |||    |||
                                AC CCTAGAC GAA    CGA
                                 T      _   ACA_
GAM109  LPIN1   3'  TGTGGATTTTCTTTCACA    42643          G    C
                                TGTGGATTT TCTT TACG
                                ||||||||| |||| ||||
                                ACACCTAAA AGAA GTGT
                                      _    A
GAM109  NCOA4   3'  AAACAGTAACTCATAATCT   24135          ATTG   C
                                AAGCAGTGG    TCA AATCT
                                |||||||||    ||| |||||
                                TTTGTCATT    AGT TTAGA
                                     G___    A
GAM109  NOS1    3'  AAGCAGTGGCAATCT       8368          ATTGTCA
                                AAGCAGTGG      CAATCT
                                |||||||||      ||||||
                                TTCGTCACC      GTTAGA
                                               _______
GAM109  NPEPPS  3'  AAGCAGTCTCACAATCT     26715        GGATTG
                                AAGCAGT     TCACAATCT
                                |||||||     |||||||||
```

```
                                TTCGTCA     AGTGTTAGA
                                   G_____
GAM109  P2RX7    3'  AGCAGTGGCACAATCT      15000        ATTGT
                                AGCAGTGG    CACAATCT
                                ||||||||    ||||||||
                                TCGTCACC    GTGTTAGA
                                     _____
GAM109  PLA2G4C  3'  AGCAGTGGAAGGCATTGGTCT  43858         TT  CACAA
                                AGCAGTGGA  GT    TCT
                                |||||||||  ||    |||
                                TCGTCACCT  CG    AGA
                                     TC  TAACC
GAM109  PTGIS    3'  AGCAATGGGGCAATCT      9669         ATTGTCA
                                AGCAGTGG      CAATCT
                                ||||||||      ||||||
                                TCGTTACC      GTTAGA
                                   CC_____
GAM109  TAL1     3'  AGCGGTTTACAATCTA      17278       A  GTC
                                AGTGG TT   ACAATCTA
                                ||||| ||   ||||||||
                                TCGCC AA   TGTTAGAT
                                  A ___
GAM110  ASPH     3'  TGAGGTGCCAACAAAGCATTT  37141     A    C     A
                                TGA GTGCC AATAGA GCATTT
                                ||| ||||| |||||| ||||||
                                ACT CACGG TTGTTT CGTAAA
                                  C   _     _
GAM110  ASPH     3'  TGAGGTGCCAACAAAGGCATTT 37142     A    C     A
                                TGA GTGCC AATAGA GCATTT
                                ||| ||||| |||||| ||||||
                                ACT CACGG TTGTTT CGTAAA
                                  C   _     C
GAM110  ESR1     3'  TGAAGTGCCATAATAGAGGC   6538         C_     A
                                TGAAGTGCC  AATAGA GC
                                |||||||||  |||||| ||
                                ACTTCACGG  TTATCT CG
                                     TA     C
GAM110  RRM2B    3'  TGAAGTGTTCAGCATTT     42727        CCCAATAGA
                                TGAAGTG       AGCATTT
                                |||||||       |||||||
                                ACTTCAC       TCGTAAA
                                   AAG_______
GAM110  ENO2     3'  TTCACATTTCTAGTTTCT    12718        C     CA
                                TTCACA TTCTAG  TCT
                                |||||| ||||||  |||
                                AAGTGT AAGATC  AGA
                                   A     AA
GAM111  CHD2     3'  TTCATCACAAAACAATGC    10454          CA_
                                TTCATCATAG   GATGC
                                ||||||||||   |||||
```

```
                                AAGTAGTGTT   TTACG
                                      TTG
GAM111  CLK2     3'  TCCATCATGGCTAGATGC    41279        A  _
                                TTCATCAT GC AGATGC
                                |||||||| || ||||||
                                AGGTAGTA CG TCTACG
                                     C  A
GAM111  GNAS     3'  TTCATCACACTCAGGATG    38668        G_  _
                                TTCATCATA  CAG ATG
                                |||||||||  ||| |||
                                AAGTAGTGT  GTC TAC
                                      GA   C
GAM111  ITK      3'  TCCATCACTTTGGGCAGATG  24445        A____
                                TTCATCAT    GCAGATG
                                ||||||||    |||||||
                                AGGTAGTG    CGTCTAC
                                     AAACC
GAM111  MLLT2    3'  TTCATCATAGGGATCTTAGATG 25516         C______
                                TTCATCATAG      AGATG
                                ||||||||||      |||||
                                AAGTAGTATC      TCTAC
                                      CCTAGAA
GAM111  PPP2R5E  3'  TTCACCATAAACTGATGC    26483         _ A
                                TTCATCATAG C GATGC
                                |||||||||| | |||||
                                AAGTGGTATT G CTACG
                                      T A
GAM111  WASF1    5'  TTCATCATCCGCAAGTGC    19449        A_   A
                                TTCATCAT  GCAG TGC
                                ||||||||  |||| |||
                                AAGTAGTA  CGTT ACG
                                     GG   C
GAM111  PREP     3'  GGATGAACAACTTA       15553        TACAC
                                GGATGAAC    GACTTA
                                ||||||||    ||||||
                                CCTACTTG    TTGAAT
                                     _____
GAM111  WHSC1L1  3'  TCTGGGATGAAATTGTACAGGA 35715         C___   C
                                TCTGGGATGAA   TACA GA
                                ||||||||||   |||| ||
                                AGACCCTACTT   ATGT CT
                                      TAAC   C
GAM112  ABCB11   3'  TGCCTGTTATAGACCCGCCT   19047     AC__  A
                                TGCC   GTA ACCCGCCT
                                ||||   ||| ||||||||
                                ACGG   TAT TGGGCGGA
                                  ACAA  C
GAM112  B3GAT1   3'  CCCACCACCCACCGCCT    33001    TG   G  AAC
                                CC  CCAC TA   CCGCCT
                                ||  |||| ||   ||||||
```

```
                              GG  GGTG GT   GGCGGA
                               GT    G ___
GAM112  B4GALT7  3'  CCCAGCCCAAGCCTGCCT    28543     T   A  TAAA  C
                              CCC GCC CG    CC GCCT
                              ||| ||| ||    || ||||
                              GGG CGG GT    GG CGGA
                                T   _  TC__  A
GAM112  BDKRB2   3'  CACCCTGCTCGACCGC      8396         CA  TAAAC   C
                              CACCCTGC  CG    CCG C
                              ||||||||  ||    ||| |
                              GTGGGACG  GC    GGC G
                                   A_  T____   A
GAM112  BLK      3'  CACCCCGCCTTCGCGGCCCGTC 11841         A_   AAA    C
            T                  CACCCTGCC  CGT   CCCG CT
                              |||||||||  |||   |||| ||
                              GTGGGGCGG  GCG   GGGC GA
                                   AA   CC_    A
GAM112  CLCN4    5'  CACGCTGCCACGTGACGCCC   12278     C       AAACC
                              CAC CTGCCACGT    CGCCT
                              ||| |||||||||    |||||
                              GTG GACGGTGCA    GCGGG
                                C        CT___
GAM112  DVL1     5'  ACCCGCCCGCCCGC       40402      T   A  TAAA
                              ACCC GCC CG    CCCGC
                              |||| ||| ||    |||||
                              TGGG CGG GC    GGGCG
                                _   _  _____
GAM112  INHA     5'  CACCCTGCCCCGTGCCCC    13536         A   AAA
                              CACCCTGCC CGT   CCC
                              ||||||||| |||   |||
                              GTGGGACGG GCA   GGG
                                   G   CG_
GAM112  KIT      3'  ACTCTGCCATGTACACATTTGC 6895     C     C   A  CC__
            CT                   AC CTGCCA GTA AC    GCCT
                              || |||||| ||| ||    ||||
                              TG GACGGT CAT TG    CGGA
                               A     A   G  TAAA
GAM112  KLF4     5'  CACCACTGTCGCGGTCGCCT   20151      _   CCA   AAACC
                              CACC CTG   CGT    CGCCT
                              |||| |||   |||    |||||
                              GTGG GAC   GCG    GCGGA
                                T   A__   CCA__
GAM112  PIG3     5'  CTGCCGCGGACCCGCCT     22194       A  TAA
                              CTGCC CG   ACCCGCCT
                              ||||| ||   ||||||||
                              GACGG GC   TGGGCGGA
                                C  C__
GAM112  REPS2    5'  CCGCCACAGCCACCGCCT    21809        _  AAAC
                              CTGCCAC GT    CCGCCT
                              ||||||| ||    ||||||
```

```
                                GGCGGTG CG   GGCGGA
                                   T  GT__
GAM112  S100A10  5'  CCCTCGCTCCCGGACCCGCCT  40389     _  CA_  TAA
                                CCCT GC   CG   ACCCGCCT
                                ||||  ||   ||   ||||||||
                                GGGA CG   GC   TGGGCGGA
                                  G  AGG  C__
GAM112  SERPINA4  3'  CCCTGCCACATCCTCCTGC   26318         AAA  C
                                CCCTGCCACGT   CC GC
                                ||||||||||   || ||
                                GGGACGGTGTA   GG CG
                                      GGA  A
GAM112  SLC9A5   3'  CACCCTGTCAGCCCCTGC    21383       C  C  AAA  _
                                CACCCTG CA GT   CCC GC
                                |||||||  || ||   ||| ||
                                GTGGGAC GT CG   GGG CG
                                   A  _  ___   A
GAM112  TRO      3'  CACCCTGCTGTCCTGCC     32071        CAC  AAA  C
                                CACCCTGC   GT   CC GCC
                                ||||||||   ||   || |||
                                GTGGGACG   CA   GG CGG
                                   A__  ___  A
GAM112  ZNF274   5'  CCCTGCCACGAAGGCGACCAC  32247         TAAAC__
                                CCCTGCCACG      CCGC
                                ||||||||||      ||||
                                GGGACGGTGC      GGTG
                                      TTCCGCT
GAM112  ATSV     3'  TGTGGCACAGGTCCCCGGGCCT 20231          GTAGAAAA
                                TGTGGTACAGG       CCT
                                ||||||||||        |||
                                ACACCGTGTCC       GGA
                                      AGGGGCCC
GAM112  CACNA2D2  3'  CATGTGGTCCCACTGGGGGC  25706        A_  ____
                                CATGTGGT  CA   GGGT
                                ||||||||  ||   ||||
                                GTACACCA  GT   CCCG
                                   GG  GACC
GAM112  CDH6     3'  CATGTGGTGGCCAAAAC     22322        ACAG   AG
                                CATGTGGT   GGT  AAAAC
                                ||||||||   |||  |||||
                                GTACACCA   CCG  TTTTG
                                   _____  G_
GAM112  DUSP6    3'  CATGGGTACAGAGCAAACC   42325      T        GAA
                                CATG GGTACAGGGTA   AACC
                                ||||  ||||||||||   ||||
                                GTAC CCATGTCTCGT   TTGG
                                  _        ___
GAM112  FTSJ2    3'  AGAGCAGGGGTGGAAAGCCT  30164    TA    TA_   A
                                GG  CAGGG   GAAA CCT
                                ||  |||||   |||| |||
```

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                                TC  GTCCC   CTTT GGA
                                 TC     CAC    C
GAM112  GNG5     3'  CATGTGTTACAGGGATAA    23607       G      _
                                CATGTG TACAGGG TAG
                                |||||| ||||||| |||
                                GTACAC ATGTCCC ATT
                                   A      T
GAM112  LRRC2    3'  TGTGGTACCCACAAGGAAGCCT 36003       ____     T  AAAA
                                TGTGGT    ACAGGG AG    CCT
                                ||||||    |||||| ||    |||
                                ACACCA    TGTTCC TC    GGA
                                   TGGG     T ____
GAM112  LZTFL1   3'  CATGTGGTAGCTTCCAGAGGAA 33770         _____    TA
             A                   CATGTGGTA     CAGGG  GAAA
                                |||||||||     |||||  ||||
                                GTACACCAT     GTCTC  CTTT
                                     CGAAG    __
GAM112  SCO1     3'  CATTTGGTATGTCACTGAAAAC 21378     G     CAGGGTA
             CT                   CAT TGGTA      GAAAACCT
                                ||| |||||      ||||||||
                                GTA ACCAT      CTTTTGGA
                                  A     ACAGTGA
GAM112  SET7     3'  ATGTGGTACAGATTTAGA     36152           G_
                                ATGTGGTACAGG  TAGA
                                ||||||||||||  ||||
                                TACACCATGTCT  ATCT
                                      AA
GAM112  XRCC5    3'  ATGTGGTAACTAGAAGGCCT   34486        CAG G     AA
                                ATGTGGTA   G TAGAA  CCT
                                ||||||||   | |||||  |||
                                TACACCAT   T ATCTT  GGA
                                     ___ G     CC
GAM113  CALCA    3'  TGAGTCCTGCTCTCTTTCC    11941     T     AGTG
                                TGA TCCTGT    CTCTTTCC
                                ||| ||||||    ||||||||
                                ACT AGGACG    GAGAAAGG
                                  C     A___
GAM113  DTNA     3'  TATGACTTTTTTCTCTTTC    37374        CCTGTAGTG
                                TATGATT        CTCTTTC
                                |||||||        |||||||
                                ATACTGA        GAGAAAG
                                    AAAAA____
GAM113  HCS      3'  TATGTTTCCTGTATCATTTCC  33234      A       GTGC  _
                                TATG TTCCTGTA    TC TTTCC
                                |||| ||||||||    || |||||
                                ATAC AAGGACAT    AG AAAGG
                                  A       _____ T
GAM113  PPARGC1  3'  TATGATATCTGTAGTGCT    29965       TC
                                TATGAT  CTGTAGTGCT
                                ||||||  ||||||||||
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                                ATACTA  GACATCACGA
                                   TA
GAM113  SHMT1    3'  TATAATTCTTGTAGACATTCT  20025        C    _ GC
                                TATGATTC TGTAG T  TCT
                                |||||||| ||||| |  |||
                                ATATTAAG ACATC G  AGA
                                     A    T TA
GAM113  SMOH     3'  TGGTTCCTCTCTTTC      24818    A    GTAGTG
                                TG TTCCT     CTCTTTC
                                || |||||     |||||||
                                AC AAGGA     GAGAAAG
                                 C    _______
GAM114  EGLN1    3'  TGTAAAACATTAACTAAAAGTT 35182    G       ____
           ATT                    TG AAAACATTAA   GAGTTGTT
                                || ||||||||||   ||||||||
                                AC TTTTGTAATT   TTCAATAA
                                 A        GATT
GAM114  IL1R1    3'  TGGAAGGCATTAAAAGTT    9375       AA
                                TGGAA  CATTAAGAGTT
                                |||||  ||||||||||
                                ACCTT  GTAATTTTCAA
                                   CC
GAM114  KPNA1    3'  TGGAAAACATTTGAGAAGTT   44319         AA   TT
                                TGGAAAACATT  GAG  GTT
                                |||||||||||  |||  |||
                                ACCTTTTGTAA  CTC  CAA
                                      A_   TT
GAM114  PSG11    3'  GAAAACATTATCCTTTTGTTAT 15813         AGAG_
           T                    GAAAACATTA    TTGTTATT
                                ||||||||||    ||||||||
                                CTTTTGTAAT    AACAATAA
                                      AGGAA
GAM114  DNASE1   5'  TGATAACAAGGCCAAAGG    23359        AA   TGTTTT
                                TGGTAACAA  CCA     AGG
                                |||||||||  |||     |||
                                ACTATTGTT  GGT     TCC
                                     CC   T_____
GAM114  GHR      3'  GTAGCAAAACCAAGTTGGGT   6715     A      T   TTA
                                GTA CAAAACCA GTT   GGT
                                ||| |||||||| |||   |||
                                CAT GTTTTGGT CAA   CCA
                                  C       T   C__
GAM114  HSPA5    3'  TGGTAACAAGCCTGTG      23790         AA  A   TTTA
                                TGGTAACAA  CC TGT   G
                                |||||||||  || |||   |
                                ACCATTGTT  GG ACA   C
                                     C_  _   ____
GAM114  LILRB4   3'  GTAACAAAGCTGCAG       27778        ACCAT   T
                                GTAACAAA    GTT TAG
                                ||||||||    ||| |||
```

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                                CATTGTTT    CGA GTC
                                     _____  C
GAM115  CLCN7    3'  GGGTTGGGGGACCAAGGCAGGG 10521      AGAATTGCT
            C                    GGGTTG       GGCAGGGC
                                 ||||||       ||||||||
                                 CCCAAC       CCGTCCCG
                                    CCCCTGGTT
GAM115  COX10    3'  GGTTGAGAATGTGTGGGG    10554        T C  GCA
                                 GGTTGAGAAT G TG   GGG
                                 |||||||||| | ||   |||
                                 CCAACTCTTA C AC   CCC
                                      _ _  AC_
GAM115  DRD2     3'  TGGCTTGGGAATCTCTGGGG  9023     G  A   TG   CA
                                 TGG TTG GAAT  CTGG  GG
                                 ||| ||| ||||  ||||  ||
                                 ACC AAC CTTA  GACC  CC
                                   G  C   GA   __
GAM115  ENG      3'  TGGGTTGAAGGTTCTGTGGGG  6510        AATTG   GCA
                                 TGGGTTGAG    CTG   GGG
                                 |||||||||    |||   |||
                                 ACCCAACTT    GAC   CCC
                                      CCAA_   AC_
GAM115  FLNA     3'  GGGTTGAGGGGAAGAGGGCGGG 11137       AATTGCT_  A
            GC                   GGGTTGAG       GGC GGGC
                                 ||||||||       ||| ||||
                                 CCCAACTC       CCG CCCG
                                      CCCTTCTC   C
GAM115  KRT5     5'  TGGGTTGGGAGGTGCTGG    7692        A  AT
                                 TGGGTTG GA  TGCTGG
                                 ||||||| ||  ||||||
                                 ACCCAAC CT  ACGACC
                                      C  CC
GAM115  MAPK8IP1 3'  GGGTTGGGGCAGGGGCAGGGC  24160       AGAATT  T__
                                 GGGTTG     GC   GGCAGGGC
                                 ||||||     ||   ||||||||
                                 CCCAAC     CG   CCGTCCCG
                                    CC_____  TCC
GAM115  MRPL49   3'  GGGTTGGGATGGGATGGCAGGG 43026       A  ATTGC
                                 GGGTTG GA    TGGCAGGG
                                 |||||| ||    ||||||||
                                 CCCAAC CT    ACCGTCCC
                                    C  ACCCT
GAM115  PCTK1    3'  TGGGTTGACAGGCCAATGGTGG 26239        GAATT  ___  CA
            GG                     TGGGTTGA    GCT   GG  GGG
                                   ||||||||    |||   ||  |||
                                   ACCCAACT    CGG   CC  CCC
                                        GTC__   TTA  AC
GAM115  SHANK2   3'  TGGGTGGGCTGGCAGG     29474      TGAGAATT
                                 TGGGT       GCTGGCAGG
                                 |||||       |||||||||
```

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                                ACCCA      CGACCGTCC
                                  CC_____
GAM115  STIM1    3' GGTTGGGACGGAGGCAGGGC  41135      A  ATTGCT
                                GGTTG GA     GGCAGGGC
                                |||||| ||     ||||||||
                                CCAAC CT     CCGTCCCG
                                  C  GCCT__
GAM116  CALD1    3' CATCTCTAGCTGTGA      37625          ACTTC
                                CATCTCTAGTT    GTGG
                                ||||||||||    ||||
                                GTAGAGATCGA    CACT
                                       _____
GAM116  LANCL1   3' TCTTTAGTTACTACCATG    25858     C      _
                                TCT TAGTTACT TCGTG
                                ||| |||||||| |||||
                                AGA ATCAATGA GGTAC
                                  A       T
GAM116  SFRS7    3' CATCTTTAATTACTTTGCA   40465      C       C
                                CATCT TAGTTACTT GTG
                                ||||| |||||||||| |||
                                GTAGA ATTAATGAA CGT
                                  A       A
GAM116  GRAF     3' CCGAAGCGGGGACAGTGACCT 31442        AACA_  A  ATAA
                                TCGAAGCG    AG GA   CCT
                                ||||||||    || ||   |||
                                GGCTTCGC    TC CT   GGA
                                     CCCTG  A  _____
GAM116  KIF3C    3' TCGAAGCAGGCAGGAGCAGCCT 13958        AA  A   AATAA
                                TCGAAGCG  CA GAG    CCT
                                ||||||||  || |||    |||
                                AGCTTCGT  GT CTC    GGA
                                     CC  C   GTC__
GAM116  PIK4CB   3' GAAGCGGGTGAGAGAACA    15313       AACA
                                GAAGCG    AGAGAATA
                                ||||||    ||||||||
                                CTTCGC    TCTCTTGT
                                  CCAC
GAM117  ARG2     3' TCCCAGGTCTAACCCC      10122        ACAG
                                TCCCAGGT    TTAATCCC
                                ||||||||    ||||||||
                                AGGGTCCA    GATTGGGG
                                       _____
GAM117  CNGB3    3' CAATCCTAGGTACAATCA    33304       C
                                TAATCC AGGTACAGTTA
                                |||||| ||||||||||
                                GTTAGG TCCATGTTAGT
                                  A
GAM117  GOLGA4   5' ATCTGGGTACAATTAAT     41054     CCA
                                ATC   GGTACAGTTAAT
                                |||   ||||||||||||
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                                TAG  CCATGTTAATTA
                                  AC_
GAM117  IL1F5   3' AATCCCAGGGGCTGTGATCC  29345       TACA  TA
                                AATCCCAGG   GT  ATCC
                                |||||||||   ||  ||||
                                TTAGGGTCC   CA  TAGG
                                    CCGA  C_
GAM117  JRKL    3' CATTTTAGCAGATTAATCCC  19089   GG_ _  _
                                CA  TA CAG TTAATCCC
                                ||  || ||| ||||||||
                                GT  AT GTC AATTAGGG
                                 AAA  C  T
GAM117  LAMP1   3' TCCCGTGTACAATCCC     24509     AG    GTTA
                                TCCC  GTACA   ATCCC
                                ||||  |||||   |||||
                                AGGG  CATGT   TAGGG
                                  CA   _____
GAM117  MAP1A   5' TAATCCCAGGTGGCTCC    14348         ACA  TAA
                                TAATCCCAGGT  GT  TCC
                                ||||||||||  ||  |||
                                ATTAGGGTCCA  CG  AGG
                                    C__  ___
GAM117  MTMR8   3' AATCACAAATATAGTTAATCC  31747     C     C
                                AATC CAGGTA AGTTAATCC
                                |||| |||||| |||||||||
                                TTAG GTTTAT TCAATTAGG
                                  T     A
GAM117  RAP1GA1  3' ATCCCAGGTCTGGACGGCT   16160        _____  A
                                ATCCCAGGT   AC GTT
                                |||||||||   || |||
                                TAGGGTCCA   TG CGA
                                    GACC  C
GAM117  SLC25A13 3' ATCCCAGGGCTGATC      30658        TACA   A
                                ATCCCAGG   GTT ATC
                                ||||||||   ||| |||
                                TAGGGTCC   CGA TAG
                                   _____  C
GAM117  TGIF    5' ATCCCAGGCGCCCGCTCC    17496        ACA   AA_
                                ATCCCAGGT  GTT  TCC
                                |||||||||  |||  |||
                                TAGGGTCCG  CGG  AGG
                                   ___  GCG
GAM117  ZNF26   3' ATCCCAAATATGGTTGGTC   43794         CA   AA
                                ATCCCAGGTA  GTT  TC
                                ||||||||||  |||  ||
                                TAGGGTTTAT  CAA  AG
                                    AC  CC
GAM118  WIG1    5' TCGGAACCCCCCGGGAC     45387        A    AA
                                TCGGAACC CCCGG  GAT
                                |||||||| |||||  |||
```

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                                AGCCTTGG GGGCC  CTG
                                      _    __
GAM118  ADAM17   3'  AGGGATCACAGGGGCAGGCTGC 34829    T   AGATTCAAA
                                AG GGAT       CAGGCTGC
                                || ||||       ||||||||
                                TC CCTA       GTCCGACG
                                 _   GTGTCCCC_
GAM118  BCAT1    3'  GTGGATAAAGATAGGCTG    42382        TTCAAAC
                                GTGGATAGA     AGGCTG
                                |||||||||     ||||||
                                CACCTATTT     TCCGAC
                                     CTA____
GAM118  FGFR1    3'  GTGGTGGGCCCAGCAGGCTG  31952     ATAGA   AA
                                GTGG    TTCA  CAGGCTG
                                ||||    ||||  |||||||
                                CACC    GGGT  GTCCGAC
                                  ACCC_   C_
GAM118  FXYD6    3'  GTGGGCAGGACCGCAGGCTGC  35121     A   AT  AAA
                                GTGG TAG  TC   CAGGCTGC
                                |||| |||  ||   ||||||||
                                CACC GTC  GG   GTCCGACG
                                  C   CT  C__
GAM118  GALR1    5'  GTGGATAGAGTCGGGTG     11207        T  AAACA  C
                                GTGGATAGA TC    GG TG
                                |||||||| ||    || ||
                                CACCTATCT AG    CC AC
                                     C  _____  C
GAM118  GRM4     3'  GCGGGGCAGGCGGGCAGGCTGC 9160      A_   ATTCAAA
                                GTGG  TAG     CAGGCTGC
                                ||||  |||     ||||||||
                                CGCC  GTC     GTCCGACG
                                  CC   CGCCC__
GAM119  HGF      3'  TTCTTACTAAAATGGTGTATTA 45327     A  ACAGCC
                                TTC TTA     ATGGTGTATTA
                                ||| |||     ||||||||||
                                AAG AAT     TACCACATAAT
                                  _   GATTT_
GAM119  NPEPPS   3'  TCATTAACAGTAGAGTGT    26722         CCAT
                                TCATTAACAG    GGTGT
                                ||||||||||    |||||
                                AGTAATTGTC    TCACA
                                     ATC_
GAM120  ALPI     3'  GGGTTGCCGGAAGCTTCTC    11581    A      TGAT
                                GG TTGCCGGG    TTTCTC
                                || ||||||||    ||||||
                                CC AACGGCCT    GAAGAG
                                 C       TC__
GAM120  AP1G1    3'  ATGGATTGCAGTCCTTTTCT   10047        CG   GA
                                ATGGATTGC  GGT  TTTTCT
                                |||||||||  |||  ||||||
```

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                                TACCTAACG  TCA  AAAAGA
                                    __   GG
GAM120  BCAT1    3'  GATTGCAATTCATTTTCTC   42380      CG   G_
                                GATTGC  GGT  ATTTTCTC
                                ||||||  |||  ||||||||
                                CTAACG  TTA  TAAAAGAG
                                   __   AG
GAM120  DTNB     3'  TAGATTGCAAAAATTTTCTCC  37608       CGGGT
                                TGGATTGC    GATTTTCTCC
                                ||||||||    ||||||||||
                                ATCTAACG    TTAAAAGAGG
                                     TTT__
GAM120  DYRK1A   3'  TGGATTTTATGATTTTCT    39006      GCCGG
                                TGGATT    GTGATTTTCT
                                ||||||    ||||||||||
                                ACCTAA    TACTAAAAGA
                                   AA___
GAM120  GGA3     3'  ATGGCAGCTGGTGATTTT    39781     ATT  CG
                                ATGG   GC  GGTGATTTT
                                ||||   ||  |||||||||
                                TACC   CG  CCACTAAAA
                                  GT_  A_
GAM120  HTR2C    3'  GGATTGCTGAAGGATTTTCT   9289       C   T
                                GGATTGC GGG GATTTTCT
                                ||||||| ||| ||||||||
                                CCTAACG CTT CTAAAAGA
                                    A   C
GAM120  ITSN1    3'  ATGGACTGCCTTCATTTTCT   16653        GGGTG
                                ATGGATTGCC    ATTTTCT
                                ||||||||||    |||||||
                                TACCTGACGG    TAAAAGA
                                     AAG__
GAM120  SLC20A2  5'  TGGGTGCCGGGTACTTTTCT   27579    AT       A
                                TGG  TGCCGGGTG TTTTCT
                                |||  ||||||||| ||||||
                                ACC  ACGGCCCAT AAAAGA
                                  C_       G
GAM120  TGFA     3'  ATGGATTTGCTAAGTTTTCTCC 17440       _ CG   GAT
                                ATGGATT GC  GGT   TTTCTCC
                                ||||||| ||  |||   |||||||
                                TACCTAA CG  TCA   AAAGAGG
                                   A  AT   ___
GAM120  TNFSF10  3'  ATGGATTGTTGCGCTTTCT   19188       CCGG   A
                                ATGGATTG    GTG TTTTCT
                                ||||||||    ||| ||||||
                                TACCTAAC    CGC GAAAGA
                                    AA__   _
GAM120  NPDC1    3'  TTACCCACCCGTTCCTG     31728       CGCATT    A  A
                                TTACCCA     CCCG TC TG
                                |||||||     |||| || ||
```

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                                AATGGGT     GGGC AG AC
                                   _______   A  G
GAM120  SIAT7D   3'  TTACCCGTACGTTCCTGA    30835       AC  A   C
                                TTACCC  GC TTCC GA
                                ||||||  || |||| ||
                                AATGGG  TG AAGG CT
                                   CA  C    A
GAM121  ADAMTS7  3'  AGTCAGTGTGGTGAGGGGCCAC 30695    C   CCCG  _  C
                                AG CAG    GG GA GGGGCCAC
                                || |||    || || ||||||||
                                TC GTC    CC CT CCCCGGTG
                                 A   ACA_  A  _
GAM121  ADORA1   3'  AGCAGCAGAGATGGGGTCACC  8587     C   CC    C    C
                                AGC AGC  GGGGA GGGG CACC
                                ||| |||  ||||| |||| ||||
                                TCG TCG  TCTCT CCCC GTGG
                                  _  __     A    A
GAM121  ATP8B2   3'  GCCAGCCCTGGGTGCTCTGGTC 42206        _   GACGG_  C
              AC                    GCCAGCCC GGG     GG CAC
                                ||||||||  |||     || |||
                                CGGTCGGG CCC     CC GTG
                                     A   ACGAGA  A
GAM121  BLK      3'  GCCAGCACGGGGGGTGCC    11845       C    AC  G
                                GCCAGC CGGGG  GG GCC
                                ||||||  |||||  || |||
                                CGGTCG GCCCC  CC CGG
                                   T     __  A
GAM121  CACNA1S  5'  AGCCAGCCAGGGGGCGGGGC   6299         C    A
                                AGCCAGCC GGGG CGGGGC
                                ||||||||  ||||  ||||||
                                TCGGTCGG CCCC GCCCCG
                                     T   C
GAM121  CAPN10   3'  AGCTGGCACAGGGGGCCAC   35781     CA  C    ACGG
                                AGC  GC CGGGG    GGCCAC
                                |||  || |||||    ||||||
                                TCG  CG GTCCC    CCGGTG
                                  AC  T    _____
GAM121  CARPX    5'  AGCCGGCCAGGGACAGTCACC  33564      A  C      G_
                                AGCC GCC GGGGACGG  GCC
                                ||||  ||| ||||||||  |||
                                TCGG CGG TCCCTGTC  TGG
                                  C  _       AG
GAM121  CDH1     5'  GCTGGCCGGGGACGCCGG    20366    CA  C     ______
                                GC  GCC GGGGACG     GG
                                ||  ||| |||||||     ||
                                CG  CGG CCCCTGC     CC
                                 AC   _      GGIII
GAM121  CDKN1A   5'  GCCGGCCCGGGGTCCCC     38509     A      ACGGGG  A
                                GCC GCCCGGGG     CC CC
                                ||| ||||||||     || ||
```

```
                                CGG CGGGCCCC     GG GG
                                  C       A_____ _
GAM121  CNTN2    5'  GCTCAGCTTGGGGACAGCC   22912    _   CC     GG
                                GC CAGC  GGGGAC  GGCC
                                || ||||  ||||||  ||||
                                CG GTCG  CCCCTG  TCGG
                                 A    AA     __
GAM121  COL4A3   5'  GCGAGTCCGGGGACCCTCAGGC 36380    C  C       G___
                                GC AG CCGGGGAC    GGGC
                                || || ||||||||    ||||
                                CG TC GGCCCCTG    TCCG
                                 C  A       GGAG
GAM121  CPE      5'  CAGCCCGCGCACTGGGGCCACC 12420        GGG  _
                                CAGCCCG   AC GGGGCCACC
                                |||||||   || |||||||||
                                GTCGGGC   TG CCCCGGTGG
                                    GCG  A
GAM121  ERBB3    5'  CCGGCCCGGGGGCCCCTAGGC  12753    A       ACG___
                                CC GCCCGGGG     GGGC
                                || ||||||||     ||||
                                GG CGGGCCCC     TCCG
                                 C       CGGGGA
GAM121  FAAH     3'  GCCAGGGACGGGGTGGGGCTGC 11053      CC_    AC    CA
          C                      GCCAG   CGGGG  GGGGC  CC
                                |||||   |||||  |||||  ||
                                CGGTC   GCCCC  CCCCG  GG
                                   CCT    A_    AC
GAM121  FBXW1B   5'  GCCAGCCCGCCCGGGCCGCC   37990         GGGA   G  A
                                GCCAGCCCG    CGGG CC CC
                                |||||||||    |||| || ||
                                CGGTCGGGC    GCCC GG GG
                                     GG__    _  C
GAM121  GARP     3'  GCAGCCCGGGAAGGGGGTCACC 24311    C        C    C
                                GC AGCCCGGGGA GGGG CACC
                                || ||||||||| |||| ||||
                                CG TCGGGCCCTT CCCC GTGG
                                 _         C    A
GAM121  GGT2     5'  GCCAGCCTGGGGGCCAC     43925        C    ACGGG
                                GCCAGCC GGGG     GCCAC
                                ||||||| ||||     |||||
                                CGGTCGG CCCC     CGGTG
                                    A   _____
GAM121  GNAS     5'  AGCTGGCCCGGAGGTCCCAGCC 38653     CA       ACGG_
                                AGC  GCCCGGGG    GGCC
                                |||  ||||||||    ||||
                                TCG  CGGGCCTC    TCGG
                                  AC       CAGGG
GAM121  GPRK5    5'  AGCCGGCCGGCGGGGC      23631      A   CGG  A
                                AGCC GCC   GG CGGGGC
                                |||| |||   || ||||||
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```
                                TCGG CGG   CC GCCCCG
                                  C  ___  _
GAM121  GSPT1    5'  GCCCGGCCCGGGGGCTTCCA  13311     A_      ACGGGG
                                GCC  GCCCGGGG     CCA
                                |||  ||||||||     |||
                                CGG  CGGGCCCC     GGT
                                  GC       CGAA__
GAM121  IRF1     3'  AGCCAGCCCTGGGATTGG    42038         G    CG
                                AGCCAGCCC GGGA  GG
                                |||||||||| ||||  ||
                                TCGGTCGGG CCCT  CC
                                     A    AA
GAM121  ITPR3    3'  GCCAGCTGGCTGGGCCAC    13689       CCGG  ACG
                                GCCAGC   GG   GGGCCAC
                                ||||||   ||   |||||||
                                CGGTCG   CC   CCCGGTG
                                   A___  GA_
GAM121  LEF1     5'  GCTGCCCCGGCGGCCAC     32213    CA   GGGGA  _
                                GC  GCCC    CGG GGCCAC
                                ||  ||||    ||| ||||||
                                CG  CGGG    GCC CCGGTG
                                 A_   ______  G
GAM121  LLGL1    3'  AGTGAGCAGAGATGGGGCCAC  42501    CC   CC    C
                                AG  AGC  GGGGA GGGGCCAC
                                ||  |||  ||||| ||||||||
                                TC  TCG  TCTCT CCCCGGTG
                                 AC  __    A
GAM121  LZTS1    3'  GCCGGCCTGGGACAGGGCC   34268     A   CG
                                GCC GCC  GGGACGGGGCC
                                ||| |||  ||||||||||
                                CGG CGG  CCCTGTCCCGG
                                  C  A_
GAM121  MUC3B    3'  GCTGCCCGCGTCCTGGGGCCAC 45339    CA    GGGAC_
           C                     GC  GCCCG     GGGGCCACC
                                ||  |||||     |||||||||
                                CG  CGGGC     CCCCGGTGG
                                 A_    GCAGGA
GAM121  MYLK2    3'  GCTGCCCTGGGGATCTGGC   37525    CA   _    CGG
                                GC  GCCC GGGGA   GGC
                                ||  |||| |||||   |||
                                CG  CGGG CCCCT   CCG
                                 A_   A    AGA
GAM121  NAV2     3'  AGCTGGCCCGGGATGCC     41139     CA      ACGGG
                                AGC  GCCCGGGG    GCC
                                |||  ||||||||    |||
                                TCG  CGGGCCCT    CGG
                                  AC       A____
GAM121  NCOR2    3'  GCCAGCCCGGGGCGGGA     26733           A
                                GCCAGCCCGGGG CGGGG
                                |||||||||||| |||||
```

```
                                CGGTCGGGCCCC GCCCT
                                          _
GAM121  NLGN2   5' GCCGCCCGGGGCGCCGCC   44755    A      A  GG
                                GCC GCCCGGGG CG  GCC
                                ||| |||||||| ||  |||
                                CGG CGGGCCCC GC  CGG
                                  _      _ GG
GAM121  NOX4    5' AGCCAGCCCGGGCGGGG    32593          GA
                                AGCCAGCCCGGG  CGGGG
                                ||||||||||||  |||||
                                TCGGTCGGGCCC  GCCCC
                                          __
GAM121  NTE     3' AGCTACCCCCACGGGGCCACC 27458    CA   GGGG
                                AGC  GCCC   ACGGGGCCACC
                                |||  ||||   ||||||||||
                                TCG  TGGG   TGCCCCGGTGG
                                  A_   GG__
GAM121  OTOF    3' GCCGGCCAGGAGGCCAC    22058    A  C  GACG
                                GCC GCC GGG   GGGCCAC
                                ||| ||| |||   |||||||
                                CGG CGG TCC   TCCGGTG
                                  C  _  ____
GAM121  PFKL    5' CAGCCCAGGGTCACAGCCA   15230         A  G
                                CAGCCCGGGG CG GGCCA
                                |||||||||| || |||||
                                GTCGGGTCCC GT TCGGT
                                      A  G
GAM121  PKNOX1  3' AGCCAACCCGTGGGGGCTGCC 21306         _  AC  G_
                                AGCCAGCCCG GGG  GG  GCC
                                |||||||||| |||  ||  |||
                                TCGGTTGGGC CCC  CC  CGG
                                      A  __ GA
GAM121  POLR2A  3' AGCTGGGCTGGGGGTGACGCC 9598     CA_ CC   AC  G
                                AGC  GC  GGGG  GG GCC
                                |||  ||  ||||  || |||
                                TCG  CG  CCCC  CT CGG
                                  ACC  A_   CA  G
GAM121  POLR2C  3' GCCAGCCCTGGGGCAAGAAC  15453        _   AC
                                GCCAGCCC GGGG  GGGGC
                                |||||||| ||||  |||||
                                CGGTCGGG CCCC  TCTTG
                                     A   GT
GAM121  PPP1R8  5' GCTAGCTCCGGCCGGGCCAC  39730   C  _   GGACG
                                GC AGC CCGG    GGGCCAC
                                || ||| ||||    |||||||
                                CG TCG GGCC    CCCGGTG
                                 A  A   GG___
GAM121  PRV1    3' CATTCGGGGGGAGCCAC    43874    GCC    AC
                                CA  CGGGG  GGGGCCAC
                                ||  |||||  ||||||||
```

```
                                GT   GCCCC  CCTCGGTG
                                 AA_    __
GAM121  PTGS1    3'  AGCCAGCTGTGGGGATGAG   38728       CC_    C
                                AGCCAGC   GGGGA GGG
                                |||||||   ||||| |||
                                TCGGTCG   CCCCT CTC
                                    ACA    A
GAM121  PTPN11   5'  GCTGGCCCGAGGGAGGCC    15919    CA      AC
                                GC  GCCCGGGG  GGGGCC
                                ||  ||||||||  ||||||
                                CG  CGGGCTCC  CTCCGG
                                 AC       __
GAM121  RECQL5   3'  GCCGGCTCTGGGACGGGGC   20167     A  CCG
                                GCC GC   GGGACGGGGC
                                ||| ||   ||||||||||
                                CGG CG   CCCTGCCCCG
                                  C  AGA
GAM121  RGS16    3'  GCCACCTGCAGGGGGCCACC   16322     G  __    ACGG
                                GCCA CC  CGGGG   GGCCACC
                                |||| ||  |||||   |||||||
                                CGGT GG  GTCCC   CCGGTGG
                                  _  AC    _____
GAM121  SIX2     5'  GCCGCCCGGGGCGCCGC     32608     A      A  GG
                                GCC GCCCGGGG CG  GC
                                ||| |||||||| ||  ||
                                CGG CGGGCCCC GC  CG
                                  _       _  GG
GAM121  SOD3     5'  AGCCAGCCCAGGAACGCAGGC  16952              _
                                AGCCAGCCCGGGGACG GGGC
                                |||||||||||||||| ||||
                                TCGGTCGGGTCCTTGC TCCG
                                          G
GAM121  SORCS2   3'  AGCCACCCCGGTGGCTACC    34044      G    _  ACGGG
                                AGCCA CCCGG GG    GCC
                                ||||| ||||| ||    |||
                                TCGGT GGGCC CC    TGG
                                   G    A  GA___
GAM121  STX1A    3'  ACCTAGCCCAAGGGGTTGC    21407     _       AC  G_
                                GCC AGCCCGGGG  GG  GC
                                ||| |||||||||  ||  ||
                                TGG TCGGGTTCC  CC  CG
                                  A        __  AA
GAM121  SYK      5'  GCGCAGCGCGGGGCCAC     17239    C   GGA
                                GC CGG   CGGGGCCAC
                                || |||   |||||||||
                                CG GTC   GCCCCGGTG
                                 C  GC_
GAM121  TCIRG1   5'  GCCAGCCTGGGGAGAGCAC   25841       C    CG    C
                                GCCAGCC GGGGA  GGGC AC
                                ||||||| |||||  |||| ||
```

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                                CGGTCGG CCCCT  CTCG TG
                                   A    __   _
GAM121  TRPC6    5' ACTGGCCCGGGGAAAAGTCACC 21479    CA       CG  GC
                                GC  GCCCGGGGA  GG  CACC
                                ||  |||||||||  ||  ||||
                                TG  CGGGCCCCT  TC  GTGG
                                 AC        TT  A_
GAM121  UPF3B    5' GCTTGGCCGGAACGGGGTTACC 38766    CA_   CG       CC
                                GC   GCC  GGGACGGGG  ACC
                                ||   |||  |||||||||  |||
                                CG   CGG  CCTTGCCCC  TGG
                                 AAC   __        AA
GAM121  WBSCR1   3' GCTGCCCGGGGACTCACC    35269    CA        GGG
                                GC  GCCCGGGGAC   GCC
                                ||  ||||||||||   |||
                                CG  CGGGCCCCTG   TGG
                                 A_        AG_
GAM121  WHSC1    3' GCCGGCCTGAGGACGGACAGC  39366     A   C      __
                                GCC GCC GGGGACGG  GGC
                                ||| ||| ||||||||  |||
                                CGG CGG CTCCTGCC  TCG
                                  C   A       TG
GAM121  ZNF140   5' ACCGCCCGGGGCCATCGGTGGC 18339     A       A G_____  GCCA
                                GCC GCCCGGGG C     GG    C
                                ||| |||||||| |     ||    |
                                TGG CGGGCCCC G     CC    G
                                  _       G TAGIII  ACCG
GAM121  ADORA1   3' CAGCAGAGATGGGGTCACCTA  8589      CC    C    C
                                CAGC  GGGGA GGGG CACCTA
                                ||||  ||||| |||| ||||||
                                GTCG  TCTCT CCCC GTGGAT
                                   __    A   A
GAM121  ADRA2A   5' CCGGCCCGGGGCTGGGGC    8632     A       AC
                                CC GCCCGGGG  GGGGC
                                || ||||||||  |||||
                                GG CGGGCCCC  CCCCG
                                 C       GA
GAM121  AXUD1    5' CCGGCCGGGGACGCCCCC    37485    A  C     GGG   A
                                CC GCC GGGGAC   GCC CCT
                                || ||| ||||||   ||| |||
                                GG CGG CCCCTG   CGG GGG
                                 C  _     ____  _
GAM121  CDKN1A   5' CCGGCCCGGGGTCCCCT     38505    A       ACGGGG  A
                                CC GCCCGGGG     CC CCT
                                || ||||||||     || |||
                                GG CGGGCCCC     GG GGA
                                 C       A_____  _
GAM121  FKBP1A   3' GCCCAGGGACAGATACCT    38279           GCC
                                GCCCGGGGACGGG   ACCT
                                ||||||||||||   ||||
```

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                                CGGGTCCCTGTCT  TGGA
                                      A__
GAM121  GNA15   5' CCGGCTCGGCGGTGGCAAGGC 40900   A C  _ A__
                                CC GC CGG GG  CGGGGC
                                || || ||| ||  ||||||
                                GG CG GCC CC  GTTCCG
                                 C A  G ACC
GAM121  GPR62   3' GCCTGGGGACCACCT     44877    C   ACGGG
                                GCC GGGG   GCCACCT
                                ||| ||||   |||||||
                                CGG CCCC   TGGTGGA
                                 A  _____
GAM121  MKI67   5' CCGGCCCGCAAGGCCAC    14517   A   GGGA
                                CC GCCCG   CGGGGCCAC
                                || |||||  |||||||||
                                GG CGGGC   GTTCCGGTG
                                 C   ____
GAM121  NFATC2  5' CCGGGGACGGCGCGCCT    29585       G CA
                                CCGGGGACGG GC CCT
                                |||||||||| ||  |||
                                GGCCCCTGCC CG GGA
                                     G C_
GAM121  OFD1    5' CCAGCCCGGGCGGTGGGGCCA 18812       GAC_
                                CCAGCCCGGG  GGGGCCA
                                |||||||||  |||||||
                                GGTCGGGCCC  CCCCGGT
                                     GCCA
GAM121  OTC     5' AGCCAGCGGGGGCCACCTA  8041     CGG AC
                                AGCC  GG GGGGCCACCTA
                                ||||  ||  ||||||||||
                                TCGG  TC CCCCGGTGGAT
                                  ___ GC
GAM121  PLIN    3' CCGGCCCGGGGCGCGGC    15398   A     A G
                                CC GCCCGGGG CG GGC
                                || |||||||| || |||
                                GG CGGGCCCC GC CCG
                                 C      _ G
GAM121  PRV1    3' CATTCGGGGGGAGCCAC    43874   GCC   AC
                                CA  CGGGG GGGGCCAC
                                ||  ||||| ||||||||
                                GT  GCCCC CCTCGGTG
                                 AA_   __
GAM121  RECQL5  3' CCGGCTCTGGGACGGGGC   20165   A CCG
                                CC GC  GGGACGGGGC
                                || ||  ||||||||||
                                GG CG  CCCTGCCCCG
                                 C AGA
GAM121  TRPC6   5' GCCCGGGGAAAAGTCACC   21483       CG GC
                                GCCCGGGGA GG CACC
                                |||||||| ||  ||||
```

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                                CGGGCCCCT  TC  GTGG
                                     TT  A_
GAM121  UBE2L3   3' AGTGCGGGGACAATCCCA    17823    CC       GG
                                AG  CGGGGACGG  CCA
                                ||  |||||||||  |||
                                TC  GCCCCTGTT  GGT
                                 AC        AG
GAM121  WHSC1    3' CCGGCCTGAGGACGGACAGC   39358    A   C      __
                                CC GCC GGGGACGG  GGC
                                || ||| ||||||||  |||
                                GG CGG CTCCTGCC  TCG
                                 C  A       TG
GAM122  ARCN1    3' GCATTCCAGCCTGGGTTA     11655        A    C
                                GCATTCCA CCTG GTTG
                                |||||||| |||| ||||
                                CGTAAGGT GGAC CAAT
                                     C    C
GAM122  LILRA3   3' ACTGCATTCCAGCCTGGT    45461    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C   _
GAM122  PIGR     3' ACTGCATTCCAGTCTGGGT   43695    C       AC   C
                                AC GCATTCCA  CTG GT
                                || ||||||||  ||| ||
                                TG CGTAAGGT  GAC CA
                                 A       CA   C
GAM122  TNFAIP1  3' CGCATTCCAGTCTCTGT     34477         AC  GCG
                                CGCATTCCA  CT   TTGT
                                |||||||||  ||   ||||
                                GCGTAAGGT  GA   GACA
                                     CA  ___
GAM122  TRPV1    3' ACTGCATTCCAGCCTGGGT   38789    C       A    C
                                AC GCATTCCA CCTG GT
                                || |||||||| |||| ||
                                TG CGTAAGGT GGAC CA
                                 A       C    C
GAM122  XRCC5    3' CCGCATCCAACTTGTTTTG    34488       T    C  CG
                                CCGCAT CCAAC TG  TTG
                                |||||| ||||| ||  |||
                                GGCGTA GGTTG AC  AAC
                                   _    A  AA
GAM122  CD34     3' TTCCTGTATTGCGGCAGA     12124         CACAGC    AA
                                TTCCTGTA     TTGCG  AGG
                                ||||||||     |||||  |||
                                AAGGACAT     AACGC  TCT
                                     _______    CG
GAM122  CNTNAP2  3' CTGTAACAGCCCATTAAGG    30486      C       CGA
                                CTGTA ACAGCTTG   AAGG
                                ||||| ||||||||   ||||
```

```
                                GACAT TGTCGGGT   TTCC
                                  _      AA_
GAM122  FBN1    3'  TTCCCGTACGTTTGCTGGAAGG 42057        ACAGC   GA_
                                TTCCTGTAC    TTGC   AAGG
                                |||||||||    ||||   ||||
                                AAGGGCATG    AACG   TTCC
                                     CA___    ACC
GAM122  NUP98   3'  TTCCTGCACATAGTAGTAGCAA 32238         C  CTT__  G
          AGG                     TTCCTGTACA AG    GC AAAGG
                                |||||||||| ||    || |||||
                                AAGGACGTGT TC    CG TTTCC
                                     A  ATCAT  _
GAM122  SFRP1   3'  TTCCTGTACATTGGACAAGAAG 16581         CAGCTT   _
          G                      TTCCTGTACA     GCGA AAGG
                                ||||||||||     |||| ||||
                                AAGGACATGT     TGTT TTCC
                                     AACC__    C
GAM122  STK24   3'  TTCCTTATGCACGCCGAAAGG  18711      GTA_   A  TTG
                                TTCCT    CAC GC   CGAAAGG
                                |||||    ||| ||   |||||||
                                AAGGA    GTG CG   GCTTTCC
                                   ATAC   _ ___
GAM123  CDH5    3'  CAAGTCAAGCTGTCCAGGCCTT 12183        AGA   A   A
                                TAAGTCAA   TGT CCA GCCTT
                                ||||||||   ||| ||| |||||
                                GTTCAGTT   ACA GGT CGGAA
                                     CG_   _   C
GAM123  PAX5    5'  GTCGGAATAATTCAAGCCTT   32518     AAA    TAC
                                GTC   GATG   CAAGCCTT
                                |||   ||||   ||||||||
                                CAG   TTAT   GTTCGGAA
                                  CC_    TAA
GAM123  ZNF35   5'  GTCAAACCCCATCCAAGC    18284       GA_   A
                                GTCAAA   TGT CCAAGC
                                ||||||   ||| |||||||
                                CAGTTT   GTA GGTTCG
                                   GGG   _
GAM123  AF3P21  3'  GGCAGCGACCCCCATG      32401       ACT
                                GGCGGT   ATCCCCATG
                                ||||||   |||||||||
                                CCGTCG   TGGGGGTAC
                                   C__
GAM123  AK2     3'  AGCCACCATCCCTATG      11561     GG       C
                                GGC  TACTATCCC ATG
                                |||  ||||||||| |||
                                TCG  GTGGTAGGG TAC
                                  __        A
GAM123  ATP1B1  3'  GGCAGTTCCCCCATG       11731       ACTA
                                GGCGGT    TCCCCATG
                                ||||||    ||||||||
```

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                                CCGTCA   GGGGGTAC
                                   A___
GAM123  ATP5G1   3'  AGGCCGGTGACCCCCCATG   23201     _  _  AT
                                AGGC GGT ACT  CCCCATG
                                |||| ||| |||  |||||||
                                TCCG CCA TGG  GGGGTAC
                                  G  C  __
GAM123  BRF1     3'  AGGGGTCTGACCCCCATG    11327    C  A  _
                                AGG GGT CT ATCCCCATG
                                ||| ||| || |||||||||
                                TCC CCA GA TGGGGGTAC
                                  _  _  C
GAM123  CALD1    3'  AGGCAGTACTTTTACCATG   37575        ATCC
                                AGGCGGTACT   CCATG
                                ||||||||||   |||||
                                TCCGTCATGA   GGTAC
                                     AAAT
GAM123  CARKL    3'  AGACGGGGTATCCCCATG    29985      TAC
                                AGGCGG  TATCCCCATG
                                ||||||  ||||||||||
                                TCTGCC  ATAGGGGTAC
                                   CC_
GAM123  CLCN7    3'  AGGCCGGGGTCCCCATG     10511     _  TACTA
                                AGGC GG    TCCCCATG
                                |||| ||    ||||||||
                                TCCG CC    AGGGGTAC
                                  G  CC___
GAM123  DLX4     5'  GGGGTGCCCCCCCATG      39618    C  A  A
                                GG GGT CT TCCCCATG
                                || ||| || ||||||||
                                CC CCA GG GGGGGTAC
                                  _  C  _
GAM123  EFNB2    3'  AGCGAGTGCCTCCCCATG    19875     _  A  A
                                GGCG GT CT TCCCCATG
                                |||| || || ||||||||
                                TCGC CA GG AGGGGTAC
                                  T  C  _
GAM123  ETV5     3'  AGGCGGGCTTTCACATG     20840      TA  A  CC
                                AGGCGG  CT TC  CATG
                                ||||||  || ||  ||||
                                TCCGCC  GA AG  GTAC
                                   C_  A  T_
GAM123  FVT1     3'  AGGCTGCCTTTCCCCATG    13026     G  A  A
                                AGGC GT CT TCCCCATG
                                |||| || || ||||||||
                                TCCG CG GA AGGGGTAC
                                  A  _  A
GAM123  GCK      3'  GGGAGCACTTCCCCATG     37929    C     A
                                GG GGTACT TCCCCATG
                                || |||||| ||||||||
```

```
                                CC TCGTGA AGGGGTAC
                                 C     _
GAM123  GYPE     3'  AGGCCACATCCTCATG      13328     GG   T    C
                                AGGC  TAC ATCC CATG
                                ||||  ||| |||| ||||
                                TCCG  GTG TAGG GTAC
                                  __  _   A
GAM123  HBE1     3'  AAGCCCAGTCCCCATG      23723     GGTA  _
                                AGGC   CTA TCCCCATG
                                ||||   ||| ||||||||
                                TTCG   GGT AGGGGTAC
                                  ____  C
GAM123  HR       5'  GGCGCCTGCTCCCCATG     32927     GTA  A_
                                GGCG   CT  TCCCCATG
                                ||||   ||  ||||||||
                                CCGC   GA  AGGGGTAC
                                  G__  CG
GAM123  HTRA3    3'  GGCGGCACTTCCATG       44835        ATCC
                                GGCGGTACT    CCATG
                                |||||||||    |||||
                                CCGCCGTGA    GGTAC
                                     A___
GAM123  KCNK6    3'  GGCAGCACCTCCCATG      22081        ATC
                                GGCGGTACT   CCCATG
                                |||||||||   ||||||
                                CCGTCGTGG   GGGTAC
                                     A__
GAM123  LOXL2    3'  AGGTAGCAGCCCCCCATG    14191     CG   CTA
                                AGG  GTA   TCCCCATG
                                |||  |||   ||||||||
                                TCC  CGT   GGGGGTAC
                                  AT   CG_
GAM123  LPIN2    3'  GGCACCCGTGTCCCCATG    31215       A___
                                GGTACT    TCCCCATG
                                ||||||    ||||||||
                                CCGTGG    AGGGGTAC
                                   GCAC
GAM123  MEIS2    3'  AGGCCGGATCCCCATG      33535     _  TACT
                                AGGC GG    ATCCCCATG
                                |||| ||    |||||||||
                                TCCG CC    TAGGGGTAC
                                  G  _____
GAM123  PAEP     3'  AGCAGCCTCCCCATG       15064       ACTA
                                GGCGGT    TCCCCATG
                                ||||||    ||||||||
                                TCGTCG    AGGGGTAC
                                   G___
GAM123  SLC31A1  3'  AGACGGGGTTTCCCCATG    12395       TACTA
                                AGGCGG    TCCCCATG
                                ||||||    ||||||||
```

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                                TCTGCC    AGGGGTAC
                                   CCAA_
GAM123  SYNGR1   3' AGCGAGTTTCCCCATG     21750     _ ACTA
                                GGCG GT   TCCCCATG
                                |||| ||   ||||||||
                                TCGC CA   AGGGGTAC
                                  T  A___
GAM124  DGCR2    3' CCCAGGATGGTGGTTTCA    23088    GCA
                                CCC   AGGATGGTGGTTTCA
                                |||   ||||||||||||||
                                GGG   TCCTACCACCAAAGT
                                 ___
GAM124  DHFR     5' CCCCTGCGAGGCAAGCGGTTT 8990      _ A   AT
                                CCCC GC AGG  GGTGGTTT
                                |||| || |||  ||||||||
                                GGGG CG TCC  TCGCCAAA
                                  A  C   GT
GAM124  IL1F5    5' CCTCCAAGGATGCCTCA     29348    G_     GGTG
                                CC  CAAGGAT   GTTTCA
                                ||  |||||||   ||||||
                                GG  GTTCCTA   CGGAGT
                                 AG     _____
GAM124  SLC2A3   5' TCTCCGCAAAGGGTGGAGCC  27982    C      AT    TT
                                TC CCGCAAGG  GGTGG  TC
                                || ||||||||  |||||  ||
                                AG GGCGTTTC  CCACC  GG
                                 A      __    TC
GAM124  TSC      3' TCTCCGCGGAGGTGGC      32835    C   AA   T
                                TC CCGC  GGA GGTGGT
                                || ||||  ||| ||||||
                                AG GGCG  CCT CCACCG
                                 A   __  _
GAM124  TTYH1    3' TCCCTCCAAGGATGGGACC    34033     CG       T GT
                                TCCC  CAAGGATGG G  T
                                ||||  |||||||| |  |
                                AGGG  GTTCCTACC C  G
                                  AG       _ TG
GAM124  ZYX      3' TCCCTGCAGGATGGGCGA     18438     C  A     _
                                TCCC GCA GGATGG TGG
                                |||| ||| |||||| |||
                                AGGG CGT CCTACC GCT
                                  A  _     C
GAM125  DDX9     3' TCAACAGATGTAGCTGGCA    44796       C  A__
                                TCAACGGA GTA   GGCA
                                |||||||| |||   ||||
                                AGTTGTCT CAT   CCGT
                                     A  CGA
GAM125  PCLO     3' GGCTGGTGGAGGCAGATTAT   45304    AC_  A_
                                GG   GT  AGGCAGATTAT
                                ||   ||  ||||||||||
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```
                                CC   CA  TCCGTCTAATA
                                 GAC  CC
GAM125  HSPA5    3'  ACTGCTAATGAAAAGCAG    23785      C   CCGTTTC
                                ACTGC TAA      AAAGCAG
                                ||||| |||      |||||||
                                TGACG ATT      TTTCGTC
                                  _   ACT____
GAM125  IHPK1    3'  ACAGCTTTAAAGTTCAAAGCAG 45478    T  CTAACCGT
              T                  AC GC       TTCAAAGCAGT
                                 || ||       ||||||||||
                                 TG CG       AAGTTTCGTCA
                                  T  AAATTTC_
GAM125  LDHB     5'  CTGCCTAACTAAACAGGCAGT  14118         CGTTT  AA
                                CTGCCTAAC    CA  GCAGT
                                |||||||||    ||  |||||
                                GACGGATTG    GT  CGTCA
                                      ATTT_  C_
GAM125  POLA     3'  CTGGAGTTGTGTTTTAAAGCAG 32614     CCTAACC   C
              T                  CTG      GTTT AAAGCAGT
                                 |||      |||| ||||||||
                                 GAC      CAAA TTTCGTCA
                                   CTCAACA   A
GAM125  STAU     3'  CCAAATTTTCAAAGCAGT    32692      CCG
                                 CTAA   TTTCAAAGCAGT
                                 ||||   ||||||||||||
                                 GGTT   AAAGTTTCGTCA
                                   TA_
GAM126  AP3B1    5'  GGTCCTGCCGGGGGT       18942      GCGGG
                                 GGTTC    GCCGGGGGT
                                 |||||    |||||||||
                                 CCAGG    CGGCCCCCA
                                    A____
GAM127  EBAG9    3'  GGATGGCCTGATCAATGTAT  20118    CC    GT_
                                 GG  GGTC   TCAATGTAT
                                 ||  ||||   |||||||||
                                 CC  CCGG   AGTTACATA
                                  TA    ACT
GAM128  AXIN1    5'  TCCGGCCGGCTCTGGCGGCG  41393        A  CC_
                                 TCCGGCCG GC   GGCGGCG
                                 |||||||| ||   |||||||
                                 AGGCCGGC CG   CCGCCGC
                                      _  AGA
GAM128  CAPZA1   5'  GGCCCAGCCCGGCTACGGGC  43717      G       ____
                                 GGCC AGCCCGGC    GGC
                                 |||| ||||||||    |||
                                 CCGG TCGGGCCG    CCG
                                   G       ATGC
GAM128  CDA      5'  TCCGGCCAGCCTGGCTGGGGC  12145        G   C  _  C
                                 TCCGGCC AGCC GGC GG GC
                                 ||||||| |||| ||| || ||
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```
                                AGGCCGG TCGG CCG CC CG
                                   _   A  A  C
GAM128  FHL2    5'  CCGGCCGAGTGGAGCGCTGC  11106        CCC  C    C
                                CCGGCCGAG   GG GGCGC GC
                                |||||||||   || ||||| ||
                                GGCCGGCTC   CC TCGCG CG
                                     A__  _    A
GAM128  FZD1    5'  TCCGTCGAGCCCAAGCCG    18619     GC       CGGC
                                TCCG  CGAGCCCGG   GCCG
                                ||||  |||||||||   ||||
                                AGGC  GCTCGGGTT   CGGC
                                  A_       _____
GAM128  FZD1    5'  GGCTCCCGGCTGGCGGCGCCGC 18616     ___  A  CC
                                GGC   CG GC  GGCGGCGCCGC
                                |||   || ||  ||||||||||
                                CCG   GC CG  CCGCCGCGGCG
                                  AGG  _  A_
GAM128  GSPT1   5'  TCCGTGGTTATTGGCGGCGCCG 13312     GCCGAGCCC
            C                    TCCG       GGCGGCGCCGC
                                ||||       ||||||||||
                                AGGC       CCGCCGCGGCG
                                  ACCAATAA_
GAM128  HD      5'  TCGGGCCGACTCGCGGCGCCGC 13362    C     G C  G
                                TC GGCCGA C CG CGGCGCCGC
                                || |||||| | || |||||||||
                                AG CCGGCT G GC GCCGCGGCG
                                 C     _ A  _
GAM128  HDGF    5'  CGGCGGTGGCGGCGCCG     21061      CGAGCCC
                                CGGC      GGCGGCGCCG
                                ||||      ||||||||||
                                GCCG      CCGCCGCGGC
                                  CCA_____
GAM128  IRS2    5'  ACCGCTCGGCGGCGCC      40693      AGCC
                                GCCG   CGGCGGCGCC
                                ||||   ||||||||||
                                TGGC   GCCGCCGCGG
                                  GA__
GAM128  NAGA    5'  TCCAGCCGGGTCCGGGTTCCCG 7044         AGC   CGGCG
            C                    TCCGGCCG  CCGG    CCGC
                                ||||||||  ||||    ||||
                                AGGTCGGC  GGCC    GGCG
                                     CCA   CAAG_
GAM128  RANBP2L1 5'  CGGCCGGGCTCGTGGCGCCGC  37023       A  C  GC
                                CGGCCG GC CG  GGCGCCGC
                                |||||| || ||  ||||||||
                                GCCGGC CG GC  CCGCGGCG
                                   C  A  A_
GAM128  RDBP    5'  TCCGGCCGCGCCCGCGCTGGCC 16232         A    _  GGC
            GC                     TCCGGCCG GCCCG GC   GCCGC
                                ||||||| ||||| ||   |||||
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                                AGGCCGGC CGGGC CG   CGGCG
                                    G    G  AC_
GAM128  RENT1   3'  TCCGGCCGCGGCAC       16258        GAGCCCG
                                TCCGGCC      GCGGCGC
                                |||||||      |||||||
                                AGGCCGG      CGCCGTG
                                         ________
GAM128  SIM2    3'  GCCGGGCTCGGTGGCGCCGC   22877      A  C   C
                                GCCG GC CGG GGCGCCGC
                                |||| || ||| ||||||||
                                CGGC CG GCC CCGCGGCG
                                  C  A   A
GAM128  SOLH    5'  CCTCCACAGCCCGGCGGCGCCG 24825    GG  _
          C                      CC  CCG AGCCCGGCGGCGCCGC
                                ||  ||| ||||||||||||||||
                                GG  GGT TCGGGCCGCCGCGGCG
                                 A_  G
GAM128  TACC1   5'  TCCCGCCGGCAGCCGGCGCCGC 26602     G   A  CC  _
                                TCC GCCG GC  GGC GGCGCCGC
                                ||| |||| ||  ||| ||||||||
                                AGG CGGC CG  TCG CCGCGGCG
                                  G   _ __   G
GAM128  TEAD3   5'  TCCGGCCGGGCCGCTCCG    17379        AGCCC  G  G
                                TCCGGCCG    GGC GC CCG
                                ||||||||    ||| || |||
                                AGGCCGGC    CCG CG GGC
                                     _____  G  A
GAM128  TLL2    5'  TCCGGCCGGGACTCGGTGG   29756        A_  C   C
                                TCCGGCCG  GC CGG GG
                                ||||||||  || ||| ||
                                AGGCCGGC  TG GCC CC
                                     CC  A   A
GAM128  TSG     5'  CGGCCGAGCCCGGGGCGC    34003           C
                                CGGCCGAGCCCGG GGCGC
                                |||||||||||| |||||
                                GCCGGCTCGGGCC CCGCG
                                          _
GAM129  ALPP    3'  CTGCCTGGTACCCACTGGGCTG 42868      A_  GGG TG
                                CTGCT  GTA   C  CTGGGCTG
                                |||||  |||   |  ||||||||
                                GACGG  CAT   G  GACCCGAC
                                   AC   G__ GT
GAM129  BIN3    3'  CTGCTGGAGGGTGCTG     33079      AGT   C
                                CTGCT   AGGG TGCTG
                                |||||   |||| |||||
                                GACGA   TCCC ACGAC
                                   CC_   _
GAM129  CYLN2   3'  CTGGTGTGGACTGGGCTGC   18049    A  AG  CT
                                CT GT  GG  GCTGGGCTGC
                                || ||  ||  ||||||||||
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                                GA CA  CC  TGACCCGACG
                                 C  CA  __
GAM129  CYP3A43  5'  CTGCTCTTTGCTGGGCTG    38398      AGTAGGGC
                                CTGCT       TGCTGGGCTG
                                |||||       ||||||||||
                                GACGA       ACGACCCGAC
                                   GAA_____
GAM129  CYP3A5   5'  CTGCTGTTTGCTGGGCTG    8930       A  AGGGC
                                CTGCT GT    TGCTGGGCTG
                                ||||| ||    ||||||||||
                                GACGA CA    ACGACCCGAC
                                   _ A____
GAM129  MKI67    3'  CTGCTGTAGGGTGGCTG     14520      A     CT
                                CTGCT GTAGGG  GCTG
                                ||||| ||||||  ||||
                                GACGA CATCCC  CGAC
                                   _     AC
GAM129  PFN1     5'  CTGCTACTGGGGCTGCTCTCGG 22715       GTA       G__
              C                  CTGCTA   GGGCTGCT   GGC
                                ||||||   ||||||||   |||
                                GACGAT   CCCGACGA   CCG
                                   GAC       GAG
GAM129  RP2      3'  CTGTTAGTAGAGTTACTTGC   27931     C       C    GG
                                CTG TAGTAGGG TGCT  GC
                                ||| |||||||| ||||  ||
                                GAC ATCATCTC ATGA  CG
                                  A       A    A_
GAM129  STK13    5'  CTGCTGGGCTGCTGGGCTG   17198      AGTA
                                CTGCT   GGGCTGCTGGGCTG
                                |||||   ||||||||||||||
                                GACGA   CCCGACGACCCGAC
                                   _____
GAM130  ATP10C   3'  CCATGTTCACACCTGCC     35977         AATT    C
                                CCATGTTCG   TACC GCC
                                |||||||||   |||| |||
                                GGTACAAGT   GTGG CGG
                                   _____    A
GAM130  DPP6     3'  CACCATGTTGAACGTCC     39127         C    TTAC
                                CACCATGTT GAAT   CC
                                ||||||||| ||||   ||
                                GTGGTACAA CTTG   GG
                                   _    CA__
GAM130  RUNX1    3'  ACCATGTTTTCCCAC       12003         CGAAT  A
                                ACCATGTT    TT CCCGC
                                ||||||||    || |||||
                                TGGTACAA    AA GGGTG
                                   ______ _
GAM130  CD34     3'  CTCAAGGTGTAGGGCCCCAAG  12115      T       AATTA
                                CTCA GGTGTAGG    CAAG
                                |||| ||||||||    ||||
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                                GAGT CCACATCC    GTTC
                                  T      CGGG_
GAM130  CLNS1A   3'  CACAGTCAAGGTAGGAATTA  10525      ____
                                CATGGT   GTAGGAATTA
                                ||||||   ||||||||||
                                GTGTCA   CATCCTTAAT
                                   GTTC
GAM130  CUBN     3'  CTCGAGTGGCTGGAATTACA  9889     AT   TA_
                                CTC  GGTG   GGAATTACA
                                |||  ||||   |||||||||
                                GAG  TCAC   CCTTAATGT
                                  C_   CGA
GAM130  FGFR2    3'  CTCCTGGGGAAGATTACAAG  35661    A   TGTA  __
                                CTC TGG   GGA  ATTACAAG
                                ||| |||   |||  ||||||||
                                GAG ACC   CCT  TAATGTTC
                                  G  ____  TC
GAM130  KCNA3    3'  CTCATGGTGGGTTTACAAG   13794       TA  AA
                                CTCATGGTG  GG  TTACAAG
                                |||||||||  ||  |||||||
                                GAGTACCAC  CC  AATGTTC
                                     __  A_
GAM130  NXF5     3'  CTCTGCTGCAGGAATTGCA   37618    A  G       A
                                CTC TG TGTAGGAATT CA
                                ||| || |||||||||| ||
                                GAG AC ACGTCCTTAA GT
                                  _ G        C
GAM130  P2RY1    3'  CTCATGGTGTTTACAA      15006         AGGAA
                                CTCATGGTGT    TTACAA
                                ||||||||||    ||||||
                                GAGTACCACA    AATGTT
                                     _____
GAM131  CACNG6   5'  ACCCTGAGGTTTAGAGA     36693       TA   A
                                ACCCTGAG  TTTA AGG
                                ||||||||  |||| |||
                                TGGGACTC  AAAT TCT
                                     C_   C
GAM131  DUT      3'  ACCCAGTCAATAGAGGATTTA  12622     TG   ATT  A
                                ACCC  AGT   TA AGGATTTA
                                ||||  |||   || ||||||||
                                TGGG  TCA   AT TCCTAAAT
                                  __  GTT  C
GAM131  ID4      3'  CCCTGCTTGAAGGATTT     11377      AGTA   A
                                CCCTG    TTT AAGGATTT
                                |||||    ||| ||||||||
                                GGGAC    GAA TTCCTAAA
                                   ____  C
GAM131  ITPR3    3'  CTCAGGCCAAAGGATTT     13687    G  TAT
                                CT AG   TTAAAGGATTT
                                || ||   ||||||||||
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                                GA TC   GGTTTCCTAAA
                                 G  C__
GAM131  KCNAB1   3'  CCTGGGTATTTTACAGGTTTAC 41401      A     AA_  A
                                CCTG GTATTT   AGG TTTAC
                                |||| ||||||   ||| |||||
                                GGAC CATAAA   TCC AAATG
                                  C     ATG  _
GAM131  MAD2L1   3'  CTGAATATTTAGACTT      14311          AAA
                                CTGAGTATTT   GGATTT
                                ||||||||||   ||||||
                                GACTTATAAA   TCTGAA
                                      ___
GAM131  MAP3K1   3'  CCCTGGTATTTAAGAAA     42699       A       AG
                                CCCTG GTATTTAA  GA
                                ||||| ||||||||  ||
                                GGGAC CATAAATT  TT
                                  _       CT
GAM131  TPMT     3'  CTGAGTAAAAGACAAGGGTTTA 7494         TTTA__    A
                                CTGAGTA     AAGG TTTA
                                |||||||     |||| ||||
                                GACTCAT     TTCC AAAT
                                    TTTCTG    C
GAM131  VPS26    3'  CCTGAAAAGAGAGGATTTA    22209       TATTTAA
                                CCTGAG      AGGATTTA
                                ||||||      ||||||||
                                GGACTT      TCCTAAAT
                                   TTCTC__
GAM132  NEB      3'  AGAGGTTTTATTAGTTGCTGGT 21231     AA        AC___
           TTGT                   GGA  TTTTATTAGT    GTTTGT
                                |||  ||||||||||    ||||||
                                TCT  AAAATAATCA    CAAACA
                                  CC         ACGAC
GAM133  ATP2A3   3'  TCCGGCGGGACCCGGTGGGCA  23198     TTT  AT  A
                                TCC   GT  GA CCCGGTGGGCA
                                |||   ||  || ||||||||||
                                AGG   CG  CT GGGCCACCCGT
                                  C__  CC  _
GAM133  DPYSL2   3'  TCCCTGTATGAGCTTGGTGGG  10757      T     ACCC
                                TCCTT GTATGA    GGTGGG
                                ||||| ||||||    ||||||
                                AGGGA CATACT    CCACCC
                                  _     CGAA
GAM133  NCAM2    3'  TTTGTATAATCCATTGTG     21229         A  CG_
                                TTTGTATGA CC   GTG
                                |||||||| ||   |||
                                AAACATATT GG   CAC
                                     A  TAA
GAM133  RAB36    3'  CCCTGGAGCTGAGCCCGGTGGG 22237      TTGTA   A
                                TCCT     TGA CCCGGTGGG
                                ||||     ||| |||||||||
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                                GGGA    ACT GGGCCACCC
                                  CCTCG   C
GAM133  ALDOB    3'  CACTGGAGCTAGGCTGGCGGG  42768     A  __   AA_
                                CATT GAG  GGGC   CGGG
                                |||| |||  ||||   ||||
                                GTGA CTC  TCCG   GCCC
                                  C   GA    ACC
GAM133  BAIAP3   3'  ACATGAGGGACATAAATGGG   19450     TA      AC___
                                ACAT  GAGGGGCA    GGG
                                ||||  ||||||||    |||
                                TGTA  CTCCCTGT    CCC
                                  __      ATTTA
GAM133  IKBKB    5'  AAAACATTAAAATGCGG     41803          GG  AAC
                                AAAACATTAGAG  GC   GG
                                ||||||||||||  ||   ||
                                TTTTGTAATTTT  CG   CC
                                       A_  ___
GAM134  EXO1     3'  CAGGGACTTCAAATTGATCAGA 25698     C    GTA  TCA__
           TT                    CAG GGAC   CA    ATCAGATT
                                |||| ||||   ||    ||||||||
                                GTC CCTG   GT    TAGTCTAA
                                  _   AA_  TTAAC
GAM134  P2RX4    3'  AGTGGAGACTCAATCAGATT   14998    C   CGT  A
                                AG GGA   AC TCAATCAGATT
                                || |||   || ||||||||||
                                TC CCT   TG AGTTAGTCTAA
                                 A  C__  _
GAM134  ADD1     3'  TGCACACAGGCCCATCTGCCGC 30512        AAGAAAA_
                                TGCACACA       TGCCGC
                                ||||||||       ||||||
                                ACGTGTGT       ACGGCG
                                     CCGGGTAG
GAM134  ATP7B    3'  TGATGCACACAGACAGGC    6282           AA  AAAT
                                TGATGCACACA  GA   GC
                                ||||||||||  ||   ||
                                ACTACGTGTGT  CT   CG
                                       __  GTC_
GAM134  AVP      5'  TGGTGCACACAGGTGGACCCCG 7942     A       AAGAAA  G
                                TG TGCACACA     AT CCG
                                || ||||||||     || |||
                                AC ACGTGTGT     TG GGC
                                 C       CCACC_  G
GAM134  NGB      3'  TGAATGAGGGAAAGGGAATGCC 34588     TGCACAC    AA
           GC                    TGA      AAAG  AATGCCGC
                                |||      ||||  ||||||||
                                ACT      TTTC  TTACGGCG
                                  TACTCCC    CC
GAM134  SLC1A4   3'  TAATGCACATAGAGAACAAAGC 16754         CAA    AAT_
                                TGATGCACA   AGAA    GC
                                |||||||||  ||||    ||
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                                ATTACGTGT  TCTT   CG
                                     ATC   GTTT
GAM134  SLC9A1   3' TGGTACACACAAGGGAAA   43243   A      A_
                                TG TGCACACAA  GAAA
                                || |||||||||  ||||
                                AC ATGTGTGTT  CTTT
                                  C       CC
GAM135  COG3     3' TCACGTACTTACTGTACAATA 36416     C   CC  AAC
                                TCACG TAC  TA  GTACAATA
                                ||||| |||  ||  ||||||||
                                AGTGC ATG  AT  CATGTTAT
                                   _  A_  GA_
GAM135  CRKL     3' GCTACTCTTTGCACAATA   23307     C  AAAC
                                GCTAC CT   GTACAATA
                                ||||| ||   ||||||||
                                CGATG GA   CGTGTTAT
                                   A  AA__
GAM135  G6PT1    5' TCACGCTACCCAGGACACGC  11166        TAA__
                                TCACGCTACCC    ACGT
                                ||||||||||    ||||
                                AGTGCGATGGG    TGCG
                                      TCCTG
GAM135  HLF      3' GCTCTAGCGTACAAT     13391    ACC   AA
                                GCT   CTA  CGTACAAT
                                |||   |||  ||||||||
                                CGA   GAT  GCATGTTA
                                  ___   C_
GAM135  PPP3CA   3' GCGACTGTAAACGTACAATA  9613    T  CC
                                GC AC  TAAACGTACAATA
                                || ||  ||||||||||||
                                CG TG  ATTTGCATGTTAT
                                 C  AC
GAM135  SEC22L1  3' TCACTTACCCTAAAGCA    22202     GC      C
                                TCAC  TACCCTAAA GTA
                                ||||  ||||||||| |||
                                AGTG  ATGGGATTT CGT
                                  A_       _
GAM135  SP3      3' ACACTTTAAACGTACAATA   44372     ACCC
                                ACGCT    TAAACGTACAATA
                                |||||    ||||||||||||
                                TGTGA    ATTTGCATGTTAT
                                  A___
GAM136  LRRC2    3' TTCGTCATGATGTCCAAGCTGT 36005    C      _  CGAT
                                TTC TCATGATG CCG    TTGT
                                ||| |||||||| |||    ||||
                                AAG AGTACTAC GGT    GACA
                                  C       A   TC__
GAM136  HNRPH1   5' CACGCGACTTCTGCGTGGCT  24327       TGGGG   A
                                TACGCGAT    CTGC TGGCT
                                ||||||||    |||| |||||
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                                GTGCGCTG    GACG ACCGA
                                    AA___   C
GAM136  RAB26    3' GCGGCTGAAGACATGGCT   30748    AT    CT
                                GCG  TGGGG  GCATGGCT
                                |||  |||||  ||||||||
                                CGC  ACTTC  TGTACCGA
                                  CG    __
GAM137  COG7     3' TTGGCAGAGTGTGGGC     42665       ATCA  AA
                                TTGGCAGA   TG  GGGT
                                ||||||||   ||  ||||
                                AACCGTCT   AC  CCCG
                                    C___  A_
GAM137  D12S2489E 3' TTGGAGAATCATGCATGT   28887     C       AAGG
                                TTGG AGAATCATG   GT
                                |||| |||||||||   ||
                                AACC TCTTAGTAC   CA
                                  _       GTA_
GAM137  DGKA     3' TTGGAGGCCAAGGGTG     10649     C  AA   TGA
                                TTGG AG  TCA   AGGGTG
                                |||| ||  |||   ||||||
                                AACC TC  GGT   TCCCAC
                                  _ C_  ___
GAM137  DRD2     3' CTGGCAGAGTGAGGGTG     9014        ATCA   A
                                TTGGCAGA   TGA GGGTG
                                ||||||||   ||| |||||
                                GACCGTCT   ACT CCCAC
                                    C___  _
GAM137  NORE1    3' TTGGCAGAATCTGTGGT     36433         A  AAG
                                TTGGCAGAATC TG   GGT
                                |||||||||||| ||   |||
                                AACCGTCTTAG AC   CCA
                                      _ A__
GAM137  OGT      5' TTGACAGAATTGTGGCTAT   18792         CA  AA  G
                                TTGGCAGAAT  TG  GG TGT
                                ||||||||||  ||  || |||
                                AACTGTCTTA  AC  CC ATA
                                     __  A_  G
GAM137  PHKB     3' TTGGCATAATCATGAGAAC   7126       G       A GG
                                TTGGCA AATCATGA G  T
                                ||||||| |||||||| |  |
                                AACCGT TTAGTACT C  G
                                   A       _ TT
GAM137  PRSS16   3' TGGTGAGTGAAGGGTG     25234     CA  ATCA
                                TGG  GA   TGAAGGGTG
                                |||  ||   |||||||||
                                ACC  CT   ACTTCCCAC
                                  A_  C___
GAM137  SCN3A    3' TTGGTGAATCATGCACTAGT  27957     CA      AAG_
                                TTGG  GAATCATG   GGT
                                ||||  ||||||||   |||
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                                AACC  CTTAGTAC   TCA
                                  A_      GTGA
GAM137  RPS6KA5  3'  CCAATGAGACCAACG      21913       TAA
                                CCGATGA   GACCAACG
                                |||||||   ||||||||
                                GGTTACT   CTGGTTGC
                                    ___
GAM138  CEACAM1  3'  TGGTTTTCTTCTCTTTGCTAGT 11837    CTTG  G  GC
                                TGG   CTT CTT  TTGCTAGT
                                |||   ||| |||  ||||||||
                                ACC   GAA GAG  AACGATCA
                                  AAAA  _  A_
GAM138  DMRT2    3'  TGGATTTGTTTGCTTGCTTGCT 27271    C_  C
                                TGG  TTG TTGCTTGCTTGCT
                                |||  ||| ||||||||||||
                                ACC  AAC AACGAACGAACGA
                                  TA  A
GAM139  B4GALT5  3'  TGTTTTATGGAAAACAAGG   21948         TT___
                                TGTTTTGTGGA    AGG
                                ||||||||||    |||
                                ACAAAATACCT    TCC
                                      TTTGT
GAM139  BTEB1    3'  TGTTTTGTGACATTTTAAAACA 10224         ATTAGG
           G                    TGTTTTGTGG     TAAAACAG
                                |||||||||     ||||||||
                                ACAAAACACT     ATTTTGTC
                                      GTAAA_
GAM139  FLOT2    3'  TGTTCTGTGGGATTAAAAC   20986        ATTAGG
                                TGTTTTGTGG     TAAAAC
                                |||||||||     ||||||
                                ACAAGACACC     ATTTTG
                                      CTA___
GAM139  GNRHR    5'  TGTTTTGTGTATTGGTAATCCA 7619         G  A   ___
           ACAG                    TGTTTTGTG ATT GGTAA   AACAG
                                |||||||| ||| |||||  |||||
                                ACAAAACAC TAA CCATT   TTGTC
                                      A  _    AGG
GAM140  BCL2A1   5'  CTGGTGGAATTTCTGTTTGCA  19730       CTTG  A__
                                CTGGTGGAA   TCT  TGCG
                                |||||||||   |||  ||||
                                GACCACCTT   AGA  ACGT
                                      AA__  CAA
GAM140  INPP5D   3'  ACTGGTGGGTTTGGGCAC    44418       AAC  TCTAT
                                ACTGGTGG  TTG   GCGC
                                ||||||||  |||   ||||
                                TGACCACC  AAC   CGTG
                                    CA_  C____
GAM140  TRPC1    5'  TGGTGGCGGCGCATGCGC    17684       AACTT  C
                                TGGTGG    GT TATGCGC
                                ||||||    || |||||||
```

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                                ACCACC    CG GTACGCG
                                   GC___  C
GAM141  GAS7    3'  CTTGATAACTGAGAACTT    25267         AC
                                CTTGATGATT  GAGAACTT
                                ||||||||||  ||||||||
                                GAACTATTGA  CTCTTGAA
                                          __
GAM142  ADCY9   3'  TTCTCTATGGCTTTGCCAAATC 10025    G    ACT     __
          GA                      TTC CTATG   CTTTGCT  GTCGA
                                ||| |||||   |||||||  |||||
                                AAG GATAC   GAAACGG  TAGCT
                                  A    C__      TT
GAM143  COX11   3'  TGTCATGTTTCACAGGCC    20423        C   C
                                TGTCATGT TCAC AGGCT
                                |||||||| |||| |||||
                                ACAGTACA AGTG TCCGG
                                     A   _
GAM143  CSHL1   3'  TGTCATACACCAGGTTG     35457       TCT     C
                                TGTCATG   CACCAGG TG
                                |||||||   ||||||| ||
                                ACAGTAT   GTGGTCC AC
                                    ___      A
GAM143  GRB10   5'  TGCCGGTCACTGGGCTGC    23671     __   CA
                                TGTC  TCAC  GGCTGC
                                ||||  ||||  ||||||
                                ACGG  AGTG  CCGACG
                                  CC    AC
GAM143  IL11    3'  TGCCATGTCTCGCAGGCCG   8481          AC
                                TGTCATGTCTC  CAGGCTG
                                ||||||||||  |||||||
                                ACGGTACAGAG  GTCCGGC
                                       C_
GAM143  IL12B   3'  TGTTATGTTTCCCAGGCTG   13522    C   C  A
                                TGT ATGT TC CCAGGCTG
                                ||| |||| || ||||||||
                                ACA TACA AG GGTCCGAC
                                  A   A  _
GAM143  IL24    5'  GTCATGTCTTGTCCCTCTG   27789        CA_  AGG
                                GTCATGTCT   CC   CTG
                                |||||||||   ||   |||
                                CAGTACAGA   GG   GAC
                                     ACA  GA_
GAM143  KAL1    3'  TGCATGTCTCGTGGCCG    6876    T      ACCA
                                TG CATGTCTC    GGCTG
                                || ||||||||    |||||
                                AC GTACAGAG    CCGGC
                                 _      CA__
GAM143  MAPRE3  3'  TGTGTGGTGAACCAGGCTGC  29543    CAT  CTC
                                TGT   GT   ACCAGGCTGC
                                |||   ||   ||||||||||
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                                ACA   CA   TGGTCCGACG
                                  CAC  CT_
GAM143  MMP2     3'  TGCCCTGTGCCAGGCTGTCG   21203      A   CTCA      C
                                TGTC TGT    CCAGGCTG CG
                                |||| |||    |||||||| ||
                                ACGG ACA    GGTCCGAC GC
                                  G   C___       A
GAM143  MTMR1    5'  GTCTCCACGCTGGGCTGCCG   43158      _  CA__
                                GTCTC AC    GGCTGCCG
                                ||||| ||    ||||||||
                                CAGAG TG    CCGACGGC
                                   G  CGAC
GAM144  ATF5     3'  TCCCAGCTGCTTCCCTGT    28941     A  AT       C
                                TTC AG  TTGCTTCCC GT
                                ||| ||  |||||||| ||
                                AGG TC  GACGAAGGG CA
                                  G  __        A
GAM144  CCNT2    3'  TTCAAGATTAGCTGATAAA    38500         T   TCCCC
                                TTCAAGATT GCT     GTAAA
                                ||||||||| |||     |||||
                                AAGTTCTAA CGA     TATTT
                                      T   C_____
GAM144  NUMA1    5'  TTCAAGATTTGCTGTCCC    45246           _
                                TTCAAGATTTGCT TCCC
                                |||||||||||| ||||
                                AAGTTCTAAACGA AGGG
                                       C
GAM145  DAAM1    3'  TCTTTCAGGAGATAGTATTGT  31431         A    TGGAG
                                TCTTTCAG AGATA     ATTGT
                                |||||||| |||||     |||||
                                AGAAAGTC TCTAT     TAACA
                                     C     CA___
GAM145  ITPR1    3'  TCTTTCAGAAGAATAACATGT  13669           T    AGAT
                                TCTTTCAGAAGA ATGG    TGT
                                |||||||||||| ||||    |||
                                AGAAAGTCTTCT TATT    ACA
                                       _    GT__
GAM145  SLC26A4  3'  TCTTTCAGAAATAGACACATTG 7763          ___     GGAG
           T                    TCTTTCAGA   AGATAT    ATTGT
                                |||||||||   ||||||    |||||
                                AGAAAGTCT   TCTGTG    TAACA
                                     TTA     _____
GAM145  ZNF195   3'  TTTCAGAAGAAATACTCTTGT  28384         T   GAGA
                                TTTCAGAAGA ATG    TTGT
                                |||||||||| |||    ||||
                                AAAGTCTTCT TAT    AACA
                                      T   GAG_
GAM146  ABP1     3'  AGCAGGTACTTAGGCAG     41788     GAAAG   C  C
                                GGC     AGG AC TAGGCAG
                                |||     ||| || |||||||
```

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                                TCG    TCC TG ATCCGTC
                                 _____  A  A
GAM146  ACCN1    3'  GGCCGGAGCGAGGTCTAGGCAG 9914     __ AA   CAC
              C                   GGC  GA  GAGG   CTAGGCAGC
                                  |||  ||  ||||   |||||||||
                                  CCG  CT  CTCC   GATCCGTCG
                                    GC  CG   A__
GAM146  ANPEP    3'  AGGTGAAAGAGGGTACAGGGCG 10095    C      CACCTA   A
              GC                   AGG GAAAGAGG     GGC GC
                                  ||| ||||||||     ||| ||
                                  TCC CTTTCTCC     CCG CG
                                    A       CATGTC   C
GAM146  CA12     3'  AGGCAAGGAGGCACCCAG    10240       AA
                                  AGGCGA  GAGGCACCTAG
                                  ||||||  ||||||||||
                                  TCCGTT  CTCCGTGGGTC
                                     C_
GAM146  CA3      5'  GGCGAAGGGGCACCCACGC   23214       A A       G
                                  GGCGAA G GGCACCTA GC
                                  |||||| | |||||||| ||
                                  CCGCTT C CCGTGGGT CG
                                     _ C       G
GAM146  CDKN1A   3'  GGGACAGGCACCTCAGAGC   38511    C  AAG      A  C
                                  GG GA   AGGCACCT GG AGC
                                  || ||   |||||||| || |||
                                  CC CT   TCCGTGGA TC TCG
                                   _ G__       G  _
GAM146  CETN1    3'  GGTGAAGAAGGGACAGGCAGC  45458    C   AG   C  CT
                                  GG GAA  AGG AC  AGGCAGC
                                  || |||  ||| ||  |||||||
                                  CC CTT  TCC TG  TCCGTCG
                                   A  CT   C  __
GAM146  CHRM1    5'  AGCGGGAGAGGCACAGC     45421      AA       CTA
                                  GGCG  AGAGGCAC   GGC
                                  ||||  ||||||||   |||
                                  TCGC  TCTCCGTG   TCG
                                    CC       ___
GAM146  CLNS1A   3'  GGAAGAGGCACCAAG       10528    CGA        T
                                  GG   AAGAGGCACC AG
                                  ||   ||||||||||  ||
                                  CC   TTCTCCGTGG TC
                                   ___          T
GAM146  DAAM2    3'  AGGCAGAAGATAGGCA      45171       A    GGCACC
                                  AGGCG AAGA     TAGGCA
                                  ||||| ||||     ||||||
                                  TCCGT TTCT     ATCCGT
                                    C   _______
GAM146  DLST     3'  AGGTAGAAGAGGCATCTTGA   12570     CGA       C  A
                                  AGG   AAGAGGCA CT GG
                                  |||   |||||||| || ||
```

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                                TCC   TTCTCCGT GA CT
                                  ATC       A  A
GAM146  DLX2     3'  GGCGAGGAAGGCGCCAGACAG  20593      AA    A  T
                                GGCGA  GAGGC CC AGGCAG
                                ||||| ||||| || ||||||
                                CCGCT  TTCCG GG TCTGTC
                                   CC    C  _
GAM146  FDX1     5'  AGGCGGGGGCGGCAGCTGCGGC 41266      AAAGA   C  A_
                                AGGCG    GGCA CT  GGC
                                |||||    |||| ||  |||
                                TCCGC    CCGT GA  CCG
                                   CCCCG   C  CG
GAM146  GALE     3'  AGGCTGGAGAGCAGGCAG    41797     GAA   GCACC
                                AGGC   AGAG    TAGGCAG
                                ||||   ||||    |||||||
                                TCCG   TCTC    GTCCGTC
                                  ACC   _____
GAM146  GGT1     3'  AGGCCAGGGAGGCACCTGGC   30203     GAAA       A
                                AGGC    GAGGCACCT GGC
                                ||||    ||||||||| |||
                                TCCG    CTCCGTGGA CCG
                                  GTCC       _
GAM146  GPC1     3'  AGCTGGGGGGGAGGGCTAGGCAG 13231     GAAA__    CAC
          C                      GGC     GAGG   CTAGGCAGC
                                |||     ||||   |||||||||
                                TCG     CTCC   GATCCGTCG
                                  ACCCCC    C__
GAM146  GRB14    5'  AGGCGAGGTGCCGCCTAGGCAG 21027       AA AG  A_
          C                      AGGCGA  G  GC  CCTAGGCAGC
                                ||||||  |  ||  ||||||||||
                                TCCGCT  C  CG  GGATCCGTCG
                                   __ CA  GC
GAM146  HSPB1    3'  GGCGGGGGAGGCACAGC     11363      AAA      CTA
                                GGCG   GAGGCAC   GGC
                                ||||   |||||||   |||
                                CCGC   CTCCGTG   TCG
                                   CCC      ___
GAM146  KIAA0857 3'  AGGAGAGAGGGCAGGCAG    42465     C  A  A   CCTA
                                AGG GA AG GGCA    GGCAG
                                ||| || || ||||    |||||
                                TCC CT TC CCGT    CCGTC
                                  T  C  _   ____
GAM146  MSLN     5'  AGGGAGGGAGGCACCGTGG   30174     C  AA      TA
                                AGG GA  GAGGCACC  GG
                                ||| ||  ||||||||  ||
                                TCC CT  CTCCGTGG  CC
                                  _  CC       CA
GAM146  MYCL1    3'  AGGGAAAGAGGCAGCA      23886     C        CCTAG
                                AGG GAAAGAGGCA    GCA
                                ||| ||||||||||    |||
```

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                              TCC CTTTCTCCGT    CGT
                                _     _____
GAM146  MYO1F    3'  GGCGAAAGAGAAGGCAG    44371         CACCT
                              GGCGAAAGAGG    AGGCAG
                              ||||||||||    ||||||
                              CCGCTTTCTCT    TCCGTC
                                           _____
GAM146  NIPSNAP1 3'  AGGTGGAGGTGTAGGCAG    18867    CGAAA   CACC
                              AGG    GAGG   TAGGCAG
                              |||    ||||   |||||||
                              TCC    CTCC   ATCCGTC
                                AC___   AC__
GAM146  NXF1     3'  AGGCGAGGAGAGGGATCAGGCA 26836      A_    CACC
             GC                 AGGCGA  AGAGG   TAGGCAGC
                              ||||||  |||||   ||||||||
                              TCCGCT  TCTCC   GTCCGTCG
                                 CC    CTA_
GAM146  PDGFRB   3'  AGTGAAAGAGGTCCCGTGG   42332    C      CA  TA
                              GG GAAAGAGG  CC  GG
                              || ||||||||  ||  ||
                              TC CTTTCTCC  GG  CC
                               A       AG  CA
GAM146  SHC1     5'  AGGTGAAAGAGGGGC      16695     C      CACCTA
                              AGG GAAAGAGG     GGC
                              ||| ||||||||     |||
                              TCC CTTTCTCC     CCG
                                A      _______
GAM146  SYNGR2   3'  AGGTGAAAGAGAGGGGCTGGCA 21742     C      CAC_  A
             G                  AGG GAAAGAGG    CT GGCAG
                              ||| ||||||||    || |||||
                              TCC CTTTCTCT    GA CCGTC
                                A       CCCC  _
GAM146  TAPBP    3'  GGCTGAAGAACTAGGCAG    17307     GA    GCAC
                              GGC  AAGAG    CTAGGCAG
                              |||  |||||    ||||||||
                              CCG  TTCTT    GATCCGTC
                                AC    _____
GAM146  TCEB3    3'  AGGCAGGGAGGCGGGGCTGTGG 17314      AAA    AC__  A_
             C                  AGGCG   GAGGC    CT  GGC
                              |||||   |||||    ||  |||
                              TCCGT   CTCCG    GA  CCG
                                CC_    CCCC  CA
GAM146  TCF19    5'  AGGCAAGGATACTTTAGGCAGC 45554      AA  G  ACC
                              AGGCGA  GA GC   TAGGCAGC
                              ||||||  || ||   ||||||||
                              TCCGTT  CT TG   ATCCGTCG
                                 C_  A  AA_
GAM146  TNFRSF6  5'  AGGCAGCTCCGCCTGGGCAGC  6220     GAAAGA   A___   A
                              AGGC     GGC    CCT GGCAGC
                              ||||     |||    ||| ||||||
```

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                                TCCG     TCG   GGA CCGTCG
                                  _______  AGGC   C
GAM146  ZNF278   5'  AGGCGAAGGCGAAGGCG     36785       AAG   ACCT   A
                                AGGCGA  AGGC   AGGC G
                                ||||||  ||||   |||| |
                                TCCGCT  TCCG   TCCG C
                                   ___   CT__   C
GAM147  CIAO1    5'  TCCCCGTTCCGCCGGAGG    43686     AGACA
                                TTCC    CGTTCCGCCGGAGG
                                ||||    ||||||||||||||
                                AGGG    GCAAGGCGGCCTCC
                                  _____
GAM147  GAA      3'  TCCTAGACACGTTGGG      6667      _       CCGCC  A
                                TCC AGACACGTT    GG G
                                ||| |||||||||    || |
                                AGG TCTGTGCAA    CC C
                                  A       _____ _
GAM147  NTSR1    3'  TCCTGGACACGTTCCGGG    14896     A_        CC
                                TCC  GACACGTTCCG  GG
                                |||  ||||||||||  ||
                                AGG  CTGTGCAAGGC  CC
                                  AC         __
GAM147  PDCL     3'  TTCCAGACTTAGTCATGCTGGA 23936        AC_  CC  C
           GGA                    TTCCAGAC   GTT  GC GGAGGA
                                |||||||   |||  || ||||||
                                AAGGTCTG   CAG  CG CCTCCT
                                     AAT   TA  A
GAM148  IHH      5'  GGCGGTCCTTGCAGCGC     43556         C   G
                                GGCGGTCCT GCAG TGT
                                ||||||||| |||| |||
                                CCGCCAGGA CGTC GCG
                                     A   _
GAM148  ITGB1    5'  GGCGGGAGACCGCAGGTGTCA  38051      TCC_
                                GGCGG   TCGCAGGTGTCA
                                |||||   ||||||||||||
                                CCGCC   GGCGTCCACAGT
                                   CTCT
GAM148  PIGB     5'  TGGCGGTCTCTGTGCTCGG   22143        _  C_  A_
                                TGGCGGTC CT  GC  GG
                                |||||||| ||  ||  ||
                                ACCGCCAG GA  CG  CC
                                     A  CA  AG
GAM149  ADAM11   3'  TCACACGGGGCAGTGGGTGTG  14389        AA G  AACAA
                                TCACACGG  C AG    GTGTG
                                ||||||||  | ||    |||||
                                AGTGTGCC  G TC    CACAC
                                     CC _  ACC__
GAM149  OLIG2    3'  CACGGAACGCAGGAAGCACG   25142        AGAAC   TG
                                CACGGAACG    AAG  TG
                                |||||||||    |||  ||
```

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                                GTGCCTTGC    TTC  GC
                                     GTCC_  GT
GAM149  RREB1    5'  TCACACGGAGTAGAAAATG   16401        ACG   CA
                                TCACACGGA  AGAA  AGTG
                                |||||||||  ||||  ||||
                                AGTGTGCCT  TCTT  TTAC
                                     CA_   __
GAM150  NR2E1    5'  ATTACCCCGTGACTTTGTGCCT 17573        A_   GCCTAC
            G                    ATTACCCT  GACT    GCCTG
                                |||||||| ||||    |||||
                                TAATGGGG CTGA    CGGAC
                                     CA   AACA__
GAM150  SMARCC1  3'  ATTACCCTAGACTCCTA    16899          G
                                ATTACCCTAGACT CCTA
                                |||||||||||| ||||
                                TAATGGGATCTGA GGAT

                                     _
GAM150  TMOD     3'  TTACCCTGTACTGCCCAC    17604       AG
                                TTACCCT  ACTGCCTAC
                                |||||||  |||||||||
                                AATGGGA  TGACGGGTG
                                     CA
GAM151  PPIG     3'  GTTTTTCTCATGTCGAG     21991     CAC  CG
                                GTT   TC  CATGTCGAG
                                |||   ||  |||||||||
                                CAA   AG  GTACAGCTC
                                  AA_  A_
GAM152  HTR2B    5'  TCCGAACAGTGGTCAGCA    9275          AC  _
                                TCCGAACGGTG  CA CA
                                ||||||||||  || ||
                                AGGCTTGTCAC  GT GT
                                      CA  C
GAM153  AHR      3'  TTAGTTCTCTAACTT      11554      TCTT
                                TTAGT   TCTCTAACTT
                                |||||   ||||||||||
                                AATCA   AGAGATTGAA

                                ____
GAM153  HFE      5'  TTAGTTCTCTCTCTCCTAC   40007          AA
                                TTAGTTCTTTCTCT  CTTAT
                                ||||||||||||  |||||
                                AATCAAGAGAGAGA  GGATG

                                     __
GAM153  PROCR    3'  TTACTTCTTTCTACCCTATTAT 26920     G      _  AAC
            A                    TTA TTCTTTCT CT   TTATA
                                ||| ||||||| ||   |||||
                                AAT AAGAAAGA GG   AATAT
                                  G       T  GAT
GAM154  CKTSF1B1 5'  TTCGACGCGTGGCGCTGAGTGC 30096     _     TA  GG
            GG                    TTCG CGCGTG  TG  GAGTGCGG
                                |||| ||||||  ||  ||||||||
```

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                                AAGC GCGCAC  GC  CTCACGCC
                                  T     C_  GA
GAM154  BARHL1   3'  CCTGGCGGGGGCGCGGGGA   33462    A  __
                                CC GGC  GGGCGCGGGGA
                                || |||  ||||||||||||
                                GG CCG  CCCGCGCCCCT
                                 A  CC
GAM154  CHRNA5   5'  CGACCGCCGCGCGGGG     40748      AG  GG
                                CGACC  GC  GCGCGGGG
                                |||||  ||  ||||||||
                                GCTGG  CG  CGCGCCCC
                                   __  G_
GAM154  COL4A4   5'  CCGCCGCGGGCGCGGG     6396     A  AG
                                CCG CC  GCGGGCGCGGG
                                ||| ||  ||||||||||||
                                GGC GG  CGCCCGCGCCC
                                 _  __
GAM154  GLUL     5'  TCGCCGAGCAGGCGGGCGGG  13158    A   C       C
                                TC CCGA CAGGCGGGCG GG
                                || |||| ||||||||||| ||
                                AG GGCT GTCCGCCCGC CC
                                 C   C       _
GAM154  GPR4     5'  GACAACGGCGCGGGG      40883     CA    G
                                GAC  GGCGG CGCGGGG
                                |||  ||||| |||||||
                                CTG  TTGCC GCGCCCC
                                   __    _
GAM154  IL12RB2  5'  CCGGGGTGGGCGCGGGG     11425     ACCA  C
                                CCG   GG GGGCGCGGGG
                                |||   || ||||||||||
                                GGC   CC CCCGCGCCCC
                                  C___  A
GAM154  ITGB4    5'  CCGAGGGCGGGCGCGGGG    6844      CCA
                                CCGA  GGCGGGCGCGGGG
                                ||||  ||||||||||||
                                GGCT  CCGCCCGCGCCCC
                                   C__
GAM154  NOVA1    3'  CGGCCAGGCGATGGGA      27058    A      GCGC
                                CG CCAGGCGG   GGGG
                                || ||||||||   ||||
                                GC GGTCCGCT   CCCT
                                 C      A___
GAM154  OPRD1    5'  CCACCGGCTGCCTGGGCGCGGG 9508        ACCAG  __
           GA                    TCACCG    GC  GGGCGCGGGGA
                                ||||||    ||  ||||||||||||
                                GGTGGC    CG  CCCGCGCCCCT
                                   CGA__  GA
GAM154  SAG      5'  TCACCAACCAGGTGGGAAGGG  8076           C  CGC
                                TCACCGACCAGG GGG  GGGG
                                |||||||||||| |||  ||||
```

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                                AGTGGTTGGTCC CCC   TCCC
                                      A  T__
GAM155  BSG     3'  GTGGCGGTGGGTGGGAGGGGG  42696          C  CGC
                                GTGGCGGTGGG GG   GGGGG
                                |||||||||| ||   |||||
                                CACCGCCACCC CC   CCCCC
                                      A  CT_
GAM155  CACNB4   5'  GTGCGGTGGGCGGAGGGGG   8801     G        CGC
                                GTG CGGTGGGCGG   GGGGG
                                ||| |||||||||   |||||
                                CAC GCCACCCGCC   CCCCC
                                  _        T__
GAM155  FHL2     5'  CGGGCGTGGGGCGCGGGG    11109    T   G   CG
                                CG GGCG TGGG  GCGCGGGG
                                || |||| ||||  ||||||||
                                GC CCGC ACCC  CGCGCCCC
                                 _   _   __
GAM155  FMNL     5'  GTGGCGGTGGCGGG        25312          GGCGGC
                                GTGGCGGTG     GCGGG
                                |||||||||     |||||
                                CACCGCCAC     CGCCC
                                      _______
GAM155  G6PD     3'  CGTGGCGGGGGGTGGAGG     7602          T   C  CGC
                                CGTGGCGG GGG GG   GGG
                                |||||||| ||| ||   |||
                                GCACCGCC CCC CC   TCC
                                     _   A  ___
GAM155  GNB2     5'  GTGGCGGTGGGACTCTGCGGCG 23604           CG___   _
           GGGG                      GTGGCGGTGGG     GCG CGGGGG
                                |||||||||||     ||| ||||||
                                CACCGCCACCC     CGC GCCCCC
                                      TGAGA   C
GAM155  HAP1     3'  GGCGGTGGGCAGGG        19503           GCGC
                                GGCGGTGGGCG    GGG
                                ||||||||||    |||
                                CCGCCACCCGT    CCC
                                      _____
GAM155  HPD      3'  CGTGGGGTGGGCGGG       41156       C      GGCGC
                                CGTGG GGTGGGC     GGG
                                ||||| |||||||     |||
                                GCACC CCACCCG     CCC
                                  _      ______
GAM155  IL6R     5'  CGGGGCGGTGGGCGGGCAGG  8174     T          C
                                CG GGCGGTGGGCGG GCGGG
                                || ||||||||||| |||||
                                GC CCGCCACCCGCC CGTCC
                                 C          _
GAM155  JUND     3'  GGGGCGGCCGCGCGGGG     23809     C     G G
                                GG GGTGG C GCGCGGGG
                                || ||||| | ||||||||
```

```
                                CC CCGCC G CGCGCCCC
                                 _    _ G
GAM155  KCNC3    3'  CGTGGCGGGGCTGGG      22501        TGGGC  GC
                                CGTGGCGG    GGC  GGG
                                ||||||||    |||  |||
                                GCACCGCC    CCG  CCC
                                     _____   A_
GAM155  KLF4     5'  CGGGGCGGTGGGCGGGCGG   20154    T         C
                                CG GGCGGTGGGCGG GCGG
                                || ||||||||||||| ||||
                                GC CCGCCACCCGCC CGCC
                                 C          _
GAM155  MSX2     3'  GGCGGTGGGGGGCGGGGG    42296         C  C
                                GGCGGTGGG GG GCGGGGG
                                ||||||||| || |||||||
                                CCGCCACCC CC CGCCCCC

                                     _ _
GAM155  PAX2     5'  CGGGGCGGTGGGCCGGGG    19625    T       GGCG
                                CG GGCGGTGGGC   CGGGG
                                || ||||||||||   |||||
                                GC CCGCCACCCG   GCCCC
                                 C       ____
GAM155  RBP1     5'  CGGGTGGTGGGCGGCCCGG   16181    T  C       G
                                CG GG GGTGGGCGGC CGG
                                || || |||||||||| |||
                                GC CC CCACCCGCCG GCC
                                 _ A        G
GAM155  SIX1     5'  TGGCGGTGGGCGGCCAAGG   25597           G
                                TGGCGGTGGGCGGC CGGGG
                                |||||||||||||| |||||
                                ACCGCCACCCGCCG GTTCC

                                      _
GAM155  SMT3H1   5'  CGCGGGGAGGCGGCGCGGGGG  40994      C  T
                                CGTGG GG GGGCGGCGCGGGGG
                                ||||| || ||||||||||||||
                                GCGCC CC TCCGCCGCGCCCCC

                                    _ _
GAM155  SPG3A    5'  TGGCGGTGGGCGGCTCCG    31978           G_
                                TGGCGGTGGGCGGC  CG
                                ||||||||||||||  ||
                                ACCGCCACCCGCCG  GC
                                       AG
GAM155  TCF7     3'  GTGGCAGTGGGGGATGGGGG   17324          C  CGC
                                GTGGCGGTGGG GG   GGGGG
                                |||||||||| ||   |||||
                                CACCGTCACCC CC   CCCCC
                                      _  TA_
GAM155  TMEPAI   5'  GCGGCGCGGGGCGCGGGGG   33610       _  C
                                GCGGTG GG GGCGCGGGGG
                                |||||| || ||||||||||
```

```
                                CGCCGC CC CCGCGCCCCC
                                   G  _
GAM155  WNT5A    5'  GGGGTGGCCAGCGCGGGGG   18124    C    G
                                GG GGTGG CGGCGCGGGGG
                                || ||||| ||||||||||
                                CC CCACC GTCGCGCCCCC
                                 _    G
GAM155  CML66    5'  GCGCGCGACGGCAAGGTCT   42818       C   CAACAC  C
                                GCGCGCG CGGC     GG CT
                                ||||||| ||||     || ||
                                CGCGCGC GCCG     CC GA
                                   T   TT____  A
GAM155  GAS1     5'  GCGCGCCGCTGGCTGATGCCC  13068      _  C  CAACACG
                                GCGCG CGC GGC      GCCT
                                ||||| ||| |||      ||||
                                CGCGC GCG CCG      CGGG
                                  G   A   ACTA___
GAM155  HMGA2    5'  GCGCGCGCTGCCCGGGCT    18520       CG   AACA   C
                                GCGCGCGC  GCC    CGG CT
                                ||||||||  |||    ||| ||
                                CGCGCGCG  CGG    GCC GA
                                   A_  ____   C
GAM155  LDB1     5'  GCGCCCGCCGGCTGCC      19340      G      CAACACG
                                GCGC CGCCGGC      GCC
                                |||| |||||||      |||
                                CGCG GCGGCCG      CGG
                                  G      A_____
GAM155  MAP4K5   5'  CGCGCGCCGGCCGGC       27302          AACAC
                                CGCGCGCCGGCC    GGC
                                ||||||||||||    |||
                                GCGCGCGGCCGG    CCG
                                       _____
GAM155  PPP3R1   5'  GCCCGCGCCGGCCGGGC     44076    G        AACAC
                                GC CGCGCCGGCC    GGC
                                || ||||||||||    |||
                                CG GCGCGGCCGG    CCG
                                 G        C____
GAM155  SORCS3   5'  GCGCGCGCCGGCGAGCGA    31420          CAACA
                                GCGCGCGCCGGC    CGG
                                ||||||||||||    |||
                                CGCGCGCGGCCG    GCT
                                      CTC__
GAM155  STUB1    5'  GCGCCGCGCGGCACGGCCTG  44062     G  _   CAAC
                                GCGC CGC CGGC   ACGGCCTG
                                |||| ||| ||||   ||||||||
                                CGCG GCG GCCG   TGCCGGAC
                                  _  C   _____
GAM155  TBL2     5'  GCACGCGGGGGCGCGGCCT   37409       CC   CAACA
                                GCGCGCG  GGC    CGGCCT
                                |||||||  |||    ||||||
```

```
                                CGTGCGC  CCG    GCCGGA
                                   CC   C____
GAM155  TESK1    5'  GCCGCGCCGGCTGGC      26613    G       CAACAC
                                GC CGCGCCGGC     GGC
                                || |||||||||     |||
                                CG GCGCGGCCG     CCG
                                 _       A_____
GAM155  TIMP3    5'  GCGCGCCGCCGGCGGGGC    7458       _     CAACAC
                                GCGCGC GCCGGC     GGC
                                |||||| ||||||     |||
                                CGCGCG CGGCCG     CCG
                                   G     CC____
GAM155  ZNF274   5'  GCGCCCGTCGGCCGGC     32249     G  C    AACAC
                                GCGC CG CGGCC     GGC
                                |||| || |||||     |||
                                CGCG GC GCCGG     CCG
                                  G  A    _____
GAM156  DISC1    3'  GCACTTTGGGAAGTGCTGC   33040    GG       C  T
                                GC  ACTTTGGGG GT TTGC
                                ||  ||||||||| || ||||
                                CG  TGAAACCCT CA GACG
                                 __       T  C
GAM156  KPNA3    3'  TTTGGAGCCTTTTGTTGC    13984        G    CC
                                TTTGGGGC TTTTG  GC
                                |||||||| |||||  ||
                                AAACCTCG AAAAC  CG
                                     G    AA
GAM156  POLG     3'  GAACTTTGGGGCTTCTGC    15445          G
                                GGACTTTGGGGC TTTTGC
                                |||||||||||| ||||||
                                CTTGAAACCCCG AAGACG
                                          _
GAM156  SLC30A3  3'  GCGGGCTTTGGGGCCCCTGC  18430     A       G
                                GCGG CTTTGGGGC TTTTGC
                                |||| ||||||||| ||||||
                                CGCC GAAACCCCG GGGACG
                                  C       _
GAM156  ANK1     3'  GCCTGGAGGCCGGGCCG     33866        AT  A  G
                                GCCTGGAG  CG GC CG
                                ||||||||  || || ||
                                CGGACCTC  GC CG GC
                                     CG  C  _
GAM156  ARNTL    5'  CGCCGGGAGCGCCCGCGCCCGC 10135     T   AT  AG
                                CGCC GGAG  CG  CGCGCCCGC
                                |||| ||||  ||  |||||||||
                                GCGG CCTC  GC  GCGCGGGCG
                                  C   __  GG
GAM156  CDKN2A   5'  CGCCTTCCCTGAGCGCGCCCGC 38472      GGAGA  _
                                CGCCT    TC GAGCGCGCCCGC
                                |||||    || ||||||||||||
```

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                                GCGGA    GG CTCGCGCGGGCG
                                  AG___  A
GAM156  CSNK2A1  5'  TGGAGATCTGGCAGTCAC    12482        GA  __
                                TGGAGATC  GCG  CGC
                                ||||||||  |||  |||
                                ACCTCTAG  CGT  GTG
                                    AC   CA
GAM156  FLG      3'  GCCTGGAGCTGTCTCGTGCCTG 43361        ATCGAG  C   C
          C                      GCCTGGAG     CG GCC GC
                                 ||||||||     || ||| ||
                                 CGGACCTC     GC CGG CG
                                    GACAGA  A   A
GAM156  FLG      5'  GCCTGGAGCTGTCTCGTGCCTG 43361        ATCGAG  C   C
          C                      GCCTGGAG     CG GCC GC
                                 ||||||||     || ||| ||
                                 CGGACCTC     GC CGG CG
                                    GACAGA  A   A
GAM156  MSF      5'  GCTGGGGCGCCGCGCCCGC   44734    C  AGAT  AG
                                GC TGG   CG  CGCGCCCGC
                                || |||   ||  |||||||||
                                CG ACC   GC  GCGCGGGCG
                                 _  CC__  G_
GAM156  PCTK3    5'  CCTGGGGGCCGCGGTGCGCCCG 43777      AGA   AGC_
          C                      CCTGG   TCG   GCGCCCGC
                                 |||||   |||   ||||||||
                                 GGACC   GGC   CGCGGGCG
                                   CCC   GCCA
GAM156  RAX      3'  GCCTGGAGGCTCCAGCGC    30244        A_  G
                                GCCTGGAG  TC AGCGC
                                ||||||||  || |||||
                                CGGACCTC  AG TCGCG
                                    CG  G
GAM156  SHB      5'  CGCCGGAGCCCGCGCGCCCG   16687     T   A  GA
                                CGCC GGAG TC  GCGCGCCCG
                                |||| |||| ||  |||||||||
                                GCGG CCTC GG  CGCGCGGGC
                                  _   _  G_
GAM156  ST14     3'  CCTGGAGATTGAGTTCAC    35061        C   CG
                                CCTGGAGAT GAG  CGC
                                ||||||||| |||  |||
                                GGACCTCTA CTC  GTG
                                    A   AA
GAM156  UBL3     3'  CCCCTGGAGATTGACTGC    28265   G       C  GC
                                C CCTGGAGAT GA  GC
                                | |||||||||  ||  ||
                                G GGACCTCTA CT  CG
                                 G        A  GA
GAM157  DXYS155E 3'  CCGTGGACGTTCGTGGC     22947        CCGCCC  A_
                                CCGTGGACG     TCG  GC
                                |||||||||     |||  ||
```

```
                                GGCACCTGC     AGC  CG
                                    A_____   AC
GAM157  FGF2     5'  CCGCGGACGCCGCCTGGGGAGA 12834           CTC___
            GCC                   CCGTGGACGCCGCC     GAGCC
                                  ||||||||||||||     |||||
                                  GGCGCCTGCGGCGG     CTCGG
                                       ACCCCT
GAM157  FGF8     5'  CCCGTGGAACGTCGTGC     37664        _ CCGCCC   A
                                  CCCGTGGA CG     TCG GC
                                  |||||||| ||     ||| ||
                                  GGGCACCT GC     AGC CG
                                     T _______  A
GAM157  PAK1     5'  CCCCGTGGGTGCGCCTAGC    15081        AC  C   CTCG
                                  CCCCGTGG  GC GCC    AGC
                                  ||||||||  || |||    |||
                                  GGGGCACC  CG CGG    TCG
                                     CA  _   A___
GAM157  PPP2R5A  5'  CCCCGGGACGCCGCCGAGC   26432      T        CTC
                                  CCCCG GGACGCCGCC   GAGC
                                  ||||| ||||||||||   ||||
                                  GGGGC CCTGCGGCGG   CTCG
                                    _        ___
GAM157  PTPN14   5'  CCCCGTGGCGCCCCGGAG    23995        ACGC     C
                                  CCCCGTGG    CGCCCT GAG
                                  ||||||||    |||||| |||
                                  GGGGCACC    GCGGGG CTC
                                     _____      C
GAM157  SORCS2   3'  CCCCGTGGGCCTGGGCGGGC   34051         AC   GCCCT  A
                                  CCCCGTGG  GCC     CG GC
                                  ||||||||  |||     || ||
                                  GGGGCACC  CGG     GC CG
                                     __   ACCC_  C
GAM157  THOP1    3'  CCTTGAGGACGCCGTCTCTAGC 43831    GT__       CC   G
            C                      CC    GGACGCCG  CTC AGCC
                                  ||    ||||||||  ||| ||||
                                  GG    CCTGCGGC  GAG TCGG
                                   AACT       A_   A
GAM157  ACTN2    5'  GCGGCGGGCGGCGGGCGGCGG  9947       A  A  CT  C_
                                  GCGG CG GC  GC  GCGGCGG
                                  |||| || ||  ||  |||||||
                                  CGCC GC CG  CG  CGCCGCC
                                    _  C  C_  CC
GAM157  ALDH3B1  3'  GCGGCGCGGCGATTGCGGCGG  45065      A  A_  CTGCC
                                  GCGG CG  GC    GCGGCGG
                                  |||| ||  ||    |||||||
                                  CGCC GC  CG    CGCCGCC
                                    _  GC  CTAA_
GAM157  CAPON    5'  GCGGCGACGCGTGGCGG     41921      A   GCC   C C
                                  GCGG CGA   TGC G GGCGG
                                  |||| |||   ||| | |||||
```

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                                CGCC GCT   GCG C CCGCC
                                  _  ___  _ A
GAM157  CHRNB2   5' GGTGGTGCCGGCCGCCGCGG  8861    ACGA  T   G
                                GG   GCC GCCGC GCGG
                                ||   ||| ||||| ||||
                                CC   CGG CGGCG CGCC
                                 ACCA  C    G
GAM157  GATA6    3' AGTGGAGTGAGGCCCGCGGCGG 23536   C  C_  CCTG
                                AG GGA  GAG   CCGCGGCGG
                                || |||  |||   |||||||||
                                TC CCT  CTC   GGCGCCGCC
                                 A  CA  CG__
GAM157  IMMT     5' GGACTCGAGCTGCCGCGGCGG  27753     __   C
                                GGAC  GAGC TGCCGCGGCGG
                                ||||  |||| ||||||||||
                                CCTG  CTCG ACGGCGCCGCC
                                  AG   _
GAM157  IMMT     5' AAGCGGACGGCGCTGCTGGTGG 27751       A  _   CGC  C
                                AAGCGGACG GC CTGC   GG GG
                                ||||||||| || ||||   || ||
                                TTCGCCTGC CG GACG   CC CC
                                     _ C   A__  A
GAM157  NFKB1    5' GGCGAGCGGGAGCGCGGCGG  19655    A    CT__  C
                                GG CGAGC   GC GCGGCGG
                                || |||||   || |||||||
                                CC GCTCG   CG CGCCGCC
                                 _    CCCT  _
GAM157  NRG2     3' GCGGAGGGGCGCGCGGCGG   30366     CGAGCCT  _
                                GCGGA      GC CGCGGCGG
                                |||||      || ||||||||
                                CGCCT      CG GCGCCGCC
                                   CCC____  C
GAM157  PAM      5' ACGGCGGGCGTCCTGCGGCGG  39882     A  A  CTG  _
                                GCGG CG GC   CC GCGGCGG
                                |||| || ||   || |||||||
                                TGCC GC CG   GG CGCCGCC
                                  _  C  CA_  A
GAM157  PYGL     5' GCGGCGGGCTGCGCGGCGG   16055     A  A  C   C
                                GCGG CG GC TGC GCGGCGG
                                |||| || || ||| |||||||
                                CGCC GC CG ACG CGCCGCC
                                  _  C  _   _
GAM157  RIMS1    5' GCAGGCGGAGGCGCGGCGG   43733     A  _  CCT  C
                                GCGG CG AG   GC GCGGCGG
                                |||| || ||   || |||||||
                                CGTC GC TC   CG CGCCGCC
                                  C  C  ___  _
GAM157  RXRA     5' AGCGGGCGGCGGGCGCGGCGG  16409      A  A  CT  C
                                AGCGG CG GC  GC GCGGCGG
                                ||||| || ||  || |||||||
```

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                                TCGCC GC CG  CG CGCCGCC
                                  C  _  CC  _
GAM157  S100A10  5'  GCGGAGAGGCGAGCGCGGCGG  40394      C  _ CT  C
                                GCGGA GAG C  GC GCGGCGG
                                ||||| ||| |  || |||||||
                                CGCCT CTC G  CG CGCCGCC
                                  _  C CT  _
GAM157  SGT      3'  AGCGGCTGCAGGGCCGCGGCGG 16606      ACGA  CT_
                                AGCGG   GC   GCCGCGGCGG
                                |||||   ||   ||||||||||
                                TCGCC   CG   CGGCGCCGCC
                                  GA__  TCC
GAM157  SOX18    5'  GCGGCGGGCGGGCGGCGG    32942     A  A  CTGCC
                                GCGG CG GC    GCGGCGG
                                |||| || ||    |||||||
                                CGCC GC CG    CGCCGCC
                                  _  C  CC___
GAM157  TBL1X    5'  GCGGGCGCGGCGGCGGCGG    24886     A  AGCCT  C
                                GCGG CG    GC GCGGCGG
                                |||| ||    || |||||||
                                CGCC GC    CG CGCCGCC
                                  C  GC___  C
GAM157  TOP1     5'  AGGGACGAGCGCGGC       17624     C      CTGCC
                                AG GGACGAGC    GCGGC
                                || ||||||||    |||||
                                TC CCTGCTCG    CGCCG
                                 _      _____
GAM157  UBE3A    5'  GCGGATGGCTACGCGGCGG    39280      CGA  C   C
                                GCGGA   GC TGC GCGGCGG
                                |||||   || ||| |||||||
                                CGCCT   CG ATG CGCCGCC
                                  AC_  _  _
GAM157  USP14    5'  GCGGCGGGAGGCGGCGG     23114     AC_   CCTGCC
                                GCGG   GAG     GCGGCGG
                                ||||   |||     |||||||
                                CGCC   CTC     CGCCGCC
                                  GCC  _______
GAM157  VIM      5'  GCGAACGAGGGCGCGGTGG    45224        CCT  C    C
                                GCGGACGAG   GC GCGG GG
                                |||||||||   || |||| ||
                                CGCTTGCTC   CG CGCC CC
                                     C__  _    A
GAM157  WNT6     5'  GCGGCGAGCGCAACGGCGG    27183     A    CT  C
                                GCGG CGAGC  GC GCGGCGG
                                |||| |||||  || |||||||
                                CGCC GCTCG  CG TGCCGCC
                                  _    __ T
GAM157  YY1      5'  AAGGGGCGGGCGCCGCGGCGG  18160     C  A  A  CT
                                AAG GG CG GC  GCCGCGGCGG
                                ||| || || ||  ||||||||||
```

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                                TTC CC GC CG  CGGCGCCGCC
                                  _ C C __
GAM157  ZFP103   5' AGCGGCGGGCACGGCGGCGG  24956      A A CT C
                                AGCGG CG GC  GC GCGGCGG
                                ||||| || ||  || |||||||
                                TCGCC GC CG  TG CGCCGCC
                                  _ C __ C
GAM158  APM1     3' TTTAGGGAAAATACCTCTACAT 22025     AT CGTT
                                TTTA GA   ATACCTCTACAT
                                ||||  ||   ||||||||||||
                                AAAT CT   TATGGAGATGTA
                                  CC TT__
GAM158  CHD2     5' TGATTGACACTCTCTACAT   10453     CGTT  _
                                TGA   ATAC CTCTACAT
                                |||   |||| ||||||||
                                ACT   TGTG GAGATGTA
                                  AAC_   A
GAM159  ABCB4    5' TCTCCAAGGACGGCGAGA    7772     CA   TTT G  A
                                TC  CAAG  GA GGC AGA
                                ||  ||||  || ||| |||
                                AG  GTTC  CT CCG TCT
                                 AG   ___ G  C
GAM159  BSG      3' TCCACAAAGGGCAAGGACC   42697      AGTTT      A
                                TCCACA    GAGGGCAAG ACC
                                ||||||    ||||||||| |||
                                AGGTGT    TTCCCGTTC TGG
                                   _____       C
GAM159  C18orf1  3' CATAAGTTTGAGCCAAAA    41215    C      G G
                                CA AAGTTTGA G CAAGA
                                || |||||||| | |||||
                                GT TTCAAACT C GTTTT
                                 A      _ G
GAM159  CDH18    3' TCCACAAGGTTGCAAGAAC   22340       TTTGAGG
                                TCCACAAG      GCAAGAAC
                                ||||||||      ||||||||
                                AGGTGTTC      CGTTCTTG
                                     CAA____
GAM159  CHD4     3' CAAGCCTGGCAGGAACC     10459       GAG   A
                                CAAGTTT   GGCA GAACC
                                |||||||   |||| |||||
                                GTTCGGA   CCGT CTTGG
                                   ___   C
GAM159  ESRRB    5' TCCACCCCAGGGTGAGGGC   42630      A__ TT
                                TCCAC   AG  TGAGGGC
                                |||||   ||  |||||||
                                AGGTG   TC  ACTCCCG
                                  GGG  CC
GAM159  F2RL3    3' CACTTGAGGGCAGGA      19511     AAGT       A
                                CAC    TTGAGGGCA GA
                                |||    ||||||||| ||
```

```
                                GTG    AACTCCCGT CT
                                  _____       C
GAM159  LARGE    3'  TCCACAGTGAAGCAGGCAAGAA 21866       A  TTGA_
              CC                    TCCACA GT    GGGCAAGAACC
                                    |||||| ||    ||||||||||
                                    AGGTGT CA    TCCGTTCTTGG
                                      _ CTTCG
GAM159  LTB4R    5'  ACAAGCTTTGGCAGGAAC    8876         GAG    A
                                    ACAAGTTT   GGCA GAAC
                                    ||||||||   |||| ||||
                                    TGTTCGAA   CCGT CTTG
                                         A__    C
GAM159  MECP2    3'  CCACTATGGGGGCAGGAGCC   22580      AAGTT  A    A  A
                                    CCAC     TG GGGCA GA CC
                                    ||||     || ||||| || ||
                                    GGTG     AC CCCGT CT GG
                                      AT___  C    C  C
GAM159  MEN1     5'  TCCAGGGTGGAAGCAAGA    39232      CAA TT  AG
                                    TCCA   G  TG  GGCAAGA
                                    ||||   |  ||  |||||||
                                    AGGT   C  AC  TCGTTCT
                                      ___ CC  CT
GAM159  NFRKB    5'  TCCATGAGTTTGAGACCA    26101      CA       G
                                    TCCA  AGTTTGAGG CA
                                    ||||  |||||||||| ||
                                    AGGT  TCAAACTCT GT
                                      AC        G
GAM159  NTRK2    3'  CAAAAGAAAGGGTAAGAA    26143      TTT    C
                                    CAAG   GAGGG AAGAA
                                    ||||   ||||| |||||
                                    GTTT   TTCCC TTCTT
                                      TCT    A
GAM159  PAICS    3'  CAGGAGTTTGAGACGAACC    26981    CA       GCAA
                                    CA  AGTTTGAGG    GAACC
                                    ||  |||||||||    |||||
                                    GT  TCAAACTCT    CTTGG
                                     CC        G___
GAM159  PSCD4    3'  CACAGGCTGACAAGAA      30122      A   TGAG
                                    CACA GTT    GGCAAGAA
                                    |||| |||    ||||||||
                                    GTGT CGA    CTGTTCTT
                                      C  _____
GAM159  WNT3A    3'  CCCGCACCTTGAGGGTGGGAGC 37540     A  AG       CAA  A
              C                      TCC CA  TTTGAGGG   GA CC
                                    ||| ||  ||||||||   || ||
                                    GGG GT  GAACTCCC   CT GG
                                      C  G_       ACC  C
GAM159  KCNA6    3'  TGAGGCTATGCAAATAAAGACT 13822    T  A   C   __
                                    TG AG CTA TGT  GTAAAGACT
                                    || || ||| |||  |||||||||
```

```
                                AC TC GAT ACG  TATTTCTGA
                                 _ C  _  TT
GAM159  ZNF141   3' TGAGGATGTGGTAAAGACT   18349   TA CTAC  _
                                TG  GA   TGTG TAAAGACT
                                ||  ||   |||| ||||||||
                                AC  CT   ACAC ATTTCTGA
                                 TC ____   C
GAM159  ZNF195   3' TCTGTAGACTCAACACAGGGA 28381        ACT TG  AA
                                TCTGTAGACT  G  TA  GA
                                ||||||||||  |  ||  ||
                                AGACATCTGA  T  GT  CT
                                      GT_ GT  CC
GAM160  CLCN4    3' GCCCAGTGCCCAAATTGGC  12284        GC__
                                GCCCGGTGCC   TTGGC
                                ||||||||||   |||||
                                CGGGTCACGG   AACCG
                                      GTTT
GAM160  EXT2     5' GCTCGGCCCCGAGCTTGG   7589    C   G __
                                GC CGGT CC  GCTTGG
                                || |||| ||  ||||||
                                CG GCCG GG  CGAACC
                                 A   G  CT
GAM160  GAB2     3' GCTTGGTCGCCCAGCTTGG  38682   CC  _  __
                                GC  GGT GCC  GCTTGG
                                ||  ||| |||  ||||||
                                CG  CCA CGG  CGAACC
                                 AA  G  GT
GAM160  INPP1    5' GCACCGGATCCGAGCTTGGC  13571   _   TG __
                                GC CCGG  CC  GCTTGGC
                                || ||||  ||  |||||||
                                CG GGCC  GG  CGAACCG
                                 T   TA  CT
GAM160  PAX2     5' GCCCGGCTGCTGCGGGGC   19627      _  C  TT
                                GCCCGG TGC GC  GGC
                                |||||| ||| ||  |||
                                CGGGCC ACG CG  CCG
                                   G  A  CC
GAM160  PNUTL1   3' GCCCAGTGCCCCGGGGGC   15431        G  T__
                                GCCCGGTGCC CT   GGC
                                |||||||||| ||   |||
                                CGGGTCACGG GG   CCG
                                      _ CCC
GAM160  RAB5B    3' ACCCGGCACCTCCTGCTTGG  16086      TG ____
                                GCCCGG  CC   GCTTGG
                                ||||||  ||   ||||||
                                TGGGCC  GG   CGAACC
                                   GT  AGGA
GAM160  SYCP1    5' GCCCGCTGCCACGCTGGC   17232     G    _
                                GCCCG TGCCGC TTGGC
                                ||||| |||||| |||||
```

```
                                CGGGC ACGGTG GACCG
                                  G     C
GAM160  TAF6    5'  GCTCGGCGCCATCTTGGC    24859    C      _
                                GC CGGTGCCG CTTGGC
                                || |||||||| ||||||
                                CG GCCGCGGT GAACCG
                                 A       A
GAM160  ADSS    5'  GTGGCGGCAACGGCCGC     43477       T   A   TCGC
                                GTGGCGG CAAC GCC    GC
                                ||||||| |||| |||    ||
                                CACCGCC GTTG CGG    CG
                                    _   C  ____
GAM160  ASIC4   5'  AGTGGTGGCAGCGGCTGC    33064      C  TCAA   CTC  _
                                AGTGG GG    CAGC   GC GC
                                ||||| ||    ||||   || ||
                                TCACC CC    GTCG   CG CG
                                   A  _____   C__  A
GAM160  CCND1   3'  GTGGCGGTGGCGCCCGC     38218       CAACA   T
                                GTGGCGGT    GCC CGC
                                ||||||||    ||| |||
                                CACCGCCA    CGG GCG
                                    CCG__  _
GAM160  CORO2A  5'  GTGGCGGTGGCGGCGGCGGC  38065       CAACA  CT  C
                                GTGGCGGT    GC  CG GC
                                ||||||||    ||  || ||
                                CACCGCCA    CG  GC CG
                                    CCGC_  CC  _
GAM160  CTBP2   5'  GTGGCGGTGGCGGCGGC     35603       CAACA  CT  C
                                GTGGCGGT    GC  CG GC
                                ||||||||    ||  || ||
                                CACCGCCA    CG  GC CG
                                    C_____  CC  _
GAM160  EFNB1   5'  GGTAGCCCGGCAGCCTCGCG  20725    CG   AA_
                                GG  GTC   CAGCCTCGCG
                                ||  |||   ||||||||||
                                CC  CGG   GTCGGAGCGC
                                 AT   GCC
GAM160  EGLN2   5'  AGTGGCGGATGACGGCGTC   38814       TCA  A  C
                                AGTGGCGG   AC GC TC
                                ||||||||   || || ||
                                TCACCGCC   TG CG AG
                                    TAC  C  C
GAM160  EHD1    5'  AGTGGCGGCTAGCGCCGC    43032       CAAC   C
                                AGTGGCGGT    AGC TCGC
                                |||||||||    ||| ||||
                                TCACCGCCG    TCG GGCG
                                    A___   C
GAM160  ELK1    5'  GTGGCGGCGGCAGCACC     23415       CAA   C
                                GTGGCGGT   CAGC TC
                                ||||||||   |||| ||
```

```
                                CACCGCCG  GTCG GG
                                    CC_   T
GAM160  ENO2    5' AGTGGCGGCGGCGGCTGCGGC 12709       CAACA CT C
                                AGTGGCGGT   GC CG GC
                                |||||||||   ||  || ||
                                TCACCGCCG   CG  GC CG
                                    CCGC_ AC  _
GAM160  ENO2    5' GTGGCGGTGGCGACGGCGGCGC 12715      CA__ A CTC
                                GTGGCGGT   AC GC  GCGC
                                ||||||||   || ||  ||||
                                CACCGCCA   TG CG  CGCG
                                    CCGC C C__
GAM160  EXT1    5' GTGGCGGCGGCGGCGCG    6551        CAACA CT
                                GTGGCGGT   GC CGCG
                                ||||||||   ||  ||||
                                CACCGCCG   CG GCGC
                                    C____ CC
GAM160  FCER2   5' AGAGGTTTAAGCAGCCTCGTGC 12809   C  CAA__     C
          C                      GG GGT   CAGCCTCG GCC
                                || |||   ||||||| |||
                                TC CCA   GTCGGAGC CGG
                                 T  AATTC      A
GAM160  FGFR1   3' GTGGCAGTCAGCGGCG     31951        ACA CTC
                                GTGGCGGTCA  GC  GCG
                                ||||||||||  ||  |||
                                CACCGTCAGT  CG  CGC
                                    ___ C__
GAM160  KISS1   5' AGGGTGGGCAGCCTCGTGCC  13963   T C TCAA     C
                                AG GG GG   CAGCCTCG GCC
                                || || ||   |||||||| |||
                                TC CC CC   GTCGGAGC CGG
                                 _ A C___      A
GAM160  KPNB1   5' GTGGCGGCGGCGGCGC     13978       CAACA CTC  _
                                GTGGCGGT   GC  GCG C
                                ||||||||   ||  ||| |
                                CACCGCCG   CG  CGC G
                                    C____ C__  T
GAM160  LAMC1   5' GTGGCGGCGGCTCGCGC    14090       CAACA C
                                GTGGCGGT   GC TCGCGC
                                ||||||||   || ||||||
                                CACCGCCG   CG AGCGCG
                                    C____ _
GAM160  LZTR1   5' AGTGGTGGTAACGGGGGGCC  27630     C  C  A____
                                AGTGG GGT AAC    GCC
                                ||||| ||| |||    |||
                                TCACC CCA TTG    CGG
                                  A  _  CCCCC
GAM160  PDHA1   5' AGTGGCGGCAGCGGCGC    7105        TCAA  CTC  _
                                AGTGGCGG   CAGC  GCG C
                                ||||||||   ||||  ||| |
```

```
                                TCACCGCC   GTCG  CGC G
                                    _____   C__   T
GAM160  PGLS    3'  AGTGGCGGCCAGCAGGGGC   28981         A  CCTCGC
                                AGTGGCGGTCA CAG     GC
                                |||||||||| |||     ||
                                TCACCGCCGGT GTC     CG
                                      C  CC_____
GAM160  PPP3R1  5'  GGGGCTGCAGCCTCGCGC   44083   C  CAA
                                GG GGT  CAGCCTCGCGC
                                || |||  ||||||||||
                                CC CCG  GTCGGAGCGCG
                                 _  AC_
GAM160  PTP4A2  5'  GTGGCGGCGGCGGCGACGAC  38637       CAACA  CT  C
                                GTGGCGGT    GC  CG GC
                                ||||||||    ||  || ||
                                CACCGCCG    CG  GC TG
                                     CCGC_  CT  _
GAM160  SEC13L1 5'  GGCGGTGGCTGCCTCGTGC   36227      CAACA    C
                                GGCGGT    GCCTCG GC
                                ||||||    |||||| ||
                                CCGCCA    CGGAGC CG
                                   CCGA_     A
GAM160  SLC20A2 3'  GTGGCGGTGGCACTGC      27577       CAACA  _  C
                                GTGGCGGT    GC CT GC
                                ||||||||    || || ||
                                CACCGCCA    CG GA CG
                                     C_____  T  _
GAM160  SLC30A4 5'  AGTGGGGTCGTGCTCGCGC   30009     C   AACA  C
                                AGTGG GGTC   GC TCGCGC
                                ||||| ||||   || ||||||
                                TCACC CCAG   CG AGCGCG
                                   _   CA__  _
GAM160  SLC6A8  5'  GTGGCGGCGGCGGCGGCGGC  24784       CAACA  CT  C
                                GTGGCGGT    GC  CG GC
                                ||||||||    ||  || ||
                                CACCGCCG    CG  GC CG
                                     CCGC_  CC  _
GAM160  SP3     5'  GTGGCGGTTAGGGTCGGGCC   44379       CAAC  CC   C
                                GTGGCGGT   AG  TCG GCC
                                ||||||||   ||  ||| |||
                                CACCGCCA   TC  AGC CGG
                                     A___  CC   C
GAM160  SQSTM1  5'  AGCGGCGAGCCTCGG       19373       GTCAAC     C
                                AGTGGCG     AGCCTCG G
                                |||||||     ||||||| |
                                TCGCCGC     TCGGAGC C
                                   _______      A
GAM160  STUB1   3'  AGTGGCGGCAATGGCCTCAGCC 44061        T  CA    C
                                AGTGGCGG CAA  GCCTCG GCC
                                |||||||| |||  |||||| |||
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                                TCACCGCC GTT  CGGAGT CGG
                                     _  AC    _
GAM160  ZNF261   3' AGTGGCGGCAGGCCCTGCGCC  22987       T  ACA  TC
                                AGTGGCGG CA  GCC  GCGCC
                                |||||||| ||  |||  |||||
                                TCACCGCC GT  CGG  CGCGG
                                     _ C__  GA
GAM160  ZNF278   5' GTGGCGGCGGCGGCGGCGGC  36818       CAACA  CT  C
                                GTGGCGGT   GC  CG GC
                                ||||||||   ||  || ||
                                CACCGCCG   CG  GC CG
                                     CCGC_  CC  _
GAM161  ALDH3B1  3' TGATTCCATGGTGTGGCCT   45068    GA_      A
                                TGA  CATGGTGTG CCT
                                |||  ||||||||| |||
                                ACT  GTACCACAC GGA
                                  AAG       C
GAM161  FGF5     3' TGGCGTGGTGGCATGA     37595       AGACA
                                TGGCGTG    TGGTGTGA
                                |||||||    ||||||||
                                ACCGCAC    ACCGTACT
                                   C____
GAM161  FIGF     3' TGGTGTGAATGGAAGGTTGGTC 20923    C   ___  CA__   G
           TG                     TGG GTGA  GA   TGGT TG
                                |||  ||||  ||   |||| ||
                                ACC CACT  CT   ACCA AC
                                  A   TAC  TCCA   G
GAM161  GPD1     3' TGGCATGAGGCTGCCAGTGGCT 40659        A____  _   G
           TG                     TGGCGTGAG    CA TGGT TG
                                |||||||||    || |||| ||
                                ACCGTACTC    GT ACCG AC
                                     CGACG  C   A
GAM161  LNK      3' TGGTGTGGACACAGCAGACCT  24211    C  A      T
                                TGG GTG GACATGGTG GACCT
                                ||| ||| ||||||||| |||||
                                ACC CAC CTGTGTCGT CTGGA
                                  A  _       _
GAM161  NORE1    3' TGGTGTGAGGTTCCAGTTTG  36432    C   ACA_   G
                                TGG GTGAG   TGGT TG
                                ||| |||||   |||| ||
                                ACC CACTC   GTCA AC
                                  A    CAAG   A
GAM161  SHOX     3' TGGTTTGGGAAACGGTGTG   27835    CG  A  C
                                TGG  TG GA ATGGTGTG
                                |||  || || ||||||||
                                ACC  AC CT TGCCACAC
                                  AA  C  T
GAM161  TRPM2    5' GCGTGAGATGTGTCCCT     17693       CATG   GA
                                GCGTGAGA   GTGT  CCT
                                ||||||||   ||||  |||
```

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                                CGCACTCT   CACA  GGA
                                   A___   G_
GAM161  XPR1    3'  TGGTGTGAAGTGTGGGATTCCT 21854    C   GACAT    A____
                                TGG GTGA   GGTGTG   CCT
                                ||| ||||   ||||||   |||
                                ACC CACT   TCACAC   GGA
                                  A  _____    CCTAA
GAM162  ABCC1   5'  GCTGCTGGCGCTAGCGCTGGCG 33404   C _   GAC T
                                GC GC GGCG  G CGCTGGCG
                                || || ||||  | ||||||||
                                CG CG CCGC  C GCGACCGC
                                 A A   GAT _
GAM162  ACTN1   5'  CCGCCGCGGCGCTGCTGGC   9930     G   A  C
                                CCGC GCGG CGT GCTGGC
                                |||| |||| ||| ||||||
                                GGCG CGCC GCG CGACCG
                                  G   _  A
GAM162  BAZ1B   5'  GCGGCGGCGGTGGGACTGGCG  37088   C     ACGTC
                                GC GCGGCGG    GCTGGCG
                                || |||||||    |||||||
                                CG CGCCGCC    TGACCGC
                                 C      ACCC_
GAM162  BID     5'  CAGCCGCGGGGGCGCGGGC   10178       C  AC T   T
                                CAGCCGCGG GG  G CGC GGC
                                ||||||||| ||  | ||| |||
                                GTCGGCGCC CC  C GCG CCG
                                     _ __ _  C
GAM162  CUL3    5'  CAGCCGCGGCGGCGG      18730         ACGTCGC
                                CAGCCGCGGCGG     TGG
                                ||||||||||||     |||
                                GTCGGCGCCGCC     GCC
                                      ________
GAM162  CYLN2   3'  CAGCCGCGTGGGGCTCTGG   18046       GC  AC  CG
                                CAGCCGCG  GG  GT  CTGG
                                ||||||||  ||  ||  ||||
                                GTCGGCGC  CC  CG  GACC
                                   A_  C_  A_
GAM162  EGR1    5'  GCTGCGGCGGCGGATGGCG   12661   C     A  TCGC
                                GC GCGGCGG CG   TGGCG
                                || ||||||| ||   |||||
                                CG CGCCGCC GC   ACCGC
                                 A     _ CT__
GAM162  HDAC4   5'  ACCGCGGCGGGCGG       25739        ACGTC  T
                                GCCGCGGCGG    GC GG
                                ||||||||||    || ||
                                TGGCGCCGCC    CG CC
                                      _____ _
GAM162  IL12A   5'  GCCGCGGCAGGTGAGGGCG   9402         AC  CGCT
                                GCCGCGGCGG  GT   GGCG
                                ||||||||||  ||   ||||
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                                CGGCGCCGTC  CA   CCGC
                                     __  CTC_
GAM162  JAG2     5'  CAGCTCCGGCTCGCTGGC    13703     CG   GGACG
                                CAGC  CGGC    TCGCTGGC
                                ||||  ||||    ||||||||
                                GTCG  GCCG    AGCGACCG
                                  AG   _____
GAM162  MAP3K4   5'  GCCGCGGCGGGCAGTAAGCTG  25429         A _  C_
                                GCCGCGGCGG C GT  GCTG
                                |||||||||| | ||  ||||
                                CGGCGCCGCC G CA  CGAC
                                      C T  TT
GAM162  PK428    5'  CAGCTGCGGCGGCGG       18796      C      ACGTCGC
                                CAGC GCGGCGG      TGG
                                |||| |||||||      |||
                                GTCG CGCCGCC      GCC
                                  A     ________
GAM162  POU4F1   5'  CAGCCGCGGCGGTCGCGGC   26381          ACG   T
                                CAGCCGCGGCGG   TCGC GGC
                                ||||||||||||   |||| |||
                                GTCGGCGCCGCC   AGCG CCG
                                      ___   _
GAM162  PTMA     5'  GCTGCGGCGAGCAAGGAGGCG  15870    C     GA  TCGCT
                                GC GCGGCG  CG    GGCG
                                || ||||||  ||    ||||
                                CG CGCCGC  GT    CCGC
                                 A     TC  TCCT_
GAM162  PTMS     5'  GCCGCGGCCGGAACCTGGCG   15886        _   CGTCG
                                GCCGCGGC GGA    CTGGCG
                                |||||||| |||    ||||||
                                CGGCGCCG CCT    GACCGC
                                    G   TG___
GAM162  RPS28    5'  CGCGGCGGCGGTCTGGCG    9751         A  TCG
                                CGCGGCGG CG   CTGGCG
                                |||||||| ||   ||||||
                                GCGCCGCC GC   GACCGC
                                     _  CA_
GAM162  SORCS2   3'  CAGCCGCCGGCTTTGCTGG   34047        _   GGACGTC
                                CAGCCGC GGC      GCTGG
                                ||||||| |||      |||||
                                GTCGGCG CCG      CGACC
                                    G   AAA_____
GAM162  BARHL1   3'  GCCGCGAGAGAGGACGCCG   33465    G    ATTCGT
                                GC CGCGA     GGACGCCG
                                || |||||     ||||||||
                                CG GCGCT     CCTGCGGC
                                 _    CTCT__
GAM162  ELF3     5'  GCCGCGAATTCGCGGCC     20754    G         GAC
                                GC CGCGAATTCGTG   GCC
                                || ||||||||||||   |||
```

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                                CG GCGCTTAAGCGC   CGG
                                  _       ___
GAM162  KNSL1    5'  GCCGCGGACCTGGGCGC     21179    G   AAT  G   A
                                GC CGCG   TC TGG CGC
                                || ||||   || ||| |||
                                CG GCGC   GG ACC GCG
                                  _   CT_ _   C
GAM162  LAMP1    5'  GCGCGCGAGACGGCGC      24507        ATTCG   A
                                GCGCGCGA    TGG CGC
                                ||||||||    ||| |||
                                CGCGCGCT    GCC GCG
                                     CT___  _
GAM162  NR2C2    5'  CAGCGGGCGAGAGACGAGACGC 17668      C   ATT_ T
              CG                   CAGCG GCGA   CG GGACGCCG
                                |||||  ||||   || ||||||||
                                GTCGC CGCT   GC TCTGCGGC
                                   C   CTCT  _
GAM162  PTPN18   5'  GCGCGCGGCGAGTGTGGACGCC 30769        AATTC_
              G                    GCGCGCG     GTGGACGCCG
                                |||||||     ||||||||||
                                CGCGCGC     CACCTGCGGC
                                     CGCTCA
GAM163  ADCY7    3'  CTGCTGCTCCCCGCCTTCTTGC 9987           _  GC
                                TTGCTGCTCTT GCT  TCTTGC
                                |||||||||| |||  ||||||
                                GACGACGAGGG CGG  AGAACG
                                       G  A_
GAM163  ANK1     3'  CTCCCCGCTTCTTGCTGCTTTT 33859     G   _      C
              G                    CTT CTGCT CTTGCTGCT TTG
                                ||| ||||| |||||||| |||
                                GAG GGCGA GAACGACGA AAC
                                  G    A       A
GAM163  BPGM     3'  TTGCTGCTTATTCTTG      11897        CTTGC  C
                                TTGCTGCT    TG TCTTG
                                ||||||||    || |||||
                                AACGACGA    AT AGAAC
                                     _____  A
GAM163  CXorf6   5'  TCTTCCTGGGCTGCTCTTG   24243     G  CTCTT
                                TCTT CTG    GCTGCTCTTG
                                |||| |||    ||||||||||
                                AGAA GAC    CGACGAGAAC
                                  G  C____
GAM163  KEL      5'  TCTGCTGCTCTTTCGCCTTG  7680     T      GC  T
                                TCT GCTGCTCTT  TGC CTTG
                                ||| |||||||||  ||| ||||
                                AGA CGACGAGAA  GCG GAAC
                                  _       A_  _
GAM163  MLLT4    3'  GCTGCTCTTAAACATTTG    43680         CT  TC
                                GCTGCTCTTG  GC  TTG
                                ||||||||||  ||  |||
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                                CGACGAGAAT  TG  AAC
                                      T_  TA
GAM163  SCA2    3'  TCTTGTTACTTCTTTTGC    16478      C   _  GC
                                TCTTG TGCT CTT  TGC
                                ||||| |||| |||  |||
                                AGAAC ATGA GAA  ACG
                                   A   A  A_
GAM164  ABCD1   3'  GGCTGCGCTGCTGTGTGGC   6199        C   CAGC
                                GGTTGCGC GCTG   GGC
                                |||||||| ||||   |||
                                CCGACGCG CGAC   CCG
                                     A   ACA_
GAM164  DPYSL3  5'  GGTGGTGGCTGCAGCGGCTGGC 10775    TGCGCC
                                GGT     GCTGCAGCGGCTGGC
                                |||     ||||||||||||||
                                CCA     CGACGTCGCCGACCG
                                  CCAC__
GAM164  RHBG    5'  GGTTGGGCTGCGATCTCGGCTG 33822     CGCC    AG___
           GC                     GGTTG   GCTGC    CGGCTGGC
                                |||||   |||||    ||||||||
                                CCAAC   CGACG    GCCGACCG
                                   C___    CTAGA
GAM164  ATOX1   5'  GGCGGCGGTGTGGCGGCG    19723       CGA_  CTTCC
                                GGCGGCGG   GCG    GCG
                                ||||||||   |||    |||
                                CCGCCGCC   CGC    CGC
                                     ACAC  _____
GAM164  BAALC   5'  GGCGGCGGCGGCGACATCGCGT 36040        A  _ TTC
                                GGCGGCGGCG GCG C   CGCGT
                                |||||||||| ||| |   |||||
                                CCGCCGCCGC CGC G   GCGCA
                                      _   T TA_
GAM164  CDK2AP1 5'  CGGCGGCGGCGAGGCCGGGCG  21596          C   TCC
                                CGGCGGCGGCGAG GCT   GCG
                                |||||||||||| |||   |||
                                GCCGCCGCCGCTC CGG   CGC
                                      _   CC_
GAM164  DLC1    5'  CGGAGGCGGCTCGGCTTCCGCG 25903    C     GAGC
           T                    CGG GGCGGC    GCTTCCGCGT
                                ||| ||||||    ||||||||||
                                GCC CCGCCG    CGAAGGCGCA
                                  T     AGC_
GAM164  FGD1    5'  CGGCGGTGGCGCGGGGCGCGCG 20902      C   A___   TTCC
           T                    CGGCGG GGCG   GCGC   GCGT
                                |||||| ||||   ||||   ||||
                                GCCGCC CCGC   CGCG   CGCA
                                   A   GCCC   _____
GAM164  FHL1    5'  CGGCGGCGGCGGCCGCTGCC   11094         AG   T
                                CGGCGGCGGCG  CGCT CC
                                ||||||||||  |||| ||
```

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                                GCCGCCGCCGC  GCGA GG
                                      CG    C
GAM164  FMNL    5'  CGGCGGCGGTGGCGCTGC    25297        CGA    TCC
                                CGGCGGCGG   GCGCT   GC
                                |||||||||   |||||   ||
                                GCCGCCGCC   CGCGA   CG
                                     AC_    ____
GAM164  FMR2    5'  CGGCGGCGGGCGGGCGCCT   12961         _ A
                                CGGCGGCGG CG GCGCTT
                                ||||||||| || ||||||
                                GCCGCCGCC GC CGCGGA
                                     C  C
GAM164  IMMT    5'  GGAGGCGTGCTTCCGG     27754    C   AGC      C
                                GG GGCG   GCTTCCG G
                                || ||||   ||||||| |
                                CC CCGC   CGAAGGC C
                                 T   A__      A
GAM164  INSM1   5'  CGGCGGCTGCGGGACTCGCGT  13575       G   AGC   TC
                                CGGCGGC GCG   GCT  CGCGT
                                ||||||| |||   |||  |||||
                                GCCGCCG CGC   TGA  GCGCA
                                   A  CC_  __
GAM164  LGMN    5'  CGGCGGCGGTGAGTGACCGCG  24682        C   CGCTT
                                CGGCGGCGG GAG    CCGCG
                                ||||||||| |||    |||||
                                GCCGCCGCC CTC    GGCGC
                                     A  ACT__
GAM164  LMO4    5'  CGGCGGCGGCGGCGCTGGCC   27652         A    T_
                                CGGCGGCGGCG GCGCT  CC
                                |||||||||| |||||  ||
                                GCCGCCGCCGC CGCGA  GG
                                      _    CC
GAM164  PIM1    5'  CGGCGGGGTGAGCGGCTC    44964       C  C    _
                                CGGCGG GG GAGCG CTT
                                |||||| || ||||| |||
                                GCCGCC CC CTCGC GAG
                                   _ A    C
GAM164  PODXL   5'  CGGCGGCGGCGGCGGCTGCGT  23969          A  _  TCC
                                CGGCGGCGGCG GCG CT   GCGT
                                |||||||||| ||| ||   ||||
                                GCCGCCGCCGC CGC GA   CGCA
                                      _  C  ___
GAM164  PPP2R5E 5'  CGGCGGCGGCGGCGACGACGT  26468          A  CTTC  _
                                CGGCGGCGGCG GCG    CG CGT
                                |||||||||| |||    || |||
                                GCCGCCGCCGC CGC    GC GCA
                                      _  T___  T
GAM164  PTP4A2  5'  CGGCGGCGGCGGCGGCGGCGCG 38627          A  CTTC
           T                    CGGCGGCGGCG GCG    CGCGT
                                |||||||||| |||    |||||
```

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                                GCCGCCGCCGC CGC   GCGCA
                                      _  CGCC
GAM164  RFX2    5'  CGGCGGCGGCAGCGGCTGCTGC 8450        G  _ TCC
          GT                  CGGCGGCGGC AGCG CT  GCGT
                              |||||||||| |||| ||  ||||
                              GCCGCCGCCG TCGC GA  CGCA
                                    _  C  CGA
GAM164  RFX2    5'  GGCGGCGGCGGCCGCTCC   8454         AG
                              GGCGGCGGCG  CGCTTC
                              ||||||||||  ||||||
                              CCGCCGCCGC  GCGAGG
                                    CG
GAM164  RREB1   5'  CGGCGGCGGCGGCGCTCGGAC  16397        A    CC
                              CGGCGGCGGCG GCGCTT  GC
                              |||||||||| ||||||  ||
                              GCCGCCGCCGC CGCGAG  TG
                                    _    CC
GAM164  SLC9A3  3'  CGGCGGCGGTGGGCGGACCG  20050       CGA  CTT
                              CGGCGGCGG  GCG  CCG
                              |||||||||  |||  |||
                              GCCGCCGCC  CGC  GGC
                                   ACC  CT_
GAM164  TPM1    5'  CGGCGGGGCGAGCGCGCG   7484      C      TTCC
                              CGGCGG GGCGAGCGC   GCG
                              |||||| |||||||||   |||
                              GCCGCC CCGCTCGCG   CGC
                                   _      ____
GAM164  USF2    3'  GGCGGCGGCGGCTGCG     17900        AGC  TCC
                              GGCGGCGGCG  GCT  GCG
                              ||||||||||  |||  |||
                              CCGCCGCCGC  CGA  CGC
                                    ___  ___
GAM164  ZNF219  5'  CGGCGGCGCGGGCGTCAGCGT  32322       G  A  CT  C
                              CGGCGGCG CG GCG  TC GCGT
                              |||||||| || |||  || ||||
                              GCCGCCGC GC CGC  AG CGCA
                                   _ C  __ T
GAM165  CD59    3'  AAAGACAGAGGAAAAACTC   8302      C  TAT
                              AAAGAC GA  GGAAACTC
                              |||||| ||  ||||||||
                              TTTCTG CT  TTTTTGAG
                                 T  CC_
GAM165  CR1     3'  TCAAAGACTTTATGAAGCTCA  8201       CGA    AA
                              TCAAAGAC  TATGGA  CTCA
                              ||||||||  ||||||  ||||
                              AGTTTCTG  ATACTT  GAGT
                                   AA_    C_
GAM165  FGA     3'  TCAAAGACTAATATGTCTCA  34840       CG   GAAA
                              TCAAAGAC  ATATG   CTCA
                              ||||||||  |||||   ||||
```

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                                AGTTTCTG  TATAC   GAGT
                                    AT    A___
GAM165  GALR1    3'  CCACTTATATGGAAACTCAA  11196    ___
                                CCG   ATATGGAAACTCAA
                                |||   ||||||||||||||
                                GGT   TATACCTTTGAGTT
                                  GAA
GAM165  NOL3     5'  AGGCCAACACGGGGAACTC   19489    A       A_
                                AG CCGATATGG  AACTC
                                || |||||||||  |||||
                                TC GGTTGTGCC  TTGAG
                                 C        CC
GAM165  NOLA1    5'  AAAGACCAGAAACT       37422       GATAT
                                AAAGACC    GGAAACT
                                |||||||    |||||||
                                TTTCTGG    TCTTTGA

                                   _____
GAM165  NOX4     5'  TCAAAGACTGAGTGGAAGCCC  32597       C  TA    A
                                TCAAAGAC GA  TGGAA CTC
                                |||||||| ||  ||||| |||
                                AGTTTCTG CT  ACCTT GGG
                                    A  C_    C
GAM165  PPP2R5C  3'  AAGACCGATGAAAACTCA    15519       TA
                                AAGACCGA  TGGAAACTCA
                                ||||||||  ||||||||||
                                TTCTGGCT  ACTTTTGAGT

                                   __
GAM165  PRDM2    3'  TCAAGAGCCAGAAACTCA    31974     A  _  GATAT
                                TCAA GA CC    GGAAACTCA
                                |||| || ||    |||||||||
                                AGTT CT GG    TCTTTGAGT
                                  _  C  _____
GAM165  RFC2     5'  CCGAGAAATGGAAACTCA    16277     T__
                                CCGA   ATGGAAACTCA
                                ||||   ||||||||||
                                GGCT   TACCTTTGAGT
                                  CTT
GAM165  SON      3'  TCATGGACCAATAGAAATTCA  38462     AA      AT    C
                                TCA  GACCGAT  GGAAA TCA
                                |||  |||||||  ||||| |||
                                AGT  CTGGTTA  TCTTT AGT
                                  AC      __    A
GAM165  VWF      5'  CCAAGGTCCCTGGGAAACTCA  8128      AGA_  GATAT
                                TCAA   CC    GGAAACTCA
                                ||||   ||    |||||||||
                                GGTT   GG    CCTTTGAGT
                                  CCAG  AC___
GAM165  ZNF80    5'  AGACTGCAGGGAAACTCAA   28329     CGA  T
                                AGAC   TA GGAAACTCAA
                                ||||   || ||||||||||
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                                TCTG   GT CCTTTGAGTT
                                  AC_  C
GAM165  B4GALT1  3'  TACAGCAGAGACCCTGTCCAG  11288      A  A__   ATGA
                                TACA TA   ACC    CTGTCCAG
                                |||| ||   |||    ||||||||
                                ATGT GT   TGG    GACAGGTC
                                  C  CTC  ____
GAM165  HUNK     3'  AATAAACCTGAGTTCAGA    31054         A   CT  C
                                AATAAACC TGA  GT CAGA
                                |||||||| |||  || ||||
                                TTATTTGG ACT  CA GTCT
                                     _   __ A
GAM165  IL10RA   3'  TACAAAAAACCATGGCTTCTCT 40625       T       A  G_  CA
           GGA                    TACAA AAACCATG CT  TC  GA
                                |||||| |||||||| ||  ||  ||
                                ATGTT TTTGGTAC GA  AG  CT
                                   T       C  AG  AC
GAM165  TNC      3'  TACAATCAGGTACTGTCCAGA  13469       AAACCATG
                                TACAAT       ACTGTCCAGA
                                ||||||       ||||||||||
                                ATGTTA       TGACAGGTCT
                                   GTCCA___
GAM165  VCP      3'  CAACAGAAACCCCCTGTCCAGA 44007       __    ATGA
                                CAATA  AACC   CTGTCCAGA
                                |||||  ||||   |||||||||
                                GTTGT  TTGG   GACAGGTCT
                                   CT   GG__
GAM166  ACP5     3'  TGCCTGTGAGCAGGGTCCCGG  11515      CA      TACAC
                                TGCC  TGAGCAGG    TTTGG
                                ||||  ||||||||    |||||
                                ACGG  ACTCGTCC    GGGCC
                                  AC      CA___
GAM166  APM1     3'  TGCCTGTAATCCCAGCACTTTG 22021      CA  G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                |||| |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG  ___
GAM166  ARCN1    3'  TGCCTGTAATCCCAACACTTTG 11659      CA   GCAGGT
           G                     TGCC  TGA     ACACTTTGG
                                |||| |||     |||||||||
                                ACGG  ATT     TGTGAAACC
                                  AC   AGGGT_
GAM166  AXL      3'  TGCCTGTAATCTCAGCACTTTG 34891      CA  G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                |||| |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGA  ___
GAM166  BAZ2B    5'  TGCCTGTAATCCCAGCACTTTG 30325      CA  G__   GTA
           G                     TGCC  TGA   CAG   CACTTTGG
                                |||| |||   |||   ||||||||
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                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM166  CBFA2T2  3' TGCCTGTAATCCTGGCACTTTG 22980    CA  GCA_ TA
          G                TGCC TGA  GG CACTTTGG
                          |||| |||  || ||||||||
                          ACGG ATT  CC GTGAAACC
                            AC  AGGA __
GAM166  CCNF    3' TGCCTGTAATCCCAGCACTTTG 12078    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM166  CLECSF11 5' TGCCTATAATCTCAGCACTTTG 39043    C   G__  GTA
          G                TGCC ATGA  CAG  CACTTTGG
                          |||| ||||  |||  ||||||||
                          ACGG TATT  GTC  GTGAAACC
                            A   AGA  ___
GAM166  COX15   3' TGCCTGTAATCTCAGCACTTTG 20425    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  AGA  ___
GAM166  CYP2B6  3' TGCCTGTAATATCAGCACTTTG 8924     CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  ATA  ___
GAM166  CYP51   3' TGCCTGTAATCCCAGCACTTTG 8960     CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM166  DFFB    3' TGCCTGTAATCCCAGCACTTTG 44603    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM166  DNASE1L1 5' TGCCTGTAATCCCAGCACTTTG 27503    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM166  DSC3    3' TGCCTGTAATCCCAGCACTTTG 12597    CA  G__  GTA
          G                TGCC TGA  CAG  CACTTTGG
                          |||| |||  |||  ||||||||
                          ACGG ATT  GTC  GTGAAACC
                            AC  AGG  ___
GAM166  FCAR    3' TGCCTATAATCTCAGCACTTTG 39338    C   G__  GTA
          G                TGCC ATGA  CAG  CACTTTGG
                          |||| ||||  |||  ||||||||
```

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                                ACGG TATT   GTC   GTGAAACC
                                  A   AGA   ___
GAM166  GPR44    3'  TGCCTTGGAAGCACTTTG    21962     CAT_   AGGTAC
                                TGCC   GAGC    ACTTTG
                                ||||   ||||    ||||||
                                ACGG   TTCG    TGAAAC
                                  AACC   _______
GAM166  HTR1D    3'  TGCCTGTAATCCCAGCACTTTG 9267      CA  G__  GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM166  LAMA4    3'  TGTCCATTGCAGACACTTTGG  14063    C   GA   GT
                                TG CCAT  GCAG  ACACTTTGG
                                || ||||  ||||  |||||||||
                                AC GGTA  CGTC  TGTGAAACC
                                 A   A_   __
GAM166  MDM2     3'  TGCCTGTAATCCCAGCACTTTG 27809     CA  G__  GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM166  MEFV     3'  TGCCTGTAATCCCAGCACTTTG 6972      CA  G__  GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM166  MEFV     3'  TGCCTGTAATCCCTGCACTTTG 6973      CA  GCAGGTA
          G                      TGCC  TGA     CACTTTGG
                                ||||  |||     ||||||||
                                ACGG  ATT     GTGAAACC
                                  AC   AGGGAC_
GAM166  MPL      3'  TGCCTGTAATCCTAACACTTTG 23883     CA  GCAGGT
          G                      TGCC  TGA     ACACTTTGG
                                ||||  |||     |||||||||
                                ACGG  ATT     TGTGAAACC
                                  AC   AGGAT_
GAM166  NAGA     3'  GCCGTGAGATTGCACTTTGG   7038     CA   CAGGTA
                                GCC  TGAG    CACTTTGG
                                |||  ||||    ||||||||
                                CGG  ACTC    GTGAAACC
                                  C_   TAAC__
GAM166  NDRG3    3'  TGCCTGTAATCCCAGCACTTTG 36748     CA  G__  GTA
          G                      TGCC  TGA   CAG   CACTTTGG
                                ||||  |||   |||   ||||||||
                                ACGG  ATT   GTC   GTGAAACC
                                  AC   AGG   ___
GAM166  PDE1B    3'  TGCTGATGACATCAAACACTTT 9568     CC   G  GGT_
          GG                     TGC  ATGA CA   ACACTTTGG
                                |||  |||| ||   |||||||||
```

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                              ACG  TACT GT   TGTGAAACC
                                AC   _ AGTT
GAM166  PIK3CD   3'  TGCCTGTAATCCCAGCACTTTG 22736     CA  G__  GTA
            G                  TGCC  TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                               ACGG  ATT  GTC  GTGAAACC
                                 AC  AGG  ___
GAM166  PPEF2    3'  TGCCTATGAGGCACTTTG    26406     C    CAGGTA
                               TGCC ATGAG    CACTTTG
                               |||| |||||    |||||||
                               ACGG TACTC    GTGAAAC
                                 A   C_____
GAM166  PPEF2    3'  TGCCTGTAATCCCAGCACTTTG 26407     CA  G__  GTA
            G                  TGCC  TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                               ACGG  ATT  GTC  GTGAAACC
                                 AC  AGG  ___
GAM166  PTGES    3'  TGCCTGTCATCCCAGCACTTTG 22185     ___  GAG  GTA
            G                  TGCC  CAT  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                               ACGG  GTA  GTC  GTGAAACC
                                 ACA  GG_  ___
GAM166  PTGIS    3'  TGCCTGTAATCCTAGCACTTTG 9679      CA  GCAGGTA
            G                  TGCC  TGA    CACTTTGG
                               |||| |||    ||||||||
                               ACGG  ATT    GTGAAACC
                                 AC  AGGATC_
GAM166  RABL2A   3'  TGCCTGTAATCCCAGCACTTTG 28209     CA  G__  GTA
            G                  TGCC  TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                               ACGG  ATT  GTC  GTGAAACC
                                 AC  AGG  ___
GAM166  RABL2B   3'  TGCCTGTAATCCCAGCACTTTG 28207     CA  G__  GTA
            G                  TGCC  TGA  CAG  CACTTTGG
                               |||| |||  |||  ||||||||
                               ACGG  ATT  GTC  GTGAAACC
                                 AC  AGG  ___
GAM166  RBBP9    3'  TGCCTGTAATCCCAACACTTTG 43143     CA  GCAGGT
            G                  TGCC  TGA    ACACTTTGG
                               |||| |||    |||||||||
                               ACGG  ATT    TGTGAAACC
                                 AC  AGGGT_
GAM166  SCNN1G   3'  TGCCTGTAATCCCTGCACTTTG 9795      CA  GCAGGTA
            G                  TGCC  TGA    CACTTTGG
                               |||| |||    ||||||||
                               ACGG  ATT    GTGAAACC
                                 AC  AGGGAC_
GAM166  SEDL     3'  TGCCTGTAATCCTAGCACTTTG 31013     CA  GCAGGTA
            G                  TGCC  TGA    CACTTTGG
                               |||| |||    ||||||||
```

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                              ACGG ATT    GTGAAACC
                                AC  AGGATC_
GAM166 SERPINB9 3' TGCCTGTAATCCTAGCACTTTG 19999    CA  GCAGGTA
          G                    TGCC TGA    CACTTTGG
                              |||| |||    ||||||||
                              ACGG ATT    GTGAAACC
                                AC  AGGATC_
GAM166 SH3BP2  3' TGCCTGTAATCCCAGCACTTTG 16643    CA  G__  GTA
          G                    TGCC TGA  CAG  CACTTTGG
                              |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGG  ___
GAM166 SHOX    3' TGCTTGTAATTCTAACACTTTG 27833    CCA  GCAGGT
          G                    TGC  TGA    ACACTTTGG
                              |||  |||    |||||||||
                              ACG  ATT    TGTGAAACC
                                AAC  AAGAT_
GAM166 SNX15   3' TGCCTGTAATCTCAGCACTTTG 43938    CA  G__  GTA
          G                    TGCC TGA  CAG  CACTTTGG
                              |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGA  ___
GAM166 STAT6   3' TGTCCAGAGCAGGTCTGTG   17160   C  T     ACA  T
                              TG CCA GAGCAGGT  CT TG
                              || ||| ||||||||  || ||
                              AC GGT CTCGTCCA  GA AC
                               A  _     ___  C
GAM166 TBXA2R  3' TGCCTGTGATCCCAGCACTTTG 9861     CA  G__  GTA
          G                    TGCC TGA  CAG  CACTTTGG
                              |||| |||  |||  ||||||||
                              ACGG ACT  GTC  GTGAAACC
                                AC  AGG  ___
GAM166 TERF2   3' TGCCTGTAATCCCAGCACTTTG 24917    CA  G__  GTA
          G                    TGCC TGA  CAG  CACTTTGG
                              |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGG  ___
GAM166 TRAF5   3' TGCCTGTAATCTCAGCACTTTG 21477    CA  G__  GTA
          G                    TGCC TGA  CAG  CACTTTGG
                              |||| |||  |||  ||||||||
                              ACGG ATT  GTC  GTGAAACC
                                AC  AGA  ___
GAM166 TSG     3' TGCCTATGTCAGCACTTTG   34011    C  AG  GTA
                              TGCC ATG  CAG  CACTTTG
                              |||| |||  |||  |||||||
                              ACGG TAC  GTC  GTGAAAC
                                A  A_  ___
GAM166 VENTX2  3' TGCCCGTAATCCCAGCACTTTG 30926    A  G__  GTA
          G                    TGCCC TGA  CAG  CACTTTGG
                              ||||| |||  |||  ||||||||
```

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                                ACGGG ATT   GTC   GTGAAACC
                                  C   AGG   ___
GAM166  WHSC1    5'  TGCCTGTAATCCCAGCACTTTG 39391     CA   G__   GTA
              G                   TGCC  TGA   CAG   CACTTTGG
                                  ||||  |||   |||   ||||||||
                                  ACGG  ATT   GTC   GTGAAACC
                                    AC   AGG   ___
GAM166  BCL9     3'  GCTTAAAACATCATGTTTCC   20242    CC         ACAC
                                  GC  AAGACATCATGT    TCC
                                  ||  ||||||||||||    |||
                                  CG  TTTTGTAGTACA    AGG
                                   AA          A___
GAM166  CENTD2   5'  GCCCAAGAATGTCGTGTACCT  31595        CA_  A    A
                                  GCCCAAGA   TC TGTAC CT
                                  ||||||||   || ||||| ||
                                  CGGGTTCT   AG ACATG GA
                                       TAC  C    _
GAM166  PABPC1   5'  GCCCGGAGCACACACTCC    15023      A_  A   CATGT
                                  GCCC  AG CAT    ACACTCC
                                  ||||  || |||    |||||||
                                  CGGG  TC GTG    TGTGAGG
                                    CC  _   _____
GAM166  TEM8     3'  CCAAGACAATGATCTC      38175         TC   TACA
                                  CCAAGACA  ATG    CTC
                                  ||||||||  |||    |||
                                  GGTTCTGT  TAC    GAG
                                       __   TA__
GAM167  GPRK5    5'  CAGCGCCTGGGGTGCTG     23632          ACGC
                                  CAGCGCCTGG    GCTG
                                  ||||||||||    ||||
                                  GTCGCGGACC    CGAC
                                        CCA_
GAM167  STARD5   5'  CCAGCGCCGGGTCCATT     36123         T  ACGCG
                                  CCAGCGCC GG    CTGTT
                                  ||||||||  ||    |||||
                                  GGTCGCGG CC    GGTAA
                                       _  CA___
GAM167  ADRBK1   5'  CGCGCGGCGCTCGGCCG     11527          C    G
                                  CGCGCGGCGC CGGC CG
                                  |||||||||| |||| ||
                                  GCGCGCCGCG GCCG GC
                                        A    _
GAM167  CABC1    5'  CTGCGCGCTGGCCACCGCGCTG 33682         _   GCC  G
                                  CTGCGCGC GGC   CG CGCGCTG
                                  ||||||||  |||   || |||||||
                                  GACGCGCG CCG   GT GCGCGAC
                                       A   ___  G
GAM167  CDO1     5'  CTGCGCGCGCGTCTCACTGCTG 12215         G  CCCGG  _
                                  CTGCGCGCG CG    CGC GCTG
                                  |||||||||  ||    ||| ||||
```

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                                GACGCGCGC GC    GTG CGAC
                                    _ AGA__   A
GAM167  GPR4    5'  CTGCGCGCGGCGACTGGACG  40881          _ CC
                                CTGCGCGCGGCG C  GGCG
                                |||||||||||| |  ||||
                                GACGCGCGCCGC G  CTGC
                                    T AC
GAM167  GRB14   5'  CTGGGCGGCCCCGGCGCGCTG  21032    CGC    G
                                CTG   GCGGC CCCGGCGCGCTG
                                |||   ||||| ||||||||||||
                                GAC   CGCCG GGGCCGCGCGAC
                                  C__    _
GAM167  KPNA3   5'  CTGCGCGCGGCTCCGGCG    13982          GC
                                CTGCGCGCGGC  CCGGCG
                                ||||||||||  ||||||
                                GACGCGCGCCG  GGCCGC
                                    A_
GAM167  MAF     5'  GCGCGGCGTCCCGCCTTCGCGC 23831        _   G___
            TG                    GCGCGGCG CCCG   CGCGCTG
                                |||||||| ||||   |||||||
                                CGCGCCGC GGGC   GCGCGAC
                                    A   GGAA
GAM167  PACE4   5'  CGCGCGGCGCCCGAGCT    15048          CGC
                                CGCGCGGCGCCCGG   GCT
                                ||||||||||||||  |||
                                GCGCGCCGCGGGCT  CGA
                                    ___
GAM167  PDGFB   5'  GCGCGCGGCGTGCCCGCT    15180        CCCG  G
                                GCGCGCGGCG   GC CGCT
                                ||||||||||   || ||||
                                CGCGCGCCGC   CG GCGA
                                    A___  G
GAM167  PTS     5'  CTGTCTGCGGTGCTCGGCCG  7226     CGC   C  C   G
                                CTG   GCGG GC CGGC CG
                                |||   |||| || |||| ||
                                GAC   CGCC CG GCCG GC
                                  AGA   A  A   _
GAM167  TCIRG1  5'  CTGCGCGCCGCGCCTCCGCTG  25839       G    CGGCG
                                CTGCGCGC GCGCC    CGCTG
                                |||||||| |||||    |||||
                                GACGCGCG CGCGG    GCGAC
                                    G    AG___
GAM168  ACCN1   3'  CAGCACTGGGGCCATCCC    9912      C  CGTC
                                CAGC GC   GCCATCCC
                                |||| ||   ||||||||
                                GTCG TG   CGGTAGGG
                                  _ ACCC
GAM168  ANK1    3'  CAGCCACCGGCCTGTCCC    33851         TC  A_
                                CAGCCGCCG  GCC  TCCC
                                |||||||||  |||  ||||
```

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                                GTCGGTGGC CGG AGGG
                                     __  AC
GAM168 ANP32A  3' ACCCCCACCCGCCATCCC   26705    G GT _
                                GCC CC  C GCCATCCC
                                ||| ||  | ||||||||
                                TGG GG  G CGGTAGGG
                                  G  TG G
GAM168 ARHGAP6  5' CAGCCGCCGATCAGGGCC   30208       _ ___
                                CAGCCGCCG TC  GCC
                                ||||||||| ||  |||
                                GTCGGCGGC AG  CGG
                                     T  TCC
GAM168 ATF5    3' CAGTACCCCGCCATCCC    28935    CC  G
                                CAG  GCC TCGCCATCCC
                                |||  ||| ||||||||||
                                GTC  TGG GGCGGTAGGG
                                  A_  _
GAM168 AXIN1   5' CAGCCGCCAGCTCC      41370       TC  CA
                                CAGCCGCCG  GC  TCC
                                |||||||||  ||  |||
                                GTCGGCGGT  CG  AGG
                                     __ __
GAM168 BDKRB2   5' CACCGTCAGGACCGTCCC   8397       ___  A
                                CGCCGTC   GCC TCCC
                                |||||||   ||| ||||
                                GTGGCAG   TGG AGGG
                                    TCC   C
GAM168 BSN     5' GCCGCTGCCGCCGCCATC   18402    ___
                                GCC   GCCGTCGCCATC
                                |||   ||||||||||||
                                CGG   CGGCGGCGGTAG
                                  CGA
GAM168 CAPN10   5' CAGCCGCCGCCGCCTCC    35764          A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG AGG
                                     _
GAM168 CHD2    5' CAGCCGCCATCTAGAGCC    10442         ____
                                CAGCCGCCGTC   GCC
                                ||||||||||    |||
                                GTCGGCGGTAG   CGG
                                      ATCT
GAM168 CKAP1   5' CAGCCGCCTCACACCC     43878       G   C
                                CAGCCGCC TCGC ATCC
                                |||||||| |||| ||||
                                GTCGGCGG AGTG TGGG
                                     _  _
GAM168 CYP21A2  5' AGCCCCAGCCATCCC      7979      G  TC
                                AGCC CCG  GCCATCCC
                                |||| |||  ||||||||
```

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                                TCGG GGT  CGGTAGGG
                                  _  __
GAM168  DCLRE1C  5' AGCGCCGCCGATCCC      35416    C     CC
                                AGC GCCGTCG  ATCCC
                                ||| |||||||  |||||
                                TCG CGGCGGC  TAGGG
                                  _     __
GAM168  DGAT1    3' GCCTGCTGTCGCCATCCC    42074    _ C
                                GCC GC GTCGCCATCCC
                                ||| || ||||||||||
                                CGG CG CAGCGGTAGGG
                                  A  A
GAM168  DMD      5' AGCCGCCGGGCTCCC       19676       TC  CA
                                AGCCGCCG  GC  TCCC
                                ||||||||  ||  ||||
                                TCGGCGGC  CG  AGGG
                                    C_  __
GAM168  DSCR3    5' CAGCAGCCGCCACTTCC     25818    C      CA
                                CAGC GCCGTCGC  TCC
                                |||| ||||||||  |||
                                GTCG CGGCGGTG  AGG
                                  T       A_
GAM168  DUSP4    5' CAGCCGCCAGGCCTTCC     38409       TC   A
                                CAGCCGCCG  GCC TCC
                                |||||||||  ||| |||
                                GTCGGCGGT  CGG AGG
                                    C_  A
GAM168  DUSP7    5' CAGCCGCCGCCGCCCCC     42261          A
                                CAGCCGCCGTCGCC TCC
                                |||||||||||||| |||
                                GTCGGCGGCGGCGG GGG
                                          _
GAM168  DXYS155E 3' CAGCCGCCGCCGCTCC      22944          CA
                                CAGCCGCCGTCGC  TCC
                                ||||||||||||  |||
                                GTCGGCGGCGGCG  AGG
                                          __
GAM168  EGLN2    5' CAGCTCACCACCATCC      38815    _   GTC
                                CAGC CGCC   GCCATCC
                                |||| ||||   |||||||
                                GTCG GTGG   TGGTAGG
                                  A   ____
GAM168  EGLN2    5' GCCCGCCAAAACCGTCCC    38826    _   TC   A
                                GCC GCCG  GCC TCCC
                                ||| ||||  ||| ||||
                                CGG CGGT  TGG AGGG
                                  G   TT   C
GAM168  EN2      5' GCCGCCGCCCGGCCGTCCC   10953        __   A
                                GCCGCCGTC  GCC TCCC
                                |||||||||  ||| ||||
```

```
                                CGGCGGCGG  CGG AGGG
                                     GC   C
GAM168  ETS2    3'  CAGCCAGAACCATCCC     23466      CCGTC
                                CAGCCG    GCCATCCC
                                ||||||    ||||||||
                                GTCGGT    TGGTAGGG
                                   CT___
GAM168  F2R     5'  CAGCCGCCGCTCGCAAGCCC  12792        _   CAT
                                CAGCCGCCG TCGC   CCC
                                ||||||||| ||||   |||
                                GTCGGCGGC AGCG   GGG
                                     G    TTC
GAM168  FBN1    5'  CCGCCGGGGTCCCGCTATCCC  42052      _____   C
                                CCGCCG    TCGC ATCCC
                                ||||||    |||| |||||
                                GGCGGC    GGCG TAGGG
                                   CCCAG   A
GAM168  FBXL7   5'  CCGCCGCCGCCGGGTCCC    29396        A__
                                CCGCCGTCGCC   TCCC
                                ||||||||||   ||||
                                GGCGGCGGCGG   AGGG
                                      CCC
GAM168  FEN1    5'  CAGCCGCCTTCCAAAGCCC   19957       GTCG   T__
                                CAGCCGCC   CCA   CCC
                                ||||||||   |||   |||
                                GTCGGCGG   GGT   GGG
                                     AA__   TTC
GAM168  FPGS    3'  CAGCCACCCTCTGTCCC     22426       G  GCCA
                                CAGCCGCC TC   TCCC
                                |||||||| ||   ||||
                                GTCGGTGG AG   AGGG
                                     G  AC__
GAM168  FSTL1   3'  CAGCCACCTTCATATCC     28213       G   CC
                                CAGCCGCC TCG  ATCC
                                |||||||| |||  ||||
                                GTCGGTGG AGT  TAGG
                                     A   A_
GAM168  FXYD6   3'  CAGCCGCCTCAGGTTCC     35114       G   CCA
                                CAGCCGCC TCG   TCC
                                |||||||| |||   |||
                                GTCGGCGG AGT   AGG
                                     _   CCA
GAM168  FZD10   5'  CAGCGCCGCCGCTCCC      28447     C      CA
                                CAGC GCCGTCGC  TCCC
                                ||||| ||||||||  ||||
                                GTCG CGGCGGCG  AGGG
                                   _      ___
GAM168  GPC1    3'  CAGCCACCAGCATCCC      13237       TC  C
                                CAGCCGCCG  GC ATCCC
                                |||||||||  || |||||
```

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                              GTCGGTGGT  CG TAGGG
                                   __ _
GAM168  GPR30    5'  GCCACCGTGCACAGTCCC    11312        _  CA
                              GCCGCCGT CGC  TCCC
                              |||||||| |||  ||||
                              CGGTGGCA GTG  AGGG
                                   C   TC
GAM168  GPR44    3'  GCTTGACCACGCCATCCC    21955    C__   T
                              GC   GCCG CGCCATCCC
                              ||   |||| |||||||||
                              CG   TGGT GCGGTAGGG
                               AAC   _
GAM168  HSF4     5'  CAGCGCGCCGCCAGCTCC    40761     _      CCA
                              CAGC CGCCGTCG   TCC
                              |||| ||||||||   |||
                              GTCG GCGGCGGT   AGG
                                C       CG_
GAM168  IDS      5'  CAGCCGCCGCCGCAGCC     25958          CAT
                              CAGCCGCCGTCGC   CC
                              ||||||||||||   ||
                              GTCGGCGGCGGCG   GG
                                     TC_
GAM168  IFNAR1   5'  CAGCCGCCATCGCCCCGTCC  8430           A__
                              CAGCCGCCGTCGCC   TCC
                              ||||||||||||   |||
                              GTCGGCGGTAGCGG   AGG
                                     GGC
GAM168  IFNAR1   5'  AGCCGCCGCAGATCCC      8428         CGCC
                              AGCCGCCGT    ATCCC
                              |||||||||    |||||
                              TCGGCGGCG    TAGGG
                                   TC__
GAM168  IFNAR2   3'  AGCCACCGCCACTTGTCC    9315          CA_
                              AGCCGCCGTCGC   TCC
                              ||||||||||||   |||
                              TCGGTGGCGGTG   AGG
                                     AAC
GAM168  ITSN1    3'  GCCTGTCTTTGCCATCCC    16658     _  ___
                              GCC GTC   GCCATCCC
                              ||| |||   ||||||||
                              CGG CAG   CGGTAGGG
                                A   AAA
GAM168  LIF      3'  CAGACCCTGGCCATCCC     14139     CC   GTC
                              CAG  GCC   GCCATCCC
                              |||  |||   ||||||||
                              GTC  TGG   CGGTAGGG
                                __   GAC
GAM168  MAN2A1   5'  CAGCCGCCGGAGGCTCCC    14331         TC_  CA
                              CAGCCGCCG   GC  TCCC
                              |||||||||   ||  ||||
```

```
                              GTCGGCGGC  CG  AGGG
                                   CTC  __
GAM168  MAP3K8   5'  CAGCCACCGCCTCC       23302          GCCA
                              CAGCCGCCGTC   TCC
                              ||||||||||   |||
                              GTCGGTGGCGG   AGG
                                    ____
GAM168  MAP4K5   5'  CAGCCGCTGCACGGCGCGTCC  27300        ____  T  CA
                              CAGCCGC   CG CGC  TCC
                              |||||||   || |||  |||
                              GTCGGCG   GC GCG  AGG
                                  ACGT  C   C_
GAM168  MAP4K5   5'  GCCGCCGCACCACGTTCC    27305        T    ___
                              GCCGCCG CGCCA   TCC
                              ||||||| |||||   |||
                              CGGCGGC GTGGT   AGG
                                  _    GCA
GAM168  MTA1L1   5'  GCCGTCGCGGTTCATCCC    21890        ____
                              GCCGTCGC   CATCCC
                              ||||||||   ||||||
                              CGGCAGCG   GTAGGG
                                   CCAA
GAM168  MYO9A    3'  CAGCTGGCACCATCCC      27904      CGCC T
                              CAGC   G CGCCATCCC
                              ||||   | |||||||||
                              GTCG   C GTGGTAGGG
                                AC__ _
GAM168  NAGA     3'  CAGCCTGTCACATGTCCC    7035       GCC   CA_
                              CAGCC  GTCGC  TCCC
                              |||||  |||||  ||||
                              GTCGG  CAGTG  AGGG
                                 A__   TAC
GAM168  NMB      5'  GCCGCCCTCCCCGCCGTCCC  43953       G  ___  A
                              GCCGCC TC  GCC TCCC
                              |||||| ||  ||| ||||
                              CGGCGG AG  CGG AGGG
                                 G  GGG  C
GAM168  NPTX1    3'  CAGTGTCCTCAGCCATCCC   14833     CCG  G  _
                              CAG  CC TC GCCATCCC
                              |||  || || ||||||||
                              GTC  GG AG CGGTAGGG
                                ACA  _  T
GAM168  NRXN3    5'  CAGCCGCCGGCTTCC       39939        TC  CA
                              CAGCCGCCG  GC  TCC
                              |||||||||  ||  |||
                              GTCGGCGGC  CG  AGG
                                   __  A_
GAM168  OGG1     5'  CAGCTGCTGCCTGCCGTC    32558      C  C  _  A
                              CAGC GC GTC GCC TC
                              |||| || ||| ||| ||
```

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                                GTCG CG CGG CGG AG
                                  A A  A  C
GAM168  OSBP    5' ACCGCCGCGCAGCGTCCC   14984      T  CA__
                                GCCGCCG CGC   TCCC
                                ||||||| |||   ||||
                                TGGCGGC GCG   AGGG
                                   _  TCGC
GAM168  PIAS3   3' AGCTCACATACCATCCC    25907    _  CGTC
                                AGC CGC   GCCATCCC
                                ||| |||   ||||||||
                                TCG GTG   TGGTAGGG
                                  A  TA__
GAM168  PRex1   3' CAGGCGGAGCCATCCC     34071    CC  C TC
                                CAG  GC G  GCCATCCC
                                |||  || |  ||||||||
                                GTC  CG C  CGGTAGGG
                                  __  _ CT
GAM168  PSAP    3' CAGCTGCTTCCAAAATCCC   42965    C  CG  CC
                                CAGC GC  TCG  ATCCC
                                |||| ||  |||  |||||
                                GTCG CG  GGT  TAGGG
                                  A  AA  TT
GAM168  RAB33A  5' CAGCCGCCGCCGCGCC     21997         CAT
                                CAGCCGCCGTCGC  CC
                                ||||||||||||  ||
                                GTCGGCGGCGGCG  GG
                                      C__
GAM168  RAB6A   5' CAGCCGCCGCCGCCTCCC   16099          A
                                CAGCCGCCGTCGCC TCCC
                                |||||||||||||| ||||
                                GTCGGCGGCGGCGG AGGG
                                      _
GAM168  RAB6A   5' CAGCTGCCGCCGCCCC     16100    C      AT
                                CAGC GCCGTCGCC  CC
                                |||| |||||||||  ||
                                GTCG CGGCGGCGG  GG
                                  A       __
GAM168  RANBP2  5' CAGCAGTCGCCACTTCC    26538    CGCC    __
                                CAGC   GTCGCCA  TCC
                                ||||   |||||||  |||
                                GTCG   CAGCGGT  AGG
                                  T___     GA
GAM168  RANBP2L1 5' CAGCAGTCGCCACTTCC   37020    CGCC    __
                                CAGC   GTCGCCA  TCC
                                ||||   |||||||  |||
                                GTCG   CAGCGGT  AGG
                                  T___     GA
GAM168  RANBP9  5' CAGCCGCCGCTGCAACTCC  24249        C  CA_
                                CAGCCGCCGT GC   TCC
                                |||||||||| ||   |||
```

```
                                GTCGGCGGCG CG   AGG
                                     A  TTG
GAM168  RB1CC1   5'  CAACCGCCGGCGTCCC     31307        T  CCA
                                CAGCCGCCG CG   TCCC
                                ||||||||| ||   ||||
                                GTTGGCGGC GC   AGGG
                                     C  ___
GAM168  RFC4     5'  ACCGCCGCCGGCTCGTTCC    16284         _ CA__
                                GCCGCCGTCG C    TCC
                                |||||||||| |    |||
                                TGGCGGCGGC G    AGG
                                     C AGCA
GAM168  RREB1    5'  TGACCGCAGTTGCCATCCC    16402    A    C  C
                                C GCCGC GT GCCATCCC
                                | ||||| || ||||||||
                                A TGGCG CA CGGTAGGG
                                 C    T  A
GAM168  RXRB     3'  CACTCGTGAAACCATCCC     35039     _   C__
                                CGC CGT   GCCATCCC
                                ||| |||   ||||||||
                                GTG GCA   TGGTAGGG
                                  A   CTT
GAM168  SLC12A4  5'  CAGCCGCCCGCCGCTGTCCC   22887        _    CA
                                CAGCCGCC GTCGC  TCCC
                                |||||||| |||||  ||||
                                GTCGGCGG CGGCG  AGGG
                                     G    AC
GAM168  SLC35A3  5'  CAGCGCCGCCGGCTCCC     29275     C      CCA
                                CAGC GCCGTCG   TCCC
                                |||| |||||||   ||||
                                GTCG CGGCGGC   AGGG
                                  _      CG_
GAM168  SLC6A12  5'  CAGCTCGCCACCATCCC     16796     CGC
                                CAGC   CGTCGCCATCCC
                                ||||   ||||||||||||
                                GTCG   GCGGTGGTAGGG
                                  A__
GAM168  SNX3     5'  CCGCCGCCGCGGGCTCCC     19136         CA__
                                CCGCCGTCGC    TCCC
                                |||||||||    ||||
                                GGCGGCGGCG    AGGG
                                     CCCG
GAM168  SOX4     3'  CCGCCGCCGCCAGCTCCC     16979          __
                                CCGCCGTCGCCA  TCCC
                                ||||||||||||  ||||
                                GGCGGCGGCGGT  AGGG
                                       CG
GAM168  STK6     5'  CAGCCGCCCCTTGTCCC      18773        G  GCCA
                                CAGCCGCC TC    TCCC
                                |||||||| ||    ||||
```

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                                GTCGGCGG GG    AGGG
                                     _ AAC_
GAM168  TBL1X    5'  CCGCCGCCGCCGAGTCCC    24875          A__
                                CCGCCGTCGCC   TCCC
                                ||||||||||   ||||
                                GGCGGCGGCGG   AGGG
                                     CTC
GAM168  TXNRD2   3'  CAGTCCCCTGAGCCATCCC   26974    _ G  GTC
                                CAG CC CC   GCCATCCC
                                ||| || ||   ||||||||
                                GTC GG GG   CGGTAGGG
                                  A _  ACT
GAM168  UBE2B    5'  CCGCCGCCTCCGGATCCC    17790        G  __
                                CCGCCGTC CC  ATCCC
                                ||||||||  ||  |||||
                                GGCGGCGG GG  TAGGG
                                     A  CC
GAM168  ATP2B2   5'  AGGGTCTGGAAACTGGGGCCCA 11751     C          CCA
                                AGG GTCTGGAAACTGG   TCCA
                                ||| ||||||||||||   ||||
                                TCC CAGACCTTTGACC   GGGT
                                  _          CC_
GAM168  BAIAP3   3'  AGGCTCTGGACCATC      19452     G    AAACTG
                                AGGC TCTGG     GCCATC
                                ||||  |||||     ||||||
                                TCCG AGACC     TGGTAG
                                  _   _______
GAM168  CANX     3'  AGCTGTCTGGGAACTGAGC   44659    _    A    _
                                GGC GTCTGG AACTG GC
                                |||  ||||||  ||||| ||
                                TCG CAGACC TTGAC CG
                                  A     C    T
GAM168  CDH3     3'  AGGCTTCTGGAAACTTGGCCTC 12170     G        _   A
                                AGGC TCTGGAAACT GGCC TC
                                ||||  ||||||||||  |||| ||
                                TCCG AGACCTTTGA CCGG AG
                                  A        A   _
GAM168  DAPK1    5'  GGCGCCTGGGAGCTCCCC    22358         AAACT   CA
                                GGCGTCTGG    GGC  TCC
                                |||||||||    |||  |||
                                CCGCGGACC    TCG  GGG
                                     C____   AG
GAM168  EHD3     3'  AGGTGGGTTGGCCATC     31104     CGTC   AAAC
                                AGG    TGG    TGGCCATC
                                |||    |||    ||||||||
                                TCC    ACC    ACCGGTAG
                                  _____  CA__
GAM168  FGFRL1   3'  GTCTGGAAGTGTGTGTCCA   34913         AC  GCCA
                                GTCTGGAA  TG    TCCA
                                ||||||||  ||    ||||
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                                CAGACCTT AC   AGGT
                                    C_ ACAC
GAM168  GSS     3' GGCGTCTAGATCTCATC    6758        AA GGC
                                GGCGTCTGGA CT  CATC
                                |||||||||| ||  ||||
                                CCGCAGATCT GA  GTAG
                                     A_ ___
GAM168  HS3ST4  3' GGTTCTGGTGGCCATC     43868   CG   AAAC
                                GG TCTGG   TGGCCATC
                                || |||||   ||||||||
                                CC AGACC   ACCGGTAG
                                 A_   ____
GAM168  IHPK1   3' GGTGTCACCTCCTGGCCATC 45494   C  TGGAAA
                                GG GTC    CTGGCCATC
                                || |||    |||||||||
                                CC CAG    GACCGGTAG
                                 A  TGGAG_
GAM168  IL1RAPL2 5' GGCGCCTGGAAATGAGCTCCA 32640         CT  CA
                                GGCGTCTGGAAA GGC TCCA
                                |||||||||||| ||| ||||
                                CCGCGGACCTTT TCG AGGT
                                      AC  __
GAM168  LMO4    5' AGGCGTCGGGGGCTGCGGCC  27646      T AAAC_
                                AGGCGTC GG   TGGCC
                                ||||||| ||   |||||
                                TCCGCAG CC   GCCGG
                                    C CCGAC
GAM168  LOXL1   3' AGGGGAGAGATTGGCCATC  41181   CGTCT  AAC__
                                AGG   GGA   TGGCCATC
                                |||   |||   ||||||||
                                TCC   CCT   ACCGGTAG
                                 ______ CTCTA
GAM168  MUC12   3' GGAGTCTGGAAGCTCC     45332   C     AACT  CA
                                GG GTCTGGA   GGC TCC
                                || |||||||   ||| |||
                                CC CAGACCT   TCG AGG
                                 T     _____ __
GAM168  NGB     3' AGGCGCTGGAAGCTCAGCCA  34578     T    A _
                                AGGCG CTGGAA CT GGCCA
                                ||||| |||||| || |||||
                                TCCGC GACCTT GA TCGGT
                                   _    C  G
GAM168  OVOL1   5' GGTTTCTGGAAACTTCCC   21276   CG       GG
                                GG TCTGGAAACT CC
                                || |||||||||| ||
                                CC AGACCTTTGA GG
                                 AA        AG
GAM168  SCA1    3' AGGCTCATTGGCCATC     7274      G TGGAAAC
                                AGGC TC     TGGCCATC
                                |||| ||     ||||||||
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                                TCCG AG      ACCGGTAG
                                  _ TA_____
GAM168  SLC21A2  3'  GGCATCTGGGGGCCTCTTCCA  24799        AAACT   A__
                                GGCGTCTGG    GGCC  TCCA
                                |||||||||    ||||  ||||
                                CCGTAGACC    CCGG  AGGT
                                     C____    AGA
GAM168  SLC22A1  3'  AGGCGTCTAGGAATTTCTG   16854        _   A__
                                AGGCGTCT GGAA  CTG
                                |||||||| ||||  |||
                                TCCGCAGA CCTT  GAC
                                     T   AAA
GAM168  TMPRSS2  5'  AGGTATCTGGAATGTTCA    24927     CG     AC  GC
                                AGG  TCTGGAA  TG  CA
                                |||  |||||||  ||  ||
                                TCC  AGACCTT  AC  GT
                                  AT      __  AA
GAM168  WSX1     5'  GGCGTCTGGGGGGTGGGGGCCTC 22118        AAACT__   A
              C                  GGCGTCTGG      GGCC TCC
                                 |||||||||      |||| |||
                                 CCGCAGACC      CCGG AGG
                                      CCCACCC   _
GAM169  ALDH1A2  3'  CTGGGCTTCATCCTCCT     19330       CCC
                                CTGGGC   CGTCCTCTT
                                ||||||   |||||||||
                                GACCCG   GTAGGAGGA
                                   AA_
GAM169  ALPPL2   3'  TCTGAGCCTCCTCT       42878        CCCG
                                TCTGGGCC    TCCTCT
                                ||||||||    ||||||
                                AGACTCGG    AGGAGA
                                     ____
GAM169  B4GALT3  5'  GATCTAGGTTCAAGCTGTCTTC 19105        CCCCC___  C
              TT                  GATCTGGG       GTC TCTT
                                  ||||||||       ||| ||||
                                  CTAGATCC       CAG AGAA
                                       AAGTTCGA   A
GAM169  C4BPB    5'  TCTGGGTTGGTCCTCTT     8739        CCCCC
                                TCTGGG    GTCCTCTT
                                ||||||    ||||||||
                                AGACCC    CAGGAGAA
                                   AAC__
GAM169  CFTR     3'  GATCTGGAAGTTCTCT      7953         CCCCC  C
                                GATCTGGG    GT CTCT
                                ||||||||    || ||||
                                CTAGACCT    CA GAGA
                                     T____  A
GAM169  COL15A1  3'  GATCTGAGTCCTCT        12354        GCCCCC
                                GATCTGG     GTCCTCT
                                |||||||     |||||||
```

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                                CTAGACT     CAGGAGA
                                        _______
GAM169  CRY2     3'  AATCTGGGCCTCGGCCT     43576          CC  T
                                GATCTGGGCC  CG CCT
                                ||||||||||  || |||
                                TTAGACCCGG  GC GGA
                                      A_  C
GAM169  ENG      3'  TCTGGGCTGGGCCCTCTT    6506         CCCC
                                TCTGGGC    GTCCTCTT
                                |||||||    ||||||||
                                AGACCCG    CGGGAGAA
                                    ACC_
GAM169  FOXF1    3'  GATCTGAGCTCTTGTCACT   11118          CCCC  _
                                GATCTGGGC    GTC CT
                                |||||||||    ||| ||
                                CTAGACTCG    CAG GA
                                      AGAA   T
GAM169  GNB3     5'  GATCTGGATAATCCTTCTT    13220         CCCCC    _
                                GATCTGGG     GTCCT CTT
                                ||||||||     ||||| |||
                                CTAGACCT     TAGGA GAA
                                     AT___     A
GAM169  HSD17B1  5'  GACCTTCTCCTGTCCTCTT   7658        GGG  CCC
                                GATCT   CC   GTCCTCTT
                                |||||   ||   ||||||||
                                CTGGA   GG   CAGGAGAA
                                   AGA  A__
GAM169  IL18     5'  TCTGAGGTTCCTTTCCTCTT   11456     _  CC  CG
                                TCTG GG  CC  TCCTCTT
                                |||| ||  ||  |||||||
                                AGAC CC  GG  AGGAGAA
                                  T  AA  AA
GAM169  KCNN4    3'  GATCCGGGCCCCTAGTACCCTC 13924           CG___
           TT                     GATCTGGGCCCC    TCCTCTT
                                  ||||||||||||    |||||||
                                  CTAGGCCCGGGG    GGGAGAA
                                        ATCAT
GAM169  LLGL1    3'  GGGCCCCACCTGTCCTCTT    42507        C___
                                GGGCCCC    GTCCTCTT
                                |||||||    ||||||||
                                CCCGGGG    CAGGAGAA
                                    TGGA
GAM169  LPIN2    3'  TCTGGGCTCCTGACAGTTCTCT 31222        _  CC___  C    III
           TA                     TCTGGGC CC    GT CTCTT   A
                                  ||||||| ||    || |||||  |
                                  AGACCCG GG    CA GAGAA   T
                                     A  ACTGT  A    III
GAM169  MEN1     5'  GATCTGGGCTCACTGCAGCCT  39183         CCC___  T
                                GATCTGGGC     CG CCT
                                |||||||||     || |||
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                                CTAGACCCG     GT GGA
                                      AGTGAC  C
GAM169  MYO7A    3'  GAGCTAGATTGTCCTCTT    7028     T    CCCCC
                                GA CTGGG    GTCCTCTT
                                || |||||    ||||||||
                                CT GATCT    CAGGAGAA
                                 C    AA___
GAM169  NDST1    5'  GATCTGGGCCCCCAGTCCT   11367          _
                                GATCTGGGCCCCC GTCCT
                                |||||||||||| |||||
                                CTAGACCCGGGGG CAGGA
                                         T
GAM169  PNUTL1   3'  GATCCTGGGAATCCTCTT    15430     _   CCCCC
                                GATC TGGG    GTCCTCTT
                                |||| ||||    ||||||||
                                CTAG ACCC    TAGGAGAA
                                  G   T____
GAM169  RNH      3'  GATCTGAGCGTTTCTCTT    40604        CCCCGTC
                                GATCTGGGC      CTCTT
                                |||||||||      |||||
                                CTAGACTCG      GAGAA
                                      CAAA___
GAM169  SECTM1   5'  GACTTGGGCCCCTGGTCCT   16542    TC       C_
                                GA  TGGGCCCC  GTCCT
                                ||  ||||||||  |||||
                                CT  ACCCGGGG  CAGGA
                                 GA       AC
GAM169  SERPINE1 3'  TGTCCCCCCCACTCCGTCCT   8293     GG     _  _
                                TG  CCCCCG TCC TCTT
                                ||  |||||| ||| ||||
                                AC  GGGGGT AGG AGGA
                                 AG     G   C
GAM169  SRRM1    3'  TCTGGGCCCTTCCAGCCT    25192         __  T
                                TCTGGGCCC  CCG CCT
                                |||||||||  ||| |||
                                AGACCCGGG  GGT GGA
                                      AA   C
GAM169  TLL2     5'  GGCGCCCCCTGTCTTCTT    29754    _    _  C
                                GG GCCCCC GTC TCTT
                                || |||||| ||| ||||
                                CC CGGGGG CAG AGAA
                                 G     A   A
GAM169  TNFSF15  3'  GATCTGGGCTCACCGCAACCT  23053         CC_   __
                                GATCTGGGC   CCGT  CCT
                                |||||||||   ||||  |||
                                CTAGACCCG   GGCG  GGA
                                      AGT    TT
GAM169  WDR1     3'  GACTGGGCCCTCCTGCCTCTT  32749    T      _  GT
                                GA CTGGGCCC CC  CCTCTT
                                || |||||||| ||  ||||||
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                                CT GACCCGGG GG  GGAGAA
                                 _      A  AC
GAM169  ZNF174   5'  GGAAGAGTTTTGTCTTCT    18362        CTTTCC  A  _
                                GGAAGAGT     TG TCT CT
                                ||||||||     || ||| ||
                                CCTTCTCA     AC AGA GA
                                    AA____  _   A
GAM170  CUL3     3'  CACTAGTTACTGAAAATGAGTA 18729     A   AT    A
                                CAC AGT  TATT AAAATGAGTA
                                ||| |||  |||| ||||||||||
                                GTG TCA  ATGA TTTTACTCAT
                                  A  __   C
GAM170  AKAP13   3'  ATCCATGCCCAAAACATGTGG  28469        _____
                                ATCCATGCT    CATGTGG
                                |||||||||    |||||||
                                TAGGTACGG    GTACACC
                                     GTTTT
GAM170  POLR2E   3'  CCCACAGGGCTGTGTGGA    40915      ___  CA
                                TCCAT   GCT  TGTGGA
                                |||||   |||  ||||||
                                GGGTG   CGA  ACACCT
                                   TCC   C_
GAM170  RAB11A   3'  ATCCATGCCTGCTGGTGGA   21679        CAT__
                                ATCCATGCT    GTGGA
                                |||||||||    |||||
                                TAGGTACGG    CACCT
                                     ACGAC
GAM170  UBE2G2   3'  ACCCATGACACTCTGTGTGG   42117       ___  A_
                                ATCCATG   CTC  TGTGG
                                |||||||   |||  |||||
                                TGGGTAC   GAG  ACACC
                                    TGT   AC
GAM171  GSPT1    5'  TGTGTGGTGGACAGAGAGC   13314    GA    AG TTGG
                                TG  TGGTG  C    AGAGAGC
                                ||  |||||  |    |||||||
                                AC  ACCAC  G    TCTCTCG
                                 AC     CT _____
GAM171  LZTFL1   3'  TGGAATGGATTTTTGGAGAGAG 33773     _  TGAGC
                                TGGA TGG    TTGGAGAGAG
                                ||||  |||   ||||||||||
                                ACCT ACC    AACCTCTCTC
                                  T   TAAA_
GAM171  POU4F1   3'  GGTGGAGGAAAGAGAGC     26393     _  CTT
                                GGTG AG   GGAGAGAGC
                                ||||  ||   |||||||||
                                CCAC TC   TTTCTCTCG
                                  C  C__
GAM171  SH3BP2   3'  TGGAAGGTGTGCCAGGGAGAG  16644     T   A   T  A
                                TGGA GGTG GCT GG GAGAG
                                |||| |||| ||| || |||||
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                                ACCT CCAC CGG CC CTCTC
                                  T   A  T  _
GAM171  TEM5    3'  GGGTGGGAGTACTTGGGGAG  37239   A  T  __   A
                                GG TGG GAG  CTTGG GAG
                                || ||| |||  ||||| |||
                                CC ACC CTC  GAACC CTC
                                 C  _  AT    C
GAM171  TNFRSF8  3'  TGGGTGGGGCCCACAGAGAGCG 10326    A  TGA   G
                                TGG TGG   GCTTG AGAGAGCG
                                ||| |||   ||||| ||||||||
                                ACC ACC   CGGGT TCTCTCGC
                                  C  C__    G
GAM172  HOXC11   3'  TCGCCGAGGTGTGTTTTC   41162     _ T   GGACGC
                                TCGC G GGTG     GTTTTC
                                |||| | ||||     ||||||
                                AGCG C CCAC     CAAAAG
                                  G T   A_____
GAM172  TNFSF4   3'  TCTGTGGCAAAGAATGTGTTTT 17755   GC   TG _ CGC_
            C                    TC  GTGG  G GA   GTTTTC
                                ||  ||||  | ||   ||||||
                                AG  CACC  T CT   CAAAAG
                                 A_   GT T  TACA
GAM172  ACHE    5'  GATGTTCCCCGGCGC      8562      _   GCCGCCGC
                                GATG TCCC       TGGCGC
                                |||| ||||       ||||||
                                CTAC AGGG       GCCGCG
                                  A  _________
GAM172  COL4A2   5'  TGTCCCGGCGCACTGCA     12324       C  C  GGC
                                TGTCCCG CGC GCT   GCA
                                ||||||| ||| |||   |||
                                ACAGGGC GCG TGA   CGT
                                    C  _  ___
GAM172  DUX4    5'  TGCCCCGCCGGCCGGCGC    43762         CC
                                TGTCCCGCCG  GCTGGCGC
                                ||||||||||  ||||||||
                                ACGGGGCGGC  CGGCCGCG
                                            __
GAM172  FOXE3    3'  GCCTGCCCGCGCGGCGCAG   29146    _  _ _
                                GCC GCC GC TGGCGCAG
                                ||| ||| || ||||||||
                                CGG CGG CG GCCGCGTC
                                  A  G  C
GAM172  GALC    5'  GTCCCGTCGCCGCCACG     6676       C      G
                                GTCCCG CGCCGCTG CG
                                |||||| |||||||| ||
                                CAGGGC GCGGCGGT GC
                                   A      _
GAM172  GNAZ    3'  TGTCCCGCGAGGCTGGCGCAG  13190        CGCC
                                TGTCCCGC   GCTGGCGCAG
                                ||||||||   ||||||||||
```

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                                ACAGGGCG   CGACCGCGTC
                                    CTC_
GAM172  GPR48   5' GATGTCCCCCGCCGCCCCCGG 32986       __    G
                                GATGTCCC  GCCGCC CTGG
                                ||||||||  |||||| ||||
                                CTACAGGG  CGGCGG GGCC
                                    GG     G
GAM172  KCNJ4   3' GATGTCCCCCGCCCAGCA   22537       G    GCT
                                GATGTCCC CCGCC   GGCG
                                |||||||| |||||   ||||
                                CTACAGGG GGCGG   TCGT
                                    _    G__
GAM172  NRG1    5' GTCCCGCCGCTGGCG      30344       GCC
                                GTCCCGCC   GCTGGCG
                                ||||||||   |||||||
                                CAGGGCGG   CGACCGC
                                    ___
GAM172  RRAD    5' CCGCCGCCGCTGCTGCTGCAG 20017         __ _
                                CCGCCGCCGCTG  GC GCAG
                                ||||||||||||  || ||||
                                GGCGGCGGCGAC  CG CGTC
                                      GA  A
GAM172  SLC1A4  5' GTCTCGCGGCCTGGCGCAG   16753    C   C   GC
                                GTC CGC GCC  TGGCGCAG
                                ||| ||| |||  ||||||||
                                CAG GCG CGG  ACCGCGTC
                                  A   C  __
GAM173  GCN5L1  5' CCATGTCACGTGCCCGCTG   11245    TC      G
                                CC  GTCACGTGC CGCTG
                                ||  ||||||||| |||||
                                GG  CAGTGCACG GCGAC
                                 TA       G
GAM173  P4HB    3' TCGGAGGCGTGCGCTGCTG   9550     TCAC   C
                                TCG   GTG GCGCTGCTG
                                |||   ||| |||||||||
                                AGC   CGC CGCGACGAC
                                  CTC_  A
GAM173  POLR2E  3' GACCTCGTCACGTCCACCTG  40919          G   G
                                GACCTCGTCACGT CGC CTG
                                |||||||||||| ||| |||
                                CTGGAGCAGTGCA GTG GAC
                                      G  _
GAM173  ASCL2   5' CGGCGCGCCGCAGGAAGGTGCA 44716     A  C  _  C
          G                      CGGC GC GCC CAG GAGGTGCAG
                                 |||| || ||| ||| |||||||||
                                 GCCG CG CGG GTC TTCCACGTC
                                   _ _  C  C
GAM173  ATP4A   3' GGCAGCCGTCCAGCCTGG   8718        C    GA
                                GGCAGCCG CCAGC  GG
                                |||||||| |||||  ||
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```
                                CCGTCGGC GGTCG  CC
                                    A    GA
GAM173  CHD2    3'  GGCAGCTACTCAGCTACA    10446      CG C   GAGG
                                GGCAGC  C CAGC   TGCA
                                ||||||  | ||||   ||||
                                CCGTCG  G GTCG   ATGT
                                   AT A   ____
GAM173  EGFL4   5'  CGGCAGCCCCTAGAGCCTGTG  41567       G  C__  GAG
                                CGGCAGCC CC   AGC   GTG
                                |||||||| ||   |||   |||
                                GCCGTCGG GG   TCG   CAC
                                    _ ATC   GA_
GAM173  FGF18   5'  CGGCAGCCGCTGTGC      19302         CCAGCGAG
                                CGGCAGCCGC      GTGC
                                ||||||||||      ||||
                                GCCGTCGGCG      CACG
                                    A_______
GAM173  FGFR1   5'  CGTGGCCGCCCAGCTCCCGG  31937   GCA       GA__
                                CG   GCCGCCCAGC   GG
                                ||   ||||||||||   ||
                                GC   CGGCGGGTCG   CC
                                 AC_       AGGG
GAM173  FMR2    5'  CGGCAGCCGCTGCGGGCTCAG  12958        CCA   A   G
                                CGGCAGCCGC   GCG GGT CAG
                                ||||||||||   ||| ||| |||
                                GCCGTCGGCG   CGC CCG GTC
                                    A__   _   A
GAM173  IL18    5'  GGCAGCCGCTTTAGCAGCCAG  11455       C____   G
                                GGCAGCCGC    CAGC AG
                                |||||||||    |||| ||
                                CCGTCGGCG    GTCG TC
                                    AAATC    G
GAM173  MBNL    5'  GGCGGTCGCCCAGCGGCG    34316    AGC      GA
                                GGC   CGCCCAGC  GGTG
                                |||   ||||||||  ||||
                                CCG   GCGGGTCG  CCGC
                                  CCA       __
GAM173  NCOR2   3'  CGGCAGCCGCCCCGCTCCTGCA 26731          A  GAGG
          G                      CGGCAGCCGCCC GC    TGCAG
                                ||||||||||| ||    |||||
                                GCCGTCGGCGGG CG    ACGTC
                                    G  AGG_
GAM173  OPCML   5'  CGGCAGCCGCACAGTCCTGG   14951        C   CGA_
                                CGGCAGCCGC CAG    GG
                                |||||||||| |||    ||
                                GCCGTCGGCG GTC    CC
                                    T   AGGA
GAM173  SLC18A1 5'  GGCAGCTGTTAGCAAGACAG   16822      CGCCC     GT
                                GGCAGC    AGCGAG  GCAG
                                ||||||    ||||||  ||||
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                                CCGTCG    TCGTTC  TGTC
                                   ACAA_     __
GAM173  SORCS3   5'  GGCGCCCGCCGAGGTGC     31423     AG    CAGC
                                GGC  CCGCC    GAGGTGC
                                |||  |||||    |||||||
                                CCG  GGCGG    CTCCACG
                                  CG    ____
GAM173  SOX11    3'  CGGCAGCCGCCTGCTCCCCGG  17017          CA  GA___
                                CGGCAGCCGCC  GC    GG
                                ||||||||||  ||    ||
                                GCCGTCGGCGG  CG    CC
                                      A_  AGGGG
GAM173  TEM5     3'  GGCAGTCAGCTGTTGAGGTGCA 37237       CCGCC    ____
           G                     GGCAG    CAGC    GAGGTGCAG
                                |||||     ||||    |||||||||
                                CCGTC    GTCG    CTCCACGTC
                                   A____    ACAA
GAM174  ABL2     5'  CCTCCTCGGCTCCGGCCTCG   28726    GG TC         C
                                CC  T  CGGCTCCGGCC CG
                                ||  |  ||||||||||| ||
                                GG  G  GCCGAGGCCGG GC
                                 A_ GA          A
GAM174  ARIH1    5'  GCCCCGGCTCTCGCTCCGGCTC 25090          CG       C
           CG                     GCCCCGGTTC  GCTCCGGC CCG
                                |||||||||  ||||||| |||
                                CGGGGCCGAG  CGAGGCCG GGC
                                      AG       A
GAM174  ARIH1    5'  CAGGCCTGGCTCCGGCCCCG   25086     TT C
                                CGG  C GGCTCCGGCCCCG
                                |||  | ||||||||||||
                                GTC  G CCGAGGCCGGGGC
                                  CG A
GAM174  COL6A2   5'  CCTGGTCCCGAGGAGGCTCCG  38437    C     _____
                                CC GGTTCC     GGCTCCG
                                || ||||||     |||||||
                                GG CCAGGG     CCGAGGC
                                 A     CTCCT
GAM174  CTSZ     5'  GGATCCCGCCCCGGCCTCG    41614    T   G       C
                                GG TCC GCTCCGGCC CG
                                || ||| |||||||| ||
                                CC AGG CGGGGCCGG GC
                                 T   G        A
GAM174  DLG5     3'  CCTGGTTCCGGATCCTTCCCC  44455    C       C   GG
                                CC GGTTCCGG TCC  CCCC
                                || |||||||| |||  ||||
                                GG CCAAGGCC AGG  GGGG
                                 A       T   AA
GAM174  DMN      5'  GCCGCGACGCTCCGGCCC    41643     C   TTCCG       C
                                GCC CGG    GCTCCGGCC C
                                ||| |||    ||||||||| |
```

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                                CGG GCT    CGAGGCCGG G
                                  C  G____      A
GAM174  GCLM    5'  GCTGCGGCTCCGGCTCCG   13132   CC
                                GC  CGGTTCCGGCTCCG
                                ||  ||||||||||||||
                                CG  GCCGAGGCCGAGGC
                                 AC
GAM174  GNA11   5'  GCCGCGGCCCTCCGGCCC   44044    C    CCGG      C
                                GCC CGGTT   CTCCGGCC C
                                |||  |||||   ||||||||  |
                                CGG GCCGG   GAGGCCGG G
                                  C    _____      A
GAM174  GOSR2   5'  GCTCCGGCTCTGGCTTCCTCG  20178         C  __  _
                                GTTCCGGCTC GGC  CC CG
                                ||||||||||  |||  ||  ||
                                CGAGGCCGAG CCG  GG GC
                                      A   AA  A
GAM174  HCN2    3'  GGTCTGGATGACGGCCCCG   10173     CC  CTC_
                                GGTT  GG   CGGCCCCG
                                ||||  ||   ||||||||
                                CCAG  CC   GCCGGGGC
                                  A_  TACT
GAM174  HDAC5   5'  GCTGCGGCTCGAGCTCCGGCTT 40170   CC    C       CC
          CG                      GC  CGGTTC GGCTCCGGC  CG
                                ||  ||||||  |||||||||  ||
                                CG  GCCGAG TCGAGGCCG  GC
                                 AC     C       AA
GAM174  IRF1    5'  GCCTCGGTTCGGCGGGGC   42043    C    C   TCC
                                GCC CGGTTC GGC   GGC
                                |||  ||||||  |||   |||
                                CGG GCCAAG CCG   CCG
                                  A     _   CC_
GAM174  KCNK4   5'  GCCCGGGTTCCAGCACGGCCTC 37836     C       TC    C
          G                      GCCC GGTTCCGGC  CGGCC CG
                                ||||  |||||||||  |||||  ||
                                CGGG CCAAGGTCG  GCCGG GC
                                  C       T_    A
GAM174  LRP3    5'  GCTCCGGTTCCGGCTGCGGCTC 42168   C        C   C
          CG                      GC CCGGTTCCGGCT CGGC CCG
                                ||  ||||||||||||  ||||  |||
                                CG GGCCAAGGCCGA GCCG GGC
                                 A         C   A
GAM174  LRP3    5'  CGGCTCCGGCTCCGGTTCCG   42163            CC
                                CGGTTCCGGCTCCGG  CCG
                                ||||||||||||||  |||
                                GCCGAGGCCGAGGCC  GGC
                                          AA
GAM174  LRP3    5'  GCTCCGGTTCCGGCTGCGGCTC 42168   C        C   C
          CG                      GC CCGGTTCCGGCT CGGC CCG
                                ||  ||||||||||||  ||||  |||
```

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                                CG GGCCAAGGCCGA GCCG GGC
                                 A         C   A
GAM174  LRP3    5'  GCCCCGCGGCTCCGGCTCCG  42166       GTTC        C
                                GCCCCG   CGGCTCCGGC CCG
                                ||||||   |||||||||| |||
                                CGGGGC   GCCGAGGCCG GGC
                                   ____       A
GAM174  MAP3K7  5'  GCCGTGTCCGGCTCTGGCTCCG 17271    ____     C
                                GCC   CCGGTTC GGCTCCG
                                |||   ||||||| |||||||
                                CGG   GGCCGAG CCGAGGC
                                  CACA     A
GAM174  MAPRE1  5'  GCTCCGGTTCCGTCTTCG    29525    C       G  C
                                GC CCGGTTCCG CT CG
                                || |||||||| || ||
                                CG GGCCAAGGC GA GC
                                 A       A  A
GAM174  MAPRE1  5'  GCCCGCAACCGGCTCCGGTTCC 29523     _  TT        CC
           G                     GCCC CGG  CCGGCTCCGG  CCG
                                |||| |||  ||||||||||  |||
                                CGGG GTT  GGCCGAGGCC  GGC
                                  C  __        AA
GAM174  MTMR1   5'  GCCCCGGGTTCGGGCCCC    43155       _  C
                                GCCCCGG TTC GGCTCC
                                ||||||| ||| ||||||
                                CGGGGCC AAG CCGGGG
                                    C  C
GAM174  NAGA    5'  GCCTACGGGCGCCTTCGGCCCC 7039     C_  TTC  G  C
           G                     GCC  CGG   CG CT CGGCCCCG
                                |||  |||   || || ||||||||
                                CGG  GCC   GC GA GCCGGGGC
                                  AT   C__  G  A
GAM174  NEU1    5'  GCCCCGGTCTGGAGGCCCC   7729         CC  CTCC
                                GCCCCGGTT  GG   GGCCCC
                                |||||||||  ||   ||||||
                                CGGGGCCAG  CC   CCGGGG
                                     A_  T____
GAM174  NFE2L2  5'  GCCCTGTTCCGGCTGCCG    26086     CG       _
                                GCCC  GTTCCGGCT CCG
                                ||||  ||||||||| |||
                                CGGG  CAAGGCCGA GGC
                                  A_       C
GAM174  NKX2H   3'  CCAGGCGTTCGGCTCCGGCCC  30756    C   TC_
                                CC GGT   CGGCTCCGGCCC
                                || |||   ||||||||||||
                                GG CCG   GCCGAGGCCGGG
                                 T   CAA
GAM174  NRBP    5'  GCTCGGGTTCCGGGGCCCC   30160    CCC      CTCC
                                GC   GGTTCCGG   GGCCCC
                                ||   ||||||||   ||||||
```

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                                CG   CCAAGGCC    CCGGGG
                                 AGC      ____
GAM174   OLFM1    5'  CGCGCTCCGGCTCTGGCCCCG  26769    _        C
                                CG GTTCCGGCTC GGCCCCG
                                || |||||||||| |||||||
                                GC CGAGGCCGAG CCGGGGC
                                 G         A
GAM174   OLFM1    5'  GCCCCGGCTCCGCTGGCTCCG  26772           ___
                                GCCCCGGTTCC   GGCTCCG
                                ||||||||||   |||||||
                                CGGGGCCGAGG   CCGAGGC
                                      CGA
GAM174   PDXK     5'  GCTCGGGCTCGGGCTCCGGCCC 18968    CCC    C
              CG                  GC   GGTTC GGCTCCGGCCCCG
                                ||   ||||| ||||||||||||
                                CG   CCGAG CCGAGGCCGGGGC
                                 AGC    C
GAM174   PPP2R5D  5'  GCCCCGCTCCGGCTCCGGC   26459       G
                                GCCCCG TTCCGGCTCCGGC
                                |||||| ||||||||||||
                                CGGGGC GAGGCCGAGGCCG
                                   _
GAM174   PVRL2    5'  GGCTCCGGCTCCGGCTCC    16002             C
                                GGTTCCGGCTCCGGC CC
                                |||||||||||||| ||
                                CCGAGGCCGAGGCCG GG
                                      A
GAM174   PVRL2    5'  GCCTGTGGGGCTCCGGCTCCG  16001    CC___
                                GCC    GGTTCCGGCTCCG
                                |||    ||||||||||||
                                CGG    CCGAGGCCGAGGC
                                  ACACC
GAM174   RAB2L    5'  CCGTCGGTCTCCGGCCCC    21918    GTTC  _
                                CCG    CGG CTCCGGCCCC
                                |||    ||| ||||||||||
                                GGC    GCC GAGGCCGGGG
                                  A___   A
GAM174   RASD1    5'  GCTTGGGGCTCCGGCTCCG   32011    CCC_
                                GC    GGTTCCGGCTCCG
                                ||    ||||||||||||
                                CG    CCGAGGCCGAGGC
                                 AACC
GAM174   SCRT1    3'  CGGTTCTAGGTCTCGCGGGGC  36364       C_ _  ____  GCCC
                                CGGTTC  GG CTC    CG    C
                                ||||||  || |||    ||    |
                                GCCAAG  CC GAG    GC    G
                                   AT  A   CIII  CCCG
GAM174   SLC22A2  5'  GGTTCCAGTCCACCTCG     40527        C    G  C
                                GGTTCCGG TCCG CC CG
                                |||||||| |||| || ||
```

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                                CCAAGGTC AGGT GG GC
                                   _   _ A
GAM174  TNFRSF11A 3'  GCCCTGGCTCCGAGCTTCG   19271     C     _  C
                                GCCC GGTTCCG GCT CG
                                |||| ||||||| ||| ||
                                CGGG CCGAGGC CGA GC
                                  A      T   A
GAM174  TRAM    5'  GCCCCGGTTCTGCTCTTCCC  30701        CG   CGG
                                GCCCCGGTTC  GCTC   CCC
                                ||||||||||  ||||   |||
                                CGGGGCCAAG  CGAG   GGG
                                     A_    AA_
GAM174  WT1     5'  GCCCCGCGGCTCCTCCGGCCC  35960      __     GGC
                                GCCCC  GGTTCC   TCCGGCCC
                                |||||  ||||||   ||||||||
                                CGGGG  CCGAGG   AGGCCGGG
                                  CG     ___
GAM174  ZNF198  5'  CCCGGTTCTGGCTGCGCTCCG  18368       C    C  G C
                                CCCGGTTC GGCT CG C CCG
                                |||||||| |||| || | |||
                                GGGCCAAG CCGA GC G GGC
                                    A   C  _ A
GAM174  ABL1    5'  CCGGGCCCGGCTCAGGCCCGGC 28710     C    A   C   T
                                CCGG CCCG CTC GGC CCGGC
                                |||| |||| ||| ||| |||||
                                GGCC GGGC GAG CCG GGCCG
                                  C   C   T  _
GAM174  ACCN2   5'  CGGCTCCGATCTGTCCGC    33442     C    C  CGGC    G
                                CGGC CCGA TC    TCCG C
                                |||| |||| ||    |||| |
                                GCCG GGCT AG    AGGC G
                                  A   _ AC__    _
GAM174  ADAR    5'  CCGGGCCCAAGATGGCTCCGG  31903     C    CTCC
                                CCGG CCCGA    GGCTCCGG
                                |||| |||||    ||||||||
                                GGCC GGGTT    CCGAGGCC
                                  C    CTA_
GAM174  ADCY6   5'  CCGCCCCCGCGGGCTCCGGCC  31612     G    ACTCC
                                CCG CCCCG    GGCTCCGGCC
                                ||| |||||    ||||||||||
                                GGC GGGGC    CCGAGGCCGG
                                 G    GC___
GAM174  ADCY6   5'  CCGGCCCGGCTCCGG      34169       CGACTCC     _
                                CCGGCCC      GGCTCCG G
                                |||||||      ||||||| |
                                GGCCGGG      CCGAGGC C
                                   ________     G
GAM174  ADK     5'  CCGGCCCCTGGCTAGCCGGCC  27482       GACTCC   __
                                CCGGCCCC     GGCT  CCGGCC
                                ||||||||     ||||  ||||||
```

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                                GGCCGGGG    CCGA  GGCCGG
                                   A_____   TC
GAM174  AF5Q31   5'  CCAGTCCCGGCTCCGCTAGGCC 30853     C   A    G  CC
                                CCGG CCCG CTCCG CT  GGCC
                                |||| |||| ||||| ||  ||||
                                GGTC GGGC GAGGC GA  CCGG
                                  A   C    _ T_
GAM174  ANK1     3'  GGCCCCGGCCTCTGGGCGTC  33869       A_  C_  _
                                GGCCCCG  CTC  GGC TC
                                |||||||  |||  ||| ||
                                CCGGGGC  GAG  CCG AG
                                   CG   AC   C
GAM174  AOC3     3'  CGGCCACGGCTCCAGGC    19017      CCGACTC     _
                                CGGCC      CGGCTCC GGC
                                |||||      ||||||| |||
                                GCCGG      GCCGAGG CCG
                                  T_______      T
GAM174  ARIH1    5'  CCGGCTCTCGCTCCGGCTCCGG 25088      CC_ A
          C                      CCGGC   CG CTCCGGCTCCGGC
                                |||||   || ||||||||||||
                                GGCCG   GC GAGGCCGAGGCCG
                                  AGA  _
GAM174  ATRN     5'  CCGGCTCCGCTTCGCCTGGCC  40290      C   A  C  G  CC
                                CCGGC CCG CT CG CT  GGCC
                                ||||| ||| || || ||  ||||
                                GGCCG GGC GA GC GA  CCGG
                                  A  _ A  G  __
GAM174  BAZ2A    3'  CCGGCCCCATTGCTACTTGGCC 30305        ACTCCG   CC
                                CCGGCCCCG     GCT  GGCC
                                |||||||||     |||  ||||
                                GGCCGGGGT     TGA  CCGG
                                    AACGA_   A_
GAM174  BCAR1    3'  CCGGCCCCTGGGCTTCGGC   41941        GACTCC   C
                                CCGGCCCC     GGCT CGGC
                                ||||||||     |||| ||||
                                GGCCGGGG     CCGA GCCG
                                    AC____   A
GAM174  CHIC2    5'  CGGCTGTCTCGGCTCCGGC   29051     CCCGA  C
                                CGGC    CTC GGCTCCGGC
                                ||||    ||| |||||||||
                                GCCG    GAG CCGAGGCCG
                                  ACA__  _
GAM174  CLCN7    3'  CCGGCCCCGGTGCCCACCGGCC 10515        AC_   GCT
                                CCGGCCCCG  TCCG  CCGGCC
                                |||||||||  ||||  ||||||
                                GGCCGGGGC  GGGT  GGCCGG
                                    CAC   ___
GAM174  CLDN14   5'  CGGCTCCGGGTCCATTGGC   29081     CCCGAC    C  ___
                                CGGC     TCCGG TCC  GGC
                                ||||     ||||| |||  |||
```

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                                GCCG     AGGCC AGG   CCG
                                  _______    C   TAA
GAM174  CLN3     5'  CCGGTCCCAGCTCCGGCT    6359       C    A
                                CCGG CCCG CTCCGGCT
                                |||| |||| ||||||||
                                GGCC GGGT GAGGCCGA
                                  A    C
GAM174  COL9A1   5'  GGCCCGGCTCTGCAGCC     38535      CGACTCC    __
                                GGCCC      GGCTC  CGGCC
                                |||||      |||||  |||||
                                CCGGG      CCGAG  GTCGG
                                  ________    AC
GAM174  CORO2A   5'  CCAGCTCCGGCTCCGCGC    38061     A         _
                                CCG CTCCGGCTCCG GC
                                ||| ||||||||||| ||
                                GGT GAGGCCGAGGC CG
                                  C          G
GAM174  CRMP1    5'  GCCCCGGCTGCTCGGC      10597       A  CCG    C
                                GCCCCG CT   GCTC GGC
                                |||||| ||   |||| |||
                                CGGGGC GA   CGAG CCG
                                   C  ___   _
GAM174  CSNK1E   3'  CCAGCCCTGACTCCAGGCT   12472        C     _
                                CCGGCCC GACTCC GGCT
                                ||||||| |||||| ||||
                                GGTCGGG CTGAGG CCGA
                                    A     T
GAM174  CTSZ     5'  CCGGCTCCCGCTCTGGATC   41612      _   A   C  C
                                CCGGC CCCG CTC GG TC
                                ||||| |||| ||| || ||
                                GGCCG GGGC GAG CC AG
                                  A    _   A  T
GAM174  DMD      3'  GGCTTCCGGCTCCGG       19687     CCCGAC
                                GGC     TCCGGCTCCGG
                                |||     ||||||||||
                                CCG     AGGCCGAGGCC
                                  A_____
GAM174  EN2      5'  CCCGCCCGGGCCGGCTCCGGCC 10931    G    CGACT
                                CC GCCC    CCGGCTCCGGCC
                                || ||||    ||||||||||||
                                GG CGGG    GGCCGAGGCCGG
                                 G   CCC__
GAM174  ENIGMA   5'  CCGGCTCCTGCTTGGCCCGGCC 41634      C  GA  CC   T
                                CCGGC CC  CT  GGC CCGGCC
                                ||||| ||  ||  ||| ||||||
                                GGCCG GG  GA  CCG GGCCGG
                                  A  AC  A_  _
GAM174  EXT2     5'  CGGCCCCGAGCTTGGTCACCGG 7587         _  CC  CT_
            C                    CGGCCCCGA CT  GG   CCGGC
                                |||||||| ||  ||   |||||
```

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                                GCCGGGGCT GA  CC   GGCCG
                                      C  A_  AGT
GAM174  FGFR1    5'  CCGCGTCCCCGGCTCCGGC   35789    C  A
                                CC CG CTCCGGCTCCGGC
                                || || ||||||||||||
                                GG GC GGGGCCGAGGCCG
                                 C  A
GAM174  FKBP1B   5'  CCGACCCCGGCTCGGCTCCGGC 19963          A   C
              C                  CCGGCCCCG CTC GGCTCCGGCC
                                 ||||||||| ||| ||||||||||
                                 GGCTGGGGC GAG CCGAGGCCGG
                                       C   _
GAM174  FOXD2    5'  CCGGCTCCGCTCCGGCAGCGGC 20960       C   A      TC
                                 CCGGC CCG CTCCGGC  CGGC
                                 ||||| ||| |||||||  ||||
                                 GGCCG GGC GAGGCCG  GCCG
                                    A  _      TC
GAM174  GAN      5'  CCGGCTCCCGACACCGTCCGGC 35142       _     T   GC
              C                  CCGGC CCCGAC CCG  TCCGGCC
                                 ||||| |||||| |||  |||||||
                                 GGCCG GGGCTG GGC  AGGCCGG
                                    A     T  __
GAM174  GATA2    5'  CGGGCCCGCCCGGCTCCGGCC  13085     C    A T
                                 CGG CCCG C CCGGCTCCGGCC
                                 ||| |||| | ||||||||||||
                                 GCC GGGC G GGCCGAGGCCGG
                                   C   _ _
GAM174  GCLM     5'  GGCTGCGGCTCCGGCTCCGGC  13133     CC  A
                                 GGC  CG CTCCGGCTCCGGC
                                 |||  || ||||||||||||
                                 CCG  GC GAGGCCGAGGCCG
                                   AC  C
GAM174  GCLM     5'  CCGGCTCCGGCTACTGCGGCC  13129     A       C___
                                 CCG CTCCGGCT    CGGCC
                                 ||| ||||||||    |||||
                                 GGC GAGGCCGA    GCCGG
                                   C       TGAC
GAM174  GNA11    5'  CCGGCCCCGGCCGACGCGGCC  44037          ACT    TC
                                 CCGGCCCCG   CCGGC  CGGCC
                                 |||||||||   |||||  |||||
                                 GGCCGGGGC   GGCTG  GCCGG
                                      C__     C_
GAM174  GOSR2    5'  CGGCTCCGGCTCTGGC      38288      CCCGAC       C
                                 CGGC     TCCGGCTC GGC
                                 ||||     |||||||| |||
                                 GCCG     AGGCCGAG CCG
                                    _______       A
GAM174  GOSR2    5'  CCGGCAGGCCACGGCTCCGGCT 20177       ___  _  A       C
              CTGGC                  CCGGC   CC CG CTCCGGCTC GGC
                                 |||||   || || |||||||| |||
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                                GGCCG   GG GC GAGGCCGAG CCG
                                   TCC  T  C       A
GAM174  GTF2IRD1  5'  CCGGCCCCGGCCCGCGGC    32253        GACTCC    _
                                CCGGCCCC     GGCTC CGGC
                                ||||||||     ||||| ||||
                                GGCCGGGG     CCGGG GCCG
                                   _______    C
GAM174  GZMM      5'  GGCCCCGGCCCCGAGC      23695       GACTCC      _
                                GGCCCC     GGCTCCG GC
                                ||||||     ||||||| ||
                                CCGGGG     CCGGGGC CG
                                   _______     T
GAM174  HCN4      5'  GCCCCGGCCCGTCCGGCC    24222       A T   GC
                                GCCCCG C CCG  TCCGGCC
                                ||||||  | |||  |||||||
                                CGGGGC G GGC  AGGCCGG
                                   C _  __
GAM174  HIF1A     5'  CCGGGCCCGGCTCCGAGC    11347     AC        _
                                CCG  TCCGGCTCCG GC
                                |||  ||||||||||  ||
                                GGC  GGGCCGAGGC CG
                                  CC         T
GAM174  HOXD13    5'  CCGGCCCCGGCCCTGGCCCTGG 8017          A   C    C
           CC                     CCGGCCCCG CTC GGCTC GGCC
                                |||||||||  |||  |||||  ||||
                                GGCCGGGGC GGG CCGGG CCGG
                                     C   A    A
GAM174  HS3ST3A1  5'  CCAGCCCCGGCTTTCTCTGG   25801         A  CCGG   C
                                CCGGCCCCG CT    CTC GG
                                |||||||||  ||    |||  ||
                                GGTCGGGGC GA    GAG CC
                                     C  AA__   A
GAM174  HSF4      5'  CCGGCTCTGCGCTCGGGCCCGG 40764       CC__  A   C   T
           CC                     CCGGC    CG CTC GGC CCGGCC
                                |||||    ||  |||  |||  ||||||
                                GGCCG    GC GAG CCG GGCCGG
                                   AGAC  _   C   _
GAM174  HSPA4     5'  GCTCAGGCCGGCTCCGGC    44852     CC  ACT
                                GC  CG   CCGGCTCCGGC
                                ||  ||   ||||||||||
                                CG  GT   GGCCGAGGCCG
                                 A_  CC_
GAM174  HSPA4     5'  CCGGCTCCGGCTCAGTGGCC   44848      A       C__
                                CCG CTCCGGCTC   GGCC
                                |||  |||||||||   ||||
                                GGC GAGGCCGAG   CCGG
                                  C        TCA
GAM174  JAG2      5'  CCGCGCTCCGGCTGCCCGGCC  13710    C  A       __
                                CC CG CTCCGGCT  CCGGCC
                                || ||  ||||||||  ||||||
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                                GG GC GAGGCCGA  GGCCGG
                                 C _       CG
GAM174  KCNJ6    5' GCTCCGGCTCCAGGTCCGGC  13858    C  A     C
                                GC CCG CTCCGG TCCGGC
                                || ||| |||||| ||||||
                                CG GGC GAGGTC AGGCCG
                                 A  C     C
GAM174  KIF5C    5' CCGGCCCCTCCGGCT       21147         GAC
                                CCGGCCCC   TCCGGCT
                                ||||||||   |||||||
                                GGCCGGGG   AGGCCGA
                                     ____
GAM174  KIFC3    5' CCGGCTCGGGCTCCGGGGC   24458     A  C     __
                                CCG CTC GGCTCC  GGC
                                ||| ||| ||||||  |||
                                GGC GAG CCGAGG  CCG
                                  C  C     CC
GAM174  LHX5     5' CCGCGCCCCGGCGGCTTCGGCC 35315     _     ACTC    C
                                CCG GCCCCG    CGGCT CGGCC
                                ||| ||||||    ||||| |||||
                                GGC CGGGGC    GCCGA GCCGG
                                  G     C___    A
GAM174  LRP3     5' GCCCCGCGGCTCCGGCTCCGG  42167       A__
                                GCCCCG   CTCCGGCTCCGG
                                ||||||   ||||||||||||
                                CGGGGC   GAGGCCGAGGCC
                                    GCC
GAM174  LRP3     5' CCTGCCCCGCGGCTCCGGCTCC 42162    G     A__
           GG                     CC GCCCCG   CTCCGGCTCCGG
                                || ||||||   ||||||||||||
                                GG CGGGGC   GAGGCCGAGGCC
                                 A     GCC
GAM174  LRP3     5' CCGGCTCCGGTTCCGGCTGCGG 42159      C  AC      C
           C                     CCGGC CCG  TCCGGCT CGGC
                                ||||| |||  ||||||| ||||
                                GGCCG GGC  AGGCCGA GCCG
                                   A  CA      C
GAM174  LRP3     5' CCGGCTCTGGCTCTGGCTGCGG 42160      CCCGA  C   C
           C                     CCGGC    CTC GGCT CGGC
                                |||||    ||| |||| ||||
                                GGCCG    GAG CCGA GCCG
                                   AGACC   A   C
GAM174  LRP3     5' CCGGCTGCGGCTCCGGCTCTGG 42161      CC  A       C
           C                     CCGGC  CG CTCCGGCTC GGC
                                |||||  || |||||||| |||
                                GGCCG  GC GAGGCCGAG CCG
                                   AC  C       A
GAM174  LRP3     5' CCGGCTGCGGCTCCGGCTCTGG 42161      CC  A       C
           C                     CCGGC  CG CTCCGGCTC GGC
                                |||||  || |||||||| |||
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                                GGCCG  GC GAGGCCGAG CCG
                                  AC  C       A
GAM174  LRP8    5'  CCCGCCCCGGCTCCTCGGC   37790     A       __
                                CCCG CTCCGGCTCC  GGC
                                |||| ||||||||||  |||
                                GGGC GGGGCCGAGG  CCG
                                  _       AG
GAM174  M11S1   5'  CGGCCCCGGCTCCCGCGGCC  25328       A   G  TCC
                                CGGCCCCG CTCC GC   GGCC
                                |||||||| |||| ||   ||||
                                GCCGGGGC GAGG CG   CCGG
                                    C   G ___
GAM174  MAPRE1  5'  CCGGCTCCGGTTCCGTCTTCG  29520     C  AC   G  C
                                CCGGC CCG  TCCG CT CG
                                ||||| |||  |||| || ||
                                GGCCG GGC  AGGC GA GC
                                  A  CA   A  A
GAM174  MAPRE1  5'  GCCCGCAACCGGCTCCGG    29522     _  CT
                                GCCC CGA  CCGGCTCCGG
                                |||| |||  ||||||||||
                                CGGG GTT  GGCCGAGGCC
                                  C  __
GAM174  MTMR1   5'  CCGGCCCCGGGTTCGGGC    43152       ACTCC  C  C
                                CCGGCCCCG    GG TC GGC
                                |||||||||    || || |||
                                GGCCGGGGC    CC AG CCG
                                     _____  A  C
GAM174  NFKB2   5'  CCGGCTCTGTCTAGTGGCTCCG 14763     CCCGA  CC_
          GCC                   CCGGC    CT   GGCTCCGGCC
                                |||||    ||   ||||||||||
                                GGCCG    GA   CCGAGGCCGG
                                  AGACA  TCA
GAM174  NKX2H   3'  CCAGGCGTTCGGCTCCGGC   30755     CCC  ACTC
                                CCGG   CG   CGGCTCCGGC
                                ||||   ||   ||||||||||
                                GGTC   GC   GCCGAGGCCG
                                  C__  AA__
GAM174  OLFM1   5'  GGCCCCGGCTCCGCTGGC    26775       A    G  CC
                                GGCCCCG CTCCG CT  GGC
                                ||||||| ||||| ||  |||
                                CCGGGGC GAGGC GA  CCG
                                   C    _ __
GAM174  OLFM1   5'  CCGGCTCTGGCCCCGGCTCCG  26767     CCCGA
                                CCGGC    CTCCGGCTCCG
                                |||||    ||||||||||
                                GGCCG    GGGGCCGAGGC
                                  AGACC
GAM174  OLIG2   3'  CCGGCTTAGACTCCGATGGGGC 25144     CCC      CTCC
                                CCGGC   GACTCCGG   GGC
                                |||||   ||||||||   |||
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                                GGCCG  CTGAGGCT   CCG
                                  AAT      ACC_
GAM174  PCDH7    5'  CCAGGCTCTGCTCCGGCTCCGG 37109    _  CCCGA
            CC                   CC GGC    CTCCGGCTCCGGCC
                                || |||    ||||||||||||||
                                GG CCG    GAGGCCGAGGCCGG
                                 T  AGAC_
GAM174  PDXK     5'  CGGCTCGGGCTCGGGCTCCGGC 18966     CC  A_  C
            C                    CGGC  CG  CTC GGCTCCGGCC
                                ||||  ||  ||| ||||||||||
                                GCCG  GC  GAG CCGAGGCCGG
                                  A_  CC   C
GAM174  PDXK     5'  CCGGCCCCGGCTCCCCTCGGC  18965        A   GG TC
                                CCGGCCCCG CTCC  C  CGGC
                                ||||||||| ||||  |  ||||
                                GGCCGGGGC GAGG  G  GCCG
                                      C   __ GA
GAM174  PEX7     5'  CCGGCCCTCGCTGCCCCGGCC  7111        _  A  CCG
                                CCGGCCC CG CT   GCTCCGGCC
                                ||||||| || ||   |||||||||
                                GGCCGGG GC GA   CGGGGCCGG
                                    A  _  ___
GAM174  PK428    5'  GGCACCGGCTCCGGAGAAGCGG 18808    C   A    CTC__
            C                    GGC CCG CTCCGG    CGGC
                                ||| ||| ||||||    ||||
                                CCG GGC GAGGCC    GCCG
                                  T   C     TCTTC
GAM174  POLG     5'  GGCTTTGGGCTCCAGCTTGGC  15448    CCCGA_     CC
                                GGC     CTCCGGCT  GGC
                                |||     ||||||||  |||
                                CCG     GAGGTCGA  CCG
                                  AAACCC       A_
GAM174  POV1     5'  GGCCCCGAGCTCCGCAGGGC   18844        _    G TCC
                                GGCCCCGA CTCCG C   GGC
                                |||||||| ||||| |   |||
                                CCGGGGCT GAGGC G   CCG
                                     C    _ TC_
GAM174  PPP1R14B 5'  CCGGCTCCGCTCCGCGCGGC   39793      C   A    G TC
                                CCGGC CCG CTCCG C  CGGC
                                ||||| ||| ||||| |  ||||
                                GGCCG GGC GAGGC G  GCCG
                                  A   _    _ C_
GAM174  PPP2R2C  5'  CCGGCTCGTGGCTCTGG     41543      CC  ACTCC    C
                                CCGGC  CG    GGCTC GG
                                |||||  ||    ||||| ||
                                GGCCG  GC    CCGAG CC
                                  A_  A_____     A
GAM174  PPP2R5A  5'  CCGGCCCCACGGCCCTCCGGCC 26433         ACTC   __
                                CCGGCCCCG   CGGC  TCCGGCC
                                |||||||||   ||||  |||||||
```

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                              GGCCGGGGT   GCCG  AGGCCGG
                                   ____   GG
GAM174  PPP2R5D  5' CCCGCTCCGGCTCCGGC    26454     A
                              CCCG CTCCGGCTCCGGC
                              |||| ||||||||||||
                              GGGC GAGGCCGAGGCCG
                                _
GAM174  PPP2R5D  5' CCGGCTCCGGCTTTGCTCGGCC 26456      C  A  CCG   C
                              CCGGC CCG CT   GCTC GGCC
                              ||||| ||| ||   |||| ||||
                              GGCCG GGC GA   CGAG CCGG
                                A  C  AA_   _
GAM174  PPP2R5D  5' CGGCCCCGCTCCGGCTCCGGC  26457       A
                              CGGCCCCG CTCCGGCTCCGGC
                              |||||||| ||||||||||||
                              GCCGGGGC GAGGCCGAGGCCG
                                 _
GAM174  PPP4C    5' CCGGTTCCGGCTCTCCGGCC   15533    AC    __
                              CCG  TCCGGC  TCCGGCC
                              |||  ||||||  |||||||
                              GGC  AGGCCG  AGGCCGG
                                CA     AG
GAM174  PPP4C    5' CCGCCGCTGCGACTCCGGTTCC 15532    G  C___      C
           GGC                  CCG CC    CGACTCCGG TCCGGC
                              ||| ||    |||||||| ||||||
                              GGC GG    GCTGAGGCC AGGCCG
                                _ CGAC       A
GAM174  PRKAR2B  5' CCGGCGCCGGCTGGCCCGGCC  15618     C  A  CC  T
                              CCGGC CCG CT  GGC CCGGCC
                              ||||| ||| ||  ||| ||||||
                              GGCCG GGC GA  CCG GGCCGG
                                C  C __  _
GAM174  PTPRA    5' CCGGCCCGCGGCTCCGAGC   15923       CGACTC      _
                              CCGGCCC     CGGCTCCG GC
                              |||||||     |||||||| ||
                              GGCCGGG     GCCGAGGC CG
                                  C_____       T
GAM174  PTPRE    5' CCGCCTCGGCTCCAGCTCCGGC 38984    G  C  A
                              CCG CC CG CTCCGGCTCCGGC
                              ||| || || ||||||||||||
                              GGC GG GC GAGGTCGAGGCCG
                                _ A  C
GAM174  PVRL2    5' CCGGCTCCGGCTCCGGGCC   16000    A        _
                              CCG CTCCGGCTCCGG CC
                              ||| |||||||||||| ||
                              GGC GAGGCCGAGGCC GG
                                C          C
GAM174  RBBP5    5' CCGGTCTCAGCTCCGGC    22806     CCCCGAC  _
                              CCGG      TC CGGCTCCGGC
                              ||||      || ||||||||||
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                                GGCC      AG GTCGAGGCCG
                                  _______ A
GAM174  ROCK2    5' CCGGCTTCGGGTCTCCAAGGC  42355      CC  ACTCC  _   __
                                CCGGC  CG    GG CTCC  GGC
                                |||||  ||    || ||||  |||
                                GGCCG  GC    CC GAGG  CCG
                                   AA  _____  A    TT
GAM174  SIAH1    5' CCGCCCCGGCTCCCCCCTGGCC 16711     G    A    GG   _
                                CCG CCCCG CTCC  CTCC GGCC
                                ||| ||||| ||||  |||| ||||
                                GGC GGGGC GAGG  GGGG CCGG
                                  _    C    __    A
GAM174  SIL      5' CCGGCCCCGCCTCTGGGACG   16727         A   C  CTC
                                CCGGCCCCG CTC GG   CG
                                |||||||| ||| ||   ||
                                GGCCGGGGC GAG CC   GC
                                     G   A  CT_
GAM174  SLC25A15 5' CGGCTCCGGGTCGCCGGC    30667     CCCGAC    CT__
                                CGGC     TCCGG    CCGGC
                                ||||     |||||    |||||
                                GCCG     AGGCC    GGCCG
                                  _______    CAGC
GAM174  SLC6A8   5' GGCCCGCGACTCCGGTGGC    24774      _       CTCC
                                GGCCC CGACTCCGG    GGC
                                ||||| |||||||||    |||
                                CCGGG GCTGAGGCC    CCG
                                   C        A___
GAM174  SLC6A9   5' GGCCCTGCCCCTCCGGC     27989      CGA    GGC
                                GGCCC   CTCC   TCCGGC
                                |||||   ||||   ||||||
                                CCGGG   GGGG   AGGCCG
                                   AC_    ___
GAM174  SLC7A8   5' CCGGCCCCATCCCTCTGG    29285         AC   GG   C
                                CCGGCCCCG  TCC  CTC GG
                                |||||||||  |||  ||| ||
                                GGCCGGGGT  AGG  GAG CC
                                     __   __   A
GAM174  TERF2    5' CCGTCCCGGCTCCCGCGGC   24907    GC    A    G  TCC
                                CCG  CCCG CTCC GC   GGC
                                |||  |||| |||| ||   |||
                                GGC  GGGC GAGG CG   CCG
                                  A_    C    G  ___
GAM174  UGCG     5' CGGCCCCGCGCTCCGG      17870         ACTCCG
                                CGGCCCCG     GCTCCGG
                                ||||||||     |||||||
                                GCCGGGGC     CGAGGCC
                                     G_____
GAM174  VEGF     5' CCGCCTCCGGGGGCGGGCTCCG 17947     G  _   ACTCC_
            GCC                    CCG CC CCG     GGCTCCGGCC
                                ||| || |||     ||||||||||
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                                GGC GG GGC     CCGAGGCCGG
                                  _ A   CCCCGC
GAM174  VEGF     5'  CCGGCTGCGGCTCCTCCCGGCC 17949      CC  A    GG T
                                CCGGC  CG CTCC  C CCGGCC
                                ||||||  || ||||  | |||||||
                                GGCCG  GC GAGG  G GGCCGG
                                   AC  C    A_ _
GAM174  VGF      5'  CCGCCTCGGCTCCGAGCGGTGG 17986     G  C  A    _  TCC
             CC                   CCG CC CG CTCCG GC   GGCC
                                ||| || || ||||| ||   ||||
                                GGC GG GC GAGGC CG   CCGG
                                  _ A  C    T  CCA
GAM174  XT3      5'  CCGGCCTCGGCGCGCTCGGCTC 33661       C  A____   C
             CGGC                  CCGGCC CG    CTC GGCTCCGGC
                                |||||| ||    ||| |||||||||
                                GGCCGG GC    GAG CCGAGGCCG
                                   A  CGCGC  _
GAM174  ZNF174   5'  GGCCCAGTGGCTCCGGC     18363      CGACTCC
                                GGCCC      GGCTCCGGC
                                |||||      |||||||||
                                CCGGG      CCGAGGCCG
                                   TCA____
GAM174  ZNF80    5'  GCCACTGCTGGCTCCGGCC   28330     CCG   CC_
                                GCC   ACT   GGCTCCGGCC
                                |||   |||   ||||||||||
                                CGG   TGA   CCGAGGCCGG
                                  ___   CGA
GAM175  ADH5     3'  GCTGTGAAGCTCTACGAGG   8579     CA   GAA      A
                                GC  TGA   AGCTCTAC AGG
                                ||  |||   |||||||| |||
                                CG  ACT   TCGAGATG TCC
                                 AC   ___       C
GAM175  ARHGEF12 3'  GCCATGAGGAAGCTGACTGTGA 31640         A    __  ACA
             GG                    GCCATGAG AAGCT  CT   AGG
                                |||||||| |||||  ||   |||
                                CGGTACTC TTCGA  GA   TCC
                                     C     CT  CAC
GAM175  CD5L     3'  ACGTCATGAAAAGGTCTA    25315     C       A C
                                ACG CATGAGAA G TCTA
                                ||| |||||||| | ||||
                                TGC GTACTTTT C AGAT
                                  A       _ C
GAM175  GNA11    5'  GCCATGAGAGAGGGCCCAGG   44043         AA__   TACA
                                GCCATGAGA   GCTC   AGG
                                |||||||||   ||||   |||
                                CGGTACTCT   CGGG   TCC
                                     CTCC   _____
GAM175  GRM6     3'  ACCCATGAGAGAGCTGCACAGG 9165     G       A   C   A
                                AC CCATGAGA AGCT TACA GG
                                || |||||||| |||| |||| ||
```

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                                TG GGTACTCT TCGA GTGT CC
                                 _      C   C   _
GAM175  NF2     3'  ACGCCATGAGAGAAATCTCTAC 7062          _  _     A
             AGGG                  ACGCCATGAGA AAG CTCTACA GG
                                   |||||||||| ||| ||||||| ||
                                   TGCGGTACTCT TTT GAGATGT CC
                                         C  A     C
GAM175  OIP2    5'  ACGCCACGGGAAATGCCAAGG  44166        A   _  TCTA
                                   ACGCCATG GAAA GC   CAAGG
                                   |||||||| |||| ||   |||||
                                   TGCGGTGC CTTT CG   GTTCC
                                        C   A ____
GAM175  SGT     3'  CGCCATGAGCGGCTGCAGG   16610        AAA   CTACA
                                   CGCCATGAG  GCT    AGG
                                   |||||||||  |||    |||
                                   GCGGTACTC  CGA    TCC
                                        GC_  CG___
GAM175  SLC39A1  3'  GCTTTGAGAAAGAGGAAGG   30886    CA      CTCTAC
                                   GC  TGAGAAAG     AAGG
                                   ||  ||||||||     ||||
                                   CG  ACTCTTTC     TTCC
                                    AA       TCC___
GAM175  SLC6A12  3'  GCCATGAGAGACTCGGAGG   16798        AA   TACA
                                   GCCATGAGA  GCTC   AGG
                                   |||||||||  ||||   |||
                                   CGGTACTCT  TGAG   TCC
                                        C_   CC__
GAM175  TIMP4    3'  GCCAAAGCTCTGCAG      17531     TGAGA     A  A
                                   GCCA    AAGCTCT CA G
                                   ||||    ||||||| || |
                                   CGGT    TTCGAGA GT C
                                     ______      C  C
GAM175  TNFSF11  3'  ACGCGTGTTCTCTACAAG   37452     CA  AGAAAG
                                   ACGC  TG     CTCTACAAG
                                   ||||  ||     |||||||||
                                   TGCG  AC     GAGATGTTC
                                     C_  AA_____
GAM175  TP63     3'  GCCATGAGGAGGTAAGCCAGTA 18999        A_____    CTAC
             AGG                    GCCATGAG    AAGCT    AAGG
                                    ||||||||    |||||    ||||
                                    CGGTACTC    TTCGG    TTCC
                                         CTCCA    TCA_
GAM176  DNASE1L1 5'  CGAGGTCAGGCGTTCA     27491      C  TGCTC
                                   CGAGG CG    GCGTTCA
                                   ||||| ||    |||||||
                                   GCTCC GT    CGCAAGT
                                     A  C_____
GAM176  PHGDH    3'  GAGGCCCGCGTTCA       42034       GTGCT
                                   GAGGCC    CGCGTTCA
                                   ||||||    ||||||||
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                                CTCCGG    GCGCAAGT
                                      _____
GAM176  ADRA1A   5'  CGCGGAGGCGGGAGCGCGGG  37807    T    __     CAGC
                                CGC GGAGGC  GAGCGCG   GG
                                ||| ||||||  |||||||   ||
                                GCG CCTCCG  CTCGCGC   CC
                                  _    CC     ____
GAM176  ARHC     5'  CGCTGGAGCCGGGAAGCGG   23168       G  AGCGCGC
                                CGCTGGAG CG     AGCGG
                                |||||||| ||     |||||
                                GCGACCTC GC     TCGCC
                                    G  CCT____
GAM176  CADPS    5'  CGCTGGAGGCAGCCG      42193        G   GCGCAG
                                CGCTGGAGGC AGC     CG
                                |||||||||| |||     ||
                                GCGACCTCCG TCG     GC
                                      _  _______
GAM176  CAV1     5'  CGCTGGAGGGGGGGCGGTGGCTG 11990        CGA   CGCA _
            GG                    CGCTGGAGG   GCG    GC GGG
                                |||||||||   |||    || |||
                                GCGACCTCC   CGC    CG CCC
                                     CCC   CAC_  A
GAM176  CDKN2C   5'  GCTGCCGGGCGTGCGGCGGG   38565     GA  CGA   C  A
                                GCTG  GG   GCG GC GCGGG
                                ||||  ||   ||| || |||||
                                CGAC  CC   CGC CG CGCCC
                                  GG  ___   A  C
GAM176  CNGB1    3'  CGCTGGGGCGAGGGGCGCAGCG 10531       A     C_
            GG                    CGCTGG GGCGAG  GCGCAGCGGG
                                ||||||  ||||||  ||||||||||
                                GCGACC CCGCTC  CGCGTCGCCC
                                   _     CC
GAM176  COL4A4   5'  TGGAGGCGGGCTGGAGGCGGG  6410        A  GCGCA
                                TGGAGGCG GC    GCGGG
                                |||||||| ||    |||||
                                ACCTCCGC CG    CGCCC
                                     C  ACCTC
GAM176  EHD2     5'  CGCTGGCGGCTGCAGCGG    31129     GGA   A  GC
                                CGCT   GGCG GC  GCAGCGG
                                ||||   |||| ||  |||||||
                                GCGA   CCGC CG  CGTCGCC
                                  ___    _ A_
GAM176  FTH1     5'  CGCTGGAGCGGCGGCG      42785        G  A   CGCA
                                CGCTGGAG CG GCG    GCG
                                |||||||| || |||    |||
                                GCGACCTC GC CGC    CGC
                                      _ _  _____
GAM176  GRM7     5'  CGCTGGAGGGAACGGTGGTGGG 9185          C    CGCAGC
                                CGCTGGAGG GAGCG     GGG
                                ||||||||| |||||     |||
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                                GCGACCTCC CTTGC     CCC
                                     _    CACCA_
GAM176  HAS3     5' GCTGAAGGGGCGCGGCGG    39774        CGA    CA
                                GCTGGAGG   GCGCG  GCGG
                                ||||||||   |||||  ||||
                                CGACTTCC   CGCGC  CGCC
                                    C__    __
GAM176  HCN2     3' GCTGGAGGGAGGCG       10170        C   CGCGCA
                                GCTGGAGG GAG     GCG
                                |||||||| |||     |||
                                CGACCTCC CTC     CGC
                                     _  _______
GAM176  ID4      5' CGCTGGGGCGAGCGAGG     11381       A      CGC  C
                                CGCTGG GGCGAGCG   AG G
                                |||||| ||||||||   || |
                                GCGACC CCGCTCGC   TC C
                                     _      ___  _
GAM176  JAG2     3' CGCTGGAGCGGGCGTTCTGGG  13713        G  A   CGCAGC
                                CGCTGGAG CG GCG     GGG
                                |||||||| || |||     |||
                                GCGACCTC GC CGC     CCC
                                     _ C   AAGA__
GAM176  LMCD1    5' CGCGAGGGCGCGCAGCGG    31044     TG   CGA
                                CGC  GAGG   GCGCGCAGCGG
                                |||  ||||   ||||||||||
                                GCG  CTCC   CGCGCGTCGCC
                                     __    ___
GAM176  MAPRE3   3' GCTGGAGGGAGTGGCTGG    29534        C   CGC  AGC
                                GCTGGAGG GAG   GC   GG
                                |||||||| |||   ||   ||
                                CGACCTCC CTC   CG   CC
                                     _   AC_  A__
GAM176  MCM5     3' CGCTAGAGGCGGGCGCCCAGAG 41006          A   G   C
          G                      CGCTGGAGGCG GCGC CAG GG
                                 |||||||||| |||| ||| ||
                                 GCGATCTCCGC CGCG GTC CC
                                       C   G   T
GAM176  PRKCI    5' CGCTGGAGGCCGGGGGGTGCGGG 15632         GAG  CGCA_
                                CGCTGGAGGC   CG    GCGGG
                                |||||||||   ||    |||||
                                GCGACCTCCG   GC    CGCCC
                                     ____ CCCCA
GAM176  PRX      3' GCTGGAGGCGCCGGCGG     34126         AG  CGCA
                                GCTGGAGGCG  CG   GCGG
                                |||||||||  ||   ||||
                                CGACCTCCGC  GC   CGCC
                                     G_  _____
GAM176  TMEFF2   5' CGCGGGGGCCGGGCAGCGG   32102     T  A   GAG  C
                                CGC GG GGC   CG GCAGCGG
                                ||| || |||   || |||||||
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                                GCG CC CCG   GC CGTCGCC
                                  C _  ___  C
GAM176  UBE2L3   3'  TGGAGGCGAGCCCGG      17834          G  CAGC
                                TGGAGGCGAGC CG   G
                                |||||||||| ||   |
                                ACCTCCGCTCG GC   C
                                      G ____
GAM176  UGCG     5'  CGCGGGAGGCGAGAGGAAGGTG 17869     T       CGCGCAGC
          GG                    CGC GGAGGCGAG       GGG
                                ||| |||||||||       |||
                                GCG CCTCCGCTC       CCC
                                  C       TCCTTCCA
GAM176  ZNF144   5'  GCTGGAGGGCTGCAGTGG    28340        CGA  GC   C
                                GCTGGAGG   GC  GCAG GG
                                ||||||||   ||  |||| ||
                                CGACCTCC   CG  CGTC CC
                                    ___  A_   A
GAM177  ALDH3A2  5'  TGGCCTGGGCGGCCCACG    42922     GC      GTGC
                                TGGC  GGGCGGCC   CGCG
                                ||||  ||||||||   ||||
                                ACCG  CCCGCCGG   GTGC
                                  GA      ____
GAM177  FZD3     5'  CTGCCGCGGGCGGCCGCGC   32629     G
                                CTG CGCGGGCGGCCGTGC
                                ||| ||||||||||||||
                                GAC GCGCCCGCCGGCGCG
                                  G
GAM177  KRTHB6   3'  CCGGCGCGGGCGGCGCGT    14032           _
                                CTGGCGCGGGCGGC CGT
                                |||||||||||||| |||
                                GGCCGCGCCCGCCG GCA
                                        C
GAM177  RAP1GDS1 5'  TGGTGCGGGCGGCGCGGC    34509     C       _  T
                                TGG GCGGGCGGC CG GC
                                ||| ||||||||| || ||
                                ACC CGCCCGCCG GC CG
                                  A       C  _
GAM177  BAI2     5'  CCGGCGCTGGCGGGGGCG     11793       C   GA
                                CCGGCGC GGC  GGGGGTG
                                ||||||| |||  |||||||
                                GGCCGCG CCG  CCCCCGC
                                    A  __
GAM177  HPCAL1   5'  CGGCGCCGGCGGCGGC      39546          GAGGG
                                CGGCGCCGGC    GGTGGT
                                ||||||||||    ||||||
                                GCCGCGGCCG    CCGCCG
                                       _____
GAM177  IRF1     3'  GCTGGGGCTTGAGGGGGTGGTG 42044    GCC  __
                                GC   GGC  GAGGGGGTGGTG
                                ||   |||  ||||||||||||
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                                CG  CCG CTCCCCCACCAC
                                 ACC  AA
GAM177  SFTPA2   3' CCGGTGGCATGGGGGGTGGTG 27962    CGCC   A_
                                CCGG   GGCG GGGGGTGGTG
                                ||||   |||| ||||||||||
                                GGCC   CCGT CCCCCACCAC
                                  A___   AC
GAM177  WNT6     5' TCCGGCGGCGGCGGGGGGG   27185      C    A
                                TCCGGCG CGGCG GGGGG
                                ||||||| ||||| |||||
                                AGGCCGC GCCGC CCCCC
                                    C    _
GAM178  ACP1     5' CTCGCGGCTCCGCGGC     28235       CCT  AA
                                CTCGCGGC  TC  CGGC
                                ||||||||  ||  ||||
                                GAGCGCCG  AG  GCCG
                                    ___  GC
GAM178  ATP10C   5' CTCGCGGCCCGGGCGCGGC   35978        TTCAA
                                CTCGCGGCCC    CGGC
                                ||||||||||    ||||
                                GAGCGCCGGG    GCCG
                                     CCCGC
GAM178  ATP11A   3' TCTCCCGGCCCTCGCA     44186     G      CAACG
                                TCTC CGGCCCTT    GCA
                                |||| ||||||||    |||
                                AGAG GCCGGGAG    CGT
                                  G      _____
GAM178  BLK      3' TCGCGGCCCGTCTGGGATGGCA 11848       T  AAC___
           C                     TCGCGGCCC TC     GGCAC
                                |||||||||  ||     |||||
                                AGCGCCGGG AG     CCGTG
                                     C  ACCCTA
GAM178  CACNB2   5' TCGCGACCCTGCAGTAC    8797         T  ACG
                                TCGCGGCCCT CA   GC
                                |||||||||| ||   ||
                                AGCGCTGGGA GT   TG
                                     C  CA_
GAM178  CDX2     5' CCTCGCGGCTCTTCTGC    10404        C   AACG
                                TCTCGCGGC CTTC   GC
                                |||||||| ||||   ||
                                GGAGCGCCG GAAG   CG
                                     A   A___
GAM178  CLC      3' TCTCCTGGCTCAACAG     29904     GC  CCT
                                TCTC  GGC  TCAACGG
                                ||||  |||  |||||||
                                AGAG  CCG  AGTTGTC
                                  GA  ___
GAM178  COL1A1   3' TCGTGGCCCTTCCTGAC    6381     C      AAC
                                TCG GGCCCTTC  GGC
                                ||| ||||||||  |||
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                                AGC CCGGGAAG   CTG
                                  A       GA_
GAM178  DLC1    5'  CCTCGCGGTCCTCAACGCA   25902        C   T    G
                                TCTCGCGG CCT CAACG CA
                                |||||||| ||| ||||| ||
                                GGAGCGCC GGA GTTGC GT
                                    A  _    _
GAM178  FPGS    3'  TCTCGCGGCCCTGCAGC     22433           TCAA
                                TCTCGCGGCCCT   CGGC
                                ||||||||||||   ||||
                                AGAGCGCCGGGA   GTCG
                                      C___
GAM178  JTB     5'  CTCGCGGCCCTAGC       27443          TCAAC
                                CTCGCGGCCCT    GGC
                                ||||||||||     |||
                                GAGCGCCGGGA    TCG

                                      _____
GAM178  NFATC1  3'  TCTCGCAGCCTTCCAGCA    26082         C   AA
                                TCTCGCGGCC TTC  CGGCA
                                |||||||||| |||  |||||
                                AGAGCGTCGG AAG  GTCGT
                                      _  __
GAM178  NHP2L1  3'  TCTTTCTGCCTTTCAACGG   22682     CGCG   C
                                TCT   GCC TTCAACGG
                                |||   ||| ||||||||
                                AGA   CGG AAGTTGCC
                                  AAGA   A
GAM178  SQLE    5'  TCCAACCCTTCTTTGGTGGCAC 17108    G       AAC___
                                TC CGGCCCTTC     GGCAC
                                || |||||||||     |||||
                                AG GTTGGGAAG     CCGTG
                                 _       AAACCA
GAM178  ABCC1   3'  CCTGGAGTCGGGGGTGGG     33400         C   TC
                                CCTGGAGTCG GGT  GG
                                |||||||||| |||  ||
                                GGACCTCAGC CCA  CC
                                      C   C_
GAM178  ASH2L   3'  CCTGGAGTCAGCGGTTGTTGGC 43432         _     C__
                                CCTGGAGTC GCGGTT   GGC
                                |||||||| ||||||   |||
                                GGACCTCAG CGCCAA   CCG
                                     T     CAA
GAM178  CARP    5'  CCTGGAGTTGGCCCTGCTGG   30793        CGC    G  C
                                CCTGGAGT   GGTTC GC GG
                                ||||||||   ||||| || ||
                                GGACCTCA   CCGGG CG CC
                                    A__     A  A
GAM178  CLDN14  5'  CTGGAGCCTGGCTGGAC     40322        GC    C
                                CTGGAGTC  GGTT GGC
                                ||||||||  |||| |||
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                                GACCTCGG  CCGA CTG
                                    A_    C
GAM178  EVX1     5'  CCTGGGTCTCCAGCGGCCGGAC 12769      A  G_  TT
                                CCTGG GTC  CGG  CGGCCGGAC
                                ||||| |||  |||  |||||||||
                                GGACC CAG  GTC  GCCGGCCTG
                                  _  AG  __
GAM178  ITGA11   3'  CCTGGAGTGTGCAGATTGG   29197       C_   TTC
                                CCTGGAGT  GCGG  GG
                                ||||||||  ||||  ||
                                GGACCTCA  CGTC  CC
                                    CA   TAA
GAM178  KNS2     5'  CCTGGAGCGCCGCCGGGC    24471       T  G  TC
                                CCTGGAG CGC GT  GGC
                                ||||||| ||| ||  |||
                                GGACCTC GCG CG  CCG
                                   _  G  GC
GAM178  LILRB1   3'  CCTGGGGTAGATCCAGGCTGG  27426      A  CGC   _  C
                                CCTGG GT   GGTTC GGC GG
                                ||||| ||   ||||| ||| ||
                                GGACC CA   CTAGG CCG CC
                                  C  T__    T  A
GAM178  NAGLU    5'  CCAGGAGTCGCGGCTTCCGG   7048     T        TCGG
                                CC GGAGTCGCGGT   CCGG
                                || ||||||||||   ||||
                                GG CCTCAGCGCCG   GGCC
                                 T         AA__
GAM178  RUNX3    3'  CCAGGAGTCGCAAGATTTGGCT 20317    T      __   C  C
          GGA                     CC GGAGTCGC  GGTT GGC GGA
                                || ||||||||  |||| ||| |||
                                GG CCTCAGCG  CTAA CCG CCT
                                 T      TT   A  A
GAM178  SERPINH2 5'  CCTGGGTCGGGCTGGGC     10295      A   C   C
                                CCTGG GTCG GGTT GGC
                                ||||| |||| |||| |||
                                GGACC CAGC CCGA CCG
                                  _   _   C
GAM178  THRB     5'  CCTGGAGCCGGTTGGG      7856        CG   C
                                CCTGGAGT  CGGTT GG
                                ||||||||  ||||| ||
                                GGACCTCG  GCCAA CC
                                    __    C
GAM178  TNNC1    3'  CTGGAGTTGGAGGCTGGGC   17617       CGC_   C
                                CTGGAGT   GGTT GGC
                                |||||||   |||| |||
                                GACCTCA   CCGA CCG
                                   ACCT   C
GAM179  ALDH3B1  3'  TTCCATGGTGTGGCCTGAGTCA 45070      AAGC  C  _
                                TTCCA   GG GTG TCTGAGTCA
                                |||||   || ||| |||||||||
```

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                                AAGGT   CC CAC GGACTCAGT
                                  A___  A  C
GAM179  BAI2    3'  TTCCAAAGTGGAGTGTGAAAAT 11799       C  C   CT
                                TTCCAAAG GG GTGT  GAGT
                                |||||||| || ||||  ||||
                                AAGGTTTC CC CACA  TTTA
                                    A  T   CT
GAM179  SPAG8   3'  TTCCGGAATGGTGTGTCCA   29696     AA  C  C
                                TTCC  AG GG GTGTCTG
                                ||||  || || |||||||
                                AAGG  TT CC CACAGGT
                                  CC  A  A
GAM179  VAPB    3'  TTCCAAAGCGCTGGGT     21878         GCGTGT   A
                                TTCCAAAGCG     CTG GT
                                ||||||||||     ||| ||
                                AAGGTTTCGC     GAC CA
                                     _______  C
GAM179  BCL11B  3'  GCGGGGCGCCGGGGCCCG   39749    T___
                                GC   CGCCGGGGCCCG
                                ||   ||||||||||||
                                CG   GCGGCCCCGGGC
                                 CCCC
GAM179  CDH1    3'  GCACATGGGTCTGGGGCCCG  20364      AGC  GCC
                                GCACAT   TC   GGGGCCCG
                                ||||||   ||   ||||||||
                                CGTGTA   AG   CCCCGGGC
                                   CCC  A__
GAM179  CHRNB2  5'  CGGGCATAGCTCGCTGCCTCG  8858    CA       CGGG  _
                                CG  CATAGCTCGC   GCC CG
                                ||  ||||||||||   ||| ||
                                GC  GTATCGAGCG   CGG GC
                                 CC        A___   A
GAM179  CSDA    5'  CGCGGCGGCCGGGGCC     18893    ACATA  TC      C
                                CGC    GC  GCCGGGGC C
                                |||    ||  |||||||| |
                                GCG    CG  CGGCCCCG G
                                  C____  C_       A
GAM179  CXorf6  3'  CACATAGCTTGGTGGCTCG   24235        CGCC  _   C
                                CACATAGCT   GG GGC CG
                                |||||||||   || ||| ||
                                GTGTATCGA   CC CCG GC
                                     A___  A  A
GAM179  DES     3'  GCTCACAGCTGGGGC      43567    A     CGCC   C
                                GC CATAGCT   GGGG C
                                || |||||||   |||| |
                                CG GTGTCGA   CCCC G
                                 A      ____   A
GAM179  EGLN2   5'  ACACACATACCTGGGGCC    38809        G  CGCC
                                ACGCACATA CT   GGGGCC
                                |||||||| ||   ||||||
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                                TGTGTGTAT GA   CCCCGG
                                     G _____
GAM179  EXT2    3'  GCATAGCTCGAGGTGC     7588     CA     CC  _
                                GCA  TAGCTCG  GGG GC
                                |||  |||||||  ||| ||
                                CGT  ATCGAGC  TCC CG
                                  __     __  A
GAM179  FGF5    3'  CACATACCGGGGCC       37583      AGCTC
                                CACAT    GCCGGGGCC
                                |||||    |||||||||
                                GTGTA    TGGCCCCGG
                                  _____
GAM179  HIF1A   5'  GCGGGCGGCAATCGCCGGGGTC 11349    ACATA __       C
           CG                     GC    GC  TCGCCGGGG CCG
                                ||    ||  ||||||||| |||
                                CG    CG  AGCGGCCCC GGC
                                 CCCGC  TT       A
GAM179  KIP2    3'  GCATAGCTCGTTAAAACCC   26890    CA     CC
                                GCA  TAGCTCG  GGGGCCC
                                |||  |||||||  |||||||
                                CGT  ATCGAGC  TTTTGGG
                                  __     AA
GAM179  LASS1   3'  CGCGCAGGCGGCAGGGGCCCG  34598    A  TA  TC  C
                                CGC CA  GC  GC GGGGCCCG
                                ||| ||  ||  || ||||||||
                                GCG GT  CG  CG CCCCGGGC
                                  C  C_  C_  T
GAM179  SLC6A8  5'  CGCGCGGGCGGCGTCGGGGCCC 24759    ACATA  T_  C
           G                     CGC    GC  CG CGGGGCCCG
                                |||    ||  || |||||||||
                                GCG    CG  GC GCCCCGGGC
                                  CGCC_  CC  A
GAM179  TDG     3'  GCATATAGCTCAGGGAACCC   17357    C      CC
                                GCA ATAGCTCG  GGGGCCC
                                ||| ||||||||  |||||||
                                CGT TATCGAGT  CCTTGGG
                                  A       C_
GAM179  UBTF    5'  CGCGTGGGGCTCGCCATTAGCC 30611    ACATA      G_
                                CGC    GCTCGCCG  GGCC
                                |||    ||||||||  ||||
                                GCG    CGAGCGGT  TCGG
                                  CACCC       AA
GAM179  WWOX    5'  CGCGCGCGTCGGGGCCCG    39112    ACATA  T  C
                                CGC    GC CG CGGGGCCCG
                                |||    || || |||||||||
                                GCG    CG GC GCCCCGGGC
                                  _____  C  A
GAM179  YWHAH   5'  CGCACTGGCTCGCCGGCC    18193      ATA      GG
                                CGCAC   GCTCGCC  GGCC
                                |||||   |||||||  ||||
```

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                                GCGTG  CGAGCGG  CCGG
                                  AC_     __
GAM180  FLII    3'  TGGAGCAGGTGGTGTCACC   12900        CGA  T   CT
                                TGGAGTAGG  TG TGTC  CC
                                |||||||||  || ||||  ||
                                ACCTCGTCC  AC ACAG  GG
                                     ___ C   T_
GAM180  PYCR1   3'  GGAGTGGGTGAAGACCCTCCG  43125      A  C  TGTTG
                                GGAGT GG GA    TCCTCCG
                                ||||| || ||    |||||||
                                CCTCA CC CT    GGGAGGC
                                  C  A  TCT__
GAM180  SPON1   3'  TGGAGTAGGTCAAAGTCTCCG  41672        _   T  TGTC
                                TGGAGTAGG CGA GT   CTCCG
                                ||||||||| ||| ||   |||||
                                ACCTCATCC GTT CA   GAGGC
                                     A  T  ____
GAM180  LTB4R   5'  GTCAGGGCAGGGTGGTGTA   8885       CAC   TCGA
                                GTCAG  GCGG   TGGTGTA
                                |||||  ||||   |||||||
                                CAGTC  CGTC   ACCACAT
                                  C__   CC__
GAM180  STAU    3'  GCAGTGGTGATGGTGT     32696     CGC  C
                                GCA  GGT GATGGTGT
                                |||  ||| ||||||||
                                CGT  CCA CTACCACA
                                 CA_  _
GAM181  BAZ2B   3'  CATTATGTATGTGCCTTGCA  30322     C   TCCTACAC
                                CAT ATGT      GCCTTGCA
                                ||| ||||      ||||||||
                                GTA TACA      CGGAACGT
                                 A   TACA____
GAM181  DMRT2   3'  CATCATGTCCTGCTCTGC    27260       T  ACAC  C
                                CATCATGT CCT   GC TTGC
                                |||||||| |||   || ||||
                                GTAGTACA GGA   CG GACG
                                     _  ____  A
GAM181  EPM2A   3'  CATCATGTTTTTAAATTAGCTT 24968        CCTACACGC_
          GCA                   CATCATGTT       CTTGCA
                                |||||||||       ||||||
                                GTAGTACAA       GAACGT
                                     AAATTTAATC
GAM181  ESR1    3'  ATCATGTTCCTACACCC    6525            G
                                ATCATGTTCCTACAC CC
                                |||||||||||||| ||
                                TAGTACAAGGATGTG GG
                                     _
GAM181  ETV5    3'  CATCATGTCCCGTTTTGC    20845         TACAC CC
                                CATCATGTTCC    G  TTGC
                                ||||||||||    |  ||||
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                                GTAGTACAGGG    C  AACG
                                      _____ AA
GAM181  MAP3K13  3'  TCATGTTCCTGTTATTGCA   21797        ACACGCC
                                TCATGTTCCT      TTGCA
                                ||||||||||      |||||
                                AGTACAAGGA      AACGT
                                     CAAT___
GAM181  PCDHB6   3'  CATCATGTTCTTACATGAGGC  33199        C   CGCCTT
                                CATCATGTTC TACA     GC
                                |||||||||| ||||     ||
                                GTAGTACAAG ATGT     CG
                                     A   ACTC__
GAM181  SKIV2L   3'  CATCATGTTTTTACATGGGGCA 27970        CC   CGCCTT
                                CATCATGTT  TACA     GCA
                                |||||||||  ||||     |||
                                GTAGTACAA  ATGT     CGT
                                     AA   ACCC__
GAM181  BCAR1    3'  TGGCACGAGGTCCTGCAG    41943    A    CGCC
                                TGG ACGAG   GTCCTGCAG
                                ||| |||||   |||||||||
                                ACC TGCTC   CAGGACGTC
                                  G   _____
GAM181  CRHR2    3'  GGATGGGCAAATGCCTGCAGAC 12441    ACGA  CCGT
                                GGA   GCG   CCTGCAGAC
                                |||   |||   |||||||||
                                CCT   CGT   GGACGTCTG
                                  ACC_  TTAC
GAM181  DNAJB1   3'  TGGAACGAGAGGTATTGC    26036       CGCC  CC
                                TGGAACGAG   GT  TGC
                                |||||||||   ||  |||
                                ACCTTGCTC   CA  ACG
                                     TC__  TA
GAM181  GAS11    3'  TGGGTGAGGGTCCTGCAG    11224    AAC  CGCC
                                TGG   GAG   GTCCTGCAG
                                |||   |||   |||||||||
                                ACC   CTC   CAGGACGTC
                                  CA_   C___
GAM181  GCH1     3'  TGGAAGCTATGGTTCTGCAGAC 6707     ACG  GCC_  C
                                TGGA   AGC   GT CTGCAGAC
                                ||||   |||   || ||||||||
                                ACCT   TCG   CA GACGTCTG
                                  ___   ATAC  A
GAM181  LENG4    3'  TGGGACGGCCGTCCCCAG    35894    A  AGC      G
                                TGG ACG   GCCGTCCT CAG
                                ||| |||   |||||||| |||
                                ACC TGC   CGGCAGGG GTC
                                  C  ___      _
GAM181  MAL      5'  GGGACGAGCGCCGCTCAGAC  35335    A        CCTG
                                GG ACGAGCGCCGT    CAGAC
                                || ||||||||||    |||||
```

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                                CC TGCTCGCGGCG   GTCTG
                                 C         A___
GAM181  RTN2    3'  TGGGGGCAGGCGTCCTGC    24728    AACG  C  C
                                TGG   AG GC GTCCTGC
                                |||   || || |||||||
                                ACC   TC CG CAGGACG
                                  CCCG  _  _
GAM181  SEPX1   3'  TGGGAAGGGCCTCCCTGCAG  32271    AAC   C   GT
                                TGG   GAG GCC  CCTGCAG
                                |||   ||| |||  |||||||
                                ACC   TTC CGG  GGACGTC
                                  C__   C   AG
GAM181  SHANK2  3'  TGGATGGGTGCTCATGGCAGAC 29473     ACGA_ GC   CCT
                                TGGA    GC  CGT   GCAGAC
                                ||||    ||  |||   ||||||
                                ACCT    CG  GTA   CGTCTG
                                   ACCCA  A_   C__
GAM181  SLC22A2 5'  TGGGCATGATCCTGCAG    40530    AACGA   CC
                                TGG    GCG  GTCCTGCAG
                                |||    |||  |||||||||
                                ACC    CGT  TAGGACGTC
                                  ______   AC
GAM182  ACADVL  3'  CTTCGGGACAAACCAGGG    6157     G   A    GT  C
                                CTT CGG ACAG  CG GG
                                ||| ||| ||||  || ||
                                GAA GCC TGTT  GT CC
                                  _   C    TG  C
GAM182  ADCY6   3'  TTGGGGACAGATCATGG     34183    C  A      C
                                TTG GG ACAGGTCG GG
                                ||| || ||||||| ||
                                AAC CC TGTCTAGT CC
                                  _ C       A
GAM182  ADRA2A  5'  CTGGCGGAACATGAACGCGG  8635     T      _ GT
                                CT GCGGAACA G  CGCGG
                                || |||||||| |  |||||
                                GA CGCCTTGT C  GCGCC
                                 C       A TT
GAM182  AGRN    5'  CTTGTGGGCTGGCCACAG    44250     C  AACA
                                CTTG GG    GGTCGCGG
                                |||| ||    ||||||||
                                GAAC CC    CCGGTGTC
                                  A  CGA_
GAM182  AHR     5'  CCTGCGGAGCTCGGG       11547        ACA G   C
                                CTTGCGGA   G TCG GG
                                ||||||||   | ||| ||
                                GGACGCCT   C AGC CC
                                     ___ G   _
GAM182  ALDH1A3 3'  CTTGCAGAACACACAG      8678           GGT
                                CTTGCGGAACA   CGCGG
                                ||||||||||   |||||
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                                GAACGTCTTGT  GTGTC
                                        ___
GAM182  CDKN2B   3'  CCTGCGGAACCCGCGG     38544        AGG
                                CTTGCGGAAC  TCGCGG
                                ||||||||||  ||||||
                                GGACGCCTTG  GGCGCC
                                       ___
GAM182  CENTD1   5'  CTTGCGCTCGGGTCGCGGA   40140      GAACA
                                CTTGCG    GGTCGCGGA
                                ||||||    |||||||||
                                GAACGC    CCAGCGCCT
                                   GAGC_
GAM182  COL4A3   3'  CCTGCGGAGTGTGCTTGGA   36377       ACAG  C  __
                                CTTGCGGA   GT GC  GGA
                                ||||||||   || ||  |||
                                GGACGCCT   CA CG  CCT
                                     CA__  _  AA
GAM182  COL6A2   3'  TTGGGGGACACCACGGA    38452    C  A   GG
                                TTG GG ACA  TCGCGGA
                                ||| || |||  |||||||
                                AAC CC TGT  GGTGCCT
                                  C  C  __
GAM182  CYP24    5'  CTTGCTGGAGCCACGG     8944      _  ACAG
                                CTTGC GGA   GTCGCGG
                                |||||| |||   |||||||
                                GAACG CCT   CGGTGCC
                                   A  _____
GAM182  FGF23    3'  CTTGGGAACAGAGTGG     33953     C     _  CGC
                                CTTG GGAACAG GT   GG
                                |||| ||||||| ||   ||
                                GAAC CCTTGTC CA   CC
                                  _     T  ___
GAM182  HK1      5'  CTGGCGGTCGGGGTCGCGG   37916   T   AACA
                                CT GCGG   GGTCGCGG
                                || ||||   ||||||||
                                GA CGCC   CCAGCGCC
                                 C   AGCC
GAM182  ISG20    3'  CCTGCGGAACGGGCTGGA    13589        A  CGC
                                CTTGCGGAAC GGT  GGA
                                |||||||||| |||  |||
                                GGACGCCTTG CCG  CCT
                                      C  A__
GAM182  MN1      5'  CTTGCGAGGCCGCGG       14579      GAAC
                                CTTGCG   AGGTCGCGG
                                ||||||   |||||||||
                                GAACGC   TCCGGCGCC
                                      _____
GAM182  NKX2E    3'  CTCGCGGAATGGGCGG      20495        CA  TC
                                CTTGCGGAA  GG  GCGG
                                |||||||||  ||  ||||
```

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                                GAGCGCCTT  CC  CGCC
                                    A_  __
GAM182  NR2C2   5'  CTCGCGGGGCAGCGG      17671       AACA   C
                                CTTGCGG   GGT GCGG
                                |||||||   ||| ||||
                                GAGCGCC   CCG CGCC
                                   ____   T
GAM182  NRXN3   3'  CCTGCGGAAGTGGTGGA    39941        CA   CGC
                                CTTGCGGAA  GGT   GGA
                                |||||||||  |||   |||
                                GGACGCCTT  CCA   CCT
                                    CA  ___
GAM182  PA2G4   3'  CTTGCAGAACTCTGG      43418        AGG  GC
                                CTTGCGGAAC   TC  GG
                                ||||||||||   ||  ||
                                GAACGTCTTG   AG  CC
                                   ___  A_
GAM182  PATE    3'  CTTGTGAACAGGTTCGG    39640     CG      CG
                                CTTG  GAACAGGT  CGG
                                ||||  ||||||||  |||
                                GAAC  CTTGTCCA  GCC
                                  A_      A_
GAM182  PGF     5'  CTTGCGGAGTCAGG       15251        ACAG   C
                                CTTGCGGA   GTCG GG
                                ||||||||   |||| ||
                                GAACGCCT   CAGT CC
                                   ____   _
GAM182  RAD50   5'  CCTGCGGATCACGTGG     39435        A  G  CGC
                                CTTGCGGA CA GT   GG
                                ||||||||| || ||   ||
                                GGACGCCT GT CA   CC
                                    A  G  ___
GAM182  RBBP9   3'  CTTACGGAACTTAACTGGA  43138         AGGTC  _
                                CTTGCGGAAC    GC GGA
                                ||||||||||    || |||
                                GAATGCCTTG    TG CCT
                                    AAT__  A
GAM182  RNASE1  5'  TTGCTGGAGTGGCCACAGA  16344     _  ACA
                                TTGC GGA   GGTCGCGGA
                                ||||  |||   |||||||||
                                AACG CCT   CCGGTGTCT
                                  A   CA_
GAM182  SCA1    3'  CTTGCAGAAAAGACCGTGGA  7278         C  GT  C
                                CTTGCGGAA AG  CG GGA
                                |||||||||  ||  || |||
                                GAACGTCTT TC  GC CCT
                                    T  TG  A
GAM182  SLC2A4  5'  CCTGCGGAGGCCGCGG     9797         ACA
                                CTTGCGGA   GGTCGCGG
                                ||||||||   ||||||||
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                              GGACGCCT  CCGGCGCC
                                 ___
GAM182  STARD5   5' CTGCGGGGTCGCGG      36126      AACA
                              TTGCGG   GGTCGCGG
                              ||||||   ||||||||
                              GACGCC   CCAGCGCC
                                 ____
GAM182  UTY      5' CTTGCGGGGCATGGCAG    28313      AACA  C__
                              CTTGCGG   GGT  GCGG
                              |||||||   |||  ||||
                              GAACGCC   CCG  CGTC
                                 ____  TAC
GAM182  BRCA1    3' CCTGACTGGCATTTG      28625     _ CCTCCA
                              CCTG CT    GGCATTTG
                              |||| ||    ||||||||
                              GGAC GA    CCGTAAAC
                                T _______
GAM182  CHST6    3' ACCTGCCTTCCAGGCACTGATC 34673       CC       T
                              ACCTGCT  TCCAGGCATT GATC
                              |||||||  |||||||||| ||||
                              TGGACGG  AGGTCCGTGA CTAG
                                 A_       _
GAM182  CIT      5' CTGCTCCTCCAGGTCTGTGAT  43047          CATT
                              CTGCTCCTCCAGG   TGAT
                              ||||||||||||   ||||
                              GACGAGGAGGTCC   ACTA
                                    AGAC
GAM182  CLCN4    5' CCTGCTCCTTTGGGTTGA    12282       CCA  CAT
                              CCTGCTCCT  GG  TTGA
                              |||||||||  ||  ||||
                              GGACGAGGA  CC  AACT
                                   AA_  C__
GAM182  DXS1283E 3' TGTTCCTCCAGTCCTGATC   43357   C     GCAT
                              TG TCCTCCAG   TTGATC
                              || ||||||||   ||||||
                              AC AGGAGGTC   GACTAG
                               A      AG__
GAM182  FGFR1    3' CTGGTACCAGGCATTTG     31938    CTCCT
                              CTG    CCAGGCATTTG
                              |||    ||||||||||
                              GAC    GGTCCGTAAAC
                                CAT__
GAM182  HCFC1    3' CTTTTCCTCCAGAAAGAT    43390    GC       CATTT
                              CT  TCCTCCAGG    GAT
                              ||  |||||||||    |||
                              GA  AGGAGGTCT    CTA
                               AA       TT___
GAM182  HDAC7A   3' CTGCTCCACCAGGGCATC    32469       T    _
                              CTGCTCC CCAGG CATT
                              ||||||| ||||| ||||
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                                GACGAGG GGTCC GTAG
                                    T    C
GAM182  HSD17B3  3' CTGCTCCTCTGGTCCTC    6809        CA  CA
                                CTGCTCCTC  GG  TTT
                                |||||||||  ||  |||
                                GACGAGGAG  CC  GAG
                                     A_  AG
GAM182  IL2RB    3' CCTCTTTCTCCAGGCGCCCTG 9381     G  C_      A_
                                CCT CT  CTCCAGGC  TTTG
                                ||| ||  ||||||||  ||||
                                GGA GA  GAGGTCCG  GGAC
                                  _ AA       CG
GAM182  NFATC1   3' CTTCTCCTCCAGGTGA     26074    G        CATT
                                CT CTCCTCCAGG    TGA
                                || ||||||||||    |||
                                GA GAGGAGGTCC    ACT
                                 A        _____
GAM182  NR0B2    3' TGCCCCTCCAGGAGCATT    35033          __
                                TGCTCCTCCAG  GCATT
                                ||||||||||  |||||
                                ACGGGGAGGTC  CGTAA
                                      CT
GAM182  ZNF38    5' CTGCTCCTTGGTGTGGATC   45362        CCA  CATTT
                                CTGCTCCT   GG    GATC
                                ||||||||   ||    ||||
                                GACGAGGA   CC    CTAG
                                    A__  ACAC_
GAM183  APG5L    3' GCTGTACTGGCTATTCTTT   22132    C   GCG  G
                                GC GTA   GG TGTTTTTT
                                || |||   || ||||||||
                                CG CAT   CC ATAAGAAA
                                 A  GA_  G
GAM183  FLRT2    5' GCCTGGCTAATTTTTTAA    29851     GTA  GGGGT
                                GCC   GC    GTTTTTTAA
                                |||   ||    |||||||||
                                CGG   CG    TAAAAAATT
                                  AC_  AT___
GAM183  TM7SF3   3' GCCTGGCTAATTTTTTAA    40655     GTA  GGGGT
                                GCC   GC    GTTTTTTAA
                                |||   ||    |||||||||
                                CGG   CG    TAAAAAATT
                                  AC_  AT___
GAM183  ANK1     3' GCATAGTATTTATTGTTTTTC  33862    TAT    C  C
                                GC   GTAT TA TGTTTTTC
                                ||   |||| || ||||||||
                                CG   CATA AT ACAAAAAG
                                 TAT    A  A
GAM183  HADHB    3' TATGTATCTAAACATTTTT    6769          CT_
                                TATGTATCTA   GTTTTT
                                ||||||||||   ||||||
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                                ATACATAGAT   TAAAAA
                                     TTG
GAM183  IMPA1    3'  TACTTTATGTATCTATTGT   24392     GC        C
                                TAC  TATGTATCTA TGT
                                |||  |||||||||| |||
                                ATG  ATACATAGAT ACA
                                  AA         A
GAM183  LBR      3'  GCTATGTATTTACATTTTC   40429         C   T
                                GCTATGTAT TAC GTTTTT
                                ||||||||| ||| ||||||
                                CGATACATA ATG TAAAAG
                                     A  _
GAM184  EGR3     3'  CGTGCGTGCGGCGGGCAGCAA  40544     T  AC        C
                                CGT GC  GCGGCGGGTA CGA
                                ||| ||  |||||||||| |||
                                GCA CG  CGCCGCCCGT GTT
                                  _ CA        C
GAM184  L1CAM    3'  GTTGTGTGGTGGGTACCGAA   35805     CACGC  C
                                GTTG    GG GGGTACCGAA
                                ||||    || ||||||||||
                                CAAC    CC CCCATGGCTT
                                  ACA__  A
GAM184  ADAMTS13 3'  ACGCGGCACTGCTCGTTGGCGC 40026         ACG  CAC__
                                ACGCGGCA   GC    GGCGC
                                ||||||||   ||    |||||
                                TGCGCCGT   CG    CCGCG
                                     GA_  AGCAA
GAM184  AXIN1    5'  GCGGCAGCGGCCACGATCGC   41380       A       _
                                GCGGCA CGGCCACGG CGC
                                |||||| ||||||||| |||
                                CGCCGT GCCGGTGCT GCG
                                   C        A
GAM184  B3GAT1   5'  CGGGCAACGGCCCCTACGC    33002    C        ACG
                                CG GGCAACGGCC   GCGC
                                || ||||||||||   ||||
                                GC CCGTTGCCGG   TGCG
                                 _         GGA
GAM184  BAZ1B    5'  GCGGAACGCCACGGCGC     37087     C   G
                                GCGG AACG CCACGGCGC
                                |||| |||| |||||||||
                                CGCC TTGC GGTGCCGCG
                                  _   _
GAM184  BCL7B    3'  ACGCGGCGCGGCCAGAAC    11800       AA     CG
                                ACGCGGC  CGGCCA  GC
                                |||||||  ||||||  ||
                                TGCGCCG  GCCGGT  TG
                                   C_     CT
GAM184  COL6A2   3'  CGCCGCCAGGCCACGGTGC   38438     G  AAC      C
                                CGC GC   GGCCACGG GC
                                ||| ||   |||||||| ||
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                                GCG CG   CCGGTGCC CG
                                  G  GT_      A
GAM184  CSNK1G2  3'  ACGCGGCAGGGCTGAGGGC   10604        AC   CAC_
                                ACGCGGCA  GGC   GGC
                                ||||||||  |||   |||
                                TGCGCCGT  CCG   CCG
                                    C_   ACTC
GAM184  EGFL4    5'  CGCAGTGGCCACGGCG     41565      CAAC
                                CGCGG   GGCCACGGCG
                                |||||   ||||||||||
                                GCGTC   CCGGTGCCGC
                                  A___
GAM184  FGFR4    5'  ACGCGGCAGGGTCCGC     35651        AC  _  ACG
                                ACGCGGCA  GG CC   GC
                                ||||||||  || ||   ||
                                TGCGCCGT  CC GG   CG
                                    C_  A  ___
GAM184  GABRB2   5'  GCGCATGGCCACGGCG     34869     G  AC
                                GCG CA  GGCCACGGCG
                                ||| ||  ||||||||||
                                CGC GT  CCGGTGCCGC
                                  _  A_
GAM184  GPC1     5'  CGGCGGCGGCGGCGGCGC    13241      AA   CA
                                CGGC  CGGC  CGGCGC
                                ||||  ||||  ||||||
                                GCCG  GCCG  GCCGCG
                                  CC    CC
GAM184  HADHSC   3'  ACGCAGCAACAGTGAGCATGGT 23716           C___  C  C
           GC                     ACGCGGCAACGG    CA GG GC
                                ||||||||||||    || || ||
                                TGCGTCGTTGTC    GT CC CG
                                      ACTC  A  A
GAM184  HDAC4    5'  CGGGACGCGGCCACGGCGC   25761    C   AA
                                CG GGC  CGGCCACGGCGC
                                || |||  ||||||||||||
                                GC CTG  GCCGGTGCCGCG
                                 C   C_
GAM184  HDAC4    5'  ACCGGCGGGTCCCACGGCGC  25741    G   AAC  __
                                AC CGGC   GG  CCACGGCGC
                                || ||||   ||  |||||||||
                                TG GCCG   CC  GGTGCCGCG
                                  _    C__  AG
GAM184  HYAL3    5'  GCGGCACGCCACGGCG      18647       A  G
                                GCGGCA CG CCACGGCG
                                |||||| || ||||||||
                                CGCCGT GC GGTGCCGC
                                    _  _
GAM184  LMO4     5'  GCGGCGGCGGACGGTGC     27654      AA   CC   C
                                GCGGC  CGG  ACGG GC
                                |||||  |||  |||| ||
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                                CGCCG  GCC  TGCC CG
                                   CC   __   A
GAM184  MECP2   3'  GCGGCAACGGCCTCCTCGC   22591          ACGG
                                GCGGCAACGGCC   CGC
                                ||||||||||||   |||
                                CGCCGTTGCCGG   GCG
                                      AGGA
GAM184  MTR     5'  CGCGGCAACTGCTGGAGC   7013         G  CAC
                                CGCGGCAAC GC   GGC
                                ||||||||| ||   |||
                                GCGCCGTTG CG   TCG
                                     A  ACC
GAM184  NAV2    5'  GGGGACTGGCCACGGCGC   41150    CA  _
                                GG  AC GGCCACGGCGC
                                ||  || ||||||||||
                                CC  TG CCGGTGCCGCG
                                 CC  A
GAM184  NHP2L1  3'  ACGTGGCAGAGGCCACAG   22677    C   AC
                                ACG GGCA  GGCCACGG
                                ||| ||||  ||||||||
                                TGC CCGT  CCGGTGTC
                                  A   CT
GAM184  NRIP1   5'  GCGGCGCTCACGGCG      40963      AACG  _
                                GCGGC   GC CACGGCG
                                |||||   || |||||||
                                CGCCG   CG GTGCCGC
                                   ____  A
GAM184  PTMS    5'  ACACGGCAGCGGCGGCCGC   15879        A   CAC  _
                                ACGCGGCA CGGC   GGC GC
                                |||||||| ||||   ||| ||
                                TGTGCCGT GCCG   CCG CG
                                     C   ___   G
GAM184  SGT     3'  GCTGGGACCACGGCG      16619    _  CAAC
                                GC GG   GGCCACGGCG
                                || ||   ||||||||||
                                CG CC   CTGGTGCCGC
                                 A  ____
GAM184  SYN2    3'  ACGCAGCAACGGCACCAG   39457          CA
                                ACGCGGCAACGGC  CGG
                                ||||||||||||  |||
                                TGCGTCGTTGCCG  GTC
                                      TG
GAM184  ZNF14   5'  ACCTGCAGGTCACGGCGC   34294   G_  AC  C
                                GC  GCA  GG CACGGCGC
                                ||  |||  || ||||||||
                                TG  CGT  CC GTGCCGCG
                                 GA  __  A
GAM185  GIPR    3'  GCCTATGCTATCGCTTCC   6724          _   GCG
                                GCCTATGCT TCGC   TC
                                |||||||| ||||   ||
```

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                                CGGATACGA AGCG   GG
                                     T    AA_
GAM185  MAP3K14  3'  GCTATGCTCCTACAGTGTCAC  19541    C       _   C_
                                GC TATGCTTC GCG  GTCAC
                                || |||||||| |||  |||||
                                CG ATACGAGG TGT  CAGTG
                                 _       A   CA
GAM185  GJA1     3'  AACTGGTAGATGTCTTCAAC   6728     G      C
                                AA TGGTAGA GTCTTCGGC
                                || ||||||| |||||||||
                                TT ACCATCT CAGAAGTTG
                                 G      A
GAM186  CMKLR1   5'  TCCTGAGCTCCCTGCT      19828     A       ACGATCC
                                TCC TGAGCTCC      GCT
                                ||| ||||||||      |||
                                AGG ACTCGAGG      CGA
                                 _       GA_____
GAM186  IGSF3    3'  TCCGTGGCCAACATCCGCTGG  11366     A  A   CC  G
                                TCC TG GCT  AC ATCCGCTGG
                                ||| || |||  || |||||||||
                                AGG AC CGG  TG TAGGCGACC
                                  C  _   T_  _
GAM186  IL21R    3'  TCCATGAGTGCCACGGGGGGTG 34757        CT    ATCCGC
           G                     TCCATGAG  CCACG     TGG
                                ||||||||  |||||     |||
                                AGGTACTC  GGTGC     ACC
                                     AC    CCCCC_
GAM186  TARBP2   3'  TCCATGAGTCCAGCT      39537        C   CGATCC
                                TCCATGAG TCCA     GCT
                                |||||||| ||||     |||
                                AGGTACTC AGGT     CGA
                                    _   _______
GAM186  ATP8A2   3'  GGACTTCTGTGGTCGT      45259        TGGC  C
                                GGACTTCT    GT GGTCGT
                                ||||||||    || ||||||
                                CCTGAAGA    CA CCAGCA
                                    _____  _
GAM186  FMNL     5'  ATGGGCTTCTTGGCCTTC    25293      A       G_
                                ATGG CTTCTTGGC  TC
                                |||| |||||||||  ||
                                TACC GAAGAACCG  AG
                                  C        GA
GAM187  B3GALT3  3'  AATTTCTTTAGCAAAAACCT  37665           CATTT
                                AATTTCTTTAGCA    CCT
                                ||||||||||||||    |||
                                TTAAAGAAATCGT    GGA
                                        TTTT_
GAM187  BCL11B   3'  TTTCTTACATTTCCT      39765       TAGC
                                TTTCTT    ACATTTCCT
                                ||||||    |||||||||
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                                AAAGAA   TGTAAAGGA
                                     ____
GAM187  C8orf1   5'  TTTCTTTGGGCATTTCCT   20275       AGCA
                                TTTCTTT   CATTTCCT
                                |||||||   ||||||||
                                AAAGAAA   GTAAAGGA
                                    CCC_
GAM187  CACNG2   3'  TTTCCCACATTTCC       25881      TTAG
                                TTTCT   CACATTTCC
                                |||||   |||||||||
                                AAAGG   GTGTAAAGG
                                     _____
GAM187  CASP2    3'  CAGTTTCTCTTGCATTTCCT  37397    A     A  CA
                                CA TTTCTTT GCA  TTTCCT
                                || ||||||| |||  ||||||
                                GT AAAGAGA CGT  AAAGGA
                                 C      A  __
GAM187  LPHH1    3'  AATTTCTTTAGCCATTT     29384          A
                                AATTTCTTTAGC CATTT
                                |||||||||||| |||||
                                TTAAAGAAATCG GTAAA
                                          _
GAM187  MTMR1    5'  AATCTCTGGACACATTTTCT  43150       TTA      C
                                AATTTCT   GCACATTT CT
                                |||||||   |||||||| ||
                                TTAGAGA   TGTGTAAA GA
                                    CC_       A
GAM187  MYH4     3'  ATTTCTTTGGTCACATTTTCT  32753       AG_     C
                                ATTTCTTT   CACATTT CT
                                ||||||||   ||||||| ||
                                TAAAGAAA   GTGTAAA GA
                                    CCA      A
GAM187  PDE4D    3'  CAATTTCTGTGGCTCATCCT  43891        TTA  A  TT
                                CAATTTCT   GC CA  TCCT
                                ||||||||   || ||  ||||
                                GTTAAAGA   CG GT  AGGA
                                    CAC  A  __
GAM187  SMARCA1  3'  TAAATTTCTTATAGACATTTC  40051   C      _  C
                                A AATTTCTT TAG ACATTTC
                                | |||||||| ||| |||||||
                                A TTAAAGAA ATC TGTAAAG
                                 T      T  _
GAM187  SORT1    3'  ATTTCTTTAGTGTAGGTCCT  16439        CACATT
                                ATTTCTTTAG     TCCT
                                ||||||||||     ||||
                                TAAAGAAATC     AGGA
                                      ACATCC
GAM187  TRHR     3'  CAATTTCTTTGTCATCCATTTT 17678        AG __    C
            CT                   CAATTTCTTT  CA  CATTT CT
                                ||||||||||  ||  ||||| ||
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                                GTTAAAGAAA  GT  GTAAA GA
                                     CA  AG    A
GAM187  ZNF6     5'  CAATTTCTTTTTATTTTTCCT  35090         AGCACA
                                CAATTTCTTT     TTTCCT
                                ||||||||||     ||||||
                                GTTAAAGAAA     AAAGGA
                                     AATAA_
GAM188  ABCC3    3'  AGCAGCTTCTCTGGTTG     33412         GCAT
                                AGCAGCTTCT    GTTG
                                ||||||||||    ||||
                                TCGTCGAAGA    CAAC
                                     GAC_
GAM188  AKAP13   3'  ACAGCTTCTGCCTGGCC     40349          A  TT
                                GCAGCTTCTGC TG  GCC
                                |||||||||| ||  |||
                                TGTCGAAGACG AC  CGG
                                      G  __
GAM188  AKAP13   5'  ACAGCTTCTGCCTGGCC     28466          A  TT
                                GCAGCTTCTGC TG  GCC
                                |||||||||| ||  |||
                                TGTCGAAGACG AC  CGG
                                      G  __
GAM188  AP1B1    3'  ACAGCTTCTGTGGCTGC     10031         CAT
                                GCAGCTTCTG   GTTGC
                                |||||||||    |||||
                                TGTCGAAGAC   CGACG
                                     AC_
GAM188  APOC3    3'  AGCAGCTTCTTGTCC       6213          GCA   TGC
                                AGCAGCTTCT   TGT   CC
                                |||||||||    |||   ||
                                TCGTCGAAGA   ACA   GG
                                     ___   ___
GAM188  B3GALT5  5'  CAGCAGATTCTGCACTCCA   37679       C       GTTGC
                                CAGCAG TTCTGCAT    CCA
                                |||||| ||||||||    |||
                                GTCGTC AAGACGTG    GGT
                                   T       A____
GAM188  BLTR2    5'  GCAGTGTGTATGTTGCC     33366      CTTC  C
                                GCAG    TG ATGTTGCC
                                ||||    || ||||||||
                                CGTC    AC TACAACGG
                                  AC__  A
GAM188  CBFA2T2  3'  CAGAGTTTTGCTCTGTTGCCCA 22970     C  C  C   A_
          G                      CAG AG TT TGC  TGTTGCCCAG
                                 ||| || || |||  ||||||||||
                                 GTC TC AA ACG  ACAACGGGTC
                                   _  _  A   AG
GAM188  CCR9     3'  CAGTGCTTCTGTGTCCCC    36296     CA      CA    G
                                CAG  GCTTCTG  TGTT CCC
                                |||  |||||||  |||| |||
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                                GTC  CGAAGAC  ACAG GGG
                                  A_     __   _
GAM188  CDC2L2   5'  GCTGGCTTCTGCGCACGCGCC  37941    A_      __   T
                                GC  GCTTCTGC  ATGT GCC
                                ||  ||||||||  |||| |||
                                CG  CGAAGACG  TGCG CGG
                                  AC       CG   _
GAM188  CHRNA5   5'  AGCAGCTTCTGGCGGGCT    40745          _ AT
                                AGCAGCTTCTG C  GTT
                                |||||||||||  |  |||
                                TCGTCGAAGAC G  CGA
                                       C CC
GAM188  CHST5    5'  GCTGCTTCTGCTGCAGCCTCAG 29078    A      A   T   _
                                GC GCTTCTGC TGT GCC CAG
                                || |||||||| ||| ||| |||
                                CG CGAAGACG ACG CGG GTC
                                  A       _   T   A
GAM188  CLTCL1   3'  CAGCAACTTCTGGGCCAGCTCA 41881           CAT   _  C
             G                   CAGCAGCTTCTG   GTT GC CAG
                                ||||||||||||   ||| || |||
                                GTCGTTGAAGAC   CGG CG GTC
                                       C__   T  A
GAM188  CPT2     3'  AGCTTTTCATCTGCCCAG    6430       CTG   G
                                AGCTT   CAT TTGCCCAG
                                |||||   ||| ||||||||
                                TCGAA   GTA GACGGGTC
                                  AA_   _
GAM188  DGSI     3'  CAACAGCTTCTGGCCC      35530           CATGTT
                                CAGCAGCTTCTG     GCCC
                                ||||||||||||     ||||
                                GTTGTCGAAGAC     CGGG
                                          _______
GAM188  EHHADH   3'  CAGGGTTTTGCTATGTTGCCCA 12682     CTTC_   _
             G                   CAG     TGC ATGTTGCCCAG
                                |||     ||| ||||||||||||
                                GTC     ACG TACAACGGGTC
                                  CCAAA   A
GAM188  GALNT7   3'  CAGCAGCTTCTGATGTT     38351           C
                                CAGCAGCTTCTG ATGTT
                                |||||||||||| |||||
                                GTCGTCGAAGAC TACAA
                                          _
GAM188  GNPI     3'  GCAGTGTCTGTTGCCC      24185      CTTC  CA
                                GCAG    TG  TGTTGCCC
                                ||||    ||  ||||||||
                                CGTC    AC  ACAACGGG
                                  _____ AG
GAM188  GP1BB    3'  GCAGGCCCGTGTTGCCCAG   7625       CT    CA
                                GCAG  TCTG  TGTTGCCCAG
                                ||||  ||||  ||||||||||
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                                CGTC  GGGC  ACAACGGGTC
                                  C_   __
GAM188  HS3ST3B1  5'  GCGGCTCTTGACATGTTGCCC  25796    A   TC  _
                                GC GCT  TG CATGTTGCCC
                                || |||  || ||||||||||
                                CG CGA  AC GTACAACGGG
                                 C   GA  T
GAM188  IFRD1    3'  CAGGGTCTCGCTATGTTGCCCA 41106     CT  _ _
           G                     CAG  TCT GC ATGTTGCCCAG
                                ||| ||| || ||||||||||||
                                GTC  AGA CG TACAACGGGTC
                                  CC   G  A
GAM188  ITCH     3'  CAGGGTCTCCCTATGTTGCCCA 36453     CAG    GC
           G                     CAG   CTTCT  ATGTTGCCCAG
                                |||   |||||  ||||||||||
                                GTC   GAGGG  TACAACGGGTC
                                  CCA    A_
GAM188  KCNK5    3'  GCGGCCTCTGCAAACGGC    19036    A       TG T
                                GC GCTTCTGCA  T GC
                                || |||||||||  | ||
                                CG CGGAGACGT  G CG
                                 C        TT C
GAM188  LZTS1    3'  GCTTCTGCTGTCCA       34270        A   TGC
                                GCTTCTGC TGT   CCA
                                |||||||| |||   |||
                                CGAAGACG ACA   GGT
                                     _  ___
GAM188  MAP3K1   3'  ACAGTTTCTGCACTAGTT    42698     C      __
                                GCAG TTCTGCAT  GTT
                                |||| ||||||||  |||
                                TGTC AAGACGTG  CAA
                                  A       AT
GAM188  MECP2    3'  AGCAGCTTCCGCCATCCA    22570          ATGTTGC
                                AGCAGCTTCTGC      CCA
                                ||||||||||||      |||
                                TCGTCGAAGGCG      GGT
                                      GTA____
GAM188  MOG      3'  AGCAGGCATGTTGCCCA     14607      CTTCT
                                AGCAG    GCATGTTGCCCA
                                |||||    ||||||||||||
                                TCGTC    CGTACAACGGGT
                                     _____
GAM188  OPA3     3'  TCTTGCTCTGTTGCCCAG    36072    _ A_
                                TCT GC  TGTTGCCCAG
                                ||| ||  ||||||||||
                                AGA CG  ACAACGGGTC
                                  A  AG
GAM188  PC       3'  ACAGCTTCTGTTGAAGGC    9553          CA  TT_
                                GCAGCTTCTG  TG   GC
                                |||||||||  ||   ||
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                                TGTCGAAGAC  AC   CG
                                      A_  TTC
GAM188  POLL     3'  GCAGCTTCTGTCCCCACCCAG  29980         CATG TG
                                GCAGCTTCTG    T  CCCAG
                                ||||||||||    |  |||||
                                CGTCGAAGAC    G  GGGTC
                                      AGG_  GT
GAM188  PPP1R12B 3'  CAGCAGCTTCAGACCAGCC    36969         T_  ATGTT
                                CAGCAGCTTC  GC    GCC
                                ||||||||||  ||    |||
                                GTCGTCGAAG  TG    CGG
                                      TC  GT___
GAM188  RFX2     5'  CAGCGGCTGCTGCGTGTTG    8448      A  T   A
                                CAGC GCT CTGC TGTTG
                                |||| ||| |||| |||||
                                GTCG CGA GACG ACAAC
                                  C   C   C
GAM188  SLC7A5   3'  CAGTAGCTCTGTTTGCCCA    18543     C   T   CATG
                                CAG AGCT CTG    TTGCCCA
                                ||| |||| |||    |||||||
                                GTC TCGA GAC    AACGGGT
                                  A   _   A___
GAM188  SMARCD2  3'  CAGCAGCCTTTGGTT       16911         C  CAT
                                CAGCAGCTT TG   GTT
                                |||||||| ||   |||
                                GTCGTCGGA AC   CAA
                                      A  ___
GAM188  UVRAG    3'  CAGAGCTTCTGCCCC       17908     C       ATGTTG
                                CAG AGCTTCTGC     CCC
                                ||| |||||||||     |||
                                GTC TCGAAGACG     GGG
                                  _       _______
GAM188  WNT3A    3'  CAGCAGCTCTGGGCAGCC    37537         T   CAT  T
                                CAGCAGCT CTG   GT GCC
                                |||||||| |||   || |||
                                GTCGTCGA GAC   CG CGG
                                      _   C__  T
GAM188  WW45     3'  GCTTCACCATGTTGCCCAG   34824      TG
                                GCTTC  CATGTTGCCCAG
                                |||||  ||||||||||||
                                CGAAG  GTACAACGGGTC
                                   TG
GAM188  YWHAG    3'  ACAGCTTCTGCACCC       29783          ATGTT
                                GCAGCTTCTGC    GCCC
                                ||||||||||    ||||
                                TGTCGAAGACG    TGGG
                                              _____
GAM188  ADD1     5'  GACTGGAGAGGCCTCGG     30520     C      T  GGCC
                                GGC GGAGAGGC CT    CGG
                                ||| ||||||| ||    |||
```

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                                CTG CCTCTCCG GA   GCC
                                  A      _ _____
GAM188  ARHGAP6  5' AGGCGGGGCTGGCCCG     30207     C  AGA   CT
                                AGGC GG   GGCT  GGCCCG
                                |||| ||   ||||  ||||||
                                TCCG CC   CCGA  CCGGGC
                                  _ ____   __
GAM188  B4GALT6  5' GACTGGGGGCTAGGGGCCCGGG 40849    C  AGA   CT_
                                GGC GG   GGCT   GGCCCGGG
                                ||| ||   ||||   ||||||||
                                CTG CC   CCGA   CCGGGCCC
                                  A  C__    TCC
GAM188  BACH2    3' GGCTGGAGTGGCCCTCGG    34794    C   A    GGCC
                                GGC GGAG GGCTCT   CGG
                                ||| |||| ||||||   |||
                                CCG CCTC CCGGGA   GCC
                                  A   A    _____
GAM188  BRF1     3' AGGCCTGGGGAGGCTCTCGGG  11326      _ A      GGCC
                                AGGCC GG GAGGCTCT   CGGG
                                ||||| || ||||||||   ||||
                                TCCGG CC CTCCGAGA   GCCC
                                   A  C      _____
GAM188  CACNG7   3' AGGTTGGGGAGCTCTGG    36686    CC  A   G
                                AGG  GG GAG CTCTGG
                                |||  || ||| ||||||
                                TCC  CC CTC GAGACC
                                  AA  C  _
GAM188  CENTD2   5' AGGCTGGGGAGGCCCCTGG   31588     C  A     _
                                AGGC GG GAGGCTC TGG
                                |||| || ||||||| |||
                                TCCG CC CTCCGGG ACC
                                  A  C      G
GAM188  CNTFR    3' GGCTGGGGGGCGGCAGGCCCGG 12303    C  AGA   TCT_
           G                     GGC GG   GGC    GGCCCGGG
                                ||| ||   |||    ||||||||
                                CCG CC   CCG    CCGGGCCC
                                  A  CC_   CCGT
GAM188  CSK      3' GGCCGGAGGGGTGCAGGCTGGG 20465        A  CTCT   CC
                                GGCCGGAG GG   GGC  GGG
                                |||||||| ||    |||  |||
                                CCGGCCTC CC    CCG  CCC
                                    C  ACGT   A_
GAM188  EEF1A2   3' GGCGGGGGCCCGGGCCCGGG  41520    C  AGA    T
                                GGC GG   GGCTC GGCCCGGG
                                ||| ||   ||||| ||||||||
                                CCG CC   CCGGG CCGGGCCC
                                  C  ___    C
GAM188  EGLN3    5' AGGCGCGGGGAGCGTGGCCCGG 35204     _  A   G TC
           G                     AGGC CGG GAG C  TGGCCCGGG
                                |||| ||| ||| |  |||||||||
```

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                                TCCG GCC CTC G  ACCGGGCCC
                                  C   C   _ C_
GAM188  FANCC    3'  GCCGGAGGCCCGGGCTTGGG  43276      GA    T   CC
                                GCCGGA  GGCTC GGC  GGG
                                ||||||  ||||| |||  |||
                                CGGCCT  CCGGG CCG  CCC
                                   __    C   AA
GAM188  FHIT     5'  GGCCGGAGCGCCGCCTGG    12873        AG   CTG   C
                                GGCCGGAG  GCT   GCC GG
                                ||||||||  |||   ||| ||
                                CCGGCCTC  CGG   CGG CC
                                    G_  ___   A
GAM188  G6PT1    5'  AGCCTGGGGAGGCTCCAAGGG  11158      _ A      TG CCC
                                GGCC GG GAGGCTC  G   GGG
                                |||| || |||||||  |   |||
                                TCGG CC CTCCGAG  T   CCC
                                  A  C      GT ___
GAM188  GAL      5'  GGTCGGGTGGGCTCTGGCGGCC 45054    C   AGA       __ _
           TGGG                   GG CGG   GGCTCTGGC  CC GGG
                                || |||   |||||||||  || |||
                                CC GCC   CCGAGACCG  GG CCC
                                 A  CAC       CC  A
GAM188  HCN4     5'  GGCCGGAGAGGCTCTGCGG   24227             GCC
                                GGCCGGAGAGGCTCTG   CGG
                                ||||||||||||||||   |||
                                CCGGCCTCTCCGAGAC   GCC
                                                  ___
GAM188  HR       5'  GGCTGGAGAGGCGCCCAGG   32929     C       TCTG
                                GGC GGAGAGGC    GCCCGGG
                                ||| ||||||||    |||||||
                                CCG CCTCTCCG    CGGGTCC
                                  A       _____
GAM188  HSPG2    3'  GGCTGGGGCGTGGCCCGGG   24366     C  AGA   TC
                                GGC GG   GGC  TGGCCCGGG
                                ||| ||   |||  |||||||||
                                CCG CC   CCG  ACCGGGCCC
                                  A  ___   C_
GAM188  IGHMBP2  3'  AGGCCGGGAGGCTCTGG     13489        A
                                AGGCCGG GAGGCTCTGG
                                ||||||| ||||||||||
                                TCCGGCC CTCCGAGACC
                                   _
GAM188  IGSF8    3'  AGGCCAGAGGGAGGGGCTTGGG 38080          A  CTCT   CC
                                AGGCCGGAG GG    GGC  GGG
                                ||||||||| ||    |||  |||
                                TCCGGTCTC CC    CCG  CCC
                                     _ TCC_   AA
GAM188  IKBKB    5'  GGCTGGGGCGGCCAAACCCGGG 41808     C  AGA    CT
                                GGC GG   GGCT  GGCCCGGG
                                ||| ||   ||||  ||||||||
```

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                                CCG CC   CCGG  TTGGGCCC
                                  A  CCG    T_
GAM188  INHBB    5'  GGCCCGAGGGGCGCGCCGGG   13560      G   A   TCTG  _
                                GGCC GAG GGC    GC CCGGG
                                |||| ||| |||    || |||||
                                CCGG CTC CCG    CG GGCCC
                                  G   C   ____  C
GAM188  INPPL1   5'  AGGCTGGGGCCGGGCCCGG    11460      C  AGA    CT
                                AGGC GG   GGCT  GGCCCGG
                                |||| ||   ||||  |||||||
                                TCCG CC   CCGG  CCGGGCC
                                  A  ___    C_
GAM188  KCNQ4    5'  GGCTGGGGGCGCCGGGGCCCGG 21733     C  AGA   T  __
            G                    GGC GG   GGC CT  GGCCCGGG
                                ||| ||   ||| ||  ||||||||
                                CCG CC   CCG GG  CCGGGCCC
                                  A  C__   C  CC
GAM188  LAMB2    5'  AGGCCGGAGCGGATTCTGG    14071         A  C_
                                AGGCCGGAG GG  TCTGG
                                |||||||||  ||  |||||
                                TCCGGCCTC CC  AGACC
                                     G  TA
GAM188  LNK      5'  GGCGGAGGCGGTGGCCCGGG   24205     CGGA    TC
                                GGC   GAGGC  TGGCCCGGG
                                |||   |||||  |||||||||
                                CCG   CTCCG  ACCGGGCCC
                                  C___    CC
GAM188  MADH7    3'  GGCAGGAGAGACACCGCTTGGG 25367     C       T   G CC
                                GGC GGAGAGGC CTG C  GGG
                                ||| ||||||| ||| |  |||
                                CCG CCTCTCTG GGC G  CCC
                                  T       T   _ AA
GAM188  MIC2     5'  GGCCGGGTGGGGCGAAGCCCGG 14505       AGA_   TCT
            G                    GGCCGG   GGC   GGCCCGGG
                                ||||||   |||   ||||||||
                                CCGGCC   CCG   TCGGGCCC
                                   CACC   CT_
GAM188  MMP14    3'  AGGCTGCGGGGAGGGGGCTCGG 22631      __   A   CTCT   C
            G                    AGGC  CGG GAGG   GGC CGGG
                                |||| ||| ||||   ||| ||||
                                TCCG  GCC CTCC   CCG GCCC
                                  AC   C   C___   A
GAM188  NTSR1    3'  GGAGTTGGGGACAGGCCCGGG  14884      A__  CTCT
                                GGAG   GG   GGCCCGGG
                                ||||   ||   ||||||||
                                CCTC   CC   CCGGGCCC
                                  AAC  CTGT
GAM188  PACE     3'  AGGCCAGAGAGGCCGGCTGGG  15029           CT   CC
                                AGGCCGGAGAGGCT  GGC  GGG
                                ||||||||||||||  |||  |||
```

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                                TCCGGTCTCTCCGG  CCG  CCC
                                      __   A_
GAM188  PACE4    5'  GGCCGAGAGCCGTCCGG     15054      G   GCT   GC
                                GGCCG AGAG   CTG  CCGG
                                ||||| ||||   |||  ||||
                                CCGGC TCTC   GGC  GGCC
                                  _   ___   A_
GAM188  PATE     3'  GGTGGGAGAGGCATCTGG     39643     CC      _
                                GG  GGAGAGGC TCTGG
                                ||  |||||||| |||||
                                CC  CCTCTCCG AGACC
                                 AC       T
GAM188  PAX2     3'  GGCTGGGGGCGGTGGGCCCGGG 19611     C  AGA   TCT_
                                GGC GG   GGC    GGCCCGGG
                                ||| ||   |||    ||||||||
                                CCG CC   CCG    CCGGGCCC
                                  A  C__   CCAC
GAM188  RAD23A   3'  AGACTGGGGAGGGGGCCTTGGG 22791     C  A   CTCT   C_
                                AGGC GG GAGG    GGCC  GGG
                                |||| || ||||    ||||  |||
                                TCTG CC CTCC    CCGG  CCC
                                  A  C    C___    AA
GAM188  RCN2     5'  AGGCTGGCGGGGGCCCGG     16210      C  AGA  CTCT
                                AGGC GG   GG    GGCCCGG
                                |||| ||   ||    |||||||
                                TCCG CC   CC    CCGGGCC
                                  A  GC_  _____
GAM188  SPOCK    3'  GGCCAGAGAGGCTTGCTTGGG  41736           CTG  CC
                                GGCCGGAGAGGCT   GC  GGG
                                ||||||||||||   ||  |||
                                CCGGTCTCTCCGA   CG  CCC
                                       A__  AA
GAM188  THRA     5'  GGCCGGTGGGGCCCG       17520       AGA  CTCT
                                GGCCGG   GG   GGCCCG
                                ||||||   ||   ||||||
                                CCGGCC   CC   CCGGGC
                                   A__  _____
GAM188  TRPV4    3'  AGGTGGAGGGGCTCTGG     41344     CC   A
                                AGG  GGAG GGCTCTGG
                                |||  |||| ||||||||
                                TCC  CCTC CCGAGACC
                                  A_   C
GAM188  VGF      3'  AGGCTGGAGGGGCTCGTGG   17983      C   A   _
                                AGGC GGAG GGCTC TGG
                                |||| |||| ||||| |||
                                TCCG CCTC CCGAG ACC
                                  A   C    C
GAM188  ZNF144   5'  AGGCTGGAGGGCTGCAGTGGG  28336     C   A   C  CCC
                                AGGC GGAG GGCT TGG   GGG
                                |||| |||| |||| |||   |||
```

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                                TCCG CCTC CCGA GTC   CCC
                                  A   _   C   A__
GAM189  CD63    5'  TGGCTGCGCGTTCCTCTCCCG  12135     G       A   GT
                                TGGC TGCGCGTTCC CTC  CCG
                                |||| |||||||||| |||  |||
                                ACCG ACGCGCAAGG GAG  GGC
                                  _       A  __
GAM189  GTF2F1  5'  TGGCGTGCGCGTCCCTCG    13321          T  A
                                TGGCGTGCGCGT CC CTCG
                                |||||||||||| || ||||
                                ACCGCACGCGCA GG GAGC
                                      _ _
GAM189  FKBP1A  3'  ACCTACCACTTGTGCTGTT   38275        ACC  C  AC
                                ACCTGCCGC   GT GC  TGTT
                                |||||||||   || ||  ||||
                                TGGATGGTG   CA CG  ACAA
                                    AA_  _  __
GAM189  FTL     5'  CTGTTCCGTCCAAACACTGTT  6629     CCGCA   ___
                                CTG    CCGTC   GCACTGTT
                                |||    |||||   ||||||||
                                GAC    GGCAG   TGTGACAA
                                  AA___    GTT
GAM189  PYCR1   5'  TGCTGCACCGTCTCCTTGTT  43129    C      GCA  _
                                TGC GCACCGTC   CT GTT
                                ||| ||||||||   || |||
                                ACG CGTGGCAG   GA CAA
                                  A       AG_  A
GAM190  EGR3    3'  ACGCAGGCGCGCGTGCGTGCG  40536      AA     A    CA
                                ACGCG  GCGCGC TGCG  CG
                                |||||  |||||| ||||  ||
                                TGCGT  CGCGCG ACGC  GC
                                   C_     C    AC
GAM190  PPP2R5C 3'  CGCTGAGGCGGACGCACGTT  15521    GA  C   CAT
                                CGC  AG GCG   GCGCACGTT
                                |||  || |||   |||||||||
                                GCG  TC CGC   TGCGTGCAA
                                  AC  _   C__
GAM190  APOBEC2 3'  TGGTTGGTGTCAAATGTTGTC  27709    C  C  C    _
                                TG GT GG GTCGG TGTTGTT
                                || || || ||||| |||||||
                                AC CA CC CAGTT ACAACAG
                                 _ A  A    T
GAM190  TCFL4   3'  TGGTTGGCTTTTGTTGTTG   41831    C  C   GTCGG
                                TG GT GGC    TGTTGTTG
                                || || |||    ||||||||
                                AC CA CCG    ACAACAAC
                                 _  A   AAA__
GAM191  ESPN    3'  ACCGTGGCGGCGTGTGC     36437         A   TTCAGG
                                ACCGTGGCG CGT     GC
                                |||||||| |||     ||
```

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                                TGGCACCGC GCA     CG
                                     C   CA____
GAM192  CR2     3'  TTGTTTATAGCCATGGCCTGGC 12425    C       GTC   A
             TT                   TTG TTATGGCCA   CCT GCTT
                                  ||| |||||||||   ||| ||||
                                  AAC AATATCGGT   GGA CGAA
                                    A       ACC   C
GAM192  EPHB2   3'  TTGCTTATGAAGCT       32685          CCAGTCCCT
                                  TTGCTTATGG       AGCT
                                  ||||||||||       ||||
                                  AACGAATACT       TCGA
                                            _________
GAM192  SORBS1  3'  TTGCTTATGGTTGTCCCC    31719          CCA
                                  TTGCTTATGG   GTCCCT
                                  ||||||||||   ||||||
                                  AACGAATACC   CAGGGG
                                       AA_
GAM192  TFDP2   3'  TTGCTTATTGTGTTTCTCTAG  26622        GGCCAG  C
                                  TTGCTTAT     TC CTAG
                                  ||||||||     || ||||
                                  AACGAATA     AG GATC
                                       ACACAA  A
GAM193  ACVR1B  3'  GGGAAAGCGCGGCTCAGAGC   33761    A      TAA  ___
                                  GG GAAAGCG   CGG   AGAGC
                                  || |||||||   |||   |||||
                                  CC CTTTCGC   GCC   TCTCG
                                    _     ___   GAG
GAM193  ANXA5   5'  GGAGAGCGGCGGAGAGC     10102      AA   TAA
                                  GGAGA  GCG   CGGAGAGC
                                  |||||  |||   ||||||||
                                  CCTCT  CGC   GCCTCTCG
                                     __  C__
GAM193  ASK     5'  GGAGAAAGTGTCGCACCGG   27477        ___   A
                                  GGAGAAAG   CGTA CGG
                                  ||||||||   |||| |||
                                  CCTCTTTC   GCGT GCC
                                       ACA    G
GAM193  ATP8A2  3'  GGAGAAAGAGCAGAG      45260        C  AAC
                                  GGAGAAAG GT   GGAG
                                  |||||||| ||   ||||
                                  CCTCTTTC CG   TCTC
                                       T  ___
GAM193  B3GALT3  5'  GGTGAGTAGTCGGAGAGC    37669    A  AAGC   A_
                                  GG GA    GTA  CGGAGAGC
                                  || ||    |||  ||||||||
                                  CC CT    CAT  GCCTCTCG
                                   A  _____   CA
GAM193  C14orf1  3'  GGGAAGGCTGGAAAAGGGAGC  28417    A   A  GT__  C  A
                                  GG GAA GC    AA GG GAGC
                                  || ||| ||    || || ||||
```

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                                CC CTT CG   TT CC CTCG
                                 _  C  ACCT  T  _
GAM193  CDC5L   5'  GGAGGGGGCGCAGAATAGC   10360     AAA   AC  G
                                GGAG  GCGTA  GGA AGC
                                ||||  |||||  ||| |||
                                CCTC  CGCGT  CTT TCG
                                  CCC    __  A
GAM193  CFL1    5'  GGAGAGGGCACCGAGAGC    24285     AA  GTA  G
                                GGAGA  GC  AC GAGAGC
                                |||||  ||  || ||||||
                                CCTCT  CG  TG CTCTCG
                                  CC  ___  G
GAM193  COL1A1  3'  GGAGAGAGGTCGGAGAGC    6376      A  C  AA
                                GGAGA AG GT  CGGAGAGC
                                ||||| || ||  ||||||||
                                CCTCT TC CA  GCCTCTCG
                                  C  _  __
GAM193  CSPG3   3'  AGAGAAAGTGTAAGCAGAG   20482       C   _
                                GGAGAAAG GTAA CGGAG
                                |||||||| |||| |||||
                                TCTCTTTC CATT GTCTC
                                    A   C
GAM193  CXADR   3'  GAAAGGAACACGGAGAGC    10640     CGTA
                                GAAAG   ACGGAGAGC
                                |||||   |||||||||
                                CTTTC   TGCCTCTCG
                                  CTTG
GAM193  CYFIP2  3'  GGAGAAAGGGTGAAACTAGGAG 43911       C  __  __
                                GGAGAAAG GT  AAC  GGAG
                                |||||||| ||  |||  ||||
                                CCTCTTTC CA  TTG  CCTC
                                    C  CT   AT
GAM193  CYP8B1  3'  GGAGAAAGCTGGCAAAG    20506       GTAA
                                GGAGAAAGC   CGGAG
                                |||||||||   |||||
                                CCTCTTTCG   GTTTC
                                     ACC_
GAM193  DLX4    5'  GAAGAAAGCGCCGAGGGC    39616        AACG  A
                                GGAGAAAGCGT   GAG GC
                                ||||||||||   ||| ||
                                CTTCTTTCGCG   CTC CG
                                     G___  C
GAM193  DPH2L1  5'  GAAGAACGCGGAGAG      10727     AA  TAA
                                GGAGA  GCG  CGGAGAG
                                |||||  |||  |||||||
                                CTTCT  TGC  GCCTCTC
                                  __  ___
GAM193  DPYSL3  3'  GGAGAAAGCCTGGGAAGC    10773       GTAAC  AG
                                GGAGAAAGC   GG  AGC
                                |||||||||   ||  |||
```

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                                CCTCTTTCG    CC  TCG
                                     GA___  CT
GAM193  DTNA    3'  GGAAAAAGCTGAGAG      37372         GTAACG
                                GGAGAAAGC    GAGAG
                                |||||||||    |||||
                                CCTTTTTCG    CTCTC
                                     A_____
GAM193  EHD2    5'  GGAGAGACGTGCAGATGGAGAG 31133      AA   AAC___
          C                      GGAGA  GCGT    GGAGAGC
                                |||||  ||||    |||||||
                                CCTCT  TGCA    CCTCTCG
                                  C_   CGTCTA
GAM193  ELF3    3'  GGAGAAAGGAGCTGGGAGC   20755        C_  AAC  A
                                GGAGAAAG  GT   GG GAGC
                                ||||||||  ||   || ||||
                                CCTCTTTC  CG   CC CTCG
                                     CT  A__  _
GAM193  ENC1    3'  AGAGATTAACGGAGAG     18859      AAGCG
                                GGAGA    TAACGGAGAG
                                |||||    ||||||||||
                                TCTCT    ATTGCCTCTC
                                  A____
GAM193  ENG     3'  GAAGGGTAGGCGCGGAGAGC  6497      AAA__   TAA
                                GGAG    GCG   CGGAGAGC
                                ||||    |||   ||||||||
                                CTTC    CGC   GCCTCTCG
                                  CCATC  ___
GAM193  FACL5   3'  GAAGAAGGCACAGAG      42014       A  GTA
                                GGAGAA GC   ACGGAG
                                |||||| ||   ||||||
                                CTTCTT CG   TGTCTC
                                   C  ___
GAM193  FOXE3   3'  GGAGAAGGATGTAGCAGGAG  29148       AGC_  A  A
                                GGAGAA    GTA CGG GAG
                                ||||||    ||| ||| |||
                                CCTCTT    CAT GTC CTC
                                    CCTA   C  _
GAM193  GPRK7   5'  GGGAAAGCACAAGAGGGC    40181    A       AC   A
                                GG GAAAGCGTA  GGAG GC
                                || |||||||||  |||| ||
                                CC CTTTCGTGT  TCTC CG
                                 _       __    C
GAM193  HR      5'  GGTAGAGCGCGGCGGAGAGC  32931    _  AA   AA
                                GG AGA  GCGT  CGGAGAGC
                                || |||  ||||  ||||||||
                                CC TCT  CGCG  GCCTCTCG
                                 A  __   CC
GAM193  HSF2BP  5'  GGGGGTCGGGAACGGAGAGC  28148    AGAAAG  T_
                                GG     CG  AACGGAGAGC
                                ||     ||  ||||||||||
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                                CC     GC  TTGCCTCTCG
                                 CCCA__  CC
GAM193  IHPK1    3'  GGAGAAAGCAGTGGCAGACAG  45492         _ AA   G
                                GGAGAAAGC GT  CGGA AG
                                ||||||||| ||  |||| ||
                                CCTCTTTCG CA  GTCT TC
                                     T  CC    G
GAM193  IHPK1    3'  GAAAGAGCAGCAGAGAGC    45486      C   A
                                GAAAG GTA CGGAGAGC
                                ||||| ||| ||||||||
                                CTTTC CGT GTCTCTCG
                                   T   C
GAM193  KAL1     3'  GGAGAAAGTGTGGATG      6871         C  AAC   GA
                                GGAGAAAG GT   GGA  G
                                |||||||| ||   |||  |
                                CCTCTTTC CA   CCT  C
                                     A ____  A_
GAM193  KRT4     5'  AGAGAGCGAGCTGGGAGC    14000      AA   TAAC  A
                                GGAGA  GCG    GG GAGC
                                |||||  |||    || ||||
                                TCTCT  CGC    CC CTCG
                                   __   TCGA  _
GAM193  LDB3     3'  GGAGAAAATGACTTAGAGC   44109        CGTA  GG
                                GGAGAAAG    AC  AGAGC
                                ||||||||    ||  |||||
                                CCTCTTTT    TG  TCTCG
                                     AC__  AA
GAM193  MATK     5'  GGGAAAGCGCGAGG        40313    A      AACG   A
                                GG GAAAGCGT    GAG G
                                || |||||||     ||| |
                                CC CTTTCGCG    CTC C
                                 _      _____  _
GAM193  MYEOV    3'  GGAGAGGGTAGGAGAG      39877      AAGC   AC
                                GGAGA   GTA  GGAGAG
                                |||||    |||  ||||||
                                CCTCT    CAT  CCTCTC
                                   CC__   __
GAM193  NKX2H    3'  GGAGGCGGACGGAGAGC     30760     AAA   TA
                                GGAG   GCG  ACGGAGAGC
                                ||||   |||  |||||||||
                                CCTC   CGC  TGCCTCTCG
                                   ____  C_
GAM193  NUMA1    3'  GGAGGCAAGGTAGGGAGAGC  45242      A_   C   AC
                                GGAG  AAG GTA  GGAGAGC
                                ||||  ||| |||  |||||||
                                CCTC  TTC CAT  CCTCTCG
                                   CG   _  C_
GAM193  POLR2E   3'  GGAGGGGACAGAGAGAGC    40922      AAA   TAAC
                                GGAG   GCG    GGAGAGC
                                ||||   |||    |||||||
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                                CCTC  TGT   TCTCTCG
                                  CCC  C___
GAM193  POU4F1   3'  GGAGAAAACAGGAGAG     26391        TAAC
                                GGAGAAAGCG   GGAGAG
                                ||||||||||   ||||||
                                CCTCTTTTGT   CCTCTC
                                     ____
GAM193  PPP3R1   5'  GGAGAGCGCGGGAGGAGC   44080     AA   AAC  _
                                GGAGA  GCGT  GGAG AGC
                                |||||  ||||  |||| |||
                                CCTCT  CGCG  CCTC TCG
                                   __   C__   C
GAM193  PSCD4    3'  AGAGAGCGCCTTCAGAG    30118     AA   AA_
                                GGAGA  GCGT  CGGAG
                                |||||  ||||  |||||
                                TCTCT  CGCG  GTCTC
                                   __   GAA
GAM193  PTGER3   5'  GGGATGGCGTCCAGAGAGC   9650    A  AA   AA
                                GG GA  GCGT  CGGAGAGC
                                || ||  ||||  ||||||||
                                CC CT  CGCA  GTCTCTCG
                                 _ AC   G_
GAM193  RAPSN    3'  GGAGAAAGAGCAGGAG     37216       C   AC
                                GGAGAAAG GTA  GGAG
                                ||||||| |||  ||||
                                CCTCTTTC CGT  CCTC
                                     T  __
GAM193  RARA     3'  AGAGAAAAGCCGGGGCGGAGGG 9702        _ GTAA_    A
          C                      GGAGAAA GC    CGGAG GC
                                |||||||  ||    ||||| ||
                                TCTCTTT CG    GCCTC CG
                                    T  GCCCC    C
GAM193  RARG     3'  GGGACTTATAACGGAGGGC   9726    A  AAGC       A
                                GG GA   GTAACGGAG GC
                                || ||   ||||||||| ||
                                CC CT   TATTGCCTC CG
                                 _ GAA_       C
GAM193  RERE     3'  GGAGAAAGTGCGTTACGG    29028       __   A
                                GGAGAAA  GCGT ACGG
                                |||||||  |||| ||||
                                CCTCTTT  CGCA TGCC
                                    CA   A
GAM193  RORA     5'  GGAGAGCGCAGGGAGAGC    39516     AA    AC
                                GGAGA  GCGTA  GGAGAGC
                                |||||  |||||  |||||||
                                CCTCT  CGCGT  CCTCTCG
                                   __    C_
GAM193  SFN      3'  GAGGAAGCGGGTGCGGAGAGC  43967    A    TAA_
                                GAG AAGCG   CGGAGAGC
                                ||| |||||   ||||||||
```

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                                CTC TTCGC   GCCTCTCG
                                  C    CCAC
GAM193  SHANK2   3'  GGAGAAAGTGCAAATTACAGGA 29460       C  ____   A
              GC                  GGAGAAAG GTA   ACGG GAGC
                                  |||||||| |||   |||| ||||
                                  CCTCTTTC CGT   TGTC CTCG
                                      A  TTAA  _
GAM193  SLBP     5'  GGCAGAGAGCGCAGAG     27196   _  A   AAC
                                  GG AGA AGCGT  GGAG
                                  || ||| |||||  ||||
                                  CC TCT TCGCG  TCTC
                                   G  C   ___
GAM193  SLC25A6  5'  GGAGAACGGGCGCGGAGAG   44864      A__  TAA
                                  GGAGAA  GCG  CGGAGAG
                                  ||||||  |||  |||||||
                                  CCTCTT  CGC  GCCTCTC
                                     GCC  ___
GAM193  SQLE     5'  AGAGGAGCACGGAGAG     17104     AA  GTA
                                  GGAG  AGC  ACGGAGAG
                                  ||||  |||  ||||||||
                                  TCTC  TCG  TGCCTCTC
                                    C_  ___
GAM193  STAC     3'  AGAGAGGAAGCCTGGAGAGC  17132      __  GTAAC
                                  GGAGA  AAGC   GGAGAGC
                                  |||||  ||||   |||||||
                                  TCTCT  TTCG   CCTCTCG
                                    CC   GA___
GAM193  SUFU     3'  GGAGGGCAGCAGAGAGC    32092     AAA  TAA
                                  GGAG  GCG  CGGAGAGC
                                  ||||  |||  ||||||||
                                  CCTC  CGT  GTCTCTCG
                                    C__  C__
GAM193  SYNGR3   3'  AGAGAAAGTGGAGAG      20091       CGTAAC
                                  GGAGAAAG    GGAGAG
                                  ||||||||    ||||||
                                  TCTCTTTC    CCTCTC
                                      A_____
GAM193  TAX1BP1  5'  GGAGAAAGTTACGCAGGC   25696       CGTA  G  A
                                  GGAGAAAG   ACG AG GC
                                  ||||||||   ||| || ||
                                  CCTCTTTC   TGC TC CG
                                      AA__   G  _
GAM193  TEAD2    5'  GGAGAAAGTTGCCGGGAGC   18765       CGTAA  A
                                  GGAGAAAG   CGG GAGC
                                  ||||||||   ||| ||||
                                  CCTCTTTC   GCC CTCG
                                      AACG_  _
GAM193  TGFBI    3'  AGAGAAATTGGCGGAGAGC   7411       GCGTAA
                                  GGAGAAA    CGGAGAGC
                                  |||||||    ||||||||
```

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                                TCTCTTT     GCCTCTCG
                                    AACC__
GAM193  THBD     3' AGAGAGAGAGACCGGAGAGC  7420       A  CGTAA
                                GGAGA AG    CGGAGAGC
                                ||||| ||    ||||||||
                                TCTCT TC    GCCTCTCG
                                  C  TCTG_
GAM193  TMC1     5' GGAGGTTGCAGAGAGC      39798      AAAGC  AA
                                GGAG    GT  CGGAGAGC
                                ||||    ||  ||||||||
                                CCTC    CA  GTCTCTCG
                                  _____  AC
GAM193  TNFRSF1B 3' GGGCAGGTCACAGAGAG     9875     AGAA  C  A
                                GG    AG GT ACGGAGAG
                                ||    || || ||||||||
                                CC    TC CA TGTCTCTC
                                 CG__  _  G
GAM193  TSPY     3' GGAGAAAGCTTAGATAG     17702        GTAAC   G
                                GGAGAAAGC    GGA AG
                                |||||||||    ||| ||
                                CCTCTTTCG    TCT TC
                                     AA___   A
GAM193  VANGL2   3' GAGAAAGTTCCGGAGAG     43458       CGTAA
                                GAGAAAG    CGGAGAG
                                |||||||    |||||||
                                CTCTTTC    GCCTCTC
                                    AAG__
GAM194  ASCL1    5' GCTTCGGGAGCCTCGCGT    43745    CG   T  A_
                                GCT  CGGG GT  TGCGT
                                |||  |||| ||  |||||
                                CGA  GCCC CG  GCGCA
                                  A_   T  GA
GAM194  DLG5     5' CAGCTCGCGGCTGACAT     44447        G  TAT
                                CAGCTCGCGG TG   GCGT
                                |||||||||| ||   ||||
                                GTCGAGCGCC AC   TGTA
                                     G  ___
GAM194  DSC2     5' CAGGTCGCGGGCCGAGCGT   35936    C      GTAT
                                CAG TCGCGGGT   GCGT
                                ||| ||||||||   ||||
                                GTC AGCGCCCG   CGCA
                                  C       GCT_
GAM194  IGF2R    3' GCTCGCACGCACGTGTGT    9338       G   TA  C
                                GCTCGCG GTG  TG GT
                                ||||||| |||  || ||
                                CGAGCGT CGT  AC CA
                                    G   GC  A
GAM194  LPIN1    3' CAACTCGTATATGCG       42632       GCGG
                                CAGCTC   GTGTATGCG
                                ||||||   |||||||||
```

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                                GTTGAG   CATATACGC
                                   ____
GAM194  RU2     5' CAGCTCGCTGCTTCGCGT   32290       GG  GTA
                                CAGCTCGC  GT   TGCGT
                                ||||||||  ||   |||||
                                GTCGAGCG  CG   GCGCA
                                    A_  AA_
GAM194  SHH     5' GCGCGGCGGGTGTGTGCGT   6796    T _     A
                                GC CG CGGGTGT TGCGT
                                || || ||||||| |||||
                                CG GC GCCCACA ACGCA
                                 C  C      C
GAM194  UBE4A   3' AGCACATGGGGTGTATGTGT  21969    T  C_       C
                                AGC CG  GGGTGTATG GT
                                ||| ||  |||||||||| ||
                                TCG GT  CCCACATAC CA
                                  T  AC        A
GAM194  WEE1    5' CAGCACGTGGGCATGCGT    18081     T  C    GT
                                CAGC CG GGGT  ATGCGT
                                |||| || ||||  ||||||
                                GTCG GC CCCG  TACGCA
                                  T  A   __
GAM194  WT1     5' GCTCCGGGACACACGT     35963     G    TGT
                                GCTC CGGG   ATGCGT
                                |||| ||||   ||||||
                                CGAG GCCC   TGTGCA
                                  _    TG_
GAM194  GPR17   3' GCTCTGGGGGTTGCAGGCTTGT 23621    _     CTTTCTA__  C
           GCG                    GC CTGGGGG        TG GCG
                                || |||||||        || |||
                                CG GACCCCC        AC CGC
                                 A      AACGTCCGA  A
GAM194  IL20RA  5' GCGCCTGGGGCTCTGCG     30877         G   TCTA
                                GCGCCTGGGG CTT    TGCG
                                |||||||||| |||    ||||
                                CGCGGACCCC GAG    ACGC
                                   _  _____
GAM194  TAF4B   5' TGGGGGCTTTCACGGCG     44552          T   C
                                TGGGGGCTTTC ATG GCG
                                |||||||||| ||| |||
                                ACCCCCGAAAG TGC CGC
                                   _  _
GAM194  TLE1    5' GCGCTCGGGGACTGTGCGC   22920     C       TTCTA
                                GCGC TGGGGGCT    TGCGC
                                |||| ||||||||    |||||
                                CGCG GCCCCTGA    ACGCG
                                  A       C____
GAM194  VEGF    3' GCCCCTGGGGGCGAGATGCGCG 17956    G       TTTCT
                                GC CCTGGGGGC    ATGCGCG
                                || |||||||||    |||||||
```

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                              CG GGACCCCCG    TACGCGC
                               G       CTC__
GAM195  ABCB4    5'  TGCTCCTGATCCTTTCCCC   7774     _    CC   CC
                              TGC CCTGG  TCC  TCCCC
                              ||| |||||  |||  |||||
                              ACG GGACT  AGG  AGGGG
                                A    __   AA
GAM195  ABCD1    3'  CCCTCTCCCCTCTCCC     6194      GGC      _
                              CCCT   CTCCCCTC CCC
                              ||||   |||||||| |||
                              GGGA   GAGGGGAG GGG
                                ___      A
GAM195  ACK1     3'  GCCCTGGCCTTGGGCCCT   25116         C___
                              GCCCTGGCCT   CCCT
                              ||||||||||   ||||
                              CGGGACCGGA   GGGA
                                    ACCC
GAM195  ACTR1B   3'  GCTCTGTCTCCCCTCCC    43346    C   GC
                              GC CTG  CTCCCCTCCC
                              || |||  ||||||||||
                              CG GAC  GAGGGGAGGG
                               A  A_
GAM195  ADAM11   3'  TGCCCTGGCCCCAGCACCCCC  34663          CCCT
                              TGCCCTGGCCTC   CCCCC
                              ||||||||||||   |||||
                              ACGGGACCGGGG   GGGGG
                                     TCGT
GAM195  ADCY6    3'  TGCTACTGACCCCTCCCC    34181    C_   CCT
                              TGC  CTGG   CCCCTCCCC
                              |||  ||||   |||||||||
                              ACG  GACT   GGGGAGGGG
                                AT   ___
GAM195  ADCY7    5'  CTGCCAACACCCTCCCCC    9986     G  TC__
                              CTG CC   CCCTCCCCC
                              ||| ||   |||||||||
                              GAC GG   GGGAGGGGG
                                _  TTGT
GAM195  ADORA1   3'  GCCACCTCCCCTCCC      8592     CTG
                              GCC   GCCTCCCCTCCC
                              |||   ||||||||||||
                              CGG   TGGAGGGGAGGG
                                    ___
GAM195  ADORA2A  3'  GCCCCAACCTCTCCCC     8603      TG    CCC
                              GCCC  GCCTC   TCCCC
                              ||||  |||||   |||||
                              CGGG  TGGAG   AGGGG
                                GT    ___
GAM195  ADRA2B   3'  TACTCTGGCCTCAACAACCC  8651     C      CCCT_
                              TGC CTGGCCTC    CCC
                              ||| ||||||||    |||
```

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                                ATG GACCGGAG    GGG
                                  A      TTGTT
GAM195  AGPAT2   3'  GCCCTCCAGGCCCCTCCTC   26927      ___     C
                                GCCCT   GGCCTC CCTC
                                |||||   |||||| ||||
                                CGGGA   CCGGGG GGAG
                                   GGT     A
GAM195  AK2      3'  CCCTTCCCCCTCCCC      30188      GGCC
                                CCCT    TCCCCTCCCC
                                ||||    ||||||||||
                                GGGA    GGGGGAGGGG
                                  A___
GAM195  ALDH3B1  3'  GCCTTGGCAATCCTTTTCCTC  45064     C    C_   ____
                                GCC TGGC  TCC    CCTC
                                ||| ||||  |||    ||||
                                CGG ACCG  AGG    GGAG
                                  A   TT   AAAA
GAM195  AP1S1    3'  TGCCCTGAACACCTTTTCCC   10502        CCT  CC_
                                TGCCCTGG   CC   TCCC
                                ||||||||   ||   ||||
                                ACGGGACT   GG   AGGG
                                     TGT  AAA
GAM195  AP2A1    3'  CCCTGGCCCCTCTCCCC     39101         T  C
                                CCCTGGCC CC CTCCCC
                                |||||||| || ||||||
                                GGGACCGG GG GAGGGG
                                     _  A
GAM195  AP2A1    5'  GCCCCCTGCCCCTCCCC     39105      TGG  _
                                GCCC   CCT CCCCTCCCC
                                ||||   ||| |||||||||
                                CGGG   GGA GGGGAGGGG
                                   ___   C
GAM195  AQP1     3'  ACCCCTCCCCTCCC       7544       TGGC
                                GCCC    CTCCCCTCCC
                                ||||    ||||||||||
                                TGGG    GAGGGGAGGG
                                   ____
GAM195  ARF3     5'  TGCCCTGGCCCACTCCC     11679          CCC
                                TGCCCTGGCCT   CTCCC
                                ||||||||||   |||||
                                ACGGGACCGGG   GAGGG
                                      T__
GAM195  ARF4L    3'  TGCCAGCCTCTTCTCC      43074      CT     CC
                                TGCC  GGCCTC  CTCC
                                ||||  ||||||  ||||
                                ACGG  TCGGAG  GAGG
                                   __     AA
GAM195  ARHGAP6  5'  TGCCATTGGGGCCTCCCCC   25966      CT___
                                TGCC    GGCCTCCCCT
                                ||||    ||||||||||
```

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                                ACGG    CCGGAGGGGG
                                  TAACC
GAM195  ASCL1    5'  CCTCCTCCCTCCCCTCCTCC  43744    _  GG        _
                                CC CT  CCTCCCCTCC CC
                                || ||  |||||||||| ||
                                GG GG  GGAGGGGAGG GG
                                 A  AG         A
GAM195  ASIC4    3'  CCCCCTCCCTCTCCTTCC    33065     TGG     _   __
                                CCC   CCTCCC CTCC  CC
                                |||   |||||| ||||  ||
                                GGG   GGAGGG GAGG  GG
                                  ___     A   AA
GAM195  ATF5     3'  GCCTTTAGCCTCCCTCCC    28937     C_       C
                                GCC  TGGCCTCCC TCCC
                                |||  ||||||||| ||||
                                CGG  ATCGGAGGG AGGG
                                  AA       _
GAM195  ATP1A1   3'  GCCCTCCCCCCTCCCCC     8696       GGC
                                GCCCT   CTCCCCTCCCCC
                                |||||   ||||||||||||
                                CGGGA   GGGGGGAGGGGG
                                  ___
GAM195  ATP8B2   3'  TGCCAGCCTCCTTTTCC     42220      CT     CC_
                                TGCC  GGCCTCC   TCC
                                ||||  |||||||   |||
                                ACGG  TCGGAGG   AGG
                                  __      AAA
GAM195  B29      5'  TGCTGTGATTTCCCCTCC    36711     CC   CC
                                TGC  TGG  TCCCCTCC
                                |||  |||  ||||||||
                                ACG  ACT  AGGGGAGG
                                  AC   AA
GAM195  B4GALT5  3'  TGCTGTGTAGACCCTCCCCC  21944     CC  GCCTC
                                TGC  TG    CCCTCCCCC
                                |||  ||    |||||||||
                                ACG  AC    GGGAGGGGG
                                  AC  ATCT_
GAM195  BCL11B   3'  CTCTCCCATTCCCTCCCCC   39748    GG   C__
                                CT  CCT   CCCTCCCCC
                                ||  |||   |||||||||
                                GA  GGG   GGGAGGGGG
                                 GA   TAA
GAM195  BCL2L2   3'  GCCAAAACATTCCCCTCCCC  19743     CT   C_
                                GCC  GGC  TCCCCTCCCC
                                |||  |||  ||||||||||
                                CGG  TTG  AGGGGAGGGG
                                  TT   TA
GAM195  BLTR2    5'  GCTCTGGCCCCAATCCTCC   33367    C       C__
                                GC CTGGCCTC   CCTCC
                                || ||||||||   |||||
```

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                                CG GACCGGGG   GGAGG
                                 A       TTA
GAM195  BLTR2    5' CTGTTCTCATCCCTCCCCC   33365     GC  __
                                CTG  CTC  CCCTCCCCC
                                |||  |||  |||||||||
                                GAC  GAG  GGGAGGGGG
                                  AA   TA
GAM195  BTEB1    3' TGGCCTTACCCCCTCCCCC   10221       ___
                                TGGCCT   CCCCTCCCCC
                                ||||||   ||||||||||
                                ACCGGA   GGGGAGGGGG
                                   ATG
GAM195  CACNA2D2 3' TGCCCCAGAGCCTCTCTCC   25726       __     CC
                                TGCCCT  GGCCTC  CTCC
                                ||||||  ||||||  ||||
                                ACGGGG  TCGGAG  GAGG
                                   TC     A_
GAM195  CACNB1   3' GCCCCTCGCTCCCTCCCC    8781       G_  CTC
                                GCCCT  GC   CCCTCCCC
                                |||||  ||   ||||||||
                                CGGGG  CG   GGGAGGGG
                                  AG  A__
GAM195  CACNB1   3' CGCTCCCTCCCCTCCCC     8779     C TGG
                                TGC C   CCTCCCCTCCCC
                                |||  |   ||||||||||||
                                GCG G   GGAGGGGAGGGG
                                  A ___
GAM195  CACNB1   3' CCCTGGCTCAGAGCCCTTCCTC 8778        C _____   _ _
           C                     CCCTGGC TC    CCCT CC CC
                                |||||||  ||    ||||  ||  ||
                                GGGACCG AG    GGGA GG GG
                                   _  TCTC    A  A
GAM195  CAV1     3' TACCCTGGAATTCTTCCCT   11995        C___  C
                                TGCCCTGG    CT CCCT
                                ||||||||    ||  ||||
                                ATGGGACC    GA GGGA
                                     TTAA  A
GAM195  CD34     3' GCCCTGGCCTCCACCGTTTTCC 12117           _  _____
                                GCCCTGGCCTCC CC    TCC
                                ||||||||||||  ||    |||
                                CGGGACCGGAGG GG    AGG
                                       T  CAAA
GAM195  CD3Z     3' GCCCTGGCTGACCCTCCCC    8820        CTC
                                GCCCTGGC   CCCTCCCC
                                ||||||||   ||||||||
                                CGGGACCG   GGGAGGGG
                                     ACT
GAM195  CDC25A   3' TGCCCTGGGCTCCAACCT    12151        C   __
                                TGCCCTGG CTCC  CCT
                                |||||||| ||||  |||
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                                ACGGGACC GAGG  GGA
                                    C    TT
GAM195  CDC25A   3'  CCCCTCCGTCTCCTCTCCCC  12147     GG  _  _  _
                                CCCT  CC TC CC CTCCCC
                                ||||  || || || ||||||
                                GGGG  GG AG GG GAGGGG
                                  A_  C  A  A
GAM195  CDH2     5'  CCCTTCCCCTCCCC       12167     GGCC
                                CCCT   TCCCCTCCCC
                                ||||   ||||||||||
                                GGGA   AGGGGAGGGG
                                 ____
GAM195  CDKN1C   3'  TGCCCCGGCAGGTTCCCTC   6338         CTC__
                                TGCCCTGGC    CCCTC
                                |||||||||    |||||
                                ACGGGGCCG    GGGAG
                                     TCCAA
GAM195  CDS1     5'  TGCCCGGGCCTCCCGCACC   10402      T      CT_
                                TGCCC GGCCTCCC   CC
                                ||||| ||||||||   ||
                                ACGGG CCGGAGGG   GG
                                   C       CGT
GAM195  CEBPA    3'  CCCTGAGCCCCCCTCCTCC   20389      _  T     _
                                CCCTG GCC CCCCTCC CC
                                ||||| ||| ||||||| ||
                                GGGAC CGG GGGGAGG GG
                                   T  _      A
GAM195  CELSR3   3'  CCCTCTATCTCCCTCCCCC   10831     GGCC  _
                                CCCT   TC CCCTCCCCC
                                ||||   || |||||||||
                                GGGA   AG GGGAGGGGG
                                  GAT_  A
GAM195  CENTD2   5'  CCTCACACTCCCCTCCCCC   31592     G  _
                                CCT GC CTCCCCTCCCCC
                                ||| || ||||||||||||
                                GGA TG GAGGGGAGGGGG
                                  G  T
GAM195  CHD4     3'  TGCCCCTCACTCCCTCCCC   10460      GGC    C
                                TGCCCT   CTCCC TCCCC
                                ||||||   ||||| |||||
                                ACGGGG   GAGGG AGGGG
                                   AGT    _
GAM195  CHRNE    3'  CCCTCCCCCCTCCCC      6343      GGC
                                CCCT   CTCCCCTCCCC
                                ||||   ||||||||||
                                GGGA   GGGGGGAGGGG
                                 ___
GAM195  CNTN2    3'  GCCCTGGCCTCTCAACTC    22911         CC__
                                GCCCTGGCCTC   CTC
                                ||||||||||    |||
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                                CGGGACCGGAG   GAG
                                      AGTT
GAM195  COL11A2  3'  GCCCTGGCCCAGGGCTCCC   38776        CCC_
                                GCCCTGGCCT   CTCCC
                                ||||||||||   |||||
                                CGGGACCGGG   GAGGG
                                      TCCC
GAM195  COL9A2   3'  TGCTCTACCTCCCCTTCCCC   12341    C  G     _
                                TGC CTG CCTCCCCT CCCC
                                ||| ||| |||||||| ||||
                                ACG GAT GGAGGGGA GGGG
                                  A  _      A
GAM195  COPG2    3'  CCCCTCCCCCCTCCCCC    44348     GG  T
                                CCCT  CC CCCCTCCCCC
                                ||||  || ||||||||||
                                GGGG  GG GGGGAGGGGG
                                  A_ _
GAM195  COPG2    3'  ACTCTGGCTTCCCCTCCCCC   44347    C    C
                                GC CTGGC TCCCCTCCCCC
                                || ||||| ||||||||||
                                TG GACCG AGGGGAGGGGG
                                 A    A
GAM195  CPNE6    5'  GCCCTGGCCCTGACTCCC    25735        CCC
                                GCCCTGGCCT   CTCCC
                                ||||||||||   |||||
                                CGGGACCGGG   GAGGG
                                      ACT
GAM195  CPNE7    3'  TGCCTTGCTGGCCCTCCCCC   30874     ___     TCCC
                                TGCC   CTGGCC   CTCCCCC
                                ||||   ||||||   |||||||
                                ACGG   GACCGG   GAGGGGG
                                  AAC    _____
GAM195  CPT2     5'  TGCTCGTCTCCCTTCCC     6433     CC  GC    C
                                TGC  TG  CTCCC TCCC
                                |||  ||  ||||| ||||
                                ACG  GC  GAGGG AGGG
                                  A_ A_    A
GAM195  CRHR1    3'  TGCCCTGGCTGTCCAGTCCC   20451        C_  CC
                                TGCCCTGGC  TCC  TCCC
                                |||||||||  |||  ||||
                                ACGGGACCG  AGG  AGGG
                                      AC   TC
GAM195  CRYBA2   5'  GCTCCCCTCCCTTCCCC     38394    _ TGG     C
                                GC CC   CCTCCC TCCCC
                                || ||   |||||| |||||
                                CG GG   GGAGGG AGGGG
                                 A ___     A
GAM195  CSF3R    3'  GCTTATGGACCCTCCCCTC   8907     CC_  __
                                GC   TGG  CCTCCCCTC
                                ||   |||  |||||||||
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                                CG   ACC  GGAGGGGAG
                                 AAT   TG
GAM195  CSH2     5'  TACCCTGGCCAGTTCTCTCTCC 35460          TCCC__  _
              C                   TGCCCTGGCC     CTC CCC
                                  ||||||||||     ||| |||
                                  ATGGGACCGG     GAG GGG
                                       TCAAGA   A
GAM195  CSRP1    3'  GCCCAGCCCTTTCCCCTTCC   19841     T   ___     C
                                  GCCC GGCC   TCCCCT CC
                                  |||| ||||   |||||| ||
                                  CGGG TCGG   AGGGGA GG
                                    _   GAA     A
GAM195  CYB561   3'  GCCAGTCCCTCCCCTCTCC   12543     CTGG       C
                                  GCC    CCTCCCCTC CC
                                  |||    |||||||||| ||
                                  CGG    GGAGGGGAG GG
                                    TCAG        A
GAM195  CYLN2    3'  TGCCCTGGGCTCCGAGCC    18066        C    CCT
                                  TGCCCTGG CTCC   CC
                                  |||||||| ||||   ||
                                  ACGGGACC GAGG   GG
                                       C    CTC
GAM195  CYP26A1  5'  CCCTGGCTCCTCCCCC      38406        CTCC
                                  CCCTGGC    CCTCCCCC
                                  |||||||    ||||||||
                                  GGGACCG    GGAGGGGG
                                     A___
GAM195  DDT      3'  TGCCCTGGATCCCTCC       10673         CCTC
                                  TGCCCTGG    CCCTCC
                                  ||||||||    ||||||
                                  ACGGGACC    GGGAGG
                                     TA__
GAM195  DIA1     3'  TGGCCAGCCCCCTCTTCC     28794       __      CC
                                  TGGCC  TCCCCTC  CC
                                  |||||  |||||||  ||
                                  ACCGG  GGGGGAG  GG
                                     TC      AA
GAM195  DIO3     3'  CCCCCACCTCTCTTTCCCC    10690      G    CCC_
                                  CCCT GCCTC    TCCCC
                                  |||| |||||    |||||
                                  GGGG TGGAG    AGGGG
                                    G     AGAA
GAM195  DISC1    3'  GCCCACCTCCCTCCCCC      33041      TG      C
                                  GCCC  GCCTCCC TCCCCC
                                  ||||  ||||||| ||||||
                                  CGGG  TGGAGGG AGGGGG
                                     __      _
GAM195  DMN      5'  TGTCCCGGTCTCGTCCTC     41645    C    C   C_
                                  TG CCTGG CTC  CCTC
                                  || ||||| |||  ||||
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```
                                AC GGGCC GAG  GGAG
                                 A    A  CA
GAM195  DMN     5'  TGCCCTGGTCTTGTCCC    41644       C  CCCC
                                TGCCCTGG CT   TCCC
                                |||||||| ||   ||||
                                ACGGGACC GA   AGGG
                                    A  AC__
GAM195  DSC1    5'  CCCTGGCCAGTCTCCTTCC   35932       __ _ C
                                CCCTGGCC  TC CC TCC
                                |||||||| || || |||
                                GGGACCGG  AG GG AGG
                                    TC  A  A
GAM195  DSC3    3'  TGCCCTGAGTTCTTTCTCCC  35947       CC  CC_
                                TGCCCTGG  TC  CTCCC
                                |||||||| ||  |||||
                                ACGGGACT  AG  GAGGG
                                    CA  AAA
GAM195  DTNB    3'  GCTCTGGCTCCCCTCTCCC   37606   C   C    _
                                GC CTGGC TCCCCTC CCC
                                || ||||| ||||||| |||
                                CG GACCG AGGGGAG GGG
                                 A    _     A
GAM195  DXYS155E 3'  GCCCGGCTCCTCTCCC    22954    T  C  C
                                GCCC GGC TCC CTCCC
                                |||| ||| ||| |||||
                                CGGG CCG AGG GAGGG
                                  _  _  A
GAM195  E2F1    3'  TGCCCTGGGCCTTGTGGGACCC 44493       _  CCCCT__
          CC                    TGCCCTGG CCT     CCCCC
                                |||||||| |||      |||||
                                ACGGGACC GGA     GGGGG
                                    C  ACACCCT
GAM195  ECE1    3'  GCCCCTTCCCCTCCTCC    10817     GGCC      _
                                GCCCT   TCCCCTCC CC
                                |||||   |||||||| ||
                                CGGGG   AGGGGAGG GG
                                  A___      A
GAM195  EDARADD  5'  CCTCCGCCTTCCCCTCCC   38846   _  G  _
                                CC CTG CCT CCCCTCCC
                                || ||| ||| ||||||||
                                GG GGC GGA GGGGAGGG
                                 A  _  A
GAM195  EDN2    3'  GCCCTGGCCACTTCTCTCCTCC 12645       _____ C
                                GCCCTGGCC    TC CCTCC
                                |||||||||    || |||||
                                CGGGACCGG    AG GGAGG
                                     TGAAG  A
GAM195  EFNA3   3'  GCCCCATCTCTCCCC      22398      GC  CCC
                                GCCCTG  CTC  TCCCC
                                ||||||  |||  |||||
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                                CGGGGT  GAG   AGGGG
                                  A_  ___
GAM195  EGLN2    5'  TGCCCTGACCTCTCTGCCC   38839          CC  C
                                TGCCCTGGCCTC  CT CCC
                                ||||||||||||  || |||
                                ACGGGACTGGAG  GA GGG
                                      A_  C
GAM195  EGR3     3'  GCTCCTTACCCCCTCCCCC   40551    _  GGCC
                                GC CCT   TCCCCTCCCCC
                                || |||   ||||||||||
                                CG GGA   GGGGGAGGGGG
                                 A  AT__
GAM195  EHD3     3'  GCCCTGGCTTTGAATCCTCTC  31113        C_____  C
                                GCCCTGGC     TCC CTC
                                ||||||||     ||| |||
                                CGGGACCG     AGG GAG
                                     AAACTT   A
GAM195  EIF4A1   3'  TGGCTCCCTTCCCTCCCCC   10870     _  __
                                TGGC CTC  CCCTCCCCC
                                ||||| |||  |||||||||
                                ACCG GGG  GGGAGGGGG
                                  A  AA
GAM195  EIF5A    3'  CCCTCTCCTCCTCTTCCC    12699     GG    C  C
                                CCCT  CCTCC CT CCC
                                ||||  ||||| || |||
                                GGGA  GGAGG GA GGG
                                  GA    A  A
GAM195  EIF5A    3'  CCCCTCCCCTCTCCTCC     12698    TGG       _ _
                                CC   CCTCCCCTC CC CC
                                ||   ||||||||| || ||
                                GG   GGAGGGGAG GG GG
                                 ___       A  A
GAM195  EMP1     3'  CCCCCTCCCCCCTCCCC     10892     GG  T
                                CCCT  CC CCCCTCCCC
                                ||||  || |||||||||
                                GGGG  GG GGGGAGGGG
                                  GA  _
GAM195  EPB41L2  3'  GCCCCCTCCCCCTCTCCC    11006      GG    C
                                GCCCT  CCTCC CTCCC
                                |||||  ||||| |||||
                                CGGGG  GGGGG GAGGG
                                   GA    A
GAM195  EPB49    5'  TGCCTGGCCCTCTCTCCC    12737     C     CCC
                                TGCC TGGCCT   CTCCC
                                |||| ||||||   |||||
                                ACGG ACCGGG   GAGGG
                                  _     AGA
GAM195  EPHB3    3'  CCTGGAGTCCCCTCCTCC    20785      CC      _
                                CCTGG  TCCCCTCC CC
                                |||||  |||||||| ||
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                                GGACC  AGGGGAGG GG
                                  TC       A
GAM195  EXT1     3'  CCCTTCTTGCTTCCCCTCCCCC 6549      G___  C
                                CCCT    GC TCCCCTCCCCC
                                ||||    || ||||||||||
                                GGGA    CG AGGGGAGGGGG
                                  AGAA  A
GAM195  FBXW1B   3'  TGCCCCCTCCCTTCCCCC    38000      TGG     C
                                TGCCC   CCTCCC TCCCCC
                                |||||   |||||| ||||||
                                ACGGG   GGAGGG AGGGGG
                                   ___     A
GAM195  FGF23    5'  GCCTTACTGGCCTTTTCCTTCT 33954     ___     ___   C_
            CC                    GCC   CTGGCC   TCC  CTCC
                                |||   ||||||   |||  ||||
                                CGG   GACCGG   AGG  GAGG
                                  AAT     AAA   AA
GAM195  FHL2     5'  GCTCTGCTCCCCTCTCC     11112    C   GC      C
                                GC CTG  CTCCCCTC CC
                                || |||  |||||||| ||
                                CG GAC  GAGGGGAG GG
                                 A  __       A
GAM195  FOS      3'  GCCGGCTGCCTCCCCTTCCC   23516     CTG_       C
                                GCC    GCCTCCCCT CCC
                                |||    ||||||||| |||
                                CGG    CGGAGGGGA GGG
                                  CCGA        A
GAM195  FOXO1A   5'  ACCCCCGCCCCTCCCCC     12881      TGG  T
                                GCCC   CC CCCCTCCCCC
                                ||||   || ||||||||||
                                TGGG   GG GGGGAGGGGG
                                   ___  C
GAM195  FRZB     5'  CTGGGAGCTTCTCCTCCCCC   11154     ___  C  C
                                CTG   GC TC CCTCCCCC
                                |||   || || ||||||||
                                GAC   CG AG GGAGGGGG
                                  CCT  A  A
GAM195  FXR2     3'  TGCCACCCCCCTCCCCC     22169      CTG   T
                                TGCC   GCC CCCCTCCCCC
                                ||||   ||| ||||||||||
                                ACGG   TGG GGGGAGGGGG
                                   ___   _
GAM195  FZD5     5'  GCCCCCTCCCTCCCC       41048      TGG     C
                                GCCC   CCTCCC TCCCC
                                ||||   |||||| |||||
                                CGGG   GGAGGG AGGGG
                                   ___     _
GAM195  GAPD     3'  CCCTAGGCCCCTCCCC       13051        CCT
                                CCCTGG   CCCCTCCCC
                                ||||||   |||||||||
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                                GGGATC  GGGGAGGGG
                                  C__
GAM195  GAS7    3'  TGCCCTGACCTTACATTCC   25286         CCCC_
                                TGCCCTGGCCT    TCC
                                ||||||||||    |||
                                ACGGGACTGGA    AGG
                                      ATGTA
GAM195  GCNT2   5'  GCCCAGCCTTCCCTCCTCC   11250     T    C    _
                                GCCC GGCCT CCCTCC CC
                                |||| ||||| |||||| ||
                                CGGG TCGGA GGGAGG GG
                                  _    A     A
GAM195  GCS1    3'  TGGCTCCCCTCCTCTCCC    26701     C      ___
                                TGGC TCCCCTCC   CCC
                                |||| ||||||||  |||
                                ACCG AGGGGAGG   GGG
                                  _       AGA
GAM195  GLDC    5'  CCTGGCCTCGGTCCCCC     42024        CCC
                                CCTGGCCTC   TCCCCC
                                |||||||||  ||||||
                                GGACCGGAG   AGGGGG
                                     CC_
GAM195  GLO1    3'  CCTTCCTCCTCCCCTTTCCC  27469    GG__      CC
                                CCT   CCTCCCCT  CCC
                                |||   ||||||||  |||
                                GGA   GGAGGGGA  GGG
                                  AGGA       AA
GAM195  GOT1    3'  TGCTTTGACCTCCAAAGGCTC  13226    CC      C____
                                TGC  TGGCCTCC    CTC
                                |||  ||||||||    |||
                                ACG  ACTGGAGG    GAG
                                  AA       TTTCC
GAM195  GPC1    3'  GCCCAGCTTCCCCTCCTCC   13245     T  C      _
                                GCCC GGC TCCCCTCC CC
                                |||| ||| |||||||| ||
                                CGGG TCG AGGGGAGG GG
                                  _  A       A
GAM195  GPR61   3'  TACCCAGGTTCCCTCCCC    44264      T  CCTC
                                TGCCC GG   CCCTCCCC
                                ||||| ||   ||||||||
                                ATGGG CC   GGGAGGGG
                                   T  AA__
GAM195  GRIA3   5'  GCTCTTACACCCCCTCCCC   9092     C  G  C
                                GC CT GC TCCCCTCCCC
                                || || || ||||||||||
                                CG GA TG GGGGGAGGGG
                                 A  A  T
GAM195  GRIK3   3'  TACCCCAAACTCCTCTTTTCC  9099       TG C    C  CC_
                                TGCCC  G CTCC CT   CC
                                |||||  | |||| ||   ||
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                                ATGGG  T GAGG GA   GG
                                   GT T    A  AAA
GAM195  GRM1     3'  TGGCCTGGCCCTTCCCTTCCCC 9147     C      __    C
                                TG CCTGGCC  TCCC TCCCC
                                || |||||||  |||| |||||
                                AC GGACCGG  AGGG AGGGG
                                 C      GA    A
GAM195  GSTM5    3'  TGCTCAGCCCCCTTCCCC    9208     CC    T  C
                                TGC  TGGCC CCC TCCCC
                                |||  ||||| ||| |||||
                                ACG  GTCGG GGG AGGGG
                                  A_    _  A
GAM195  H1F0     3'  GCCCACTCCCCCTCCCCC    23700     TG  CT
                                GCCC  GC  CCCCTCCCCC
                                ||||  ||  ||||||||||
                                CGGG  TG  GGGGAGGGGG
                                   __ AG
GAM195  HCCS     5'  TGCACCTAAGCCCTCCCCC   23735    _    CCTC
                                TGC CCTGG    CCCTCCCCC
                                ||| |||||    |||||||||
                                ACG GGATT    GGGAGGGGG
                                  T    C___
GAM195  HCN4     3'  CCCTCCTCCCTCCCC      24219      GG     C
                                CCCT  CCTCCC TCCCC
                                ||||  |||||| |||||
                                GGGA  GGAGGG AGGGG
                                   __    _
GAM195  HEM1     3'  GCTCCTGACCCTCTCTCC    23740    _      CCC
                                GC CCTGGCCT   CTCC
                                || ||||||||   ||||
                                CG GGACTGGG   GAGG
                                 A       AGA
GAM195  HIRA     3'  TGCCAGTGTCTCCTCCCCC   17744     CT  CC  C
                                TGCC  GG  TC CCTCCCCC
                                ||||  ||  || ||||||||
                                ACGG  TC  AG GGAGGGGG
                                   __ AC  A
GAM195  HIS1     3'  CCCCTTTGCCCCCTCCCCC   26990     GGCC
                                CCCT    TCCCCTCCCCC
                                ||||    ||||||||||
                                GGGG    GGGGGAGGGGG
                                  AAAC
GAM195  HOXA7    3'  TACTACTGGTCCCCTCCTCC  27889     C_   CC      _
                                TGC  CTGG  TCCCCTCC CC
                                |||  ||||  |||||||| ||
                                ATG  GACC  AGGGGAGG GG
                                  AT    __       A
GAM195  HOXC13   5'  GCTCCTGTTTCCCCTCCCCC  40667    _   GCC
                                GC CCTG   TCCCCTCCCCC
                                || ||||   ||||||||||
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                                CG GGAC   AGGGGAGGGGG
                                 A   AA_
GAM195  HOXC13   5'  CCCCCCATCCCTCCCC     40663     GG  TC
                                CCCT  CC  CCCTCCCC
                                ||||  ||  ||||||||
                                GGGG  GG  GGGAGGGG
                                  __  TA
GAM195  HOXD4    3'  GCCCTACCCCTTCCC      31174      GCCT    C
                                GCCCTG   CCCCT CCC
                                ||||||   ||||| |||
                                CGGGAT   GGGGA GGG
                                   ____    A
GAM195  HOXD4    3'  TGCACAGCCCCTCCCC     31181     CCTG  CT
                                TGC   GC  CCCCTCCCC
                                |||   ||  |||||||||
                                ACG   TG  GGGGAGGGG
                                  ____  TC
GAM195  HYAL2    3'  CCCAGGGACTTCCCCTCCCCC  37635    T_  _ C
                                CCC  GG C TCCCCTCCCCC
                                |||  || | ||||||||||
                                GGG  CC G AGGGGAGGGGG
                                  TC  T A
GAM195  ICAM1    3'  TACCTTGGCCCCCTTCCCC   43433     C    T   C
                                TGCC TGGCC CCC TCCCC
                                |||| ||||| ||| |||||
                                ATGG ACCGG GGG AGGGG
                                  A    _  A
GAM195  IFNGR2   5'  CCCCCGCCCCCCTCCCC    24379     G   T
                                CCCT GCC CCCCTCCCC
                                |||| ||| |||||||||
                                GGGG CGG GGGGAGGGG
                                  G  _
GAM195  IGF2R    3'  TGGCCTCCCTCCTCCTCC    9344         __   _
                                TGGCCTCCC  CTCC CC
                                |||||||||  |||| ||
                                ACCGGAGGG  GAGG GG
                                     AG   A
GAM195  IGHMBP2  3'  GCCCTCCGCTCCTCCCCC   13492     GG  TCC
                                GCCCT  CC   CCTCCCCC
                                |||||  ||   ||||||||
                                CGGGA  GG   GGAGGGGG
                                  __  CGA
GAM195  IL18R1   3'  TGCCAGCCCCTCCTCC     19298     CT    C
                                TGCC  GGCCTC CCTCC
                                ||||  |||||| |||||
                                ACGG  TCGGGG GGAGG
                                  __     A
GAM195  IL2RB    3'  CCCTGACAGCTTCTCCCTC   9379       C___  _
                                CCCTGGC    TC CCCTC
                                |||||||    || |||||
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                                GGGACTG   AG GGGAG
                                   TCGA  A
GAM195  INHBA   5'  GCCCTGCTTTTCCTCCCCC   13537      G CTCC
                                GCCCTG C   CCTCCCCC
                                |||||| |   ||||||||
                                CGGGAC G   GGAGGGGG
                                  _ AAAA
GAM195  INHBB   3'  GCCCCCTCTTCTCTCCC    13558    TGG   CC  _
                                GCCC  CCTC  CTC CCC
                                ||||  ||||  ||| |||
                                CGGG  GGAG  GAG GGG
                                  ___   AA  A
GAM195  INSRR   3'  GCCCTGGCCCAGTTCCC    42845        CCCC
                                GCCCTGGCCT   TCCC
                                ||||||||||   ||||
                                CGGGACCGGG   AGGG
                                     TCA_
GAM195  ITPKA   3'  GCCCTTTGCCCCCTCCCC   13637     GGCC
                                GCCCT   TCCCCTCCCC
                                |||||   ||||||||||
                                CGGGA   GGGGGAGGGG
                                  AAC_
GAM195  JAG2    5'  TGCCCGGCCCGGCTCCC    13735     T   CCC
                                TGCCC GGCCT  CTCCC
                                ||||| |||||  |||||
                                ACGGG CCGGG  GAGGG
                                  _   CC_
GAM195  JAM2    5'  TGCCCCAACTCCTTTCTTCC  34551     TG  C  CC  CC
                                TGCCC  GC TCC  TC  CC
                                |||||  || |||  ||  ||
                                ACGGG  TG AGG  AG  GG
                                  GT  _  AA  AA
GAM195  JJAZ1   5'  CCTGCCTCCTCCCCC     31686     G   CC
                                CCTG CCTCC  TCCCCC
                                |||| |||||  ||||||
                                GGAC GGAGG  AGGGGG
                                  _   __
GAM195  KLF1    5'  GCCTCAAGCCTCCTCTTCC   27291    CT_     C  C
                                GCC  GGCCTCC CT CC
                                |||  ||||||| || ||
                                CGG  TCGGAGG GA GG
                                  AGT     A  A
GAM195  KRTHA7  5'  TGCTTTGACCTCCTGCCT   19086    CC     __
                                TGC  TGGCCTCC  CCT
                                |||  ||||||||  |||
                                ACG  ACTGGAGG  GGA
                                  AA      AC
GAM195  KRTHA8  5'  TGCTTTGACCTCCTGCCT   27670    CC     __
                                TGC  TGGCCTCC  CCT
                                |||  ||||||||  |||
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                                ACG  ACTGGAGG  GGA
                                  AA       AC
GAM195  LAPTM5   5'  TGCTGCCGTCCCCTCC     27609     CCTG  _
                                TGC    GCC TCCCCTCC
                                |||    ||| ||||||||
                                ACG    CGG AGGGGAGG
                                  A___   C
GAM195  LETM1    5'  TGCGCTGCCTCCTTCTCC    29505     C  G    C_
                                TGC CTG CCTCC  CTCC
                                ||| ||| |||||  ||||
                                ACG GAC GGAGG  GAGG
                                  C  _    AA
GAM195  LHX4     5'  TGGCCGGCCCCCTCCCCC    37854      __
                                TGGCC  TCCCCTCCCCC
                                |||||  ||||||||||
                                ACCGG  GGGGGAGGGGG
                                   CC
GAM195  LIF      3'  TGCTGCCTCCTTCCCTCCCC  14155     CCTG    ___
                                TGC    GCCTCC   CCTCCCC
                                |||    ||||||   |||||||
                                ACG    CGGAGG   GGAGGGG
                                  A___     AAG
GAM195  LIF      3'  TGCAGCCTCCCTCTCCTCC   14154     CCT      _   _
                                TGC   GGCCTCCC CTCC CC
                                |||   |||||||| |||| ||
                                ACG   TCGGAGGG GAGG GG
                                  ___       A   A
GAM195  LMNB1    3'  CCCTCCACCTCCCTCCCCC   24532      G_     C
                                CCCT  GCCTCCC TCCCCC
                                ||||  ||||||| ||||||
                                GGGA  TGGAGGG AGGGGG
                                  GG      _
GAM195  LMO2     5'  TGCCTGTGCCATCTCCCC    24553      C  _   TCCC
                                TGCC TG GCC    CTCCCC
                                |||| || |||    ||||||
                                ACGG AC CGG    GAGGGG
                                  _  A   TA__
GAM195  LMO4     3'  CCCCAGCTCCCTCCCCC     27647     TG  CTC
                                CCC  GC   CCCTCCCCC
                                |||  ||   |||||||||
                                GGG  CG   GGGAGGGGG
                                  GT  A__
GAM195  LNK      5'  GCCCTGGGCGCGTCCTCTCCC  24203        _ C__   C
                                GCCCTGG C   TCC CTCCC
                                ||||||| |   ||| |||||
                                CGGGACC G   AGG GAGGG
                                    C CGC   A
GAM195  LPIN2    3'  GCCCAGTTCCTCCCTTCTCC   31211      TGG_     __
                                GCCC    CCTCCC  CTCC
                                ||||    ||||||  ||||
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                                CGGG   GGAGGG  GAGG
                                  TCAA     AA
GAM195  LYL1     5'  TGCCCTGGCTCTGTCCC     24581         C  CCC
                                TGCCCTGGC TC   TCCC
                                ||||||||| ||   ||||
                                ACGGGACCG AG   AGGG
                                     _ AC_
GAM195  LZTS1    3'  TGCCTGTCTCTCCCCTCC    34277      C  GC_
                                TGCC TG   CTCCCCTCC
                                |||| ||   |||||||||
                                ACGG AC   GAGGGGAGG
                                  _ AGA
GAM195  MAD2L2   3'  TGCCCTAGGCGGGGATCCCCC  26808       _  CTCCCC
                                TGCCCT GGC     TCCCCC
                                |||||| |||     ||||||
                                ACGGGA CCG     AGGGGG
                                   T  CCCCT_
GAM195  MAF      5'  GCCCGCCCTCCCTCCCCC    23830     TG  TC
                                GCCC  GCC  CCCTCCCCC
                                ||||  |||  |||||||||
                                CGGG  CGG  GGGAGGGGG
                                  __  GA
GAM195  MAGEA4   3'  GCCCTGCCCCTTCCCC      14324       GCCT   _
                                GCCCTG   CCCCT CCCC
                                ||||||   ||||| ||||
                                CGGGAC   GGGGA GGGG
                                   _____    A
GAM195  MAML1    3'  GCCTACGGCCTCCTTCCCC   31285    C_     CC
                                GCC  TGGCCTCC  TCCCC
                                |||  ||||||||  |||||
                                CGG  GCCGGAGG  AGGGG
                                  AT       A_
GAM195  MAP3K10  3'  CCCTGCCCACCCTCCCCC    42754      G  TC
                                CCCTG CC  CCCTCCCCC
                                ||||| ||  |||||||||
                                GGGAC GG  GGGAGGGGG
                                  _ GT
GAM195  MAP3K11  3'  CCCTGCACCTCCCCTCCTCC  14530      _       _
                                CCCTG GCCTCCCCTCC CC
                                ||||| ||||||||||| ||
                                GGGAC TGGAGGGGAGG GG
                                   G         A
GAM195  MAP3K12  3'  GCCTTAGCCTCCCTCCTCC   26685     C       C  _
                                GCC TGGCCTCCC TCC CC
                                ||| ||||||||| ||| ||
                                CGG ATCGGAGGG AGG GG
                                  A       _  A
GAM195  MAP3K12  3'  CCCACCGCCCCTCCCCC     26682     TG  T
                                CCC  GCC CCCCTCCCCC
                                |||  ||| ||||||||||
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                                GGG  TGG GGGGAGGGGG
                                  __  C
GAM195  MAPK1    3'  TGCCCTAGGTAGTAGCCTTCCC 15656       _______    C
              T                   TGCCCT      GGCCT CCCT
                                  ||||||      ||||| ||||
                                  ACGGGA      TCGGA GGGA
                                     TCCATCA     A
GAM195  MAPK12   5'  GCTCCCGGCCCTTCCCTC    16471    _      C_
                                  GC CCTGGCCT  CCCTC
                                  || ||||||||  |||||
                                  CG GGGCCGGG  GGGAG
                                   A       AA
GAM195  MAPK12   5'  TGCGCACGGCCCCTCCCCC   16473    CC_    TCC
                                  TGC   TGGCC   CCTCCCCC
                                  |||   |||||   ||||||||
                                  ACG   GCCGG   GGAGGGGG
                                    CGT    ____
GAM195  MAPRE3   3'  TGCCCCCCTCCCTTTCCC    29541      GG     C_
                                  TGCCCT  CCTCCC  TCCC
                                  ||||||  ||||||  ||||
                                  ACGGGG  GGAGGG  AGGG
                                     __      AA
GAM195  MASP1    5'  TGCCCGGCCTTGGTCCTCC    40112      T    CC__
                                  TGCCC GGCCT    CCTCC
                                  ||||| |||||    |||||
                                  ACGGG CCGGA    GGAGG
                                     _     ACCA
GAM195  MAZ      3'  TACTCCATTCTCCCCTCTCCC  43855     C   GC       _
                                  TGC CTG  CTCCCCTC CCC
                                  ||| |||  |||||||| |||
                                  ATG GGT  GAGGGGAG GGG
                                    A   AA       A
GAM195  MBD1     5'  CGCCCTCCTCCCCTTCC     31921       GG       C
                                  TGCCCT  CCTCCCCT CC
                                  ||||||  |||||||| ||
                                  GCGGGA  GGAGGGGA GG
                                     __       A
GAM195  MBD3     3'  TGCCCTGGCCCTTGAGCCC    19425          CCCCT
                                  TGCCCTGGCCT    CCC
                                  ||||||||||    |||
                                  ACGGGACCGGG    GGG
                                         AACTC
GAM195  MBNL     5'  CTGCGCGGCCCCTCCCCC    34311     _ CT
                                  CTG GC  CCCCTCCCCC
                                  ||| ||  ||||||||||
                                  GAC CG  GGGGAGGGGG
                                    G  CC
GAM195  MDFI     3'  CCCTTCCCTTCCTTTCCCC   24615      GG  _  CC
                                  CCCT  CCT CC  TCCCC
                                  ||||  ||| ||  |||||
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                                GGGA  GGA GG  AGGGG
                                  AG   A  AA
GAM195  MEN1    5'  CCTGGCCTCGGTCCCCC    39172        CCC
                                CCTGGCCTC  TCCCCC
                                |||||||||  ||||||
                                GGACCGGAG  AGGGGG
                                     CC_
GAM195  MEST    3'  GCCCCCCTTCTCCTCCTCC   43080     GGC_  _
                                GCCCT   CTCC CCTCC
                                |||||   |||| |||||
                                CGGGG   GAGG GGAGG
                                  GGAA   A
GAM195  MGAT1   5'  TGCCCTGGGCTTGCCCGGCTCC 14440       C __  __
          C                      TGCCCTGG CT  CCC  CTCCC
                                |||||||| ||  |||  |||||
                                ACGGGACC GA  GGG  GAGGG
                                     C  AC   CC
GAM195  MGAT1   5'  GCCCGCCTCCTTTCCC     14434     TG    CC
                                GCCC  GCCTCC  TCCC
                                ||||  ||||||  ||||
                                CGGG  CGGAGG  AGGG
                                  __     AA
GAM195  MGAT3   5'  GCCCCGATCCCCTCCCCC    14459       CC
                                GCCCTGG  TCCCCTCCCCC
                                |||||||  ||||||||||
                                CGGGGCT  AGGGGAGGGGG
                                     __
GAM195  MGEA5   5'  CCGGCTCCTTCCCCTCCCCC  29213      _ __
                                CTGGC C  TCCCCTCCCCC
                                |||||  |  ||||||||||
                                GGCCG G  AGGGGAGGGGG
                                  A GA
GAM195  MLLT7   3'  CCCCTCCCAGTCCCTTCCC   25529     GG __   C
                                CCCT  CC  TCCC TCCC
                                ||||  ||  |||| ||||
                                GGGG  GG  AGGG AGGG
                                  AG  TC   A
GAM195  MNT     3'  CCCTGACTCCTCCCCC     33707       CTCC
                                CCCTGGC   CCTCCCCC
                                |||||||   ||||||||
                                GGGACTG   GGAGGGGG
                                   A___
GAM195  MOG     5'  TACAGGGCTTTCCTCCCCC   14614    CCT   CTCC
                                TGC   GGC   CCTCCCCC
                                |||   |||   ||||||||
                                ATG   CCG   GGAGGGGG
                                  TC_   AAA_
GAM195  MTA1L1  3'  TGCACGCCCCCCTCCCCC   21896    CCTG   T
                                TGC   GCC CCCCTCCCCC
                                |||   ||| ||||||||||
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                                ACG   CGG GGGGAGGGGG
                                  TG__  _
GAM195  MYLK2   3'  TGGCTTCTCCCCTCCCCC   37530     __
                                TGGC  CTCCCCTCCCCC
                                ||||  ||||||||||||
                                ACCG  GAGGGGAGGGGG
                                  AA
GAM195  MYO10   3'  GCGTGGTTCCTCCCCTCC   29571   CC  __
                                GC  TGG  CCTCCCCTCC
                                ||  |||  ||||||||||
                                CG  ACC  GGAGGGGAGG
                                 C_  AA
GAM195  MYOC    3'  GCCCTGGCTGGCTGGCTCTCCC 7031        ________  _
          T                      GCCCTGGC      CTC CCCT
                                 ||||||||      ||| ||||
                                 CGGGACCG      GAG GGGA
                                      ACCGACC   A
GAM195  MYOD1   5'  TGTCCCCCACCCCTCCCTC   42134   _   G   _
                                TG CCCT GCCTC CCCTC
                                || |||| ||||| |||||
                                AC GGGG TGGGG GGGAG
                                 A   G    A
GAM195  NCOR2   3'  CCCCGGCCCCTTCCCC     26727       T  CC
                                CCCTGGCC CC  TCCCC
                                |||||||| ||  |||||
                                GGGGCCGG GG  AGGGG
                                     _  A_
GAM195  NCOR2   3'  GCCCCTTCCCCTCCC      26734      GGCC
                                GCCCT   TCCCCTCCC
                                |||||   |||||||||
                                CGGGG   AGGGGAGGG
                                  A___
GAM195  NDRG2   3'  GCCCCAAATCCCCTCCCC   32196     TG CC
                                GCCC  G  TCCCCTCCCC
                                ||||  |  ||||||||||
                                CGGG  T  AGGGGAGGGG
                                  GT T_
GAM195  NDST1   3'  GCCAGGCTCTCCTCCCC    11369    CT   C  C
                                GCC  GGC TC CCTCCCC
                                |||  ||| || |||||||
                                CGG  CCG AG GGAGGGG
                                  T_  _ A
GAM195  NDUFB10 5'  TGCCCTGGCCTCTACCTCC   21237          C_
                                TGCCCTGGCCTC  CCTCC
                                ||||||||||||  |||||
                                ACGGGACCGGAG  GGAGG
                                       AT
GAM195  NEURL   3'  TGCGGCCTCCTCTCCTCC   20106    CCT     C   _
                                TGC   GGCCTCC CTCC CC
                                |||   ||||||| |||| ||
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                                ACG   CCGGAGG GAGG GG
                                 ___      A   A
GAM195  NEURL    3'  TGCCTGATACCCCCCTCTCCC  20104     CTG_     _
                                TGCC    GCCTCCC CTCCC
                                ||||    ||||||| |||||
                                ACGG    TGGGGGG GAGGG
                                  ACTA      A
GAM195  NIPSNAP1 3'  TGGCCTGGCCTCCTCTCTTCCG 18876    C        C   CC  III
                                TG CCTGGCCTCC CTC  CC   G
                                || ||||||||| |||  ||   |
                                AC GGACCGGAGG GAG  GG   C
                                 C        A   AA  III
GAM195  NLGN1    5'  TGCACCCCCCCCCTCC      31391     _ TGG
                                TGC CC   CCTCCCCTCC
                                ||| ||   ||||||||||
                                ACG GG   GGGGGGGAGG
                                  T  ___
GAM195  NOTCH3   3'  TGCCCTGGCTCCCATTTCCC   7742          C    C__
                                TGCCCTGGC TCCC   TCCC
                                |||||||| ||||   ||||
                                ACGGGACCG AGGG   AGGG
                                      _   TAA
GAM195  NOTCH3   5'  GCCGCGACCCTCCCCTCCTCC  7735      C    _      _
                                GCC TGGCC TCCCCTCC CC
                                ||| ||||| |||||||| ||
                                CGG GCTGG AGGGGAGG GG
                                  C    G       A
GAM195  NPR1     3'  TGCGCCACCCCTCTTCTCCCC  44588     CCTG   T     ____
                                TGC    GCC CCCCTC    CCCC
                                |||    ||| ||||||    ||||
                                ACG    CGG GGGGAG    GGGG
                                  ____  T     AAGA
GAM195  NRD1     5'  GGCCTGAACCCCTCCCCC    14856      ___
                                GGCCT   CCCCTCCCCC
                                |||||   ||||||||||
                                CCGGA   GGGGAGGGGG
                                   CTT
GAM195  NT5C2    3'  GCCCCCTCCCTCCCC       29230      TGG     C
                                GCCC   CCTCCC TCCCC
                                ||||   |||||| |||||
                                CGGG   GGAGGG AGGGG
                                  ___     _
GAM195  OPHN1    5'  TGCACTGTCCCCTCCCC     14974     C   GCC
                                TGC CTG   TCCCCTCCCC
                                ||| |||   ||||||||||
                                ACG GAC   AGGGGAGGGG
                                  T  ___
GAM195  OPHN1    3'  TGCCTGGCCTCAATCC      14975      C      CCC
                                TGCC TGGCCTC   TCC
                                |||| |||||||   |||
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                                ACGG ACCGGAG   AGG
                                  _      TT_
GAM195  P2RY6    3'  CTGTGTACCCCCTCCCCC    19990     GCC_
                                CTG    TCCCCTCCCCC
                                |||    ||||||||||
                                GAC    GGGGGAGGGGG
                                  ACAT
GAM195  PAFAH1B1 5'  GCCCGAGCGCTCCCCTCC    7710      T  _
                                GCCC GGC CTCCCCTCC
                                |||| ||| |||||||||
                                CGGG TCG GAGGGGAGG
                                  C   C
GAM195  PAX5     3'  TGCTCTCCTGCCCCTCCC    32523     C  GG  _
                                TGC CT  CCT CCCCTCCC
                                ||| ||  ||| ||||||||
                                ACG GA  GGA GGGGAGGG
                                  A  __   C
GAM195  PAX8     5'  GCCCGGTGTCTCTCCTCC    30335     T  C__   C
                                GCCC GG   CTC CCTCC
                                |||| ||   ||| |||||
                                CGGG CC   GAG GGAGG
                                  _ ACA   A
GAM195  PCDH7    5'  CCCCGAGTCCTCTCCCC     37111       CC   C
                                CCCTGG  TCC CTCCCC
                                ||||||  ||| ||||||
                                GGGGCT  AGG GAGGGG
                                   C_   A
GAM195  PDE7A    3'  CCAACCTTCCCCTCCCCC    42285   TG   _
                                C  GCCT CCCCTCCCCC
                                |  |||| ||||||||||
                                G  TGGA GGGGAGGGGG
                                 GT    A
GAM195  PDGFB    3'  TGCCTGGAGGTGCCTCCCC   15198     C   CCTCC
                                TGCC TGG    CCTCCCC
                                |||| |||    |||||||
                                ACGG ACC    GGAGGGG
                                  _   TCCAC
GAM195  PGR      5'  CCCCTTTTCTCCTCCCCC    9569      GGCC  C
                                CCCT    TC CCTCCCCC
                                ||||    || ||||||||
                                GGGG    AG GGAGGGGG
                                  AAA_  A
GAM195  PIG3     5'  TGCCCTGGTCTGCCGCGGACCC 22198        C  _  CCT__
                                TGCCCTGG CT CC    CCC
                                |||||||| || ||    |||
                                ACGGGACC GA GG    GGG
                                    A  C  CGCCT
GAM195  PIM1     3'  ACAGAAGCTTCCCCTCCC    44960    CCT   C
                                GC   GGC TCCCCTCCC
                                ||   ||| |||||||||
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                                TG   TCG AGGGGAGGG
                                 TCT   A
GAM195  PIN1     3'  TGCCCTGGGTCTGGGAGCCTCC 26322        C_  CC___
                                TGCCCTGG  CT    CCTCC
                                ||||||||  ||    |||||
                                ACGGGACC  GA    GGAGG
                                    CA  CCCTC
GAM195  PK428    5'  CCCTTCCAGCCCTCCCCC    18798     GG  TC
                                CCCT  CC  CCCTCCCCC
                                ||||  ||  |||||||||
                                GGGA  GG  GGGAGGGGG
                                  A_  TC
GAM195  PK428    5'  CCCCCGCCTTCCCTCTCC    18797     G   C    C
                                CCCT GCCT CCCTC CC
                                |||| |||| ||||| ||
                                GGGG CGGA GGGAG GG
                                  G   A    A
GAM195  PLA2G10  5'  CCCCAGCCCCTCCCCC     18672     TG   TCC
                                CCC  GCC   CCTCCCCC
                                |||  |||   ||||||||
                                GGG  CGG   GGAGGGGG
                                 GT   ___
GAM195  PLA2G2A  5'  TGCCCCGGCCGTCGCTCCCC   7154          _  CC
                                TGCCCTGGCC TC  CTCCCC
                                |||||||||| ||  ||||||
                                ACGGGGCCGG AG  GAGGGG
                                     C  C_
GAM195  PLA2G5   5'  TGGCCTGGCCTCAAATCC    9580     C       CCC
                                TG CCTGGCCTC   TCC
                                || |||||||||   |||
                                AC GGACCGGAG   AGG
                                 C        TTT
GAM195  PNOC     5'  GCACAGCCCTCCCCTTCCC    26350    CCT   _     C
                                GC   GGCC TCCCCT CCC
                                ||   |||| |||||| |||
                                CG   TCGG AGGGGA GGG
                                 TG_    G     A
GAM195  PNUTL2   3'  TGCCCTGGGTTTTCCACTTCC  38650        CC__   C  C
                                TGCCCTGG    TCC CT CC
                                ||||||||    ||| || ||
                                ACGGGACC    AGG GA GG
                                    CAAA   T  A
GAM195  PODXL    3'  CCCCAGTCTTTCCCTTCCCC   23962     TG C __    C
                                CCC  G C  TCCC TCCCC
                                |||  | |  |||| |||||
                                GGG  C G  AGGG AGGGG
                                  GT A AA    A
GAM195  PODXL    3'  CCCTGGCCTTCCTTTTCCC    23963         _  CC_
                                CCCTGGCCT CC   TCCC
                                |||||||| ||   ||||
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                                GGGACCGGA GG   AGGG
                                     A  AAA
GAM195  PODXL    3'  CCCCAGCCCCTCCCCC     23961     TG   TCC
                                CCC  GCC   CCTCCCCC
                                |||  |||   ||||||||
                                GGG  CGG   GGAGGGGG
                                  GT  ___
GAM195  POU3F2   3'  GCTCTGCCCCTCCCC      24672    C   GCCT
                                GC CTG    CCCCTCCCC
                                || |||    |||||||||
                                CG GAC    GGGGAGGGG
                                 A  ____
GAM195  PPP2R5B  3'  TGCCCTCCCCCTCCCCC     26450       GGCC
                                TGCCCT    TCCCCTCCCCC
                                ||||||    ||||||||||
                                ACGGGA    GGGGGAGGGGG
                                          ____
GAM195  PPP5C    3'  TGCTCCACCTCCTTCCTC    26495     _  TG     __
                                TGC CC  GCCTCC  CCTC
                                ||| ||  ||||||  ||||
                                ACG GG  TGGAGG  GGAG
                                  A  __     AA
GAM195  PRELP    5'  CCTCTTCCACCCCCTCCC    15548    _  GG  _
                                CC CT  CC TCCCCTCCC
                                || ||  || |||||||||
                                GG GA  GG GGGGGAGGG
                                 A  A_  T
GAM195  PRX      3'  TGTCCCGGCCTCTGACCCC   34137    C       CCCT
                                TG CCTGGCCTC    CCCC
                                || |||||||||    ||||
                                AC GGGCCGGAG    GGGG
                                 A        ACT_
GAM195  PRX      5'  GCTCCTGTGTCCTCTCCCC   34125    _   GCC   C
                                GC CCTG   TCC CTCCCC
                                || ||||   ||| ||||||
                                CG GGAC   AGG GAGGGG
                                 A    AC_   A
GAM195  PTER     5'  CCCTGGCCTTTTTAGTCTCCC  36215         CCC____
                                CCCTGGCCT      CTCCC
                                |||||||||      |||||
                                GGGACCGGA      GAGGG
                                     AAAATCA
GAM195  PTGIR    3'  TGCAGCAGCCTCCCCTTCC   9665     CC        C
                                TGC  TGGCCTCCCCT CC
                                |||  |||||||||| ||
                                ACG  GTCGGAGGGGA GG
                                  TC         A
GAM195  PTGS1    3'  GCCCTGGCCTCAGCACTC    38736          CC__
                                GCCCTGGCCTC    CTC
                                ||||||||||    |||
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                                CGGGACCGGAG   GAG
                                      TCGT
GAM195  PTPRN    3'  TGCCCTGGGCTCTGGGATGCCC 15983        C  CCCT___
             C                   TGCCCTGG CTC      CCCC
                                 |||||||| |||      ||||
                                 ACGGGACC GAG      GGGG
                                     C   ACCCTAC
GAM195  PVR      3'  CCCCTGCATCCCTTCCCCC   27107     G  C   C
                                 CCCT GC TCCC TCCCCC
                                 |||| || |||| ||||||
                                 GGGG CG AGGG AGGGGG
                                   A  T   A
GAM195  RAB1A    5'  CCCTGCTCCCCTCCCC      43185      GC
                                 CCCTG  CTCCCCTCCCC
                                 |||||  ||||||||||
                                 GGGAC  GAGGGGAGGGG
                                   __
GAM195  RBL1     5'  CCCCGACTTCTTTCTCCC    16174       C  CC_
                                 CCCTGGC TC   CTCCC
                                 |||||||  ||   |||||
                                 GGGGCTG AG   GAGGG
                                     A  AAA
GAM195  RBL1     3'  GCCTTGGCCTCCCAAAGTCC   16177     C       C___
                                 GCC TGGCCTCCC    TCC
                                 ||| |||||||||    |||
                                 CGG ACCGGAGGG    AGG
                                   A        TTTC
GAM195  REQ      3'  TGGCCTGGCCCCCTGATCCTTC 26551    C       ____  _
             CCC                   TG CCTGGCCTCC    CCT CCCC
                                   ||  ||||||||||    ||| ||||
                                   AC GGACCGGGGG    GGA GGGG
                                    C         ACTA   A
GAM195  REQ      3'  CTGATCCTTCCCCTCTCCC   26543     _  _     _
                                 CTGG CCT CCCCTC CCC
                                 |||| ||| |||||| |||
                                 GACT GGA GGGGAG GGG
                                   A  A     A
GAM195  RPL10    3'  TGCCGGACCCCTCCC       25673      CT  CCT
                                 TGCC  GG   CCCCTCCC
                                 ||||  ||   ||||||||
                                 ACGG  CC   GGGGAGGG
                                   __  T__
GAM195  RTN4     3'  CCCTGACCCTCCCC        42491       CCTC
                                 CCCTGG    CCCTCCCC
                                 ||||||    ||||||||
                                 GGGACT    GGGAGGGG
                                     ____
GAM195  RUNX3    3'  CCTATCCCCCCTCCCCC     20319      GC
                                 CCTG  CTCCCCTCCCCC
                                 ||||  ||||||||||||
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                                GGAT  GGGGGGAGGGGG
                                  A_
GAM195  S100A10  5'  GCCCTGTCTCCTCCCCC    40392      GC   CC
                                GCCCTG  CTCC  TCCCCC
                                ||||||  ||||  ||||||
                                CGGGAC  GAGG  AGGGGG
                                  A_   __
GAM195  SAS     5'  TGCACCGTCCCTCCCC     25590    CCTG  TC
                                TGC   GCC  CCCTCCCC
                                |||   |||  ||||||||
                                ACG   TGG  GGGAGGGG
                                  _____  CA
GAM195  SDC2    3'  TGCCTACCCTCCTTCCC    42576    C  G   CC
                                TGCC TG CCTCC  TCCC
                                |||| || |||||  ||||
                                ACGG AT GGAGG  AGGG
                                  _ G    A_
GAM195  SDC4    3'  CCCTGGCTTCCCTCCCC    16522      CTC
                                CCCTGGC   CCCTCCCC
                                |||||||   ||||||||
                                GGGACCG   GGGAGGGG
                                   AA_
GAM195  SERPINF2 3'  GCCCTCTCCCCCTCCC     9591      GGC    TC
                                GCCCT   CTCCCC  CCC
                                |||||   ||||||  |||
                                CGGGA   GAGGGG  GGG
                                  ____    GA
GAM195  SFRP5   3'  TGCCCTGAGCCCCTCC     16598      CCT
                                TGCCCTGG   CCCCTCC
                                ||||||||   |||||||
                                ACGGGACT   GGGGAGG
                                    C__
GAM195  SHH     3'  CCCGCGCCCCTCCCC      6793     TG  CT
                                CCC  GC  CCCCTCCCC
                                |||  ||  |||||||||
                                GGG  CG  GGGGAGGGG
                                  __  C_
GAM195  SIAT4C  3'  TGCCCTGGCCGGGCTCCC    26580        TCCC
                                TGCCCTGGCC   CTCCC
                                ||||||||||   |||||
                                ACGGGACCGG   GAGGG
                                     CCC_
GAM195  SIT     3'  GCCCTTACCCCTCCCCC     30898      GGCCT
                                GCCCT    CCCCTCCCCC
                                |||||    ||||||||||
                                CGGGA    GGGGAGGGGG
                                  AT___
GAM195  SLA2    3'  GCCCTGGTCCCACCTTCTC   37015       _  TC  __
                                GCCCTGG CC  CC  CTC
                                ||||||| ||  ||  |||
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                                CGGGACC GG  GG  GAG
                                    A  GT  AA
GAM195  SLC14A2  5'  TGCCCCTGGCCCCTCC     28402      _    TCC
                                TGCCC TGGCC   CCTCC
                                ||||| |||||   |||||
                                ACGGG ACCGG   GGAGG
                                   G    ___
GAM195  SLC18A3  5'  GCCGCTGCGCTCCCCTCCCC   16835    _  _ C
                                GCC CTG GC TCCCCTCCCC
                                ||| ||| || ||||||||||
                                CGG GAC CG AGGGGAGGGG
                                  C   G  _
GAM195  SLC19A2  5'  GCCCGGCCCCTTCCTTCTCC   42888     T     __ __
                                GCCC GGCCTC  CC  CTCC
                                |||| ||||||  ||  ||||
                                CGGG CCGGGG  GG  GAGG
                                   _     AA  AA
GAM195  SLC6A8   3'  TGCCCCTCCCCTGCCTCCC   24790      TGGC     _ _
                                TGCCC    CTCCCCT CC CCC
                                |||||    ||||||| || |||
                                ACGGG    GAGGGGA GG GGG
                                   _____      C  A
GAM195  SMAC     5'  TGCCGTGTCCCTCCTCC     39900      C  GC   C
                                TGCC TG  CTC CCTCC
                                |||| ||  ||| |||||
                                ACGG AC  GGG GGAGG
                                  C  A_   A
GAM195  SMARCC1  3'  TGCCAAACTCCCTCCCC     16906      CT   CTC
                                TGCC  GGC   CCCTCCCC
                                ||||  |||   ||||||||
                                ACGG  TTG   GGGAGGGG
                                  T_   A__
GAM195  SMURF1   3'  CCCCATCCCCCTCCCCC     45187      GC T
                                CCCTG  C CCCCTCCCCC
                                |||||  | ||||||||||
                                GGGGT  G GGGGAGGGGG
                                   A_ _
GAM195  SNK      3'  CCCTTCTCCCTCCCC       27360      GGC    C
                                CCCT   CTCCC TCCCC
                                ||||   ||||| |||||
                                GGGA   GAGGG AGGGG
                                  A__    _
GAM195  SOX11    3'  CCTACCTCCCCTCCCCC     17013      G
                                CCTG CCTCCCCTCCCCC
                                |||| ||||||||||||
                                GGAT GGAGGGGAGGGGG
                                  _
GAM195  SOX4     3'  CCCTCAACATCTCCTCCTCC   16978      _  __   _
                                CCCT GGC  CTCC CCTCC
                                |||| |||  |||| |||||
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                                GGGA TTG  GAGG GGAGG
                                  G  TA   A
GAM195  SPK     3'  TGTCCCACCCCCTTTCCC    22073   _  TG    CC
                                TG CCC  GCCTCC  TCCC
                                || |||  ||||||  ||||
                                AC GGG  TGGGGG  AGGG
                                 A  __     AA
GAM195  SPK     5'  GCTCTGGCCTCCGTTCCCC   22071   C       CC
                                GC CTGGCCTCC  TCCCC
                                || |||||||||  |||||
                                CG GACCGGAGG  AGGGG
                                 A       CA
GAM195  SPTBN4  3'  CCCTCGCCCCTCCCC      36086    G  TCC
                                CCCT GCC   CCTCCCC
                                |||| |||   |||||||
                                GGGA CGG   GGAGGGG
                                  G  ___
GAM195  SRC     3'  TGCTTGGCCTCCTTCCCC    24039    CC      CC
                                TGC  TGGCCTCC  TCCCC
                                |||  ||||||||  |||||
                                ACG  ACCGGAGG  AGGGG
                                  A_      A_
GAM195  SRRM2   3'  CTGTATCCTCCCCTCCCCC   32274    G__
                                CTG   CCTCCCCTCCCCC
                                |||   |||||||||||||
                                GAC   GGAGGGGAGGGGG
                                  ATA
GAM195  TBL1X   3'  GCCCTGACCCTTCCCC     24883         CCCC
                                GCCCTGGCCT   TCCCC
                                ||||||||||   |||||
                                CGGGACTGGG   AGGGG
                                     A___
GAM195  TCF15   3'  GCTCCTGGCCTCCTTCTCC   21422   _       C_
                                GC CCTGGCCTCC  CTCC
                                || ||||||||||  ||||
                                CG GGACCGGAGG  GAGG
                                 A         AA
GAM195  TEM5    3'  CCCACTCCCCTCCCCC     37229    TGGC
                                CCC   CTCCCCTCCCCC
                                |||   ||||||||||||
                                GGG   GAGGGGAGGGGG
                                  T___
GAM195  TEM5    3'  CCCTCCCTCCCCTTTCCC   37231     GG      CC
                                CCCT  CCTCCCCT  CCC
                                ||||  ||||||||  |||
                                GGGA  GGAGGGGA  GGG
                                  G_       AA
GAM195  TES     5'  CCTATGGGTCCCCTCCTCC   43537     GCC_      _
                                CCTG   TCCCCTCC CC
                                ||||   |||||||| ||
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                                GGAT    AGGGGAGG GG
                                  ACCC       A
GAM195  TGFB1    5'  CCTCCTCCCCCTCCTCC     8537      GG      TC  _
                                CCT  CCTCCCC  CC CC
                                |||  |||||||  || ||
                                GGA  GGAGGGG  GG GG
                                  __       GA  A
GAM195  TGFB3    3'  TGCCCTTCCTTCTCCC       17462       GG   CCC
                                TGCCCT  CCT   CTCCC
                                ||||||  |||   |||||
                                ACGGGA  GGA   GAGGG
                                  A_   A__
GAM195  THBS1    3'  TGCTTTGGCCTCTGCTCC    17514     CC      CC
                                TGC  TGGCCTC  CTCC
                                |||  |||||||  ||||
                                ACG  ACCGGAG  GAGG
                                  AA       AC
GAM195  TNFRSF6B 5'  GCCCTGACCGCCCCCTCTCC   32356         _      C
                                GCCCTGGCC TCCCCTC CC
                                |||||||||| ||||||| ||
                                CGGGACTGG GGGGGAG GG
                                     C       A
GAM195  TNFRSF8  3'  GCCTCACGACCTCTCCCTC    10322     C__      _
                                GCC   TGGCCTC CCCTC
                                |||   ||||||| |||||
                                CGG   GCTGGAG GGGAG
                                  AGT       A
GAM195  TNS      3'  CCCCACAAGCCCCTTCCCC    35470     G  CT_    _
                                CCT GC   CCCCT CCCC
                                ||| ||   ||||| ||||
                                GGG TG   GGGGA GGGG
                                  G  TTC     A
GAM195  TNXB     3'  ACCCCTCCCCTCCCCC       37147      TGGC
                                GCCC    CTCCCCTCCCCC
                                ||||    ||||||||||||
                                TGGG    GAGGGGAGGGGG
                                        ____
GAM195  TRPS1    5'  CCCCCCCCTTTCCCTCCCCC   30459      GG   C_
                                CCCT  CCT  CCCTCCCCC
                                ||||  |||  |||||||||
                                GGGG  GGA  GGGAGGGGG
                                  GG   AA
GAM195  TRPS1    3'  TGCCCTGGACCTTCAATTTCTC 30473         _   _ CC___
              C                  TGCCCTGG CCT C     CTCC
                                 |||||||| ||| |     ||||
                                 ACGGGACC GGA G     GAGG
                                     T   A TTAAA
GAM195  UBE2B    3'  CCTGGCCTCAAGTGATCCTCC  17792         C_______
                                CCTGGCCTC       CCTCC
                                |||||||||       |||||
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                                GGACCGGAG      GGAGG
                                     TTCACTA
GAM195  UBTF    3'  CCTGGCCTGGGCTCCTCC    30610        CCC   _
                                CCTGGCCT   CTCC CC
                                ||||||||   |||| ||
                                GGACCGGA   GAGG GG
                                     CCC    A
GAM195  UNC13   3'  TGCCCTGGCCATACTCC     26867         TCCC
                                TGCCCTGGCC    CTCC
                                ||||||||||    ||||
                                ACGGGACCGG    GAGG
                                      TAT_
GAM195  USP7    3'  CCACTAACCTCTTCTCCCCC   18449    _      CC
                                CC CTGGCCTC  CTCCCCC
                                || ||||||||  |||||||
                                GG GATTGGAG  GAGGGGG
                                 T       AA
GAM195  VEGF    5'  TGCGGCCCCCTCTCC       17974     CCT      C
                                TGC   GGCCTCC CTCC
                                |||   ||||||| ||||
                                ACG   CCGGGGG GAGG
                                  ___      A
GAM195  YWHAG   3'  CCCTCCCTTTCCCTCCCCC   29791     GG   C_
                                CCCT  CCT  CCCTCCCCC
                                ||||  |||  |||||||||
                                GGGA  GGA  GGGAGGGGG
                                  G_   AA
GAM195  YWHAG   3'  TGCCCCCCCCCTCCCCC     29802      TGGC
                                TGCCC    CTCCCCTCCCCC
                                |||||    ||||||||||||
                                ACGGG    GGGGGGAGGGGG
                                   _____
GAM195  YY1     5'  GCCCTGGCCGCGCCTCCTCC   18173         TCC    _
                                GCCCTGGCC   CCTCC CC
                                |||||||||   ||||| ||
                                CGGGACCGG   GGAGG GG
                                     CGC    A
GAM195  ZIC1    3'  CCCCCTCCCCCTCCCCC     18227     TGG      _
                                CCC   CCTCCCC TCCCCC
                                |||   ||||||| ||||||
                                GGG   GGAGGGG AGGGGG
                                  ___      G
GAM195  ZIC1    3'  CCCTCCCCCCTCCCCC      18228      GGC
                                CCCT   CTCCCCTCCCCC
                                ||||   ||||||||||||
                                GGGA   GGGGGGAGGGGG
                                   ___
GAM195  ZNF179  3'  CCCTGGCATCACCCTCCCCC   28375        C  _
                                CCCTGGC TC CCCTCCCCC
                                ||||||| || |||||||||
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                                GGGACCG AG GGGAGGGGG
                                    T  T
GAM195  ZNF184   5'  TACCCTGAGCTCCCCTCCCCC  45132       GC
                                TGCCCTG  CTCCCCTCCCCC
                                |||||||  ||||||||||||
                                ATGGGAC  GAGGGGAGGGGG
                                    TC
GAM195  ZNF205   3'  CGCCCTCGCCCTCCCCC     18380       G   TCCC
                                TGCCCT GCC    CTCCCCC
                                ||||||| |||    |||||||
                                GCGGGA CGG    GAGGGGG
                                   G  ____
GAM195  ZNF278   5'  TGCCCGCCCCCTCCCTTCCCC  36811      T G   _   _
                                TGCCC G CCTC CCCT CCCC
                                ||||| | |||| |||| ||||
                                ACGGG C GGGG GGGA GGGG
                                  _ G   A   A
GAM195  CAST     5'  GGGTGCGGCGGGCGGCG     11983       TT
                                GGGTGCGG  CGGGCGGCG
                                ||||||||  |||||||||
                                CCCACGCC  GCCCGCCGC
                                    __
GAM195  CDK2AP1  5'  CCTCCGGGTGCGCTCGGCG   21595   _       G    G
                                CC CCGGGTGCG TTCGG CG
                                || |||||||| ||||| ||
                                GG GGCCCACGC GAGCC GC
                                 A       _   _
GAM195  CDKN2D   5'  CCCGGGGCGCGGCCGCGG    38609    C       CGG
                                CCC GGGTGCGGTT   GCGG
                                ||| ||||||||||   ||||
                                GGG CCCGCGCCGG   CGCC
                                  C       ___
GAM195  GMPR     5'  CCTGGCTGCGGCGGCG      44954    C  G    TCG
                                CC GG TGCGGT   GGCG
                                || || ||||||   ||||
                                GG CC ACGCCG   CCGC
                                 A  G    ___
GAM195  INS      3'  GGTGCAGGAGGCGGCG      6822        TTC
                                GGTGCGG   GGGCGGCG
                                |||||||   ||||||||
                                CCACGTC   TCCGCCGC
                                    C__
GAM195  IRS2     5'  CCTCGGGCTCTCGGGCGGCG  40698   C    GCGGT
                                CC CGGGT    TCGGGCGGCG
                                || |||||    ||||||||||
                                GG GCCCG    AGCCCGCCGC
                                 A    AG___
GAM195  ITGB1    5'  CCCGGGTGTCGGGCGCGGCG  38045       CGGT    __
                                CCCGGGTG   TCGGGC  GGCG
                                ||||||||   ||||||  ||||
```

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                                GGGCCCAC   AGCCCG  CCGC
                                    ____     CG
GAM195  NR2F2   5' CCCCTGGCTGCGGGCGGC   34231     C  G   GGTTC
                                CCCC GG TGC    GGGCGGC
                                |||| || |||    |||||||
                                GGGG CC ACG    CCCGCCG
                                  A  G  _____
GAM195  TRAF5   5' CCTGGCTGCGGCCGGCG    21468    C  G     CG
                                CC GG TGCGGTT  GGCG
                                || || |||||||  ||||
                                GG CC ACGCCGG  CCGC
                                 A  G     __
GAM195  TRAF5   3' CCTGGGTGTGGTGACGGGCG  21469    C    C  T_
                                CC GGGTG GGT  CGGGCG
                                || ||||| |||  ||||||
                                GG CCCAC CCA  GCCCGC
                                 A    A  CT
GAM195  VPREB1  3' CCTCGGCGCTTCGGGCGGCG  28322    G_    GG
                                CC  GGTGC  TTCGGGCGGCG
                                ||  |||||  ||||||||||
                                GG  CCGCG  AAGCCCGCCGC
                                 AG    __
GAM196  CAV2    3' ATCTACTTTCACATTTATTT  10285    _      GTG
                                ATC ACTTTCACG   ATTT
                                ||| |||||||||   ||||
                                TAG TGAAAGTGT   TAAA
                                  A        AAA
GAM196  CENPB   3' ACTTCCACGGTGGGGGGCCTCT 43010          ATTTA_
                                ACTTTCACGGTG     TTCT
                                ||||||||||||     ||||
                                TGAAGGTGCCAC     GAGA
                                      CCCCCG
GAM196  GPR63   3' ATCACTTTCCTATTATTTATTC 36264        ACG  G
           T                    ATCACTTTC   GT ATTTATTCT
                                |||||||||   || |||||||||
                                TAGTGAAAG   TA TAAATAAGA
                                     GA_  A
GAM196  HGF     3' ATCATGACAAGTGATTTATT   45317     CTTT  C
                                ATCA    CA GGTGATTTATT
                                ||||    || ||||||||||||
                                TAGT    GT TCACTAAATAA
                                  ACT_  _
GAM196  POLR2E  3' CTTTCACAGGCACGTTTATT   40918       _   A_
                                CTTTCAC GGTG  TTTATT
                                ||||||| ||||  ||||||
                                GAAAGTG CCGT  AAATAA
                                    T   GC
GAM196  ZNF36   3' ATCACTTTCGTGGAGCCAATCT 45287        AC  TGAT   T
                                ATCACTTTC  GG    TTA TCT
                                |||||||||  ||    ||| |||
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                                TAGTGAAAG  CC   GGT AGA
                                     CA  TC__   T
GAM196  DHFR    3'  AGTGGGGAATAAAAACAA   8988    C   T
                                AG GGG AATAAAAACAA
                                || ||| ||||||||||
                                TC CCC TTATTTTTGTT
                                 A   C
GAM197  FMN2    3'  GAACTGTCTAGAAAACA    44285       CAAC  CT
                                GAACTGTCT   GA  GCA
                                |||||||||   ||  |||
                                CTTGACAGA   CT  TGT
                                     T___  TT
GAM197  IL1A    3'  GAACTGTCAACACTGC     41675       TC   G
                                GAACTGTC  AAC ACTGC
                                ||||||||  ||| |||||
                                CTTGACAG  TTG TGACG
                                     __   _
GAM197  SLC30A3  5'  CGAACTGCAGCGACTG     18428       CTCAA
                                CGAACTGT    CGACTG
                                ||||||||    ||||||
                                GCTTGACG    GCTGAC
                                     TC___
GAM197  TMEPAI   3'  GAGGACTGTCTCAGCCTG    33608   __      ACGA
                                GA  ACTGTCTCA   CTG
                                ||  |||||||||   |||
                                CT  TGACAGAGT   GAC
                                 CC       CG__
GAM197  TOX     3'  GAACTGCCTTGACTG      31272       CAAC
                                GAACTGTCT   GACTG
                                |||||||||   |||||
                                CTTGACGGA   CTGAC
                                     A___
GAM197  FGFRL1   3'  GCCTTCGTCTGCAGCTCCGT   34910   _      CT  GAC
                                GC TTCGTCTGC  GC   CCGT
                                || |||||||||  ||   ||||
                                CG AAGCAGACG  CG   GGCA
                                 G       T_  A__
GAM197  TCAP    3'  CAGCTTCTTCTGCCTAGAGCG  18946       G    ___
                                CAGCTTC TCTGCCT   GCG
                                ||||||| |||||||   |||
                                GTCGAAG AGACGGA   CGC
                                    A      TCT
GAM198  SLC17A5  3'  CATAGAACAGGCTGGGCACA  29686    TA       ACAT
                                CAT  AACAGGCTGG   GCGCG
                                |||  ||||||||||   |||||
                                GTA  TTGTCCGACC   CGTGT
                                  TC       _____
GAM198  APOB    3'  CAGGTCCAGTTCATATGTGC   7542        C   AAG__
                                CAGGTCCAG TTA    GC
                                |||||||||  |||    ||
```

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                                GTCCAGGTC AGT    CG
                                     A  ATACA
GAM198  CDK6    3'  CAGGATCAGCTTAAGGCGGC  10383     TC      A  _
                                CAGG  CAGCTTAA GGCG C
                                ||||  |||||||| |||| |
                                GTCC  GTCGAATT CCGC G
                                  TA      _   C
GAM198  DXYS155E  3'  CAGGCCCAGCGCGC       22945         TTAAAG
                                CAGGTCCAGC     GCGC
                                ||||||||||     ||||
                                GTCCGGGTCG     CGCG
                                       ______
GAM198  FGFR3   3'  ACAGGTCCAGTTTTAAAACA  6610          C  A
                                ACAGGTCCAG TT AAGGCG
                                |||||||||| || ||||||
                                TGTCCAGGTC AA TTTTGT
                                     A  A
GAM198  GRAF    3'  CAGGCTTAGCTACACA     31440      CC   TAAAG
                                CAGGT  AGCT    GCGCA
                                |||||  ||||    |||||
                                GTCCG  TCGA    TGTGT
                                  AA   ______
GAM198  KCNAB1   3'  ACAGGTTTACTTAAAAA     41398       CCA
                                ACAGGT   GCTTAAAGG
                                ||||||   |||||||||
                                TGTCCA   TGAATTTTT
                                   AA_
GAM198  MAP3K7IP1 3'  ACAGGTCCAGTCTGCA      25920          _  TAAAGGC
                                ACAGGTCCAG CT      GCA
                                |||||||||| ||      |||
                                TGTCCAGGTC GA      CGT
                                     A  ________
GAM198  PI3     5'  AGTCCAGCTTGGCCTGGC    15278          AAA  ___
                                GGTCCAGCTT   GGC   GC
                                ||||||||||   |||   ||
                                TCAGGTCGAA   CCG   CG
                                     ___  GAC
GAM198  SLC25A17  3'  ACAGGTCCAGTTGGCCA     26822          CTTAAA   G
                                ACAGGTCCAG     GGC CA
                                ||||||||||     ||| ||
                                TGTCCAGGTC     CCG GT
                                     AA____  _
GAM199  ASTN    3'  CAGAACTGGGTATCCCAGAGT  42940        AT   CAG
                                CAGAACT  GTAT   CCTAGAGT
                                |||||||  ||||   ||||||||
                                GTCTTGA  CATA   GGGTCTCA
                                   CC   ___
GAM199  BMP1    3'  CAGAACTTGCCATGCAGCTTGG 25974        A  AT__   CTA
           AGT                   CAGAACT TGT   CAGC   GAGT
                                |||||||  |||   ||||   ||||
```

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                                GTCTTGA ACG   GTCG  CTCA
                                   _  GTAC   AAC
GAM199  HMOX2   3'  CAGAAGTGTGGAAGCCTGGAGT 42172     CTA  ATC   A
                                CAGAA  TGT  AGCCT GAGT
                                ||||||  |||  ||||| ||||
                                GTCTT  ACA  TCGGA CTCA
                                   C__  CCT   C
GAM199  PRSS16  3'  CAGAATCATGAATCCCTAGAGT 25233     C   T  AG
                                CAGAA TATG ATC  CCTAGAGT
                                ||||| |||| |||  ||||||||
                                GTCTT GTAC TAG  GGATCTCA
                                   A   T  __
GAM200  HTR2A   3'  GAACCCCGCTTTTCATTGACA  8388      TG  A_  C
                                GAACT  CC  TT TCATTGACA
                                |||||  ||  || |||||||||
                                CTTGG  GG  AA AGTAACTGT
                                   __  CG  A
GAM200  KMO     3'  TAGAACTCAAGGTTTTCATTGA 18957       GCCATTC
            CA                    TAGAACTT     TCATTGACA
                                |||||||      |||||||||
                                ATCTTGAG     AGTAACTGT
                                     TTCCAAA
GAM200  MMP13   3'  TAAATTATGCTCTCATTGACA  14554     ACT  CAT
                                TAGA  TGC  TCTCATTGACA
                                ||||  |||  ||||||||||
                                ATTT  ACG  AGAGTAACTGT
                                  AAT  ___
GAM200  PEX10   3'  CTGCTGTTCTCACTGCA     15218     CA      A
                                TTGC  TTCTCATTG CA
                                ||||  ||||||||| ||
                                GACG  AAGAGTGAC GT
                                  AC       _
GAM200  PGAM1   3'  TAGAACTGCTATTCTGAC    44059       T  C    CATT
                                TAGAACT GC ATTCT   GAC
                                ||||||| || |||||   |||
                                ATCTTGA CG TAAGA   CTG
                                     _  A    ____
GAM201  MARK3   5'  GGCCGCCGCGGGCTGTGG    14360      T A  TTCAC  C
                                GGCCGC C CG    GC GTGG
                                ||||||  | ||    || ||||
                                CCGGCG G GC    CG CACC
                                   _ C  C____  A
GAM201  PML     3'  GGCCGCTCTGACCGTG     37731        ACGTTCAC
                                GGCCGCTC      GCCGTG
                                ||||||||      ||||||
                                CCGGCGAG      TGGCAC
                                     AC_____
GAM201  PRKCI   5'  GGCGCTTCGGGCGCCGTGG   15634    C   CA  TTCA
                                GGC GCT  CG   CGCCGTGG
                                |||  |||  ||   ||||||||
```

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                                CCG CGA  GC    GCGGCACC
                                  _  A_  CC__
GAM201  SHB      5'  GGCCGTACGCCCCTCGCCGTGG 16690      CTC     A_
             A                    GGCCG   ACGTTC  CGCCGTGGA
                                  |||||   ||||||  |||||||||
                                  CCGGC   TGCGGG  GCGGCACCT
                                    A__     GA
GAM201  WHSC1    3'  GGCAGCTCACACAGCTGTGGA  39371     C      TT  C  C
                                  GGC GCTCACG  CA GC GTGGA
                                  |||  |||||||  ||  ||  |||||
                                  CCG CGAGTGT  GT CG CACCT
                                    T      __  _  A
GAM201  WHSC1    5'  GGCAGCTCACACAGCTGTGGA  39371     C      TT  C  C
                                  GGC GCTCACG  CA GC GTGGA
                                  |||  |||||||  ||  ||  |||||
                                  CCG CGAGTGT  GT CG CACCT
                                    T      __  _  A
GAM202  ANK1     3'  AGCTGCGGGGTCCGCGGGG   33848      _     AC
                                  GGTT CGGGG  CCGCGGGG
                                  ||||  |||||  ||||||||
                                  TCGA GCCCC  GGCGCCCC
                                    C    A_
GAM202  DDX3     3'  ATGCAGTTTGGGATGGGG    35812        CG    CCCGC
                                  ATGCGGTT  GGGA    GGGG
                                  ||||||||  ||||    ||||
                                  TACGTCAA  CCCT    CCCC
                                      A_    A____
GAM202  IL12RB2  5'  CGCGGTCCCGGGCCTGCGGGGA 11427        G   A  C
                                  TGCGGTTC GGG CC GCGGGGA
                                  |||||||| ||| ||  |||||||
                                  GCGCCAGG CCC GG CGCCCCT
                                      G   _  A
GAM202  IRS2     5'  GTCCGGGGAGGCCCGCGGGG   40712         __
                                  GTTCGGGGA  CCCGCGGGG
                                  |||||||||  |||||||||
                                  CAGGCCCCT  GGGCGCCCC
                                       CC
GAM202  MTA1L1   5'  GTCCGGGAGGCTCGCGGGG   21893        ACC_
                                  GTTCGGGG   CGCGGGG
                                  ||||||||   |||||||
                                  CAGGCCCT   GCGCCCC
                                      CCGA
GAM202  PDLIM1   5'  GCGGGCGACGACCCGCGGGGA  34192     TT   G
                                  GCGG  CGG GACCCGCGGGGA
                                  ||||  |||  ||||||||||||
                                  CGCC  GCT CTGGGCGCCCCT
                                    C_   G
GAM202  RUNX3    3'  GCAGCTGGGGGTCCGCGGGG   20322      C    AC
                                  GCGGTT GGGG  CCGCGGGG
                                  ||||||  ||||  ||||||||
```

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                                CGTCGA CCCC  GGCGCCCC
                                   _   CA
GAM202  CTSF    3'  TCCCGAGCTGGGGGCCCC    45367       C  ATCAGA
                                TCCCGAGC GG     GCCCT
                                |||||||| ||     |||||
                                AGGGCTCG CC     CGGGG
                                    A  CC_____
GAM202  FGF4    3'  TTCCCGAGGCTGAGGCAAGGGT 12854       CCG  TCA   C__
          CCTC                    TTCCCGAG   GA   GAG   CCTC
                                |||||||||   ||   |||   ||||
                                AAGGGCTC   CT   TTC   GGAG
                                    CGA  CCG   CCA
GAM202  GFRA1   5'  CCGAGCAGAGCCCT       23564       CGGATC
                                CCGAGC     AGAGCCCT
                                ||||||     ||||||||
                                GGCTCG     TCTCGGGA
                                  _______
GAM202  HTR1E   5'  CTCCTGAGCTGGATCAGAGC   9271      C    C
                                TTCC GAGC GGATCAGAGC
                                |||| |||| ||||||||||
                                GAGG CTCG CCTAGTCTCG
                                  A   A
GAM202  TLX1    5'  TTCCCGGCCTGTTGGAGCCCTC 24351       A   GGATCA
                                TTCCCG GCC     GAGCCCTC
                                |||||| |||     ||||||||
                                AAGGGC CGG     CTCGGGAG
                                   _  ACAAC_
GAM202  TOP3B   5'  CTCCCGAGCTCGCGGGTC    19463        ___   A
                                TTCCCGAGC   CGG TC
                                |||||||||   ||| ||
                                GAGGGCTCG   GCC AG
                                     AGC   C
GAM202  WARS    3'  GAACCCTCGGAGTCCTC     42621       GGA  A   C
                                GAGCC   TC GAG CCTC
                                |||||   || ||| ||||
                                CTTGG   AG CTC GGAG
                                  G__  C   A
GAM203  ACN     3'  TGGTATGTATGTAGGGATAGG  31413          GCTACTA
                                TGGTATGTGTG      ATAGG
                                ||||||||||       |||||
                                ACCATACATAC      TATCC
                                     ATCCC__
GAM203  KCNS3   5'  TGGAATGTGTGGTGCACATAGG 13937     T       CTACTA
          C                      TGG ATGTGTGG     ATAGGC
                                ||| ||||||||     ||||||
                                ACC TACACACC     TATCCG
                                  T       ACGTG_
GAM203  MNT     3'  TGGAATGTGTGGAGCTGGTGGG 33726     T       CTA  AATA
                                TGG ATGTGTGG   CT    GG
                                ||| ||||||||   ||    ||
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                                ACC TACACACC   GA    CC
                                  T       TC_  CCAC
GAM203  PTBP1    3'  TGGGTGTGTGGCTGCAGGAAGG 36724     TA       ACTAAT
              C                   TGG  TGTGTGGCT     AGGC
                                  |||  |||||||||      ||||
                                  ACC  ACACACCGA     TCCG
                                    C_       CGTCCT
GAM204  BSN      3'  CAAGGGCTGTGCCTTGAA    18393     T  A    CTTT
                                  CAA GG CTGT    GTCTTGAA
                                  ||| || ||||    ||||||||
                                  GTT CC GACA    CGGAACTT
                                    C  _   _____
GAM204  DDX3     3'  AATGTACTGCGAGTTCTTGAAA 35809      G     CTTTG
                                  AATG ACTGT     TCTTGAAA
                                  |||| |||||     ||||||||
                                  TTAC TGACG     AGAACTTT
                                    A     CTCA_
GAM204  DXF68S1E 3'  TGATGTTCCATTTTGTCTTG   41040    A   GA    C
                                  C ATG  CTGT TTTGTCTTG
                                  | |||  |||| |||||||||
                                  A TAC  GGTA AAACAGAAC
                                   C   AA   _
GAM204  EIF2C1   3'  CAATGGATTTTAACCATCTTGA 29173         CTGTCT TG
                                  CAATGGA     T  TCTTGA
                                  |||||||     |  ||||||
                                  GTTACCT     G  AGAACT
                                       AAAATT GT
GAM204  GAN      3'  AATGAACTGTCTCCTTG     35135            TGT
                                  AATGGACTGTCTT   CTTG
                                  ||||||||||||   ||||
                                  TTACTTGACAGAG   GAAC
                                                 ___
GAM204  GSPT1    5'  CAATGACTGTTCCTCTTGA    13304      G     CT  G
                                  CAATG ACTGT  TT TCTTGA
                                  ||||| |||||  || ||||||
                                  GTTAC TGACA  AG AGAACT
                                     _     __  G
GAM204  PCDH9    3'  GGGGCCCTTTGTCTTGAA    44403    ACTG
                                  GG    TCTTTGTCTTGAA
                                  ||    ||||||||||||
                                  CC    GGAAACAGAACTT
                                    CCG_
GAM204  PTGS1    3'  GGGCTGTCTGCCCTGA      38739    A     TT
                                  GG CTGTCT  GTCTTGA
                                  || ||||||  |||||||
                                  CC GACAGA  CGGGACT
                                    C      __
GAM204  RP42     3'  AATGGACTGTTTGTCTGAAA  33977          CT     T
                                  AATGGACTGT  TTGTCT GAAA
                                  ||||||||||  |||||| ||||
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                                TTACCTGACA  AACAGA CTTT
                                   __     _
GAM204  SLC1A4   3'  CAATGTGATTGTTTCCCTTGAA 16741      _ C   CT  G
            A                    CAATG GA TGT  TT TCTTGAAA
                                 ||||| || |||  || ||||||||
                                 GTTAC CT ACA  AA GGAACTTT
                                    A  A   __ G
GAM204  ZNF268   3'  ATGAGGTTTTTGTCTTGAAA   41758     ACT  C
                                 ATGG   GT TTTGTCTTGAAA
                                 ||||   || ||||||||||||
                                 TACT   CA AAACAGAACTTT
                                   C__  A
GAM205  AKAP13   3'  AGGGGTGGTATGTGCCCGGGAT 28468    A   __ C        C
            GG                     AG GGGT  TA GTGCCCGGGA GG
                                 || ||||  || ||||||||||| ||
                                 TC CCCA  AT CACGGGCCCT CC
                                  _   CC  A        A
GAM205  CD3E     3'  AGAGGGCTGCAAAAGGGGACGG 8812         A  TGCCC
                                 AGAGGGTT CG    GGGACGG
                                 |||||||| ||    |||||||
                                 TCTCCCGA GT    CCCTGCC
                                      C  TTTC_
GAM205  IGF1     3'  AGAGGATTATGTGTTGG     8333          C   CCCG
                                 AGAGGGTTA GTG    GG
                                 ||||||||| |||    ||
                                 TCTCCTAAT CAC    CC
                                       A   AA__
GAM205  OTOF     3'  AGGGTGTGCCCGGGATGG    22055      TAC        C
                                 AGGGT   GTGCCCGGGA GG
                                 |||||   |||||||||| ||
                                 TCCCA   CACGGGCCCT CC
                                    ____         A
GAM205  RAB3A    3'  GAGGGGCAGGGCTTGGGGCGG  16061      T  CGT  CC   A
                                 GAGGG TA   GC  GGG CGG
                                 ||||| ||   ||  ||| |||
                                 CTCCC GT   CG  CCC GCC
                                    C  CC_  AA   C
GAM205  SCG3     5'  GAGGGTGGGTGTGGGGCGG   29888       TAC   CCC   A
                                 GAGGGT   GTG   GGG CGG
                                 ||||||   |||   ||| |||
                                 CTCCCA   CAC   CCC GCC
                                    CC_   AC_   _
GAM205  SYBL1    5'  GAGGGCGCGCGGGCTCGGGACG 24847       TA_  T  C
            G                     GAGGGT   CG GC CGGGACGG
                                 ||||||   || || ||||||||
                                 CTCCCG   GC CG GCCCTGCC
                                    CGC  C  A
GAM205  UTY      5'  AAAAGGGTAGTCTCTGGGATGG 28307         TACGTGCCC   C
                                 AAGAGGGT        GGGA GG
                                 ||||||||        |||| ||
```

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                                TTTTCCCA       CCCT CC
                                    TCAGAGA__    A
GAM205  AXL     3'  ACCACATAATGTCAGAGCTTTA 34877          CCCTACT
              G                  ACCACATGATG      TTTTAG
                                 ||||||||||       ||||||
                                 TGGTGTATTAC      GAAATC
                                     AGTCTC_
GAM205  CBFA2T2  3'  CACATGTTGCATCTCTTTTTAG 22969       A   C_  A
                                 CACATG TGC  CT CTTTTTAG
                                 |||||| |||  || ||||||||
                                 GTGTAC ACG  GA GAAAAATC
                                    A   TA  _
GAM205  MAPRE1   3'  CAACGATGCCTCTTGCTTTTTA 29519    C       _  A_
              G                  CA ATGATGCC CT  CTTTTTAG
                                 || |||||||| ||  ||||||||
                                 GT TGCTACGG GA  GAAAAATC
                                  _       A  AC
GAM205  NOLA1    3'  CATGATGCTGACATTTTAG   37423        CCT  T
                                 CATGATGC   AC TTTTAG
                                 ||||||||   || ||||||
                                 GTACTACG   TG AAAATC
                                      AC_  T
GAM205  PPP1R3D  3'  CCACCTGAGGCTACTTTTTAG  26424      A   T  CC
                                 CCAC TGA GC  TACTTTTTAG
                                 |||| ||| ||  ||||||||||
                                 GGTG ACT CG  ATGAAAAATC
                                   G   C  __
GAM205  PSMB7    3'  CCACATGAGTGTCTTACT    15824         _  CCC
                                 CCACATGA TG   TACT
                                 |||||||| ||   ||||
                                 GGTGTACT AC   ATGA
                                      C  AGA
GAM205  RTN1     3'  ACATGCTGGTACTTTTTAG   34470       A  CCC
                                 ACATG TG   TACTTTTTAG
                                 ||||| ||   ||||||||||
                                 TGTAC AC   ATGAAAAATC
                                    G  C__
GAM205  SUDD     3'  ACCTATGATGCCTTTTCTTAG  19259     AC       CTAC
                                 ACC  ATGATGCC    TTTTTAG
                                 |||  ||||||||    |||||||
                                 TGG  TACTACGG    AAGAATC
                                   A_       AA__
GAM206  NFYA     3'  TAAGTGGTTTCTGTCCTGTAG  14768    T     AGG   C
                                 A AGTGG   TTG CCTGTAG
                                 | |||||   ||| |||||||
                                 A TCACC   GAC GGACATC
                                  T    AAA   A
GAM207  GJA5     3'  CTCCTGACCTCGTAC       23581      AAACG
                                 CTCC     TGACCTCGTAC
                                 ||||     ||||||||||
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                                GAGG    ACTGGAGCATG
                                  _____
GAM208  NPY1R   3'  TGATTTCAACCCCATTCCTTGG 9484      _ TG  A  CC
            GA                    TGAT T  GCT TCA  CCTTGGGA
                                  |||| |  ||| |||  ||||||||
                                  ACTA A  TGG GGT  GGAACCCT
                                    A GT  _  AA
GAM208  PROX1   3'  TAATTTGGCCTTTTGG      15723          ATCACCCC
                                  TGATTTGGCT       TTGG
                                  ||||||||||       ||||
                                  ATTAAACCGG       AACC
                                       AA_______
GAM208  TRIM    3'  TGATTTGGTTATCAGTGGG   32302        C    CCCCT
                                  TGATTTGG TATCA    TGGG
                                  |||||||| |||||    ||||
                                  ACTAAACC ATAGT    ACCC
                                       A    C____
GAM209  ABCB11  3'  TATTATGGAAGGCCATTAGAAA 19045    C       GCTG
                                  TAT ATGGGAGGC   GGAGA
                                  ||| |||||||||   |||||
                                  ATA TACCTTCCG   TCTTT
                                    A       GTAA
GAM209  ATRX    3'  CATCATGGGAAAGTGGGGGAGA 39604          CGCT
                                  TATCATGGGAGG   GGGAGA
                                  ||||||||||||   ||||||
                                  GTAGTACCCTTT   CCCTCT
                                       CACC
GAM209  CD72    3'  TACCATGGGAAGTTCTTGGGGG 12141          CG ____
            GAG                   TATCATGGGAGG  CT   GGGAG
                                  ||||||||||||  ||   |||||
                                  ATGGTACCCTTC  GA   CCCTC
                                       AA  ACCC
GAM209  EGFL4   3'  TCATAGGAGGTGGAGA     41584          CGCTG
                                  TCATGGGAGG    GGAGA
                                  ||||||||||    |||||
                                  AGTATCCTCC    CCTCT
                                       A____
GAM209  EHD3    3'  TCCTGGGAGGCTGCAGGG    31115    A      _  T
                                  TC TGGGAGGC GC GGG
                                  || |||||||| || |||
                                  AG ACCCTCCG CG CCC
                                    G       A  T
GAM209  FRDA    3'  TATCATGTGAGGGAGGAA    6626        G   CGCT
                                  TATCATG GAGG   GGGAG
                                  ||||||| ||||   |||||
                                  ATAGTAC CTCC   TCCTT
                                       A   C___
GAM209  GPR86   3'  TATTATGGGAGATACCAAGAAA 35796    C      GC  TG
                                  TAT ATGGGAG  GC  GGAGA
                                  ||| |||||||  ||  |||||
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                                ATA TACCCTC  TG  TCTTT
                                  A      TA  GT
GAM209  IHPK1    3'  CATGGGGCAGGGAGAA      45484       AGGC  T
                                CATGGG    GC GGGAGAA
                                ||||||    || |||||||
                                GTACCC    CG CCCTCTT
                                   ____  T
GAM209  KMO      3'  TGGGAGGCTGAAGTGGGAG    18962        GC___
                                TGGGAGGC    TGGGAG
                                ||||||||    ||||||
                                ACCCTCCG    ACCCTC
                                     ACTTC
GAM209  LUZP1    3'  TCTGGGGGGCAAAAGAAA    37965    A   A   CT
                                TC TGGG GGCG  GGGAGA
                                || |||| ||||  ||||||
                                AG ACCC CCGT  TTCTTT
                                 _   C   T_
GAM209  MAP4     3'  CATGGGAGGAGGGAA       36270        CGCT
                                CATGGGAGG   GGGAG
                                |||||||||   |||||
                                GTACCCTCC   CCCTT
                                     T___
GAM209  MPL      3'  ACTCTAGGTGCTGGGGGAAA  23878    GGG  C    A
                                AT  AGG GCTGGG GAAA
                                ||  ||| |||||| ||||
                                TG  TCC CGACCC CTTT
                                 AGA  A    C
GAM209  MYBL2    3'  ACGTGGGCTTGGGAGAA     14700     GGA  GC
                                ATG  GGC  TGGGAGAA
                                |||  |||  ||||||||
                                TGC  CCG  ACCCTCTT
                                 AC_  A_
GAM209  NCOA6    5'  CATGGGAGGTGGGAG       30434        CGC
                                CATGGGAGG  TGGGAG
                                |||||||||  ||||||
                                GTACCCTCC  ACCCTC
                                    ___
GAM209  NTSR1    3'  TCATGGGAGCTCTGTGGGGGAG 14894         G G  _____
                                TCATGGGAG C CT   GGGAG
                                ||||||||| | ||   |||||
                                AGTACCCTC G GA   CCCTC
                                     _ A  CACC
GAM209  PVR      3'  ATGGCTCCACTGGGAGA     27106      GAGG
                                ATGG   CGCTGGGAGA
                                ||||   ||||||||||
                                TACC   GTGACCCTCT
                                  GAG_
GAM209  TCF1     3'  TCATGGGGCCTGGGAGA     8093         AG  G
                                TCATGGG  GC CTGGGAGA
                                |||||||  || ||||||||
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                                AGTACCC  CG GACCCTCT
                                   __ _
GAM209  TFE3     3'  TCATGGGAGGGTGGGGGAAA  27172         CGC    A
                                TCATGGGAGG   TGGG GAAA
                                ||||||||||   |||| ||||
                                AGTACCCTCC   ACCC CTTT
                                   C__    C
GAM210  BHLHB3   3'  TCTGTACAGATAGATATCTA  36260         TAACT
                                TCTGTACGG    GATATCTA
                                |||||||||    ||||||||
                                AGACATGTC    CTATAGAT
                                   TAT__
GAM210  FLRT2    3'  TCTGTACAGTGACATTTAC   29858         AACT    C
                                TCTGTACGGT   GATAT TAC
                                ||||||||||   ||||| |||
                                AGACATGTCA   CTGTA ATG
                                   _____     A
GAM210  RCN1     3'  TCTGTACAGGTTGTGTCTGCC  16208       _  AAC  ATA   A
                                TCTGTAC GGT   TG   TCT CC
                                |||||||  |||   ||   ||| ||
                                AGACATG CCA   AC   AGA GG
                                   T   ___  AC_   C
GAM211  DKK1     3'  TCAGAAAATAAGCTAGTATTTT 29271        _    TAA
                                TCAGAAAG AGGTT   TATTTT
                                ||||||||  |||||   ||||||
                                AGTCTTTT TTCGA   ATAAAA
                                   A     TC_
GAM211  KERA     3'  AGAAAGCATTCAATATTTT   28152       AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
                                TCTTTC  TAAGTTATAAAA
                                  G_
GAM211  PPP1R12A 3'  CCAGAAAGATGTAGTATTTT  14726         G  TTAA
                                TCAGAAAGA GT    TATTTT
                                |||||||||  ||    ||||||
                                GGTCTTTCT CA    ATAAAA
                                   A  TC__
GAM211  S100B    3'  GAAAGAGGTTTTCAATTTT   26568          AAT
                                GAAAGAGGTTT   ATTTT
                                ||||||||||   |||||
                                CTTTCTCCAAA   TAAAA
                                   AGT
GAM212  DSC3     3'  TAAGTCTAAAACACATAGATTT 35946       AGT      A
          TA                    TAAGTT   AATACATA ATTTTA
                                ||||||   |||||||| ||||||
                                ATTCAG   TTGTGTAT TAAAAT
                                  ATT       C
GAM213  ABL2     5'  CAGCCCAGGCCCTGGCCCT   28722        A_   A
                                CAGCCTA  CCCT GCCCT
                                |||||||  |||| |||||
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                                GTCGGGT  GGGA CGGGA
                                    CC   C
GAM213  ACK1    3'  CCTTGGTCTCCTTCCAGCCCT  25111    GCAG__  AACC
                                CCT    CCT   CTAGCCCT
                                |||    |||   ||||||||
                                GGA    GGA   GGTCGGGA
                                  ACCAGA  A___
GAM213  ADAM12  3'  CCTGAAGCCCCTTGGCTCT  18469    C   TAAC  A_ C
                                CCTG AGCC   CCT  GC CT
                                |||| ||||   |||  || ||
                                GGAC TCGG   GGA  CG GA
                                  T   _____  AC  A
GAM213  ADAMTS13 5'  CCTGCAGCCCAGTCCTGC   40030         AC  A
                                CCTGCAGCCTA  CCT GC
                                ||||||||||  ||| ||
                                GGACGTCGGGT  GGA CG
                                      CA  _
GAM213  ADAMTS4  5'  CCTCCACACCCTAGC      23003    G  G CTA
                                CCT CA C   ACCCTAGC
                                ||| || |   ||||||||
                                GGA GT G   TGGGATCG
                                  G  _ ___
GAM213  BACE2    3'  CCTGCAGCCCAATCCACT    39988          _ _
                                CCTGCAGCCTAA CC CT
                                |||||||||||| || ||
                                GGACGTCGGGTT GG GA
                                      A  T
GAM213  BLTR2    5'  CCTGCAGCCTGCCTCTTTTCTG 33364         AA  _  A____
           CC                     CCTGCAGCCT  CC CT    GCC
                                ||||||||||  || ||    |||
                                GGACGTCGGA  GG GA    CGG
                                      C_  A  AAAGA
GAM213  BPI     3'  CTGCAGCCTTAGCCCT      11899         AACCC
                                CTGCAGCCT    TAGCCCT
                                |||||||||    |||||||
                                GACGTCGGA    ATCGGGA
                                             _____
GAM213  BRCA1    3'  CTGTGCTTCCAGCCCTA     28630    CA  CTAACC
                                CTG  GC     CTAGCCCTA
                                |||  ||     |||||||||
                                GAC  CG     GGTCGGGAT
                                  A_  AA____
GAM213  CACNG3   5'  CTGCAGCCGGGTAACCTAG   27235        ___    C
                                CTGCAGCC   TAACC TAG
                                ||||||||   ||||| |||
                                GACGTCGG   ATTGG ATC
                                     CCC    _
GAM213  CSPG3    3'  CTGGGCTCATCTAGCCCTAA  20486    CA  C  ACC
                                CTG  GC TA   CTAGCCCTAA
                                |||  || ||   ||||||||||
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                                GAC  CG GT   GATCGGGATT
                                  C_  A  A__
GAM213  DGKG    3'  CCTGCAGCCTGCTCCTCGC   10651         AAC   A
                                CCTGCAGCCT   CCT GC
                                ||||||||||   ||| ||
                                GGACGTCGGA   GGA CG
                                     CGA   G
GAM213  DPYSL2  3'  CTGCAGCCTCATACCTCTAA   10748         A__   _
                                CTGCAGCCT   ACC CTAG
                                |||||||||   ||| ||||
                                GACGTCGGA   TGG GATT
                                     GTA   A
GAM213  DUSP4   5'  CTGGTGGCCTAACCAGGACC   38417     CA_      CTA
                                CTG   GCCTAACC   GCC
                                |||   ||||||||   |||
                                GAC   CGGATTGG   TGG
                                  CAC       TCC
GAM213  HSPA4   3'  CCTGCAGCCAGCACT       44849         TAACCCT   C
                                CCTGCAGCC      AGC CT
                                |||||||||      ||| ||
                                GGACGTCGG      TCG GA
                                     ________  T
GAM213  HTRA3   3'  CCTACAGCTTGGTAAGTCCTA  44826        CTAACCCT  C
                                CCTGCAGC       AG CCTA
                                ||||||||       || ||||
                                GGATGTCG       TC GGAT
                                    AACCAT__  A
GAM213  LBR     5'  CCTGCAACCTACAAGCC     40428          ACCCT
                                CCTGCAGCCTA    AGCC
                                ||||||||||     ||||
                                GGACGTTGGAT    TCGG
                                     GT___
GAM213  MID1    5'  CCTGCAGCCCTAGTTCTA     7539          TAACC    CC
                                CCTGCAGCC    CTAG  CTA
                                |||||||||    ||||  |||
                                GGACGTCGG    GATC  GAT
                                     _____   AA
GAM213  NOV     3'  TGCAGCCTACCTTGTAGCC    14814         A  C__
                                TGCAGCCTA CC   TAGCC
                                |||||||| ||   |||||
                                ACGTCGGAT GG   ATCGG
                                     _  AAC
GAM213  NYX     3'  TGTGGCTAGGGCCAGCCCT    35450     CA  C  ACC
                                TG  GC TA   CTAGCCCT
                                ||  || ||   ||||||||
                                AC  CG AT   GGTCGGGA
                                  AC  _  CCC
GAM213  OTX1    3'  CCTCCGGCGGGCCTAGCCCT   30985     GCA  CTAAC
                                CCT   GC    CCTAGCCCT
                                |||   ||    |||||||||
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                              GGA  CG    GGATCGGGA
                                GGC  CCC__
GAM213  PTGFRN   3'  CTTTAGCCTAACTTGCACCT  42590    GC      CCTA  _
                              CT  AGCCTAAC    GC CCT
                              ||  ||||||||    || |||
                              GA  TCGGATTG    CG GGA
                               AA       AA__  T
GAM213  PTPN1    3'  TACAGCCTGGCACCTA      15904        AACCCTA  _
                              TGCAGCCT      GC CCTA
                              ||||||||      || ||||
                              ATGTCGGA      CG GGAT
                                   C_______  T
GAM213  SH3BP2   3'  CCTCCAGAGCCCTAACCCTAGC 16628     G  ___
            CCT                  CCT CAG   CCTAACCCTAGCCCT
                              ||| |||   ||||||||||||||||
                              GGA GTC   GGATTGGGATCGGGA
                                G   TCG
GAM213  SOX11    3'  CAGCCTAACCCCCTA       17007          TAGC
                              CAGCCTAACCC    CCTA
                              ||||||||||    ||||
                              GTCGGATTGGG    GGAT
                                        ____
GAM213  STIM1    3'  CTGCAGCCTAGCACCCTCCTAA 41126          __    AGC
                              CTGCAGCCTA  ACCCT   CCTAA
                              |||||||||  |||||  |||||
                              GACGTCGGAT  TGGGA   GGATT
                                    CG    ___
GAM213  TEM7     3'  CTGCAGCCTTGAACTCCT    33808         __  _
                              CTGCAGCCT  AAC CCT
                              |||||||||  ||| |||
                              GACGTCGGA  TTG GGA
                                   AC   A
GAM213  WSX1     3'  CCTGCAGCTTCGAACTCCT    22116        CT__  _
                              CCTGCAGC    AAC CCT
                              ||||||||    ||| |||
                              GGACGTCG    TTG GGA
                                   AAGC   A
GAM213  XPC      3'  CCTCAGCTTGGCCTCGTCTCCC 21549     G   CTAAC   AG___
            C                  CCT CAGC    CCT    CCCT
                              ||| ||||    |||    ||||
                              GGA GTCG    GGA    GGGG
                                _   AACC_   GCAGA
GAM214  FSTL1    3'  TGAGATCAAATCTGGTCATCT  28223   A     TCCAAC   TG
                              C AGATCAA     GGT  TTT
                              | |||||||     |||  |||
                              A TCTAGTT     CCA  AGA
                               C      TAGA__   GT
GAM214  LYZ      3'  CAAGATTAAGTCTGGGTTATTT 6952        C  _  CAAC
            C                  CAAGAT AA TC    GGTTGTTTC
                              |||||| || ||    |||||||||
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                                GTTCTA TT AG   CCAATAAAG
                                   A  C  AC__
GAM214  TSGA10   5'  TGAGATCAATCTTGGCT    36112   A      CAAC
                                C AGATCAATC   GGTT
                                | |||||||||   ||||
                                A TCTAGTTAG   CCGA
                                 C       AA__
GAM214  ADARB1   3'  TTCAAACATGTCTTTGATA   31887   TG  T  C
                                TT  GAT ATG CTTTGATA
                                ||  ||| ||| ||||||||
                                AA  TTG TAC GAAACTAT
                                 GT  _  A
GAM214  CCNT2    3'  AGTCCTTGGATTATGTACCACT 38490   C        __ T
           G                     AG CTTTGGATTATG  CC TTG
                                || ||||||||||||  || |||
                                TC GGAACCTAATAC  GG GAC
                                 A         AT  T
GAM214  CLASPIN  3'  TTTGGCACCTTTGAT      35226      ATTA
                                TTTGG   TGCCTTTGAT
                                |||||   ||||||||||
                                AAACC   GTGGAAACTA
                                  _____
GAM214  H3FL     3'  AGCCTTTGGGTTTTAAGACTGA 18638        ATTATGCCT
           T                     AGCCTTTGG       TTGAT
                                |||||||||       |||||
                                TCGGAAACC       GACTA
                                     CAAAATTCT
GAM215  FANCC    3'  TAGCATTGCCACATACCAAAA  43279    ATCAT
                                TAG    TTATATACCAAAA
                                |||    ||||||||||||
                                ATC    GGTGTATGGTTTT
                                  GTAAC
GAM215  KNSL1    3'  CCAGATCAAAAATACCA     21177       TTTAT
                                CTAGATCA    ATACCA
                                ||||||||    ||||||
                                GGTCTAGT    TATGGT
                                     TTT__
GAM215  PPAT     3'  AGACTATATACCAAA      15480     CATT
                                AGAT   TATATACCAAA
                                ||||   ||||||||||
                                TCTG   ATATATGGTTT
                                  _____
GAM215  PRKG1    3'  CTAGTCATTTACTTCCA     26515     A      ATA
                                CTAG TCATTTAT   CCA
                                |||| ||||||||   |||
                                GATC AGTAAATG   GGT
                                  _      AA_
GAM215  SSRP1    3'  TAAATCATTTTCACAGACCA  17131       __    T
                                TAGATCAT  TTATA ACCA
                                ||||||||  ||||| ||||
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                                ATTTAGTA  AGTGT TGGT
                                    AA    C
GAM216  DKK1     3'  TCAGAAAATAAGCTAGTATTTT 29271       _    TAA
                                TCAGAAAG AGGTT   TATTTT
                                |||||||| |||||   ||||||
                                AGTCTTTT TTCGA   ATAAAA
                                    A    TC_
GAM216  KERA     3'  AGAAAGCATTCAATATTTT   28152      AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM216  PPP1R12A 3'  CCAGAAAGATGTAGTATTTT  14726       G  TTAA
                                TCAGAAAGA GT    TATTTT
                                ||||||||| ||    ||||||
                                GGTCTTTCT CA    ATAAAA
                                     A  TC__
GAM216  S100B    3'  GAAAGAGGTTTTCAATTTT   26568         AAT
                                GAAAGAGGTTT   ATTTT
                                ||||||||||   |||||
                                CTTTCTCCAAA   TAAAA
                                      AGT
GAM217  HYAL2    3'  GGGTGCGAGCTGGTATGGAT  37638     A      TTGAGT
                                GGG GCGAGCTG     TGGAT
                                ||| ||||||||     |||||
                                CCC CGCTCGAC     ACCTA
                                  A       CAT___
GAM217  MPDZ     3'  AGGAGGTGAGCTAGGGGTTGG  19254      C_     TTGA
                                GGGAG  GAGCTG    GTTGG
                                |||||  ||||||    |||||
                                TCCTC  CTCGAT    CAACC
                                   CA     CCC_
GAM217  SLC35A2  3'  GGGGGCTGAGCTGAGGTGG   24952     A _    GTT   T
                                GGG GC GAGCT   GAG TGG
                                ||| || |||||   ||| |||
                                CCC CG CTCGA   CTC ACC
                                  C  A    ___   C
GAM217  TMEM4    5'  AGGGAGCAGGGCTGTCCGGGAT 30673        A_     GAGTT
                                AGGGAGCG  GCTGTT    GGAT
                                ||||||||  ||||||    ||||
                                TCCCTCGT  CGACAG    CCTA
                                     CC     GC____
GAM217  ABCG5    5'  GCCCTGCCTGCTCCACCTGACC 35329     _  C  _
                                GCCC GCC GC CCACCTGACC
                                |||| ||| || ||||||||||
                                CGGG CGG CG GGTGGACTGG
                                  A  A  A
GAM217  ACCN2    5'  CCGCCCGCCCGCGCGCGCTG  33440          CCAC_
                                CCGCCCGCCCGC    CTG
                                ||||||||||||    |||
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                                GGCGGGCGGGCG   GAC
                                      CGCGC
GAM217  ACTN4   5' GCCTCTCGCTCGCCCACCAGCC 22276    ___  C      CA
                                GCC  CGC CGCCCGCC  CC
                                |||  ||| ||||||||  ||
                                CGG  GCG GCGGGTGG  GG
                                  AGA  A      TC
GAM217  ADARB1  3' GCCCGCCGCGCTCCTGAC   31877      _  CCA
                                GCCCGCC CGC  CCTGAC
                                |||||||  |||  ||||||
                                CGGGCGG GCG  GGACTG
                                    C  A__
GAM217  ADCY8   5' CCCGCCCGCCCAGAC      10000         CCT
                                CCCGCCCGCCCA  GAC
                                ||||||||||||  |||
                                GGGCGGGCGGGT  CTG
                                      ___
GAM217  ADORA2B 5' GCCCGCGCGCCCGCCCGTCT  8613      C      AC
                                GCCCGC CGCCCGCCC  CT
                                ||||||  |||||||||  ||
                                CGGGCG GCGGGCGGG  GA
                                   C       CA
GAM217  ADRBK1  3' GCTGCCCGCCCACCTGGCC   11533   CC         A
                                GC  GCCCGCCCACCTG CC
                                ||  ||||||||||||| ||
                                CG  CGGGCGGGTGGAC GG
                                 A_          C
GAM217  AP2M1   5' CCCTGCTCGTCTGCCCGCTGCC 19818    _ C  CCC   AC  A
                                CCC GC CG   GCCC  CTG CC
                                |||  ||  ||   ||||  |||  ||
                                GGG CG GC   CGGG  GAC GG
                                  A  A  AGA   C_  _
GAM217  AP2M1   5' GCCCGCCCCCTGCTCGTCTGCC 19819       G  C  CCAC  A
                                GCCCGCCC CC GC   CTG CC
                                ||||||||  ||  ||   |||  ||
                                CGGGCGGG GG CG   GAC GG
                                     _  A  AGCA  _
GAM217  ATBF1   5' GCCCGCCCGCCCGCAGGGACC  27847          CCACCT
                                GCCCGCCCGCCCGC    GACC
                                ||||||||||||||    ||||
                                CGGGCGGGCGGGCG    CTGG
                                      TCC___
GAM217  BCL7A   5' GCCCGCCCGCCGCTCAC    34211         C  C
                                GCCCGCCCGCC GC CAC
                                ||||||||||| ||  |||
                                CGGGCGGGCGG CG GTG
                                      _  A
GAM217  BCL7B   5' GCCCGCCCGCCGCCGCC    11806         C   CA
                                GCCCGCCCGCC GCC  CC
                                |||||||||| |||  ||
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```
                                CGGGCGGGCGG CGG  GG
                                      _  C_
GAM217  BIN1    5'  GCCCCCCGCCCGCCCCC    40296     G        A
                                GCCC CCCGCCCGCCC CC
                                |||| |||||||||| ||
                                CGGG GGGCGGGCGGG GG
                                  _        _
GAM217  BIRC7   3'  GCCCACTCTGCAGCCCACCTGG 40253      CC_ CC       A
            CC                    GCCCGC  GC  GCCCACCTG CC
                                |||||| || |||||||| ||
                                CGGGTG  CG  CGGGTGGAC GG
                                   AGA  T_       C
GAM217  CAPN10  5'  GCCCGCCCCGCCCGTTCCCCGC 35787        _   ___  A
            C                     GCCCGCCC GCCCG  CCC CC
                                |||||||| |||||  ||| ||
                                CGGGCGGG CGGGC  GGG GG
                                    G    AAG  C
GAM217  CAPN10  5'  GCCCGTTCCCCGCCCGGCC   35773      ___      C
                                GCCCG  CCCGCCCG CC
                                |||||  |||||||| ||
                                CGGGC  GGGCGGGC GG
                                   AAG       C
GAM217  CCND1   3'  GCCCGCCTGCCTGGCGCC    38208       C  ___
                                GCCCGCC GCC  CGCC
                                ||||||| |||  ||||
                                CGGGCGG CGG  GCGG
                                    A  ACC
GAM217  CLCN7   3'  CCGCCTGCCCGCCCAGCT    10513      C       C
                                CCGCC GCCCGCCCA CT
                                ||||| ||||||||| ||
                                GGCGG CGGGCGGGT GA
                                   A       C
GAM217  COG8    3'  GCCCACCCGCTCGCCTGCCACA 37039         C   CA  TG
            CC                    GCCCGCCCGC CGCC  CC  ACC
                                |||||||||| ||||  ||  |||
                                CGGGTGGGCG GCGG  GG  TGG
                                     A   AC  TG
GAM217  CXCL16  5'  GCCTGGCCCGTCCGCCGACC  35200    C_   C   C
                                GCC  GCCCG CCGCC ACC
                                |||  ||||| ||||| |||
                                CGG  CGGGC GGCGG TGG
                                  AC    A    C
GAM217  CXCL16  5'  GCCCGCCTGGCCCGTCCGCC  35199       C_   C  A
                                GCCCGCC  GCCCG CC CC
                                |||||||  ||||| || ||
                                CGGGCGG  CGGGC GG GG
                                    AC    A  C
GAM217  CYB561  3'  GCCCGCCTGCTGCCAGAGCC  12544       C  CC   CA__
                                GCCCGCC GC  GCC   CC
                                |||||||  ||  |||   ||
```

```
                                CGGGCGG CG  CGG   GG
                                    A  A_   TCTC
GAM217  DNM2    5'  CCTCGCCCGCCGCCGACC   22378   _     C   C
                                CC CGCCCGCC GCC ACC
                                || |||||||| ||| |||
                                GG GCGGGCGG CGG TGG
                                 A       _  C
GAM217  DNMT3B  5'  CCGCCCGCTCGCCCGACC   27872       C   _
                                CCGCCCGC CGCCC ACC
                                |||||||| ||||| |||
                                GGCGGGCG GCGGG TGG
                                    A    C
GAM217  DNMT3B  5'  GCCCGCTCGCCCGACCGCC   27876      C    C  A
                                GCCCGC CGCCCG CC CC
                                |||||| |||||| || ||
                                CGGGCG GCGGGC GG GG
                                   A     T  C
GAM217  DSCAM   5'  GCCCGCCCGCCGCCCGCC   10801         C   A
                                GCCCGCCCGCC GCCC CC
                                |||||||||||| |||| ||
                                CGGGCGGGCGG CGGG GG
                                      _   C
GAM217  DSCAM   5'  GCCCGCCGCCCGCCGCC    10802      C     CA
                                GCCCGCC GCCCGCC  CC
                                ||||||| |||||||  ||
                                CGGGCGG CGGGCGG  GG
                                   _     C_
GAM217  DUSP7   5'  CCCGCCCGCCCGCCCGGCC   42263          A_
                                CCCGCCCGCCCGCCC  CC
                                ||||||||||||||  ||
                                GGGCGGGCGGGCGGG  GG
                                      CC
GAM217  DVL1    5'  ACCCGCCCGCCCGCCTGCGCC  40403          CA__
                                GCCCGCCCGCCCGCC   CC
                                ||||||||||||||   ||
                                TGGGCGGGCGGGCGG   GG
                                      ACGC
GAM217  E2F1    3'  GCCCACCCCACCATCTGAC   44488       GC  C
                                GCCCGCCC  CCA CTGAC
                                ||||||||  ||| |||||
                                CGGGTGGG  GGT GACTG
                                    GT   A
GAM217  E2F4    5'  GCCCGCCCGCCGCCTCC    12637         C  CA
                                GCCCGCCCGCC GCC  CC
                                |||||||||| |||  ||
                                CGGGCGGGCGG CGG  GG
                                      _  A_
GAM217  FKRP    3'  GCCCCCCCAGGCCCACCTG   35897     G   CCC
                                GCCC CCCG   GCCCACCTG
                                |||| ||||   |||||||||
```

```
                                CGGG GGGT   CGGGTGGAC
                                  G   C__
GAM217  GJB3     5'  ACCCGCCTGCCTGTCCAC    35833        C   CGC
                                GCCCGCC GCC   CCAC
                                ||||||| |||   ||||
                                TGGGCGG CGG   GGTG
                                   A   ACA
GAM217  GPRC5B   5'  GCACGCCCGCCTGCGA     32174    C      C  CCACCT
                                GC CGCCCGCC GC     GA
                                || |||||||| ||     ||
                                CG GCGGGCGG CG     CT
                                 T       A _______
GAM217  GRB10    3'  GCCAGCTTGCCCGCCCCC    23658     C  CC       A
                                GCC GC  GCCCGCCC CC
                                ||| ||  |||||||| ||
                                CGG CG  CGGGCGGG GG
                                  T  AA       _
GAM217  HNF3G    5'  GCCCGCCCGTCCGACCGCC   43647         C   C  A
                                GCCCGCCCG CCG CC CC
                                ||||||||| ||| || ||
                                CGGGCGGGC GGC GG GG
                                     A   T  C
GAM217  HOXD4    5'  GCCTGCCCGCCCTGCCTGCAGC 31175     C       _   __  _
              C                  GCC GCCCGCCC GCC  CA CC
                                ||| ||||||| |||  || ||
                                CGG CGGGCGGG CGG  GT GG
                                  A       A   AC  C
GAM217  HS2ST1   5'  GCCCGCCTGCTTGCCCGCCT  29332        C  CC    A
                                GCCCGCC GC  GCCC CCT
                                ||||||| ||  |||| |||
                                CGGGCGG CG  CGGG GGA
                                   A  AA    C
GAM217  HS2ST1   5'  GCCCGCCTGCTTGCCCGCC   29331        C  CC    A
                                GCCCGCC GC  GCCC CC
                                ||||||| ||  |||| ||
                                CGGGCGG CG  CGGG GG
                                   A  AA    C
GAM217  HYAL1    5'  GCCCGCTCGTCCCTGCTGACC  37641       C  _   AC
                                GCCCGC CG CCC  CTGACC
                                |||||| || |||  ||||||
                                CGGGCG GC GGG  GACTGG
                                   A  A   AC
GAM217  IL12RB2  5'  GCCCGCCCTCCCGCCTCCGCC  11430         G     CAC   A
                                GCCCGCCC CCCGCC   CTG CC
                                |||||||| ||||||   ||| ||
                                CGGGCGGG GGGCGG   GGC GG
                                   A     A__   _
GAM217  IL21R    3'  CCCGCCCGCCTCGGCTCTGGCC 34753          _  CCCAC   A
                                CCCGCCCGCC CG    CTG CC
                                |||||||||| ||    ||| ||
```

```
                                GGGCGGGCGG GC    GAC GG
                                     A  CGA__   C
GAM217  ITGA7    5'  GCCCTCCCGCCCGCCCGCC   13609     G        A
                                GCCC CCCGCCCGCCC CC
                                |||| |||||||||| ||
                                CGGG GGGCGGGCGGG GG
                                  A         C
GAM217  JAG2     5'  GCCCGCCCGCCCTCCGA     13722          A  T
                                GCCCGCCCGCCC CC GA
                                |||||||||||| || ||
                                CGGGCGGGCGGG GG CT
                                       A  _
GAM217  KCNK1    5'  GCGCGCCCGCCCGCCCCGCT  13892    C         AC
                                GC CGCCCGCCCGCCC  CT
                                || ||||||||||||  ||
                                CG GCGGGCGGGCGGG  GA
                                 C          GC
GAM217  KCNK1    5'  GCCCGCCCGCCCCGCTCC    13889          _ _
                                GCCCGCCCGCCC GC CC
                                |||||||||||| || ||
                                CGGGCGGGCGGG CG GG
                                       G  A
GAM217  KIF5C    5'  GCCCACCTGCCCGCGA      21153       C     CCACCT
                                GCCCGCC GCCCGC     GA
                                ||||||| ||||||     ||
                                CGGGTGG CGGGCG     CT
                                    A     _______
GAM217  LASS1    5'  GCCCGCTCGCCCGCCGTGCC  34606      C      CA_
                                GCCCGC CGCCCGCC   CC
                                |||||| ||||||||   ||
                                CGGGCG GCGGGCGG   GG
                                   A       CAC
GAM217  LASS2    5'  GCCCGCCCGCCGGCCCGCGCC 42675         C    A__
                                GCCCGCCCGCC GCCC   CC
                                |||||||||| ||||   ||
                                CGGGCGGGCGG CGGG   GG
                                       C    CGC
GAM217  LDB1     5'  GCCCGCCCGCCCTCCCCAGGCC 19339         G_   __
                                GCCCGCCCGCCC  CCCA  CC
                                |||||||||||  ||||  ||
                                CGGGCGGGCGGG  GGGT  GG
                                       AG    CC
GAM217  MAP3K14  3'  GCTCGCCCACCCCTTCTGACC  19542    C       AC_
                                GC CGCCCGCCC   CTGACC
                                || |||||||||   ||||||
                                CG GCGGGTGGG   GACTGG
                                 A        GAA
GAM217  MAPK12   5'  GCTCGCCCGCCCGCCCGCC   16472    C         A
                                GC CGCCCGCCCGCCC CC
                                || ||||||||||||| ||
```

```
                                CG GCGGGCGGGCGGG GG
                                 A           C
GAM217  MAPK12   5'  GCCCGCCCGCCCGCCGGCC   16469            CA
                                GCCCGCCCGCCCGCC  CC
                                |||||||||||||||  ||
                                CGGGCGGGCGGGCGG  GG
                                         CC
GAM217  MLLT1    5'  GCCCGCTCGCCCGCCAGCC   25486       C       CA
                                GCCCGC CGCCCGCC  CC
                                ||||||| ||||||||  ||
                                CGGGCG GCGGGCGG  GG
                                   A       TC
GAM217  MLLT1    5'  GCTCGCCCGCCAGCCCCGCGGA 25487    C       C    ACCT_
            ACC                    GC CGCCCGCC GCCC     GACC
                                || ||||||||| ||||     ||||
                                CG GCGGGCGG CGGG     TTGG
                                 A       T    GCGCC
GAM217  MSF      5'  GCTCCGCCCGCCTGTCAAGGCC 44732    _       C_______
                                GC CCGCCCGCC       GCC
                                || |||||||||       |||
                                CG GGCGGGCGG       CGG
                                 A        ACAGTTC
GAM217  MSR1     3'  CCCGCCCAACCCACCTGA    14658         _
                                CCCGCCCG CCCACCTGA
                                |||||||| |||||||||
                                GGGCGGGT GGGTGGACT
                                     T
GAM217  MTNR1A   5'  GCCCGCCTCGTCCGCCCGCCCG 25549        _ C     A
            ACC                    GCCCGCC CG CCGCCC CCTGACC
                                ||||||| || |||||| |||||||
                                CGGGCGG GC GGCGGG GGGCTGG
                                    A A     C
GAM217  MYC      5'  GCCCGCTCGCTCCCTCTGC    14708       C  _ AC   A
                                GCCCGC CGC CC  CTG C
                                |||||| ||| ||  ||| |
                                CGGGCG GCG GG  GAC G
                                   A   A  GA  _
GAM217  NCOR2    3'  CCGCCCACCTGGCCTGAC    26729          CA_
                                CCGCCCGCC   CCTGAC
                                |||||||||   ||||||
                                GGCGGGTGG   GGACTG
                                     ACC
GAM217  NCOR2    3'  GCCCTTTTGTCCGCCCACCTGG 26736      GCCCGC         A
            CC                     GCCC     CCGCCCACCTG CC
                                ||||     |||||||||||| ||
                                CGGG     GGCGGGTGGAC GG
                                  AAAACA          C
GAM217  NFIA     5'  GCCCGCTCGCGCCGCCGCC    43215       C  _    CA
                                GCCCGC CGC CCGCC  CC
                                |||||| ||| |||||  ||
```

```
                                CGGGCG GCG GGCGG  GG
                                   A  C    C_
GAM217  NFIA    5'  GCCCGCGCGCCCGCCTCCGCC  43214       C      CAC  A
                                GCCCGC CGCCCGCC  CTG CC
                                |||||| ||||||||  ||| ||
                                CGGGCG GCGGGCGG  GGC GG
                                   C       A__  _
GAM217  NIPSNAP1  5'  GCTCGCCCGCCCCCTCAC    18871    C       A  G
                                GC CGCCCGCCC CCT AC
                                || |||||||| ||| ||
                                CG GCGGGCGGG GGA TG
                                 A        _  G
GAM217  NR0B2    3'  GCCAGCCTCTGCCCACCTGA  35032    C  C__
                                GCC GCC  GCCCACCTGA
                                ||| |||  ||||||||||
                                CGG CGG  CGGGTGGACT
                                  T  AGA
GAM217  PITPN    5'  GCCCGCTGCCCGCCGGCC    26337      CC     CA
                                GCCCGC  GCCCGCC  CC
                                ||||||  |||||||  ||
                                CGGGCG  CGGGCGG  GG
                                   A_      CC
GAM217  PKD1    5'  GCTCGGCCGCCCGCTCGGAC  7140    C  C      CCACCT
                                GC CG CCGCCCGC     GAC
                                || || ||||||||     |||
                                CG GC GGCGGGCG     CTG
                                 A  C       AGC___
GAM217  PKD1    5'  GCCCGCCCGCGCGCGGAGACC  7138          C  CCACCT
                                GCCCGCCCGC CGC     GACC
                                |||||||||| |||     ||||
                                CGGGCGGGCG GCG     CTGG
                                      C  CCT___
GAM217  PRSS8    5'  GCCCGCCCCTCCCCTGC     15760        GC  A   A
                                GCCCGCCC  CC CCTG C
                                ||||||||  || |||| |
                                CGGGCGGG  GG GGAC G
                                     GA  _   C
GAM217  PTEN    5'  GCCTGCCCGCCCCCTCCGC   7214     C      G  CAC  A
                                GCC GCCCGCCC CC  CTG C
                                ||| ||||||| ||  ||| |
                                CGG CGGGCGGG GG  GGC G
                                  A       _  A__  _
GAM217  PTEN    5'  GCCGGCCTGCCCGCCCCC    7213     C  C      A
                                GCC GCC GCCCGCCC CC
                                ||| ||| |||||||| ||
                                CGG CGG CGGGCGGG GG
                                  C  A       _
GAM217  PTEN    5'  GCCCGCCGGCCTGCCCGCC   7212       C  C   A
                                GCCCGCC GCC GCCC CC
                                ||||||| ||| |||| ||
```

```
                                CGGGCGG CGG CGGG GG
                                    C  A   C
GAM217  PTPRE    5'  CCGCCCGCTCGTCCGCAGCC  38981       C _ _ _
                                CCGCCCGC CG CC CA CC
                                |||||||| || || || ||
                                GGCGGGCG GC GG GT GG
                                    A  A  C  C
GAM217  RGS3     5'  GCCCGTCCTTCTGCCCACC   39126     C  GCCC
                                GCCCG CC   GCCCACC
                                ||||| ||   |||||||
                                CGGGC GG   CGGGTGG
                                  A  AAGA
GAM217  SCNN1B   3'  GCCCACCCGCCTGTTCCT    7337         CA__
                                GCCCGCCCGCC   CCT
                                ||||||||||   |||
                                CGGGTGGGCGG   GGA
                                     ACAA
GAM217  SLC18A3  5'  GCCCGCCCGCTTGCCCGCC   16832        CC   A
                                GCCCGCCCGC  GCCC CC
                                ||||||||||  |||| ||
                                CGGGCGGGCG  CGGG GG
                                     AA   C
GAM217  SLC18A3  5'  GCCCGCCCGCTTGCCCGCCCG  16833        CC   A
                                GCCCGCCCGC  GCCC CCTG
                                ||||||||||  |||| ||||
                                CGGGCGGGCG  CGGG GGGC
                                     AA   C
GAM217  SLC18A3  5'  GCCCGCCCGTTAGCCCCGCC   16834        _____
                                GCCCGCCCG    CCCGCC
                                |||||||||    ||||||
                                CGGGCGGGC    GGGCGG
                                     AATCG
GAM217  SLC22A3  5'  GCCCGCCGCCCGCCGCC    35050       C     CA
                                GCCCGCC GCCCGCC  CC
                                ||||||| |||||||  ||
                                CGGGCGG CGGGCGG  GG
                                   _     C_
GAM217  SMARCD1  5'  GCCCGCCTGTTCCCCCGGCC  40085       CG__  G  CA
                                GCCCGCC   CCC CC  CC
                                |||||||   ||| ||  ||
                                CGGGCGG   GGG GG  GG
                                    ACAA  _  CC
GAM217  SRRM2    5'  GCCGGTCCGCCCGCCTCAGCC  32276    CGC      _ _
                                GCC   CCGCCCGCC CA CC
                                |||   ||||||||| || ||
                                CGG   GGCGGGCGG GT GG
                                  CCA       A  C
GAM217  STAT5B   5'  GCCCGCTCGCTCCCTCC    29720      C  CCG  A
                                GCCCGC CGC   CCC CC
                                |||||| |||   ||| ||
```

```
                                CGGGCG GCG   GGG GG
                                   A  A__  A
GAM217  TACC3   5' GCCCGCCCGCCCGTTGCC   26809          C__
                                GCCCGCCCGCCCG  CC
                                |||||||||||||  ||
                                CGGGCGGGCGGGC  GG
                                       AAC
GAM217  TIMP3   5' GCCTGCTGCCCGCTCTGCGCC 7457     C  CC     CCAC  A_
                                GCC GC  GCCCGC   CTG  CC
                                ||| ||  ||||||   |||  ||
                                CGG CG  CGGGCG   GAC  GG
                                  A  A_     A___   GC
GAM217  TIMP3   5' GCTCGCTCGCCCGCCGGGCC  7459    C  C      CA_
                                GC CGC CGCCCGCC  CC
                                || ||| ||||||||  ||
                                CG GCG GCGGGCGG  GG
                                 A  A      CCC
GAM217  TJP1    5' GCCCGCCCGCTCCTCACGCC  17544         _ ____
                                GCCCGCCCGC CC   GCC
                                |||||||||| ||   |||
                                CGGGCGGGCG GG   CGG
                                      A  AGTG
GAM217  TNP2    5' GCCCTGGCAGGCCCACCTG   24056     GCCC  CC
                                GCCC   GC  GCCCACCTG
                                ||||   ||  |||||||||
                                CGGG   CG  CGGGTGGAC
                                  AC__  TC
GAM217  TPR     5' GCGCGCCCGCCCGCCGGAGAC  17655   C        CACCT
                                GC CGCCCGCCCGCC    GAC
                                || ||||||||||||    |||
                                CG GCGGGCGGGCGG    CTG
                                 C         CCT__
GAM217  UBE2E3  5' GCCCGCCCGGCCGCTCGCGCGC 26819        C   CCACC  A
           C                     GCCCGCCCG CCGC    TG CC
                                |||||||| ||||    || ||
                                CGGGCGGGC GGCG    GC GG
                                      C   AGCGC  _
GAM217  ZNF76   5' GCCCGCCCGCCCGCGCGCAGCC 18306          C__  _
                                GCCCGCCCGCCCGC  CA CC
                                ||||||||||||||  || ||
                                CGGGCGGGCGGGCG  GT GG
                                       CGC  C
GAM218  MME     3' TATTTCTGTAACTTTTTTT   28603        AA
                                TATTTTTGTA  ACTTTTTTT
                                |||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                          __
GAM219  NCOA3   3' GATAAAGGGAATTAAACT    27216        T   CTCT
                                GATAAAGG GAAT   ACT
                                |||||||| ||||   |||
```

```
                                CTATTTCC CTTA    TGA
                                     _   ATT_
GAM220  DGCR2    3'  CCCCAGGGACCGGTGTT     23089       AACTCTA
                                TCCCAG      GACCGGTGTT
                                ||||||      ||||||||||
                                GGGGTC      CTGGCCACAA
                                   C_______
GAM220  HPS1     3'  TCTCAGGGTTTAGACCAACAT  6805     C   AACTC       TG
                                TC CAG    TAGACCGG  T
                                || |||    ||||||||  |
                                AG GTC    ATCTGGTT  A
                                 A  CCAA_       GT
GAM220  LOX      3'  CCAGCACTTTAGAAAAGT    14189      A  C    CC
                                CCAG ACT TAGA  GGT
                                |||| ||| ||||  |||
                                GGTC TGA ATCT  TCA
                                  G   A    TT
GAM221  FGF2     3'  AAAAAGCAGCCACAAAAATAT  12822        T_
                                AAAAAGT  TTACAAAAATAT
                                |||||||  ||||||||||||
                                TTTTTCG  GGTGTTTTTATA
                                    TC
GAM221  MPHOSPH1 3'  AAAAAAGCCTTATAAAAATAT  32111           C
                                AAAAAAGTTTTA AAAAATAT
                                |||||||||||| ||||||||
                                TTTTTTCGGAAT TTTTTATA
                                       A
GAM222  DMD      5'  TAGTGGTCAGTCCAGGAGCTAG 19707        C ___   A   A
           GT                     TAGTGGTC GT  GGGA GCTA GT
                                ||||||||  ||  ||||  ||||  ||
                                ATCACCAG CA  TCCT CGAT CA
                                     T  GG   _   C
GAM222  SCAMP3   3'  TTAGGGACGGGAGCTAAG    25035     T  TCCG    A
                                TTAG GG    TGGGA GCTAAG
                                |||| ||    ||||| ||||||
                                AATC CC    GCCCT CGATTC
                                  _ T____    _
GAM223  LMCD1    3'  TGTGTCTTTAGTTGGTTGT   31048    _  C__
                                TG GTT   AGTTGGTTGT
                                || |||   ||||||||||
                                AC CAG   TCAACCAACA
                                 A  AAA
GAM223  PCDHGA11 5'  CTCGAGCTGGTTGGTTGT    36881    AT    CA
                                CT  GGTT  GTTGGTTGT
                                ||  ||||  |||||||||
                                GA  TCGA  CAACCAACA
                                 GC   C_
GAM224  BAIAP3   3'  CTCTGTGTCCTGCCTCGGCG   19455     A  CA      CA
                                CTCT TG  CTGCTTCG  GCG
                                |||| ||  ||||||||  |||
```

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                                GAGA AC  GACGGAGC  CGC
                                  C AG      __
GAM224  SLC16A1  5' TATGCGCGGATCGCAGCG    16816      AC  CT
                                TATGC  TG  TCGCAGCG
                                |||||  ||  ||||||||
                                ATACG  GC  AGCGTCGC
                                   C_  CT
GAM225  APAF1    5' TCTCTCTGAGCTGTCAACCAT  29828    C      C    TT
                                TC CTCTGAGC GTTAG  GT
                                || ||||||||  |||||  ||
                                AG GAGACTCG CAGTT  TA
                                 A       A    GG
GAM225  CFTR     5' CTCTGACCTGCTGTGA      7951       G  GTTA
                                CTCTGA CC    GTTGTGA
                                ||||||  ||    |||||||
                                GAGACT GG    CGACACT
                                   _  A___
GAM226  ANK3     3' GTATACTGTAGTGTTTGCAAA  34187         ACA  C__
                                GTGTACTGTA   TGT   CAAA
                                ||||||||||   |||   ||||
                                CATATGACAT   ACA   GTTT
                                      C__   AAC
GAM227  APLP2    3' TCTCTCACGTGCTTCAGTGG   44924       AAT  GC_
                                TCTCTCAC   CT   GTGG
                                ||||||||   ||   ||||
                                AGAGAGTG   GA   CACC
                                     CAC  AGT
GAM227  ARSD     3' TCTCTCACAGTCCTGG      28929        A   GCG
                                TCTCTCACA TCT   TGG
                                |||||||||  |||   |||
                                AGAGAGTGT AGG   ACC
                                      C  ___
GAM227  C18orf2  3' TCTCCCACAGTCTCACAG    36409        A   G  TG
                                TCTCTCACA TCT CG  G
                                |||||||||  ||| ||  |
                                AGAGGGTGT AGA GT  C
                                      C  _  GT
GAM227  CA3      5' TCTCTTCCCCTGCGTGG     23217      CACAA
                                TCTCT    TCTGCGTGG
                                |||||    |||||||||
                                AGAGA    GGACGCACC
                                   AGG__
GAM227  DLG5     5' TCTTCACCTGCGTGG       44469     C   AAT
                                TCT TCAC   CTGCGTGG
                                |||  ||||   ||||||||
                                AGA AGTG   GACGCACC
                                  _   ____
GAM227  DNAJB1   3' CCTCTCATGGTCCACAACTGG  26030       CAA  TG  __
                                TCTCTCA   TC  CG  TGG
                                |||||||   ||  ||  |||
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                                GGAGAGT  AG  GT  ACC
                                    ACC  GT  TG
GAM227  EPHB6   3'  TCTCTCACAGAGGCTGTTGG  20804        AT__  CG
                                TCTCTCACA   CTG  TGG
                                |||||||||   |||  |||
                                AGAGAGTGT   GAC  ACC
                                     CTCC   A_
GAM227  GYPC    3'  TCTCCCACCTCCGTGG     13326        AAT  G
                                TCTCTCAC   CT CGTGG
                                ||||||||   || |||||
                                AGAGGGTG   GA GCACC
                                    ___  G
GAM227  LAMA5   3'  TCTCTCACAATTAAAAATGG  24501         CTGC_
                                TCTCTCACAAT    GTGG
                                ||||||||||    ||||
                                AGAGAGTGTTA    TACC
                                      ATTTT
GAM227  PARK2   3'  TCTCTTCTGCGTAG       30375      CACAA
                                TCTCT    TCTGCGTGG
                                |||||    |||||||||
                                AGAGA    AGACGCATC
                                  _____
GAM227  PSMD7   3'  TCTCATACAATCTGAAGG    15839     TC      CGT
                                TCTC  ACAATCTG   GG
                                ||||  ||||||||   ||
                                AGAG  TGTTAGAC   CC
                                  TA      TT_
GAM227  RPA3    5'  TCTTGCCAGTTCTGCGTGG   16384    C_  CAA
                                TCT  TCA   TCTGCGTGG
                                |||  |||   |||||||||
                                AGA  GGT   AGACGCACC
                                  AC   CA_
GAM227  SHOX2   3'  TCCCTGGTCCTGCGTGG     27841      CACAA
                                TCTCT    TCTGCGTGG
                                |||||    |||||||||
                                AGGGA    GGACGCACC
                                   CCA__
GAM227  SIM1    3'  TCTCTAACAATCTGTGG     22871      C      GC
                                TCTCT ACAATCT  GTGG
                                ||||| |||||||  ||||
                                AGAGA TGTTAGA  CACC
                                   T     __
GAM227  SLC6A1  3'  CCCCTCTCTGCGTGG      40488       ACAA
                                TCTCTC   TCTGCGTGG
                                ||||||   |||||||||
                                GGGGAG   AGACGCACC
                                    ____
GAM227  TPI1    3'  TCCCTCACATGGGTGG      7478         ATC  C
                                TCTCTCACA   TG GTGG
                                |||||||||   || ||||
```

```
                                AGGGAGTGT  AC CACC
                                    ___ C
GAM227  UCP3    3'  TCTCCCACTCCATTGTGG   17857       AA  GC_
                                TCTCTCAC  TCT  GTGG
                                ||||||||  |||  ||||
                                AGAGGGTG  AGG  CACC
                                   __  TAA
GAM227  VIL2    3'  TCTCTGCCAGCTGCGTGG   18001     CA  AT
                                TCTCT  CA  CTGCGTGG
                                |||||  ||  ||||||||
                                AGAGA  GT  GACGCACC
                                  CG  C_
GAM227  CD83    3'  GAAAAAATGTCCAGGAGGT   20138          CTC
                                GAAAAGATGTCCAGG  GT
                                ||||||||||||||  ||
                                CTTTTTTACAGGTCC  CA
                                        TC_
GAM227  EGFL5   5'  GAAAAGATAGTCTGCAGG   44526       _  __
                                GAAAAGAT GTC  CAGG
                                |||||||| |||  ||||
                                CTTTTCTA CAG  GTCC
                                     T  AC
GAM227  HS2ST1  3'  AAAATGTCCATCAGTGTCA   29317        GGCTC
                                AAGATGTCCA   GTCA
                                ||||||||||   ||||
                                TTTTACAGGT   CAGT
                                      AGTCA
GAM227  MNT     3'  CCTGGGAGGTGTCCAGGACC  33710   GAAA  A     _
                                CC   AG TGTCCAGG CT
                                ||   || |||||||| ||
                                GG   TC ACAGGTCC GG
                                 ACCC  C      T
GAM227  NRG1    5'  CCAAACCATCCCGGGCTCGTCA 30339     AAGATG  A
                                CCGAA    TCC GGCTCGTCA
                                |||||    ||| |||||||||
                                GGTTT    GGG CCGAGCAGT
                                  GGTA__  C
GAM227  ONECUT1 3'  AAAAGATGTCCGCTCA    41624        AG
                                AAAAGATGTCC  GCTCG
                                ||||||||||  |||||
                                TTTTCTACAGG  CGAGT
                                     __
GAM227  PCDHA1  3'  GAAAAGATGATTAGACAAGT  36396       TCC  TC
                                GAAAAGATG  AGGC  GT
                                |||||||||  ||||  ||
                                CTTTTCTAC  TCTG  CA
                                      TAA  TT
GAM227  TMEPAI  3'  CCTGGGAGAAACCCAGGCTTGT 33599   GAAA  TG     C
            CA                   CC   AGA  TCCAGGCT GTCA
                                ||   |||  |||||||| ||||
```

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                                GG    TCT  GGGTCCGA CAGT
                                 ACCC   TT       A
GAM228  BRCA1    3'  TCTCTTGAGGCCAAGCCACTCT 28648    _  CA       _ AA
             GTG                    TC CTT  AGGCCAAGT GC  TGTG
                                || |||  ||||||||| ||  ||||
                                AG GAA  TCCGGTTCG TG  ACAC
                                 A   C_       G  AG
GAM228  DPP4     3'  TCCTTCAAGTTAAGATTTGTG  12582         GCC   TGCAA
                                TCCTTCAAG   AAG    TGTG
                                |||||||||   |||    ||||
                                AGGAAGTTC   TTC    ACAC
                                      AA_   TAA__
GAM228  SH3BP2   3'  TTCAAGGCTGGGCGCCGTG   16645        CAA    AA
                                TTCAAGGC   GTGC  TGTG
                                ||||||||   ||||  ||||
                                AAGTTCCG   CGCG  GCAC
                                     ACC   __
GAM228  TGFBR2   3'  CAAAAGCAAGTGCAATGTG   17472      C
                                CAAGG CAAGTGCAATGTG
                                ||||| ||||||||||||
                                GTTTT GTTCACGTTACAC
                                   C
GAM229  BMPR1B   3'  TGTTGGCTTTCTGCAGAGATG  10208    C   A       AT_
                                TG TGG TTTCTGCA   GTG
                                || ||| ||||||||   |||
                                AC ACC AAAGACGT   TAC
                                 A   G       CTC
GAM229  CHRNA2   5'  TGCTGGATTCTGTGAGG     8832          T   CAA  T
                                TGCTGGATT CTG   TG GG
                                ||||||||| |||   || ||
                                ACGACCTAA GAC   AC CC
                                      _  ____  T
GAM229  EGFL4    3'  GCTGGAGCAGCAGTGTGGCCA  41573       TTTCT   A
                                GCTGGA    GCA TGTGGCCA
                                ||||||    ||| ||||||||
                                CGACCT    CGT ACACCGGT
                                   CGT__   C
GAM229  KIF5C    3'  TGTTGGATTTCTTCAGCA    21170    C       ___
                                TG TGGATTTCT   GCA
                                || |||||||||   |||
                                AC ACCTAAAGA   CGT
                                 A        AGT
GAM229  PCDH11X  3'  TGCTGAATTTCTGTGAACAGCC 37313           CAAT TG
             A                   TGCTGGATTTCTG   G  GCCA
                                ||||||||||||    |  ||||
                                ACGACTTAAAGAC    T  CGGT
                                       ACT_ GT
GAM229  PCDH9    5'  TACTGGATTTCTGTGGAGTG   44408           CAAT
                                TGCTGGATTTCTG    GTG
                                ||||||||||||    |||
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                                ATGACCTAAAGAC   CAC
                                      ACCT
GAM229  PTGER4   5'  TGCTGGATTTCTTACTCGC   9656          GCAA
                                TGCTGGATTTCT   TGT
                                ||||||||||||  |||
                                ACGACCTAAAGA   GCG
                                      ATGA
GAM229  SCNN1A   3'  TACTGGAGAGCAGTGTGGCCA  9784        TTTCT  A
                                TGCTGGA    GCA TGTGGCCA
                                |||||||    ||| ||||||||
                                ATGACCT    CGT ACACCGGT
                                    CT___  C
GAM229  SDC2     5'  TGTTGGTTTCTGCACTCC    42577    C  A      ATGTGG
                                TG TGG TTTCTGCA     CC
                                || ||| ||||||||     ||
                                AC ACC AAAGACGT     GG
                                 A  _      GA_____
GAM229  SLC7A8   3'  GCTGGGTTTCTGCAATCTG   29289      A        G
                                GCTGG TTTCTGCAAT TG
                                ||||| ||||||||||  ||
                                CGACC AAAGACGTTA AC
                                   C        G
GAM229  SNAI1    3'  TGTGGGGCTGATGTGGCC    25610    C  ATTT  CA
                                TG TGG   CTG  ATGTGGCC
                                || |||   |||  ||||||||
                                AC ACC   GAC  TACACCGG
                                 _  CC__  __
GAM229  TSLP     5'  CTGGATTTCAGTAAGGCAATGT 39696        T_____
            GGC                   CTGGATTTC     GCAATGTGGC
                                |||||||||     ||||||||||
                                GACCTAAAG     CGTTACACCG
                                      TCATTC
GAM230  GRIN2A   3'  CAGAAATGACAAATACTTT   9105       CGC
                                TAGAGA   CAAATACTTT
                                ||||||   ||||||||||
                                GTCTTT   GTTTATGAAA
                                   ACT
GAM230  KMO      3'  TCTAAGACGCCAGCTCTTT   18960    A      AATA
                                TCT GAGACGCCA   CTTT
                                ||| |||||||||   ||||
                                AGA TTCTGCGGT   GAAA
                                  _       CGA_
GAM231  AQP6     3'  GTCCTCTCTGGACCAAGGGTTT 11645       GGC GT  __  C
            CC                   GTCCTCTT  G  CA  GGT TCC
                                ||||||||  |  ||  ||| |||
                                CAGGAGAG  C  GT  CCA AGG
                                     AC_ TG  TC  A
GAM231  CDH20    3'  GCCCTCTTCCTTCTGGGTTTCC 36682       GGCGG  A_  C
                                GTCCTCTT    TC  GGT TCC
                                ||||||||    ||  ||| |||
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                                CGGGAGAA    AG  CCA AGG
                                    GGA__  AC   A
GAM231  DBY     3'  TCTTTTGGTCAAGTTTC    21663     GGC      C
                                TCTT   GGTCAGGT TC
                                ||||   |||||||| ||
                                AGAA   CCAGTTCA AG
                                  AA_       A
GAM231  DDX3    3'  TCTTTTGGTCAAGTTTC    35824     GGC      C
                                TCTT   GGTCAGGT TC
                                ||||   |||||||| ||
                                AGAA   CCAGTTCA AG
                                  AA_       A
GAM231  DLEC1   3'  GTCTTCTGGAACATAGGTCTCC 28836    C   T  CGGTC
                                GTC TCT GG    AGGTCTCC
                                ||| ||| ||    ||||||||
                                CAG AGA CC    TCCAGAGG
                                  A  _ TTGTA
GAM231  MAP3K9  5'  GCCTCTTGGCGAACATTCTC   41355   T       GT  GG
                                G CCTCTTGGCG  CA  TCTC
                                | ||||||||||  ||  ||||
                                C GGAGAACCGC  GT  AGAG
                                _        TT  A_
GAM231  NOS1    3'  CGTTTCTTGGCATTGAGGGTCT 8373     CC      GTCA_
                                CGT  TCTTGGCG    GGTCT
                                |||  ||||||||    |||||
                                GCA  AGAACCGT    CCAGA
                                  A_       AACTC
GAM231  SACS    3'  GTTGTCTTGGCAAGCAGTTTCC 45436    CC       T   GTC
                                GT  TCTTGGCGG CAG   TCC
                                ||  ||||||||| |||   |||
                                CA  AGAACCGTT GTC   AGG
                                 AC        C   AA_
GAM231  SIX3    3'  GTCCTCGTGGTGGTGATTGATC 24027       T   C   CA__
           T                     GTCCTC TGG GGT    GGTCT
                                ||||||| ||| |||    |||||
                                CAGGAG ACC CCA    CTAGA
                                   C   A   CTAA
GAM231  SOLH    3'  CGTCCTCTGTCGGGGTCTC    24828        TGG   TCA
                                CGTCCTCT   CGG   GGTCTC
                                ||||||||   |||   ||||||
                                GCAGGAGA   GCC   CCAGAG
                                    CA_   ____
GAM231  STAC    3'  GTCTTTAGGCAGGTCAGGTCT  17137     CTCTT  _
                                GTC    GGC GGTCAGGTCT
                                |||    ||| ||||||||||
                                CAG    CCG CCAGTCCAGA
                                  AAAT_   T
GAM231  TBX5    3'  GTTCTCTTGGCTACTGTCTC   38808    C      GGTCAG
                                GT CTCTTGGC     GTCTC
                                || ||||||||     |||||
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                                CA GAGAACCG     CAGAG
                                 A       ATGA__
GAM231  TM4SF2   3'  TCCTTTTTAAAACAGGTCTC  21452      C  GGCGGT
                                TCCT TT     CAGGTCTC
                                |||| ||     ||||||||
                                AGGA AA     GTCCAGAG
                                  A  ATTTT_
GAM232  DMD      3'  TATAATAAGTCCTGTGTA    19692        A  G
                                TATAATAA TC TGTGTA
                                |||||||| || ||||||
                                ATATTATT AG ACACAT
                                     C  G
GAM233  ABR      3'  ACACACCGACACTCGGATGCC  9910         _ _____  AC
                                GCACACCG CA   GA  GCC
                                |||||||| ||   ||  |||
                                TGTGTGGC GT   CT  CGG
                                     T  GAGC  A_
GAM233  CNTN2    3'  ACACACCAGCATGAATGC    22908        _  _  C
                                GCACACC GCA GAA GC
                                ||||||| ||| ||| ||
                                TGTGTGG CGT CTT CG
                                    T   A   A
GAM233  COL4A2   5'  GCACACCGGCAGGGCGGCC   12317         _  AA  _
                                GCACACCG CAG  CG CC
                                |||||||| |||  || ||
                                CGTGTGGC GTC  GC GG
                                     C   CC  C
GAM233  CRYBA4   3'  CACAGCCTCCAGAGCGCC    12457      _  G_   A
                                CACA CC  CAGA CGCC
                                |||| ||  |||| ||||
                                GTGT GG  GTCT GCGG
                                  C  AG   C
GAM234  SLC17A4  3'  TACTATCTTGCTCCCATTAGT  24256          GA_
                                TACTATCTTGC   TATTAGT
                                ||||||||||   |||||||
                                ATGATAGAACG   GTAATCA
                                      AGG
GAM235  FUT7     3'  GGGCCGGATGCCTGGTGG    20994      TCA       C
                                GGGTC   GATGCCTGG GG
                                |||||   ||||||||| ||
                                CCCGG   CTACGGACC CC
                                  C__       A
GAM236  EGFL5    3'  AAGAGTTCAAAGATTT      44508        TATCT
                                AAGAGTTT    AAAGATTT
                                ||||||||    ||||||||
                                TTCTCAAG    TTTCTAAA
                                      _____
GAM237  B4GALT2  3'  AGCCAAACTTGTCCAT      36133          TATAAAGA
                                AGCCAAACTT      CCAT
                                ||||||||||      ||||
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                                TCGGTTTGAA       GGTA
                                     CA_______
GAM237  CHC1     3'  AGCCAGGGCCAACCAGGACCAT 10422       AACTTT  AAA
            GG                    AGCCA     AT   GACCATGG
                                  |||||     ||   ||||||||
                                  TCGGT     TG   CTGGTACC
                                    CCCGGT  GTC
GAM237  CYP27B1  3'  GCCAAGCAAGCAGAGAGACCAT 8954        ACTTTATAA_
            GG                    GCCAA        AGACCATGG
                                  |||||        |||||||||
                                  CGGTT        TCTGGTACC
                                    CGTTCGTCTC
GAM237  EMP1     3'  GCCTAGCAAAGACCATG     10896     AAACTTTA
                                  GCC       TAAAGACCATG
                                  |||       ||||||||||
                                  CGG       GTTTCTGGTAC
                                    ATC_____
GAM237  FRAP1    3'  AGTCAAACTTTCTCACCATGG  22436    C       ATAAAG
                                  AG CAAACTTT     ACCATGG
                                  || ||||||||     |||||||
                                  TC GTTTGAAA     TGGTACC
                                   A       GAG___
GAM237  LYAAT1   3'  AGCCCAGCTTTATAAAGA    38525      AAA
                                  AGCC   CTTTATAAAGA
                                  ||||   ||||||||||
                                  TCGG   GAAATATTTCT
                                    GTC
GAM237  MFAP4    3'  AGCACTCATGGAGACCATG   42908     CAA    TATAA
                                  AGC   ACTT    AGACCATG
                                  |||   ||||    ||||||||
                                  TCG   TGAG    TCTGGTAC
                                    ___   TACC_
GAM237  MYD88    3'  GCACAGACACCTAAGACCATGG 14716    _  A  TTTATA
                                  GC CA AC     AAGACCATGG
                                  || || ||     ||||||||||
                                  CG GT TG     TTCTGGTACC
                                   T  C  TGGA__
GAM237  RASGRP1  3'  ACCAGACTTTATAGGCATG   25071      A       AAGAC
                                  GCCA ACTTTATA     CATG
                                  |||| ||||||||     ||||
                                  TGGT TGAAATAT     GTAC
                                    C       CC___
GAM237  SLN      3'  AGTCAATCCCAGGACCATG   16876    C   A   TATAAA
                                  AG CAA CTT     GACCATG
                                  || ||| |||     |||||||
                                  TC GTT GGG     CTGGTAC
                                   A   A   TC_____
GAM238  BACH2    3'  TCCAGAATCAGTATGTAATA   34808          A  T  A
                                  TCCAGAATTA GT TG TAATA
                                  |||||||||| || || |||||
```

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                                AGGTCTTAGT CA AC ATTAT
                                      _  T  _
GAM238  GYPA     3'  TCCAGAACTAGGAAGAAAATA  44626          AGTTT  T
                                TCCAGAATTA     GA AATA
                                ||||||||||     || ||||
                                AGGTCTTGAT     CT TTAT
                                     CCTT_  T
GAM238  RAB5A    5'  TCCAGAATTCAAGGGGCCAATA 20014         _    T__ TG
                                TCCAGAAT TAAG   T  ATA
                                |||||||| ||||   |  |||
                                AGGTCTTA GTTC   G  TAT
                                    A    CCC GT
GAM238  RAB7     5'  TCCAGAATCTCCCAGGATGATA 21579         A___  TT
                                TCCAGAATT    AG  TGATA
                                |||||||||    ||  |||||
                                AGGTCTTAG    TC  ACTAT
                                     AGGG  CT
GAM238  SPO11    3'  CAGAATTAAGAATATAATA   29706          TTTG
                                CAGAATTAAG    ATAATA
                                ||||||||||    ||||||
                                GTCTTAATTC    TATTAT
                                     TTA_
GAM239  ATP1A2   3'  TGCAAGGTCTGAAGG      8712       CAGTCTC   C
                                TGCA      GGG CTGAAGG
                                ||||      ||| |||||||
                                ACGT      TCC GACTTCC
                                  ________  A
GAM239  CASP3    3'  TACACAGTCTTAAGTGGGGGGA 37417           CG  CC  AA
                                TGCACAGTCT  GG  TG  GGGA
                                ||||||||||  ||  ||  ||||
                                ATGTGTCAGA  TC  AC  CCCT
                                     AT  __  CC
GAM239  JPH3     5'  GCGCGGTCTCGGGCGCGGG   34020    ACA       CTGAA
                                GC   GTCTCGGGC    GGG
                                ||   |||||||||    |||
                                CG   CAGAGCCCG    CCC
                                 CGC       CG___
GAM239  MAP3K14  3'  CAGTGCTGGGCCTGAAGGG   19538     _  C
                                CAGT CT GGGCCTGAAGGG
                                |||| || ||||||||||||
                                GTCA GA CCCGGACTTCCC
                                  C  _
GAM239  RBP5     3'  GCACAATCTGGGCTTGAAGGG  36461         C   C
                                GCACAGTCT GGGC TGAAGGG
                                ||||||||| |||| |||||||
                                CGTGTTAGA CCCG ACTTCCC
                                     _   A
GAM239  RDS      3'  CAGCGGGCCTGAAGGG      7242      TCT
                                CAG   CGGGCCTGAAGGG
                                |||   ||||||||||||
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                                GTC   GCCCGGACTTCCC
                                  ___
GAM239  TRPM2    3'  CACAGACATAGGCCTGAGGGG  17688      TCTC      A
                                CACAG    GGGCCTGA GGG
                                |||||    |||||||| |||
                                GTGTC    TCCGGACT CCC
                                   TGTA       C
GAM239  ZNF144   3'  TGCCTAAAGCTTTGGGTCTGAA 28345     AC__   CTC   C
           GGG                    TGC    AGT   GGG CTGAAGGG
                                |||    |||   ||| ||||||||
                                ACG    TCG   CCC GACTTCCC
                                  GATT   AAA   A
GAM240  AIM1     3'  AGGTTCGAGATCAGCCTGGGC  45077     ACCAAA  T      A
                                AGG     AG TTAGCCTG GC
                                |||     || |||||||| ||
                                TCC     TC AGTCGGAC CG
                                  AAGC__  T       C
GAM240  CD9      5'  AGGGCTAACTTAGCCTGGGC   12095     ACCAAAAG       A
                                AGG       TTTAGCCTG GC
                                |||       ||||||||| ||
                                TCC       GAATCGGAC CG
                                  CGATT___        C
GAM240  CLCN4    3'  AAGGAGTAAAAGTTTCTTGAG  12275      CC       AGCC
                                AAGGA  AAAAGTTT    TGAG
                                |||||  ||||||||    ||||
                                TTCCT  TTTTCAAA    ACTC
                                   CA       GA__
GAM240  CST      5'  AGGATTGCTTGAGCCTGAG    22170      CCAAAA   _
                                AGGA     GTTT AGCCTGAG
                                ||||     |||| ||||||||
                                TCCT     CGAA TCGGACTC
                                  AA_____    C
GAM240  DSCR3    3'  GGAGGTCTTTGGCCTGAG     25828     CCAAAA    A__
                                GGA     GTTT   GCCTGAG
                                |||     ||||   |||||||
                                CCT     CAGA   CGGACTC
                                  C______    AAC
GAM240  EIF5A2   3'  AACGATCAAAACTTGGCCTGAG 33784    G  C    G   A
           C                     AA GA CAAAA TTT GCCTGAGC
                                || || ||||| ||| ||||||||
                                TT CT GTTTT GAA CGGACTCG
                                 G  A    _  C
GAM240  FABP2    3'  AGGGGTTCAAGACCAGCCTGGG 6584      ACCAA   T      A
           C                     AGG     AAG TTAGCCTG GC
                                |||     ||| |||||||| ||
                                TCC     TTC GGTCGGAC CG
                                  CCAAG   T       C
GAM240  FLT1     3'  AGGAGCCAAAAGTATGGGC    12905      _       TTA_
                                AGGA CCAAAAGT    GC
                                ||||  ||||||||    ||
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                                TCCT GGTTTTCA   CG
                                  C       TACC
GAM240  FMO5    3'  GACTAAAAGAGTACCTGAGC  11143    C    TTTA
                                GAC AAAAG   GCCTGAGC
                                ||| |||||   ||||||||
                                CTG TTTTC   TGGACTCG
                                  A    TCA_
GAM240  GBE1    5'  AGGGTCGAGTGGGGCCTGAGC  6687     ACCAAA   TTA
                                AGG     AGT   GCCTGAGC
                                |||     |||   ||||||||
                                TCC     TCA   CGGACTCG
                                  CAGC__   CCC
GAM240  GGT1    3'  AAGGCCAGGAGGCCACCTGAGC 23570     A   AA  TTTA
                                AAGG CCA  AG   GCCTGAGC
                                |||| |||  ||   ||||||||
                                TTCC GGT  TC   TGGACTCG
                                  _   CC  CGG_
GAM240  GPRC5C  3'  AGGAGCAAGATCCAGGCCTGAG 33011     C   AA    _
            C                    AGGA CAA  GTTTAG CCTGAGC
                                |||| |||  |||||| |||||||
                                TCCT GTT  TAGGTC GGACTCG
                                  C  C_    C
GAM240  LAMC1   3'  AGGATCAAAAGTTGAGAAGC  14078     C      T  CCT
                                AGGA CAAAAGTT AG   GAGC
                                |||| |||||||| ||   ||||
                                TCCT GTTTTCAA TC   TTCG
                                  A      C  ___
GAM240  LENG4   3'  AAGGGGCAGCTAGGCGGCCTGA 35874     ACCAAA   TA___
            GC                    AAGG     AGTT    GCCTGAGC
                                ||||     ||||    ||||||||
                                TTCC     TCGA    CGGACTCG
                                  CCG___    TCCGC
GAM240  MAPK8IP1 3'  AGGTGGCTGGGCTCAGCCTGAG 24151     ACCAAAA
            C                    AGG      GTTTAGCCTGAGC
                                |||      ||||||||||||
                                TCC      CGAGTCGGACTCG
                                  ACCGACC
GAM240  MPP2    3'  AAGGACCAGGGCTTTGGAG   40788       AAA   AGCCT
                                AAGGACCA   GTTT    GAG
                                ||||||||   ||||    |||
                                TTCCTGGT   CGAA    CTC
                                    CC_    AC___
GAM240  NFE2L1  5'  AAGGACCAGAATGTTTATGC  17327       A _   _
                                AAGGACCA AA GTTTA GC
                                |||||||| || ||||| ||
                                TTCCTGGT TT CAAAT CG
                                    C A    A
GAM240  NPR2L   3'  AAGACCAGACCAGCCTGG    27249       AAAGT      A
                                AGGACCA    TTAGCCTG G
                                |||||||    |||||||| |
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                                TTCTGGT    GGTCGGAC C
                                   CT___       C
GAM240  RAB11A   3'  AAGACCAATAGGTCTGAG    21674        AAGTT   C_
                                AGGACCAA    TAG  CTGAG
                                ||||||||    |||  |||||
                                TTCTGGTT    ATC  GACTC
                                    _____   CA
GAM240  ROCK2    5'  AGGCTGAAGCCCAGGCCTGGGC 42349     ACCAA      _   A
                                AGG    AAGTTTAG CCTG GC
                                |||    |||||||| |||| ||
                                TCC    TTCGGGTC GGAC CG
                                  GAC__       C   C
GAM240  SH3BP2   3'  GGATTGGGGCTGGGCCTGAGC  16635    CCAAAA   TA
                                GGA     GTT  GCCTGAGC
                                |||     |||  ||||||||
                                CCT     CGA  CGGACTCG
                                  AACCC_   CC
GAM240  SIRT1    3'  AAGAATCAAAAGTTTAGC    29251      C
                                AAGGA CAAAAGTTTAGC
                                ||||| ||||||||||||
                                TTCTT GTTTTCAAATCG
                                   A
GAM240  SLC7A5   3'  GGAGACCAAAAGCTGCTCCTGG 18549   A         TAG   A
           GC                     A GGACCAAAAGTT   CCTG GC
                                | ||||||||||||   |||| ||
                                C TCTGGTTTTCGA   GGAC CG
                                 C          CGA   C
GAM240  SOX10    3'  AAGGGTTAGGGCCTGAG     27991     ACCAAAA   TA_
                                AAGG      GTT   GCCTGAG
                                ||||      |||   |||||||
                                TTCC      CAA   CGGACTC
                                  ________  TCC
GAM240  TGFA     3'  AGGGCAGGGGTCTCCTGAGC   17439     AC  AAA   AG
                                AGG  CA   GTTT  CCTGAGC
                                |||  ||   ||||  |||||||
                                TCC  GT   CAGA  GGACTCG
                                  C_  CCC   __
GAM240  TK1      3'  GGCCAGCTCCAGCCTGGGC   17554    A   AAAG       A
                                GG CCA    TTTAGCCTG GC
                                || |||    ||||||||| ||
                                CC GGT    AGGTCGGAC CG
                                 _   CG__        C
GAM240  TRPM2    3'  AGGGCCCAGGAACAGCCTGAG  17685     A  AAAAGTT
                                AGG CC      TAGCCTGAG
                                ||| ||      |||||||||
                                TCC GG      GTCGGACTC
                                  C  GTCCTT_
GAM240  UMPS     3'  AGGAGTTGAGACCAGCCTG   7500       CCAAA  T
                                AGGA    AG TTAGCCTG
                                ||||    || ||||||||
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                                TCCT    TC GGTCGGAC
                                  CAAC_ T
GAM240  FANCC   3' TGCCCGGCCGCCACCTGTC  43283      A   TCACTG
                                TGCCTG CCGCC    CTGTC
                                |||||| |||||    |||||
                                ACGGGC GGCGG    GACAG
                                   C    TG____
GAM240  GAD1    5' TGCCTGACCGCCTCTGGAGCT 30296          ACT_
                                TGCCTGACCGCCTC   GCT
                                ||||||||||||||  |||
                                ACGGACTGGCGGAG   CGA
                                        ACCT
GAM240  HAMP    5' TGTCTGGCTGTCCCACTGCT  34513   C  ACCGC
                                TG CTG    CTCACTGCT
                                || |||    |||||||||
                                AC GAC    GGGTGACGA
                                 A  CGACA
GAM240  HIP1    3' GCCATGATTTTGTTGCTGTCC 23754    _  CCGCCTCAC
                                GCC TGA       TGCTGTCC
                                ||| |||       ||||||||
                                CGG ACT       ACGACAGG
                                  T  AAAACA___
GAM240  IRTA2   3' GCCTATGCTTGCTGCTGTCC  36340     ACC  CTCA
                                GCCTG  GC   CTGCTGTCC
                                |||||  ||   |||||||||
                                CGGAT  CG   GACGACAGG
                                   A__  AAC_
GAM240  KIF5C   3' TGTCTACTACCTGCTGT    21167   C  A CG  CACT
                                TG CTG C  CCT   GCTGT
                                || ||| |  |||   |||||
                                AC GAT G  GGA   CGACA
                                 A  _ AT  ____
GAM240  MAP4    3' TGCCTGACCGGCTCACCAGCC 36276        C    _
                                TGCCTGACCG CTCACT GCT
                                |||||||||| |||||| |||
                                ACGGACTGGC GAGTGG CGG
                                      C     T
GAM240  NRXN2   5' TGTCTGCCGCCTCGCGCC   31495   C  A     AC
                                TG CTG CCGCCTC  TGCT
                                || ||| |||||||  ||||
                                AC GAC GGCGGAG  GCGG
                                 A  _     C_
GAM240  PMX1    5' TGCCTGACGTTTCACAGACC  27912       C CC   T_
                                TGCCTGAC G  TCAC  GCT
                                |||||||| |  ||||  |||
                                ACGGACTG C  AGTG  TGG
                                     _ AA   TC
GAM240  PTPN6   5' TGCCGGGCCGCCTCACCACC  15918    TGA      TG
                                TGCC  CCGCCTCAC  CT
                                ||||  |||||||||  ||
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                                ACGG  GGCGGAGTG  GG
                                  CCC       GT
GAM240  SLC22A11  5'  TGCTGACCTAACTGCTGT   32966    C   GCCTC
                                TGC TGACC    ACTGCTGT
                                ||| |||||    ||||||||
                                ACG ACTGG    TGACGACA
                                  _    AT___
GAM241  ATRX    3'  TGAGAAGAGTGTATACAAAG  39613     T   ACAC
                                TGAG AGAGT   ATGCGGAG
                                |||| |||||   ||||||||
                                ACTC TCTCA   TATGTTTC
                                  T    CA__
GAM241  BMP1    3'  TGAGCAGAGTAGCCATTGG   25995        CA  GC
                                TGAGTAGAGTA  CAT  GG
                                ||||||||||  |||  ||
                                ACTCGTCTCAT  GTA  CC
                                      CG   A_
GAM241  DBH     3'  GAGTAGAGTGCACAGTGTGCTC 8969        A  A_______  GGA
          G                     GAGTAGAGT CAC     TGC   G
                                |||||||| |||      |||  |
                                CTCATCTCA GTG     ACG   C
                                     C   TCACIII  AGG
GAM241  DYRK2   3'  TGAGTAGAGTTATTGAGC   27044        ACACA  CG
                                TGAGTAGAGT   TG  GAGC
                                ||||||||||   ||  ||||
                                ACTCATCTCA   AT  CTCG
                                     ______  AA
GAM241  EIF2C1  3'  TGAGTAGAGTAAGGGAGAGCA  29186        CACATGC
                                TGAGTAGAGTA     GGAGCA
                                ||||||||||      ||||||
                                ACTCATCTCAT     TCTCGT
                                      TCCC___
GAM241  PTPRCAP  3'  TGAGCGGGGTACACATGGA   24693     AGA      C
                                TGAGT   GTACACATG GG
                                |||||   ||||||||| ||
                                ACTCG   CATGTGTAC CT
                                  CCC       _
GAM241  THPO    5'  TGGGCAGAGTAGGGTGGGGCA  7854    A      CACA  C  A
                                TG GTAGAGTA   TG GG GCA
                                || ||||||||   || || |||
                                AC CGTCTCAT   AC CC CGT
                                 C       CCC_  _  _
GAM241  VAT1    3'  TGGTGGGGTACACAAAAGC   26856    A  AGA     TGC
                                TG GT   GTACACA   GGAGC
                                || ||   |||||||   |||||
                                AC CA   CATGTGT   TTTCG
                                 _ CCC      ____
GAM242  CYP1B1  3'  TGTTATAAAAATAAGAACA   6456          A
                                TGTTATAAAAA TAAGAATA
                                |||||||||| ||||||||
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                                ACAATATTTTT ATTCTTGT
                                          _
GAM242  MME     3'  TGTTAGGAAAAATAAGAAT   28608      TA
                                TGTTA  AAAAATAAGAAT
                                |||||  ||||||||||||
                                ACAAT  TTTTTATTCTTA
                                   CC
GAM243  ACP2    3'  CGTGGAGGAGGCAAATCCTGT  11506    C      G____
                                CG GGAGGAGG    CCTGT
                                || ||||||||    |||||
                                GC CCTCCTCC    GGACA
                                 A       GTTTA
GAM243  ATRX    5'  TCGTGGAGGAGAACTTGT    39612    C       C
                                TCG GGAGGAGGGC TGT
                                ||| |||||||||| |||
                                AGC CCTCCTCTTG ACA
                                  A         A
GAM243  CAPNS1  3'  CCGTGGACAGAGCTTGT    11977    C  GG   C
                                TCG GGA  AGGGC TGT
                                ||| |||  ||||| |||
                                GGC CCT  TCTCG ACA
                                  A  G_    A
GAM243  DTX1    5'  CCGCCAGACAGGGCCTGT    20650     _  GG
                                TCGC GGA  AGGGCCTGT
                                |||| |||  |||||||||
                                GGCG TCT  TCCCGGACA
                                  G  G_
GAM243  DVL1    3'  TCCAGACAGGGGGCCTGT    40416   G  __ A
                                TC CGGA  GG GGGCCTGT
                                || ||||  || ||||||||
                                AG GTCT  CC CCCGGACA
                                 _   GT  _
GAM243  EHD2    5'  CCGCGGAGCGGCCTGT     31128       GAG
                                TCGCGGAG   GGCCTGT
                                ||||||||   |||||||
                                GGCGCCTC   CCGGACA
                                     G__
GAM243  EMP1    3'  TCACCCAAGGGCCTGT     10899     GGAG
                                TCGC   GAGGGCCTGT
                                ||||   ||||||||||
                                AGTG   TTCCCGGACA
                                  GG__
GAM243  GM2A    3'  CGTGGTGGCAGGGCCTGT    42686    C  A  _
                                CG GG GG AGGGCCTGT
                                || || || |||||||||
                                GC CC CC TCCCGGACA
                                 A  A  G
GAM243  HRH1    3'  TCTGGAGAAAGCTGT      9257    GC      GC
                                TC  GGAGGAGG  CTGT
                                ||  ||||||||  ||||
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                                AG  CCTCTTTC  GACA
                                 A_      __
GAM243  MMP25    3'  TCGCAGTCAGGCCTGT     35393      AGGA
                                TCGCGG   GGGCCTGT
                                ||||||   ||||||||
                                AGCGTC   TCCGGACA
                                   AG__
GAM243  OSCAR    5'  TCGAGGTGGGGGCCTGT    39311    C  A  A
                                TCG GG GG GGGCCTGT
                                ||| || || ||||||||
                                AGC CC CC CCCGGACA
                                  T  A  _
GAM243  PIG3     5'  TCGCGGAGCAGCCAGCCT   22197       G  __
                                TCGCGGAG AG  GGCCT
                                |||||||| ||  |||||
                                AGCGCCTC TC  TCGGA
                                     G  GG
GAM243  PIK3CD   3'  TCGGGAGGAGAACAGT    22735    C       CT
                                TCG GGAGGAGGGC  GT
                                ||| ||||||||||  ||
                                AGC CCTCCTCTTG  CA
                                  _       T_
GAM243  PLA2G2D  3'  TCTGGAGAAACCTGT     29639    GC    GG
                                TC  GGAGGA  GCCTGT
                                ||  ||||||  ||||||
                                AG  CCTCTT  TGGACA
                                 A_    __
GAM243  POU2AF1  5'  CCGCGGGGACCTGC      26366      AGGA
                                TCGCGG   GGGCCTGT
                                ||||||   ||||||||
                                GGCGCC   CCTGGACG
                                   ____
GAM243  PROS1    5'  CCGCGGAGCTGCGAGCCTGT  44611       GA__
                                TCGCGGAG   GGGCCTGT
                                ||||||||   ||||||||
                                GGCGCCTC   CTCGGACA
                                     GACG
GAM243  RAB36    3'  TCACGGAAATTCCTGT     22244       AGGG
                                TCGCGGAGG   CCTGT
                                |||||||||   |||||
                                AGTGCCTTT   GGACA
                                     AA__
GAM243  RUNX3    3'  TCACGGAACTATACCTGT   20326       GAGG
                                TCGCGGAG   GCCTGT
                                ||||||||   ||||||
                                AGTGCCTT   TGGACA
                                     GATA
GAM243  SIL      5'  CCGCGGAGCTGAGGTCTGT  16726       __   GC
                                TCGCGGAG  GAGG  CTGT
                                ||||||||  ||||  ||||
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                                GGCGCCTC  CTCC  GACA
                                    GA    A_
GAM243  SLC21A3  3'  TCACACACCAGGGCCTGT    39579      GAGG
                                TCGCG    AGGGCCTGT
                                |||||    |||||||||
                                AGTGT    TCCCGGACA
                                   GTGG
GAM243  ZFHX1B   5'  TCCCGGAGCAAACTGT     31341    G    G   GC
                                TC CGGAG AGG  CTGT
                                || ||||| |||  ||||
                                AG GCCTC TTT  GACA
                                 G    G  __
GAM243  ADAMTS5  3'  CCTCCTGTTCACCACGA     28178      C  C
                                CCTCC TG TCACCATGA
                                ||||| || |||||||||
                                GGAGG AC AGTGGTGCT
                                   _ A
GAM243  ADH1B    5'  TCTCTGCCCACCAGCAGA    43742    C        TGA
                                TC CTGCTCACCA   AGA
                                || ||||||||||   |||
                                AG GACGGGTGGT   TCT
                                 A         CG_
GAM243  ALX3     3'  TCCATCTCATCATGAAGA    27067    CTG    C
                                TCC   CTCA CATGAAGA
                                |||   |||| ||||||||
                                AGG   GAGT GTACTTCT
                                  TA_    A
GAM243  APPBP2   3'  CCTGACACAATGAAGAACC   26877     CT   C
                                CCTG  CAC ATGAAGAACC
                                ||||  ||| ||||||||||
                                GGAC  GTG TACTTCTTGG
                                  T_   T
GAM243  APTX     3'  CCTCTTTTCTCACTGTGAAGAA 32808     CCTG    CA
            C                    CCTC    CTCAC  TGAAGAAC
                                ||||    |||||  ||||||||
                                GGAG    GAGTG  ACTTCTTG
                                   AAAA     AC
GAM243  ARHGEF12 3'  CTGCCACACTGTGAAGAAC   31637      _   CA
                                CTGCT CAC  TGAAGAAC
                                ||||| |||  ||||||||
                                GACGG GTG  ACTTCTTG
                                   T   AC
GAM243  CHD3     5'  CTCCCTGCTCCCTTTGGGAAC  10458         A  ATGAA
                                CTCCCTGCTC CC     GAAC
                                |||||||||| ||     ||||
                                GAGGGACGAG GG     CTTG
                                      _ AAACC
GAM243  ETV5     3'  CCTCCCTGTTCCCACTCCCC   20849        C  A   GAAGAA
                                CCTCCCTG TC CCAT      CC
                                |||||||| || ||||      ||
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                                GGAGGGAC AG GGTG     GG
                                    A _    AGG___
GAM243  FKBP6   3' CCTCGTTGGTAGGTGAAGAACC 44089     CC  CTCACCA
                                CCTC  TG      TGAAGAACC
                                ||||  ||      |||||||||
                                GGAG  AC      ACTTCTTGG
                                  CA  CATCC__
GAM243  FNTA    3' TCCCTGCTTACTGAAC      12995        C  CATGAA
                                TCCCTGCT AC     GAAC
                                |||||||| ||     ||||
                                AGGGACGA TG     CTTG
                                    A  A_____
GAM243  GJB1    5' CCTCCCTGTCACTGCCACACC  41008        C    CA  AAGA
                                CCTCCCTG TCAC  TG    ACC
                                |||||||| ||||  ||    |||
                                GGAGGGAC AGTG  AC    TGG
                                    _   __  GGTG
GAM243  HAS3    3' CCCCTGCTCACCATTGGAGAA  39770           GA_
                                TCCCTGCTCACCAT   AGAA
                                ||||||||||||||   ||||
                                GGGGACGAGTGGTA   TCTT
                                      ACC
GAM243  HFE     3' CTCTCCTGAAACATGAAGA   40005    _   CTCAC
                                CTC CCTG    CATGAAGA
                                ||| ||||    ||||||||
                                GAG GGAC    GTACTTCT
                                  A   TTT__
GAM243  KIF3B   3' TCCCTGCCCACTGCACTGAG   22043          __   GA
                                TCCCTGCTCAC  CAT  AG
                                ||||||||||  |||  ||
                                AGGGACGGGTG  GTG  TC
                                      AC   AC
GAM243  MLLT7   3' CCATCCCTGCTCATTTCCCAGA 25528    _        CCATGA   A
            CC                    CC TCCCTGCTCA     AGA CC
                                || ||||||||||     ||| ||
                                GG AGGGACGAGT     TCT GG
                                 T        AAAGGG  _
GAM243  PITX2   5' TCCCCGCTGCGGGGAGAGCC  7254        CACCAT  A  A
                                TCCCTGCT     GA GA CC
                                ||||||||     || || ||
                                AGGGGCGA     CT CT GG
                                    CGCCC_ _  C
GAM243  PKD1    3' CCTGCCTGCTCTCTGGGGAACC 7135     C      ACCA  AA
                                CCT CCTGCTC   TG  GAACC
                                ||| |||||||   ||  |||||
                                GGA GGACGAG   AC  CTTGG
                                  C      AG__  CC
GAM243  PLXNA2  3' CCTCTCGGCTTGAAGAAC    36076     CCT   CACCA
                                CCTC   GCT    TGAAGAAC
                                ||||   |||    ||||||||
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                                GGAG  CGA    ACTTCTTG
                                  AGC  _____
GAM243  PML     3'  CCTCTCTGCCCACCAGAGA   37725     C       T  A
                                CCTC CTGCTCACCA GA GA
                                |||| |||||||||| || ||
                                GGAG GACGGGTGGT CT CT
                                  A       _ _
GAM243  PODXL   5'  CCTCCCTGCCGCTGCAGCAGAG 23965         CACCATGA  A
          CC                    CCTCCCTGCT       AGA CC
                                ||||||||||       ||| ||
                                GGAGGGACGG       TCT GG
                                     CGACGTCG   C
GAM243  POU5F1  3'  CCTTCCTTAGTGAATGAAGAAC 15473    C  GCTCACC
                                CCT CCT      ATGAAGAAC
                                ||| |||      |||||||||
                                GGA GGA      TACTTCTTG
                                  A  ATCACT_
GAM243  PPP2R2B 3'  TCCCTTTCATTGAAAAAC    21338     GC  CCA
                                TCCCT  TCA  TGAAGAAC
                                |||||  |||  ||||||||
                                AGGGA  AGT  ACTTTTTG
                                  A_  A__
GAM243  RNPEPL1 3'  CTCCCTGCCTGGGAGAC    32880       CACCA  A_  A
                                CTCCCTGCT    TG  AGA C
                                |||||||||    ||  ||| |
                                GAGGGACGG    AC  TCT G
                                     _____  CC  C
GAM243  SCA1    3'  TCCCTGTCCACCACAACACC  7288      CT    TG AGA
                                TCCCTG  CACCA  A  ACC
                                ||||||  |||||  |  |||
                                AGGGAC  GTGGT  T  TGG
                                   AG    GT G__
GAM243  SERPINH2 3'  CCTCCCTATCTTTGAAGAAC  10294       C  ACCA
                                CCTCCCTG TC   TGAAGAAC
                                |||||||| ||   ||||||||
                                GGAGGGAT AG   ACTTCTTG
                                     _  AA__
GAM243  SGCA    3'  CTCCCTGCTTGTTTAGAGCC  6172        CACCATGA  A
                                CTCCCTGCT      AGA CC
                                |||||||||      ||| ||
                                GAGGGACGA      TCT GG
                                     ACAAA___  C
GAM243  SLC21A9 3'  CTCCCCGCTTCAGCTAAGGA  28562       _  CCA  A
                                CTCCCTGCT CA  TGA GA
                                ||||||||| ||  ||| ||
                                GAGGGGCGA GT  ATT CT
                                     A  CG_  C
GAM243  TEM8    3'  CCCTGCTTATGAGGAAC    38176       CACC   A
                                CCCTGCT   ATGA GAAC
                                |||||||   |||| ||||
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                                GGGACGA   TACT CTTG
                                   A___   C
GAM243  YWHAZ   3'  TCCCTGCTCTTGAGGA     18203       ACCA  A
                                TCCCTGCTC   TGA GA
                                |||||||||   ||| ||
                                AGGGACGAG   ACT CT
                                   A___   C
GAM243  ZNF41   3'  CCTCCCTGCTATTAGATAC   41914       CACC  GA  _
                                CCTCCCTGCT   AT  AGA AC
                                ||||||||||   ||  ||| ||
                                GGAGGGACGA   TA  TCT TG
                                     _____ A_  A
GAM244  APOL1   3'  GGCCATGGCCCACCACCTG   18936     __
                                GGCCA  GCTCGCCACCTG
                                |||||  ||||||||||||
                                CCGGT  CGGGTGGTGGAC
                                   AC
GAM244  BRF1    3'  GCTGTGGGACAGGTGCCACCTG 11336   CAC_  C  CTC
                                GC   GG CAG   GCCACCTG
                                ||   || |||   ||||||||
                                CG   CC GTC   CGGTGGAC
                                 ACAC  T   CA_
GAM244  CARPX   5'  GCGGCGGCAGCAGCCACCTG  33573   CA   C  TC
                                GC  CGGC AGC  GCCACCTG
                                ||  |||| |||  ||||||||
                                CG  GCCG TCG  CGGTGGAC
                                 CC   _   T_
GAM244  CSF2    3'  GCTTGGCCAGCCTCATCTG   8898    CAC     T GC  C
                                GC   GGCCAGC C  CA CTG
                                ||   ||||||| |  || |||
                                CG   CCGGTCG G  GT GAC
                                 AA_      _ A_  A
GAM244  EP300   5'  GCCACGGCCGGCCCCT      10986       AGCTC  A
                                GCCACGGCC    GCC CCT
                                |||||||||    ||| |||
                                CGGTGCCGG    CGG GGA
                                     C_____  _
GAM244  HCCS    5'  GCCGCGGCCAGCCTGCCCTTCT 23734    A      TC  AC_
          G                      GCC CGGCCAGC  GCC   CTG
                                |||  ||||||||  |||   |||
                                CGG GCCGGTCG  CGG   GAC
                                  C       GA   GAA
GAM244  LEP     3'  AGTCCTGGTCCTGCCACCTG   6909    _  AC  _  AGCTC
                                AG CC  GG CC    GCCACCTG
                                || ||  || ||    ||||||||
                                TC GG  CC GG    CGGTGGAC
                                 A  A_  A  A____
GAM244  MMP14   3'  CAGCGTGGCCAGCCAGGCC   22633     CAC      C_
                                CAGC   GGCCAGCT  GCC
                                ||||   ||||||||  |||
```

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                                GTCG  CCGGTCGG CGG
                                  CA_      TC
GAM244  MMP15   3' CAGCCACGGCCTCTTGC    14557         AG C
                                CAGCCACGGCC CT GC
                                |||||||||| || ||
                                GTCGGTGCCGG GA CG
                                      A_ A
GAM244  MYCL2   5' GCTCACGCAGCTTGCCACCTG 23903   _  GC   C
                                GC CACG CAGCT GCCACCTG
                                || |||| ||||| ||||||||
                                CG GTGC GTCGA CGGTGGAC
                                 A  __   A
GAM244  MYO7A   5' CAGCCTGGTACAGCTGCCACCT 7027      AC C_   C
          G                      CAGCC GG CAGCT GCCACCTG
                                ||||| || ||||| ||||||||
                                GTCGG CC GTCGA CGGTGGAC
                                  A_ AT   _
GAM244  PRX     3' GCGGCGGCCAGCCGGGCTGCCT 34123   CA      C_ CA
          G                      GC CGGCCAGCT GC CCTG
                                || ||||||||| || ||||
                                CG GCCGGTCGG CG GGAC
                                 CC       CC AC
GAM244  SEPN1   3' CAGCCATGGTGGCATGCACCTG 42423     C CCA TC C
                                CAGCCA GG  GC GC ACCTG
                                |||||| ||  ||  || |||||
                                GTCGGT CC  CG CG TGGAC
                                   A AC_ TA _
GAM244  SIGLEC11 3' CAGCTGTGGTGGCTCACGTCTG 38084    CAC CCA    CAC
                                CAGC  GG  GCTCGC  CTG
                                ||||  ||  ||||||  |||
                                GTCG  CC  CGAGTG  GAC
                                  ACA AC_    CA_
GAM244  SLC22A11 3' GCCACGGCTGCCTGGCCTCTG 32963      CA  C_  AC
                                GCCACGGC GCT GCC CTG
                                |||||||| ||| ||| |||
                                CGGTGCCG CGG CGG GAC
                                    A_  AC  A_
GAM244  STARD5  5' GCCACAGCCTCGCTCATCTG  36127       AGC  _ C
                                GCCACGGCC  TCGC CA CTG
                                |||||||||  |||| || |||
                                CGGTGTCGG  AGCG GT GAC
                                     ___   A A
GAM244  TMPRSS2  3' CAGCCGCTGCAGGTGCCACCTG 24930     ACG C CTC
                                CAGCC  GC AG  GCCACCTG
                                |||||  || ||  ||||||||
                                GTCGG  CG TC  CGGTGGAC
                                  CGA _ CA_
GAM244  TOP1    5' ACCACGGCGGCGACGCTGCCTG 17623       CA T_  CA
                                GCCACGGC GC CGC CCTG
                                |||||||| || ||| ||||
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                                TGGTGCCG CG GCG GGAC
                                    C_ CT  AC
GAM244  AES     5' CGCGGGCTGCGCCCCGGC   10053       T   GCCA
                                CGCGGGCT CGCCT   CGGC
                                |||||||| |||||   ||||
                                GCGCCCGA GCGGG   GCCG
                                    C   _____
GAM244  APBB1   5' CGGGCTCCGCCGCGGC     10114         T CAC
                                CGGGCTTCGCC GC  GGC
                                |||||||||| ||  |||
                                GCCCGAGGCGG CG  CCG
                                      _ ___
GAM244  BCL7A   5' GCGGCTCCGCGCCGCGGCC  34215     G    CT  A
                                GCGG CTTCGC  GCC CGGCC
                                |||| ||||||  ||| |||||
                                CGCC GAGGCG  CGG GCCGG
                                  _    __  C
GAM244  CA12    5' CGCGGGCTGTGCCGGGGGC  10243       TCGCC  AC_
                                CGCGGGCT   TGCC  GGC
                                ||||||||   ||||  |||
                                GCGCCCGA   ACGG  CCG
                                    C____  CCC
GAM244  CRABP2  3' GGGCTTCGGCCGCGG      12430       CCT  A
                                GGGCTTCG  GCC CGG
                                ||||||||  ||| |||
                                CCCGAAGC  CGG GCC
                                    ___  C
GAM244  DNMT3L  5' GGGCTGCTGCCACGGC     30067      TC  C
                                GGGCT  GC TGCCACGGC
                                |||||  || |||||||||
                                CCCGA  CG ACGGTGCCG
                                  __ _
GAM244  DUOX2   3' GCTTGCCACGCCTGCCATGGC 30445   GG  T      C
                                GC  GCT CGCCTGCCA GGC
                                ||  ||| ||||||||| |||
                                CG  CGG GCGGACGGT CCG
                                 AA  T       A
GAM244  ETV5    3' GCGGGCTTTCACATGGCC    20852       _  CT_
                                GCGGGCTT CGC  GCC
                                |||||||| |||  |||
                                CGCCCGAA GTG  CGG
                                    A  TAC
GAM244  FRAT2   5' GCGGGCTTCGCTGGGGGC    28973        C  CCAC
                                GCGGGCTTCGC TG   GGC
                                |||||||||| ||   |||
                                CGCCCGAAGCG AC   CCG
                                      _ CC__
GAM244  MAML1   5' GCGGGCTTCGCTCCCCGCGGC 31287         _  G  A
                                GCGGGCTTCGC CT CC CGGC
                                |||||||||| || || ||||
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                                CGCCCGAAGCG GG GG GCCG
                                      A  _  C
GAM244  MRPL49   3'  CGGGCTCCTTGCTGTGGC    43023        GCC   CAC
                                CGGGCTTC   TGC   GGC
                                ||||||||   |||   |||
                                GCCCGAGG   ACG   CCG
                                    A__    ACA
GAM244  PSMA1    5'  CGCGGGCCTGGTTGCGGC    40613        CGCC   CAC
                                CGCGGGCTT    TGC   GGC
                                |||||||||    |||   |||
                                GCGCCCGGA    ACG   CCG
                                     CCA_   ___
GAM244  RBL1     5'  CGCGGGCTGCGCGCCACGGCC  16176        T   CT
                                CGCGGGCT CGC  GCCACGGCC
                                |||||||| |||  |||||||||
                                GCGCCCGA GCG  CGGTGCCGG
                                     C   __
GAM244  RET      5'  GCGCGCTGGGGCCACGGC    33936     G   TCGCCT
                                GCG GCT     GCCACGGC
                                ||| |||     ||||||||
                                CGC CGA     CGGTGCCG
                                  G   CCC___
GAM244  TPD52L2  3'  GCGGGAGCTGCCACGG      17636      CTTC  C
                                GCGGG    GC TGCCACGG
                                |||||    || ||||||||
                                CGCCC    CG ACGGTGCC
                                   T___  _
GAM244  TRAF5    5'  CGCGGGCTCCGCGAGGCCGG  21470          CT_   AC
                                CGCGGGCTTCGC   GCC  GG
                                ||||||||||||   |||  ||
                                GCGCCCGAGGCG   CGG  CC
                                       CTC   __
GAM244  XRCC1    5'  CGTGGGCTTCGCCTGGCC    26668    C         _
                                CG GGGCTTCGCCTG CC
                                || ||||||||||||  ||
                                GC CCCGAAGCGGAC GG
                                 A          C
GAM245  DLG5     5'  CATCCAGGCTGCGCAGGG    44448      A__  C
                                CGTC   GC GCGCAGGG
                                ||||   || ||||||||
                                GTAG   CG CGCGTCCC
                                  GTC  A
GAM245  LEP      3'  TCTTTGGGGTCAGCCAGGG   6918      CCGAC      GCGC
                                TCT    GTCAGCC    AGGG
                                |||    |||||||    ||||
                                AGA    CAGTCGG    TCCC
                                  AACCC      _____
GAM245  MMP19    3'  CCTCTGACTCTCCTGCGCAGGG 35582      C   GTCAG  _
                                TCTC GAC    CC GCGCAGGG
                                |||| |||    || ||||||||
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                                GGAG CTG    GG CGCGTCCC
                                  A  AGA__  A
GAM245  NLGN2   3'  TCGTCCGGTGCCCGGCGCAGGG 44762   _   AC  AGCC
              C                   TC TCCG  GTC   GCGCAGGGC
                                  || ||||  |||   |||||||||
                                  AG AGGC  CGG   CGCGTCCCG
                                   C   CA  GC__
GAM245  RARA    3'  CCTCTGACGTCAGCCCAGG   9706      C       GCG
                                  TCTC GACGTCAGCC   CAGG
                                  |||| ||||||||||   ||||
                                  GGAG CTGCAGTCGG   GTCC
                                    A       ___
GAM246  GNA14   5'  GGGGGCCGACTTGAGCTTTGGA 20193   A   C_ _   C
                                  GG GGGTT  CT GAGCT TGGA
                                  || |||||  || ||||| ||||
                                  CC CCCGG  GA CTCGA ACCT
                                   _    CT  A    A
GAM246  HSD17B1  5'  GGGGAGAGGCTGGGGCTCTGG  7660       TTC  A_
                                  GGGGAGGG  CTG  GCTCTGG
                                  ||||||||  |||  |||||||
                                  CCCCTCTC  GAC  CGAGACC
                                       C__  CC
GAM246  ID4     5'  GGGAGGGTCGCTCTGG     11384        CCTGA
                                  GGGAGGGTT    GCTCTGG
                                  |||||||||    |||||||
                                  CCCTCCCAG    CGAGACC
                                             _____
GAM246  JUNB    5'  GGGGAGGGTCCCTGCGG    13761           AGCTC
                                  GGGGAGGGTTCCTG    TGG
                                  ||||||||||||||    |||
                                  CCCCTCCCAGGGAC    GCC
                                             _____
GAM246  MYBPH   3'  AGGCCCATTCCTGAGTTCTGGA 22648    AGG       C
                                  GGG   GTTCCTGAG TCTGGA
                                  |||   ||||||||| ||||||
                                  TCC   TAAGGACTC AGACCT
                                    GGG       A
GAM246  PAEP    5'  GGGTGGCTCTGAGCTCTGGA  15069    AG    C
                                  GGG  GGTTC TGAGCTCTGGA
                                  |||  ||||| ||||||||||
                                  CCC  CCGAG ACTCGAGACCT
                                    A_    _
GAM246  POMC    3'  GGGGAGAGCAAGGGGCTTTGG  9604        TCCTGA  C
                                  GGGGAGGGT     GCT TGG
                                  |||||||||     ||| |||
                                  CCCCTCTCG     CGA ACC
                                        TTCCC_  A
GAM246  PTPRS   5'  GGGGAGGGTCCTGCAGG    39305        T   AGCTCT
                                  GGGGAGGGT CCTG     GG
                                  ||||||||| ||||     ||
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                                CCCCTCCCA GGAC     CC
                                     _   GT____
GAM247  APLP1    5'  TGCGCCCTCACGTCCCCTG   23163          G    T
                                TGCGCCCTCA GTCCC CTG
                                |||||||||| ||||| |||
                                ACGCGGGAGT CAGGG GAC
                                     G    _
GAM247  ATP10C   3'  TGTGCTCTGCCCTCTGCCA   35985    C  C  CAG T
                                TG GC CT   G CCCTCTGCCA
                                || || ||   | ||||||||||
                                AC CG GA   C GGGAGACGGT
                                 A  A  ___ _
GAM247  B4GALT6  5'  CTGCGCTCTCAGGCCGGACTC  40848       C       C__
                                CTGCGC CTCAGGTC   CTC
                                |||||| ||||||||   |||
                                GACGCG GAGTCCGG   GAG
                                    A       CCT
GAM247  BCL7C    5'  CCGCGCTCTCGGCCTGCC    21922       C   A   CCCT
                                CTGCGC CTC GGT    CTGCC
                                |||||| ||| |||    |||||
                                GGCGCG GAG CCG    GACGG
                                    A   _  _____
GAM247  CARD15   3'  TGCTCCCTCCTCTGCCA     35261     G    CAGGTC
                                TGC CCCT      CCTCTGCCA
                                ||| ||||      |||||||||
                                ACG GGGA      GGAGACGGT
                                  A   _______
GAM247  DDB2     3'  CTGCTTGATCCCTCTGC      6461       GCCCTCA
                                CTGC       GGTCCCTCTGC
                                ||||       ||||||||||
                                GACG       CTAGGGAGACG
                                  AA_____
GAM247  DNM2     3'  CTGGTCCCCCCTCTGC       22381     CG   TCAGGT
                                CTG  CCC      CCCTCTGC
                                |||  |||      ||||||||
                                GAC  GGG      GGGAGACG
                                  CA  _______
GAM247  EFNB1    5'  CGCCTCGCCTTCCTCTGCC    20714      C  AG   __
                                CGCC TC  GTC  CCTCTGCC
                                |||| ||  |||  ||||||||
                                GCGG AG  CGG  GGAGACGG
                                  _ __   AA
GAM247  FBXL11   3'  TGGCCCAGTCCTCTGCC     29443    C    TCA    C
                                TG GCCC   GGTCC TCTGCC
                                || ||||   ||||| ||||||
                                AC CGGG   TCAGG AGACGG
                                 _   ____    _
GAM247  GAN      5'  GCGCCCGCTCCTCTGCC      35148        TCAG TC
                                GCGCCC    G  CCTCTGCC
                                ||||||    |  ||||||||
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                                CGCGGG   C  GGAGACGG
                                   ____ GA
GAM247  HAO1    3'  CTGCACAGTGTCTCTTTGTCA  32760      CCTC  _  C  C  C
                                CTGCGC   AG GTC CT TG CA
                                ||||||   || ||| || || ||
                                GACGTG   TC CAG GA AC GT
                                   ____  A  A  A  A
GAM247  HMGCL   3'  CTGGGCAGGAGGTCCTTCTGCC 6791     C  CCTC     C
          A                      CTG GC   AGGTCC TCTGCCA
                                ||| ||   ||||||| |||||||
                                GAC CG   TCCAGG AGACGGT
                                  C  TCC_    A
GAM247  HYAL1   5'  GCCTCTCAGACCAGGCCTCTGC 37642    _    GT ___
          CA                     GCC CTCAG  C   CCTCTGCCA
                                ||| |||||  |   |||||||||
                                CGG GAGTC  G   GGAGACGGT
                                  A    TG TCC
GAM247  IL10RA  3'  CTGCCCTTCTCAGCTCTGCCA  40622     G  __    GTCC
                                CTGC CC  CTCAG   CTCTGCCA
                                |||| ||  |||||   ||||||||
                                GACG GG  GAGTC   GAGACGGT
                                  _ AA    _____
GAM247  ISG20   5'  CTGCGCCCTCAGCTCACGTCTG 13590          G  CC_
                                CTGCGCCCTCAG TC   TCTG
                                |||||||||||| ||   ||||
                                GACGCGGGAGTC AG   AGAC
                                      G  TGC
GAM247  KRT16   5'  TGTGCCTCAGGTCCTC     45454    C  C      C
                                TG GCC TCAGGTCC TC
                                || ||| |||||||| ||
                                AC CGG AGTCCAGG AG
                                 A  _      _
GAM247  LMO2    5'  CTGTGCCATCTCCCCTCTCTGC 24541    C  C  AGG  _
          CA                     CTG GCC TC   TCC CTCTGCCA
                                ||| ||| ||   ||| ||||||||
                                GAC CGG AG   GGG GAGACGGT
                                  A  T  AG_  A
GAM247  PABPN1  5'  CTGGCCCCCCTTTGC      21606    C   TCAGGT   C
                                CTG GCCC     CCCT TGC
                                ||| ||||     |||| |||
                                GAC CGGG     GGGA ACG
                                  _   _______   A
GAM247  PAX5    3'  GCCCTGGCTCTCTGCCA    32510      CA  CC
                                GCCCT  GGT  CTCTGCCA
                                |||||  |||  ||||||||
                                CGGGA  CCG  GAGACGGT
                                   __   A_
GAM247  PLXNB3  3'  CTGTGCCCCCAGGCTCTGCCA  23946    C       TCC
                                CTG GCCCTCAGG   CTCTGCCA
                                ||| |||||||||   ||||||||
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                                GAC CGGGGGTCC   GAGACGGT
                                  A       ___
GAM247  PRX      5'  CTGTGTCCTCTCCCCTTTCTGC 34118    CGC    AGG   ___
                                CTG   CCTC   TCCC   TCTGC
                                |||   ||||   ||||   |||||
                                GAC   GGAG   AGGG   AGACG
                                  ACA   ___    GAA
GAM247  PTGS1    3'  CTGTCCTCTCTCTCTGC     38734     CGC    AGG  C
                                CTG   CCTC   TC CTCTGC
                                |||   ||||   || ||||||
                                GAC   GGAG   AG GAGACG
                                  A__    ___ A
GAM247  PTK2B    3'  CTGTGCCCCAGGTCCTCCCT   19917     C    T      _
                                CTG GCCC CAGGTCC CTCT
                                ||| |||| ||||||| ||||
                                GAC CGGG GTCCAGG GGGA
                                  A   _      A
GAM247  PTPRF    5'  CTGCTCCCACTCCTCTGCC    39033     G   TCAG TC
                                CTGC CCC    G  CCTCTGCC
                                |||| |||    |  ||||||||
                                GACG GGG    T  GGAGACGG
                                  A   _____ GA
GAM247  RAB13    3'  CTGCTCACTCCCTCTGCC     16114     GCCC   GG
                                CTGC    TCA  TCCCTCTGCC
                                ||||    |||  ||||||||||
                                GACG    AGT  AGGGAGACGG
                                  _____  G_
GAM247  RARA     3'  CTGTCCCACCCCCTCTGC     9708      CG   TCAGG      C
                                CTG  CCC    TCCCTCTG C
                                |||  |||    |||||||| |
                                GAC  GGG    GGGGAGAC G
                                  A_   TG___       A
GAM247  RNPEPL1  3'  CTGTGTCCTTGTTCCTCTGCCA 32881     CGC   CAG  C
                                CTG   CCT   GT CCTCTGCCA
                                |||   |||   || |||||||||
                                GAC   GGA   CA GGAGACGGT
                                  ACA   A__  A
GAM247  RPS6KA2  3'  CTGCGCCCTCGCACTGCC    34461          AG  CCCT
                                CTGCGCCCTC  GT    CTGCC
                                ||||||||||  ||    |||||
                                GACGCGGGAG  CG    GACGG
                                      __  T___
GAM247  RPS6KA2  3'  CTGCCCCTCAGTCTGC      34460      G      GTCCC
                                CTGC CCCTCAG     TCTGC
                                |||| |||||||     |||||
                                GACG GGGAGTC     AGACG
                                  _     ______
GAM247  RUNX3    3'  CTCAAACCATCTCTGCCA    20321       GT C_
                                CTCAG  C  CTCTGCCA
                                |||||  |  ||||||||
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                                GAGTT  G  GAGACGGT
                                   TG TA
GAM247  SEPN1    3'  GCCTTCCTTCTTCCTCTGCCA  42427     C  AGG  __
                                GCC TC   TC  CCTCTGCCA
                                ||| ||   ||  |||||||||
                                CGG AG   AG  GGAGACGGT
                                  A  GA_  AA
GAM247  SLC18A3  5'  CTGTGCCTCAGGTGGGCC    16830     C  C     CCCTCT
                                CTG GCC TCAGGT     GCC
                                ||| ||| ||||||     |||
                                GAC CGG AGTCCA     CGG
                                  A  _     CC____
GAM247  SLC2A2   3'  TGCATCCTCAGGTTTCTA    7351      C       CCC
                                TGCG CCTCAGGT   TCTG
                                |||| ||||||||   ||||
                                ACGT GGAGTCCA   AGAT
                                  A       A__
GAM247  SLC6A6   3'  CTGTGGCCTCCTGTGCCTCTGC 16786     CGC    AG  C
            CA                    CTG   CCTC  GT CCTCTGCCA
                                |||   ||||  || |||||||||
                                GAC   GGAG  CA GGAGACGGT
                                  ACC    GA  C
GAM247  SPO11    5'  CTGCGCCCTTGGGGCGTGGCTG 29707         CA_   CCCT
                                CTGCGCCCT   GGT    CTG
                                |||||||||   |||    |||
                                GACGCGGGA   CCG    GAC
                                     ACC   CACC
GAM247  STAT6    5'  GCCTCGGCAACCCCTCTGC    17154     C  A   ___
                                GCC TC GGT   CCCTCTGC
                                ||| || |||   ||||||||
                                CGG AG CCG   GGGAGACG
                                  _  _   TTG
GAM247  SURF5    3'  TGCGCCCTGCTCTGC       39511         CAGGTCC
                                TGCGCCCT      CTCTGC
                                ||||||||      ||||||
                                ACGCGGGA      GAGACG
                                     C_______
GAM247  TERF2    3'  TGTGCCTGTCATCTCTGCCA  24918    C  CTCAG  C_
                                TG GCC    GTC  CTCTGCCA
                                || |||    |||  ||||||||
                                AC CGG    CAG  GAGACGGT
                                 A  A____   TA
GAM247  VIPR1    3'  GCCCTCAGGTCACACCA     21508          CCTC
                                GCCCTCAGGTC    TGCCA
                                ||||||||||    |||||
                                CGGGAGTCCAG    GTGGT
                                       T___
GAM248  ACADS    3'  CCCCAGGGAGCCCCCGCCG    6152        TCCCT
                                CCCCAG    GGCCCCCGCCG
                                ||||||    ||||||||||
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                                GGGGTC    TCGGGGGCGGC
                                   CC___
GAM248  ADARB1   3'  TCCACCAGTCCCTGGAACCCG  31883     C        CC
                                TCC CCAGTCCCTGG  CCCG
                                ||| ||||||||||  ||||
                                AGG GGTCAGGGACC  GGGC
                                  T         TT
GAM248  AKT1     3'  TCCCCCATCCCTGGTCCC    23141       G     _
                                TCCCCCA TCCCTGG CCC
                                ||||||| ||||||| |||
                                AGGGGGT AGGGACC GGG
                                   _      A
GAM248  ALDH3B1  3'  TCCCACAGAAGCCCCCGC    45067     C   TCCCT
                                TCCC CAG    GGCCCCCGC
                                |||| |||    |||||||||
                                AGGG GTC    TCGGGGGCG
                                  T  T_____
GAM248  ANK1     3'  TCTCCTGGCCCTGGGGGCGCCC 33876    C  CA T   ___   C
           GCCG                    TC CC  G CCCT   GGC CCCGCCG
                                || ||  | ||||   ||| |||||||
                                AG GG  C GGGA   CCG GGGCGGC
                                 A  AC _   CCC   C
GAM248  BLTR2    5'  TCCCCCAGCTCTGGCCCC    33373         CC
                                TCCCCCAGT  CTGGCCCC
                                |||||||||  ||||||||
                                AGGGGGTCG  GACCGGGG
                                     A_
GAM248  BYSL     5'  TCTCCTGTCCCGCGACCCCGCC 19758    C  CA    _     C
           G                     TC CC  GTCCC TGGCCCC GCCG
                                || ||  ||||| ||||||| ||||
                                AG GG  CAGGG GCTGGGG CGGC
                                 A  A_    C     _
GAM248  EP300    5'  CCACTGTTCTGGCCCCTGCCG  10974     __ CC      C
                                CCA  GT  CTGGCCCC GCCG
                                |||  ||  |||||||| ||||
                                GGT  CA  GACCGGGG CGGC
                                  GA  A_       A
GAM248  EPHA8    3'  TCCTCTGGTCCCTGATCCTAGG 33901     CCCA     GC  CC_
           CC                    TCC   GTCCCTG  CC   GCC
                                |||   |||||||  ||   |||
                                AGG   CAGGGAC  GG   CGG
                                  AGAC      TA  ATC
GAM248  GNL1     5'  CCCCCCGGGGCAGCCCCCGCCG 45561       AGTCCCT
                                CCCCC      GGCCCCCGCCG
                                |||||      ||||||||||
                                GGGGG      TCGGGGGCGGC
                                   GCCCCG_
GAM248  HR       3'  TCCCCTAGCGCCATCCCCTGC  32933       C  C  TGG   C
                                TCCCC AGT CC   CCCC GC
                                ||||| ||| ||   |||| ||
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                                AGGGG TCG GG   GGGG CG
                                  A   C  TA_   A
GAM248  JUN     5'  GTCTCCGGTCCTCCCCGCCG  13747    C   _ __
                                GTC CTGG CC  CCCGCCG
                                ||| |||| ||  |||||||
                                CAG GGCC GG  GGGCGGC
                                  A   A  AG
GAM248  JUNB    5'  TCCCCCAGCTCCCAGCTCCCTG 13766       TC  TG  _   C
            C                    TCCCCCAG  CC  GC CCC GC
                                ||||||||  ||  || ||| ||
                                AGGGGGTC  GG  CG GGG CG
                                     GA  GT  A   A
GAM248  MAN2B1  5'  CCCCGGCCCTGGAAAGGCCG  8030      A T     CCCCC
                                CCCC G CCCTGG    GCCG
                                |||| | ||||||    ||||
                                GGGG C GGGACC    CGGC
                                  C _     TTTC_
GAM248  MPDU1   3'  CCTCCCAGTCCCTCCACTCTGC 22176   _       GG  CCC__
            CG                   CC CCCAGTCCCT  CC    GCCG
                                || ||||||||||  ||    ||||
                                GG GGGTCAGGGA  GG    CGGC
                                 A        __  TGAGA
GAM248  MPP6    5'  CCCGGTCGCTCCCCGCCG   32392    A  CCTG  _
                                CCC GTC   GC CCCCGCCG
                                ||| |||   || ||||||||
                                GGG CAG   CG GGGGCGGC
                                  C  _____  A
GAM248  PAPOLA  5'  TCTCCCGCACCGCTCCCGCCG  37207   C   A TC  TG  C
                                TC CCC G  CC  GC CCCGCCG
                                || ||| |  ||  || |||||||
                                AG GGG C  GG  CG GGGCGGC
                                 A  _ GT  __  A
GAM248  PAX5    3'  TCCCCCAGATCTTCCCTG   32522       _____
                                TCCCCCAG   TCCCTG
                                ||||||||   ||||||
                                AGGGGGTC   AGGGAC
                                     TAGA
GAM248  ROM1    3'  CCCCAGTCCAGCTCGC     7259         CT   CCC
                                CCCCAGTCC  GGC   CGC
                                |||||||||  |||   |||
                                GGGGTCAGG  TCG   GCG
                                     __   A__
GAM248  TGFB1   5'  CCCCCGGCCGGGGCCCTCGC  8536      A   CCT    C
                                CCCCC GTC   GGCCC CGC
                                ||||| |||   ||||| |||
                                GGGGG CGG   CCGGG GCG
                                  C   CC_    A
GAM249  ADCY4   5'  GGGTTGAAGTCCTTCGAC   40203    CCA   TCG
                                GGG   TGG   CCTTCGAC
                                |||   |||   ||||||||
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                                CCC  ACT  GGAAGCTG
                                 A__  TCA
GAM249  DVL1    3'  GCGGGCCATGGTCCCTCC   40412          G
                                GCGGGCCATGGTC CCTTC
                                ||||||||||||| |||||
                                CGCCCGGTACCAG GGAGG
                                                _
GAM249  POLR2J  3'  GCGGGCCATGGCTGGGACC   26358          CGCCTTC
                                GCGGGCCATGGT     GACC
                                ||||||||||||     ||||
                                CGCCCGGTACCG     CTGG
                                      ACC____
GAM250  LAMP2   3'  TCTAAATTTTAAAAAGCTT   30390        A
                                TCTAAATTT AAAAAGTTT
                                ||||||||| |||||||||
                                AGATTTAAA TTTTTCGAA
                                     A
GAM251  PTPN22  3'  GAAGATTTACAAGGTATAC   31984        TATCT
                                GAAGATTTAT    GTATAC
                                ||||||||||    ||||||
                                CTTCTAAATG    CATATG
                                      TTC__
GAM251  CD1D    3'  TTTACAATAGAAACTGT     44302        T   A
                                TTTACAATAG AACT GT
                                ||||||||| |||| ||
                                AAATGTTATC TTGA CA
                                      T   _
GAM252  CHES1   3'  TGACAATTCCAGTGGCTTTC  23286          ATAC
                                TGACAATTCCGG   CTTTT
                                ||||||||||||   |||||
                                ACTGTTAAGGTC   GAAAG
                                      ACC_
GAM252  CUL4B   3'  TATGACAATTCATTTCTCTTTT 18727         CGGATAC
          C                      TATGACAATTC     CTTTTC
                                ||||||||||      ||||||
                                ATACTGTTAAG     GAAAAG
                                      TAAAGA_
GAM252  DTNA    3'  ATGACAATTCGTTCCCTTTTC  37396        C GATA
                                ATGACAATTC G   CCTTTTC
                                ||||||||| |   |||||||
                                TACTGTTAAG C   GGAAAAG
                                      _ AAG_
GAM252  HNRPDL  3'  CATAACCAAGATACCTTTTC  24170      AATTCC
                                TATGAC     GGATACCTTTTC
                                ||||||     ||||||||||||
                                GTATTG     TCTATGGAAAAG
                                   GT_____
GAM252  RFPL1   5'  TGACAAGTGACAACCTTTTC  34286      TTCCG  _
                                TGACAA    GATA CCTTTTC
                                ||||||    |||| |||||||
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                                ACTGTT    CTGT GGAAAAG
                                   CA___    T
GAM252  RFPL2    5'  TGACAAGTGACAACCTTTTC  27353      TTCCG   _
                                TGACAA    GATA CCTTTTC
                                ||||||    |||| |||||||
                                ACTGTT    CTGT GGAAAAG
                                   CA___    T
GAM252  RFPL3    5'  TGACAAGTGACAACCTTTTC  27350      TTCCG   _
                                TGACAA    GATA CCTTTTC
                                ||||||    |||| |||||||
                                ACTGTT    CTGT GGAAAAG
                                   CA___    T
GAM252  CMAR     5'  TGGGGAGATCAATGAAGA    23298      A       _
                                TGGG AGATCAAT AAGA
                                |||| |||||||| ||||
                                ACCC TCTAGTTA TTCT
                                  C       C
GAM252  MN1      3'  TGGGGAGCGAGAAAGTTT    14599      A  ATCAATA
                                TGGG AG      AGAAAGTTT
                                |||| ||      |||||||||
                                ACCC TC      TCTTTCAAA
                                  C  GC_____
GAM252  PSMD9    3'  TGGGAGGGTCATAAGAAA    15849      AGA   A
                                TGGGA   TCA TAAGAAA
                                |||||   ||| |||||||
                                ACCCT   AGT ATTCTTT
                                   CCC  _
GAM252  SAS      3'  TGGAGAGAGAGGAAGAAAGTTT 25591     GA   TCAAT
           T                     TGG  AGA    AAGAAAGTTTT
                                |||  |||    ||||||||||
                                ACC  TCT    TTCTTTCAAAA
                                  TC   CTCC_
GAM253  GBAS     3'  TGCTATTCAAGGTG       11237       CGGGAGA
                                TGCTAT      TCAAGGTG
                                ||||||      ||||||||
                                ACGATA      AGTTCCAC
                                            _______
GAM253  GLRB     3'  TGCCATTCAAAATTAAGGTGCC 9071        _    GATC
                                TGCTAT CGGGA    AAGGTGCC
                                |||||| |||||    ||||||||
                                ACGGTA GTTTT    TTCCACGG
                                   A    AA__
GAM253  IL1A     3'  TGCTATTGTGGAGGATGC    41678       CG_   ATCAA
                                TGCTAT   GGAG    GGTGC
                                ||||||   ||||    |||||
                                ACGATA   CCTC    CTACG
                                   ACA   _____
GAM253  IQGAP1   3'  TGTATCAGATTGAGGTGC    42899    C   GGG   CA
                                TG TATC   AGAT  AGGTGC
                                || ||||   ||||  ||||||
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                                AC ATAG   TCTA  TCCACG
                                 _   ___    AC
GAM253  TCF2     3'  TATCGGGAAAGGTG       7846         GATC
                                TATCGGGA    AAGGTG
                                ||||||||    ||||||
                                ATAGCCCT    TTCCAC
                                     ____
GAM253  ATP8B2   3'  TGCTTACTGAAGAAGGGAGCAG 42221     C  ATCTTAC
           A                     TGC TA      AGGGAGCAGA
                                |||  ||      ||||||||||
                                ACG AT      TCCCTCGTCT
                                  A  GACTTCT
GAM253  CCND1    3'  TGCCTATTCTTACAACAGA    38226       A      GGGA
                                TGCCTA TCTTACA    GCAGA
                                ||||||  |||||||    |||||
                                ACGGAT AGAATGT    TGTCT
                                   A     ____
GAM253  COG7     3'  TGCCCAATCTTGGGCAGA     42662          ACAG  A
                                TGCCTAATCTT    GG GCAGA
                                ||||||||||    || |||||
                                ACGGGTTAGAA    CC CGTCT
                                     ____  _
GAM253  CPN1     3'  CTGATCTGAGAGCAG       10571    A    TACA
                                CT ATCT    GGGAGCAG
                                || ||||    ||||||||
                                GA TAGA    CTCTCGTC
                                 C   ____
GAM253  CRHR2    3'  TGCCTAATCTGTGGACTAGGCA 12445          TACAG  ____
           GA                     TGCCTAATCT     GGA    GCAGA
                                ||||||||||     |||    |||||
                                ACGGATTAGA     CCT    CGTCT
                                     CA___   GATC
GAM253  CTNNA2   3'  TGCCCAATTTTATGAGAA    20497        C   CA
                                TGCCTAAT TTA  GGGAG
                                ||||||||  |||  |||||
                                ACGGGTTA AAT  CTCTT
                                    A   A_
GAM253  MPP2     3'  GCCTGGCCCTGTGGGGAGCAG  40797      AA    ACA
                                GCCT  TCTT   GGGAGCAG
                                ||||  ||||   ||||||||
                                CGGA  GGGA   CCCTCGTC
                                  CC    CAC
GAM253  PTPRZ1   3'  TGCCTAATTTTAGGAAGAG    15987        C  AC     C
                                TGCCTAAT TT  AGGGAG AG
                                ||||||||  ||  ||||||  ||
                                ACGGATTA AA  TCCTTC TC
                                    A  __     _
GAM253  RORC     5'  TGCCCAGGAGGGCAGGGAGCAG 22814        ATCTTA
                                TGCCTA     CAGGGAGCAG
                                ||||||     ||||||||||
```

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                                ACGGGT     GTCCCTCGTC
                                   CCTCCC
GAM253  VIPR2    3'  GCGGAGCTTGCAGGGAGCAGA  18017    CTAAT   A
                                GC     CTT CAGGGAGCAGA
                                ||     ||| ||||||||||
                                CG     GAA GTCCCTCGTCT
                                 CCTC_   C
GAM254  CBFA2T2  3'  TACATTATTGGCTTTCTTTTGT 22975           CCGAG__  C
           GAGC                   TATATTATTGGC      TG GAGC
                                |||||||||||       || ||||
                                ATGTAATAACCG      AC CTCG
                                      AAAGAAA  A
GAM254  CHRNA3   3'  TATGTCATTGGCATCTAGTG   8838      A       CCG_
                                TAT TTATTGGC    AGTG
                                ||| ||||||||    ||||
                                ATA AGTAACCG    TCAC
                                  C       TAGA
GAM254  NEBL     3'  TATTATTGGCTGCATTACAGAG 26910          CCGAG  _
                                TATTATTGGC     TGC GAG
                                ||||||||||     ||| |||
                                ATAATAACCG     ATG CTC
                                      ACGTA   T
GAM254  CDC7L1   5'  TGAGATGCAAAATGCCAG     18605       ACGCTG
                                TGAGA     GCAGAATGCCAG
                                |||||     ||||||||||||
                                ACTCT     CGTTTTACGGTC
                                   A_____
GAM254  FGFR1    3'  TGAGGGCACTGCATGCCAG    31958      AA    G  GAA
                                TGAG  CGCTG CA   TGCCAG
                                ||||  ||||| ||   ||||||
                                ACTC  GTGAC GT   ACGGTC
                                   CC    _ ___
GAM254  GALNT7   3'  GAGGGCACTGGGAATGCCAG   38357     AA     CA
                                GAG  CGCTGG  GAATGCCAG
                                |||  ||||||  |||||||||
                                CTC  GTGACC  CTTACGGTC
                                  CC     __
GAM254  GCGR     3'  ACACTGGCACGCAG        6690          GAA   C
                                ACGCTGGCA   TGC AG
                                |||||||||   ||| ||
                                TGTGACCGT   GCG TC
                                      ___   _
GAM254  HPCAL1   5'  TGAGAACGCTGCCAGAGGCCAG 39550           G    AT
           C                     TGAGAACGCTG CAGA  GCCAGC
                                ||||||||||| ||||  ||||||
                                ACTCTTGCGAC GTCT  CGGTCG
                                      G    C_
GAM254  HTR2A    3'  TGAAATGCAGCAAATGCCAGC  8390       AC  T     A
                                TGAGA  GC GGCAGA TGCCAGC
                                |||||  || |||||| |||||||
```

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                                ACTTT  CG TCGTTT ACGGTCG
                                  A_ _     _
GAM254  ITPKA    3'  TGGGAACGCTGGGGCC      13639    A       CAGAAT
                                TG GAACGCTGG     GCC
                                || |||||||||     |||
                                AC CTTGCGACC     CGG
                                 C       C_____
GAM254  JPH2     5'  GAGGGGGGAAGCAGGATGCCAG 45377     AACGCT    A
            C                    GAG     GGCAG ATGCCAGC
                                |||     ||||| ||||||||
                                CTC     TCGTC TACGGTCG
                                  CCCCCT    C
GAM254  NESG1    5'  GAGGAGCTCAGGATGCCAGC   29581     AAC   GG   A
                                GAG   GCT  CAG ATGCCAGC
                                |||   |||  ||| ||||||||
                                CTC   CGA  GTC TACGGTCG
                                  CT_   __   C
GAM254  NESG1    3'  GAGGTAGCTGGCAGGATGTTAG 29582     AAC       A   CC
            C                    GAG   GCTGGCAG ATG  AGC
                                |||   |||||||| |||  |||
                                CTC   CGACCGTC TAC  TCG
                                  CAT       C   AA
GAM254  PACE     3'  TGAGAACGTGGGTAGTCCAGC  15038        C   CAGAATG
                                TGAGAACG TGG      CCAGC
                                |||||||| |||      |||||
                                ACTCTTGC ACC      GGTCG
                                     _  CATCA__
GAM254  RPS6KA2  3'  GAGGATGCTGGCAGGGGACGC  34462     AAC       A__
                                GAG   GCTGGCAG   ATGC
                                |||   ||||||||   ||||
                                CTC   CGACCGTC   TGCG
                                  CTA       CCC
GAM254  TEM6     3'  TGAGGATCTGCTGAAAATGCCA 35562      AAC__     CA
            GC                    TGAG    GCTGG  GAATGCCAGC
                                ||||    |||||  ||||||||||
                                ACTC    CGACT  TTTACGGTCG
                                  CTAGA    __
GAM254  TFDP2    3'  GCTGGCAAAGGCAGTGCTGGC  26619         A____   CA
                                GCTGGCAGA    TGC  GC
                                |||||||||    |||  ||
                                CGACCGTTT    ACG  CG
                                     CCGTC   AC
GAM255  CDC25B   5'  GGCAGAAGGCTGGCTGGA    34854         C   CGGTC
                                GGCAGAAGGC GGC    GGA
                                |||||||||| |||    |||
                                CCGTCTTCCG CCG    CCT
                                     A   A____
GAM255  DGCR2    3'  TGGCAGAAGGCGGGCTGTGG   23100          C   CG  C
                                TGGCAGAAGGC GGC  GT GG
                                |||||||||| |||  || ||
```

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                                ACCGTCTTCCG CCG  CA CC
                                      C   A_ _
GAM255  DNMT3B   5'  TGGCGGGAGGCCGGCTGG    27883     AGA      C
                                TGGC   AGGCCGGC GG
                                ||||   |||||||| ||
                                ACCG   TCCGGCCG CC
                                  CCC       A
GAM255  FACL5    5'  GGCAGAAGGCCGGCCCAGAG   42015           GGT
                                GGCAGAAGGCCGGCC   CGGAG
                                ||||||||||||||   |||||
                                CCGTCTTCCGGCCGG   GTCTC
                                                  ____
GAM255  KCNK4    5'  TGGCAGAGGAGCCGGAGAG   37841       A  CC     TC
                                TGGCAGA GG  GGCCGG  GGAG
                                |||||||  ||  ||||||  ||||
                                ACCGTCT CC  TCGGCC  TCTC
                                  _  __     __
GAM255  LIMK1    3'  TGGCAGGTGGCCGGCCAG    14174       AA
                                TGGCAG  GGCCGGCCGG
                                ||||||  ||||||||||
                                ACCGTC  CCGGCCGGTC
                                    CA
GAM255  LMO1     3'  TGGTAGAGTGGCTGGCTGG    14188     C   A_   C   C
                                TGG AGA  GGC GGC GG
                                ||| |||  ||| ||| ||
                                ACC TCT  CCG CCG CC
                                  A   CA   A   A
GAM255  LMO1     5'  TGGCGGGGCGGCCGGTC     14187      AGAA   C
                                TGGC    GGC GGCCGGTC
                                ||||    ||| ||||||||
                                ACCG    CCG CCGGCCAG
                                  CC__   _
GAM255  PGM1     5'  TGGCGGAGGGGCGGCCGG    15260      A  A  C
                                TGGC GA GG CGGCCGG
                                |||| || || |||||||
                                ACCG CT CC GCCGGCC
                                  C  C  C
GAM255  PPP4C    3'  TGGTGCGAGGGCCAGAAGGGTT 15539     CA_  A     CC_   C
          GGAG                    TGG   GA GGCCGG   GGT GGAG
                                |||   || ||||||   ||| ||||
                                ACC   CT CCGGTC   CCA CCTC
                                  ACG  C     TTC   A
GAM255  BLAME    3'  TGGCTGCCCAGGCTGCTCCTT  33500       G   CTTT
                                TGGCTG CCGG    CTGCTCCTT
                                ||||||  ||||    |||||||||
                                ACCGAC GGTC    GACGAGGAA
                                    G   C___
GAM255  FETUB    5'  TGGCTGGCTTGTAAGGCTCT   30775        C_____
                                TGGCTGGC     GGCTTT
                                ||||||||     ||||||
```

```
                                ACCGACCG     CCGAGA
                                    AACATT
GAM255  LAIR1    3'  TGCCTGGCTGGCTTTCTA    14056    G    C
                                TG CTGGC GGCTTTCTG
                                || ||||| |||||||||
                                AC GACCG CCGAAAGAT
                                 G    A
GAM255  PPP1R12B  5'  GGCTGAATGTCCTTTCTGCTTC 36977       CCGG_       C
           TT                    GGCTGG    CTTTCTGCT CTT
                                ||||||    ||||||||| |||
                                CCGACT    GAAAGACGA GAA
                                   TACAG       A
GAM256  ADAMTS8   5'  GGCTGCGGCGGTGGCTGC    28166    ACCC      A  AA
                                GG   CGGCGGTG GC  GC
                                ||   |||||||| ||  ||
                                CC   GCCGCCAC CG  CG
                                 GAC_       _ A_
GAM256  AGRN     3'  GGACACCGTGGGGCAGGC    44252     C   GC  TGA   A
                                GGAC CCG  GG   GCA GC
                                |||| |||  ||   ||| ||
                                CCTG GGC  CC   CGT CG
                                  T   A_  C__   C
GAM256  ALOX12B   5'  GGAGCCCAGCTGGTGGTGAGTG 10071     C     ____     CA
           AGCA                   GGA CCCGGC    GGTGAG  AGCA
                                ||| ||||||   ||||||  ||||
                                CCT GGGTCG    CCACTC  TCGT
                                  C     ACCA     AC
GAM256  BIN1     3'  GAGGACCCTTGCCCGGGTG    20196        CG ___
                                GAGGACCC  GC   GGTG
                                ||||||||  ||   ||||
                                CTCCTGGG  CG   CCAC
                                     AA  GGC
GAM256  CLTCL1    5'  GGGACCTCGGCGGCGGC     41884    A    C       A
                                G GGACC CGGCGGTG GC
                                | ||||| |||||||| ||
                                C CCTGG GCCGCCGC CG
                                _     A       _
GAM256  COL6A1    3'  GAGGACCCTGCACAAAGCAGGC 12329         CG   GT    A
           A                     GAGGACCC  GCG  GAGCA GCA
                                ||||||||  |||  ||||| |||
                                CTCCTGGG  CGT  TTCGT CGT
                                     A_   GT    C
GAM256  CRYBA2    5'  GAGGGCATTCACCGGGTGGGTG 38393      ACC____    C__
           AGC                    GAGG      CCGG   GGTGAGC
                                ||||      ||||   |||||||
                                CTCC      GGCC   CCACTCG
                                  CGTAAGT    CAC
GAM256  DLX2     3'  GAACCCCGGCTCGGGGTAAGCA 20589          ____
                                GGACCCCGGC    GGTGAGCA
                                ||||||||||    ||||||||
```

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                                CTTGGGGCCG   CCATTCGT
                                      AGCC
GAM256  DLX2    3'  GGCCCCGGGAGTGAGCA    20591   A    C
                                GG CCCCGG GGTGAGCA
                                || |||||| ||||||||
                                CC GGGGCC TCACTCGT
                                 _     C
GAM256  EIF4G1  3'  AAGGACCCCAGGGGCAGGC   22405         C   GA
                                GAGGACCCCGG GGT  GC
                                |||||||||| |||  ||
                                TTCCTGGGGTC CCG  CG
                                      C   TC
GAM256  ESPN    3'  AAGGGTCCCGGCAGCGAG    36436     AC
                                GAGG  CCCGGCGGTGAG
                                ||||  ||||||||||||
                                TTCC  GGGCCGTCGCTC
                                  CA
GAM256  EXTL1   5'  GAGGCCTCTGCCAGCAAGC   20866     A  CCGGCG  G
                                GAGG CC     GT AGCAAGC
                                |||| ||     || |||||||
                                CTCC GG     CG TCGTTCG
                                  _ AGA___  G
GAM256  FDX1    5'  GAGGGCCGCGGCGAGGGGC   41267     A  CCG      CAA
                                GAGG CC   GCGGTGAG   GC
                                |||| ||   ||||||||   ||
                                CTCC GG   CGCCGCTC   CG
                                  C ____       CC_
GAM256  FSTL3   3'  GGGGCCAGTGGGTGAGCA    25221    ACC   C_
                                GG   CCGG  GGTGAGCA
                                ||   ||||  ||||||||
                                CC   GGTC  CCACTCGT
                                 CC_   AC
GAM256  FUT3    3'  GAGGTTCCCGGCAGCCCAGGCA 6640      AC       GAG  A
                                GAGG  CCCGGCGGT   CA GCA
                                ||||  |||||||||   || |||
                                CTCC  GGGCCGTCG   GT CGT
                                  AA        G__  C
GAM256  GFRA2   3'  GGGTCCCCAGAGTGGGCA    11268   A  A     C   A
                                G GG CCCCGG GGTG GCA
                                | || |||||| |||| |||
                                C CC GGGGTC TCAC CGT
                                 _ A     _   C
GAM256  GNA11   5'  GGACCCGGCGGCTCGCCAGGC  44046       C     GA  AA_
                                GGACCC GGCGGT  GC   GC
                                |||||| ||||||  ||   ||
                                CCTGGG CCGCCG  CG   CG
                                   _     AG  GTC
GAM256  HPN     3'  GAGGACCCTGGAGGGAG     13457         C  C  T
                                GAGGACCC GG GG GAG
                                |||||||| || || |||
```

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                                CTCCTGGG CC CC CTC
                                    A  T  _
GAM256  HTR6    5'  GAGGGCCCCGGCGAAGC    9307      A      GT
                                GAGG CCCCGGCG  GAGC
                                |||| ||||||||  ||||
                                CTCC GGGGCCGC  TTCG
                                  C       __
GAM256  ITGA3   5'  GGGGTCCCGGCGAGAGC    24267   A  AC      T
                                G GG  CCCGGCGG GAGC
                                | ||  |||||||| ||||
                                C CC  GGGCCGCT CTCG
                                 _  CA       _
GAM256  JAM2    5'  GAGGGTCCCGGCGGCAGGAGC  34542     AC       __
                                GAGG  CCCGGCGGT  GAGC
                                ||||  |||||||||  ||||
                                CTCC  GGGCCGCCG  CTCG
                                  CA        TC
GAM256  JJAZ1   5'  GGCCCCGGAGAGCAAGC    31692   A    CGGT
                                GG CCCCGG    GAGCAAGC
                                || ||||||    ||||||||
                                CC GGGGCC    CTCGTTCG
                                 _     T____
GAM256  JPH3    3'  GGGACCCACAGTGAGTGGGCA  34022   A    CG      CAA
                                G GGACCC  GCGGTGAG   GCA
                                | ||||||  ||||||||   |||
                                C CCTGGG  TGTCACTC   CGT
                                _     __       ACC
GAM256  MCM7    3'  GAGGACCCCAGGGTTGCAAGCA 25408          C   GA
                                GAGGACCCCGG GGT  GCAAGCA
                                |||||||||| |||  |||||||
                                CTCCTGGGGTC CCA  CGTTCGT
                                      _  A_
GAM256  NF2     5'  GAGGACCCTGCCTGAGC     7066         CG  GG
                                GAGGACCC  GC  TGAGC
                                ||||||||  ||  |||||
                                CTCCTGGG  CG  ACTCG
                                    A_  G_
GAM256  NPAS1   3'  GGACCCCGGTTGTCGCA     40872        CG  GA
                                GGACCCCGG  GT  GCA
                                |||||||||  ||  |||
                                CCTGGGGCC  CA  CGT
                                     AA  G_
GAM256  NUCB1   3'  GGATTCCAGTAGCTGTGGGCA  26157     CC  ___   G   A
                                GGA  CC   GGC GTG GCA
                                |||  ||   ||| ||| |||
                                CCT  GG   TCG CAC CGT
                                  AA  TCA   A   C
GAM256  PIK3R2  3'  GGACCTGCGGTGGGCA      22749      CCG     A
                                GGACC   GCGGTG GCA
                                |||||   |||||| |||
```

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                                CCTGG   CGCCAC CGT
                                  A__     C
GAM256  RAB3B    3'  GAGAACCCCAGGGGCAGGCA   16081          C   GA
                                GAGGACCCCGG GGT  GCA
                                |||||||||| |||  |||
                                CTCTTGGGGTC CCG  CGT
                                      C   TC
GAM256  RUNX1    3'  GAGATCCTGGCCGTCGGGC    12022      A  CC   G  _ A
                                GAGG CC  GGC GT G GC
                                |||| ||  ||| || | ||
                                CTCT GG  CCG CA C CG
                                  A A_   G  G C
GAM256  SLC19A2  3'  AGGACTTTGGTGATAAGCA    42884       CCC  C
                                AGGAC   GG GGTGAGCA
                                |||||   || ||||||||
                                TCCTG   CC CTATTCGT
                                   AAA  A
GAM256  SLC25A1  3'  GAGGACCCAGGCCACACGGGCA 25602         C   G __  A
                                GAGGACCC GGC G  TG GCA
                                |||||||| ||| |  || |||
                                CTCCTGGG CCG T  GC CGT
                                     T   G GT  C
GAM256  SLC29A1  5'  AGACTTTGGAGTGAGCA     22410      CCC  C
                                GGAC   GG GGTGAGCA
                                ||||   || ||||||||
                                TCTG   CC TCACTCGT
                                  AAA  _
GAM256  SSRP1    5'  GAGGGCCCCGGCGCGAGAGGTG 17122      A       G    CAA___
           GGC                    GAGG CCCCGGCG TGAG     GC
                                |||| |||||||| ||||      ||
                                CTCC GGGGCCGC GCTC     CG
                                  C       _    TCCACC
GAM256  TBX1     5'  GAGGACCCTGAGCCCTGGTGGG 38768         C _ ___    A
           C                     GAGGACCC G GC   GGTG GC
                                |||||||| | ||   |||| ||
                                CTCCTGGG C CG   CCAC CG
                                     A T  GGA    C
GAM256  TNFRSF6B 5'  GGAGCCCTGTGGGTAAGCA   32359     C   GGC_
                                GGA CCC    GGTGAGCA
                                ||| |||    ||||||||
                                CCT GGG    CCATTCGT
                                  C   ACAC
GAM256  TRPC6    3'  GGATCCACAGAGCAGGC     21484     C  CG   GT    A
                                GGA CC  GCG  GAGCA GC
                                ||| ||  |||  ||||| ||
                                CCT GG  TGT  CTCGT CG
                                  A __  __     C
GAM256  VEGF     3'  GAGGACCCTGGCCCCACCAAG  17954         C   GG  AG
                                GAGGACCC GGC  TG  CAAG
                                |||||||| |||  ||  ||||
```

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                                CTCCTGGG CCG  GT  GTTC
                                    A   GG  G_
GAM256  WNT6     5'  GAGGGATCCGGCGGCGGC    27180      ACC        A
                                GAGG   CCGGCGGTG GC
                                ||||   ||||||||| ||
                                CTCC   GGCCGCCGC CG
                                  CTA        _
GAM256  ALDH3A2  5'  GCTGTTCACGGCCTCGCC    42917     T C       __
                                GCT G TCACGGCC  GCC
                                ||| | ||||||||  |||
                                CGA C AGTGCCGG  CGG
                                  _ A       AG
GAM256  ARRB2    5'  GCTCGCTCGCAGCCTCCTCGCC 41410         A    GCC    A
                                GCTTGCTC CGGCC   CCTC CC
                                |||||||| |||||   |||| ||
                                CGAGCGAG GTCGG   GGAG GG
                                    C    A__    C
GAM256  BIN3     3'  GCTTGCTCAGGCCGTGGGCC   33081         C    CC__
                                GCTTGCTCA GGCCG    CC
                                ||||||||| |||||    ||
                                CGAACGAGT CCGGC    GG
                                    _    ACCC
GAM256  CDH13    3'  GCCTGCTCTGCTCCTCAC    10369         ACGGCC  C
                                GCTTGCTC     GC CCTCAC
                                ||||||||     || ||||||
                                CGGACGAG     CG GGAGTG
                                    A_____  A
GAM256  CDKN2A   5'  GCTTGTGTAGAGCCCCCTCACC 38475      CTCAC    GC
                                GCTTG    GGCC  CCCTCACC
                                |||||    ||||  ||||||||
                                CGAAC    TCGG  GGGAGTGG
                                  ACATC    __
GAM256  DGKI     3'  GCTTGCTCATGTCCTCTTTGCC 21785         CGG  _____
                                GCTTGCTCA   CC    GCC
                                |||||||||   ||    |||
                                CGAACGAGT   GG    CGG
                                     ACA  AGAAA
GAM256  FLG      3'  GCCTGCTCGTGGCGGGATCCT  43360         AC   CGCC_
                                GCTTGCTC  GGC    CCT
                                ||||||||  |||    |||
                                CGGACGAG  CCG    GGA
                                    CA   CCCTA
GAM256  MGAT1    5'  GCTTGCCCGGCTCCCTTC    14435       T A    CGC    CA
                                GCTTGC C CGGC   CCCT  C
                                |||||| | ||||   ||||  |
                                CGAACG G GCCG   GGGA  G
                                   _ _   A__    AC
GAM256  MYC      5'  GCTCGCTCCCTCTGCCTCTC   14710         ACGGCC   C
                                GCTTGCTC     GCC CTC
                                ||||||||     ||| |||
```

```
                                CGAGCGAG     CGG GAG
                                     GGAGA_   A
GAM256   MYCL2    5'  GCTTGCTCACGCAGCTTGCC   23904          __ C_
                                GCTTGCTCACG  GC  GCC
                                ||||||||||  ||  |||
                                CGAACGAGTGC  CG  CGG
                                      GT  AA
GAM256   RBBP2    3'  CTTGCTCATGGCCATGCC    22802        C   __
                                CTTGCTCA GGCC  GCC
                                ||||||||  ||||  |||
                                GAACGAGT CCGG  CGG
                                     A    TA
GAM256   RTN3     5'  GCTCGCTCAAGTCCCT      43959         C  CCGC
                                GCTTGCTCA GG    CCCT
                                |||||||||  ||    ||||
                                CGAGCGAGT TC    GGGA
                                     _  A___
GAM256   SURF4    5'  GCTCGCTCGCTGGCTCTCGCC  37655        AC_  ___
                                GCTTGCTC   GGC   CGCC
                                ||||||||   |||   ||||
                                CGAGCGAG   CCG   GCGG
                                     CGA   AGA
GAM256   TMPO     5'  GCTTGCTCCTGGCCGGGGACC  17606        AC    CC__
                                GCTTGCTC  GGCCG    CC
                                ||||||||  |||||    ||
                                CGAACGAG  CCGGC    GG
                                     GA    CCCT
GAM257   ABCA2    3'  GGGGGCCAAGCTGGGTGGG    45526       G   G
                                GGGGGT GGG CTGGGTGGG
                                ||||||  ||| |||||||||
                                CCCCCG TTC GACCCACCC
                                   G   _
GAM257   ABL1     3'  CGGGGGACCTGGGTGG       28711        TGGG G
                                CGGGGG    G CTGGGTGG
                                ||||||    | ||||||||
                                GCCCCC    T GACCCACC
                                   _____ G
GAM257   AEGL1    3'  AGGCGGGGGTGGGAGTTG     10060    A          C
                                AG CGGGGGTGGGGG TG
                                || ||||||||||| ||
                                TC GCCCCCACCCTC AC
                                 C          A
GAM257   AGRN     3'  GATGGGGGTGGGGAAGGG     44251    C          CT
                                GA GGGGGTGGGGG  GGG
                                || ||||||||||  |||
                                CT CCCCCACCCCT  CCC
                                 A          T_
GAM257   AGRN     3'  GGGGATGGGATGGGGGTGGG   44254          GCT
                                GGGGGTGGGG   GGGTGGG
                                |||||||||   |||||||
```

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                                CCCCTACCCT   CCCACCC
                                     ACC
GAM257  ALX3     3'  AGGCGGGGGTGGGCTGGG    27064    A     GG
                                AG CGGGGGT  GGGCTGGG
                                || |||||||  ||||||||
                                TC GCCCCCA  CCCGACCC
                                 C      __
GAM257  AR       5'  GGGCGGGGGGGGCGGGTGG    6238     _ T    T
                                GGG GG GGGGGC GGGTGG
                                ||| || |||||| ||||||
                                CCC CC CCCCCG CCCACC
                                  G _    _
GAM257  ATP1A2   3'  GATGGGAGTGGGCAGGGTGGG  8706    C       GGCT
                                GA GGGGGTGGG   GGGTGGG
                                || |||||||||   |||||||
                                CT CCCTCACCC   CCCACCC
                                 A       GT__
GAM257  ATRN     3'  ACGGGGGTGGGGGGCAGGG    40262           T
                                ACGGGGGTGGGGGGC GGG
                                |||||||||||||| |||
                                TGCCCCCACCCCCG CCC
                                         T
GAM257  AXIN1    3'  GGGTGGGGTGGCATGGTGG   41389        __ TG
                                GGGTGGGG  GC  GGTGG
                                ||||||||  ||  |||||
                                CCCACCCC  CG  CCACC
                                     AC  TA
GAM257  AXIN1    3'  GGGTTGGGAGCTGGGTGG    41390    GG
                                GGG  TGGGGGCTGGGTGG
                                |||  ||||||||||||||
                                CCC  ACCCTCGACCCACC
                                  A_
GAM257  AXL      3'  AGGCGTGGGGTGGGAAAGTGGG 34880    A _       CTG
                                AG CG GGGGTGGGGG   GGTGGG
                                || || ||||||||||   ||||||
                                TC GC CCCCACCCTT   TCACCC
                                 C  A        ____
GAM257  BARX1    3'  AGACGGGGTGGGGGTGCG    34624        G     CTGG TG
                                AGACGGGG TGGGGG   G  G
                                |||||||| ||||||   |  |
                                TCTGCCCC ACCCCC   C  C
                                     _     A___ GT
GAM257  BCL3     3'  AGATGGGGGGGGGGGGG     23204    C    T    CT
                                AGA GGGGG GGGGG  GGG
                                ||| ||||| |||||  |||
                                TCT CCCCC CCCCC  CCC
                                  A    _    __
GAM257  BCL7A    3'  GGGCGAGGGGTGCAGGGTGGG  34217     _ T   _ T
                                GGG GG GGGG GC GGGTGGG
                                ||| || |||| || |||||||
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```
                                CCC CT CCCC CG CCCACCC
                                  G _   A  T
GAM257  BCL7A   3'  GATGGGGGTGGTGGTGGTGGG  34209   C      G  CTG
                                GA GGGGGTGG GG  GGTGGG
                                || |||||||| ||  ||||||
                                CT CCCCCACC CC  CCACCC
                                 A      A  A__
GAM257  BIG1    5'  AGAGGGGGTGGAGGTGGG    26955    C        C
                                AGA GGGGGTGGGGG TGGG
                                ||| |||||||||| ||||
                                TCT CCCCCACCTCC ACCC
                                  _        _
GAM257  BSN     3'  GGGGTGGGGAGGGGTGGG    18407         CT
                                GGGGTGGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCACCCCT  CCCACCC
                                      C_
GAM257  C1QG    3'  GGGGGTGGGTCAGGGTGGG   41690        GGCT
                                GGGGGTGGG   GGGTGGG
                                |||||||||   |||||||
                                CCCCCACCC   CCCACCC
                                     AGT_
GAM257  CALM3   3'  GGGTGGGGGGGTGGGGTGG    23243        CT_
                                GGGTGGGGG   GGGTGG
                                |||||||||   ||||||
                                CCCACCCCC   CCCACC
                                     CAC
GAM257  CALM3   3'  GGGGTGGGGAGGTGGTGGG   23239         CTG
                                GGGGTGGGGG  GGTGGG
                                ||||||||||  ||||||
                                CCCCACCCCT  CCACCC
                                      CCA
GAM257  CLC     3'  GGGTGGGGCTGGGGGG      29899        G    T
                                GGGTGGGG CTGGG GGG
                                |||||||| ||||| |||
                                CCCACCCC GACCC CCC
                                   _    _
GAM257  COPE    3'  AGATGGGGGTGCTGGGGGTGGG 28575    C      GG  CT
                                AGA GGGGGTG  GG  GGGTGGG
                                ||| |||||||  ||  |||||||
                                TCT CCCCCAC  CC  CCCACCC
                                  A      GA  __
GAM257  CSPG3   3'  GGGGTGGGGCAGGAGTGGG   20489        G T  _
                                GGGGTGGGG C GG GTGGG
                                ||||||||| | || |||||
                                CCCCACCCC G CC CACCC
                                     _T  T
GAM257  CYP26A1 5'  AGGCGGCGGTGGGGGAGGG   38402    A  G      CT
                                AG CGG GGTGGGGG  GGG
                                || ||| ||||||||  |||
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                                TC GCC CCACCCCC  CCC
                                 C  G      T_
GAM257  DBH     3'  CGGGGGCGGGGGGCGTTCCCGG  8968          TGGG_
                                CGGGGGTGGGGGC    TGG
                                |||||||||||||    |||
                                GCCCCCGCCCCCG    GCC
                                     CAAGG
GAM257  DCTN1    5'  AGGGGTGGGGGGCAGTGATGGG  35696          TG_
                                GGGGGTGGGGGC  GGTGGG
                                ||||||||||||  ||||||
                                TCCCCACCCCCG  CTACCC
                                     TCA
GAM257  DIA1    3'  AGGCGGGAGTGGGGGGTGACAGG 28782    A         CTG  TG
                                AG CGGGGGGTGGGGG  GG  GG
                                || ||||||||||||  ||  ||
                                TC GCCCTCACCCCC  CT  CC
                                 C         A__  GT
GAM257  DMPK    3'  CGGGGGGTGGGGGGTCCTAGGTGG 20610          __
          G                      CGGGGGGTGGGGG  CTGGGTGGG
                                ||||||||||||  |||||||||
                                GCCCCCCACCCCC  GATCCACCC
                                     AG
GAM257  DMPK    5'  GGGGGGTTGGGGGCTGGGTGGG  20620       G
                                GGGGGGT GGGGGCTGGGTGGG
                                |||||||| ||||||||||||
                                CCCCCCA CCCCGACCCACCC
                                   A
GAM257  DRIL1   5'  CGGGGGGCGGGGGGCCGCCGGG  23367           GG
                                CGGGGGGTGGGGGGCTG  TGGG
                                ||||||||||||||||  ||||
                                GCCCCCCGCCCCCCGGC  GCCC
                                     G_
GAM257  EMX2    5'  GGGGGTGGGGGGTGGGGGTGG   44693         CT_
                                GGGGGTGGGGGG   GGGTGG
                                ||||||||||   ||||||
                                CCCCCACCCCC   CCCACC
                                     ACC
GAM257  FZD7    3'  GGGGGTGGGAAAGGTGGG     18634         CT
                                GGGGGTGGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCCACCCTT  TCCACCC
                                     __
GAM257  GLI4    3'  GACGGGGGTGGAGGGGTGGG    39690        G     C
                                GACGGGG TGGGGG TGGG
                                ||||||| |||||| ||||
                                CTGCCCC ACCTCC ACCC
                                   _     C
GAM257  HCFC1   3'  GACGGGGGTGGGAGGGGTGGG   43391        G     CT
                                GACGGGG TGGGGG  GGGTGGG
                                ||||||| ||||||  |||||||
```

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                                CTGCCCC ACCCTC  CCCACCC
                                        _    __
GAM257  HIP2    3'  AGGCGGGGGTGGGGGGGG   23765   A        CT
                                AG CGGGGGTGGGGG  GGG
                                || ||||||||||||  |||
                                TC GCCCCCACCCCC  CCC
                                 C         __
GAM257  HOXC13  3'  GATGGGGGTGGAGGCTGGG  40666   C
                                GA GGGGGTGGGGGCTGGG
                                || ||||||||||||||||
                                CT CCCCCACCTCCGACCC
                                 A
GAM257  HSF4    5'  GGGGTGGAGTGGGGTGGG   40767       GCT
                                GGGGTGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCACCTC  CCCACCC
                                      AC_
GAM257  HSF4    5'  GGGGTGGGGTGGAGTGGG   40768       GCT
                                GGGGTGGGG  GGGTGGG
                                |||||||||  |||||||
                                CCCCACCCC  CTCACCC
                                      AC_
GAM257  HYOU1   3'  GGGGGTGGGGTGAGGGGTGGG 40635        GCT_
                                GGGGGTGGGG  GGGTGGG
                                ||||||||||  |||||||
                                CCCCCACCCC  CCCACCC
                                       ACTC
GAM257  IL1F5   3'  GAAGGGGGTGGGGCTGGG   29351   C       G
                                GA GGGGGTGGGG CTGGG
                                || ||||||||||  |||||
                                CT CCCCCACCCC GACCC
                                 T       _
GAM257  JAM2    5'  GGGGGTGGGGGGGATTGGG   34547        CT GG
                                GGGGGTGGGGG  G  TGGG
                                ||||||||||  |  ||||
                                CCCCCACCCCC  C  ACCC
                                      __ TA
GAM257  KCNE1L  3'  GGGGGTGGAAGGTGG      29374       GGCT
                                GGGGGTGGG  GGGTGG
                                |||||||||  ||||||
                                CCCCCACCT  TCCACC
                                       _____
GAM257  KPNB1   5'  GATGGGGGTTGGGGGTCGGGTG 13968   C    _   C
          GG                    GA GGGGGT GGGGG TGGGTGGG
                                || |||||| ||||| |||||||||
                                CT CCCCCA CCCCC GCCCACCC
                                 A    A   A
GAM257  LAG3    5'  GGGGGCGGGGGGTGTCCCAGGG  14047        C  GGT__
                                GGGGGTGGGGG TG   GGG
                                |||||||||||  ||   |||
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                                CCCCCGCCCCC AC    CCC
                                      _ AGGGT
GAM257  LMO6    3' CGGGGCGTGGGGGTGAGGG  26043     _     C   T
                                CGGGG GTGGGGG TGGG GG
                                ||||| ||||||| |||| ||
                                GCCCC CACCCCC ACTC CC
                                   G     _  _
GAM257  LY64    3' GGGGGTGGGTAGTGG      24569         GGCTG
                                GGGGGTGGG   GGTGG
                                |||||||||   |||||
                                CCCCCACCC   TCACC
                                     A____
GAM257  LY6E    3' GGAGGTGCAGGGGGTGGG   14280       G  CT
                                GGGGGTG GGG  GGGTGGG
                                ||||||| |||  |||||||
                                CCTCCAC TCC  CCCACCC
                                    G  __
GAM257  MAPRE3  3' GGGCAGGGGGCCTTGGGTGGG 29536     _     __
                                GGGT GGGGGCT  GGGTGGG
                                |||| |||||||  |||||||
                                CCCG CCCCCGG  CCCACCC
                                  T      AA
GAM257  MAPRE3  3' GGGGGTGGGGAGGGCAGGTGGG 29538         ___ T
                                GGGGGTGGGG  GC GGGTGGG
                                ||||||||||  || |||||||
                                CCCCCACCCC  CG TCCACCC
                                      TCC _
GAM257  MEOX1   3' GATTGGGGTGGGGGTAGTTGGG 30398   CG       C  G
                                GA  GGGGTGGGGG TGG TGGG
                                ||  |||||||||| ||| ||||
                                CT  CCCCACCCCC ATC ACCC
                                 AA        _  A
GAM257  MPP3    5' AGAAGGGGGTGGAGGTGGG   12566    C        C
                                AGA GGGGGTGGGGG TGGG
                                ||| |||||||||| ||||
                                TCT CCCCCACCTCC ACCC
                                  T        _
GAM257  MUS81   3' AGACGGGGGCTGGGGGCTG   36059        _
                                AGACGGGGG TGGGGGCTG
                                ||||||||| |||||||||
                                TCTGCCCCC ACCCCCGAC
                                     G
GAM257  NGFR    3' GGGGGTGCGGGCTCCACAGG  14789       G    GG TG
                                GGGGGTG GGGCT  G  GG
                                ||||||| |||||  |  ||
                                CCCCCAC CCCGA  T  CC
                                    G    GG GT
GAM257  PAX2    3' AGGCGGGGCTGGGGGCGGTGGG 19617   A   G     TG
                                AG CGGGG TGGGGGC  GGTGGG
                                || ||||| |||||||  ||||||
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                                TC GCCCC ACCCCCG  CCACCC
                                 C    G     __
GAM257  PBX2    3'  CGGGGGTGGGGATGCATGGG  15103          C  G
                                CGGGGGTGGGGG TG GTGGG
                                |||||||||||| || |||||
                                GCCCCCACCCCT AC TACCC
                                       _  G
GAM257  PES1    3'  CAGTAGGTAGGGGGCTGGGTGG 30713    _   _
                 G                CGG GGGT GGGGGCTGGGTGGG
                                ||| |||| ||||||||||||||
                                GTC TCCA CCCCCGACCCACCC
                                 A   T
GAM257  PFKFB4  3'  GGGGTGGGGGCTCTGGG    21294          GGG
                                GGGGTGGGGGCT  TGGG
                                ||||||||||||  ||||
                                CCCCACCCCCGA  ACCC
                                       G__
GAM257  PLXNB3  3'  GGGGGGAAGGTGGGTGGG    23951     T    C
                                GGGGG GGGGG TGGGTGGG
                                ||||| ||||| ||||||||
                                CCCCC CTTCC ACCCACCC
                                  _    _
GAM257  PRKACA  3'  GGGATGGGGGTGTGGGTGG   15583        C_
                                GGGGTGGGGG  TGGGTGG
                                |||||||||  |||||||
                                CCCTACCCCC  ACCCACC
                                      AC
GAM257  PRKACA  3'  GGGGCCTGTGGTTGGGTGGG  15586     GGG_  C
                                GGGGT   GG TGGGTGGG
                                |||||   || ||||||||
                                CCCCG   CC ACCCACCC
                                   GACA  A
GAM257  RAB3A   3'  AGGCGGGGGGGGGGTTCAGG  16059    A    T    CT_
                                AG CGGGGG GGGGG  GGG
                                || |||||| |||||  |||
                                TC GCCCCC CCCCC  TCC
                                 C    _    AAG
GAM257  RAD54L  5'  GGGGTGGGATTGGGGGTGGG  18715        GCT_
                                GGGGTGGGG   GGGTGGG
                                |||||||||   |||||||
                                CCCCACCCT   CCCACCC
                                      AACC
GAM257  RARA    3'  CGGGGGTGGGGGGCAGCTCGGG 9707          TGGG
                                CGGGGGTGGGGGC   TGGG
                                ||||||||||||   ||||
                                GCCCCCACCCCCG   GCCC
                                       TCGA
GAM257  RTN4R   3'  AGATGGGGGTGGCGGGCGG   35691    C      _   T
                                AGA GGGGGTGG GGGC GG
                                ||| |||||||| |||| ||
```

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                                TCT CCCCCACC CCCG CC
                                  A       G   _
GAM257  RYR1     3'  GGGGGTGGAGGGCCAGCTGGG  8073          _    TG G
                                GGGGGTGG GGGC  G TGGG
                                |||||||| ||||  | ||||
                                CCCCCACC CCCG  C ACCC
                                     T    GT G
GAM257  S100A1   3'  GGGTGGGGTGGGCAAGGGTGGG 26563     _ T _    T_
                                GGG GG GG GGGC  GGGTGGG
                                ||| || || ||||  |||||||
                                CCC CC CC CCCG  CCCACCC
                                  A  _  A    TT
GAM257  S100A1   3'  GGGGTGGGGGGTGGGGTGG    26561          CT
                                GGGGTGGGGGG  GGGTGG
                                ||||||||||  ||||||
                                CCCCACCCCC  CCCACC
                                      AC
GAM257  SEPN1    3'  GGGGTGAGGGGGTGG      42433          CTG
                                GGGGTGGGGG   GGTGG
                                ||||||||||   |||||
                                CCCCACTCCC   CCACC
                                      ___
GAM257  SLC22A1LS 5'  GGGGGTGGGGGGTTTCATG    28255          CTGG
                                GGGGGTGGGGG    GTG
                                ||||||||||    |||
                                CCCCCACCCCC    TAC
                                      AAAG
GAM257  SOX13    3'  GAGGGGCAGGGCTGGGTGGG   25012      TG
                                GGGGG  GGGGCTGGGTGGG
                                |||||  ||||||||||||
                                CTCCC  TCCCGACCCACCC
                                   CG
GAM257  SPTBN4   3'  GGGTGGGGGTGGTGAGTGG   36090        C__
                                GGGTGGGGG   TGGGTGG
                                |||||||||   |||||||
                                CCCACCCCC   ACTCACC
                                      ACC
GAM257  TCF2     5'  AGAAGGGGGTGAGGGGGTGGG  27017     C        CTG
                                AGA GGGGGTGGGGG   GGTGGG
                                ||| ||||||||||   ||||||
                                TCT CCCCCACTCCC   CCACCC
                                  T       ___
GAM257  TFAP4    3'  AGGTGGGGGGCTGGGGGG     17409           T
                                GGGTGGGGGCTGGG GGG
                                |||||||||||||| |||
                                TCCACCCCCGACCC CCC
                                      _
GAM257  THY1     3'  GGGTGGGGGGCTGGGGGTTGGG  26627           ___
                                GGGTGGGGGGCTGGG   TGGG
                                ||||||||||||||   ||||
```

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                                CCCACCCCCGACCC  ACCC
                                      CCA
GAM257  TJP1    5'  GAGGGTGGGGAGGACCTGGG  17542          ____
                                GGGGGTGGGGG  CTGGG
                                ||||||||||  |||||
                                CTCCCACCCCT  GACCC
                                     CCTG
GAM257  TNNI3   3'  GGGGGTGGCGGGTACTGAGTGG 7473        _  __
          G                      GGGGGTGG GGG  CTGGGTGGG
                                ||||||||| |||  |||||||||
                                CCCCCACC CCC  GACTCACCC
                                    G  AT
GAM257  TP53    3'  AGATGGGGGTGGGAGGCTGTCA 8094     C      _   __
          GTGGG                  AGA GGGGGTGGG GGCTG  GGTGGG
                                ||| |||||||| |||||  ||||||
                                TCT CCCCCACCC CCGAC  TCACCC
                                  A       T    AG
GAM257  VDR     3'  GGGGTGGGAGCTGTGGG    7525           GG
                                GGGGTGGGGGCT  GTGGG
                                ||||||||||||  |||||
                                CCCCACCCTCGA  CACCC
                                      __
GAM257  ZAP70   3'  GGGTGGGGCTGAGGGTGG   43339       G __
                                GGGTGGGG CT  GGGTGG
                                |||||||| ||  ||||||
                                CCCACCCC GA  CCCACC
                                    _ CT
GAM257  ZFP36L1 3'  GGGGGTGGGGGGGGCGG    22289         CTG
                                GGGGGTGGGGG  GGTGG
                                ||||||||||  |||||
                                CCCCCACCCCC  CCGCC
                                      ___
GAM257  ZFP36L1 3'  CAGGGGTGGGGGGGGTGGG  22282          CT
                                CGGGGGTGGGGG  GGGTGGG
                                ||||||||||||  |||||||
                                GTCCCCACCCCC  CCCACCC
                                      __
GAM257  ADPRT   5'  GCGTGCGCTCACCCAGC    11520    A  TCC  C
                                GTG GC   GC CACCCAGC
                                ||| ||   || ||||||||
                                CGC CG   CG GTGGGTCG
                                  A  ___  A
GAM257  ADRBK1  3'  GTGCTGCCCGCCCACCTGGCC  11538    A_  T      CA
                                GTG  GC CCGCCCACC  GCC
                                |||  || |||||||||  |||
                                CAC  CG GGCGGGTGG  CGG
                                  GA  _       AC
GAM257  ALPL    3'  CAGGTGGCTCTTCCCGGCC   7884    A  A   CG   AC
                                CA GTG GCTC  CCC  CC
                                || ||| ||||  |||  ||
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                                GT CAC CGAG  GGG  GG
                                 C  _   AA  CC
GAM257  ANXA9    5'  TGAGTGAACTCCACTCAGC   18695   A        CCACC
                                C AGTGAGCTCCGC    CAGC
                                | ||||||||||||    ||||
                                A TCACTTGAGGTG    GTCG
                                 C          A____
GAM257  ARHGEF7  3'  CAAGGTGGCGCCCCACCCAGCC 19360     _ A  T  GC
                                CAAG TG GC CC  CCACCCAGCC
                                |||| || || ||  ||||||||||
                                GTTC AC CG GG  GGTGGGTCGG
                                  C  _  C  __
GAM257  BSG      3'  GTGCCGCCCACCCG       42695     AGCT       A
                                GTG   CCGCCCACCC G
                                |||   |||||||||| |
                                CAC   GGCGGGTGGG C
                                  _____        C
GAM257  CALM3    3'  CAAATGAGCAGTCCCCACCCAG 23227        TCCG
              C                  CAAGTGAGC   CCCACCCAGC
                                |||||||||   ||||||||||
                                GTTTACTCG   GGGTGGGTCG
                                     TCAG
GAM257  EGR3     3'  ATGGGCTCCGCCTTCAG     40540     A      CACC
                                GTG GCTCCGCC   CAG
                                ||| ||||||||   |||
                                TAC CGAGGCGG   GTC
                                  C       AA__
GAM257  EVX1     5'  CAAGTGAGTTCCTAACCCCGGC 12768        C  GCCCA  A
                                CAAGTGAG TCC    CCC GC
                                |||||||| |||    ||| ||
                                GTTCACTC AGG    GGG CG
                                     A  ATTG_  C
GAM257  FTSJ2    3'  ATGAGTGGCCTCACCCAGC   30165      CTCC  _
                                GTGAG   GCC CACCCAGC
                                |||||   ||| ||||||||
                                TACTC   CGG GTGGGTCG
                                   AC__  A
GAM257  GRF2     3'  GCATTCTGCCCACCCAGC    23676    __ C
                                GC  TC GCCCACCCAGC
                                ||  || ||||||||||
                                CG  AG CGGGTGGGTCG
                                 TA  A
GAM257  HLA-DMB  5'  TGAGTGATGTGGGGATACCCAG 13383   A   GCTCCGCCC
              CC                  C AGTGA       ACCCAGCC
                                | |||||       ||||||||
                                A TCACT       TGGGTCGG
                                 C    ACACCCCTA
GAM257  HLA-G    3'  GTGAGCTCCCCCATGGC     13401         G   CCCA
                                GTGAGCTCC CCCA   GC
                                ||||||||| ||||   ||
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                                CACTCGAGG GGGT   CG
                                     _   AC__
GAM257  HOXB6   3'  CAAGTGAGTCCGCTCCTCAG  40820       C   _ ACC
                                CAAGTGAG TCCGC CC  CAG
                                |||||||| ||||| ||  |||
                                GTTCACTC AGGCG GG  GTC
                                     _    A  A__
GAM257  HR      5'  GTGAGCTCCGACACCGGC   23109        CC   CA
                                GTGAGCTCCG  CACC  GC
                                ||||||||||  ||||  ||
                                CACTCGAGGC  GTGG  CG
                                      T_   C_
GAM257  NOS1    5'  ATGAGCCCGTCCGCTCGGCC  8370      T  C  ACCCA
                                GTGAGC CCG CC    GCC
                                |||||| ||| ||    |||
                                TACTCG GGC GG    CGG
                                   _  A  CGAGC
GAM257  POLG    5'  GTGGCCTCCACCCGGC     15450    A  CCGC    A
                                GTG GCT   CCACCC GC
                                ||| |||   |||||| ||
                                CAC CGG   GGTGGG CG
                                  _  A___    C
GAM257  POLK    3'  CAAGTGATCTGCCCATTCGGCC 32135      GC  C   CCCA
                                CAAGTGA  TC GCCCA   GCC
                                |||||||  || |||||   |||
                                GTTCACT  AG CGGGT   CGG
                                    __ A    AAGC
GAM257  PTGFRN  5'  AGGACGCTCCGCCTGGCC   42585   T _     CAC
                                AG GA GCTCCGCC  CC
                                || || ||||||||  ||
                                TC CT CGAGGCGG  GG
                                 _ G      ACC
GAM257  YWHAZ   3'  AAGTGAGCTTTGGGTATAACTT 18197       CCGCCC___  CC
            AGCC                AAGTGAGCT      AC  AGCC
                                |||||||||       ||  ||||
                                TTCACTCGA       TG  TCGG
                                     AACCCATAT  AA
GAM258  BDP1    5'  AGGCAGCCTCACGGCCGC   32946       __
                                AGGCAGCC  GCGGCCGC
                                ||||||||  ||||||||
                                TCCGTCGG  TGCCGGCG
                                    AG
GAM258  C8orf1  5'  AGGTGCCCGGGACCCGCC   20270    CA  G  ___
                                AGG  GCC CGG  CCGCC
                                |||  ||| |||  |||||
                                TCC  CGG GCC  GGCGG
                                  A_  _  CTG
GAM258  CACNA1B 5'  AGCAGCCACGGAGCCGCC   8740         __
                                GGCAGCCGCG  GCCGCC
                                ||||||||||  ||||||
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```
                                TCGTCGGTGC  CGGCGG
                                     CT
GAM258  CDKN2C   5' GGCAGCCAGTCCGGTCGCC   38566       ___  C
                                GGCAGCCG   CGG CGCC
                                ||||||||   ||| ||||
                                CCGTCGGT   GCC GCGG
                                    CAG   A
GAM258  COL18A1  3' AGACAGCCAATGACTGCC    39051       C_  C
                                AGGCAGCCG  GGC GCC
                                |||||||||  ||| |||
                                TCTGTCGGT  CTG CGG
                                     TA   A
GAM258  FKBP2    5' AGCAGCCAGGGACCCGCC    38387       C __
                                GGCAGCCG GG  CCGCC
                                |||||||| ||  |||||
                                TCGTCGGT CC  GGCGG
                                    C  TG
GAM258  HLA-DQA1 5' AGGCAGCCTTAGCAGTTGC   45567       ___  CC
                                AGGCAGCC   GCGG  GC
                                ||||||||   ||||  ||
                                TCCGTCGG   CGTC  CG
                                    AAT    AA
GAM258  ING1L    5' GCACCGGCCGCGGCCGCC    11458   ___
                                GCA   GCCGCGGCCGCC
                                |||   ||||||||||||
                                CGT   CGGCGCCGGCGG
                                  GGC
GAM258  LANGERIN 3' AGCCAGCTGCTAGCTGCC    31842   G   C _  C
                                AG CAGC GC GGC GCC
                                || |||| || ||| |||
                                TC GTCG CG TCG CGG
                                 G   A A  A
GAM258  LEF1     5' GGCAGCCGGAGCAGCTGCC   32214      ___   C
                                GGCAGCC   GCGGC GCC
                                |||||||   ||||| |||
                                CCGTCGG   CGTCG CGG
                                    CCT    A
GAM258  MAG      3' GGTCAGCCACGCAGGCTGCC  38748   _    ___  C
                                GG CAGCCGC   GGC GCC
                                || |||||||   ||| |||
                                CC GTCGGTG   CCG CGG
                                 A      CGT   A
GAM258  NDRG1    3' GGCAGCCGCACTGGCCGCC   40579       ___
                                GGCAGCCGC   GGCCGCC
                                |||||||||   |||||||
                                CCGTCGGCG   CCGGCGG
                                    TGA
GAM258  PDYN     3' GGCAGCCAATTCAGCTGC    35922       ___  C
                                GGCAGCCG   CGGC GC
                                ||||||||   |||| ||
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```
                                CCGTCGGT   GTCG CG
                                     TAA    A
GAM258  PIK3R2   5'  AGGCGACCACAGGGGCCGC   22740      A    ___
                                AGGC GCCGC   GGCCGC
                                |||| |||||   ||||||
                                TCCG TGGTG   CCGGCG
                                  C     TCC
GAM258  PTBP1    3'  GCAGCCGCGGCCGCCG      36719             III
                                GCAGCCGCGGCCGCC   G
                                ||||||||||||||   |
                                CGTCGGCGCCGGCGG   C
                                         III
GAM258  PTEN     5'  AGCCGCCGCGGCCGCCG     7198      A         III
                                GGC GCCGCGGCCGCC   G
                                ||| ||||||||||||   |
                                TCG CGGCGCCGGCGG   C
                                  G          III
GAM258  RORC     3'  AGCCAGCCGCAGCATCTGC   22809    G        C___
                                AG CAGCCGCGGC    GC
                                || ||||||||||    ||
                                TC GTCGGCGTCG    CG
                                 G         TAGA
GAM258  SLC19A1  3'  AGGCAGCCCCCCCCAAGGCTGCC 16844         GC_____  C  III
           G                     AGGCAGCC      GGC GCC   G
                                ||||||||      ||| |||   |
                                TCCGTCGG      CCG CGG   C
                                     GGGGGTT   A   III
GAM258  SLC9A5   5'  GGCACCGCAGCGGCCGCC    21390     __ C
                                GGCA  GC GCGGCCGCC
                                ||||  || |||||||||
                                CCGT  CG CGCCGGCGG
                                  GG  T
GAM258  TCIRG1   5'  AGGAAGCCGCGGCAGGCC    25835     C       C_
                                AGG AGCCGCGGC  GCC
                                ||| |||||||||  |||
                                TCC TCGGCGCCG  CGG
                                  T        TC
GAM258  CCND2    3'  GCTGCTTGCTGCAGGTTCATC  12048     C   C  CCGG  _
                                GCT GCT GC    GC GGTTCATC
                                ||| ||| ||    || ||||||||
                                CGA CGA CG    CG CCAAGTAG
                                  _   A  A___  T
GAM258  DBCCR1   5'  TCGCTCGCCTGCGCTC      31147         CGG   G
                                TCGCTCGCC   GCG TTC
                                |||||||||   ||| |||
                                AGCGAGCGG   CGC GAG
                                     A__   _
GAM258  YY1      5'  GCTCGCTCGGCCGCTGCTCGTC 18175         C   G_  GGT
                                GCTCGCTCG CCG  GC   TC
                                ||||||||| |||  ||   ||
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                                CGAGCGAGC GGC  CG   AG
                                     C   GA  AGC
GAM259  ANKRD3   3'  TGATTCTGACCCACGG     33971     CG      ACA
                                TGA  CTGACTT   ACGG
                                |||  |||||||   ||||
                                ACT  GACTGGG   TGCC
                                  AA     ___
GAM259  ATF6     5'  TAACGCTGACGAGACGGTGGCC 41916         TT_  AAC
                                TGACGCTGAC   AC   GGCC
                                ||||||||||   ||   ||||
                                ATTGCGACTG   TG   CCGG
                                     CTC  CCA
GAM259  BSG      3'  TGGCACTGACTCCGGC      11904    A       ACAA
                                TG CGCTGACTT    CGGC
                                || |||||||||    ||||
                                AC GTGACTGAG    GCCG
                                 C       _____
GAM259  CKTSF1B1 3'  TGAGCAGATTGCAACGGCC   30090    C  T  C  A
                                TGA GC GA TT CAACGGCC
                                ||| || || || ||||||||
                                ACT CG CT AA GTTGCCGG
                                  _  T  _  C
GAM259  CSNK1G2  3'  TGACGCTAACGGGGGCGGC   10620         TTACAA
                                TGACGCTGAC     CGGC
                                ||||||||||     ||||
                                ACTGCGATTG     GCCG
                                     CCCCC_
GAM259  FBXL11   3'  TGACGCTGGCCTCAGAGCC   29442        A   A  AC
                                TGACGCTG CTT CA  GGCC
                                |||||||| ||| ||  ||||
                                ACTGCGAC GGA GT  TCGG
                                    C   _  C_
GAM259  IL10RA   3'  TGAGCTGACTTCAGCC      40627     C      ACAA
                                TGA GCTGACTT    CGGCC
                                ||| ||||||||    |||||
                                ACT CGACTGAA    GTCGG
                                  _      _____
GAM259  LPIN2    3'  TGACGCTGCTTCCACGGGCC  31223        A   ACA   _
                                TGACGCTG CTT   ACGG CC
                                |||||||| |||   |||| ||
                                ACTGCGAC GAA   TGCC GG
                                    _   GG_    C
GAM259  PFKFB4   3'  TGACATGGATACAACGGCC   21297      C  ACT
                                TGACG TG   TACAACGGCC
                                ||||| ||   ||||||||||
                                ACTGT AC   ATGTTGCCGG
                                  _ CT_
GAM259  PRX      3'  TGACCTTGGCTACCTTGGCC  34136     G  GAC    AAC
                                TGAC CT   TTAC   GGCC
                                |||| ||   ||||   ||||
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                                ACTG GA   GATG   CCGG
                                  _ ACC    GAA
GAM259  PRY      3'  TGACTTGTAGCAACGGCC    41257       A___
                                TGACTT    CAACGGCC
                                ||||||    ||||||||
                                ACTGAA    GTTGCCGG
                                   CATC
GAM259  SLC7A5   3'  TGACGCTGGACCACTTGGC    18557        _  T  AAC
                                TGACGCTG ACT AC   GGC
                                |||||||| ||| ||   |||
                                ACTGCGAC TGG TG   CCG
                                     C   _  AA_
GAM259  WHSC1    3'  TGAGCTGGGCTCAGACGG    39387     C    A_   CA
                                TGA GCTG  CTTA  ACGG
                                ||| ||||  ||||  ||||
                                ACT CGAC  GAGT  TGCC
                                  _    CC    C_
GAM259  DDEF1    3'  TGTGTGAAGGGTTGAC      40570      C  TATG    C
                                TGTG GG    GGGGT GAC
                                ||||  ||    |||||  |||
                                ACAC CT    TCCCA CTG
                                  A  _____     A
GAM259  FOLR1    3'  ACATGTGCGGTGTCTGGT    32501           ATGGG
                                ACATGTGCGGT    GGT
                                ||||||||||     |||
                                TGTACACGCCA    CCA
                                      CAGA_
GAM260  ABL1     3'  AGCCCGCATGTGCTGCAG    28700      T  C  A
                                AGCCT GC AT TGCTGCAG
                                ||||| ||  ||  ||||||||
                                TCGGG CG TA ACGACGTC
                                  _  _  C
GAM260  ALOX12   3'  GCCTTCATGCTGCA       8688       GCCA
                                GCCTT    TATGCTGCA
                                |||||    |||||||||
                                CGGAA    GTACGACGT
                                   _____
GAM260  ARHGEF5  3'  CCAGCCCTTGCCATGAGCAG   24125       _     ATGCT
                                CCAGCC TTGCCAT    GCAG
                                |||||| |||||||    ||||
                                GGTCGG AACGGTA    CGTC
                                   G      CT___
GAM260  DLEC1    3'  GACTAATTTTGCCATACTG    28846     C  CC      AT
                                GAC AG  TTGCCAT  GCTG
                                |||  ||  |||||||  ||||
                                CTG TT  AACGGTA  TGAC
                                  A  AA      __
GAM260  KCNA6    3'  AACCTTGAATGCTGCAG     13802        CCAT
                                AGCCTTG    ATGCTGCAG
                                |||||||    |||||||||
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                                TTGGAAC   TACGACGTC
                                   T___
GAM260  LETM1    3'  CCAGCCTGGCCATGCTGC    29498       T   TA
                                CCAGCCT GCCA  TGCTGC
                                ||||||| ||||  ||||||
                                GGTCGGA CGGT  ACGACG
                                   C   __
GAM260  MPP2     3'  CCAGCTTTGGCTGACGCTGCAG 40794      C   CCAT
                                CCAGC TTG   ATGCTGCAG
                                ||||| |||   |||||||||
                                GGTCG AAC   TGCGACGTC
                                  A  CGAC
GAM260  MYCL2    3'  GACCAGCCTGGCCAATGTG   23900       T   T   C
                                GACCAGCCT GCCA ATG TG
                                ||||||||| |||| ||| ||
                                CTGGTCGGA CGGT TAC AC
                                     C   _  _
GAM260  RABIF    3'  CCACCTTGCACTGC       16123     G     CATAT
                                CCA CCTTGC    GCTGC
                                ||| ||||||    |||||
                                GGT GGAACG    TGACG
                                 _    _____
GAM260  RECQL    5'  GACCGGCCTCGCCCTGCA    37274     A      ATATG
                                GACC GCCTTGCC    CTGCA
                                |||| ||||||||    |||||
                                CTGG CGGAGCGG    GACGT
                                  C      _____
GAM260  SLC14A2  5'  GACCAGCCTGGCCAATGTG   28397       T   T   C
                                GACCAGCCT GCCA ATG TG
                                ||||||||| |||| ||| ||
                                CTGGTCGGA CGGT TAC AC
                                     C   _  _
GAM260  SLC22A1L 5'  CCTGGCCTTGCCTGCCTTTGCA 14982    A_      ATA   ___
           G                     CC  GCCTTGCC   TGCT   GCAG
                                ||  ||||||||  ||||  ||||
                                GG  CGGAACGG   ACGG   CGTC
                                 AC       ___   AAA
GAM260  SNRPN    5'  GCCTTGCCACTGCAG       35611        ATAT
                                GCCTTGCC   GCTGCAG
                                ||||||||   |||||||
                                CGGAACGG   TGACGTC
                                     _____
GAM260  TDG      5'  GACTGATCCTATATGCTG    17355     CAG_  TGCC
                                GAC   CCT   ATATGCTG
                                |||   |||   ||||||||
                                CTG   GGA   TATACGAC
                                  ACTA  _____
GAM260  TNFSF15  3'  AGCTTTTCTCATATGCTG    23050     C  GC_
                                AGC TT   CATATGCTG
                                ||| ||   |||||||||
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                                TCG AA   GTATACGAC
                                  A  AGA
GAM260  TRIM37   3'  AACCAGCCTTCTGCTG      31623          GCCATA
                                GACCAGCCTT     TGCTG
                                ||||||||||     |||||
                                TTGGTCGGAA     ACGAC
                                     G_____
GAM261  ADRBK1   3'  CAGCCAAGCCCCGCAGTG    11524      CCCT    _
                                TAGCC    GGCCC GCAGTG
                                ||||||   ||||| ||||||
                                GTCGG    TCGGG CGTCAC
                                   T___     G
GAM261  BCAR1    3'  ACCCAACCCGGGCCCGTGGTGC 41939      __    _   CA
                                GCCC  CCTGG CCCG  GTGC
                                ||||  ||||| ||||  ||||
                                TGGG  GGGCC GGGC  CACG
                                  TT    C    AC
GAM261  BCAT1    5'  TAGCCCCTGGCCGTG       42384        C     CGCA
                                TAGCCCC TGGCC    GTG
                                ||||||| |||||    |||
                                ATCGGGG ACCGG    CAC
                                   _    _____
GAM261  BCL2L2   3'  GCTCTCCTGGCCCCCAGC    19746    CC_      G
                                GC   CCTGGCCC CAGT
                                ||   |||||||| ||||
                                CG   GGACCGGG GTCG
                                 AGA       G
GAM261  BLTR2    5'  CAGCCCACCTTCTGCAGTG    33362       _   GGCCC
                                TAGCCC CCT     GCAGTG
                                |||||| |||     ||||||
                                GTCGGG GGA     CGTCAC
                                   T   AGA__
GAM261  CBFA2T2  3'  GCCATCTGGCCCGTGC      22973     CC      GCA
                                GCC  CTGGCCC   GTGC
                                |||  |||||||   ||||
                                CGG  GACCGGG   CACG
                                  TA      ____
GAM261  CDH7     5'  CAGCCCACTCCGCGGTGC     38001       C  GGC    A
                                TAGCCC CT   CCGC GTGC
                                |||||| ||   |||| ||||
                                GTCGGG GA   GGCG CACG
                                   T ____    C
GAM261  CDX2     5'  GCGCCCCAGCCCCGCGGTGC   10407    C   TG     A
                                GC CCC  GCCCGC GTGC
                                || |||  |||||| ||||
                                CG GGG  CGGGCG CACG
                                 C  GT     C
GAM261  CHRNA3   3'  CAGCCCAAAATGTCCGTAGTGC 8834        CC__  GC   C
                                TAGCCC    TG  CCG AGTGC
                                ||||||    ||  ||| |||||
```

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                                GTCGGG   AC  GGC TCACG
                                   TTTT  A_   A
GAM261  CREBL2   3'  GCCCACTAGCTGCGGTGC    10581     C    CC  A
                                GCCC CTGGC  GC GTGC
                                |||| |||||  || ||||
                                CGGG GATCG  CG CACG
                                  T    A_  C
GAM261  CRSP6    5'  AGCCCGCAGCCGCGGTGC    20175     CCT   C  A
                                AGCCC   GGCC GC GTGC
                                |||||   |||| || ||||
                                TCGGG   TCGG CG CACG
                                   CG_   _  C
GAM261  DISC1    3'  GCTCCCCTGGCAGTG      33044   _      CCGC
                                GC CCCCTGGC    AGTG
                                || ||||||||    ||||
                                CG GGGGACCG    TCAC
                                 A      _____
GAM261  DNM2     3'  GCCCCTTTGCGCAGTGC     22383     CTG  CC
                                GCCCC   GC  GCAGTGC
                                |||||   ||  |||||||
                                CGGGG   CG  CGTCACG
                                   AAA  __
GAM261  ELAC2    3'  CAGCCTCCTGGCCCGCGGC   32851     C       A
                                TAGCC CCTGGCCCGC GT
                                ||||| ||||||||| ||
                                GTCGG GGACCGGGCG CG
                                   A        C
GAM261  FLT4     3'  TAACCCCTCCCTGTGGTGC   12918      CTGG   GCA_
                                TAGCCCC    CCC    GTGC
                                |||||||    |||    ||||
                                ATTGGGG    GGG    CACG
                                    A___   ACAC
GAM261  GNB2     3'  CAGCCCCGCAGCCCTGGCCTGT 23596       C     __ ____
           AGTG                    TAGCCCC TGGCCC  GC    AGTG
                                |||||||  ||||||  ||    ||||
                                GTCGGGG GTCGGG  CG    TCAC
                                    C     AC  GACA
GAM261  GNL1     5'  GCCCTCTGGCCCGAGAGC    45565     C      C  T
                                GCCC CTGGCCCG AG GC
                                |||| ||||||| || ||
                                CGGG GACCGGGC TC CG
                                  A      _  T
GAM261  HOXD3    3'  AGTCCCTTGGTCCGCAGT    27893    C   C   C
                                AG CCC TGG CCGCAGT
                                || ||| ||| |||||||
                                TC GGG ACC GGCGTCA
                                 A  A  A
GAM261  IGFBP4   3'  TAGCCCTCTGTGCTTCAA    11407      C   _  CCG
                                TAGCCC CTG GC   CAG
                                |||||| ||| ||   |||
```

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                                ATCGGG GAC CG   GTT
                                   A   A  AA_
GAM261   JUND    3'  AGCCCCCTTGCGGCGCGGTG   23795        G  C_   A
                                AGCCCCCT GC  CGC GTG
                                |||||||| ||  ||| |||
                                TCGGGGGA CG  GCG CAC
                                    A  CC   C
GAM261   KCNK5   5'  AGCTCCGCATGCGCAGTGC    19028     C  CTG  C__
                                AGC CC   GC   CGCAGTGC
                                ||| ||   ||   ||||||||
                                TCG GG   CG   GCGTCACG
                                  A  ___  TAC
GAM261   KCNK5   3'  CAGCTCCCTGGCCACCAGC    19031      C       CG
                                TAGC CCCTGGCC  CAGT
                                |||| ||||||||  ||||
                                GTCG GGGACCGG  GTCG
                                   A       TG
GAM261   LARS2   3'  AGCCCTCTGGGGCGTGC     31670      C    CCC  A
                                AGCCC CTGG   GC GTGC
                                ||||| ||||   || ||||
                                TCGGG GACC   CG CACG
                                   A    C__  _
GAM261   LOXL1   5'  GCCCCCTGGGCGTG        41183         CCC  A
                                GCCCCCTGG   GC GTG
                                |||||||||   || |||
                                CGGGGGACC   CG CAC
                                          ___  _
GAM261   MATK    5'  CAGCCCCCTGCAGCCTGGTG   40305          __   CGCA
                                TAGCCCCCTG  GCC   GTG
                                ||||||||||  |||   |||
                                GTCGGGGGAC  CGG   CAC
                                     GT   AC__
GAM261   NCOR2    3'  GCCGCCCTGGCCGCCTG     26737     _      C  AG
                                GCC CCCTGGCC GC  TG
                                ||| |||||||| ||  ||
                                CGG GGGACCGG CG  AC
                                  C       _  G_
GAM261   NGFR     3'  GCCCACCTAGCAGTG       14779      _     CCGC
                                GCCC CCTGGC    AGTG
                                |||| ||||||    ||||
                                CGGG GGATCG    TCAC
                                  T     _____
GAM261   NOLA2    3'  TAGCTTCCAGCGGCAGGTGC   45397      CC  T   CC   _
                                TAGC  CC GGC  GCAG TGC
                                ||||  || |||  |||| |||
                                ATCG  GG TCG  CGTC ACG
                                   AA  _   C_    C
GAM261   NTSR1    3'  AGCCCCCTCCCATGTG      14874         GG    CA
                                AGCCCCCT  CCCG  GTG
                                ||||||||  ||||  |||
```

```
                                TCGGGGGA  GGGT  CAC
                                   __   A_
GAM261  OPHN1   3'  GCTCCCTGGCCTCCAGGC   14967   C     CG  T
                                GC CCCTGGCC  CAG GC
                                || ||||||||  ||| ||
                                CG GGGACCGG  GTC CG
                                 A       AG  _
GAM261  PBX2    3'  TAGCCCCCCGGCCCATGC   15109          GCA
                                TAGCCCCCTGGCCC  GTGC
                                ||||||||||||||  ||||
                                ATCGGGGGGCCGGG  TACG
                                      ___
GAM261  RAD52   3'  CAGCCCTCTTCAGCTGCAGTG  39556      C __  CC
                                TAGCCC CT  GGC  GCAGTG
                                |||||| ||  |||  ||||||
                                GTCGGG GA  TCG  CGTCAC
                                    A  AG  A_
GAM261  SMARCC1 5'  GCCCACCCCGGCCCTCGCGGTG 16902     __     __ A
                                GCCC  CCTGGCCC  GC GTG
                                ||||  ||||||||  || |||
                                CGGG  GGGCCGGG  CG CAC
                                  TG       AG  C
GAM261  SOX10   3'  TAGCCCTTAGGCACTG     28015      CC  CCC  G
                                TAGCCC  TGG   GCA TG
                                ||||||  |||   ||| ||
                                ATCGGG  ATC   CGT AC
                                   A_  ___  G
GAM261  SREBF1  3'  GCTCGGCCCCTGCAGTGC   45372   CCCC    __
                                GC   TGGCCC  GCAGTGC
                                ||   ||||||  |||||||
                                CG   GCCGGG  CGTCACG
                                 A___     GA
GAM261  TNFSF9  3'  TAGCCCCCTAGCCTGGGC   19195          C__
                                TAGCCCCCTGGCC  GC
                                ||||||||||||  ||
                                ATCGGGGGATCGG  CG
                                       ACC
GAM261  VRK2    5'  GCGTCGGCCTCGCAGTGC   26666   CCCC   _
                                GC   TGGCC CGCAGTGC
                                ||   ||||| ||||||||
                                CG   GCCGG GCGTCACG
                                 CA__    A
GAM261  RRM2B   3'  TGGCCTGCTCCTTTTGCA   42728     CGCCT  G_
                                TGGCC   TGC  CTTTTGCA
                                |||||    |||  ||||||||
                                ACCGG    ACG  GAAAACGT
                                   _____  AG
GAM262  CARD4   3'  TTGCTCACAGCTTTATTCCTC  25895       C  CGGGG
                                TTGCTCAC GC    TCCTC
                                |||||||| ||    |||||
```

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                                AACGAGTG CG    AGGAG
                                    T  AAATA
GAM262  FAAH    3'  GCCTGCTCACTGGCTTCTC   11054        CGCC  GG  C
                                GCTTGCTCAC   GG  TC TC
                                ||||||||||   ||  || ||
                                CGGACGAGTG   CC  AG AG
                                     A___  GA  _
GAM262  FCMD    5'  GCTGCTCACTTGGTTGTC    27521    T    CGCC  G_
                                GCT GCTCAC   GG  GTC
                                ||| ||||||   ||  |||
                                CGA CGAGTG   CC  CAG
                                  _    AA__  AA
GAM262  FGF18   5'  GCTCGCTCACTGCTGGCCGG  38008        C  C  _____
                                GCTTGCTCAC GC GG    GG
                                |||||||||| || ||    ||
                                CGAGCGAGTG CG CC    CC
                                     A  A  GGIII
GAM262  FGF18   3'  TTCCTCATTCAAGTCCTCC   38011   G   CCGCCG
                                TT CTCA     GGGTCCTCC
                                || ||||     |||||||||
                                AA GAGT     TTCAGGAGG
                                 G   AAG___
GAM262  LMO4    5'  GCTTGCTCGCTCCGGGAT    27655       ACCG
                                GCTTGCTC   CCGGGGT
                                ||||||||   |||||||
                                CGAACGAG   GGCCCTA
                                     CGA_
GAM262  P2RX3   3'  CTTGCTCAGGCAGGGTCCTC   14994       CC  C
                                CTTGCTCA  GC GGGGTCCTC
                                ||||||||  || |||||||||
                                GAACGAGT  CG TCCCAGGAG
                                     C_  _
GAM262  PDGFB   5'  GCCTGCTCGCCGCTCTGGGCGT 15179       A   C__  _
            CCTC                GCTTGCTC CCGC   GGG GTCCTC
                                |||||||| ||||   ||| ||||||
                                CGGACGAG GGCG   CCC CAGGAG
                                     C   AGA   G
GAM262  REQ     3'  GCTTGCTCGCTCCCAGCTCC   26547       ACCG  G  G
                                GCTTGCTC   CC GG TCC
                                ||||||||   || || |||
                                CGAACGAG   GG TC AGG
                                     CGA_  G  G
GAM262  RHCG    3'  GCTTGCTCACTCTTGCATCC   32242        C___  CGGG
                                GCTTGCTCAC   GC   GTCC
                                ||||||||||   ||   ||||
                                CGAACGAGTG   CG   TAGG
                                     AGAA  ____
GAM262  SYNGR1  3'  GCTGGCTGGGGTCCT      21760    T  CACCGCC
                                GCT GCT      GGGGTCCT
                                ||| |||      ||||||||
```

```
                                CGA CGA      CCCCAGGA
                                  C  _______
GAM262  TLX1     5'  GCTCGCTCGCTGTTGACTC   24339        ACC  CG__  G
                                GCTTGCTC   GC    GG TC
                                ||||||||   ||    || ||
                                CGAGCGAG   CG    CT AG
                                     ___  ACAA  G
GAM262  ACPT     3'  TGAGAGGCAGGGGCAGGTG   38893         ___   C_
                                TGAGGGGC   GGC  GTG
                                ||||||||   |||  |||
                                ACTCTCCG   CCG  CAC
                                     TCC   TC
GAM262  ADAM23   5'  TGCGGGGCGGCCGCGGGC    19208    A          A
                                TG GGGGCGGCCGTG GC
                                || ||||||||||| ||
                                AC CCCCGCCGGCGC CG
                                 G          C
GAM262  AQP1     3'  TGAGGGGCGACTAGCA      7549           CGTG
                                TGAGGGGCGGC    AGCA
                                ||||||||||    ||||
                                ACTCCCCGCTG    TCGT
                                      A___
GAM262  AQP1     3'  AGGGGCTTGGGAGCAAGCAG   7546        GGCCGT
                                AGGGGC     GAGCAAGCAG
                                ||||||     ||||||||||
                                TCCCCG     CTCGTTCGTC
                                   AACC__
GAM262  ATP11A   3'  TGGGTGGTGGCCGGGCAAGCAG 44190    A  _  C     TGA
                                TG GG GG GGCCG   GCAAGCAG
                                || || || |||||   ||||||||
                                AC CC CC CCGGC   CGTTCGTC
                                 _  A  A    C__
GAM262  ATP8A2   3'  TGAGGGGCGCCTGGACACGGC  45269         G  G  AG  A_
                                TGAGGGGCG CC TG  CA  GC
                                ||||||||| || ||  ||  ||
                                ACTCCCCGC GG AC  GT  CG
                                     _  _  CT  GC
GAM262  CBFA2T3  3'  TGAGGGGTGGCTGGGCA     23271        C   CG  A
                                TGAGGGG GGC  TG GCA
                                ||||||| |||  || |||
                                ACTCCCC CCG  AC CGT
                                    A   __  C
GAM262  CDKN1B   5'  GCAGAGCCGTGAGCAAGC    19800    __
                                GC  GGCCGTGAGCAAGC
                                ||  ||||||||||||||
                                CG  TCGGCACTCGTTCG
                                 TC
GAM262  CHGA     5'  GAGGGGCGGCTGGACTGGC    10465          CG  AG AA
                                GAGGGGCGGC  TG  C  GC
                                ||||||||||  ||  |  ||
```

```
                                CTCCCCGCCG  AC  G  CG
                                      __  CT AC
GAM262  CTNNA1   3'  TGGGGGCGGCCGGCCTGGGCAG 42324    A       TGA  AA__
                                TG GGGGCGGCCG   GC    GCAG
                                || ||||||||||   ||    ||||
                                AC CCCCGCCGGC   CG    CGTC
                                 _        ____  GACC
GAM262  DVL3     3'  TGAGGGGCTGCTGAAGCA    20691        G  CGT
                                TGAGGGGC GC   GAGCA
                                |||||||| ||   |||||
                                ACTCCCCG CG   TTCGT
                                     A  AC_
GAM262  GRM4     3'  GAGGGGCAGGCGGGCAGGC   9158         CC   A   A
                                GAGGGGCGG  GTG GCA GC
                                |||||||||  ||| ||| ||
                                CTCCCCGTC  CGC CGT CG
                                      __   C   C
GAM262  GTF2I    5'  TGAGGGGAGCTGGCGAGC    37443       C   C_
                                TGAGGGG GGC  GTGAGC
                                |||||||  |||  ||||||
                                ACTCCCC TCG  CGCTCG
                                     _   AC
GAM262  HOXB7    3'  TGGGGGACGGGAAGCAAGCAG  21070    A      CCGT
                                TG GGGGCGG    GAGCAAGCAG
                                || |||||||    ||||||||||
                                AC CCCTGCC    TTCGTTCGTC
                                 C      C___
GAM262  JAG2     3'  GAGGGGCGGCCGGGGCCGGCAG 13721           TGA  AA
                                GAGGGGCGGCCG   GC  GCAG
                                ||||||||||||   ||  ||||
                                CTCCCCGCCGGC   CG  CGTC
                                       CC_  GC
GAM262  KCNC3    3'  GGGGGGCGGTGAGGC       22519      C   C     CAA
                                GGGG GGC GTGAG   GC
                                |||| ||| |||||   ||
                                CCCC CCG CACTC   CG
                                  _   C     ___
GAM262  LRP1     3'  GGGGGTGCCAAGGAGCAGGCAG 14223      CG    T_    A
                                GGGG  GCCG  GAGCA GCAG
                                ||||  ||||  ||||| ||||
                                CCCC  CGGT  CTCGT CGTC
                                  CA    TC    C
GAM262  MATK     5'  TGAGAGGCACACTGAGCAAG   40318         G CG
                                TGAGGGGCG C  TGAGCAAG
                                |||||||||  |  ||||||||
                                ACTCTCCGT G  ACTCGTTC
                                      _ TG
GAM262  NEK4     5'  TGGGGGCGGCTGTTGAGGCAG  17195    A      CG_   CAA
                                TG GGGGCGGC   TGAG   GCAG
                                || ||||||||   ||||   ||||
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                                AC CCCCGCCG  ACTC  CGTC
                                 _      ACA   ___
GAM262  PLIN    3'  GAAATGTGGCTGTGAGCAAGCA 15399     GGC  C
          G                      GAGG  GGC GTGAGCAAGCAG
                                 ||||  ||| ||||||||||||
                                 CTTT  CCG CACTCGTTCGTC
                                   ACA  A
GAM262  POLR2J  3'  TGAGGGGTGGCCACAAGGC   26360       C    TG  CAA
                                 TGAGGGG GGCCG  AG  GC
                                 ||||||| |||||  ||  ||
                                 ACTCCCC CCGGT  TC  CG
                                     A   GT  ___
GAM262  PTPRA   5'  TGAGGGGCGACTGGGC     38917          CG  A
                                 TGAGGGGCGGC  TG GC
                                 ||||||||||  || ||
                                 ACTCCCCGCTG  AC CG
                                       __ C
GAM262  SIRPB2  3'  GGAGCCTGTGGGCAGGCA   38898   C   _  A  A
                                 GG GGCC GTG GCA GCA
                                 || |||| ||| ||| |||
                                 CC TCGG CAC CGT CGT
                                  _   A  C  C
GAM262  SLBP    5'  TGAGGCGGCGGCGGCGCGGGCA 27198      _    __   A
                                 TGAGG GGCGGC  CGTG GCA
                                 ||||| ||||||  |||| |||
                                 ACTCC CCGCCG  GCGC CGT
                                    G     CC   C
GAM262  SLC6A8  5'  CGGGGGGCGGCGGTCAGGC   24763   A      C  G  CAA
                                 TG GGGGCGGC GT AG  GC
                                 || |||||||| || ||  ||
                                 GC CCCCGCCG CA TC  CG
                                  C       C  G  ___
GAM262  VIPR1   5'  GGGCGGCGCACCAGGC     21513       C  AG  A
                                 GGGCGGC GTG  CA GC
                                 ||||||| |||  || ||
                                 CCCGCCG CGT  GT CG
                                     _  G_  C
GAM262  ZFP36   5'  TGAGGGGTGTCGGCCGAGAG  18211       ___    T
                                 TGAGGGG  CGGCCG GAG
                                 |||||||  |||||| |||
                                 ACTCCCC  GCCGGC CTC
                                     ACA    T
GAM263  ABL1    3'  GGGGAAAGAGGTGATGTGC   28718         AA  CGCC
                                 GGGGAAGGAG  GG   GC
                                 |||||||||  ||   ||
                                 CCCCTTTCTC  CT   CG
                                       CA  ACA_
GAM263  ACTB    3'  GGGGAAGGGGGGGGCACGAAGGC 9927         AGAA   C___
                                 GGGGAAGG   GGCGC   GC
                                 ||||||||   |||||   ||
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                                CCCCTTCC  CCGTG  CG
                                    CCC_   CTTC
GAM263  ADRBK1   3' AGGGGCGGGAGGGCTGTGC  11523     AA  AA  GCC
                                AGGGG GGAG GGC  GC
                                ||||| |||| |||  ||
                                TCCCC CCTC CCG  CG
                                  GC  __  ACA
GAM263  ALMS1    5' AGGGGAAGGGGAGAGCCC   31529       A AG G
                                AGGGGAAGG GA GC CC
                                ||||||||| ||  || ||
                                TCCCCTTCC CT CG GG
                                     C CT _
GAM263  AP2A1    3' AAGGGAGGGAGGGGGAC    39099      A  AA C
                                AGGGGA GGAG GG GC
                                |||||| |||| || ||
                                TTCCCT CCTC CC TG
                                   C  CC _
GAM263  ARL4     3' GGGGTAGGGAGAAGAGACCAC 25067     AA_     C
                                GGGG  GGAGAAGG GCCGC
                                ||||  |||||||| |||||
                                CCCC  CCTCTTCT TGGTG
                                  ATC      C
GAM263  ATP7A    3' GGGAGGGAGAAGGAGGCATGC 6262      A      C_ C_
                                GGGA GGAGAAGG GC GC
                                |||| |||||||| ||  ||
                                CCCT CCTCTTCC CG CG
                                  C      TC TA
GAM263  BACE     3' AGGGGTGAGGAGGGGGCTTAAC 39949     A_   AA  ___ C
           TGC                    AGGGG AGGAG GGC  GC GC
                                |||||  |||||  |||  || ||
                                TCCCC TCCTC CCG  TG CG
                                  AC   CC  AAT A
GAM263  BLAME    3' AGGGAAGGGGGAGGTGTGAAAC 33485       A_ _______   CC
           GTGC                   GGGGAAGG GA    AGGCG GC
                                |||||||| ||    ||||| ||
                                TCCCTTCC CT    TTTGC CG
                                    CC CCACAC   A_
GAM263  BMP1     3' AGGGGAGGAGAAGTTGCCTGTG 25970      A     GC  ___
           C                     AGGGGA GGAGAAG GCC  GC
                                |||||| |||||||  |||  ||
                                TCCCCT CCTCTTC CGG  CG
                                  _     AA  ACA
GAM263  CADPS    5' AGGGGAAGGGAGAGGTGC   42190       _ A C
                                AGGGGAAGG AGA GG GC
                                ||||||||| ||| || ||
                                TCCCCTTCC TCT CC CG
                                    C  _ A
GAM263  CDC42    3' GGGGAAGGGGGGGGCCATACC 12159       AGAA C  C
                                GGGGAAGG   GG GCCG ACT
                                ||||||||   || |||| |||
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                                CCCCTTCC   CC CGGT TGG
                                    CCC_ _   A
GAM263  CENTD2   5' GGGGAAGGGGAAGCC      31599       A  GGC
                                GGGGAAGG GAA  GCC
                                |||||||| |||  |||
                                CCCCTTCC CTT  CGG
                                    C  ___
GAM263  CLTC     5' AGGGGAGGGGGGAGGCTGGGC 22148      A AGA   GCC
                                AGGGGA GG  AGGC  GC
                                |||||| ||  ||||  ||
                                TCCCCT CC  TCCG  CG
                                   C CCC   ACC
GAM263  CLTC     5' AGGAGAAGGGGAGGGGGGAGGC 22147        A _______
                                AGGGGAAGG GA     AGGC
                                ||||||||| ||     ||||
                                TCCTCTTCC CT     TCCG
                                     C CCCCCC
GAM263  DGUOK    3' AGGGAAGGGCTCCAGC     38966       AGAAG G _
                                GGGGAAGG    GC CC GC
                                ||||||||    || || ||
                                TCCCTTCC    CG GG CG
                                    _____ A T
GAM263  DRIL1    5' GGGGAGGGGGCCCGGCCGCACT 23372     A AGAA  ___
                                GGGGA GG   GGC  GCCGCACT
                                ||||| ||   |||  ||||||||
                                CCCCT CC   CCG  CGGCGTGA
                                  C ____  GGC
GAM263  EIF2C1   3' AGGGGAAGGAAAAAGATGCACT 29170          CGCC
                                AGGGGAAGGAGAAGG   GCACT
                                ||||||||||||||   |||||
                                TCCCCTTCCTTTTTC   CGTGA
                                       TA__
GAM263  FMNL     3' GGGGAAGGGGCGGGCGATGC  25306       AGAA   CC
                                GGGGAAGG   GGCG  GC
                                ||||||||   ||||  ||
                                CCCCTTCC   CCGC  CG
                                    CCGC   TA
GAM263  FOSL1    3' GGGGAAGGGGAGGAGACA    24139       A __
                                GGGGAAGG GA  AGGCG
                                |||||||| ||  |||||
                                CCCCTTCC CT  TCTGT
                                    C  CC
GAM263  GLI2     5' GGGGAAGGTGAAGGCTGGGC  36118       A    GCC
                                GGGGAAGG GAAGGC  GC
                                |||||||| ||||||  ||
                                CCCCTTCC CTTCCG  CG
                                    A    ACC
GAM263  GNAS     3' GGGGAAGGGAAAGGTTGC    38663       AG   C_
                                GGGGAAGG  AAGG  GC
                                ||||||||  ||||  ||
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                                CCCCTTCC  TTCC  CG
                                     CT    AA
GAM263  GRB2     5'  AAGGGAGGGAGGAGGGC     13286       A   A  C
                                AGGGGA GGAG AGG GC
                                |||||| |||| ||| ||
                                TTCCCT CCTC TCC CG
                                   C   C  _
GAM263  GRM6     5'  GGGGAAGGAGAGCGCGGGC   9173          AG   C_
                                GGGGAAGGAGA  GCGC  GC
                                ||||||||||  ||||  ||
                                CCCCTTCCTCT  CGCG  CG
                                       __   CC
GAM263  HMGA2    5'  GAGGAGAGGAGGAGGCGC    18517      _    A
                                GGGGA AGGAG AGGCGC
                                ||||| ||||| ||||||
                                CTCCT TCCTC TCCGCG
                                   C    C
GAM263  HOXC10   3'  AGGGAGGAGGAGAGGCCGCGCT 41484      A   A  C    A
                                GGGGA GGAG AGG GCCGC CT
                                ||||| |||| ||| ||||| ||
                                TCCCT CCTC TCT CGGCG GA
                                   _   C  C    C
GAM263  IGHMBP2  3'  AGGGGAAGGGACGTGCA     13490        AGAA   CC
                                AGGGGAAGG   GGCG  GCA
                                |||||||||   ||||  |||
                                TCCCCTTCC   CTGC  CGT
                                      ____   A_
GAM263  LANGERIN 3'  GGAAGGAGAAGGGAGGC     31845         CGCC
                                GGAAGGAGAAGG   GC
                                ||||||||||||   ||
                                CCTTCCTCTTCC   CG
                                       CTC_
GAM263  LBX1     5'  GGTGGAAGGAGGCCGCAC    27289   _     AAGGC
                                GG GGAAGGAG    GCCGCAC
                                || ||||||||    |||||||
                                CC CCTTCCTC    CGGCGTG
                                 A      _____
GAM263  LGALS3BP 3'  AGGGGAAGGAGGAGGTGC    42928         A  C
                                AGGGGAAGGAG AGG GC
                                |||||||||| ||| ||
                                TCCCCTTCCTC TCC CG
                                      C  A
GAM263  MADH4    5'  AGGGGAGTGGGAAGGCGC    23817      A_  A
                                AGGGGA  GG GAAGGCGC
                                ||||||  || ||||||||
                                TCCCCT  CC CTTCCGCG
                                   CA  _
GAM263  MKI67    5'  AGGAGGAGCCGGCGCCGCGCT  14514     A   AA      A
                                GGGA GGAG  GGCGCCGC CT
                                |||| ||||  |||||||| ||
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                                TCCT CCTC  CCGCGGCG GA
                                  _   GG      C
GAM263  MLC1    5'  AGGGGAAGGAGAGCTGC    40148          AGGC  C
                                AGGGGAAGGAGA   GC GC
                                ||||||||||||   || ||
                                TCCCCTTCCTCT   CG CG
                                      _____ A
GAM263  MNT     3'  AGGGGAAGCAGGAGCGGCACT  33702        G  AA   CC
                                AGGGGAAG AG  GGCG  GCACT
                                ||||||||  ||  ||||  |||||
                                TCCCCTTC TC  TCGC  CGTGA
                                    G  C_   __
GAM263  NRBP    3'  AGGGGAGGGGAAAGGATGATGC 30159       A  AG   CGCC_
                                AGGGGA GG  AAGG    GC
                                ||||||  ||  ||||    ||
                                TCCCCT CC  TTCC    CG
                                   C  CT   TACTA
GAM263  NUCB1   3'  AGGGGAGGGGGCGGGC     26151       A  AGAA   CC
                                AGGGGA GG   GGCG  GC
                                ||||||  ||   ||||  ||
                                TCCCCT CC   CCGC  CG
                                   C  _____   C_
GAM263  PAFAH1B1 5'  AGGGGGGAGGATGGCGCGC   7699       AA   AA_   C
                                AGGGG  GGAG   GGCGC GC
                                |||||  ||||   ||||| ||
                                TCCCC  CCTC   CCGCG CG
                                  __    CTA    _
GAM263  PDGFB   3'  AGGGGTGGGGGAAGCACCA   15168      AA  A   G
                                AGGGG  GG GAAG CGCCG
                                |||||  || |||| |||||
                                TCCCC  CC CTTC GTGGT
                                  AC  C   _
GAM263  PLXNB3  3'  GGGGAAGGAGGGGGATCC    23949         AA  CG
                                GGGGAAGGAG  GG  CC
                                ||||||||||  ||  ||
                                CCCCTTCCTC  CC  GG
                                      CC  TA
GAM263  PML     3'  AGGGAGGAGGAGGAAGGGGC  37722       __   _   C
                                GGGGA  AGGAG AAGG GC
                                |||||  ||||| |||| ||
                                TCCCT  TCCTC TTCC CG
                                   CC    C   C
GAM263  PPFIA3  3'  AGGAGAAGGGGAAGCGCCA   41413         A   G
                                AGGGGAAGG GAAG CGCCG
                                |||||||||  |||| |||||
                                TCCTCTTCC CTTC GCGGT
                                      C   _
GAM263  PPT2    5'  GGGGAAGGGCGGGCTGC     39923         AGAA  C  C
                                GGGGAAGG   GG GC GC
                                ||||||||   || || ||
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                                CCCCTTCC   CC CG CG
                                    CG__  _  A
GAM263  SLC21A3  3'  GGGGAAGGGGGGAGGGATAGCA 39576        AGA_  CGCC
                                GGGGAAGG   AGG   GCA
                                ||||||||   |||   |||
                                CCCCTTCC   TCC   CGT
                                    CCCC  CTAT
GAM263  SNX15    3'  GGGGAGAGGAGAAGGGGC    43936      _       C
                                GGGGA AGGAGAAGG GC
                                ||||| ||||||||| ||
                                CCCCT TCCTCTTCC CG
                                   C       C
GAM263  SOLH     3'  AGGGGAAGGAGGGGGGCG    24821          AA_
                                AGGGGAAGGAG  GGCG
                                ||||||||||  ||||
                                TCCCCTTCCTC  CCGC
                                      CCC
GAM263  SUV39H2  5'  AGGCGAGGGGGCCGC      36009     G  A  AGAA  C
                                AGG GA GG   GG GCCGC
                                ||| || ||   || |||||
                                TCC CT CC   CC CGGCG
                                  G  _  ____  _
GAM263  TRIM14   3'  GGGGCAGGGAGAGGGCCC    31330      AA_    A   G
                                GGGG  GGAGA GGC CC
                                ||||  ||||| ||| ||
                                CCCC  CCTCT CCG GG
                                  GTC    C  _
GAM263  TULP3    3'  AGGGGAAGGGGAGGCCAC    17734         A  AG C
                                AGGGGAAGG GA  G GCCGC
                                ||||||||| ||  | |||||
                                TCCCCTTCC CT  C CGGTG
                                     C  __ _
GAM263  UBE2V1   3'  GGGGAAGGGGAAGGGCC     35350        A    C
                                GGGGAAGG GAAGG GCC
                                |||||||| ||||| |||
                                CCCCTTCC CTTCC CGG
                                     C    _
GAM263  YY1      5'  GGGGAAGGGGCGGGCGCC     18180        AGAA
                                GGGGAAGG   GGCGCC
                                ||||||||   ||||||
                                CCCCTTCC   CCGCGG
                                     CCGC
GAM263  ABP1     5'  GCTCCCAGTTCGCTCTGC     41790        CC   CG  C
                                GCTCCCGG  CGC  TC GT
                                ||||||||  |||  || ||
                                CGAGGGTC  GCG  AG CG
                                     AA   __  A
GAM263  ADAMTS8  5'  GCCCCGGCCCGCGTGCGCCCGT 28162    T        ___
             CC                   GC CCCGGCCCGC   CGTCCGTCC
                                || ||||||||||  |||||||||
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                                CG GGGCCGGGCG  GCGGGCAGG
                                 _       CAC
GAM263  AMMECR1  5' GCTCCCGGCCCCGTCTGCC  31699         GC   C
                                GCTCCCGGCCC  CGTC GTC
                                |||||||||||  |||| |||
                                CGAGGGCCGGG  GCAG CGG
                                      __   A
GAM263  APTX     5' GCTCCCAGGTTCCAGCCCTGTC 32809       CCCG _   _
           CC                    GCTCCCGG   CC GTCC GTCCC
                                |||||||    || |||| |||||
                                CGAGGGTC   GG CGGG CAGGG
                                    CAA_ T   A
GAM263  ARHGAP6  5' GCTCCCGGCGCCGCGAGAACTT 30218        _   CGTCCG_
           CC                    GCTCCCGGC CCGC     TCC
                                |||||||| ||||      |||
                                CGAGGGCCG GGCG     AGG
                                     C   CTCTTGA
GAM263  ASC      5' GCCCCGGTCCGTTGCCC    29942   T   C  CC
                                GC CCCGG CCG  GTCC
                                || ||||| |||  ||||
                                CG GGGCC GGC  CGGG
                                 _   A  AA
GAM263  ATP2C1   5' GCTCCCGGCCACGCGTCC   30786        _  C
                                GCTCCCGGCC CGC GTCC
                                |||||||||| ||| ||||
                                CGAGGGCCGG GCG CAGG
                                      T  _
GAM263  BMPR1B   5' GCTCCCGGCTCCCGCGTCC  10205        __  C
                                GCTCCCGGC  CCGC GTCC
                                |||||||||  |||| ||||
                                CGAGGGCCG  GGCG CAGG
                                     AG   _
GAM263  CAPN10   5' GCCTCCGGCCCGCCCCGCCCGT 35775   TC       __    _
           TCC                   GC  CCGGCCCGCC  GTCCGT CC
                                ||  ||||||||||  |||||| ||
                                CG  GGCCGGGCGG  CGGGCA GG
                                 GA        GG     A
GAM263  CAV2     5' GCTCCCGGTCCGCGCGGCC   10291       C   _ T
                                GCTCCCGG CCGC CG CC
                                |||||||| |||| || ||
                                CGAGGGCC GGCG GC GG
                                    A   C  C
GAM263  CAV2     5' GCTCCCAGCCCGGCCGTCC   10290         _
                                GCTCCCGGCCCG CCGTCC
                                |||||||||||| ||||||
                                CGAGGGTCGGGC GGCAGG
                                       C
GAM263  CHI3L1   3' GCTCCCGGCCAGCTGGAGCC  10475        C  CGTCC
                                GCTCCCGGCC GC    GTC
                                |||||||||| ||    |||
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```
                                CGAGGGCCGG CG    CGG
                                     T  ACCT_
GAM263  CHN2    5'  CCGTCCCGCTCCGCGCC    19811    G    CG    C
                                CCG CCCGC  TCCGT CC
                                ||| |||||  ||||| ||
                                GGC GGGCG  AGGCG GG
                                  A    __    C
GAM263  CHRNA4  5'  GCTCCCGGCTCCCCGCCGC   8851        _ G   T
                                GCTCCCGGC CC CCG CCGT
                                ||||||||| || ||| ||||
                                CGAGGGCCG GG GGC GGCG
                                     A  _  _
GAM263  CLCN1   5'  GCCTTGGCCTGCTTGCCCCTGT 6353     CCC   C  C_   __
           CC                     GCT   GGCC GC  GTCC  GTCC
                                |||   |||| ||  ||||  ||||
                                CGG   CCGG CG  CGGG  CAGG
                                  AA_   A  AA   GA
GAM263  COL11A2 5'  GCTCCCGGCACTGCTCC    38777        CC  C  CCG
                                GCTCCCGGC  GC GT   TCC
                                |||||||||  || ||   |||
                                CGAGGGCCG  TG CG   AGG
                                     __  A  ___
GAM263  CRHR1   5'  GCTCTCGCTCGCCCCTTCC   20445     C  G C   GT  G
                                GCTC CG C CGCC  CC TCC
                                |||| || | ||||  || |||
                                CGAG GC G GCGG  GG AGG
                                  A  _ A   __  A
GAM263  CSNK1D  5'  GCTCCCGGCTCCGCCCCC   40068        _    G
                                GCTCCCGGC CCGCC TCC
                                ||||||||| ||||| |||
                                CGAGGGCCG GGCGG GGG
                                     A    _
GAM263  DIA1    3'  GCTCCCGGCTGGCCAGGGCCC  28789        CC   TCC
                                GCTCCCGGC  GCCG   GTCC
                                |||||||||  ||||   ||||
                                CGAGGGCCG  CGGT   CGGG
                                     AC   CC_
GAM263  DNM2    5'  GCTCCCGCCCGCCCGGGCC   22385       G    GTC  TC
                                GCTCCCG CCCGCC   CG  CC
                                ||||||| ||||||   ||  ||
                                CGAGGGC GGGCGG   GC  GG
                                     _    ___  CC
GAM263  DUSP7   5'  CTCCCGGCCTCCGTCC     42271         CGCCG
                                CTCCCGGCC    TCCGTCC
                                |||||||||    |||||||
                                GAGGGCCGG    AGGCAGG
                                     _____
GAM263  DUX4    5'  CCTCCCCCCGTCCGTCC     43757    GG   G
                                CC  CCC CCGTCCGTCC
                                ||  ||| ||||||||||
```

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                                GG  GGG GGCAGGCAGG
                                 A_  G
GAM263  DXYS155E  3'  GCTGGCCCGCCTGGCCC    22958    CCC      __
                                GCT  GGCCCGCC  GTCC
                                |||  ||||||||  ||||
                                CGA  CCGGGCGG  CGGG
                                  ___      AC
GAM263  DXYS155E  3'  GCTCCCGGTTGCACTTGTCC  22957       CC_  C_
                                GCTCCCGG  CGC  GTCC
                                ||||||||  |||  ||||
                                CGAGGGCC  GTG  CAGG
                                    AAC  AA
GAM263  DXYS155E  3'  GCTCCCGGCTCCGCTCCC    22956       _   CG
                                GCTCCCGGC CCGC  TCC
                                ||||||||| ||||  |||
                                CGAGGGCCG GGCG  GGG
                                     A   A_
GAM263  EFNA3    5'  GCTCCCGGCTTCTCCGCTTCC  22402       ____   CG
                                GCTCCCGGC   CCGC  TCC
                                |||||||||   ||||  |||
                                CGAGGGCCG   GGCG  AGG
                                     AAGA   A_
GAM263  EGFL4    3'  CTTCCGGCCCGCACCAGTCCC  41569    C      CGT  _
                                CT CCGGCCCGC   CC GTCCC
                                || |||||||||   || |||||
                                GA GGCCGGGCG   GG CAGGG
                                 A       T__  T
GAM263  ENG      5'  GCTCCCGGCTCATCCAGCCC   6499        CCGC    T
                                GCTCCCGGC   CGTCCG CCC
                                |||||||||   |||||| |||
                                CGAGGGCCG   GTAGGT GGG
                                     A___    C
GAM263  EPB41    5'  TCTCGGTCGCCGCCCGTC    20770    C   CC
                                TC CGG  CGCCGTCCGTC
                                || |||  ||||||||||
                                AG GCC  GCGGCGGGCAG
                                 A  A_
GAM263  EPHA2    5'  GCTCCCGCCCGCCGGCC     20739      G     T
                                GCTCCCG CCCGCCG CC
                                ||||||| ||||||| ||
                                CGAGGGC GGGCGGC GG
                                   _     C
GAM263  EPOR     5'  GCTCCTGCCCCTCCGTCC    6520      CG   GCCG
                                GCTCC  GCCC   TCCGTCC
                                |||||  ||||   |||||||
                                CGAGG  CGGG   AGGCAGG
                                  A_   G___
GAM263  FGD1     3'  GCTCCCAGTTTGTCCCAAACCC 20906       CCCGCC   GT__
                                GCTCCCGG    GTCC   CCC
                                ||||||||    ||||   |||
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                                CGAGGGTC     CAGG   GGG
                                   AAA___   GTTT
GAM263  FGFR1   5' GCTCCCGTCCGCCACCC    31944       GC    GT
                                GCTCCCG  CCGCC  CC
                                |||||||  |||||  ||
                                CGAGGGC  GGCGG  GG
                                   A_    TG
GAM263  FGFR1   5' GCTCCGGCCCGCCGCCC    31945      C
                                GCTCC GGCCCGCCGTCC
                                ||||| ||||||||||||
                                CGAGG CCGGGCGGCGGG
                                  _
GAM263  FZD1    5' GCTTTCGGCCCGCTCCC    18615    CC       CG
                                GCT  CGGCCCGC  TCC
                                |||  ||||||||  |||
                                CGA  GCCGGGCG  GGG
                                  AA       A_
GAM263  GATA4   5' GCTCCCGGCTTCGGTGTCC   13112        C_  CC
                                GCTCCCGGC  CG  GTCC
                                |||||||||  ||  ||||
                                CGAGGGCCG  GC  CAGG
                                     AA  CA
GAM263  GRM4    3' GCCCCGGCCCCTCGTCC    9159    T      GC
                                GC CCCGGCCC  CGTCC
                                || ||||||||  |||||
                                CG GGGCCGGG  GCAGG
                                 _       GA
GAM263  HCN2    3' GCCCCTGGCCCGCCTGGGCCC 10167      C      GTCC
                                GCTCC GGCCCGCC   GTCC
                                |||||  ||||||||   ||||
                                CGGGG CCGGGCGG   CGGG
                                   A       ACC_
GAM263  HCN4    5' GCCCCGGCCCGTCCGGCCCGTC 24223    T       _  _
            CC                    GC CCCGGCCCG CCG TCCGTCCC
                                || |||||||| ||| ||||||||
                                CG GGGCCGGGC GGC GGGCAGGG
                                 _       A  C
GAM263  HNRPM   5' GCTCCCGGCTGCCTCC     25569        CC  G
                                GCTCCCGGC  GCC TCC
                                |||||||||  ||| |||
                                CGAGGGCCG  CGG AGG
                                     A_  _
GAM263  KCNK1   5' GCTCCCGCCCGCCGCCC    13894       G
                                GCTCCCG CCCGCCGTCC
                                ||||||| ||||||||||
                                CGAGGGC GGGCGGCGGG
                                  _
GAM263  KIFC3   5' GCTCCCAGGTTCCACGTCC   24461       C__   C
                                GCTCCCGG  CCGC GTCC
                                ||||||||  |||| ||||
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                                CGAGGGTC   GGTG CAGG
                                     CAA   _
GAM263  LRP2     5'  CCCCGGCCTCGCCGTTCC    21183        _     _
                                TCCCGGCC CGCCGT CC
                                |||||||| |||||| ||
                                GGGGCCGG GCGGCA GG
                                     A     A
GAM263  MAPK12   5'  GCTCCCGGCCCTTCCC      16470          GCCG
                                GCTCCCGGCCC    TCC
                                ||||||||||    |||
                                CGAGGGCCGGG    GGG
                                      AA__
GAM263  MAPK7    5'  GCTCGCCGGCCTCCCGTCC    40047      _     CG
                                GCTC CCGGCC  CCGTCC
                                |||| ||||||  ||||||
                                CGAG GGCCGG  GGCAGG
                                  C     AG
GAM263  MARK3    5'  GCTTCGGCCCGCCGGCGTCCC  14358     CC        TC
                                GCT  CGGCCCGCCG  CGTCCC
                                |||  ||||||||||  ||||||
                                CGA  GCCGGGCGGC  GCAGGG
                                  A_         C_
GAM263  MASP1    5'  GCTCCCGGCTGCCCGGCC    40102         CCGCC    T
                                GCTCCCGGC    GTCCG CC
                                |||||||||    ||||| ||
                                CGAGGGCCG    CGGGC GG
                                     A_____    C
GAM263  MPP6     5'  GCTCCCGGTCGCTCCC      32394         CC   CG
                                GCTCCCGG  CGC  TCC
                                ||||||||  |||  |||
                                CGAGGGCC  GCG  GGG
                                     A_   A_
GAM263  MSI1     3'  GCTCCTGCCACCGTCC      14644       CG   C
                                GCTCC  GCC GCCGTCC
                                |||||  ||| |||||||
                                CGAGG  CGG TGGCAGG
                                   A_   _
GAM263  NGFR     3'  TCCTTGGCCCGCCAAACCC    14792     C_       TCCGT
                                TCC  GGCCCGCCG    CCC
                                |||  |||||||||    |||
                                AGG  CCGGGCGGT    GGG
                                  AA        TT____
GAM263  ODC1     5'  GCTCCCGCCCGCCGGAGACGCC 14920         G      TC__
                                GCTCCCG CCCGCCG    CGTC
                                ||||||| |||||||    ||||
                                CGAGGGC GGGCGGC    GCGG
                                     _      CTCT
GAM263  PACSIN3  5'  GCTCCGGCCCGAGTCC      32143       C     CC
                                GCTCC GGCCCG  GTCC
                                ||||| ||||||  ||||
```

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                                CGAGG CCGGGC  CAGG
                                  _     T_
GAM263  PAX7    5'  GCTTCCCGTCCGCTCCC     30333     _   GC    CG
                                GCT CCCG  CCGC  TCC
                                ||| ||||  ||||  |||
                                CGA GGGC  GGCG  GGG
                                  A   A_   A_
GAM263  PIAS1   5'  GCCCCGGCCCGCCCCC      32077    T        G
                                GC CCCGGCCCGCC TCC
                                || ||||||||||| |||
                                CG GGGCCGGGCGG GGG
                                  _        _
GAM263  PRKCABP 3'  GCTCCCAGGCTCCGTCC     29671       _  CCG
                                GCTCCC GGC   CCGTCC
                                |||||| |||   ||||||
                                CGAGGG CCG   GGCAGG
                                   T   A__
GAM263  PRKCL1  5'  GCTCCGGCCTGCTCGGCTCCC  41702      C   C  _  TCCG
                                GCTCC GGCC GC CG    TCCC
                                ||||| |||| || ||    ||||
                                CGAGG CCGG CG GC    AGGG
                                  _    A  A  CG__
GAM263  PTGES   3'  GCTCCCGGTCCTCCACCC    22182        C  G  GT
                                GCTCCCGG CC CC  CC
                                |||||||| || ||  ||
                                CGAGGGCC GG GG  GG
                                     A  A  TG
GAM263  ROR1    5'  GCTCCCGGCCGCCTCGTCCC   22700         C   GTC
                                GCTCCCGGCC GCC   CGTCCC
                                |||||||||| |||   ||||||
                                CGAGGGCCGG CGG   GCAGGG
                                      _   A__
GAM263  RRM2    5'  GCTCCCGGCCCTTCCC      9759           GCCG
                                GCTCCCGGCCC    TCC
                                ||||||||||    |||
                                CGAGGGCCGGG    GGG
                                      AA__
GAM263  SART2   5'  GCTCCCAGCCGAGGCTTCGT   30037         C__  __
                                GCTCCCGGCC   GC  CGT
                                |||||||||   ||  |||
                                CGAGGGTCGG   CG  GCA
                                     CTC  AA
GAM263  SCRT1   3'  GCTCCTGCTCCGCCCCGGCC   36366      CG  _    GT   T
                                GCTCC  GC CCGCC  CCG CC
                                |||||  || |||||  ||| ||
                                CGAGG  CG GGCGG  GGC GG
                                  A_  A     __   C
GAM263  SERPINF2 3' GCTCCCGGCTCCCCGATGCC   9592          _  G   TCC
                                GCTCCCGGC CC CCG   GTC
                                |||||||| || |||   |||
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                                CGAGGGCCG GG GGC   CGG
                                     A  _   TA_
GAM263  SLC20A2  3'  GCTCCCGTCCCGCTGTCATCCC 27575       G    C   C
                                GCTCCCG CCCGC GTC GTCCC
                                ||||||| ||||| ||| |||||
                                CGAGGGC GGGCG CAG TAGGG
                                   A    A  _
GAM263  SNL      3'  GCTCCCAGCCCCCAACCGTCCC 16943          G   T
                                GCTCCCGGCCC CCG CCGTCCC
                                |||||||||||| ||| |||||||
                                CGAGGGTCGGG GGT GGCAGGG
                                      _  T
GAM263  SOD3     5'  CTCCCGACGTCTGTCC      16955         CCGCC   C
                                CTCCCGGC    GTC GTCC
                                ||||||||    ||| ||||
                                GAGGGCTG    CAG CAGG
                                     _____  A
GAM263  SURF4    5'  GCTCTCGCCCGTCGGCGCCC  37656     C  G    C  TC
                                GCTC CG CCCG CG  CGTCC
                                |||| || |||| ||  |||||
                                CGAG GC GGGC GC  GCGGG
                                  A  _    A  C_
GAM263  T        5'  GCTCTTGGCCGCCGCCC     17246     CC    C
                                GCTC  GGCC GCCGTCC
                                ||||  |||| |||||||
                                CGAG  CCGG CGGCGGG
                                  AA   _
GAM263  TCF4     5'  GCTCCTGCGCCCGCTCCC    17318      CG_    CG
                                GCTCC   GCCCGC  TCC
                                |||||   ||||||  |||
                                CGAGG   CGGGCG  GGG
                                   ACG     A_
GAM263  TNFRSF6B 5'  GCTCCCGGCGGAAACTGTTCC 32358         CC__  CG_
                                GCTCCCGGC   GC   TCC
                                |||||||||   ||   |||
                                CGAGGGCCG   TG   AGG
                                     CCTT  ACA
GAM263  ZIC1     3'  GCTTTCGGCCGCCCACC     18238     CC    CGCC    T
                                GCT  CGGCC   GTCCG CC
                                |||  |||||   ||||| ||
                                CGA  GCCGG   CGGGT GG
                                  AA    ____    _
GAM263  ZNF236   3'  GCTCCCGGCCATGCACCTCC   28862          ___   G
                                GCTCCCGGCC   CGCC TCC
                                ||||||||||   |||| |||
                                CGAGGGCCGG   GTGG AGG
                                     TAC   _
GAM264  BAP1     3'  GGCTGGACAGAGGCTCTTC   21646     ACC   CT   C
                                GGC   GCGG  GGGC CTTC
                                |||   ||||  |||| ||||
```

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                              CCG   TGTC  TCCG GAAG
                                ACC   __   A
GAM264  CACNA1A  3'  AGGGTTCGTGCAGGCCCTTC  35725    CACCG  _  T
                              AGG    CG GC GGGCCCTTC
                              |||    || || |||||||||
                              TCC    GC CG TCCGGGAAG
                                CAA__  A  _
GAM264  CD7      3'  GGCACGGCTGGGCCCTTC    26004    ACC
                              GGC   GCGGCTGGGCCCTTC
                              |||   ||||||||||||||
                              CCG   TGCCGACCCGGGAAG
                                ___
GAM264  CTBP1    3'  GGCACCGCCCAAGCTTTTC   42749       GG TG   CC
                              GGCACCGC  C  GGC  TTC
                              ||||||||  |  |||  |||
                              CCGTGGCG  G  TCG  AAG
                                   __ GT   AA
GAM264  EFEMP2   3'  GGCCCCTGGGCCTTT      32620    A  GCGG     C
                              GGC CC    CTGGGCC TT
                              ||| ||    ||||||| ||
                              CCG GG    GACCCGG AA
                                _ ____      A
GAM264  FRAT2    3'  TAAAGCACCAACAGGGCTCTTC 28974         CG  T   C
                              TAAGGCACCG  GC GGGC CTTC
                              ||||||||||  || |||| ||||
                              ATTTCGTGGT  TG CCCG GAAG
                                   __ T   A
GAM264  GABPA    5'  AGGTCCCAGGGCCCTT     13036    CA   CGGCT
                              AGG  CCG    GGGCCCTT
                              |||  |||    ||||||||
                              TCC  GGT    CCCGGGAA
                                AG  _____
GAM264  PCDHA9   3'  TAAGGTGTTCACAGCCCTT   36550      CAC_  GGCTG
                              TAAGG   CGC    GGCCCTT
                              |||||   |||    |||||||
                              ATTCC   GTG    TCGGGAA
                                 ACAA  _____
GAM264  RAD9     3'  TAAGACACTGCCTGGCAGCTCT 21375       C  __  TG  C
           TC                   TAAGGCAC GC  GGC  GGC CTTC
                              ||||||||  ||  |||  ||| ||||
                              ATTCTGTG CG  CCG  TCG GAAG
                                  A  GA  __  A
GAM264  SLC7A7   3'  GGAGCATTGTGGGCCCTT    19578    CACC   GC_
                              GG   GCG   TGGGCCCTT
                              ||   |||   |||||||||
                              CC   CGT   ACCCGGGAA
                               T___  AAC
GAM264  UBE2G2   3'  AAGGGTGCCGGGCCCT      42116     CACCGCG
                              AAGG     GCTGGGCCCT
                              ||||     ||||||||||
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                                TTCC      CGGCCCGGGA
                                  CA_____
GAM264  CAPZA1   3'  AGGCAGGACTGAGGAAGAGTAA 43709         CGC  C_
           TTT                    AGGCAGGGC   GG  GAGTAATTT
                                  |||||||||   ||  |||||||||
                                  TCCGTCCTG   CC  CTCATTAAA
                                      ACT  TT
GAM264  HLCS     5'  AGGCAGAGGTTGTGGTGAGC   7635         CCGC_  C
                                  AGGCAGGG    GG GAGT
                                  ||||||||    || ||||
                                  TCCGTCTC    CC CTCG
                                      CAACA  A
GAM264  NEDD4L   3'  AGGAAGGGTTAAGTAATT    31616    C   CCGCGGC
                                  AGG AGGG      GAGTAATT
                                  ||| ||||      ||||||||
                                  TCC TCCC      TTCATTAA
                                    T   AA_____
GAM264  SAS      3'  AGGCAGAGGTTGCGGTGAGC   25584         CC_   C
                                  AGGCAGGG   GCGG GAGT
                                  ||||||||   |||| ||||
                                  TCCGTCTC   CGCC CTCG
                                      CAA    A
GAM264  VBP1     3'  AGGCAGAGTTTTGAATGAGTAA 17925         CCGCGGC_
           TTT                    AGGCAGGG       GAGTAATTT
                                  ||||||||       |||||||||
                                  TCCGTCTC       CTCATTAAA
                                      AAAACTTA
GAM265  AK1      3'  GAGGTGGGGGTGAGGGGGACA  7876     A  A       CT  GT
                                  GAG TG GGGTGGGGGG  GG  G
                                  ||| || |||||||||  ||  |
                                  CTC AC CCCACTCCC  CC  T
                                    C  C        __  TG
GAM265  ALPI     3'  GAGGCAGGGTGGGGGGTTGGGTG 11577     ATG        C     III
           C                       GAG   AGGGTGGGGG TGGGTG   C
                                  |||   |||||||||| ||||||   |
                                  CTC   TCCCACCCCC ACCCAC   G
                                    CG_         A     III
GAM265  ALPL     5'  GAGGGGGTGGGCTGGCAGTG   7887       T  _      __
                                  GAGGG GG GGGCTGG  GTG
                                  ||||| || |||||||  |||
                                  CTCCC CC CCCGACC  CAC
                                     _ A      GT
GAM265  ARHGEF1  3'  TGGGGGGTGGGGGTGGAGGGGTG 21738    A       CT___
                                  TG GGGTGGGGGG     GGGTG
                                  || |||||||||     |||||
                                  AC CCCACCCCC     CCCAC
                                    C        ACCTC
GAM265  CACNA2D2 3'  GAGGTGGGAGTGGAGGTG    25714     A  A       C
                                  GAG TG GGGTGGGGGG TG
                                  ||| || ||||||||| ||
```

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                                CTC AC CTCACCTCC AC
                                  C  C       _
GAM265  CALR     3'  GAGGGGGTGGGGGGAGAGTG   41769     ATGA       CT
                                GAG   GGGTGGGGGG  GGGTG
                                |||   ||||||||||  |||||
                                CTC   CCCACCCCCC  CTCAC
                                  C___       T_
GAM265  CDKN1A   3'  GAGCTGGGGGGTGGGGGGTG    38507     A  A       C
                                GAG TG GGGTGGGGGG TG
                                ||| || |||||||||| ||
                                CTC AC CCCACCCCCC AC
                                  G  C       _
GAM265  COPE     3'  AGATGGGGGGTGCTGGGGGGTG   28574       A    GG  CT
                                AGATG GGGTG  GG  GGGTG
                                ||||| |||||  ||  |||||
                                TCTAC CCCAC  CC  CCCAC
                                   C    GA  __
GAM265  DES      3'  GAGGGGAGGACTGAGGCTGGGT 43565     AT    TG
              G                  GAG  GAGGG  GGGGCTGGGTG
                                |||  |||||  ||||||||||||
                                CTC  CTCCT  CTCCGACCCAC
                                  CC    GA
GAM265  DMPK     5'  TGGGGGGTTGGGGCTGGGT    20626    A   G
                                TG GGGT GGGGCTGGGT
                                || |||| ||||||||||
                                AC CCCA CCCCGACCCA
                                 C   A
GAM265  EFNA1    3'  CGAGGTGAAGGTGGGGATG    20698     A         C
                                CGAG TGAGGGTGGGGG TG
                                |||| |||||||||||| ||
                                GCTC ACTTCCACCCCT AC
                                  C          _
GAM265  EGR3     3'  GAGGTAGGGTGGGGAGAAGGTG 40546     ATG        CT
                                GAG   AGGGTGGGGG  GGGTG
                                |||   ||||||||||  |||||
                                CTC   TCCCACCCCT  TCCAC
                                  CA_        CT
GAM265  EMX2     5'  TGGGGTGGGGGGTGGGGGT    44704    A       CT_
                                TG GGGTGGGGG   GGGT
                                || |||||||||   ||||
                                AC CCCACCCCC   CCCA
                                  _        ACC
GAM265  EPB49    3'  GAGTATGGGAGGGCTGGGTG   12730     ATGAG  T
                                GAG    GG GGGGGCTGGGTG
                                |||    || ||||||||||||
                                CTC    CC CTCCCGACCCAC
                                  ATA__  _
GAM265  FASN     3'  TGGGGTGGGGTGGGGATG    19948    A       GCT
                                TG GGGTGGGG   GGGTG
                                || ||||||||   |||||
```

```
                                AC CCCACCCC   CCTAC
                                 _       ACC
GAM265  HEPH     5'  GAGGGAGGGGGAAGGGCTGGGT 39857     AT    T __
              G                   GAG  GAGGG GG  GGGCTGGGTG
                                  |||  ||||| ||  ||||||||||
                                  CTC  CTCCC CC  CCCGACCCAC
                                    C_    _ TT
GAM265  HOXC4    3'  GAGGGGAGGGTGGGGGGCATGGG 31152     AT         T__
              GTG                   GAG  GAGGGTGGGGGC   GGGTG
                                  |||  ||||||||||||   |||||
                                  CTC  CTCCCACCCCCG   CCCAC
                                    CC          TAC
GAM265  IGFBP5   3'  TGGGGGTGGGAGGGGGTG    8277     A       CT
                                  TG GGGTGGGGG  GGGTG
                                  || |||||||||  |||||
                                  AC CCCACCCTC  CCCAC
                                   C        C_
GAM265  JAM2     5'  TGGGGGTGGGGGGGATTGGGTG  34552    A       C__
                                  TG GGGTGGGGG   TGGGTG
                                  || |||||||||   ||||||
                                  AC CCCACCCCC   ACCCAC
                                   C        CTA
GAM265  KCNC3    3'  CGGGGGGTGGGGGGGCGGTG    22500    A       CTG
                                  TG GGGTGGGGG   GGTG
                                  || |||||||||   ||||
                                  GC CCCACCCCC   CCAC
                                   C        CG_
GAM265  KCNE1L   3'  GGGGTAGGGGGTGGAAGGGT    29375   A       CT__
                                  G GGGTGGGGG    GGGT
                                  | |||||||||    ||||
                                  C CCCATCCCC    TCCA
                                   _       ACCT
GAM265  KRT5     3'  GATTGGGGTGGGGATTCTG    7688      GA       __
                                  GAT  GGGTGGGGG  CTG
                                  |||  |||||||||  |||
                                  CTA  CCCACCCCT  GAC
                                    AC        AA
GAM265  MAP3K7IP1 3'  CGAGGTGAGGGAGGTGATGGTG 25925     A     T   GGCTG
                                  CGAG TGAGGG GGG     GGTG
                                  |||| |||||| |||     ||||
                                  GCTC ACTCCC TCC     CCAC
                                    C     _   ACTA_
GAM265  MEOX1    3'  GATTGGGGTGGGGGGTAG     30397     GA       C
                                  GAT  GGGTGGGGG TGG
                                  |||  ||||||||| |||
                                  CTA  CCCACCCCC ATC
                                    AC        _
GAM265  PER2     3'  GATGTGGGCTTGGCTGGGTG   35617      A   GGG
                                  GATG GGGT   GGCTGGGTG
                                  |||| ||||   |||||||||
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                                CTAC CCCG   CCGACCCAC
                                  A   AA_
GAM265  PRKACA   3'  TGGGATGGGGGGTGTGGGT    15589    A       C_
                                TG GGGTGGGGGG  TGGGT
                                || |||||||||  |||||
                                AC CCTACCCCC  ACCCA
                                  _       AC
GAM265  PTPN7    3'  GAGATGGGGTTGGGGGGACAGT 38712       A   _    CTG
          G                      GAGATG GGGT GGGGG   GGTG
                                |||||| |||| |||||   ||||
                                CTCTAC CCCA CCCCC   TCAC
                                   _   A    CTG
GAM265  RABL2B   3'  GAGGGGGTGGGGAAGGTG    28203     ATGA       CT
                                GAG   GGGTGGGGGG  GGGTG
                                |||   |||||||||  |||||
                                CTC   CCCACCCCT  TCCAC
                                  C___       __
GAM265  RANBP3   3'  TGGGGTGGGGGGCGGGTG     28774    A       T
                                TG GGGTGGGGGC GGGTG
                                || ||||||||| |||||
                                AC CCCACCCCCG CCCAC
                                  _       _
GAM265  REST     5'  GAGGGTGGTAAAGTTGGGTG   24709        __  C
                                GAGGGTGG  GGG TGGGTG
                                ||||||||  ||| ||||||
                                CTCCCACC  TTC ACCCAC
                                     AT   A
GAM265  RYR1     3'  GAGGTGGGGGTGGAGGGCCAG  8068      A  A    _   TG
                                GAG TG GGGTGG GGGC  G
                                ||| || |||||| ||||  |
                                CTC AC CCCACC CCCG  C
                                  C  C     T    GT
GAM265  S100A1   3'  TGGGGGTGGGGGGTGGGGT    26565    A       CT
                                TG GGGTGGGGGG  GGGT
                                || |||||||||  ||||
                                AC CCCACCCCC  CCCA
                                  C        AC
GAM265  SOX13    3'  AGGTGAGGGGCAGGGCTGGGTG 25009    A     TG
                                AG TGAGGG  GGGGCTGGGTG
                                || ||||||  ||||||||||
                                TC ACTCCC  TCCCGACCCAC
                                  C     CG
GAM265  SPTBN4   3'  TGGGGTGGGGGGTGGTGAGT   36093    A       C__
                                TG GGGTGGGGGG   TGGGT
                                || |||||||||   |||||
                                AC CCCACCCCC   ACTCA
                                  _       ACC
GAM265  TCF3     3'  TGGGGTGGGGGTGGGGGGT    43334    A       GCT_
                                TG GGGTGGGG    GGGT
                                || ||||||||    ||||
```

```
                                AC CCCACCCC   CCCA
                                 _      ACCC
GAM265  TJP1    5'  AGGTGAGGGTGGGGAGGACCTG 17533    A        ____
                                AG TGAGGGTGGGGG   CTG
                                || ||||||||||||   |||
                                TC ACTCCCACCCCT   GAC
                                 C         CCTG
GAM265  TLR9    3'  GAGGTGAGTGTGGAGGTG    32660    A   G     C
                                GAG TGAG GTGGGGG TG
                                ||| |||| ||||||| ||
                                CTC ACTC CACCTCC AC
                                  C   A     _
GAM265  TNC     5'  TGGAGGTGGGTTTGGCTGGGTG 13473    AG    ___
                                TG  GGTGGG   GGCTGGGTG
                                ||  ||||||   |||||||||
                                AC  CCACCC   CCGACCCAC
                                 CT     AAA
GAM265  TNNI3   3'  GGGGTGGGGGTGGCGGGTA   7474    A      C__
                                G GGGTGGGGG   TGGGTG
                                | |||||||||   ||||||
                                C CCCACCCCC   GCCCAT
                                 _       ACC
GAM265  TRAF1   3'  AGGATGTGGGGGCTGGGT    24941    __
                                AGG  GTGGGGGCTGGGT
                                |||  ||||||||||||
                                TCC  CACCCCCGACCCA
                                  TA
GAM265  TRIM14  3'  TGAGGGTGCGGAGGTCTG    31331       _ _ _
                                TGAGGGTG GG GG CTG
                                |||||||| || || |||
                                ACTCCCAC CC CC GAC
                                     G  T  A
GAM265  TRIM14  3'  CCAGATGAGATCTGGCTGGGTG 37698   G      GTGGG
                                C AGATGAGG    GGCTGGGTG
                                | ||||||||    |||||||||
                                G TCTACTCT    CCGACCCAC
                                 G       AGA__
GAM265  UNC13   3'  GATGAGGAGTGGAGAGGTG   26864       _    GCT
                                GATGAGG GTGGGG   GGGTG
                                ||||||| ||||||   |||||
                                CTACTCC CACCTC   TCCAC
                                     T    ___
GAM265  VARS2   3'  TGAGGGGTGAAGCTGGGTG   26663      TG
                                TGAGGG  GGGGCTGGGTG
                                ||||||  ||||||||||||
                                ACTCCC  CTTCGACCCAC
                                   CA
GAM265  YWHAH   3'  GATGATGGGGGTGGTGGGTG  18194     G  T  _  C
                                GATGA GG GGG GG TGGGTG
                                ||||| || ||| || ||||||
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                                CTACT CC CCC CC ACCCAC
                                  A _  A _
GAM265  ABR     3'  TGAGCTCCCCAGCC      35017        GCCCAC
                                TGAGCTCC    CCAGCC
                                ||||||||    ||||||
                                ACTCGAGG    GGTCGG
                                        _______
GAM265  AGRN    3'  AGTGAGCTCCTCTCGATAGCCC 44246         GCCCACCC
            C                    AGTGAGCTCC      AGCCCC
                                ||||||||||      ||||||
                                TCACTCGAGG      TCGGGG
                                     AGAGCTA_
GAM265  AMT     3'  AGTGAGTTCTGCCTCAGC    7905       C  C   CACC
                                AGTGAG TC GCC   CAGC
                                |||||| || |||   ||||
                                TCACTC AG CGG   GTCG
                                   A  A  A___
GAM265  ANXA9   5'  AGTGAACTCCACTCAGCC    18689          CCACC
                                AGTGAGCTCCGC    CAGCC
                                ||||||||||||    |||||
                                TCACTTGAGGTG    GTCGG
                                      A____
GAM265  AP1B1   3'  GCGCACCCGCTTACCCAGCCCC 10037    A  T   CC
                                GTG GC CCGC  ACCCAGCCCC
                                ||| || ||||  ||||||||||
                                CGC TG GGCG  TGGGTCGGGG
                                  G  _   AA
GAM265  ARHGEF7 3'  GTGGCGCCCCACCCAGCCC   19366    A  T  GC
                                GTG GC CC  CCACCCAGCCC
                                ||| || ||  ||||||||||||
                                CAC CG GG  GGTGGGTCGGG
                                  _  C  __
GAM265  AVPR2   3'  AGTGGCTCCCAGGACCAGCCCC 6284      A    GCCCAC
                                AGTG GCTCC     CCAGCCCC
                                |||| |||||     ||||||||
                                TCAC CGAGG     GGTCGGGG
                                  _    GTCCT_
GAM265  BAZ2A   5'  GCTGGGACCACCCAGCTCC   30309    CCGC       _
                                GCT   CCACCCAGC CC
                                |||   ||||||||| ||
                                CGA   GGTGGGTCG GG
                                  CCCT       A
GAM265  CLASP1  3'  AGGGAGTCAGCCCGCCCAGCCC 42233   T  C  C   A
            C                    AG GAG TC GCCC CCCAGCCCC
                                || ||| || |||| |||||||||
                                TC CTC AG CGGG GGGTCGGGG
                                 C  _ T   C
GAM265  CRLF1   5'  TGGCCCCGCCCGGCCC     21903    A       ACCCA
                                TG GCTCCGCCC    GCCC
                                || |||||||||    ||||
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                                AC CGGGGCGGG    CGGG
                                 _       C____
GAM265  EFNB1   3'  AGCGGGCTGGCCCAGCCC   20706     A  CCGCCCA
                                AGTG GCT      CCCAGCCC
                                |||| |||      ||||||||
                                TCGC CGA      GGGTCGGG
                                  C  CC_____
GAM265  EGR3    3'  ATGGGCTCCGCCTTCAGTCCC  40541     A      CACC  _
                                GTG GCTCCGCC   CAG CCC
                                ||| ||||||||   ||| |||
                                TAC CGAGGCGG   GTC GGG
                                  C       AA__  A
GAM265  EVX1    5'  AGTGAGTTCCTAACCCCGGCTC 12767       C  GCCCA  A  _
           C                     AGTGAG TCC    CCC GC CC
                                ||||||| |||    ||| || ||
                                TCACTC AGG    GGG CG GG
                                   A  ATTG_  C  A
GAM265  FMOD    3'  AGTGAGCTTCTGCCTATGTCC  12927        _ C  CACCCAG
                                AGTGAGCT C GCC      CC
                                |||||||| | |||      ||
                                TCACTCGA G CGG      GG
                                    A A  ATACA__
GAM265  FTSJ2   3'  ATGAGTGGCCTCACCCAGCCCC 30166      CTCC  _
                                GTGAG   GCC CACCCAGCCCC
                                |||||   ||| ||||||||||
                                TACTC   CGG GTGGGTCGGGG
                                  AC__  A
GAM265  FUS1    3'  AGGGAGAAGCCCCCACCCAGTC 28582    T  CT_ G      _
           CC                     AG GAG  CC CCCACCCAG CCC
                                || |||  || ||||||||| |||
                                TC CTC  GG GGGTGGGTC GGG
                                 C  TTC  _       A
GAM265  GBF1    3'  GTGGGCAGTCCCCCACCCAGCC 20080    A  __  G
           CC                     GTG GC  TCC CCCACCCAGCCCC
                                ||| ||  ||| ||||||||||||
                                CAC CG  AGG GGGTGGGTCGGGG
                                  C  TC  _
GAM265  GGCX    3'  GTGAGCCACGGCACCCAGCCCC 9060       TC  CC
                                GTGAGC  CG  CACCCAGCCCC
                                ||||||  ||  ||||||||||
                                CACTCG  GC  GTGGGTCGGGG
                                   GT  C_
GAM265  GUCY2F  3'  AGTGAGCTTTCCCATTGCC   11341       CCG   CCCA
                                AGTGAGCT   CCCA   GCC
                                ||||||||   ||||   |||
                                TCACTCGA   GGGT   CGG
                                    AA_    AA__
GAM265  HLA-DMB 5'  AGTGATGTGGGGATACCCAGCC 13380     GCTCCGCCC
           CC                     AGTGA       ACCCAGCCCC
                                |||||       ||||||||||
```

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                                TCACT       TGGGTCGGGG
                                  ACACCCCTA
GAM265  HLA-G    3'  GTGAGCTCCCCCATGGCTCC   13402        G   CCCA _
                                GTGAGCTCC CCCA   GC CC
                                ||||||||| ||||   || ||
                                CACTCGAGG GGGT   CG GG
                                      _   AC__  A
GAM265  HR       5'  GTGAGCTCCGACACCGGCTCC  32932        CC   CA _
                                GTGAGCTCCG  CACC  GC CC
                                ||||||||||  ||||  || ||
                                CACTCGAGGC  GTGG  CG GG
                                      T_   C_  A
GAM265  IL15     5'  GAGGGTGCGGCCACCCAGTTCC 8225     CTC_ C      CC
                                GAG   CG CCACCCAG  CC
                                |||   || ||||||||  ||
                                CTC   GC GGTGGGTC  GG
                                  CCAC  C       AA
GAM265  IMPDH1   5'  TGGGCTCCGCCTGGGCTCC   9416    A      CACCCA _
                                TG GCTCCGCC     GC CC
                                || ||||||||     || ||
                                AC CGAGGCGG     CG GG
                                 C       ACC___  A
GAM265  KCNF1    3'  AGGAGTCTTACCCAGCC     13825    T   C  CGCCC
                                AG GAG TC    ACCCAGCC
                                || ||| ||    ||||||||
                                TC CTC AG    TGGGTCGG
                                 _  _  AA___
GAM265  MAPRE3   3'  GTGAGTCCTACCCCAGCCCC   29539      C   GCCCA
                                GTGAG TCC    CCCAGCCCC
                                ||||| |||    |||||||||
                                CACTC AGG    GGGTCGGGG
                                   _  ATG__
GAM265  NDUFS6   3'  AGCGAGCTTCACGTGCTCAGC  21243        C   CCACC
                                AGTGAGCT CGC    CAGC
                                |||||||| |||    ||||
                                TCGCTCGA GTG    GTCG
                                     A   CACGA
GAM265  PDE4A    3'  GCTCTGCCCAGCCCC      26259     C    CCCA
                                GCTC GCCCA   GCCCC
                                |||| |||||   |||||
                                CGAG CGGGT   CGGGG
                                  A    _____
GAM265  POLK     3'  AGTGATCTGCCCATTCGGCC  32134     GC  C    CCCA
                                AGTGA  TC GCCCA   GCC
                                |||||  || |||||   |||
                                TCACT  AG CGGGT   CGG
                                   __  A    AAGC
GAM265  PPP5C    3'  GTGAGCCCCAGCCTAGCCCC  26492        _  CACCC
                                GTGAGCTCC GCC    AGCCCC
                                ||||||||| |||    ||||||
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                                CACTCGGGG CGG    TCGGGG
                                     T  A____
GAM265  PRSS8   5'  TGGGCTCCGCCAGCTCC    15762   A     CACCC  _
                                TG GCTCCGCC    AGC CC
                                || ||||||||    ||| ||
                                AC CGAGGCGG    TCG GG
                                 C      _____  A
GAM265  SCA1    3'  AATGAGCCCACCCAGC     7271      GCTCC
                                AGTGA    GCCCACCCAGC
                                |||||    ||||||||||
                                TTACT    CGGGTGGGTCG
                                     _____
GAM265  SCNN1B  3'  AGTGAGTTTCACCCACCC   7333      CTC
                                AGTGAG   CGCCCACCC
                                ||||||   |||||||||
                                TCACTC   GTGGGTGGG
                                   AAA
GAM265  SHANK2  3'  GCTGTGCCCGCCCAGCTCC  29458    CC   A    _
                                GCT  GCCC CCCAGC CC
                                |||  |||| |||||| ||
                                CGA  CGGG GGGTCG GG
                                  CA   C     A
GAM265  SHOX    5'  GCGACCTCGCCCAGCCC    27820     G  C    CCCA
                                GTGA CTC GCCCA   GCCC
                                |||| ||| |||||   ||||
                                CGCT GAG CGGGT   CGGG
                                  G  _   ____
GAM265  SIAH2   5'  TGGCTCCGCCCGGCTCC    22869    A      ACCCA _
                                TG GCTCCGCCC    GC CC
                                || |||||||||    || ||
                                AC CGAGGCGGG    CG GG
                                 _      C____  A
GAM265  SLC2A8  3'  AGTGAGCCTCCTAGCC     31027       CCGCCCA  C
                                AGTGAGCT     CC AGCC
                                ||||||||     || ||||
                                TCACTCGG     GG TCGG
                                   A______  A
GAM265  SYNGR2  3'  GTGGCTCTGCCAGCCC     21744    A   C  CACCC
                                GTG GCTC GCC    AGCCC
                                ||| |||| |||    |||||
                                CAC CGAG CGG    TCGGG
                                  _   A  _____
GAM265  TBX1    5'  GTGCGCTCCGCCGCC      25626    A     CACCCA
                                GTG GCTCCGCC     GCC
                                ||| ||||||||     |||
                                CAC CGAGGCGG     CGG
                                  G      _______
GAM265  TGM3    3'  GTGAGCTCTCCCTGCTCC   17505       CG  ACCCA _
                                GTGAGCTC  CCC    GC CC
                                ||||||||  |||    || ||
```

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                                CACTCGAG  GGG    CG GG
                                    A_  A____  A
GAM265  TRPV3   3'  GTGACTCCGCCTGCAGCGCC  45443     G     CACC  _
                                GTGA CTCCGCC   CAGC CC
                                |||| |||||||   |||| ||
                                CACT GAGGCGG   GTCG GG
                                  _     AC__   C
GAM265  UBE2G2  3'  GTGAGCCACAGCACCCAGCC  42126      TC  CC
                                GTGAGC  CG  CACCCAGCC
                                ||||||  ||  |||||||||
                                CACTCG  GT  GTGGGTCGG
                                   GT  C_
GAM265  WHSC1   3'  AGTGCAGCTTCTTCCCAGCCC  39352     _   CCGCCCA
                                AGTG AGCT      CCCAGCCC
                                |||| ||||      ||||||||
                                TCAC TCGA      GGGTCGGG
                                  G   AGAA___
GAM265  WHSC1   3'  TGAGCTCCGAGCAGCTTAGCTC 39386        CC  CCC_  _
            C                    TGAGCTCCG  CA   AGC CC
                                |||||||||  ||   ||| ||
                                ACTCGAGGC  GT   TCG GG
                                     TC  CGAA   A
GAM265  YWHAZ   3'  AGTGAGCTTTGGGTATAACTTA 18199        CCGCCC___  CC
            GCCCC                AGTGAGCT       AC  AGCCCC
                                |||||||       ||  ||||||
                                TCACTCGA       TG  TCGGGG
                                     AACCCATAT  AA
GAM266  ARHGDIA  3'  CCGTCGTCCGTCCGTCAG   20200    C  C  A   CC
                                CCG CG CC TCCG  TAG
                                ||| || || ||||  |||
                                GGC GC GG AGGC  GTC
                                  A  A  C   A_
GAM266  CDKN2A   5'  CCGCCGCCCGCTGCCTGC   38470        ATCC   A
                                CCGCCGCCC   GCCT GC
                                |||||||||   |||| ||
                                GGCGGCGGG   CGGA CG
                                     CGA_   _
GAM266  CEBPD    5'  CCGCCGCCTTTTCTAGCCCCGG 45515       CA_  C_   AG
            CT                   CCGCCGCC   TC  GCCT  CGGCT
                                |||||||   ||  ||||  |||||
                                GGCGGCGG   AG  CGGG  GCCGA
                                     AAA  AT   __
GAM266  CLCN7    3'  GCCGCCTGCCCGCCCAGC    10518      CA
                                GCCGCC  TCCGCCTAGC
                                ||||||  ||||||||||
                                CGGCGG  GGGCGGGTCG
                                   AC
GAM266  COL4A4   5'  CCGCTGCCTCTTCGCGGC    6397     C   CA  CGCCTA
                                CCGC GCC  TC     GCGGC
                                |||| |||  ||     |||||
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                                GGCG CGG  AG     CGCCG
                                  A   __  AAG___
GAM266  FBN1     5'  CCGCCGCCCGTCCCCCGGGCCG 42051         A   G  TA  __
              GGCT                    CCGCCGCCC TCC CC  GC  GGCT
                                |||||||| ||| ||  ||  ||||
                                GGCGGCGGG AGG GG  CG  CCGA
                                    C   G  CC  GC
GAM266  FOXD2    5'  CCCTCCCGCCTAGCGGCT    20958     AT
                                CCC  CCGCCTAGCGGCT
                                |||  ||||||||||||
                                GGG  GGCGGATCGCCGA
                                  AG
GAM266  FUS1     5'  CCGCCGCCTTCCGCAGGC    28584        CA    CTAGC
                                CCGCCGCC  TCCGC    GGC
                                ||||||||  |||||    |||
                                GGCGGCGG  AGGCG    CCG
                                    A_    T____
GAM266  HIP12    5'  CCGCCGCCCGCTTTTGTCCGGC 42397         ATCCGCCTAG
              T                  CCGCCGCCC        CGGCT
                                |||||||||        |||||
                                GGCGGCGGG        GCCGA
                                    CGAAAACAG_
GAM266  HRB      5'  CCGCCGCCCTCCGTCTGC    21084         A   C  A
                                CCGCCGCCC TCCG CT GC
                                ||||||||| |||| || ||
                                GGCGGCGGG AGGC GA CG
                                    _   A  _
GAM266  IVD      5'  CGCCGCCCACCAAACCGGCT   13695          C_   TAGC
                                CGCCGCCCATC  GCC   GGCT
                                ||||||||||  |||   ||||
                                GCGGCGGGTGG  TGG   CCGA
                                    TT  ____
GAM266  LRP8     5'  GCCGCCCGCCCCGG       37795        ATCC   AG
                                GCCGCCC   GCCT  CGG
                                |||||||   ||||  |||
                                CGGCGGG   CGGG  GCC
                                    ____   __
GAM266  MAP3K1   5'  CCGCCGCCAGTCCGCCCGC   42702        CA     A
                                CCGCCGCC  TCCGCCT GC
                                ||||||||  ||||||| ||
                                GGCGGCGG  AGGCGGG CG
                                    TC     _
GAM266  PHLDA1   5'  CGCCGCCCACTTGCTTCCGCGC 28874          CC  CTA_   G
              T                  CGCCGCCCAT  GC   GCG CT
                                ||||||||||  ||   ||| ||
                                GCGGCGGGTG  CG   CGC GA
                                    AA  AAGG  _
GAM266  PRX      3'  CCTTGCCCATTTTAGCGGCT  34113    GCC    CCGCC
                                CC   GCCCAT    TAGCGGCT
                                ||   ||||||    ||||||||
```

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                                GG  CGGGTA   ATCGCCGA
                                 AA_    AA___
GAM266  PTPRA   5'  CCGCCGCCCGGCCCGCGGC  38908       ATCC   A
                                CCGCCGCCC   GCCT GCGGC
                                |||||||||   |||| |||||
                                GGCGGCGGG   CGGG CGCCG
                                    C___   _
GAM266  RB1CC1  5'  CCGCCGCCTAGTCCTCGGCAGC 31310       CA_  GCC_
          GG                  CCGCCGCC  TCC   TAGCGG
                              ||||||||  |||   ||||||
                              GGCGGCGG  AGG   GTCGCC
                                  ATC  AGCC
GAM266  SH3BP4  5'  CCGCTCGTCGGCCAGCGGCT  30959    _ CCCA  C   T
                              CCGC CG   TC GCC AGCGGCT
                              |||| ||   || ||| |||||||
                              GGCG GC   AG CGG TCGCCGA
                                A  ____  C  _
GAM266  SLC25A15 5'  CCGCCGCCCGCTCTCGGC   30666       ATCC  C AG
                              CCGCCGCCC   GC T  CGGC
                              |||||||||   || |  ||||
                              GGCGGCGGG   CG A  GCCG
                                   ____  _ GA
GAM266  SUPT6H  3'  CACCCATCCGGGTTAGCCGCTA 41286       _________  TAGC
          GG                  CGCCCATCC       GCC   GG
                              |||||||||       |||   ||
                              GTGGGTAGG       CGG   CC
                                   CCCAAIIIT  CGAT
GAM266  TIAL1   3'  GCCACCCATTTGCCATATACT  35296       CC   TAGCG
                              GCCGCCCAT  GCC    GCT
                              |||||||||  |||    |||
                              CGGTGGGTA  CGG    TGA
                                   AA   TATA_
GAM266  TIMP3   5'  CCGCCGCCTGCCTGCTGCC   7446       CATCC   A  G
                              CCGCCGCC    GCCT GC GCT
                              ||||||||    |||| || |||
                              GGCGGCGG    CGGA CG CGG
                                  A____   _  A
GAM266  TIMP3   5'  GCTGCCCGCTCTGCGCCGCT  7460    C   A_  C  CTA  G
                              GC GCCC  TC GC   GC GCT
                              || ||||  || ||   || |||
                              CG CGGG  AG CG   CG CGA
                               A   CG  A  ___  G
GAM266  TPD52L2 3'  GCTCATCCGCCCTGGCT    17637    C       AGC
                              GC CATCCGCCT   GGCT
                              || |||||||||   ||||
                              CG GTAGGCGGG   CCGA
                               A       A__
GAM266  ADCY3   5'  GGGGCGGAGGGGAGGCCA    19719    AA
                              GGG  GGAGGGGAGGCTA
                              |||  ||||||||||||
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                                CCC  CCTCCCCTCCGGT
                                  CG
GAM266  ANKH     5'  GGGAGGCGAGGGGCGACGGGGG 38323      AG_     A   TAGAA
              C                   GGGA   GAGGGG GGC     GC
                                  ||||   |||||| |||     ||
                                  CCCT   CTCCCC CTG     CG
                                    CCG     G   CCCC_
GAM266  ARD1     3'  GGTGAGGAGGGGATGGGGC   18574    GA       ___
                                  GG  AGGAGGGGA   GGC
                                  ||  |||||||||   |||
                                  CC  TCCTCCCCT   CCG
                                   AC        ACC
GAM266  ARHGDIA  3'  AGGAGGGGGGGTCGGAGGC    20197        A  CTA  A
                                  AGGAGGGG GG   GA GC
                                  |||||||| ||   || ||
                                  TCCTCCCC CC   CT CG
                                       _  AGC  C
GAM266  ARIH1    5'  AGGAGGGAGGGAGGGAGC    25084      A     GA  CTAGA
                                  GGGA GGAGGG  GG    AGC
                                  |||| ||||||  ||     |||
                                  TCCT CCTCCC  CC     TCG
                                    C     TC  _____
GAM266  ASNS     5'  GGGAGGAGGAGGGTGAGC    11717      __      GA
                                  GGGA  AGGAGGG  GGC
                                  ||||  |||||||  |||
                                  CCCT  TCCTCCC  TCG
                                    CC      AC
GAM266  BACE     5'  GAGAGGGAGCTTGGGGGC    39960      A   ___   A
                                  GGGA GGAG   GGG GGC
                                  |||| ||||   ||| |||
                                  CTCT CCTC   CCC CCG
                                    C   GAA  _
GAM266  BACE2    5'  GGGAGGCGGGCGCGGAGGC    39992      A  A  _____
                                  GGGA GG GGG    GAGGC
                                  |||| || |||    |||||
                                  CCCT CC CCC    CTCCG
                                    _  G   GCGC
GAM266  BAT2     3'  GGGAAGGGGGAGGAGGGGAAG  38785        A  _    CTA
                                  GGGAAGG GG GGAGG   GAAG
                                  ||||||| || |||||   ||||
                                  CCCTTCC CC CCTCC   CTTC
                                      C  T    C__
GAM266  BTEB1    5'  GGGAGGCAGGGAAGGGGC    10218      A  _       CTAGAA
                                  GGGA GG AGGGGAGG     GC
                                  |||| || ||||||||     ||
                                  CCCT CC TCCCTTCC     CG
                                    _  G       C_____
GAM266  CADPS    5'  GGGAGGAGGGGAAGGGAGA   42195      A        CT
                                  GGGA GGAGGGGAGG  AGA
                                  |||| ||||||||||  |||
```

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                                CCCT CCTCCCCTTC  TCT
                                  _        CC
GAM266  CAPON    5'  GGGAGGAGGTGGCGGCGGGAGC 41926      A    _ A   TA  A
                                GGGA GGAGG GG GGC  GA GC
                                |||| ||||| || |||  || ||
                                CCCT CCTCC CC CCG  CT CG
                                  _    A  G   CC  _
GAM266  CEBPA    3'  GGAAGGGAGGGGACACGCGGAG 20396      A       G  TAGA
          CA                      GGGA GGAGGGGA GC    AGCA
                                |||| |||||||| ||    ||||
                                CCTT CCTCCCCT TG    TCGT
                                  C       G  CGCC
GAM266  CHST1    3'  GGGAGTGGGGTGAGCTGGGGGC 18912      A GA   GA    AGAA
          A                      GGGA G  GGG  GGCT    GCA
                                |||| |  |||  ||||    |||
                                CCCT C  CCC  TCGA    CGT
                                  _ AC   AC    CCCC
GAM266  COL9A2   3'  GGGAGGCAGGGAAGGAAG    12340      A _       CT
                                GGGA GG AGGGGAGG  AG
                                |||| || ||||||||  ||
                                CCCT CC TCCCTTCC  TC
                                  _ G       T_
GAM266  CRABP2   3'  GGGACGGAGGGGGGCAGTGAAGC 12429      A      AG  TA_
          A                      GGGA GGAGGGG  GC   GAAGCA
                                |||| |||||||  ||   ||||||
                                CCCT CCTCCCC  CG   CTTCGT
                                  G       __  TCA
GAM266  CRY1     5'  GGAACGGAGGCTAGAGGC     19834      G        A
                                GGAG GGAGGCTAGA GC
                                |||| |||||||||| ||
                                CCTT CCTCCGATCT CG
                                  G         C
GAM266  CRY2     3'  GGGAAGGAGGTCTAGGGAGGC  43584          _____
                                GGGAAGGAGG     GGAGGC
                                ||||||||||     ||||||
                                CCCTTCCTCC     CCTCCG
                                      AGATC
GAM266  CSK      5'  GGGAGGAGGGACCGCCAGGCA  20466      A      AG     AA
                                GGGA GGAGGGG  GCTAG  GCA
                                |||| |||||||  |||||  |||
                                CCCT CCTCCCT  CGGTC  CGT
                                  _       GG    __
GAM266  DBN1     3'  GGGAAGGAGGGGTGGAATTTGC 38939           A  CTAGAA
          A                      GGGAAGGAGGGG GG      GCA
                                ||||||||||| ||      |||
                                CCCTTCCTCCCC CC      CGT
                                      A  TTAAA_
GAM266  DDX20    5'  GGGAGGCGGGGATCTTGGGAGC 28507      A  A    GG  AGA_
                                GGGA GG GGGGA  CT    AGC
                                |||| || |||||  ||    |||
```

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                                CCCT CC CCCCT  GA    TCG
                                  _ G     A_  ACCC
GAM266  DNMT1    5'  GGGAGGAGGGGATGTACCA   10716     A       G__
                                GGG AGGAGGGGA   GCTA
                                ||| |||||||||   ||||
                                CCC TCCTCCCCT   TGGT
                                  _       ACA
GAM266  DUSP4    5'  GGGAGGGAGGCGGCGAAGGC   38422     A    _____
                                GGGA GGAGG    GGAGGC
                                |||| |||||    ||||||
                                CCCT CCTCC    CTTCCG
                                  C     GCCG
GAM266  EGLN2    5'  GGGAGCAGGGGACAGGGC    38830     A G     ___
                                GGGA G AGGGGA   GGC
                                |||| | ||||||   |||
                                CCCT C TCCCCT   CCG
                                  _ G     GTC
GAM266  EGR3     3'  GGGAAGGAGTGGGAGGGC    40554         _     CTAGAA
                                GGGAAGGAG GGGAGG     GC
                                |||||||||| ||||||     ||
                                CCCTTCCTC CCCTCC     CG
                                     A     _______
GAM266  EMX2     5'  GGGAGGGAGAGGGAGAGGC   44691     A__     _
                                GGGA   GGAGGG GAGGC
                                ||||   |||||| |||||
                                CCCT   TCTCCC CTCCG
                                  CCC     T
GAM266  EPS15    5'  GGGAGGAGGCGGAGGGAGC   12744     A    _    CTA  A
                                GGGA GGAGG GGAGG   GA GC
                                |||| ||||| |||||   || ||
                                CCCT CCTCC CCTCC   CT CG
                                  _    G    ___  _
GAM266  F2RL3    3'  GGAGGCGGGGCTGGAGGAGC   19522      _ A    A __
                                GGAGG GG GGCT GA  AGC
                                ||||| || |||| ||  |||
                                CCTCC CC CCGA CT  TCG
                                  G  _   C  CC
GAM266  FCER2    3'  GGGAAGGCAGGGGCCATAGAGG 12815       _    AGGC   __
            AGC                   GGGAAGG AGGGG    TAGA  AGC
                                ||||||| |||||    ||||  |||
                                CCCTTCC TCCCC    ATCT  TCG
                                   G    GGT_    CC
GAM266  FSTL1    3'  GGAAAGAGGCTGGAAGC     28219       G    A
                                GGAGGG AGGCT GAAGC
                                |||||| ||||| |||||
                                CCTTTC TCCGA CTTCG
                                  _    C
GAM266  FXYD2    3'  GGGAAGAAGGGGAGGCGCCAGA 34651             __   A
            GGCA                  GGGAAGGAGGGGAGGC  TAGA GCA
                                ||||||||||||||||  |||| |||
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                                CCCTTCTTCCCCTCCG  GTCT CGT
                                          CG    C
GAM266  GA      5'  GGGAAGGAGGGGCGGAGC    29968          A  CTAGA
                                GGGAAGGAGGGG GG    AGC
                                |||||||||||| ||    |||
                                CCCTTCCTCCCC CC    TCG
                                      G _____
GAM266  GALNT7   3'  GGGCAGGGGGAATAGA     38359     A  A    GGC
                                GGG AGG GGGGA   TAGA
                                ||| ||| |||||   ||||
                                CCC TCC CCCTT   ATCT
                                  G  _    ___
GAM266  GAS7     3'  GGGATGAGGGGGGAAAGA    25275     AG     A  CT
                                GGGA  GAGGGG GG  AGA
                                ||||  |||||| ||  |||
                                CCCT  CTCCCC CC  TCT
                                   A_     _ TT
GAM266  GFAP     3'  AGGAGGGAGGGGAGCAGCT   13118     A       __
                                GGGA GGAGGGGAG  GCT
                                |||| |||||||||  |||
                                TCCT CCTCCCCTC  CGA
                                   C       GT
GAM266  GLRA1    5'  GGGAGGCGGGGAACAGGGGC  6737      A  A     GC   AA
                                GGGA GG GGGGAG  TAG  GC
                                |||| || ||||||  |||  ||
                                CCCT CC CCCCTT  GTC  CG
                                   _ G     __  CC
GAM266  GRB10    3'  GGGGCGGAGGGGACCAA     23664     AA     AG
                                GGG  GGAGGGG  GCTAG
                                |||  |||||||  |||||
                                CCC  CCTCCCC  TGGTT
                                  CG     __
GAM266  GRB14    5'  GGGAGAGGGGAGGAG       21045      AG       CTAGA
                                GGGA  GAGGGGAGG    AG
                                ||||  |||||||||    ||
                                CCCT  CTCCCCTCC    TC
                                      __      _____
GAM266  GRIK5    3'  GGGAAGGAGTGACCGGAGAAG  13296          _  GA  CT
                                GGGAAGGAG GG  GG  AGAAG
                                ||||||||| ||  ||  |||||
                                CCCTTCCTC CT  CC  TCTTC
                                     A  GG  __
GAM266  GRIN2C   5'  GGGAGGAGGGGGCGCGAGCA  9127      A     AG  TAGA
                                GGGA GGAGGGG  GC   AGCA
                                |||| |||||||  ||   ||||
                                CCCT CCTCCCC  CG   TCGT
                                   _     CG  C___
GAM266  GTF2IRD1  5'  GGGAAGGAGAGGCAGAGGGAGG 32263          _______
             C                   GGGAAGGAG      GGGAGGC
                                 |||||||||      |||||||
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                                CCCTTCCTC      CCCTCCG
                                     TCCGTCT
GAM266  HAMP    3'  GGAAGGGAGGGGACGGGGGC  34512     A      ____
                                GGGA GGAGGGGA   GGC
                                |||| ||||||||   |||
                                CCTT CCTCCCCT   CCG
                                  C       GCCC
GAM266  HNF3A   3'  GGTAAGGAGGGGGAAAAAGCA  40730   G       A  CT
                                GG AAGGAGGGG GG  AGAAGCA
                                || |||||||| ||  |||||||
                                CC TTCCTCCCC CT  TTTTCGT
                                 A       _ __
GAM266  HOXC5   3'  GGGACAGGAACCGGCTAGGGGC 33247     _    GGGA     AA
                                GGGA AGGAG   GGCTAG  GC
                                |||| |||||   ||||||  ||
                                CCCT TCCTT   CCGATC  CG
                                  G    GG__    CC
GAM266  IGSF8   3'  GGGAAGGAGTGGGGAAGGGGAG 38082       _________
            GC                    GGGAAGGA       GGGGAGGC
                                |||||||||       ||||||||
                                CCCTTCCT       CCCCTCCG
                                     CACCCCTT
GAM266  IKBKB   5'  GGGAAGGCGGGGCTGGGGC   41809       A   A___
                                GGGAAGG GGGG   GGC
                                ||||||| ||||   |||
                                CCCTTCC CCCC   CCG
                                    G   GACC
GAM266  IL2RB   3'  GGGAAGGAGGAGGCTGGGGCA  9390        GG     AGAA
                                GGGAAGGA  GGAGGCT   GCA
                                ||||||||  |||||||   |||
                                CCCTTCCT  CCTCCGA   CGT
                                     __      CCC_
GAM266  ILF1    5'  GGGAGGAGGGGAGGAGGC   21115     A       CT  AA
                                GGGA GGAGGGGAGG  AG  GC
                                |||| ||||||||||  ||  ||
                                CCCT CCTCCCCTCC  TC  CG
                                  _       __  __
GAM266  IRS1    5'  GGGAGGAGGGGAGGGGACAAGG 24425     A       CTA_  A_
            GC                    GGGA GGAGGGGAGG   GA  GC
                                |||| ||||||||||   ||  ||
                                CCCT CCTCCCCTCC   TT  CG
                                  _       CCTG  CC
GAM266  ITGA11  3'  GGGAAGGATGGGAGGCAG   29200       G     T
                                GGGAAGGA GGGAGGC AG
                                |||||||| ||||||| ||
                                CCCTTCCT CCCTCCG TC
                                     A     _
GAM266  KCNQ3   5'  GGGGGCAGGGGAGGCCAGGCA  21129    AA  _         AA
                                GGG  GG AGGGGAGGCTAG  GCA
                                |||  || ||||||||||||  |||
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                                CCC  CC TCCCCTCCGGTC  CGT
                                  __  G         __
GAM266  KIAA0442 5'  GGGGAGGAGGGACGGGGAGC   31792     A      GA  CTA  A
                                GGG AGGAGGG  GG   GA GC
                                ||| |||||||  ||   || ||
                                CCC TCCTCCC  CC   CT CG
                                  C      TG  C__  _
GAM266  KIAA0442 5'  GGGAGCGAGGGCGAGAGGC    31791      AG    ___
                                GGGA  GAGGG   GAGGC
                                ||||  |||||   |||||
                                CCCT  CTCCC   CTCCG
                                   CG    GCT
GAM266  KIF3B    3'  GGGAAGGGGGAGAAGAAGGCA  22038        AG     CT    _
                                GGGAAGG  GGGAGG  AGAAG CA
                                |||||||  ||||||  ||||| ||
                                CCCTTCC  CCCTCT  TCTTC GT
                                   __     __     C
GAM266  KRT2A    3'  GGGAATGGGCATGGCTAGAAGC 7685       GGA   GA_
            A                    GGGAA   GGG   GGCTAGAAGCA
                                |||||   |||   ||||||||||
                                CCCTT   CCC   CCGATCTTCGT
                                   A__   GTA
GAM266  LAD1     3'  GGGAAGGGAGGGGAGAACCAAG 24491        _       _   GA
            CA                    GGGAAGG AGGGGAGG CTA  AGCA
                                ||||||| |||||||| |||  ||||
                                CCCTTCC TCCCCTCT GGT  TCGT
                                    C       T   __
GAM266  LIMK1    5'  GGGAGGCGGGGGGCGGAGGGC   32533      A  AG   A   TAGAA
                                GGGA GG  GGG GGC     GC
                                |||| ||  ||| |||     ||
                                CCCT CC  CCC CCG     CG
                                  _  G_   _   CCTCC
GAM266  LLGL1    3'  GGGGGGGAGGTGGCACAG    42508     AA    GGA   _
                                GGG  GGAGG   GGC TAG
                                |||  |||||   ||| |||
                                CCC  CCTCC   CCG GTC
                                  CC    A__   T
GAM266  LLGL1    3'  GGAGGGGGGGAGGTGGC     42505     A  A      CTAGAA
                                GGA GG GGGGAGG      GC
                                ||| || |||||||      ||
                                CCT CC CCCCTCC      CG
                                  C  _       AC_____
GAM266  LMO2     5'  GGGAGGCGGGGTGCCGGGC    24546      A  A    AG   AGAA
                                GGGA GG GGGG  GCT    GC
                                |||| || ||||  |||    ||
                                CCCT CC CCCC  CGG    CG
                                  _  G    A_   CC__
GAM266  LMO4     5'  GGAGAGGAGGGGGCTAAGGGC  27656    GA       AG     AA
                                GG  AGGAGGGG  GCTAG  GC
                                ||  ||||||||  |||||  ||
```

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                                CC  TCCTCCCC  CGATT  CG
                                 TC       __     CC
GAM266  LRP1     3'  GGGCAGGAGGCTTTCTGGGGGC 14220     A     _______ A
                                GGG AGGAGG     GG GGC
                                ||| ||||||     || |||
                                CCC TCCTCC     CC CCG
                                  G     GAAAGA  C
GAM266  LTBR     3'  GGAGGGGAGGGAAGGAGC    14256          CT  A
                                GGAGGGGAGG  AG AGC
                                ||||||||||  || |||
                                CCTCCCCTCC  TC TCG
                                      CT  C
GAM266  LTF      3'  GGGAGAAGAGCTGGGGGC    14261     _    __  A
                                GGGA AGGAG  GGG GGC
                                |||| |||||  ||| |||
                                CCCT TTCTC  CCC CCG
                                  C    GA  _
GAM266  LU       3'  GGGAAGGCGGGGGCGGGC    24564        A   A__
                                GGGAAGG GGGG   GGC
                                ||||||| ||||   |||
                                CCCTTCC CCCC   CCG
                                    G   CGC
GAM266  MADH2    5'  GGGAAGAGGGGAATGGGC    25344       G    ___
                                GGGAAG AGGGGA   GGC
                                |||||| ||||||   |||
                                CCCTTC TCCCCT   CCG
                                   _     TAC
GAM266  MMP14    3'  GGGAGGGAGGCGGTCAGG    22640      A    _ __
                                GGGA GGAGG GG  AGG
                                |||| ||||| ||  |||
                                CCCT CCTCC CC  TCC
                                  C    G  AG
GAM266  MMP14    3'  GGGCAGGAGGGAGGGAGGC   22641     A     ___
                                GGG AGGAGGG   GAGGC
                                ||| |||||||   |||||
                                CCC TCCTCCC   CTCCG
                                  G      TCC
GAM266  MNT      3'  GGTAGGGAGGGGAAGCAGGAGC 33722    GAA        T  A
                                GG   GGAGGGGAGGC AG AGC
                                ||   ||||||||||| || |||
                                CC   CCTCCCCTTCG TC TCG
                                 ATC         _  C
GAM266  MSL3L1   3'  AGAGGGAACCGTTAGAAGCA  38575        GGC_
                                GGAGGGGA    TAGAAGCA
                                ||||||||    ||||||||
                                TCTCCCTT    ATCTTCGT
                                     GGCA
GAM266  MTNR1B   3'  GGGGGGAAGGGGAGAAAGC   25554     AA       GCTA
                                GGG  GGAGGGGAG    GAAGC
                                |||  |||||||||    |||||
```

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                                CCC  CTTCCCCTC    TTTCG
                                  CC       ____
GAM266  MYO1C    3'  GGGAAGGGGAGGAGGAGAAAAG 41471        A      CT
              CA                    GGGAAGG GGGGAGG  AGAAGCA
                                    ||||||| |||||||  |||||||
                                    CCCTTCC CTCCTCC  TTTTCGT
                                       C      TC
GAM266  NCOR2    3'  GGGAGGGAGGGAGGACACAGC  26740      A     GA   TAGA
                                    GGGA GGAGGG  GGC    AGC
                                    |||| ||||||  |||    |||
                                    CCCT CCTCCC  CTG    TCG
                                      C     TC   TG__
GAM266  NEUROD2  5'  GGGGAGGGGGGGGAGGGGGCA   26066     A   A      CTAGAA
                                    GGG AGG GGGGAGG      GCA
                                    ||| ||| |||||||      |||
                                    CCC TCC CCCCTCC      CGT
                                      C   C      CC_____
GAM266  NF1      5'  GGGAGAGGGAAAGGGGGC    7058       A__      A
                                    GGGA   GGAGGGG GGC
                                    ||||   ||||||| |||
                                    CCCT   CCTTTCC CCG
                                      CTC      C
GAM266  NGFR     3'  GGGAAGGGGAGGATGGGGGAGC 14783        A    _  CTA  A
              A                      GGGAAGG GGGGA GG   GA GCA
                                    ||||||| ||||| ||   || |||
                                    CCCTTCC CTCCT CC   CT CGT
                                       C     A  CC_  _
GAM266  NPEPPS   5'  GGGAAGGAGGCGGTGCGGGC   26719          _  A___
                                    GGGAAGGAGG GG    GGC
                                    |||||||||| ||    |||
                                    CCCTTCCTCC CC    CCG
                                          G  ACGC
GAM266  NRXN2    3'  GGGAAGGAGGGTGGGGACAG   31487          GA  C_
                                    GGGAAGGAGGG  GG  TAG
                                    |||||||||||  ||  |||
                                    CCCTTCCTCCC  CC  GTC
                                          AC  CT
GAM266  OSM      3'  GGAAAGGAGGAAGTCTGGGGGC 33913          _______  A
                                    GGGAAGGAGG     GG GGC
                                    ||||||||||     || |||
                                    CCTTTCCTCC     CC CCG
                                          TTCAGA  C
GAM266  P23      3'  GGGAAGGAGGGGCGTGGGC    27345          A___
                                    GGGAAGGAGGGG    GGC
                                    ||||||||||||    |||
                                    CCCTTCCTCCCC    CCG
                                          GCAC
GAM266  PABPC1   5'  GGGGGGAGGGGAGCGGGGAGCA 15026     AA       G TAGA
                                    GGG  GGAGGGGAG C    AGCA
                                    |||  ||||||||| |    ||||
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                                CCC  CCTCCCCTC G    TCGT
                                  C_        _ CCCC
GAM266  PAFAH1B1  5'  GGGAAGGAGGGGGGAGGATGGC 7712            A  CTAGAA
                                GGGAAGGAGGGG GG      GC
                                |||||||||||| ||      ||
                                CCCTTCCTCCCC CC      CG
                                       _  TCCTAC
GAM266  PAFAH1B1  5'  GGGGGAGGGGAGGGGAGC    7716      AA        CTA  A
                                GGG  GGAGGGGAGG   GA GC
                                |||  ||||||||||   || ||
                                CCC  CCTCCCCTCC   CT CG
                                  __         C__  _
GAM266  PCDH7     5'  GAGAGGGAGGGGAGGGAGGGGG 37116      A         CTAGAA
              CA                  GGGA GGAGGGGAGG      GCA
                                |||| ||||||||||      |||
                                CTCT CCTCCCCTCC      CGT
                                  C         CTCCCC
GAM266  PCDH7     5'  GGGAGGGAGGGGGCAAAAGC   15113      A      AG  T
                                GGGA GGAGGGG  GC AGAAGC
                                |||| |||||||  || ||||||
                                CCCT CCTCCCC  CG TTTTCG
                                  C      __  _
GAM266  PCTK3     5'  GGGAGGGAGTGGAGGAAG    43782      A    G     CT
                                GGGA GGAG GGAGG  AG
                                |||| |||| |||||  ||
                                CCCT CCTC CCTCC  TC
                                  C    A    T_
GAM266  PDGFB     5'  GGGGGCAGGGGAGGACCTGGGC 15192      AA  _       _  AGAA
                                GGG  GG AGGGGAGG CT    GC
                                |||  || ||||||||  ||    ||
                                CCC  CC TCCCCTCC GG    CG
                                  __  G       T  ACC_
GAM266  PDGFB     3'  GGGAGGAAGGGGGTGGCAGGAGG 15189      A      A   TA  A
              CA                  GGGA GGAGGGG GGC  GA GCA
                                |||| ||||||| |||  || |||
                                CCCT CTTCCCC CCG  CT CGT
                                  C      A   TC  C
GAM266  PHF1      3'  GGGAGAAGGGGGTGCTGAGC   15272      A      AG   A  A
                                GGGA GGAGGGG  GCT GA GC
                                |||| |||||||  ||| || ||
                                CCCT CTTCCCC  CGA CT CG
                                  _      CA   _ _
GAM266  PHKA1     3'  GGGAAGGATGGGACAGAAAGGG 15277         _  GA  CT  AA
              GCA                   GGGAAGGA GGG  GG  AG  GCA
                                |||||||| |||  ||  ||  |||
                                CCCTTCCT CCC  TC  TC  CGT
                                     A   TG  TT  CC
GAM266  POU2AF1   3'  GGGGGAGAGGGAGGAAG     26372      AA   _     CT
                                GGG  GGAG GGGAGG  AG
                                |||  |||| ||||||  ||
```

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                                CCC  CCTC CCCTCC  TC
                                  __   T     T_
GAM266  PPP1R11  3'  GGGAAGGAGGGGGCTGGAGAAG 45510          AG  __
                                GGGAAGGAGGGG  GCT  AGAAG
                                ||||||||||||  |||  |||||
                                CCCTTCCTCCCC  CGA  TCTTC
                                      __  CC
GAM266  PPP2R2B  5'  GGGGGCAGGGGAGCCAG    21335    AA _     G
                                GGG  GG AGGGGAG CTAG
                                |||  || |||||||  ||||
                                CCC  CC TCCCCTC GGTC
                                  __ G     _
GAM266  PRKACA   3'  AGGAAGGAGGGAGGGAGGC   15574          ___
                                GGGAAGGAGGG   GAGGC
                                ||||||||||   |||||
                                TCCTTCCTCCC   CTCCG
                                      TCC
GAM266  PRKACG   3'  GGGCGGGGGGGTGAGGGAGCA  15602    AA  A  _   CTA  A
                                GGG  GG GGG GAGG   GA GCA
                                |||  || ||| ||||   || |||
                                CCC  CC CCC CTCC   CT CGT
                                  GC  _   A   ___  _
GAM266  PTMS     3'  GGGAGGGGAGGGGGGCAGC   15894     A_     A   TAGA
                                GGGA  GGAGGGG GGC    AGC
                                ||||  ||||||| |||    |||
                                CCCT  CCTCCCC CCG    TCG
                                  CC      _  _____
GAM266  PTPRG    5'  GGGAAGGGGAGGGGAGAGGCA  15938     AGG      CT   A
                                GGGA   AGGGGAGG  AGA GCA
                                ||||   ||||||||  ||| |||
                                CCCT   TCCCCTCC  TCT CGT
                                  ___      CC   C
GAM266  RAB3A    3'  GGGAAGAGGGGAAAGGGAG    16072       GA      CT
                                GGGAAG  GGGGAGG  AG
                                ||||||  |||||||  ||
                                CCCTTC  CCCTTTC  TC
                                    TC      CC
GAM266  RAB6A    5'  GGGAAGGAGGGCGGTGTCGGCA 16106          GA  CTAGAA
                                GGGAAGGAGGG  GG     GCA
                                ||||||||||  ||     |||
                                CCCTTCCTCCC  CC     CGT
                                      G_  ACAGC_
GAM266  RAP1GA1  3'  GGGAGGGTGGGGAGGCAGGGGG 16168      A  A      TAGAA
          CA                    GGGA GG GGGGAGGC    GCA
                                ||||  || ||||||||    |||
                                CCCT CC CCCCTCCG    CGT
                                  C  A       TCCCC
GAM266  RBM10    5'  GGGGGGAGGGGAGAAGC     24984    A      CT
                                GG GGGGAGG  AGAAGC
                                ||  |||||||  ||||||
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                                CC CCCCTCC  TCTTCG
                                 _      CC
GAM266  S100A5   3'  GGGAGGGAGAGGAGGG      16444      A        CTAGAA
                                GGGA GGAGGGGAGG      G
                                |||| ||||||||||      |
                                CCCT CCTCTCCTCC      C
                                  C         _______
GAM266  SIX3     5'  GGAAAGGAGGGGGGAG      24024           A  CTAGA
                                GGGAAGGAGGGG GG     AG
                                |||||||||||| ||     ||
                                CCTTTCCTCCCC CC     TC
                                          _ ______
GAM266  SIX3     3'  AGGAGGAGGGCTAGGAGGC    24015        A     AA_
                                AGGAGGGG GGCTAG   GC
                                |||||||| ||||||   ||
                                TCCTCCTC CCGATC   CG
                                     _     CTC
GAM266  SIX3     3'  GGGAAGGAGAGGGAGGAGGGC  24026         _     CT  AA
                                GGGAAGGAG GGGAGG  AG  GC
                                ||||||||| ||||||  ||  ||
                                CCCTTCCTC CCCTCC  TC  CG
                                      T      __  C_
GAM266  SLC39A1  3'  GGGAGGGAAGGGAGAACAGGGG 30888      A        GC   AA
           CA                     GGGA GGAGGGGAG  TAG  GCA
                                |||| |||||||||  |||  |||
                                CCCT CCTTCCCTC  GTC  CGT
                                  C        TT   CC
GAM266  SLC7A5   3'  GGAGGGGGAGGGGGAAGC     18550        _  CTA
                                GGAGGGG AGG   GAAGC
                                |||||||| |||   |||||
                                CCTCCCC TCC   CTTCG
                                    C   CC_
GAM266  SLC8A2   3'  GGAAGGGAGACTTTGGGGGCA  42416           AGAA__
                                GGAGGGGAGGCT      GCA
                                ||||||||||||      |||
                                CCTTCCCTCTGA      CGT
                                       AACCCC
GAM266  SNK      5'  GGGAGGCGGGAAGGGGGC     27363      A___      A
                                GGGA    GGAGGGG GGC
                                ||||    ||||||| |||
                                CCCT    CCTTCCC CCG
                                  CCGC      _
GAM266  SORBS1   3'  GGGGAGGGGAAAGGCTGAAG   31710     A   A  GG    A
                                GGG AGG GG  AGGCT GAAG
                                ||| ||| ||  ||||| ||||
                                CCC TCC CC  TCCGA CTTC
                                  C   _  TT     _
GAM266  SOX12    3'  GGGAAGGGAGGGGCGCAGGAGG 28047         _    AG  TA  A
           C                      GGGAAGG AGGGG  GC  GA GC
                                ||||||| |||||  ||  || ||
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                                CCCTTCC TCCCC  CG  CT CG
                                    C    G_  TC  C
GAM266  SOX9    5'  AGGAGGAGGGGAGGAAAAAGAG 7371      A       CT  _
          CA                      GGGA GGAGGGGAGG  AGA AGCA
                                  |||| ||||||||||  ||| ||||
                                  TCCT CCTCCCCTCC  TTT TCGT
                                    _       TT   C
GAM266  SRD5A1  5'  GGGAGGAGGGGCGGCTA    9830      A     A
                                  GGGA GGAGGGG GGCTA
                                  |||| ||||||| |||||
                                  CCCT CCTCCCC CCGAT
                                    _     G
GAM266  SYNGR1  3'  GGGAGGGGCGGGGGCAGGC   21763     A  A_   __
                                  GGGA GG  GGGG  AGGC
                                  |||| ||  ||||  ||||
                                  CCCT CC  CCCC  TCCG
                                    C  CG   CG
GAM266  TAF4    3'  GGGAAGGGAGGGGAGGGGAGGG 17263       _      CT  AA
          CA                      GGGAAGG AGGGGAGG  AG  GCA
                                  ||||||| ||||||||  ||  |||
                                  CCCTTCC TCCCCTCC  TC  CGT
                                    C       CC  C_
GAM266  TAF4    3'  GGAGGGGAGGGCAGGGGGCA   17262         C   AA_
                                  GGAGGGGAGG TAG   GCA
                                  |||||||||| |||   |||
                                  CCTCCCCTCC GTC   CGT
                                       C   CCC
GAM266  TEM8    3'  GAGAAGGCTAGGGTTGGAGG   38180       __   ___
                                  GGGAAGG  AGGG   GAGG
                                  |||||||  ||||   ||||
                                  CTCTTCC  TCCC   CTCC
                                    GA   AAC
GAM266  TFEB    3'  GGGAGGAGGGAGGCAGGGCA   45137     A    G   T  AA
                                  GGGA GGAGGG AGGC AG  GCA
                                  |||| |||||| |||| ||  |||
                                  CCCT CCTCCC TCCG TC  CGT
                                    _    _   _ C_
GAM266  TIMP3   3'  GGGAAGGGAGGGAAGTGAG   7462        AG    CT
                                  GGGAAGG  GGGAGG  AG
                                  |||||||  ||||||  ||
                                  CCCTTCC  CCCTTC  TC
                                    CT     AC
GAM266  TMEPAI  3'  GGGAAGGGAGGGGGTAGC    33614       _   A_
                                  GGGAAGG AGGGG  GGC
                                  ||||||| |||||  |||
                                  CCCTTCC TCCCC  TCG
                                    C    CA
GAM266  TP53BP2 5'  GGGGGAGGGGAGCGGAGAGC  24062     AA      GCT  A
                                  GGG  GGAGGGGAG   AGA GC
                                  |||  |||||||||   ||| ||
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                                CCC  CCTCCCCTC   TCT CG
                                  __       GCC  _
GAM266  TRA1    3'  GGGAGAAGGGGATTAGGGGGC  17677      A      _______
                                GGGA GGAGGGGA     GGC
                                |||| ||||||||      |||
                                CCCT CTTCCCCT     CCG
                                  _       AATCCC
GAM266  TULP1   3'  GGGAGGAGGGGGGCACAGC   17729      A      A   TAGA
                                GGGA GGAGGGG GGC    AGC
                                |||| ||||||| |||    |||
                                CCCT CCTCCCC CCG    TCG
                                  _      _  TG__
GAM266  UBE2B   5'  GGGAGGAGGGGGCGGGACGC   17794      A      A_  CTA  A
                                GGGA GGAGGGG  GG   GA GC
                                |||| |||||||  ||   || ||
                                CCCT CCTCCCC  CC   CT CG
                                  _      CG  ___  G
GAM266  UNRIP   5'  GGGAGGGAGGGAGGAAAG    28422      A  AG     CT
                                GGGA GG  GGGAGG  AG
                                |||| ||  ||||||  ||
                                CCCT CC  CCCTCC  TC
                                  _ CT     TT
GAM266  WNT7A   5'  AGGAGGGAGGGAGGAGC     21522      A  AG     CTAGA
                                GGGA GG  GGGAGG    AGC
                                |||| ||  ||||||    |||
                                TCCT CC  CCCTCC    TCG
                                  _ CT     _____
GAM266  ZNF216  5'  GGGAAGCGAGGGGGGGCC    25657       _     A
                                GGGAAG GAGGGG GGCT
                                |||||| |||||| ||||
                                CCCTTC CTCCCC CCGG
                                   G     C
GAM267  CREBL2  3'  GCAAAAATACAATCTTCATCGA 10580            AGC  _
                                GCAAAAATACAAT   TC TCGA
                                ||||||||||||   || ||||
                                CGTTTTTATGTTA   AG AGCT
                                        GA_  T
GAM267  ETV1    3'  GCGCAAAAAACGCCCT      22419          TACAATA
                                GCGCAAAAA      GCTCT
                                |||||||||      |||||
                                CGCGTTTTT      CGGGA
                                     TG_____
GAM267  ZNF200  5'  GCCAGAGAGCCAAGCTCTCG   18373    G  AAAATA  AT
                                GC CA     CA  AGCTCTCG
                                || ||     ||  ||||||||
                                CG GT     GT  TCGAGAGC
                                 _ CTCTCG  __
GAM268  ABCC3   3'  CAGCTGTCCTCCAGGTGC    33417       C  C  C  C
                                CAGCTG CC CC GG GC
                                |||||| || || || ||
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                                GTCGAC GG GG CC CG
                                   A  A  T  A
GAM268  ACO1     3'  GCTTCCTCCCTGGGCGCACGA  13582     G  C   C  C
                                GCT CC CCC GG GCGCGCGA
                                ||| || ||| || ||||||||
                                CGA GG GGG CC CGCGTGCT
                                  A  A   A  _
GAM268  ADRA2A   5'  CAGCTGCCTTCCGGCCCG    8628         CCC    G
                                CAGCTGCC   CCGGC CG
                                ||||||||   ||||| ||
                                GTCGACGG   GGCCG GC
                                     AA_    G
GAM268  ANKTM1   5'  CAGCTGCTCACCACGCGCGCG  28802        CCCC   G
                                CAGCTGC    CCG CGCGCGCG
                                |||||||    ||| ||||||||
                                GTCGACG    GGT GCGCGCGC
                                     AGT_  _
GAM268  BID      5'  CAGCGTCTCCCAGGCGCGCG   10179      TGCCCC    C
                                CAGC     CCCGG GCGCGCG
                                ||||     ||||| |||||||
                                GTCG     GGGTC CGCGCGC
                                  CAGA__    _
GAM268  CHRNA5   5'  CAGCCGCCTCTCGACCGCCGCG 40747         CCC___   G
           CG                     CAGCTGCC     CCG CGCGCG
                                ||||||||     ||| ||||||
                                GTCGGCGG     GGC GCGCGC
                                     AGAGCT   G
GAM268  DIO3     3'  CAGCTGCGCTCAGGGCGCGCG  10689        CCCCCC
                                CAGCTGC     GGCGCGCG
                                |||||||     ||||||||
                                GTCGACG     CCGCGCGC
                                     CGAGTC
GAM268  DYRK2    5'  GCCGCCCCTCGCGCG       18721         CCCGG
                                GCTGCCCC    CGCGCG
                                ||||||||    ||||||
                                CGGCGGGG    GCGCGC
                                     A____
GAM268  FBXL7    5'  GCTGCCCCTGCGCGCCCGCG   29406        CC  G   G
                                GCTGCCCC  CG CGC CGCG
                                ||||||||  || ||| ||||
                                CGACGGGG  GC GCG GCGC
                                     AC  _   G
GAM268  FCAR     3'  CAGCTGCCTCCTGGGTTCA   39335        C  CC  CG
                                CAGCTGCC CC  GG  CG
                                |||||||| ||  ||  ||
                                GTCGACGG GG  CC  GT
                                     A  AC  AA
GAM268  FKBP6    5'  AGCTGCCCTCCCTGTGGCG   44088         _  C__
                                AGCTGCCC CCC   GGCG
                                |||||||| |||   ||||
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                                TCGACGGG GGG   CCGC
                                    A   ACA
GAM268  GPC1     5'  AGCCAAGGTCCCGGCGCGCGCG 13230      GCCCC
                                AGCT    CCCGGCGCGCGCG
                                ||||    ||||||||||||
                                TCGG    GGGCCGCGCGCGC
                                  TTCCA
GAM268  LASS2    5'  GCTGCCCCTTCGCCCCGGCGCG 42679        _____
                                GCTGCCCC    CCCGGCGCG
                                ||||||||    |||||||||
                                CGACGGGG    GGGCCGCGC
                                    AAGCG
GAM268  MADD     5'  CAGTCGCTCCCCAGCGCG    39073     C   CC
                                CAG TGC  CCCCGGCGCG
                                ||| |||  ||||||||||
                                GTC GCG  GGGGTCGCGC
                                  A   A_
GAM268  MADH7    5'  GCTGCCCCACCCCGCGCG    25366        _   G
                                GCTGCCCC CCC GCGCG
                                |||||||| ||| |||||
                                CGACGGGG GGG CGCGC
                                    T   G
GAM268  MAPT     5'  TGACTGCGAGGGCGCGCGCG   32586   A    CCCCCC
                                C GCTGC     GGCGCGCGCG
                                | |||||     ||||||||||
                                A TGACG     CCGCGCGCGC
                                 C    CTC___
GAM268  N33      5'  CAGTGTCTCCTCCACGCGCG   27628    C  CCCCC  GG
                                CAG TG    CC  CGCGCGCG
                                ||| ||    ||  ||||||||
                                GTC AC    GG  GTGCGCGC
                                  _  AGA__  AG
GAM268  NAGLU    5'  CAGCTGCCGCCTCCGGCCACG  7047        _ C    G
                                CAGCTGCC CC CCGGC CGCG
                                |||||||| || ||||| ||||
                                GTCGACGG GG GGCCG GTGC
                                    C  A    _
GAM268  PDGFB    5'  GCTGCTCCGCGCGCGCG     15182      C  CCCG
                                GCTGC CC    GCGCGCGCG
                                ||||| ||    |||||||||
                                CGACG GG    CGCGCGCGC
                                  A  _____
GAM268  PTGER3   5'  GCTGCCCCCCATGGTGCG    9648         C_  C
                                GCTGCCCCCC  GG GCG
                                ||||||||||  || |||
                                CGACGGGGGG  CC CGC
                                    TA  A
GAM268  PTPN11   5'  CAGCTGCCCCCCGGCCCG    38752          C   G
                                CAGCTGCCCCCC GGC CG
                                |||||||||||| ||| ||
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                                GTCGACGGGGGG CCG GC
                                      _  G
GAM268  RAPSN    5'  CAGCTGCCCCCCGAAACG    37214          C  C
                                CAGCTGCCCCCC GG GCG
                                |||||||||||| || |||
                                GTCGACGGGGGG CT TGC
                                      _  T
GAM268  SGT      3'  CAGCTGCCTTCCCTGTGCCCG  16608        CC   GGC  G
                                CAGCTGCC  CCC   GC CG
                                ||||||||  |||   || ||
                                GTCGACGG  GGG   CG GC
                                    AA   ACA  G
GAM268  SLC1A2   5'  GCTCTCCACGGCGCGCG     41598     GC  CCC
                                GCT  CC   CGGCGCGCG
                                |||  ||   |||||||||
                                CGA  GG   GCCGCGCGC
                                  GA  T__
GAM268  SLC9A5   5'  CAGCCGCCCTCCCGGCACCGCA 21384         C      _ _
            GCG                    CAGCTGCCC CCCGGCGC GC GCG
                                |||||||||  |||||||| || |||
                                GTCGGCGGG GGGCCGTG CG CGC
                                     A       G  T
GAM268  SORBS1   3'  TGTCCCCCCAGCAGCCA     31716    C        C  G
                                TG CCCCCCGGCG GC CG
                                || ||||||||| || ||
                                AC GGGGGGTCGT CG GT
                                 A        _ _
GAM268  HTRA3    3'  CTCGGGGGGGGCGCTGCCCTCCG 44830              TG  G
                                CTCGGGGGGGGCGCTGT  CC CCG
                                ||||||||||||||||  || |||
                                GAGCCCCCCCCGCGACG  GG GGC
                                          __  A
GAM268  IRS1     5'  CTCGGGAGGGCGCTGCCGC   24417
                                CTCGGGGGGGGCGCTGTTGC
                                ||||||||||||||||||
                                GAGCCCTCCCGCGACGGCG

GAM268  SIX2     3'  CTCGGGGGGGCGCGCTCAGCCG  32604          _    GTT
                                CTCGGGGGG GCGCT   GCCG
                                |||||||| |||||   ||||
                                GAGCCCCCC CGCGA   CGGC
                                     G    GT_
GAM268  TEAD3    5'  CTCGCGGGGGGCGCTCCGGCCG  17374     G       GTTG  _
                                CTCG GGGGGCGCT    CCG CCG
                                ||||  |||||||||    ||| |||
                                GAGC CCCCCGCGA    GGC GGC
                                  G        _____  C
GAM269  ACTB     3'  CCTTAGAGAGAAGT       9923           GGGTT
                                CCTTAGAGAGG    AGT
                                ||||||||||     |||
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                                GGAATCTCTCT    TCA
                                      _____
GAM269  AKAP13   5' CTTGGAGGGGCTATGTGG   28481    A  GAG     _
                                CTT GA   GGGGTTA GTGG
                                ||| ||   ||||||| ||||
                                GAA CT   CCCCGAT CACC
                                  C ___      A
GAM269  APOC3    3' TGCCTGGAGGGGGGCCAG   6215      TA  A
                                TGCCT  GAG GGGGGTTAG
                                |||||  ||| |||||||||
                                ACGGA  CTC CCCCCGGTC
                                   C_  _
GAM269  ESRRA    3' TGCTTTGAAGAGGGGGTAG  20839    C  AG      T
                                TGC TT  AGAGGGGGT AG
                                ||| ||  ||||||||| ||
                                ACG AA  TCTCCCCCA TC
                                  A  CT       _
GAM269  LOXL3    3' TGCCATTAGGGGCCAGTGG  37203    TTAGAGA
                                TGCC      GGGGGTTAGTGG
                                ||||      ||||||||||||
                                ACGG      TCCCCGGTCACC
                                   TAA____
GAM269  MLLT3    3' CCTTGGAGAGAAGAGTGG   21190    A      GTT
                                CCTT GAGAGGGG   AGTGG
                                |||| ||||||||   |||||
                                GGAA CTCTCTTC   TCACC
                                  C      ___
GAM269  P4HB     3' TGCTGTAGAGAGGCCAGTGG  9552    CT     GGG
                                TGC  TAGAGA   GGTTAGTGG
                                |||  ||||||   |||||||||
                                ACG  ATCTCT   CCGGTCACC
                                  AC     ___
GAM269  RYR1     3' TGCCTTAGGGGGAGGGGCTT  8075       A__     G
                                TGCCTTAG   GAGGGG TT
                                ||||||||   |||||| ||
                                ACGGAATC   CTCCCC AA
                                     CCC     G
GAM269  STAT6    3' TGCCTTGAGAGGGAGAATGG  17159      A       TT
                                TGCCTT GAGAGGGGG  AGTGG
                                ||||||| |||||||||  |||||
                                ACGGAA CTCTCCCTC  TTACC
                                   _       __
GAM269  ANKH     3' AAGAGGCCACCGGGGCTC    38307     __   TACCT
                                AAGA  CCAT    CGGGGCTC
                                ||||  ||||    ||||||||
                                TTCT  GGTG    GCCCCGAG
                                  CC   _____
GAM269  BCR      3' TGAGGCCAGCCTGGGGCTC   34643   A  A   TTA   C
                                A AG CCA   CCT GGGGCTC
                                | || |||   ||| |||||||
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                                A TC GGT   GGA CCCCGAG
                                 C  C   C__   _
GAM269  BCR     3'  TGAGGCCAGCTTGGGGCTC   20249   A  A   TTAC  C
                                A AG CCA    CT GGGGCTC
                                | || |||    || |||||||
                                A TC GGT    GA CCCCGAG
                                 C  C   C___  A
GAM269  CERD4    3'  AAGACCATTACACACAGCT   28942          CT  G
                                AAGACCATTAC  CG GGCT
                                ||||||||||  || ||||
                                TTCTGGTAATG  GT TCGA
                                       T_  G
GAM269  CSNK1A1  5'  GACGGAGGCCTCGGGGCTCC  12463    CATTA
                                GAC    CCTCGGGGCTCC
                                |||    ||||||||||||
                                CTG    GGAGCCCCGAGG
                                  CCTCC
GAM269  DLEC1    3'  TGAGACCATTGTGGAAGGGGGT 28839   A      ACCTC__   C
           TC                     A AGACCATT      GGGG TC
                                | ||||||||      |||| ||
                                A TCTGGTAA      CCCC AG
                                 C       CACCTTC    A
GAM269  FPRL1    3'  AGACCATTACAAGTTTC     11144         CTC   GC
                                AGACCATTAC   GGG  TC
                                ||||||||||   |||  ||
                                TCTGGTAATG   TTC  AG
                                      ___   AA
GAM269  FXYD6    3'  AAGACCACTGCCCGTGCTC   35111        A  T  GG
                                AAGACCATT CC CG  GCTC
                                ||||||||| || ||  ||||
                                TTCTGGTGA GG GC  CGAG
                                     C  _  A_
GAM269  MHC2TA   3'  AGAGAAGGCCTCGGGGCTCC  6979     CCATTA
                                AGA     CCTCGGGGCTCC
                                |||     ||||||||||||
                                TCT     GGAGCCCCGAGG
                                  CTTCC_
GAM269  PRKACA   3'  AAAGACTTGGGCTTGGGGCTCC 15569       CATTAC  C
                                AAAGAC     CT GGGGCTCC
                                ||||||     || ||||||||
                                TTTCTG     GA CCCCGAGG
                                   AACCC_  A
GAM269  TEM8     3'  GACCATTGTCTCTCAGCTC   38179       AC   GG
                                GACCATT  CTC  GGCTC
                                |||||||  |||  |||||
                                CTGGTAA  GAG  TCGAG
                                   CA   AG
GAM269  TNS      5'  GAGCCGTTGTCCTCGAGGCT   35475    _  ATTA_
                                GA CC    CCTCGGGGCT
                                || ||    ||||||||||
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                                CT GG    GGAGCTCCGA
                                 C  CAACA
GAM270  BCL11A   3'  TATTTCTTTTGGTGCCAGTATT 39720       CCCAACACC
                                TATTTCT       CCAGTATT
                                |||||||       ||||||||
                                ATAAAGA       GGTCATAA
                                    AAACCAC__
GAM270  KCNJ3    3'  TATTTCTCCCCAGTACT    13850       CCCAACA
                                TATTTCT     CCCCAGTATT
                                |||||||     ||||||||||
                                ATAAAGA     GGGGTCATGA
                                        _______
GAM270  PPP1R12B 3'  TTTCTCTTGGCACCCCAAT   36960      CCAA
                                TTTCTC   CACCCCAGT
                                ||||||   |||||||||
                                AAAGAG   GTGGGGTTA
                                    AACC
GAM270  RANBP9   3'  ATTTCTCCTAACACTAAGT   24247       C    CCC
                                ATTTCTCC AACAC   AGT
                                |||||||| |||||   |||
                                TAAAGAGG TTGTG   TCA
                                     A    AT_
GAM270  ADAMTS4  5'  AGGGGTCTGGCTTCTCCA    23000      G   AG
                                AGGGGT TGG  TCTCCA
                                |||||| |||  ||||||
                                TCCCCA ACC  AGAGGT
                                   G   GA
GAM270  ADCY7    3'  AGGGAGAGGGAGTCTCCA    9979      TGT
                                AGGGG   GGAGTCTCCA
                                |||||   ||||||||||
                                TCCCT   CCTCAGAGGT
                                  CTC
GAM270  AGRP     5'  AGGAGTGCCTATCTCCA     28731       GGA
                                AGGGGTGT   GTCTCCA
                                ||||||||   |||||||
                                TCCTCACG   TAGAGGT
                                     GA_
GAM270  APLP1    3'  AGAGGGTGAATTCCA      23161      T    GTC
                                AGGGG GTGGA   TCCA
                                ||||| |||||   ||||
                                TCTCC CACTT   AGGT
                                  _    A__
GAM270  ARHC     5'  AGGGGTGGGAGCCCCA     23165       T     T
                                AGGGGTG GGAGTC CCA
                                ||||||| |||||| |||
                                TCCCCAC CCTCGG GGT
                                     _    _
GAM270  ATRX     3'  AGGGGCGTGGATCCA      39601          GTC
                                AGGGGTGTGGA   TCCA
                                ||||||||||   ||||
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                                TCCCCGCACCT  AGGT
                                    ___
GAM270  BCL7A    3'  AGGGTGTGCAAATCTTTCCA  34200       _   __
                                GGGGTGTG GAGTC  TCCA
                                |||||||| |||||  ||||
                                TCCCACAC TTTAG  AGGT
                                    G    AA
GAM270  BMP1     3'  AGGGGCGCCTTCCTCCA    25971       GGAG
                                AGGGGTGT   TCTCCA
                                ||||||||   ||||||
                                TCCCCGCG   GGAGGT
                                    GAA_
GAM270  C18orf2  3'  AGGGGTTGGATATTCCA    36406      G   GTC
                                AGGGGT TGGA  TCCA
                                |||||| ||||  ||||
                                TCCCCA ACCT  AGGT
                                   _  ATA
GAM270  C5       3'  AGGAGTATCTGTCTTCA    11915       GGA   C
                                AGGGGTGT  GTCT CA
                                ||||||||  |||| ||
                                TCCTCATA  CAGA GT
                                    GA_   A
GAM270  CHAT     5'  AGAGGTGTGGACATTTCCA  34184         _ C
                                AGGGGTGTGGA GT TCCA
                                |||||||||| || ||||
                                TCTCCACACCT TA AGGT
                                     G  A
GAM270  CHD3     5'  AGGAGAAAGTCTCCA      10457      TGT
                                AGGGG  GGAGTCTCCA
                                |||||  ||||||||||
                                TCCTC  TTTCAGAGGT
                                   ___
GAM270  COLQ     3'  AAGGGTGTCCCTCCA      38690       GGAG
                                AGGGGTGT   TCTCCA
                                ||||||||   ||||||
                                TTCCCACA   GGAGGT
                                    G___
GAM270  CTSF     3'  AGGGGCTGTGCCCCA      45364      _   GAGT
                                AGGGG TGTG   CTCCA
                                ||||| ||||   |||||
                                TCCCC ACAC   GGGGT
                                  G  ____
GAM270  DIA1     3'  AGGGATGTGGCCCCA      28783        AGT
                                AGGGGTGTGG  CTCCA
                                ||||||||||  |||||
                                TCCCTACACC  GGGGT
                                    ___
GAM270  DLG4     3'  AGGAGTGTCCCCCCTCCA   10699       GGAG
                                AGGGGTGT   TCTCCA
                                ||||||||   ||||||
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                                TCCTCACA   GGAGGT
                                    GGGG
GAM270  E48     3'  AGAGGTGTGGAATCCCCA    18977
                                AGGGGTGTGGAGTCTCCA
                                ||||||||||||||||||
                                TCTCCACACCTTAGGGGT

GAM270  ENTPD6  3'  AGAGGTGTCTCCCTCCA     10334       GGAG
                                AGGGGTGT   TCTCCA
                                ||||||||   ||||||
                                TCTCCACA   GGAGGT
                                    GAG_
GAM270  FACL4   5'  GGTGGTGTGGCAGAGCCA    35683   _     _ TCT
                                GG GGTGTGG AG   CCA
                                || ||||||| ||   |||
                                CC CCACACC TC   GGT
                                 A      G  TC_
GAM270  FGFR1   3'  AGGGGTGTTGGTCCA       31928       _ AGTC
                                AGGGGTGT GG   TCCA
                                |||||||| ||   ||||
                                TCCCCACA CC   AGGT
                                    A _____
GAM270  FXYD6   3'  GGAGCCTGCTGAGTCTCCA   35119      G __
                                GGGGT TG  GAGTCTCCA
                                ||||| ||  |||||||||
                                CCTCG AC  CTCAGAGGT
                                   G  GA
GAM270  GCNT3   5'  AGGCGTGATTCTGTTTCCA   21905       A___  C
                                GGGTGTGG   GT TCCA
                                ||||||||   || ||||
                                TCCGCACT   CA AGGT
                                    AAGA  A
GAM270  GRN     3'  AGGGCTGCAGAGTCTTCA    13290     G  TG    C
                                AGGG TG  GAGTCT CA
                                |||| ||  |||||| ||
                                TCCC AC  CTCAGA GT
                                  G  GT     A
GAM270  HLA-C   3'  GGGGTGGGCTGTCTCTCCA   45134      T  AG___
                                GGGGTG GG    TCTCCA
                                |||||| ||    ||||||
                                CCCCAC CC    AGAGGT
                                   _  GACAG
GAM270  HMGB3   3'  AGGGAGGCCAGTCTCCA     23776      T  GG
                                AGGGG GT  AGTCTCCA
                                ||||| ||  ||||||||
                                TCCCT CG  TCAGAGGT
                                   C  G_
GAM270  HOXB7   3'  AGGGGAGGTAAATTCCA     21068      T_    GTC
                                AGGGG  GTGGA   TCCA
                                |||||  |||||   ||||
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                                TCCCC  CATTT   AGGT
                                  TC    A__
GAM270  IL12RB2  3'  AGAGGTAGAACATTTCCA    11420       T  _  C
                                AGGGGTG GGA GT TCCA
                                ||||||| ||| || ||||
                                TCTCCAT CTT TA AGGT
                                   _  G  A
GAM270  INSRR    3'  GGGTGTGGACTCCTCTCCA   42846        G___
                                GGGTGTGGA   TCTCCA
                                |||||||||   ||||||
                                CCCACACCT   AGAGGT
                                     GAGG
GAM270  KCNA3    3'  AGGGGGCACGTTCCA      13789      T  GA  C
                                AGGGG GTG  GT TCCA
                                ||||| |||  || ||||
                                TCCCC CGT  CA AGGT
                                   _  G_  _
GAM270  KHK      3'  AGCGGTGTGGACTCCCA    27052    G      G  T
                                AG GGTGTGGA TC CCA
                                || |||||||| || |||
                                TC CCACACCT AG GGT
                                 G       G  _
GAM270  KIR2DL1  3'  AGGAGTGTGTTTTTTCTCCA  30568        GAG__
                                AGGGGTGTG    TCTCCA
                                |||||||||    ||||||
                                TCCTCACAC    AGAGGT
                                     AAAAA
GAM270  KIR2DL2  3'  AGGAGTGTGTTTTTTCTCCA  30570        GAG__
                                AGGGGTGTG    TCTCCA
                                |||||||||    ||||||
                                TCCTCACAC    AGAGGT
                                     AAAAA
GAM270  KIR2DL3  3'  AGGAGTGTGTTTTCTCTCCA  30952        GAG__
                                AGGGGTGTG    TCTCCA
                                |||||||||    ||||||
                                TCCTCACAC    AGAGGT
                                     AAAAG
GAM270  KIR2DL5  3'  AGGAGTGTGTCTTCTCTCCA  33920        GAG__
                                AGGGGTGTG    TCTCCA
                                |||||||||    ||||||
                                TCCTCACAC    AGAGGT
                                     AGAAG
GAM270  KIR2DS2  3'  AGGAGTGTGTTTTCTCTCCA  29478        GAG__
                                AGGGGTGTG    TCTCCA
                                |||||||||    ||||||
                                TCCTCACAC    AGAGGT
                                     AAAAG
GAM270  KIR2DS4  3'  AGGAGTGTGTTTTCTCTCCA  29483        GAG__
                                AGGGGTGTG    TCTCCA
                                |||||||||    ||||||
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                                TCCTCACAC    AGAGGT
                                     AAAAG
GAM270  KLRC4   3'  AGAAGCATGGGTTTCCA    30235        A  C
                                AGGGGTGTGG GT TCCA
                                |||||||||| || ||||
                                TCTTCGTACC CA AGGT
                                     _  A
GAM270  LILRB4  3'  AGGAGAACTGAGTCTCCA   27773     TGTG
                                AGGGG   GAGTCTCCA
                                |||||   |||||||||
                                TCCTC   CTCAGAGGT
                                   TTGA
GAM270  LNK     3'  AGGGGTTTGTTCCCCCA    24194      G  GAG
                                AGGGGT TG   TCTCCA
                                |||||| ||   ||||||
                                TCCCCA AC   GGGGGT
                                    A  AA_
GAM270  LSS     3'  AGGGGTATGCGGCTCCA    14246       GA T
                                AGGGGTGTG  G CTCCA
                                |||||||||  | |||||
                                TCCCCATAC  C GAGGT
                                     GC _
GAM270  MATK    5'  AGGGGTGTTGCTTCTCCA   40304       GGAG
                                AGGGGTGT   TCTCCA
                                ||||||||   ||||||
                                TCCCCACA   AGAGGT
                                     ACGA
GAM270  MMP15   3'  GGGGCCAGACAGTCTCCA   14563     GT  _
                                GGGGT  GG AGTCTCCA
                                |||||  || ||||||||
                                CCCCG  CT TCAGAGGT
                                   GT  G
GAM270  MPV17   3'  AAGGGTTCCGGGAGTCTC   43260     GT__
                                AGGGGT   GGAGTCTC
                                ||||||   ||||||||
                                TTCCCA   CCTCAGAG
                                    AGGC
GAM270  MRPL49  3'  AGGAGTGAGGGTTTCCA    43022      T  A  C
                                AGGGGTG GG GT TCCA
                                ||||||| || || ||||
                                TCCTCAC CC CA AGGT
                                     T  _  A
GAM270  NCOA3   3'  AGGGATGTCTCTTCCA     27213      GGAG  _
                                AGGGGTGT   TCT CCA
                                ||||||||   ||| |||
                                TCCCTACA   AGA GGT
                                     G___  A
GAM270  NDUFA6  3'  AGAGGTACACCAGGGTTTCCA 14740       T____  A  C
                                AGGGGTG    GG GT TCCA
                                |||||||    || || ||||
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                                TCTCCAT    CC CA AGGT
                                   GTGGT  _  A
GAM270  NSF     3'  GGGGTGTATGCTTTTTCCA   41784       GA  C___
                                GGGGTGTG  GT   TCCA
                                ||||||||  ||   ||||
                                CCCCACAT  CG   AGGT
                                   A_  AAAA
GAM270  NXF2    5'  AGGGCTGTGGAAGACCA    35186     G     TCT
                                AGGG TGTGGAG   CCA
                                |||| |||||||   |||
                                TCCC ACACCTT   GGT
                                  G      CT_
GAM270  OAS1    3'  AGGGATGTGAAAATTCCA    32544         TC
                                AGGGGTGTGGAG  TCCA
                                ||||||||||||  ||||
                                TCCCTACACTTT  AGGT
                                      TA
GAM270  ODF2    5'  AGGGGTGTTCTCATCCA     14926       GGAG  _
                                AGGGGTGT   TC TCCA
                                ||||||||   || ||||
                                TCCCCACA   AG AGGT
                                   AG__  T
GAM270  OPHN1   3'  AGGGGCATCATGGAGTTTC   14961      ___     C
                                AGGGGT  GTGGAGT TC
                                ||||||  ||||||| ||
                                TCCCCG  TACCTCA AG
                                   TAG     A
GAM270  PACSIN1 3'  AGGGGCGTGGCCCCCA     45140        AG
                                AGGGGTGTGG  TCTCCA
                                ||||||||||  ||||||
                                TCCCCGCACC  GGGGGT
                                      __
GAM270  PCTK1   3'  AGGGGTGTGGCATCCCTCCA  37464        AG__
                                AGGGGTGTGG   TCTCCA
                                ||||||||||   ||||||
                                TCCCCACACC   GGAGGT
                                     GTAG
GAM270  POU2AF1 5'  GGGGTGTGTTTTCCTCCA   26373       GAG_
                                GGGGTGTG   TCTCCA
                                ||||||||   ||||||
                                CCCCACAC   GGAGGT
                                   AAAA
GAM270  PPP1R12B 3' GGTGCTCATGAGTCTCCA   36978     G___
                                GGTGT   GAGTCTCCA
                                |||||   |||||||||
                                CCACG   CTCAGAGGT
                                  AGTA
GAM270  PPP3CB  3'  GAGGTGTGGATGCCCTCCA  34448        _  _
                                GGGGTGTGGA GTC TCCA
                                |||||||||| ||| ||||
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                                CTCCACACCT CGG AGGT
                                     A   G
GAM270  PPT1     3'  GGAGTGTGTAGTATTTTCCA  41553        G   C___
                                GGGGTGTG AGT    TCCA
                                |||||||| |||    ||||
                                CCTCACAC TCA    AGGT
                                     A   TAAA
GAM270  PSCD4    3'  GGGGTGGGAGGTGGGTCTCCA 30129       T   _____
                                GGGGTG GGA     GTCTCCA
                                |||||| |||     |||||||
                                CCCCAC CCT     CAGAGGT
                                   _   CCACC
GAM270  PTPN7    3'  GAGGTGTGGGCAAGTCCA    38713         A  C__
                                GGGGTGTGG GT   TCCA
                                ||||||||| ||   ||||
                                CTCCACACC CG   AGGT
                                     _  TTC
GAM270  RAP1GA1  3'  AGGGGTGATGGAGGCCCA   16158         _    T T
                                AGGGGTG TGGAG C CCA
                                ||||||| ||||| | |||
                                TCCCCAC ACCTC G GGT
                                     T    C _
GAM270  RFX1     3'  AGGAGAAGCGTGGTCTCC    16289       T_   GA
                                AGGGG  GTG  GTCTCC
                                |||||  |||  ||||||
                                TCCTC  CGC  CAGAGG
                                   TT   AC
GAM270  RNASE1   5'  AGGGCTGTGGAGCTTCCA    16339      G      TC
                                AGGG TGTGGAG  TCCA
                                ||||  |||||||  ||||
                                TCCC ACACCTC  AGGT
                                  G      GA
GAM270  SAC      5'  AGGAAGCAGTCTCCA       32940       T  GG
                                AGGGG GT  AGTCTCCA
                                ||||| ||  ||||||||
                                TCCTT CG  TCAGAGGT
                                   _  __
GAM270  SCA1     3'  AGAGGTGTGAAAGGTTCC    7272           _ TC
                                AGGGGTGTGGA G  TCC
                                |||||||||||  |  |||
                                TCTCCACACTT C  AGG
                                     T CA
GAM270  SH2D2A   5'  AGGGTGTGTGTATGTGTTCC  19564      _    GA_  C_
                                AGGG GTGTG   GT  TCC
                                ||||  |||||   ||  |||
                                TCCC CACAC   CA  AGG
                                  A    ATA  CA
GAM270  SOX12    3'  AGGGGGTGGGCCCCA       28026       T   A   T
                                AGGGG GTGG GTC CCA
                                ||||| |||| ||| |||
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                                TCCCC CACC CGG GGT
                                  _   _  _
GAM270  SOX13    3'  AGGGGTGTTGGTCCCA      25008        GGA  T
                                AGGGGTGT  GTC CCA
                                ||||||||  ||| |||
                                TCCCCACA  CAG GGT
                                    AC_  _
GAM270  ST14     3'  AGCGGTCCAGTCTCCA      35056    G  G GG
                                AG GGT T  AGTCTCCA
                                || ||| |  ||||||||
                                TC CCA G  TCAGAGGT
                                 G  G __
GAM270  TIMP3    3'  AGAGGTGTCCCTCCA       7439         GGAG
                                AGGGGTGT   TCTCCA
                                ||||||||   ||||||
                                TCTCCACA   GGAGGT
                                    G___
GAM270  UBE2L3   3'  GGGCACAAGGGAGTCTCCA   17830     TG ___
                                GGG  T  GGAGTCTCCA
                                |||  |  ||||||||||
                                CCC  G  CCTCAGAGGT
                                 GT TTC
GAM271  ADCY8    5'  CGGGCCGGGGGGTGGCGGAGGG  10005     A  CACAT  C
                                CGG CC    GG GGCGGAGGG
                                ||| ||    || |||||||||
                                GCC GG    CC CCGCCTCCC
                                 C  CCC__  A
GAM271  AQP6     5'  ACGGGGCTGCATGGCGGCTCCA 11637     ACCCA       GG_
           AG                    ACGG    CATGGCGGC  AGG
                                ||||    |||||||||  |||
                                TGCC    GTACCGCCG  TTC
                                  CCGAC       AGG
GAM271  ARHC     5'  CGGCCCGTGTCCGGGGGG    23169     A  ACA  G_  C  A
                                CGG CCC   TG  CGG GG GG
                                ||| |||   ||  ||| || ||
                                GCC GGG   AC  GCC CC CC
                                  _  C__  AG  _ _
GAM271  CGTHBA   5'  ACGGAGCCGGAGGCGGAGG   28957      C  ACAT  C
                                ACGGA CC    GG GGCGGAGG
                                ||||| ||    || ||||||||
                                TGCCT GG    CC CCGCCTCC
                                  C  ____  T
GAM271  CRYAA    3'  GGGCCCGCCGCGGAGG      7564     A  ACATG  G
                                GG CCC     GC GCGGAGG
                                || |||     || |||||||
                                CC GGG     CG CGCCTCC
                                 C  _____  G
GAM271  ECH1     5'  ACGTGCCCGTTAGCGGAGG   40862     GA  ACAT GC
                                ACG  CCC   G  GGCGGAGG
                                |||  |||   |  ||||||||
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                                TGC  GGG   C  TCGCCTCC
                                  AC  ____ AA
GAM271  EGLN2   5'  ACGGCGTCCACATGGGCCATGA 38812     AC_      CGGCG
              GGG                  ACGG  CCACATGG   GAGGG
                                ||||  ||||||||   |||||
                                TGCC  GGTGTACC   CTCCC
                                  GCA      CGGTA
GAM271  FABP5   5'  CGGGCTGGCGTGCAGAGAG   11065    ACCCACA   _
                                CGG     TGGCG GCGGAGGG
                                |||      ||||| ||||||||
                                GCC      ACCGC CGTCTCTC
                                  CG_____    A
GAM271  G6PD    5'  CGGCCTCGCGCGCTCGCGGAGG 7601     A  CACA  _  G_
              G                   CGG CC   TG GC  GCGGAGGG
                                ||| ||   || ||  ||||||||
                                GCC GG   GC CG  CGCCTCCC
                                  _ AGC_  G  AG
GAM271  GAS41   5'  CGGGCCCAGGCGGAGG     27200    A   CATGGC
                                CGG CCCA     GGCGGAGG
                                ||| ||||     ||||||||
                                GCC GGGT     CCGCCTCC
                                  C  _______
GAM271  HK2     5'  CGCCCGGCTGGCGGAGGG    6786    GA  ACAT  _
                                CG  CCC   GGC GGCGGAGGG
                                ||  |||   ||| |||||||||
                                GC  GGG   CCG CCGCCTCCC
                                  __  _____  A
GAM271  HMX1    3'  GGACCCACAGGTCCAGGG    33212       T  CGG  A
                                GGACCCACA GG  CGG GG
                                ||||||||| ||  ||| ||
                                CCTGGGTGT CC  GTC CC
                                     _ AG_  _
GAM271  IGFBP4  5'  CGGGCGAGCGGCGGAGG     11399    ACCCACAT
                                CGG      GGCGGCGGAGG
                                |||      ||||||||||
                                GCC      TCGCCGCCTCC
                                  CGC_____
GAM271  MAPK1   5'  CGGGCCGGCGGGCGGGCGGAGG 15650    A  CACAT   _
              G                   CGG CC    GGCGG CGGAGGG
                                ||| ||    ||||| |||||||
                                GCC GG    CCGCC GCCTCCC
                                  C  CCGC_    C
GAM271  MAPRE3  5'  CGGCTCCGGGGCGGAGG    29530    AC  ACAT  C
                                CGG  CC   GG GGCGGAGG
                                |||  ||   || ||||||||
                                GCC  GG   CC CCGCCTCC
                                  GA  ____  _
GAM271  MBD1    5'  GGACCCATGGCGAG       31922       CA   GGCG
                                GGACCCA  TGGC   GAG
                                |||||||  ||||   |||
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                                CCTGGGT  ACCG   CTC
                                   __   ____
GAM271  NF1     5'  CGGCCGGGGGGCGGCGGAGGG  7055     A  CACAT
                                CGG CC    GGCGGCGGAGGG
                                ||| ||    ||||||||||||
                                GCC GG    CCGCCGCCTCCC
                                  _ CCCC_
GAM271  OPTN    5'  CGGCGGCGGTGGCGGAGG    35066    ACCCACA  C
                                CGG      TGG GGCGGAGG
                                |||      ||| ||||||||
                                GCC      GCC CCGCCTCC
                                  GCC____  A
GAM271  PGM1    5'  CGGACTTGGCTGGCGGAGGG   15258      CCACA   _
                                CGGAC    TGGC GGCGGAGGG
                                |||||    |||| |||||||||
                                GCCTG    ACCG CCGCCTCCC
                                   A____   A
GAM271  PLXNA1  3'  CGGCCCGCAGGTCGGGGGGG   43619    A  A  T  _  C  A
                                CGG CCC CA GG CGG GG GG
                                ||| ||| || || ||| || ||
                                GCC GGG GT CC GCC CC CC
                                  _  C  _  A  _  _
GAM271  PTPRF   3'  GGGTCTGGTGGACAGAAGG   39037    ACCCACA  C  _
                                GG      TGG GG CGGAGGG
                                ||      ||| || |||||||
                                CC      ACC CC GTCTTCC
                                 CAG____  A  T
GAM271  SIX2    3'  ACTGACCCACATGGGCGAGGG  32599    G        CG   G
                                AC GACCCACATGG  GCG AGGG
                                || ||||||||||  ||| ||||
                                TG CTGGGTGTACC  CGC TCCC
                                 A        __  _
GAM271  SOX12   5'  CGGGCCCAACGGACGGCGGGGG 28035    A   C   _    A
                                CGG CCCA ATGG CGGCGG GGG
                                ||| |||| |||| |||||| |||
                                GCC GGGT TGCC GCCGCC CCC
                                  C   _   T    _
GAM271  SYBL1   5'  CGGGCTCGGGACGGAGG    24846    ACCCACA  C
                                CGG      TGG GGCGGAGG
                                |||      ||| ||||||||
                                GCC      GCC CTGCCTCC
                                  CGA____  _
GAM271  TARBP2  5'  GGACATGCGTACTAGCGGAGGG 39533     CCACATG  _
                                GGAC      GC GGCGGAGGG
                                ||||      || |||||||||
                                CCTG      TG TCGCCTCCC
                                  TACGCA_  A
GAM271  TLL1    5'  GGCCCACGGGTGGGCGGAGGG  29739    A    AT  C_
                                GG CCCAC  GG  GGCGGAGGG
                                || |||||  ||  |||||||||
```

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                                CC GGGTG  CC  CCGCCTCCC
                                 _    C_  AC
GAM271  UBE3A   5' GGCTACGCGGCGGAGG     7862     ACCC  ATG
                                GG   AC   GCGGCGGAGG
                                ||   ||   ||||||||||
                                CC   TG   CGCCGCCTCC
                                 GA__  ___
GAM271  WEE1    5' CGAGCCTGGGGCGGCGGGGG  18088    GA  CACAT      A
                                CG  CC    GGCGGCGG GGG
                                ||  ||    |||||||| |||
                                GC  GG    CCGCCGCC CCC
                                 TC  ACC__       _
GAM271  WNT1    3' GACCCCATGGCGGAGG      24081      A     GGC
                                GACCC CATGGC   GGAGG
                                ||||| ||||||   |||||
                                CTGGG GTACCG   CCTCC
                                   _    ___
GAM271  WNT6    5' GGATCCGGCGGCGGCGGGGG  27184     C  ACA       A
                                GGA CC   TGGCGGCGG GGG
                                ||| ||   ||||||||| |||
                                CCT GG   GCCGCCGCC CCC
                                 A  CC_       _
GAM271  ZRF1    5' CGGCTCACGTCCCGGGCGGAGG 45349     ACC   ATGGC_
          G                      CGG   CAC     GGCGGAGGG
                                 |||   |||     |||||||||
                                 GCC   GTG     CCGCCTCCC
                                  GA_  CAGGGC
GAM271  BNC     3' AAAGCCACCCCCAGGTCC    11850        ATG_  A
                                AGAGCCAC    AGG TCC
                                ||||||||    ||| |||
                                TTTCGGTG    TCC AGG
                                    GGGG  _
GAM271  CACNA1G  3' ACCCAGAGCCACTGAGG     33127           A
                                ACCCAGAGCCAC TGAGG
                                |||||||||||| |||||
                                TGGGTCTCGGTG ACTCC
                                           _
GAM271  CDK10   3' CAGAGCCACGGCCTCC      38146         ATGA  A_
                                CAGAGCCAC    GG  TCC
                                |||||||||    ||  |||
                                GTCTCGGTG    CC  AGG
                                     _____  GG
GAM271  CELSR3  3' CCTAGGGCCACGGAGGATCC  10836    C  A    AT
                                CC AG GCCAC  GAGGATCC
                                || || |||||  ||||||||
                                GG TC CGGTG  CTCCTAGG
                                 A  C    C_
GAM271  CLN3    3' ACCTGCGTCCTGAGGATCCCG  6358     CAGA  CACA
                                ACC   GC   TGAGGATCCCG
                                |||   ||   ||||||||||
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                                TGG   CG   ACTCCTAGGGC
                                  A___  CAGG
GAM271  DAP3    3'  CCAGAGCCAACTGCAGTCC   38012        CA  A  A
                                CCAGAGCCA  TG GG TCC
                                |||||||||  || || |||
                                GGTCTCGGT  AC TC AGG
                                     TG  G  _
GAM271  DCTN1   5'  ACCCAGAGACACAGAATCC   35695        C   TGA
                                ACCCAGAG CACA   GGATCC
                                |||||||| ||||   ||||||
                                TGGGTCTC GTGT   CTTAGG
                                     T   ___
GAM271  DNASE1  5'  AGGCCCAGGGGATCCCG    23350    A   A  TGA
                                AG GCC CA   GGATCCCG
                                || ||| ||   ||||||||
                                TC CGG GT   CCTAGGGC
                                 _  _  CC_
GAM271  DPH2L2  3'  CCAGGGTCCTTCAAGGATC   10734     AG_  ACA
                                CCAG   CC   TGAGGATC
                                ||||   ||   ||||||||
                                GGTC   GG   GTTCCTAG
                                  CCA  AA_
GAM271  EGFL3   3'  CCCAGAGCGTGCCCC      41705        CACA  AGGA
                                CCCAGAGC   TG   TCCC
                                ||||||||   ||   ||||
                                GGGTCTCG   AC   GGGG
                                     C___  ____
GAM271  FAT2    3'  ACCCAGAGTTCCATGAGGTC   11069        CCA     A
                                ACCCAGAG   CATGAGG TC
                                ||||||||   ||||||| ||
                                TGGGTCTC   GTACTCC AG
                                     AAG     _
GAM271  FGF5    3'  CAGGGCCACATACCACTCCCG  37584    A       AGGA
                                CAG GCCACATG   TCCCG
                                ||| ||||||||   |||||
                                GTC CGGTGTAT   AGGGC
                                  C       GGTG
GAM271  IGF1    3'  CAGAGCAAAGGATCC       8336        CACAT
                                CAGAGC    GAGGATCC
                                ||||||    ||||||||
                                GTCTCG    TTCCTAGG
                                   T____
GAM271  JAG2    3'  CCTGGAGCCACAGAGAAACCCG 13711    CA      T    T
                                CC  GAGCCACA GAGGA CCCG
                                ||  |||||||| ||||| ||||
                                GG  CTCGGTGT CTCTT GGGC
                                 AC       _    T
GAM271  MIC2    5'  CCCAGAGCGCGCAGGGACGGTC 14500        CA_  T_  _  A
            CCG                   CCCAGAGC   CA  GA GG TCCCG
                                ||||||||   ||  || || |||||
```

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                                GGGTCTCG  GT  CT CC AGGGC
                                    CGC  CC  G  _
GAM271  NOX4    5'  ACCCAGAGCCGGGTTTTCC   32592        ACAT A  A__
                                ACCCAGAGCC   G GG   TCC
                                ||||||||||   | ||   |||
                                TGGGTCTCGG   C CC   AGG
                                     _____ _  AAA
GAM271  NTSR1   3'  CCCAGAGCCCATTTCCC    14878        A  GAGGA
                                CCCAGAGCC CAT    TCCC
                                ||||||||| |||    ||||
                                GGGTCTCGG GTA    AGGG
                                     _  A____
GAM271  PFKFB3  5'  CCCGGGGCCGAGATCCC    44433    AGA  ACAT  G
                                CCC  GCC   GAG ATCCC
                                |||  |||   ||| |||||
                                GGG  CGG   CTC TAGGG
                                  CCC  _____  _
GAM271  PFKFB4  3'  CAGGGCCCCATGAAGACC    21287    A  A
                                CAG GCC CATGAGGATC
                                ||| ||| ||||||||||
                                GTC CGG GTACTTCTGG
                                  C  G
GAM271  PLA2G2D 3'  CCTGGAGCCACAAGACC    29632    CA      TGA
                                CC  GAGCCACA  GGATC
                                ||  ||||||||  |||||
                                GG  CTCGGTGT  TCTGG
                                 AC      ___
GAM271  PNUTL1  3'  CCTAGGCTCAGGATCCC    15427    C  A  _  CATGA
                                CC AG GC CA    GGATCCC
                                || || || ||    |||||||
                                GG TC CG GT    CCTAGGG
                                 A  _  A  _____
GAM271  PTPN11  5'  CCAGGCCTGGGGATCCC    38753    A  ACA  A
                                CCAG GCC  TG GGATCCC
                                |||| |||  || |||||||
                                GGTC CGG  AC CCTAGGG
                                  _  ___  C
GAM271  PYGO2   3'  CCATGGCAATGAGGATCCCG  41948    GA  CAC
                                CCA  GC  ATGAGGATCCCG
                                |||  ||  ||||||||||||
                                GGT  CG  TACTCCTAGGGC
                                  AC  T__
GAM271  RAB36   3'  ACCCAGAACCATAAGTCC    22230        CA   GA
                                ACCCAGAGCCA  TGAG  TCC
                                ||||||||||  ||||  |||
                                TGGGTCTTGGT  ATTC  AGG
                                     __   __
GAM271  REPS2   5'  CCCGGAGCCACAGCCCCC    21808    A      TGAGGA
                                CCC GAGCCACA     TCCC
                                ||| ||||||||     ||||
```

```
                                GGG CTCGGTGT     GGGG
                                  C       CG____
GAM271  RERE    3'  CAGAGCCACGGGAACAAGCC  29022         AT A   TC___
                                CAGAGCCAC  G GGA     CC
                                |||||||||  | |||     ||
                                GTCTCGGTG  C CCT     GG
                                     __ _   TGTTC
GAM271  RUNX1   3'  CCCAGGGCCCGGGATCCCG   12015      A   ACA  A
                                CCCAG GCC   TG GGATCCCG
                                ||||| |||   || ||||||||
                                GGGTC CGG   GC CCTAGGGC
                                  C  ___ _
GAM271  SFRS7   3'  ACCCAGAGCTACAAGG      40464         C   TG
                                ACCCAGAGC ACA  AGG
                                ||||||||| |||  |||
                                TGGGTCTCG TGT  TCC
                                     A  __
GAM271  SRD5A1  3'  ACCCAGAGCTTGAAATTC    9825          CACA    A
                                ACCCAGAGC    TGAGG TC
                                |||||||||    ||||| ||
                                TGGGTCTCG    ACTTT AG
                                     A___     A
GAM271  SRR     3'  ACCCATGGCCACATGAAA    34962       GA
                                ACCCA  GCCACATGAGG
                                |||||  ||||||||||
                                TGGGT  CGGTGTACTTT
                                  AC
GAM271  TIMP3   5'  CCCAGAGCAAACGGGGTTC   7445          CAC   A  A
                                CCCAGAGC   ATG GG TC
                                ||||||||   ||| || ||
                                GGGTCTCG   TGC CC AG
                                     TT_   C  A
GAM271  TRPV1   5'  CAGAGCCATCTGTGGTTC    38792         CA  A  A
                                CAGAGCCA  TG GG TC
                                ||||||||  || || ||
                                GTCTCGGT  AC CC AG
                                     AG  A  A
GAM271  UBE3A   5'  CCGGGGCCGCCGAAATCCCG  7860      AGA   ACA   G
                                CC   GCC   TGAG ATCCCG
                                ||   |||   |||| ||||||
                                GG   CGG   GCTT TAGGGC
                                 CCC   CG_   _
GAM271  WNT3A   3'  ACCCAGAGCCACAGCCCCC   37532           TGAGGA
                                ACCCAGAGCCACA     TCCC
                                ||||||||||||     ||||
                                TGGGTCTCGGTGT     GGGG
                                       CG____
GAM271  ZYX     3'  CCCAGGGCGGGGATCC      18433       A  CACAT A
                                CCCAG GC    G GGATCC
                                ||||| ||    | ||||||
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                                GGGTC CG    C CCTAGG
                                  C _____ C
GAM272  CACNA1C  5'  TCAATGGTTTGTGGCCCTT   8759       G
                                TCAATGG TTTGTGGCCTTT
                                ||||||| ||||||||||||
                                AGTTACC AAACACCGGGAA
                                  _
GAM272  FABP6    3'  TGGGTTTGTAGCTCCCTG    11068        _
                                TGGGTTTGTGGC CTTTG
                                |||||||||||| |||||
                                ACCCAAACATCG GGGAC
                                      A
GAM272  ITSN1    3'  GGGCCTGTCTTTGCCA      16660       GGC
                                GGGTTTGT   CTTTGCCA
                                ||||||||   ||||||||
                                CCCGGACA   GAAACGGT
                                  ___
GAM272  MGEA5    3'  TCAATTGTAGGCTTTTGCC    29217      GGGTT  _  C
                                TCAAT    TGT GGC TTTGCC
                                |||||    ||| ||| ||||||
                                AGTTA    ACA CCG AAACGG
                                  _____  T  A
GAM272  PTER     3'  AATTAAATTGTGGCCTTTG    36212     GGGT
                                AAT    TTGTGGCCTTTG
                                |||    ||||||||||||
                                TTA    AACACCGGAAAC
                                  ATTT
GAM272  UNG      3'  TCAAAGGGTAGCCTTTG     38947     T    TTGT
                                TCAA GGGT    GGCCTTTG
                                |||| ||||    ||||||||
                                AGTT CCCA    TCGGAAAC
                                  T  _____
GAM272  APOBEC2  3'  GTCCAGTATGATTGG       27706       CCCA    AC
                                GTCCAGTA    TGAT  TGG
                                ||||||||    ||||  |||
                                CAGGTCAT    ACTA  ACC
                                  _____   __
GAM272  NEU3     3'  ATCCAGTACTACTGGC      27399        CCATGA
                                GTCCAGTAC     TACTGGC
                                |||||||||     |||||||
                                TAGGTCATG     ATGACCG
                                  _______
GAM273  CD28     3'  ATAGTTGAAGAACCATCATCT  26016     AA_
                                ATGG   GGGGATCATCATCT
                                ||||   ||||||||||||||
                                TATC   TTCTTGGTAGTAGA
                                  AAC
GAM273  GRPR     3'  TATAATGGTGATCCATCAT    23683        AAGGG   _
                                TATAATGG    GATC ATCAT
                                ||||||||    |||| |||||
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                                ATATTACC    CTAG TAGTA
                                   A____    G
GAM273  LRP4    3'  TGATAGGGGACCCAGTTATCT  42069    A      ATC__
                                TGG AGGGGATC    ATCT
                                ||| ||||||||    ||||
                                ACT TCCCCTGG    TAGA
                                  A       GTCAA
GAM273  NID     3'  TGGTGGGACATCATC      14800    AAG   T
                                TGG   GGGA CATCATC
                                |||   |||| |||||||
                                ACC   CCCT GTAGTAG
                                  A__   _
GAM273  ABCD2   5'  AACAGAAGAGCAAGCAGAAA  23146      T  GT  TC
                                AACAGA GAG  CG  GCAGAAA
                                |||||| |||  ||  |||||||
                                TTGTCT CTC  GT  CGTCTTT
                                   T   __  T_
GAM273  ACCN2   3'  CAGATGAGGTTGTTGAGA    33433        C  CGC
                                CAGATGAGGT GT   AGA
                                |||||||||| ||   |||
                                GTCTACTCCA CA   TCT
                                     A  AC_
GAM273  BTNL3   3'  CAAATGAGGAGCCTGGGA    27464        TC   GCA
                                CAGATGAGG  GTC   GA
                                |||||||||  |||   ||
                                GTTTACTCC  CGG   CT
                                     T_   ACC
GAM273  CALM3   3'  AGATGAGGGGCATGGAGA    23225        T_   CGC
                                AGATGAGG  CGT   AGA
                                ||||||||  |||   |||
                                TCTACTCC  GTA   TCT
                                   CC   CC_
GAM273  CD38    5'  GAAGATGAGGCCGGCAG     40506   C        TC
                                A AGATGAGGTCG  GCAG
                                | ||||||||||  ||||
                                C TCTACTCCGGC  CGTC
                                 T         __
GAM273  COL19A1  3'  AACAGATGAGACAGACTGCAGA 12365          T  TC__
          AA                    AACAGATGAGG CG    GCAGAAA
                                |||||||||| ||    |||||||
                                TTGTCTACTCT GT    CGTCTTT
                                     _  CTGA
GAM273  COPE    3'  AACAGATGGGGGTGC       28573        A  TC  C
                                AACAGATG GG  GT GC
                                |||||||| ||  || ||
                                TTGTCTAC CC  CA CG
                                   _  C_  _
GAM273  DLEC1   3'  CAGATGAGGTTGTCCCAG    28817         C   G
                                CAGATGAGGT GTC CAG
                                |||||||||| ||| |||
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                                GTCTACTCCA CAG GTC
                                      A   G
GAM273  EIF2C1   3'  AGTAAGGTGGGGCAGAAA    29171    A     CGTC
                                AG TGAGGT    GCAGAAA
                                || ||||||    |||||||
                                TC ATTCCA    CGTCTTT
                                 _     CCC_
GAM273  EIF4EBP2 3'  CAGGGAGGAGTGGCAGAA    19891     AT    TC  C
                                CAG  GAGG  GT GCAGAA
                                |||  ||||  || ||||||
                                GTC  CTCC  CA CGTCTT
                                  C_   T_  C
GAM273  FDX1     3'  AACAGATGAGATTATATGAAAA 41265           CG CGCA
                                AACAGATGAGGT  T    GAAAA
                                ||||||||||||  |    |||||
                                TTGTCTACTCTA  A    CTTTT
                                       AT TA__
GAM273  GAGEB1   5'  CAGATGAGTCTCAGTAGA    19119        G  G   C_
                                CAGATGAG TC TCG  AGA
                                ||||||||  || |||  |||
                                GTCTACTC AG AGT  TCT
                                     _ _   CA
GAM273  GPRC5B   3'  AGGTGACATCATCGCGGAAAA  32172    A   G       A
                                AG TGA GTCGTCGC GAAAA
                                || ||| ||||||||  |||||
                                TC ACT TAGTAGCG CTTTT
                                 C   G       C
GAM273  HIVEP3   3'  AACAGATGGGGCCGTGAGA   35988         A     CGC
                                AACAGATG GGTCGT   AGA
                                ||||||||  ||||||   |||
                                TTGTCTAC CCGGCA   TCT
                                     C     C__
GAM273  HMG20A   3'  AACAGATGGGAACAGAA     32861         A  TCGTC
                                AACAGATG GG    GCAGAA
                                ||||||||  ||    ||||||
                                TTGTCTAC CC    TGTCTT
                                     _  T_____
GAM273  HTR2A    5'  CAGATGAGGTGTAGAA      8387           C  CGC
                                CAGATGAGGT GT   AGAA
                                ||||||||||  ||   ||||
                                GTCTACTCCA CA   TCTT
                                          _  ____
GAM273  JUN      3'  ACAGATGATGCAGAA       13736         GGTCGTC
                                ACAGATGA      GCAGAA
                                ||||||||      ||||||
                                TGTCTACT      CGTCTT
                                     A_______
GAM273  MAN2A2   3'  CAGTGAGGAAGCCAGAG     25941     A    TC   C
                                CAG TGAGG  GTCG AG
                                ||| |||||  |||| ||
```

```
                                GTC ACTCC  CGGT TC
                                  _    TT   C
GAM273  MT1H    3'  CAAATGAGTCGGAGTTGTAGAA 25542       G  TCGC___
             AA                   CAGATGAG TCG      AGAAAA
                                  |||||||| |||      ||||||
                                  GTTTACTC AGC      TCTTTT
                                     _  CTCAACA
GAM273  NDUFC1  3'  AACAGATGGTGAATCCAGA   14746       GA  C_  G
                                  AACAGAT  GGT  GTC CAGA
                                  |||||||  |||  ||| ||||
                                  TTGTCTA  CCA  TAG GTCT
                                     __  CT  _
GAM273  NUCB1   3'  CAGATGAGGCCAGAAA     26152         CGTCG
                                  CAGATGAGGT    CAGAAA
                                  ||||||||||    ||||||
                                  GTCTACTCCG    GTCTTT
                                                _____
GAM273  PCDHB7  3'  ATGGGTGACTGCAGAAA    33202    A  C TC
                                  ATG GGT G  GCAGAAA
                                  ||| ||| |  |||||||
                                  TAC CCA T  CGTCTTT
                                    _  C GA
GAM273  RGL     3'  AACAGATGATGGAGATGCAGAA 31536        _ TC  C
             A                    AACAGATGA GG  GT GCAGAAA
                                  |||||||| ||  || |||||||
                                  TTGTCTACT CC  TA CGTCTTT
                                       A  TC  _
GAM273  SLC14A2 3'  GATGAGGCTTATTTCGCAGAA  28399       CG___
                                  GATGAGGT    TCGCAGAA
                                  ||||||||    ||||||||
                                  CTACTCCG    AGCGTCTT
                                       AATAA
GAM273  STAT6   3'  GATGGGGCAACAGAAAA    17153     A  TC  C
                                  GATG GG  GT GCAGAAAA
                                  |||| ||  || ||||||||
                                  CTAC CC  CG TGTCTTTT
                                    _ __  T
GAM273  STK13   3'  ACAAATGAGGTGGCAGAGCAG  17197         C  C__
                                  ACAGATGAGGT GT   GCAG
                                  |||||||||| ||   ||||
                                  TGTTTACTCCA CG   CGTC
                                        C  TCT
GAM273  TEGT    3'  ACAGATGGGGTTGACAAAA   42092       A  CGTC
                                  ACAGATG GGT    GCAGAA
                                  ||||||| |||    ||||||
                                  TGTCTAC CCA    TGTTTT
                                     C  AC__
GAM273  TK1     3'  CAGTGAAAGCCGCAGA     17550    A    TC
                                  CAG TGAGG  GTCGCAGA
                                  ||| |||||  ||||||||
```

```
                                GTC ACTTT  CGGCGTCT
                                  _    __
GAM273  TRIM34   3'  CAGATGAGTCAGTTGCAG    38971        G  _  C
                                CAGATGAG TC GT GCAG
                                |||||||| || || ||||
                                GTCTACTC AG CA CGTC
                                     _  T  A
GAM273  UCP2     3'  AGATGAGAATGTAGAAA     17843        TC  CGC
                                AGATGAGG  GT   AGAAA
                                ||||||||  ||   |||||
                                TCTACTCT  CA   TCTTT
                                     TA  ___
GAM273  YWHAG    3'  ACAGATGAGATAGAA       29782          CGTCGC
                                ACAGATGAGGT     AGAA
                                ||||||||||     ||||
                                TGTCTACTCTA     TCTT

                                _______
GAM273  ZNF74    5'  AACAAATGATTGGGCGCGGGGA 18296         __  T  T  CA
            A                    AACAGATGA  GG CG CG  GAA
                                |||||||||  || || ||  |||
                                TTGTTTACT  CC GC GC  CTT
                                     AA  C  _  CC
GAM274  GYS1     3'  AATTTGTAAGCCACACGG    44781        CC      _
                                AATTTGTG  AGTCACA GG
                                ||||||||  ||||||| ||
                                TTAAACAT  TCGGTGT CC
                                     __       G
GAM274  KCNJ10   3'  AACAACTTGTGTTAGTCAC   13864          CC
                                AACAATTTGTG  AGTCAC
                                ||||||||||  ||||||
                                TTGTTGAACAC  TCAGTG
                                      AA
GAM274  MAP3K8   3'  ACATTCATGGGTCACAGGAG  23300     A  TG  CCA
                                ACA TT  TG   GTCACAGGAG
                                ||| ||  ||   ||||||||||
                                TGT AA  AC   CAGTGTCCTC
                                  _  GT  C__
GAM274  MLLT4    3'  AACATATACCAGTTATGGGAG  25520     ATT       CACA
                                AACA   TGTGCCAGT    GGAG
                                ||||   |||||||||    ||||
                                TTGT   ATATGGTCA    CCTC
                                  ___        ATAC
GAM274  UQCRFS1  5'  AACCGCCCAACCGGTCACAGG  25634     AATTTGT   A
                                AAC      GCC GTCACAGG
                                |||      ||| ||||||||
                                TTG      TGG CAGTGTCC
                                  GCGGGT_   C
GAM275  MYO1C    3'  CATCCACTGTGTCCTTGGGTG  41464      A  GG  GG
                                CATC CA  TG  GTCCTTGGGTG
                                ||||  ||  ||  ||||||||||
```

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                                GTAG GT  AC  CAGGAACCCAC
                                  _ G_  A_
GAM275  OAS2    3'  GGCAGACATCCTTGGGTG    32552    TG  _
                                GG  GG GTCCTTGGGTG
                                ||  || ||||||||||
                                CC  CT TAGGAACCCAC
                                 GT  G
GAM275  XDH     5'  TCACAGGTTGGGGTCCCCG   40460        _
                                TCACAGGT GGGGTCCTTG
                                |||||||| ||||||||||
                                AGTGTCCA CCCCAGGGGC
                                     A
GAM275  AIM1    3'  CTACCTGTGACAAGAGCA    45082       ACGA  _
                                CTGCCT   GT ATAGGAGCA
                                ||||||   || |||||||||
                                GATGGA   CA TGTTCTCGT
                                   ____  C
GAM275  HLCS    3'  CTGCCTGTTAAGAGC       7639        ACGA  A
                                CTGCCT   GT TAGGAGC
                                ||||||   || |||||||
                                GACGGA   CA ATTCTCG
                                   ____  _
GAM275  HOXD4   5'  CCCTGCCTGCAGCCGGCGGGAG 31171         A G   ATA__
          CA                      CCCTGCCT C AGT    GGAGCA
                                ||||||||  | |||    ||||||
                                GGGACGGA G TCG    CCTCGT
                                     C _  GCCGC
GAM275  HUNK    3'  CCCTGCCTGTGGGCCACAGCA  31060        ACGA  ATAGG
                                CCCTGCCT   GT    AGCA
                                ||||||||   ||    ||||
                                GGGACGGA   CG    TCGT
                                     CACC  GTG__
GAM275  IGFBP4  3'  ACTCTCCTTATAGGAG      11391    C  G   ACGAG
                                AC CT CCT    TATAGGAG
                                || || |||    ||||||||
                                TG GA GGA    ATATCCTC
                                 A  _  _____
GAM275  MEN1    5'  CCCTGCCTGTGAGATGG     39168        AC   T  A
                                CCCTGCCT  GAG AT GG
                                ||||||||  ||| || ||
                                GGGACGGA  CTC TA CC
                                     CA  _ _
GAM276  ABCA2   5'  CCTCTGCGCGCCCCGCC    45522    GCC       C
                                CC  GCGCGCCCC GCC
                                ||  ||||||||| |||
                                GG  CGCGCGGGG CGG
                                 AGA       _
GAM276  ABCC8   5'  CCGCCGCCCGGCCCGGCC    7397      G    CC
                                CCGC CGCCC  GCCCGGCC
                                |||| |||||  ||||||||
```

```
                                GGCG GCGGG  CGGGCCGG
                                  _    C_
GAM276  ADARB1   5'  CCGCACGCGCGCCCCACGCTTC 31874     _       _  C_
            GGCCG                  CCGC CGCGCGCCCC CGC  CGGCCG
                                   |||| |||||||||| |||  ||||||
                                   GGCG GCGCGCGGGG GCG  GCCGGC
                                     T        T   AA
GAM276  ADORA1   5'  CCGCCGCAGCGCTCCCAGCCCG 8591        _   _  C
                                   CCGCCGC GCGC CCC GCCCG
                                   ||||||| |||| ||| |||||
                                   GGCGGCG CGCG GGG CGGGC
                                      T   A   T
GAM276  ADRBK1   3'  GCTGCCCGCCCACCTGGCCG   11534    C  G    CC   C
                                   GC GC CGCCC  GCC GGCCG
                                   || || |||||  ||| |||||
                                   CG CG GCGGG  TGG CCGGC
                                    A  G    __   A
GAM276  AHR      5'  CCGCCGCGCGCACCGGC     11546          CCCCGC
                                   CCGCCGCGCGC     CCGGC
                                   ||||||||||      |||||
                                   GGCGGCGCGCG     GGCCG
                                         T_____
GAM276  ALX4     5'  CCACCGCGCGCCTTGGC     34951          CCCGCCC
                                   CCGCCGCGCGCC      GGC
                                   ||||||||||||      |||
                                   GGTGGCGCGCGG      CCG
                                         AA_____
GAM276  APP      5'  CCTCCGCGTGCTCTCGCCTACC 7913     G    C  CCC    CG
            G                       CC CCGCG GC   CGCC  GCCG
                                    || ||||| ||   ||||  ||||
                                    GG GGCGC CG   GCGG  TGGC
                                     A    A  AGA   A_
GAM276  ATP1B1   5'  GCGGCGCGCCCCTGGC      11730    C       CGCCC
                                   GC GCGCGCCCC    GGC
                                   || |||||||||    |||
                                   CG CGCGCGGGG    CCG
                                    C       A____
GAM276  ATRN     5'  CCGGCTCCGCTTCGCCTGGCCG 40270     C  G  CC__   C
                                   CCG GC CC    CGCC GGCCG
                                   ||| || ||    |||| |||||
                                   GGC CG GG    GCGG CCGGC
                                     _ A  CGAA    A
GAM276  BCL7B    5'  CCGCCGCAGCGTCACAGCGGCC 11803       _  CCCC  C_
            G                       CCGCCGC GCG   CGC  CGGCCG
                                    ||||||| |||   |||  ||||||
                                    GGCGGCG CGC   GTG  GCCGGC
                                       T  A___   TC
GAM276  BIN1     5'  GCCGCGCGTCCAGACCGGC   40297        C  CCGC
                                   GCCGCGCG CC   CCGGC
                                   |||||||| ||   |||||
```

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                                CGGCGCGC GG   GGCCG
                                    A  TCT_
GAM276  BRF1    5'  CGCCGCGCGCGCCCGGGCCG  11330        C   CCC
                                CGCCGCGCGC CCCG  GGCCG
                                |||||||||| ||||  |||||
                                GCGGCGCGCG GGGC  CCGGC
                                    C   ___
GAM276  CALM3   5'  CCGCCGCGCGTCCGCGCC   23230        C  C
                                CCGCCGCGCG CC CGCC
                                |||||||||| || ||||
                                GGCGGCGCGC GG GCGG
                                    A  C
GAM276  CAPN10  3'  GCTGCCCCCCCGCCGTCTGGCCG 35788   _  G     C___
                                GC GC CCCCCGCC   GGCCG
                                || || ||||||||   |||||
                                CG CG GGGGGCGG   CCGGC
                                 A  _     CAGA
GAM276  CDH23   5'  CCGCCGCGTCTTCCCGCC   38072       CGCC
                                CCGCCGCG   CCCGCC
                                ||||||||   ||||||
                                GGCGGCGC   GGGCGG
                                    AGAA
GAM276  CDK2AP1 5'  CCGCGCGCGTCCGGGCGGC   21594       CC  CC
                                CCGCGCGC  CCG  CGGC
                                |||||||  |||  ||||
                                GGCGCGCG  GGC  GCCG
                                    CA  CC
GAM276  CDK9    5'  CCGCCGCCGCCCCCAGTCG   10389       G     CC
                                CCGCCGC CGCCCCCG  CG
                                |||||||  ||||||||  ||
                                GGCGGCG GCGGGGGT  GC
                                    _     CA
GAM276  CHN2    5'  CCGCCGCTGCCCTCGCCCGGCC 19808       GC   C
          G                      CCGCCGC  GCCC CGCCCGGCCG
                                |||||||  |||| ||||||||||
                                GGCGGCG  CGGG GCGGGCCGGC
                                    A_   A
GAM276  CHN2    5'  CCGCGCGCCCCTCGCGTCG   19809         _  C_
                                CCGCGCGCCCC CGC  CG
                                ||||||||||| |||  ||
                                GGCGCGCGGGG GCG  GC
                                    A  CA
GAM276  CRK     5'  CCGCCGCGCGCGCCCCTCCG  40827         _   GC
                                CCGCCGCGCGC CCCC  CCG
                                |||||||||| ||||  |||
                                GGCGGCGCGCG GGGG  GGC
                                    C   A_
GAM276  CRMP1   5'  CCGCCGCCGCTCCGGC     10594       GCGCCCC  _
                                CCGCCGC     CGC CCGGC
                                |||||||     ||| |||||
```

```
                                GGCGGCG      GCG GGCCG
                                   ________  A
GAM276  DNMT3A   5'  GCTGCGCGCCCTGGTGCCG   35430    C      CCGCCCG
                                GC GCGCGCCC      GCCG
                                || ||||||||      ||||
                                CG CGCGCGGG      CGGC
                                 A       ACCA___
GAM276  DUSP7    5'  CCGCCGCCGCCCCCGAAGTCG  42266        G      CCC  C
                                CCGCCGC CGCCCCCG   GG CG
                                ||||||| ||||||||   || ||
                                GGCGGCG GCGGGGGC   TC GC
                                   _       T__  A
GAM276  DUSP7    5'  CCGCCGCGCGCCTCCAGCTCCT 42267          _  C  _  GG
           CC                     CCGCCGCGCGCC CC GC CC  CC
                                ||||||||||| || || ||  ||
                                GGCGGCGCGCGG GG CG GG  GG
                                      A  T  A  A_
GAM276  DYRK2    5'  CCGCCGCCGCCGCCTCCCGGCC 18720        G    C  G
           G                     CCGCCGC CGCC CC CCCGGCCG
                                ||||||| |||| || ||||||||
                                GGCGGCG GCGG GG GGGCCGGC
                                   _   C  A
GAM276  EFNB1    5'  CGCTCTTCTCCGCCCGGCCG   20715     GCGCCC
                                CGC     CCGCCCGGCCG
                                |||     ||||||||||
                                GCG     GGCGGGCCGGC
                                  AGAAGA
GAM276  EHD3     5'  CCGCCGCTCGCCCCCGGCACG  31111        G      _ C
                                CCGCCGC CGCCCCCG C CG
                                ||||||| |||||||| | ||
                                GGCGGCG GCGGGGGC G GC
                                   A       C T
GAM276  EN2      5'  GCCGCCGCCGCCGCCCGGCCG  10954      G    C
                                GCCGC CGCC CCGCCCGGCCG
                                ||||| |||| ||||||||||
                                CGGCG GCGG GGCGGGCCGGC
                                   _   C
GAM276  EN2      5'  CCGCCCGCGCTCCCCGGCCG   10935      G    _    C
                                CCGCC CGCGC CCCCG CCG
                                ||||| ||||| ||||| |||
                                GGCGG GCGCG GGGGC GGC
                                   _    A    C
GAM276  ENPP1    5'  CCGCCGCGGCTCCCGCCCCCCG 26296        C  C      GG
                                CCGCCGCG GC CCCGCCC  CCG
                                |||||||| || |||||||  |||
                                GGCGGCGC CG GGGCGGG  GGC
                                   _ A      G_
GAM276  ESR2     5'  CCGGCGCGCGCGCCCCGCC     11012     C        C
                                CCG CGCGCGCCCC GCC
                                ||| |||||||||| |||
```

```
                                GGC GCGCGCGGGG CGG
                                  C       _
GAM276  FGFR1   5'  CCTCCGCGCGCTGCGGC    31934   G     CCCCGCC
                                CC CCGCGCGC     CGGC
                                || ||||||||     ||||
                                GG GGCGCGCG     GCCG
                                 A      AC_____
GAM276  GNA11   5'  CCGCCGCGGCCCTCCGGCC   44035       C   CCGC
                                CCGCCGCG GCCC   CCGGCC
                                |||||||| ||||   ||||||
                                GGCGGCGC CGGG   GGCCGG
                                     _   A___
GAM276  GNAI2   5'  CCGCCGTCCGCCGGCCCGGCCG 42648      CG   CCC
                                CCGCCG  CGCC   GCCCGGCCG
                                ||||||  ||||   |||||||||
                                GGCGGC  GCGG   CGGGCCGGC
                                   AG    C__
GAM276  GRB10   5'  CCCCGCGGGGCGCCCGGC    23649   G   CCCC
                                CC CGCG    CGCCCGGC
                                || ||||    ||||||||
                                GG GCGC    GCGGGCCG
                                 G   CCC_
GAM276  H3F3B   5'  CCGCCGCGCCGCTTCCGC    23704       _ CC
                                CCGCCGCGC GC  CCGC
                                ||||||||| ||  ||||
                                GGCGGCGCG CG  GGCG
                                     G  AA
GAM276  HERC2   5'  ACGCGCAGGGCCCGGCCG    21690      CCCC
                                GCGCGC    GCCCGGCCG
                                ||||||    |||||||||
                                TGCGCG    CGGGCCGGC
                                   TCC_
GAM276  HRB     5'  CCGCCCGCGCCGGACCCGGCCG 21083      G    CCC
                                CCGCC CGCGCC   GCCCGGCCG
                                ||||| ||||||   |||||||||
                                GGCGG GCGCGG   TGGGCCGGC
                                   _     CC_
GAM276  ID4     5'  CCGCCGCGCTCCCCTAGCCCG  11378       G   C_
                                CCGCCGCGC CCCC  GCCCG
                                ||||||||| ||||  |||||
                                GGCGGCGCG GGGG  CGGGC
                                     A    AT
GAM276  IFNGR2  5'  CCGCCCGCGCCCCCGCCCCCG  24382     G         GG
                                CCGCC CGCGCCCCCGCCC  CCG
                                ||||| ||||||||||||  |||
                                GGCGG GCGCGGGGGCGGG  GGC
                                   _        __
GAM276  ING1    5'  GCCCGCGCCCCCCCG     24396    G      GC
                                GCC CGCGCCCCC  CCG
                                ||| |||||||||  |||
```

```
                                CGG GCGCGGGGG  GGC
                                  _      __
GAM276  KCNF1    5'  CCGCCCCGCGCCCCCTGCAGCC 13829      G       GCC
              G                   CCGCC CGCGCCCCC   CGGCCG
                                  ||||| |||||||||   ||||||
                                  GGCGG GCGCGGGGG   GTCGGC
                                    G       AC_
GAM276  KCNF1    5'  CCGCGCGCGCCCTCGCAGCC   13830     C      C   CC
                                  CCGC GCGCGCCC CGC  GGCC
                                  |||| |||||||| |||  ||||
                                  GGCG CGCGCGGG GCG  TCGG
                                    _      A  __
GAM276  KCNK1    5'  CCGCCGCCCGCTCCCCCG    13886       G   CC  G
                                  CCGCCGC CGC  CC CCCG
                                  ||||||| |||  || ||||
                                  GGCGGCG GCG  GG GGGC
                                     G  A_ _
GAM276  KIFC3    5'  CCGCTCGCGCCCCTCCCG    24457     CG      CG
                                  CCGC  CGCGCCCC  CCCG
                                  ||||  ||||||||  ||||
                                  GGCG  GCGCGGGG  GGGC
                                    A_      A_
GAM276  KLHL2    5'  CCGCGGCCATGGCCCGCTCGGC 28526      C  ____    C
              CG                    CCGCG GCC    CCCGC CGGCCG
                                  ||||| |||    ||||| ||||||
                                  GGCGC CGG    GGGCG GCCGGC
                                    _  TACC    A
GAM276  LAD1     5'  CCGCCCGCGCCCCGCCGGCCG  24484      G      C  C
                                  CCGCC CGCGCCCC GCC GGCCG
                                  ||||| |||||||| ||| |||||
                                  GGCGG GCGCGGGG CGG CCGGC
                                    _      _  _
GAM276  LAD1     5'  CCCCCGCGCGCCCCGGCC    24483    G        CGCCC
                                  CC CCGCGCGCCCC    GGCC
                                  || ||||||||||    ||||
                                  GG GGCGCGCGGGG    CCGG
                                   G        _____
GAM276  LEF1     5'  CCGCCGCGCTTTCCCGCTTCG  32203        GCC    C_
                                  CCGCCGCGC   CCCGC  CG
                                  |||||||||   |||||  ||
                                  GGCGGCGCG   GGGCG  GC
                                       AAA    AA
GAM276  LENG4    3'  CCGTCCGTGCTCCCAGCC    35881    _  C  GCCCCCG
                                  CCG CCG GC      CCCGGCC
                                  ||| ||| ||      |||||||
                                  GGC GGC CG      GGGTCGG
                                    A  A  A_____
GAM276  LMO4     5'  CCGCCCGCGCTCCTCCCG    27649      G    CC  G
                                  CCGCC CGCGC  CC CCCG
                                  ||||| |||||  || ||||
```

```
                                GGCGG GCGCG  GG GGGC
                                  _    A_  A
GAM276  LNK     5'  CGTCGCGCGCCCCCGGGCC   24200    C         CCC
                                CG CGCGCGCCCCCG   GGCC
                                || ||||||||||||   ||||
                                GC GCGCGCGGGGGC   CCGG
                                 A          ____
GAM276  LRP8    5'  GCCGCTGCCCCCGCCGCCG   37796      GC       CG
                                GCCGC  GCCCCCGCC  GCCG
                                |||||  |||||||||  ||||
                                CGGCG  CGGGGGCGG  CGGC
                                  A_       __
GAM276  MAPK12  5'  CGGCGCGCGCCTCGGGCC    16467    C      CC  CCC
                                CG CGCGCGCC  CG   GGCC
                                || ||||||||  ||   ||||
                                GC GCGCGCGG  GC   CCGG
                                 C       A_  ____
GAM276  MGAT1   5'  CCGCCGCGCCCCGCCCCCCGGC 14428         G   _  G
                  CG                  CCGCCGCGC CCC CC CCCGGCCG
                                |||||||||  ||| ||  ||||||||
                                GGCGGCGCG GGG GG GGGCCGGC
                                     _  C  G
GAM276  MLLT1   5'  CCGCCGCCGCCGATCCCGGCCG 25481        G    CCCG
                                CCGCCGC CGCC   CCCGGCCG
                                |||||||  ||||   ||||||||
                                GGCGGCG GCGG   GGGCCGGC
                                     _   CTA_
GAM276  MVK     5'  CCGCCGCCGCCTCCCCGGCCG  41340        G    CCCG
                                CCGCCGC CGCC   CCCGGCCG
                                |||||||  ||||   ||||||||
                                GGCGGCG GCGG   GGGCCGGC
                                     _   AG__
GAM276  MYO1C   5'  CCGGTAGCGCATCCTGCCCGGC 41468    CC_    C  CC
                  CG                  CCG   GCGCG CC  GCCCGGCCG
                                |||   |||||  ||  |||||||||
                                GGC   CGCGT GG  CGGGCCGGC
                                  CAT    A  A_
GAM276  NCOR2   3'  GCCGTGCCCCCTCCCCG    26738     CGC     G_
                                GCCG   GCCCCC  CCCG
                                ||||   ||||||  ||||
                                CGGC   CGGGGG  GGGC
                                  A__     AG
GAM276  NEO1    5'  CCGCGCGCCTCAGCC       14751          CCCGCC
                                CCGCGCGCC     CGGCC
                                |||||||||     |||||
                                GGCGCGCGG     GTCGG
                                     A_____
GAM276  NFIA    5'  CCCGCGCCGGCCCGGCC     43208    G     CCC
                                CC CGCGCC   GCCCGGCC
                                || ||||||   ||||||||
```

```
                                GG GCGCGG   CGGGCCGG
                                 _     C__
GAM276  NOS1     5'  CCGCTGCTCGCTGCCCGGCCG  8372      C  G   CCCC
                                CCGC GC CGC    GCCCGGCCG
                                |||| || |||    |||||||||
                                GGCG CG GCG    CGGGCCGGC
                                  A  A   A___
GAM276  NRXN2    5'  CCGCCGCGGTGCCTCTCCG   31479        C_   CCCGC
                                CCGCCGCG  GCC    CCG
                                ||||||||  |||    |||
                                GGCGGCGC  CGG    GGC
                                    CA   AGA__
GAM276  OPRD1    5'  CCGCCGCGTCCCTCTCCACCGG 9509         CG   ___    C
              C                  CCGCCGCG  CCC   CCGCC GGC
                                ||||||||  |||   ||||| |||
                                GGCGGCGC  GGG   GGTGG CCG
                                    A_   AGA    _
GAM276  OPRD1    5'  CCGCCGCGTGCCGCGCCCCGGC 9510         C   CC    _
              CG                   CCGCCGCG GCC  CGCCC GGCCG
                                ||||||||  |||  ||||| |||||
                                GGCGGCGC CGG  GCGGG CCGGC
                                    A  C_    G
GAM276  PDGFB    5'  CCGCTGCGCGCTCGGC      15172      C     CCCCGCC
                                CCGC GCGCGC      CGGC
                                |||| ||||||      ||||
                                GGCG CGCGCG      GCCG
                                  A     A_______
GAM276  PKIA     5'  CCGCCGCGGAGCTCCGGC    27739         CGCCCCC  _
                                CCGCCGCG      GC CCGGC
                                ||||||||      || |||||
                                GGCGGCGC      CG GGCCG
                                    CT_____  A
GAM276  PPP3CA   5'  CCGCCGCGCTGCAAACCGCTCG 9610          _  CC_   C
              GC                   CCGCCGCGC GC   CCGC CGGC
                                |||||||||  ||   |||| ||||
                                GGCGGCGCG CG   GGCG GCCG
                                     A  TTT    A
GAM276  PTP4A2   5'  CCTCGCGCCGTGCCCGGCC   38624    G     CCC
                                CC CGCGCC   GCCCGGCC
                                || ||||||   ||||||||
                                GG GCGCGG   CGGGCCGG
                                 A     CA_
GAM276  RAD23B   5'  CCGCCGCGCAGCTCGGC     16135          CCCCC  C
                                CCGCCGCGCG    GC CGGC
                                ||||||||||    || ||||
                                GGCGGCGCGT    CG GCCG
                                      _____  A
GAM276  RASD1    3'  CCGCGCGCGCTCCCGGCC    32009     C     CCCCG
                                CCGC GCGCGC    CCCGGCC
                                |||| ||||||    |||||||
```

```
                                GGCG CGCGCG    GGGCCGG
                                  _     A____
GAM276  RBP4    5'  CCGCGCGCAAGCCTGGCC    40592       CCCC  C
                                CCGCGCGC   GCC GGCC
                                ||||||||   ||| ||||
                                GGCGCGCG   CGG CCGG
                                    TT__   A
GAM276  RELN    5'  CCGCCGCGCGCCCTACGCGCCG 45353          C_  _
                                CCGCCGCGCGCCC  CGC CCG
                                ||||||||||||  ||| |||
                                GGCGGCGCGCGGG  GCG GGC
                                       AT   C
GAM276  RET     5'  GCTGCGCGCCCTGCTTCGGTCG 33938    C      CC  C_  C
                                GC GCGCGCCC  GC  CGG CG
                                || ||||||||  ||  ||| ||
                                CG CGCGCGGG  CG  GCC GC
                                 A       A_  AA   A
GAM276  SCN4A   3'  GCTGCACGCCCCAGGGTCG   7323    C       CGCCC  C
                                GC GCGCGCCCC    GG CG
                                || |||||||||    || ||
                                CG CGTGCGGGG    CC GC
                                 A       TC___  A
GAM276  SFRP5   5'  CCGGCGTGCGCCCCCGGCCC   16592    C  C       _
                                CCG CG GCGCCCCCG CCC
                                ||| || |||||||| |||
                                GGC GC CGCGGGGGC GGG
                                  C  A       C
GAM276  SIX2    5'  CCGCGCGCGCCCTCACC     32602     C      C
                                CCGC GCGCGCCC CGCC
                                |||| |||||||| ||||
                                GGCG CGCGCGGG GTGG
                                  _      A
GAM276  SLC12A4 5'  CCGCCGCTGTCCCCGCCC    22893       GCGC
                                CCGCCGC    CCCCGCCC
                                |||||||    ||||||||
                                GGCGGCG    GGGGCGGG
                                    ACA_
GAM276  SLC25A4 5'  CCGCCGCGCAGTCCCCGACCC  40507         C_    _
                                CCGCCGCGCG  CCCCG CCC
                                ||||||||||  ||||| |||
                                GGCGGCGCGT  GGGGC GGG
                                      CA    T
GAM276  SLC9A3R2 3' GCCGCGCGCTCGCTCG      41527        CCC   C
                                GCCGCGCGC   CGC CG
                                |||||||||   ||| ||
                                CGGCGCGCG   GCG GC
                                     A__   A
GAM276  SNX3    5'  CCGCCGCGGGCTCCCTCCTCG  19138        C  C   G  _
                                CCGCCGCG GC CCC CC CG
                                |||||||| || ||| || ||
```

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                                GGCGGCGC CG GGG GG GC
                                    C A  A A
GAM276  SOX4    3' CCGCCGCGCTCCTTGATCCG  16980       G CCCGC
                                CCGCCGCGC CC   CCG
                                ||||||||| ||   |||
                                GGCGGCGCG GG   GGC
                                    A AACTA
GAM276  SRR     5' CCTCCGCGCGCCTCCCCGGCCG 34965   G      CCCG
                                CC CCGCGCGCC  CCCGGCCG
                                || |||||||||  ||||||||
                                GG GGCGCGCGG  GGGCCGGC
                                 A       AG__
GAM276  STIP1   5' CCGCTCCGCGTTCCCAACC  27732    CG  CCCCCG
                                CCGC CGCG    CCCGGCC
                                ||||  ||||    |||||||
                                GGCG  GCGC    GGGTTGG
                                  AG   AA____
GAM276  TBL1X   5' CGCCGCGCGCCCGGC     24878         CCGCCC
                                CGCCGCGCGCCC    GGC
                                ||||||||||||    |||
                                GCGGCGCGCGGG    CCG
                                      _______
GAM276  TERF2   5' CGCCGCGCGCCCTCCCCG   24908         CCG
                                CGCCGCGCGCCC  CCCG
                                ||||||||||||  ||||
                                GCGGCGCGCGGG  GGGC
                                      AG_
GAM276  TESK1   5' CCGCCGCGCCGGCTGGC    26611        GCCC C  CC
                                CCGCCGCGC   C GC  GGC
                                |||||||||   | ||  |||
                                GGCGGCGCG   G CG  CCG
                                    _____ C  A_
GAM276  TPX1    5' GCTGCGCGCCCCTCTCACC   17665   C      ___
                                GC GCGCGCCCC  CGCC
                                || |||||||||  ||||
                                CG CGCGCGGGG  GTGG
                                 A       AGA
GAM276  TRPC1   5' CCGCCGGCGCCCCGGC     17682      C     CGCCC
                                CCGCCG GCGCCCC   GGC
                                |||||| |||||||   |||
                                GGCGGC CGCGGGG   CCG
                                   _    ______
GAM276  UGCG    5' CCGCCCGCGCGCTCTCGCC   17865     _    CCC
                                CCGCC GCGCGC  CGCC
                                ||||| ||||||  ||||
                                GGCGG CGCGCG  GCGG
                                  G     AGA
GAM276  WRN     5' CCGCCGTCGCTCTCCCCG   8135       _  GC_
                                CCGCCG CGC  CCCCG
                                |||||| |||  |||||
```

```
                                GGCGGC GCG   GGGGC
                                   A   AGA
GAM276  XYLB     5'  CCGCCCCTAGCTCCGCCCGGCC 23021      GCGC  CC
                G                   CCGCC   GC  CCGCCCGGCCG
                                    |||||   ||  ||||||||||
                                    GGCGG   CG  GGCGGGCCGGC
                                      GGAT  A_
GAM276  ABCC8    5'  CCGGCCCGGCCGTCAGGCCCCC 7399     _      C  CGC
                G                   CCG CCCGGCCG CG   GCCCCCG
                                    ||| |||||||| ||   |||||||
                                    GGC GGGCCGGC GT   CGGGGGC
                                      C       A  C__
GAM276  ABL1     5'  CCGCCCAGGGCGGCCGCGTCTC 28706       __   C     CG_
                C                   CCGCCC  GGC GCCGCG   CC
                                    ||||||  ||| ||||||   ||
                                    GGCGGG  CCG CGGCGC   GG
                                       TC   C     AGA
GAM276  ACCN2    5'  CCGCCCGGCCCCGCTCG     33441         G   G
                                    CCGCCCGGCC CCGC CG
                                    |||||||||| |||| ||
                                    GGCGGGCCGG GGCG GC
                                          _   A
GAM276  ADARB1   5'  CCGCTTGGCCGCCGCTGCC   31875     CC       GC
                                    CCGC  GGCCGCCGC  GCC
                                    ||||  |||||||||  |||
                                    GGCG  CCGGCGGCG  CGG
                                      AA        A_
GAM276  ADK      5'  CCGCGCGGCCGGCCCC      27481      C     CCGCGC
                                    CCGC CGGCCG     GCCCC
                                    |||| ||||||     |||||
                                    GGCG GCCGGC     CGGGG
                                      C     _______
GAM276  AGRP     5'  CCCGGCCACCCCGTGCCC    28732         G  C
                                    CCCGGCCGCC CG GCCC
                                    |||||||||| || ||||
                                    GGGCCGGTGG GC CGGG
                                          G  A
GAM276  ALG6     5'  CCGCCGGCCGCTGCTCG     30033      C     C  G
                                    CCGCC GGCCGC GC CG
                                    ||||| |||||| || ||
                                    GGCGG CCGGCG CG GC
                                      _     A  A
GAM276  ATP2B2   5'  CCGCTGCGGCTGCGGCTCC   11756     C_   CGCC   C  C
                                    CCGC  CGGC    GCG GC CC
                                    ||||  ||||    ||| || ||
                                    GGCG  GCCG    CGC CG GG
                                      AC    A___   _  A
GAM276  ATP8B2   5'  CCTCCCGGCCGCCGGCGC    42203    G         C
                                    CC CCCGGCCGCCG GCGC
                                    || ||||||||||| ||||
```

```
                                GG GGGCCGGCGGC CGCG
                                 A         _
GAM276  AUP1    5'  CGCCCGGCCGTCGCCGCC    29042          C   G
                                CGCCCGGCCG CGC CGCC
                                |||||||||| ||| ||||
                                GCGGGCCGGC GCG GCGG
                                     A   _
GAM276  BARX1   5'  CCCCCGGCCGCTGCATCC    34625    G       C   CG
                                CC CCCGGCCGC GCG  CC
                                || |||||||| |||  ||
                                GG GGGCCGGCG CGT  GG
                                 _       A   A_
GAM276  BCL7B   5'  CCGCCCGCCCGCCGCCGCC    11801        G      G
                                CCGCCCG CCGCCGC CGCC
                                ||||||| ||||||| ||||
                                GGCGGGC GGCGGCG GCGG
                                    G      _
GAM276  BCRP2   5'  CCGCTCGCGCCGCCGCCCCTCC 41652      C _       GCG _
            C                    CCGC CG GCCGCCGC   CC CCC
                                ||||  || ||||||||   || |||
                                GGCG GC CGGCGGCG   GG GGG
                                  A  G       G__  A
GAM276  BMP6    5'  CCGCCCGGCCGGGCTGCCCCCG 11861           CC  GC
                                CCGCCCGGCCG  GC  GCCCCCG
                                ||||||||||  ||  |||||||
                                GGCGGGCCGGC  CG  CGGGGGC
                                      C_  A_
GAM276  BRF1    5'  CCGCCCAGGCCTCGCCGC    11329        _   GC   G
                                CCGCCC GGCC  CGC CGC
                                |||||| ||||  ||| |||
                                GGCGGG CCGG  GCG GCG
                                   T   A_  _
GAM276  BUB3    5'  CGCTCGGCCGCCGCCGCCTCC  21803     C        G   C
                                CGC CGGCCGCCGC CGCC CC
                                ||| |||||||||| |||| ||
                                GCG GCCGGCGGCG GCGG GG
                                  A         _   A
GAM276  C21orf2 5'  CCGACCGGCGGGCGCCCCC   22300        C  C
                                CCGGCCG CG GCGCCCCC
                                ||||||| || ||||||||
                                GGCTGGC GC CGCGGGGG
                                    C  C
GAM276  C7orf2  5'  CGTCCGCCCGCCGCAGGGGC  35369    C   G       C__
                                CG CCG CCGCCGCG   GC
                                || ||| ||||||||   ||
                                GC GGC GGCGGCGT   CG
                                 A  G       CCC
GAM276  CACNG2  3'  CCGCCCCGCCCCGCCCCC    25879        G   G  GCGC
                                CCGCCC GCC CC    GCCCCC
                                |||||| ||| ||    ||||||
```

```
                                GGCGGG CGG GG   CGGGGG
                                   G  _ _____
GAM276  CALM1   5' CCGCCTGCGCCGCCGCC    27856      CG C   G
                                CCGCC  GC GCCGC CGCC
                                |||||  || ||||| ||||
                                GGCGG  CG CGGCG GCGG
                                   A_ _    _
GAM276  CCNT1   5' CCGCCGGGTTGTTACTTGCCTC 10302      C  CCGCC  GC   C
           CG                    CCGCC GG    GC  GCC CCG
                                |||||  ||    ||  ||| |||
                                GGCGG CC    TG  CGG GGC
                                   C  AACAA  AA   A
GAM276  CDC2L1  5' CCGCCCGTGCCGCCGCCGCC  37911        _      G
                                CCGCCCG GCCGCCGC CGCC
                                ||||||| |||||||| ||||
                                GGCGGGC CGGCGGCG GCGG
                                   A       _
GAM276  CDH6    5' CCGCCCAGGCTGCTCCTGCCTC 22325       _  C  CGCGC   C
           CG                    CCGCCC GGC GC    GCC CCG
                                ||||||  ||| ||    ||| |||
                                GGCGGG CCG CG    CGG GGC
                                   T   A  AGGA_   A
GAM276  CDKN1B  5' GCCCGGCCGCCGAGTCTCC   19802          CGCG_
                                GCCCGGCCGCCG    CC
                                ||||||||||||    ||
                                CGGGCCGGCGGC    GG
                                      TCAGA
GAM276  CHN2    5' CGCCCGGCCGCTCGCAGCCTCC 19812          _   C   C
           G                    CGCCCGGCCGC CGCG GCC CCG
                                |||||||||| |||| ||| |||
                                GCGGGCCGGCG GCGT CGG GGC
                                      A   _  A
GAM276  CHRNA3  5' CCGCTGGGTTTCCAGCGCCCTC 8835     CC  CCG   C     C
           G                    CCGC  GG   CCG GCGCCC CG
                                ||||  ||   ||| |||||| ||
                                GGCG  CC   GGT CGCGGG GC
                                   AC  AAA  _     A
GAM276  COL11A1 5' CCCTCCGGCCGCGACCC    38759    GG  _    C
                                CCC  CCG CCGCG GCCC
                                |||  ||| ||||| ||||
                                GGG  GGC GGCGC TGGG
                                   A_   C    _
GAM276  CRMP1   5' CCGCCCGCCGCCGCTCCG    10593       G     G_
                                CCGCCCG CCGCCGC  CG
                                |||||||  |||||||  ||
                                GGCGGGC GGCGGCG  GC
                                      _      AG
GAM276  DGAT1   5' GCCGGCCGCCGTAGCCC    42073    C      CGC
                                GCC GGCCGCCG   GCCC
                                ||| ||||||||   ||||
```

```
                                CGG CCGGCGGC  CGGG
                                  _      AT_
GAM276  DLG5    5'  CCGCACGGTCCCGCTCCC   44454     C  CCG  G  G
                                CCGC CGG  CC CGC CCC
                                |||| |||  || ||| |||
                                GGCG GCC  GG GCG GGG
                                  T  A__  _  A
GAM276  DNCI1   5'  CCGCTCGGCTCGCGCTCCTCCG 44989     C   CGC    G  C
                                CCGC CGGC  CGCGC CC CCG
                                |||| ||||  ||||| || |||
                                GGCG GCCG  GCGCG GG GGC
                                  A   A__    A  A
GAM276  DSCAM   5'  CCGCCCGCCCGCCGCCCG   10791       G     G
                                CCGCCCG CCGCCGC CG
                                ||||||| ||||||| ||
                                GGCGGGC GGCGGCG GC
                                    G     G
GAM276  DSCAM   5'  CCGCCCGCCGCCGCCGCC   10792       G     G
                                CCGCCCG CCGCCGC CGCC
                                ||||||| ||||||| ||||
                                GGCGGGC GGCGGCG GCGG
                                  _     _
GAM276  DSCR1   5'  CCGCCTCGGCCGCCCCCGCC  20637     _     GCG
                                CCGCC CGGCCGCC  CGCC
                                ||||| ||||||||  ||||
                                GGCGG GCCGGCGG  GCGG
                                  A      GG_
GAM276  DTR     5'  CCGCGCGGCCGCCCGACCCC  12610     C     G  C
                                CCGC CGGCCGCC CG GCCCC
                                |||| |||||||| || |||||
                                GGCG GCCGGCGG GC TGGGG
                                  C      _ _
GAM276  DUSP4   5'  CCGCTCAGCCGCCAGGCCTTCC 38413     C      CGC  C_
          G                      CCGC CGGCCGCCG  GCC  CCG
                                |||| |||||||||  |||  |||
                                GGCG GTCGGCGGT  CGG  GGC
                                  A      C__  AA
GAM276  DVL3    5'  CCGCCGCGGCCGCGCTTCC   20676     _    C  GCG
                                CCGCC CGGCCGC GC  CC
                                ||||| ||||||| ||  ||
                                GGCGG GCCGGCG CG  GG
                                  C      _  AA_
GAM276  DVL3    5'  CCGCCCGCCGCCGCCGCGGCC  20675      __      C
                                CCGCCCG  GCCGCCGCG GCC
                                |||||||  ||||||||| |||
                                GGCGGGC  CGGCGGCGC CGG
                                    GG      _
GAM276  DYRK2   5'  CCTCCCGGCCGCCCCTCG   27036   G      GCG
                                CC CCCGGCCGCC  CG
                                || ||||||||||  ||
```

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                                GG GGGCCGGCGG   GC
                                 A         GGA
GAM276  E2F1     5'  CCCCCGGCCGCCGCTGCC    44485    G         GC
                                CC CCCGGCCGCCGC  GCC
                                || ||||||||||||  |||
                                GG GGGCCGGCGGCG  CGG
                                 _          A_
GAM276  ECHS1    5'  CGCCCGGCCCCGCGGAGCC    19872         G    C_
                                CGCCCGGCC CCGCG  GCC
                                |||||||| |||||  |||
                                GCGGGCCGG GGCGC  CGG
                                      _    CT
GAM276  EGLN1    5'  CCCCTCGGCCGCCGCCGCC    35162    G _        G
                                CC CC CGGCCGCCGC CGCC
                                || || |||||||||| ||||
                                GG GG GCCGGCGGCG GCGG
                                 _ A        _
GAM276  EIF2C1   5'  CCGCTCGCGCCGCCGCCCCCG  29176     C  GC     G
                                CCGC CG  CGCCGC CGCCCCCG
                                |||| ||  |||||| ||||||||
                                GGCG GC  GCGGCG GCGGGGGC
                                  A __     _
GAM276  EN1      5'  CCGCCCCGGCCGCCGCGC     10907       _
                                CCGCCC GGCCGCCGCGC
                                |||||| ||||||||||
                                GGCGGG CCGGCGGCGCG
                                   G
GAM276  EN2      5'  CCCGGCCGTCCGCCGCCCTCG  10933         _   G    C
                                CCCGGCCG CCGC CGCCC CG
                                |||||||| |||| ||||| ||
                                GGGCCGGC GGCG GCGGG GC
                                     A   _    A
GAM276  EP300    5'  CCGCCACGGCCGGCCCC      10976      _     CCGCGC
                                CCGCC CGGCCG     GCCCC
                                ||||| ||||||     |||||
                                GGCGG GCCGGC     CGGGG
                                   T     _______
GAM276  FBXW1B   5'  CCGCCCGGGCCGCCGGCAGCTC 37998         _     C  _  C
             C                   CCGCCCGG CCGCCG GC GC CC
                                 |||||||| |||||| || || ||
                                 GGCGGGCC GGCGGC CG CG GG
                                     C     _ T  A
GAM276  FLT1     5'  CGCCGCCGCCGGCCCC      12909      CG      CGC
                                CGCC  GCCGCCG   GCCCC
                                ||||  |||||||   |||||
                                GCGG  CGGCGGC   CGGGG
                                   __     ____
GAM276  FMR1     5'  CCCCCTGGCAGCGGCGCCTCCG 12937    G  _  C  C C    C
                                CC CCC GGC GC G GCGCC CCG
                                || ||| ||| || | ||||| |||
```

```
                                GG GGG CCG CG C CGCGG GGC
                                 _  A  T _ _   A
GAM276  FXR2    5' CCGTCCGCCGCCGCCGCC   22159    C  G     G
                                CCG CCG CCGCCGC CGCC
                                ||| ||| ||||||| ||||
                                GGC GGC GGCGGCG GCGG
                                  A  _     _
GAM276  GAN     5' CCGCCCGGCCCGGCTCTCC   35140         GC  C  GCCC
                                CCGCCCGGCC  CG GC   CC
                                ||||||||||  || ||   ||
                                GGCGGGCCGG  GC CG   GG
                                      __ _ AGA_
GAM276  GATA2   5' CCGCCCGGCTCCGGCCCCTCG  13083        CG  CGC   _
                                CCGCCCGGC  CCG  GCCCC CG
                                |||||||||  |||  ||||| ||
                                GGCGGGCCG  GGC  CGGGG GC
                                     A_  ___   A
GAM276  GNA11   5' CCGCCTGCCCGCCGCCGCCCCC 44036     CG  _   G
                                CCGCC  GCC GCCGC CGCCCCC
                                |||||  ||| ||||| |||||||
                                GGCGG  CGG CGGCG GCGGGGG
                                  A_  G   _
GAM276  GNA11   5' CCGCCCGCCGCGGCCCTCC   44034    G     C   _
                                CCG CCGCCGCG GCCC CC
                                ||| |||||||| |||| ||
                                GGC GGCGGCGC CGGG GG
                                  G      _   A
GAM276  GNA11   5' CCGCCTCGGCCGCCGCCCG   13162     _      G
                                CCGCC CGGCCGCCGC CG
                                ||||| |||||||||| ||
                                GGCGG GCCGGCGGCG GC
                                  A       G
GAM276  GNAQ    5' CCGCCCGGTCGCGCGTCC    13174       CCGC    _
                                CCGCCCGG   CGCGCG CC
                                ||||||||   |||||| ||
                                GGCGGGCC   GCGCGC GG
                                    A___    A
GAM276  GNB1    5' CCGCCTCGGCCGCCGCTCG   13202     _      G
                                CCGCC CGGCCGCCGC CG
                                ||||| |||||||||| ||
                                GGCGG GCCGGCGGCG GC
                                  A       A
GAM276  GRF2    3' CCGCCCGGCCCCGCTGAGGGC  23674        G   GC___
                                CCGCCCGGCC CCGC    GC
                                |||||||||| ||||    ||
                                GGCGGGCCGG GGCG    CG
                                      _   ACTCC
GAM276  HCN4    5' CCGCCCGGCTCCAGGCGCCCC  24220       CG  C
                                CCGCCCGGC  CCG GCGCCCC
                                |||||||||  ||| |||||||
```

```
                                GGCGGGCCG  GGT CGCGGGG
                                     A_   C
GAM276  HD      5'  CCGCCCGGCACGGCAGTCCCC  13345         C  C   CG
                                CCGCCCGGC GC GCG  CCCC
                                ||||||||| || |||  ||||
                                GGCGGGCCG TG CGT  GGGG
                                     _ C   CA
GAM276  HDAC4   3'  CCGCCGGGCTGCAGCCCC    25752      C   CGCC   C
                                CCGCC GGC    GCG GCCCC
                                ||||| |||    ||| |||||
                                GGCGG CCG    CGT CGGGG
                                   C   A___   _
GAM276  HIRA    5'  CCTCCGGCCGCCGCCCG     17739     GC         G
                                CC  CCGGCCGCCGC CG
                                ||  ||||||||||| ||
                                GG  GGCCGGCGGCG GC
                                 A_          G
GAM276  HIRA    5'  CGCTCGGCCGCCGCCGCC    17740     C        G
                                CGC CGGCCGCCGC CGCC
                                ||| |||||||||| ||||
                                GCG GCCGGCGGCG GCGG
                                  A         _
GAM276  HMX1    3'  CCGCCGGCCGCGGCCTGCGCTC 33208       C     C __    C
            CCG                   CCGCC GGCCGC GC  GCGC CCCG
                                ||||| |||||| ||  |||| ||||
                                GGCGG CCGGCG CG  CGCG GGGC
                                   _     C  GA    A
GAM276  ICA1    5'  CCGTCCCGGCTGCCGGGCGTCT 22464     _     C    C   CCC
            CC                    CCG CCCGGC GCCG GCG   CC
                                ||| |||||| |||| |||   ||
                                GGC GGGCCG CGGC CGC   GG
                                  A     A   C   AGA
GAM276  IFNGR2  5'  GCTCGGCCGCCCGCGCCCCCG  24387    C       G
                                GC CGGCCGCC CGCGCCCCCG
                                || |||||||| ||||||||||
                                CG GCCGGCGG GCGCGGGGGC
                                 A       _
GAM276  IFNGR2  5'  CCGCCCGCGCCCCCGCCCCCG  24382         _  G  GCG
                                CCGCCCG GCC CC   CGCCCCCG
                                ||||||| ||| ||   ||||||||
                                GGCGGGC CGG GG   GCGGGGGC
                                    G  _ ___
GAM276  ILF1    5'  CGTCGGCCGCCGCGCACC    21106    CC
                                CG  CGGCCGCCGCGCGCC
                                ||  ||||||||||||||
                                GC  GCCGGCGGCGCGTGG
                                 A_
GAM276  INHBB   5'  CCGCCCCGCCCCGCCCCC    13547       G  G  GCGC
                                CCGCCC GCC CC    GCCCCC
                                |||||| ||| ||    ||||||
```

```
                                GGCGGG CGG GG   CGGGGG
                                   G  _ _____
GAM276  ITGA4   5' CGCCCGGCCCCACTCCC    9421         G   GCG
                                CGCCCGGCC CCGC  CCC
                                ||||||||| ||||  |||
                                GCGGGCCGG GGTG  GGG
                                     _   A__
GAM276  JAG2    5' CCGCCCGGCCCCGCCGCC    13707        G   G
                                CCGCCCGGCC CCGC CGCC
                                |||||||||| |||| ||||
                                GGCGGGCCGG GGCG GCGG
                                     _  _
GAM276  KCNA7   5' CCGCCTCGGCCGCCGCCGCC  36647      _       G
                                CCGCC CGGCCGCCGC CGCC
                                ||||| |||||||||| ||||
                                GGCGG GCCGGCGGCG GCGG
                                   A       _
GAM276  KCNA7   5' GCCCCGCCGCCGCCGCC    36657     G      G
                                GCCC GCCGCCGC CGCC
                                |||| |||||||| ||||
                                CGGG CGGCGGCG GCGG
                                  G      _
GAM276  KCNF1   5' CCTCCCCGCGCGCGCCCC    13831    G  G  CGCC      C
                                CC CCC GC   GCGCGCCC C
                                || ||| ||   |||||||| |
                                GG GGG CG   CGCGCGGG G
                                 A  G ____      A
GAM276  KCNH2   5' CCGACCGGCCGCTGGAGGCC  6946     C      CGCGC
                                CCG CCGGCCGC    GCC
                                ||| ||||||||    |||
                                GGC GGCCGGCG    CGG
                                  T      ACCTC
GAM276  KCNH3   5' CCAGCTCGGCCGCCCCCC    42084   _ C      GCGCGC
                                CC GC CGGCCGCC     CCCC
                                || || ||||||||     ||||
                                GG CG GCCGGCGG     GGGG
                                 T  A      ______
GAM276  KCNK1   5' GGCCCCGCCGCCCCCG     13895     G   G
                                GGCC CCGC CGCCCCCG
                                |||| |||| ||||||||
                                CCGG GGCG GCGGGGGC
                                     _   _
GAM276  KCNK1   5' CCGCCCGCCGCCCGCTCCCCCG 13884       G    G  G
                                CCGCCCG CCGCC CGC CCCCCG
                                ||||||| ||||| ||| ||||||
                                GGCGGGC GGCGG GCG GGGGGC
                                     _   _  A
GAM276  KCNK3   5' CCGCCCGGGCCGCCGCCGGCCC 13900       _     GC
              CC                  CCGCCCGG CCGCCGC  GCCCCC
                                ||||||||| |||||||  ||||||
```

```
                                GGCGGGCC GGCGGCG  CGGGGG
                                    C      GC
GAM276  KCNK4    5'  GCCCGGCCCTCAGCCCC     37835        GCCG  C
                                GCCCGGCC    CG GCCCC
                                ||||||||    || |||||
                                CGGGCCGG    GT CGGGG
                                    GA__  _
GAM276  KIAA0857 5'  CCGACCGGCCGCCGCCTCCCC  42470     C         GCG
                                CCG CCGGCCGCCGC   CCCC
                                ||| ||||||||||   ||||
                                GGC GGCCGGCGGCG   GGGG
                                  T         GA_
GAM276  KIF5C    5'  CGCCCGGCTCAGACCTCCCG   21151        CGCCG  C  _
                                CGCCCGGC     CG GCC CCCG
                                ||||||||     || ||| ||||
                                GCGGGCCG     GT TGG GGGC
                                    A_____  C   A
GAM276  LAD1     5'  CCGCGTGGCCGCCCGCGCCCC  24486      CC      G
                                CCGC  GGCCGCC CGCGCCCC
                                ||||  ||||||| ||||||||
                                GGCG  CCGGCGG GCGCGGGG
                                  CA      _
GAM276  LAD1     5'  CCGCCGGCCGCCGCCTCACC   24485      C        G_
                                CCGCC GGCCGCCGC  CGCC
                                |||||| |||||||||  ||||
                                GGCGG CCGGCGGCG  GTGG
                                  _        GA
GAM276  LDOC1    3'  GCCAGGCACACCGCGCCCC    29488     C  _      G
                                GCC GGC CGCCGCGC CCC
                                ||| ||| |||||||| |||
                                CGG CCG GTGGCGCG GGG
                                  T  T       _
GAM276  LMO2     5'  CCGCCCGGCCGCCCGGAGCCCC 24537            G  C_
                                CCGCCCGGCCGCC CG  GCCCC
                                |||||||||||| ||  |||||
                                GGCGGGCCGGCGG GC  CGGGG
                                      _ CT
GAM276  LMO4     5'  CCGCCCGGCGGCCCC       27650          CGCCGC C
                                CCGCCCGGC      G GCCCC
                                |||||||||      | |||||
                                GGCGGGCCG      C CGGGG
                                      _______ _
GAM276  LRP2     5'  CCGCACCGGCAGCGCC       21184      _    CGCCGC
                                CCGC CCGGC     GCGCC
                                |||| |||||     |||||
                                GGCG GGCCG     CGCGG
                                  T    T_____
GAM276  LYN      5'  CCGCCCGCTTGCCGCGGGC    14284        GCC     C
                                CCGCCCG   GCCGCG GC
                                |||||||   |||||| ||
```

```
                                GGCGGGC  CGGCGC CG
                                   GAA    C
GAM276  MADH2   5' CCCGGCCGCCGTCTTCCC   25342         CGCG
                                CCCGGCCGCCG   CCC
                                ||||||||||   |||
                                GGGCCGGCGGC   GGG
                                      AGAA
GAM276  MAFK    5' CCGCCTGGCGCTCGGGCTCC  14316     C  C _ C G
                                CCGCC GGC GC CG GC CC
                                ||||| ||| || || || ||
                                GGCGG CCG CG GC CG GG
                                  A  _ A C A
GAM276  MAFK    5' CCCCTCGGCCGCCGCCGCC   14314   G _       G
                                CC CC CGGCCGCCGC CGCC
                                || || |||||||||| ||||
                                GG GG GCCGGCGGCG GCGG
                                 _ A       _
GAM276  MAP3K1  5' CCGCCCGCTCGCGGCCCCC   42701    G  _  C
                                CCG CCGC CGCG GCCCCC
                                ||| |||| |||| ||||||
                                GGC GGCG GCGC CGGGGG
                                  G  A  _
GAM276  MAPK1   5' GCCGGGCCGCCGCCGCCTCCG 15652    C      G  C
                                GCC GGCCGCCGC CGCC CCG
                                ||| ||||||||| |||| |||
                                CGG CCGGCGGCG GCGG GGC
                                  C       _  A
GAM276  MAPK12  5' CCGCCGGCCGCTGGGGCGCTCC 16463     C    CGC_  C
           CG                    CCGCC GGCCGC   GCGC CCCG
                                ||||| ||||||   |||| ||||
                                GGCGG CCGGCG   CGCG GGGC
                                  _    ACCC   A
GAM276  MDM1    5' CGCCCGGCGCCGGAGCCCCCG 33515       C  CGC
                                CGCCCGGC GCCG  GCCCCCG
                                |||||||| ||||  |||||||
                                GCGGGCCG CGGC  CGGGGGC
                                     _  CT_
GAM276  MGEA5   5' CCCCCGGCCGCTGCCACC   29212   G      C G
                                CC CCCGGCCGC GC CGCC
                                || |||||||| || ||||
                                GG GGGCCGGCG CG GTGG
                                 _       A _
GAM276  MKPX    5' GCCGGTCCCCGCCCCC     33639    C _ G GCGC
                                GCC GG CC CC   GCCCCC
                                ||| || || ||   ||||||
                                CGG CC GG GG   CGGGGG
                                  _ A _ _____
GAM276  MKPX    5' CCTGGCTGCCGCGCCCCACTCC 33637   C  C     G  ___
           G                     CC GGC GCCGCGC CCC  CCG
                                || ||| ||||||| |||  |||
```

```
                                GG CCG CGGCGCG GGG   GGC
                                 A  A      _  TGA
GAM276  MLLT1    5'  CGCTCGCCGCCGCCGCC    25485    C  G     G
                                CGC CG CCGCCGC CGCC
                                ||| || ||||||| ||||
                                GCG GC GGCGGCG GCGG
                                  A  _     _
GAM276  MLLT1    5'  CCGCTCGCCCGCCAGCCCC   25482    C  G    CGC
                                CCGC CG CCGCCG  GCCCC
                                |||| || ||||||  |||||
                                GGCG GC GGCGGT  CGGGG
                                  A  G    ____
GAM276  MUCDHL   3'  CCCTCTGGCCGCCGCTCC   34932    ____      GCG
                                CCC  GGCCGCCGC  CC
                                |||  |||||||||  ||
                                GGG  CCGGCGGCG  GG
                                  AGA       A__
GAM276  MVK      5'  CCCGGCCGCCGCCCCTCCG   41339         GCG  _
                                CCCGGCCGCCGC  CCC CCG
                                ||||||||||||  ||| |||
                                GGGCCGGCGGCG  GGG GGC
                                      ____  A
GAM276  NCKAP1   5'  CCGCCCGCCGCCCTTCC    30253      G   GCGCG
                                CCGCCCG CCGCC    CC
                                ||||||| |||||    ||
                                GGCGGGC GGCGG    GG
                                   _    GAA__
GAM276  NRG2     5'  CCGCTCAGCCGCCGCCGCC   30363    C       G
                                CCGC CGGCCGCCGC CGCC
                                |||| |||||||||| ||||
                                GGCG GTCGGCGGCG GCGG
                                  A       _
GAM276  NRXN2    5'  CCGCCCGGCCCCCGGCCCCCG  31477        G  G  C
                                CCGCCCGGCC CC CG GCCCCCG
                                |||||||||| || || |||||||
                                GGCGGGCCGG GG GC CGGGGGC
                                      _  _  _
GAM276  PACE4    5'  CCCCCGGGCCCGCGCTCC    15045   G    CC  G    C
                                CC CCCGG  GCC CGCGC CC
                                || |||||  ||| ||||| ||
                                GG GGGCC  CGG GCGCG GG
                                 _    __  _    A
GAM276  PAFAH1B1 5'  CCGCCCCGCCGCTCCAGCTCC  7704       G    CG  C  C
                                CCGCCC GCCGC  CG GC CC
                                |||||| |||||  || || ||
                                GGCGGG CGGCG  GT CG GG
                                   G    AG  _  A
GAM276  PAX2     5'  CGCCCGGCTGCTGCGGGGC   19621        C  C   C_
                                CGCCCGGC GC GCG  GC
                                |||||||| || |||  ||
```

```
                                GCGGGCCG CG CGC  CG
                                    A A   CC
GAM276  PAX9    5'  CCGACCGGCCGGCGCCTCC   26202       _  C    C
                                CCGGCCG CCG GCGCC CC
                                ||||||| ||| ||||| ||
                                GGCTGGC GGC CGCGG GG
                                   C  _    A
GAM276  PEX7    5'  CCGCCCGCCGCCCCCGGCCCTC 7110       G   _ G  C   C
          G                      CCGCCCG CCGC C CG GCCC CG
                                ||||||| |||| | || |||| ||
                                GGCGGGC GGCG G GC CGGG GC
                                   _   G G  _   A
GAM276  PIAS1   5'  CCGCCCCGGCCCGCCCCC    32074       _   GCCGCG
                                CCGCCC GGCC     CGCCCCC
                                |||||| ||||     |||||||
                                GGCGGG CCGG     GCGGGGG
                                   G   _______
GAM276  PIK3R3  3'  CCGGCCGGCTGCTGCTCG    41441     C    C  C  G
                                CCG CCGGC GC GC CG
                                ||| ||||| || || ||
                                GGC GGCCG CG CG GC
                                  C    A  A  A
GAM276  PITPN   5'  CCGCCGGCCGCTCTCCCC    26330      C     CGCGCG
                                CCGCC GGCCGC     CCCC
                                ||||| ||||||     ||||
                                GGCGG CCGGCG     GGGG
                                   _     AGA___
GAM276  PITPN   5'  CCGGCCCGGCTGCCTGTGCG   26331     _     C   GC_
                                CCG CCCGGC GCC   GCG
                                ||| |||||| |||   |||
                                GGC GGGCCG CGG   CGC
                                  C     A   ACA
GAM276  PITX1   5'  CCGCCTGGCTGCGACC      15317      C  CGCC   C
                                CCGCC GGC    GCG GCC
                                ||||| |||    ||| |||
                                GGCGG CCG    CGC TGG
                                   A  A___   _
GAM276  PITX1   3'  CCCCCGGCCGCTGGGCC     15316    G       CGCGC
                                CC CCCGGCCGC     GCC
                                || |||||||||     |||
                                GG GGGCCGGCG     CGG
                                  _        ACC__
GAM276  PKIB    5'  GCCTGCCTGCCGGTGCCC    37164     CG  _   CGC
                                GCC  GCC GCCG   GCCC
                                |||  ||| ||||   ||||
                                CGG  CGG CGGC   CGGG
                                  A_   A    CA_
GAM276  POLD1   3'  CCCTGGTCCCGCCCCC      15438     _ _  GCCGCG
                                CCC GG CC     CGCCCCC
                                ||| || ||     |||||||
```

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                                GGG CC GG     GCGGGGG
                                  A  A _______
GAM276  PRDM1    5'  CGTCCGGCCGCCCGGGC     10182    C       G  C
                                CG CCGGCCGCC CG GC
                                || ||||||||| || ||
                                GC GGCCGGCGG GC CG
                                 A       _  C
GAM276  PRKAR2B  5'  GCCCGGCCGCCGGCTCCC    15620           C  G
                                GCCCGGCCGCCG GC CCC
                                |||||||||||| || |||
                                CGGGCCGGCGGC CG GGG
                                       _  A
GAM276  PTEN     5'  CCGCCGCGGCCGCCGCCGCC  7205       _        G
                                CCGCC CGGCCGCCGC CGCC
                                ||||| |||||||||| ||||
                                GGCGG GCCGGCGGCG GCGG
                                   C        _
GAM276  PTP4A2   5'  GCCCGGCCGCCGCTGCC     38633           GC
                                GCCCGGCCGCCGC  GCC
                                ||||||||||||  |||
                                CGGGCCGGCGGCG  CGG
                                       A_
GAM276  PTPRF    5'  CCACCTGGTCCCGCTCCC     39029      C  CCG  G   G
                                CCGCC GG   CC CGC CCC
                                ||||| ||   || ||| |||
                                GGTGG CC   GG GCG GGG
                                   A  A__  _   A
GAM276  RAB18    5'  CCGCCCGGGTGCGCCTCTCCG  34571        CCGCCGC    C__
                                CCGCCCGG      GCGCC   CCG
                                ||||||||      |||||   |||
                                GGCGGGCC      CGCGG   GGC
                                     CA_____     AGA
GAM276  RASD1    3'  CCAGTCCGCGCGCGCTCCC    32008     _   C     C
                                CCGG CCGC GCGCGC CCC
                                |||| |||| |||||| |||
                                GGTC GGCG CGCGCG GGG
                                   A   _     A
GAM276  RBBP5    5'  CCGCCCGGTCTCAGCTCC     22805        CCGC  C  G
                                CCGCCCGG    CG GC CC
                                ||||||||    || || ||
                                GGCGGGCC    GT CG GG
                                     AGA_ _  A
GAM276  REPS2    5'  CCGCGCGGCCGCTTCCTCCCG  21810      C      CGCGCG  _
                                CCGC CGGCCGC     CC CCCG
                                |||| |||||||      || ||||
                                GGCG GCCGGCG     GG GGGC
                                   C      AA_____  A
GAM276  RGS19IP1 5'  GCTCCGCCGCCGCCGCC     41698    _  G      G
                                GC CCG CCGCCGC CGCC
                                || ||| ||||||| ||||
```

```
                                CG GGC GGCGGCG GCGG
                                 A  _     _
GAM276  RIMS1    5'  CCGCCCGGCCGCCTCCC    43731          GCGCG
                                CCGCCCGGCCGCC    CCC
                                |||||||||||||    |||
                                GGCGGGCCGGCGG    GGG
                                       A____
GAM276  ROR1     5'  CCCGGCCGCCTCGTCCC    22696         G  CG
                                CCCGGCCGCC CG  CCC
                                |||||||||| ||  |||
                                GGGCCGGCGG GC  GGG
                                      A  A_
GAM276  ROR1     5'  CGTCCCGGCCGCTGGCGC    22698    _       C_
                                CG CCCGGCCGC  GCGC
                                || |||||||||  ||||
                                GC GGGCCGGCG  CGCG
                                 A        AC
GAM276  RPS6KA1  5'  CCGTCCGCCGCCGCCGCC    40381    C  G     G
                                CCG CCG CCGCCGC CGCC
                                ||| ||| ||||||| ||||
                                GGC GGC GGCGGCG GCGG
                                 A  _     _
GAM276  RRM2     5'  CCCGCGCCGCGCGCTCCCG   9757      GC       C
                                CCCG  CGCCGCGCGC CCCG
                                ||||  |||||||||| ||||
                                GGGC  GCGGCGCGCG GGGC
                                  __         A
GAM276  RU2      5'  CCGCTGGCCGCCGCCTCAGC   32291     CC       G_ _
                                CCGC  GGCCGCCGC  C GC
                                ||||  |||||||||  | ||
                                GGCG  CCGGCGGCG  G CG
                                  A_        GA T
GAM276  SKI      5'  CCCCCGGCCGCTCCCGCTCCCG 16732    G       CGCG  C
                                CC CCCGGCCGC    CGC CCCG
                                || |||||||||    ||| ||||
                                GG GGGCCGGCG    GCG GGGC
                                 _        AGG_  A
GAM276  SKI      3'  CCGCCCAGCCGCGCCCCCC    16733          CGC  G
                                CCGCCCGGCCGC   GC CCCCC
                                ||||||||||||   || |||||
                                GGCGGGTCGGCG   CG GGGGG
                                       ____ _
GAM276  SLC12A4  5'  CCGCCCGCCGCTGTCCCC    22892     G     GCG
                                CCG CCGCCGC   CCCC
                                ||| |||||||   ||||
                                GGC GGCGGCG   GGGG
                                  G      ACA
GAM276  SLC9A3R1 5'  CCGTCGGCCGCCGCGAGCC   43247     CC       C
                                CCG  CGGCCGCCGCG GCC
                                |||  |||||||||| |||
```

```
                                GGC  GCCGGCGGCGC CGG
                                  A_         T
GAM276  SLC9A5   5'  GCCCAGCCGCCCTCCC      21388          GCGCG
                                GCCCGGCCGCC    CCC
                                ||||||||||    |||
                                CGGGTCGGCGG    GGG
                                      GA___
GAM276  SMARCD1  5'  CCGCCCGGGCCGCCATCTTCCC 40083        _     CGCG
                                CCGCCCGG CCGCCG    CCC
                                |||||||| ||||||    |||
                                GGCGGGCC GGCGGT    GGG
                                     C     AGAA
GAM276  SNX15    5'  CCGCCCGCCGCCGCCTCG    43932       G      G_
                                CCGCCCG CCGCCGC  CG
                                ||||||| |||||||  ||
                                GGCGGGC GGCGGCG  GC
                                   _      GA
GAM276  SOX10    5'  CCGCCTCGGCCGCCTCCCCCG  28001      _      GCGCG
                                CCGCC CGGCCGCC    CCCCCG
                                ||||| ||||||||    ||||||
                                GGCGG GCCGGCGG    GGGGGC
                                  A       A_____
GAM276  SOX10    5'  CCCCCGGCCGCCGCCGCC    28000    G         G
                                CC CCCGGCCGCCGC CGCC
                                || ||||||||||| ||||
                                GG GGGCCGGCGGCG GCGG
                                 _         _
GAM276  SPAG4    5'  CCGCTGCGGTCGCCAAGGCCC  17058     C_  C    CGC
                                CCGC  CGG CGCCG   GCCC
                                ||||  ||| |||||   ||||
                                GGCG  GCC GCGGT   CGGG
                                  AC   A    TC_
GAM276  ST14     5'  CCGACCGGCGGCGGTGCCCTCG 35060       _ C   C_   C
                                CCGGCCG C GCG  GCCC CG
                                ||||||| | |||  |||| ||
                                GGCTGGC G CGC  CGGG GC
                                    C C   CA    A
GAM276  ST7      5'  CCGCCGCGGCCCGGGCGCCCCC 30266      _    GC  C
           G                     CCGCC CGGCC  CG GCGCCCCCG
                                ||||| |||||  || |||||||||
                                GGCGG GCCGG  GC CGCGGGGGC
                                   C     __  C
GAM276  STK11    3'  GCCCGGCCCTGCAGGGCGCTCC 7834         __  CGC    C
                                GCCCGGCC  GC   GCGC CC
                                ||||||||  ||   |||| ||
                                CGGGCCGG  CG   CGCG GG
                                     GA  TCC    A
GAM276  T        5'  GGCCGCCGCCCTTCCG      17247         GCG  C_
                                GGCCGCCGC   CC  CCG
                                |||||||||   ||  |||
```

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                                CCGGCGGCG  GG  GGC
                                     ___  AA
GAM276  TBCD    5'  GCCTGGGGACCGCGCCCCC  25628    C  CC     G
                                GCC GG  GCCGCGC CCCC
                                ||| ||  ||||||| ||||
                                CGG CC  TGGCGCG GGGG
                                  A  CC     _
GAM276  TBL1X   5'  CCGCCCCGCCGCCGCCGAGTCC 24874       G      G  CC_
           CG                     CCGCCC GCCGCCGC CG   CCCG
                                ||||||| |||||||| ||   ||||
                                GGCGGG CGGCGGCG GC   GGGC
                                   G       _ TCA
GAM276  TGFB1   5'  CCCCCGGCCGGGGCCCC    8535    G      CCGCGC   C
                                CC CCCGGCCG     GCCC C
                                || ||||||||     |||| |
                                GG GGGCCGGC     CGGG G
                                 _       CC____    A
GAM276  TJP1    5'  CGCCCGGTCGCCCGCCC     17540        C   GCG
                                CGCCCGG CGCC   CGCCC
                                ||||||| ||||   |||||
                                GCGGGCC GCGG   GCGGG
                                   A   ___
GAM276  TNFRSF6B 3'  CCGCGCGGCCCGCCC      32350     C    GCCGCG
                                CCGC CGGCC     CGCCC
                                |||| |||||     |||||
                                GGCG GCCGG     GCGGG
                                  C    _______
GAM276  TRRAP   5'  CCGCTCGGCCGCGCGCAGTCCC 18590     C     C    CC
           G                     CCGC CGGCCGC GCGCG  CCCG
                                |||| ||||||| |||||  ||||
                                GGCG GCCGGCG CGCGT  GGGC
                                  A      _    CA
GAM276  TYK2    5'  CCTCCGGCCGCGCTCCTTCCG  40857    GC      CGC  G  C_
                                CC  CCGGCCGC   GC CC  CCG
                                ||  ||||||||   || ||  |||
                                GG  GGCCGGCG   CG GG  GGC
                                 A_       ___  A  AA
GAM276  UBE2E3  5'  CCGCCCGGCCGCTCGCGCGCC  26818          _
                                CCGCCCGGCCGC CGCGCGCC
                                |||||||||||| ||||||||
                                GGCGGGCCGGCG GCGCGCGG
                                       A
GAM276  UGCG    5'  CGCCCCCGCCCGCGCGC     17868      GG    _
                                CGCCC  CCGCC GCGCGC
                                |||||  ||||| ||||||
                                GCGGG  GGCGG CGCGCG
                                   __    G
GAM276  VBP1    5'  CCGCCGGCCGCCGGGATTCC   17927      C      CGCG_
                                CCGCC GGCCGCCG    CC
                                ||||| ||||||||    ||
```

```
                                GGCGG CCGGCGGC    GG
                                  _       CCTAA
GAM276  WHSC1    3'  CCGCCCAGGTTGCCTAGGTCCC 39357        CC_  GCGCG
                                CCGCCCGG  GCC    CCC
                                ||||||||  |||    |||
                                GGCGGGTC  CGG    GGG
                                    CAA   ATCCA
GAM276  WNT11    5'  GCACGGCCGCCGCTGGTCC   21532    C       GCG_
                                GC CGGCCGCCGC   CC
                                || ||||||||||   ||
                                CG GCCGGCGGCG   GG
                                 T        ACCA
GAM276  WNT2     5'  CCGCCTCGCCGCGCCCCC    18102      CGGC      G
                                CCGCC   CGCCGCGC CCCC
                                |||||   |||||||| ||||
                                GGCGG   GCGGCGCG GGGG
                                  A___      _
GAM276  ZNF219   5'  CCCGGTCCCCCGCCCCCG    32319      _  G  GCG
                                CCCGG CC CC   CGCCCCCG
                                ||||| || ||   ||||||||
                                GGGCC GG GG   GCGGGGGC
                                  A  _  ___
GAM276  ZNF278   5'  GCCCGGCCGCTGCACC      36793         CGC
                                GCCCGGCCGC   GCGCC
                                ||||||||||   |||||
                                CGGGCCGGCG   CGTGG
                                     A__
GAM277  ABCC11   5'  GCCTGCTCTTTCCTCTCC    37616    GC  C   C
                                GC  GC CTT TCCTCTCC
                                ||  || ||| ||||||||
                                CG  CG GAA AGGAGAGG
                                 GA  A  _
GAM277  ABCD1    3'  GTGCGTCCCTCTCCCCTC    6205    C   CCCT  T
                                G GCG    TC CCTCTCCCCTC
                                | |||    || ||||||||||
                                C CGC    AG GGAGAGGGGAG
                                 A  _____  _
GAM277  ADAMTS8  3'  GCCGCCCCATACCCTCTCCTCT 28164    G     TC_      C
                                GC CGCCCT   TCCTCTCC CT
                                || ||||||   |||||||| ||
                                CG GCGGGG   GGGAGAGG GA
                                  _     TAT       A
GAM277  ADRA1D   3'  GCCCGCAGCCTCTCCCTTC   8617      TTCT      C
                                GCCC    CCTCTCCC TC
                                ||||    |||||||| ||
                                CGGG    GGAGAGGG AG
                                  CGTC       A
GAM277  AES      3'  GCCTCTGTCTCCCCTC      10055     CT   CC
                                GCC  TCT  TCTCCCCTC
                                |||  |||  |||||||||
```

```
                                CGG  AGA  AGAGGGGAG
                                  __   C_
GAM277  AKAP2    3'  GCTGCTTTTTTCCCCTCC    28496    GC  CC  C
                                GC  GC  TT TCCTCTCC
                                ||  ||  || ||||||||
                                CG  CG  AA AGGGGAGG
                                 A_  AA  A
GAM277  AQP6     5'  CGCTCTCCACCTCTCCTCC   38240     C   T     _
                                CGC CTTC CCTCTCC CC
                                ||| |||| ||||||| ||
                                GCG GAGG GGAGAGG GG
                                  A   T      A
GAM277  ARHG     5'  GCAGTGCCTCCTCTCTCT    11684     CGC     _
                                GCG   CCTTCTC CTCT
                                |||   ||||||| ||||
                                CGT   GGAGGAG GAGA
                                  CAC      A
GAM277  ARSD     3'  GCGGCTCTTCCTCTCCTCTC  28927     C  C  TC      C
                                GCG GC CT  TCCTCTCC CTC
                                ||| || ||  |||||||| |||
                                CGC CG GA  AGGAGAGG GAG
                                  _ A __       A
GAM277  ATP8A2   3'  GCTCGCCCTTCTTTTCTGCTCC 45258    G       CC   CCC
                                GC CGCCCTTCT  TCT   CTCC
                                || |||||||||  |||   ||||
                                CG GCGGGAAGA  AGA   GAGG
                                 A        AA   C__
GAM277  B4GALT4  3'  CGTCGCCTTTTCTCCCCTC   19100    _   C  CTCC
                                CG CGCC TT    TCTCCCCTC
                                || |||| ||    |||||||||
                                GC GCGG AA    AGAGGGGAG
                                 A   A  _____
GAM277  CARPX    3'  GCTGTATTTTCTCCTCTCTCT 33575    GCGCCC       CC
                                GC     TTCTCCTCTC  CT
                                ||     ||||||||||  ||
                                CG     AAGAGGAGAG  GA
                                 ACATAA         A_
GAM277  CD34     5'  ACGCGCTCTTCCCGCCCCCTCC 12108       C    T  T T
                                GCGCGC CTTC CC C CCCCTCC
                                |||||| |||| || | |||||||
                                TGCGCG GAAG GG G GGGGAGG
                                   A    _ C _
GAM277  CNP      3'  GCACGTTTCCCTCTCCCCT   37557      CCC   T
                                GCGCG   TTC CCTCTCCCCT
                                |||||   ||| ||||||||||
                                CGTGC   AAG GGAGAGGGGA
                                  A__   _
GAM277  COL1A1   3'  GCCCTTCCTGACTCTCCTCC   6375         CCT   C
                                GCCCTTCT   CTC CCTCC
                                ||||||||   ||| |||||
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```
                                CGGGAAGG   GAG GGAGG
                                     ACT   A
GAM277  CRTL1    5'  GCGCTCTTTCTCCTCACC    12450      C  _     T
                                GCGC CTT CTCCTC CC
                                |||| ||| |||||| ||
                                CGCG GAA GAGGAG GG
                                  A  A     T
GAM277  DES      3'  GCCTCTCTCCTCTCCTCTC   43566     C         C
                                GCC TTCTCCTCTCC CTC
                                ||| |||||||||| |||
                                CGG GAGAGGAGAGG GAG
                                  A         A
GAM277  DLX4     5'  GCCCCCCCATGACTTTCCCCTC 39617         C___  C
              C                  GCCCTTCT   CT TCCCCTCC
                                |||||||    || ||||||||
                                CGGGGGGG   GA AGGGGAGG
                                     TACT  A
GAM277  DXYS155E 3'  GCGCTCCTTCTCCTCCTCC   22955     _        TC
                                GCGC CCTTCTCCTC  CC
                                |||| ||||||||||  ||
                                CGCG GGAAGAGGAG  GG
                                  A        GA
GAM277  EGR3     3'  GCGCTCCTTACCCCCTCC    40550     _   CT
                                GCGC CCTT  CCTCTCC
                                |||| ||||  |||||||
                                CGCG GGAA  GGGGAGG
                                  A   TG
GAM277  EPHB2    3'  GCGGCCCCTGTCTCTCCCCT   32673     C     CTC
                                GCG GCCCTT   CTCTCCCCT
                                ||| ||||||   |||||||||
                                CGC CGGGGA   GAGAGGGGA
                                  _     CA_
GAM277  EPHB2    3'  GCCCCTGTCTCTCCCCT     32671       CTC
                                GCCCTT   CTCTCCCCT
                                ||||||   |||||||||
                                CGGGGA   GAGAGGGGA
                                   CA_
GAM277  FKBP6    3'  GCTGCGCTTTCCCCTCCCTTC  44091    _   CCTTC       C
                                GC GCGC    TCCTCTCCC TC
                                || ||||    ||||||||| ||
                                CG CGCG    AGGGGAGGG AG
                                 A   AA___       A
GAM277  GDI2     3'  CGCTTCCTCTCCCCT      11257     CCTTC
                                CGC    TCCTCTCCCCT
                                |||    ||||||||||
                                GCG    AGGAGAGGGGA
                                  A____
GAM277  GNA15    3'  GCGTTCCTTCTCCTGTCC    40901     C_       C
                                GCG  CCTTCTCCT TCC
                                |||  ||||||||| |||
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                                CGC  GGAAGAGGA AGG
                                  AA        C
GAM277  HCFC1    3'  GCGCGCTCCTCTCTCTGCTTTC 43395       C     _ _  CC
              C                   GCGCGC CTTCTC CT CT  CC
                                  |||||| |||||| || ||  ||
                                  CGCGCG GGAGAG GA GA  GG
                                     A     A  C  AA
GAM277  HEXB     3'  GCTGTGGCCTTTTTCCCCTCC  8016     GC__   C  C
                                  GC    GCC TT TCCTCTCC
                                  ||    ||| || ||||||||
                                  CG    CGG AA AGGGGAGG
                                   ACAC   A  A
GAM277  HOXB6    3'  CGCGTCCTCCCTCCC       40821      CCC     T
                                  CGCG   TTCTCC CTCCC
                                  ||||   |||||| |||||
                                  GCGC   AGGAGG GAGGG
                                    ____     _
GAM277  HOXC9    3'  CGCAAGAGTTTTCTTTTCCCCT 41480      CCC___    CCTC
                                  CGCG     TTCT    TCCCCT
                                  ||||     ||||    ||||||
                                  GCGT     AAGA    AGGGGA
                                    TCTCAA    AA__
GAM277  HOXD13   5'  GCGCGCCTCCTCCCTCCTCTCC 8018         C     T    C
                                  GCGCGCC TTCTCC CTCC CTCC
                                  ||||||| |||||| |||| ||||
                                  CGCGCGG AGGAGG GAGG GAGG
                                     _     _    A
GAM277  ITPR1    5'  GCGGCTTTCTCTCTCC      13667     C  CC    C
                                  GCG GC  TTCTC TCTCC
                                  ||| ||  ||||| |||||
                                  CGC CG  AAGAG AGAGG
                                   _ A_    _
GAM277  KCNA4    5'  GCACGCCCCATGCTCTCTCT   13799         T__   _
                                  GCGCGCCCT   CTC CTCT
                                  |||||||||   ||| ||||
                                  CGTGCGGGG   GAG GAGA
                                       TAC   A
GAM277  KPNB1    5'  GCTCCCCTTCCTCTCCTCT    13970    G    C       C
                                  GC CCCTT TCCTCTCC CT
                                  || ||||| |||||||| ||
                                  CG GGGGA AGGAGAGG GA
                                   A     _       A
GAM277  LRP1     5'  GCTGCTCTTTCCCCCTCC     14213    GC  C   CT
                                  GC  GC CTT  CCTCTCC
                                  ||  || |||  |||||||
                                  CG  CG GAA  GGGGAGG
                                   A_  A   AG
GAM277  LZTS1    3'  GCTGCCTGTCTCTCCCCTC    34269    GC   CTTCTC
                                  GC  GCC     CTCTCCCCTC
                                  ||  |||     ||||||||||
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                                CG  CGG     GAGAGGGGAG
                                 A_   ACA___
GAM277  MYLK2    3'  CCCTTGGCTTCTCCCCTCC   37520       CTCC
                                CCCTT    TCTCCCCTCC
                                |||||    ||||||||||
                                GGGAA    AGAGGGGAGG
                                   CCGA
GAM277  NNMT     5'  GCCCTCCTTCTCTTTCCTC   26121         C    CC
                                GCCCTTCT CTCT  CCTC
                                |||||||| ||||  ||||
                                CGGGAGGA GAGA  GGAG
                                     A    AA
GAM277  NR2F6    5'  GCGCCCCCACCGCGCTCTTCCC 23450        TC ___    C
           TCC                    GCGCCCT  TC   CTCT CCCTCC
                                |||||||  ||   |||| ||||||
                                CGCGGGG  GG   GAGA GGGAGG
                                    GT  CGC    A
GAM277  OGG1     5'  GCTCGCCTTTCCCCCTCC    32570    G    C     T
                                GC CGCC TTCTCC CTCC
                                || |||| |||||| ||||
                                CG GCGG AAGGGG GAGG
                                 A    A     _
GAM277  OSCAR    5'  CGCACCCTCTCCCCTCC     39308         T
                                CGCGCCCT CTCCTCTCC
                                |||||||| |||||||||
                                GCGTGGGA GAGGGGAGG
                                        _
GAM277  PAWR     5'  GCCGCTGCCTCCTCTTCCTTCC 15097     _ _       C  C
                                GCC CT TCTCCTCT CC TCC
                                ||| || |||||||| || |||
                                CGG GA GGAGGAGA GG AGG
                                  C  C       A  A
GAM277  PIK3CG   5'  CGTGCCCTCCCTTTTCCTCC   15303    C       CCTCTCC
                                CG GCCCTTCT      CCTCC
                                || ||||||||      |||||
                                GC CGGGAGGG      GGAGG
                                 A       AAAA___
GAM277  POMC     5'  GCGGCTCTTCTTCCCCTC    9602      C  C    CCTC
                                GCG GC CTTCT    TCCCCTC
                                ||| || |||||    |||||||
                                CGC CG GAAGA    AGGGGAG
                                  _ A    _____
GAM277  POU3F1   3'  GCGGCTCTCGCGACCTCCCCTC 40373     C  C   CTCC
           C                     GCG GC CTT    TCTCCCCTCC
                                ||| || |||    ||||||||||
                                CGC CG GAG    GGAGGGGAGG
                                  _ A   CGCT
GAM277  POU3F2   5'  GCTCGCTCTTTCTGTCTCCTCT 24671    G   C _____
           C                     GC CGC CT     TCTCCTCTC
                                || ||| ||     |||||||||
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                                CG GCG GA    AGAGGAGAG
                                 A  A  AAGAC
GAM277  PPIL1    3'  GGCGCTTCTCCTTTC      32000   C   CC     C
                                G GCGC  TTCTCCT TC
                                | ||||  ||||||| ||
                                C CGCG  AAGAGGA AG
                                _   __      A
GAM277  PPP1R11  3'  CGTCCTCCTCTTCCTCTTCCCT 45508   _ _   _    C
            C                    CG CC CTTCT CCTCT CCCTC
                                 || || ||||| ||||| |||||
                                 GC GG GGAGA GGAGA GGGAG
                                  A A    A    A
GAM277  RFC2     5'  CGCGCCTCCTCTTCCCTC    16281       CTTC    C
                                 CGCGCC   TCCTCT CCCTC
                                 ||||||   |||||| |||||
                                 GCGCGG   AGGAGA GGGAG
                                    ____     A
GAM277  SGCE     5'  CCGTCCTCGATTCTCCCCTCC  19394    C    C__
                                 CC TTCTC   TCTCCCCTCC
                                 || |||||   ||||||||||
                                 GG AGGAG   AGAGGGGAGG
                                  C    CTA
GAM277  SLC22A7  3'  GCCTGCCCTTCTGCTCTCC   27431    GC      C
                                 GC  GCCCTTCT CTCTCC
                                 ||  |||||||| ||||||
                                 CG  CGGGAAGA GAGAGG
                                  GA       C
GAM277  SLC25A6  3'  GCGCCCCTTTTCTAGAGCCTTC 44863     G    C  CTCTC  C
            C                    GCGC CCCTT TC    CC TCC
                                 |||| ||||| ||    || |||
                                 CGCG GGGAA AG    GG AGG
                                   _    A  ATCTC  A
GAM277  SLC6A8   5'  GCGCGCCTCGCCCTCTCC    24769       C  C
                                 GCGCGCC TT TCCTCTCC
                                 ||||||| || ||||||||
                                 CGCGCGG AG GGGAGAGG
                                     _ C
GAM277  SOX11    3'  GCATCTTCTTCTCTCCCCTCC  17021    CC    C
                                 GCG  CTTCT CTCTCCCCTCC
                                 |||  ||||| ||||||||||
                                 CGT  GAAGA GAGAGGGGAGG
                                   A_    A
GAM277  SOX11    3'  GCGGGTCCTACCTCCCCTCC   17023    CG_  CT
                                 GCG   CC  TCTCCTCTCC
                                 |||   ||  ||||||||||
                                 CGC   GG  GGAGGGGAGG
                                   CCA  AT
GAM277  SOX4     3'  GCGCTGGGTTCTCCCCTCC   16987    GCCC
                                 GCGC    TTCTCCTCTCC
                                 ||||    ||||||||||
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                                CGCG   AAGAGGGGAGG
                                  ACCC
GAM277  SPAG8   3'  GCCTGCTTTCCTCCTCTC   29694   GC  CC
                                GC  GC  TTCTCCTCTC
                                ||  ||  ||||||||||
                                CG  CG  AGGAGGAGAG
                                 GA  AA
GAM277  T       5'  GCGCGCCTCCCTCCCCTC   17245       CTTC   T
                                GCGCGCC   TCC CTCCCCTC
                                |||||||   ||| ||||||||
                                CGCGCGG   AGG GAGGGGAG
                                      ____  _
GAM277  TEAD3   3'  CGCTGAGCCCTCCTCTCCTCTC 17372    ___   TTC      C
                                CGC   GCCC   TCCTCTCC CTC
                                |||   ||||   |||||||| |||
                                GCG   CGGG   AGGAGAGG GAG
                                  ACT   ___      A
GAM277  TNS     3'  GCACTTTCTTCTCTCCTCC   35476     GCC     CT
                                GCGC   CTTCTC  CTCC
                                ||||   ||||||  ||||
                                CGTG   GAAGAG  GAGG
                                  AAA     AG
GAM277  TRHDE   5'  GCTGCTCTTCTCGGCCCCCTCC 30108   GC  C     CTC
                                GC  GC CTTCTC   TCCCCTCC
                                ||  || ||||||   ||||||||
                                CG  CG GAAGAG   GGGGGAGG
                                 A_  A     CC_
GAM277  TRIM34  5'  GCTTCCTCCTCTTCCTTC   38974   CC      C  C
                                GC  TTCTCCTCT CC TC
                                ||  ||||||||| || ||
                                CG  AGGAGGAGA GG AG
                                 A_       A  A
GAM277  VEGF    5'  GCCCCCTCTCCTCTTCCTTC  17955   G        C  C
                                GC CCCTTCTCCTCT CC TC
                                || |||||||||||| || ||
                                CG GGGGAGAGGAGA GG AG
                                 _         A  A
GAM277  VEGFB   3'  GCTGCCTCCCAGTCTCCTCT  17980   _ G_  T_
                                GC GC  CCC  TCTCCTCT
                                || ||  |||  ||||||||
                                CG CG  GGG  AGAGGAGA
                                 A  GA   TC
GAM277  ZNF278  5'  GCGCCACTCTCTCCTCTCC   36794     _ _
                                GCGCC CT TCTCCTCTCC
                                ||||| || ||||||||||
                                CGCGG GA AGAGGAGAGG
                                   T  G
GAM277  ACP1    5'  CCTGGAGGAGGAAGGGCCGC  28234   _   A     _
                                CC GGAG AGGAAGG CTGC
                                || |||| ||||||| ||||
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                                GG CCTC TCCTTCC GGCG
                                 A   C      C
GAM277  ARHC     5'  TCCGGGCAGGGGGTCCGC    23174      AGA   AA  _
                                TCCGG   AGG  GG CTGC
                                |||||   |||  || ||||
                                AGGCC   TCC  CC GGCG
                                   CG_   C_  A
GAM277  ARHGDIA  3'  CCTGGAGAATGGCTGCTCCGC  20202    _     GGAA
                                CC GGAGAA    GGCTGCTCCGC
                                || ||||||    ||||||||||
                                GG CCTCTT    CCGACGAGGCG
                                 A     A___
GAM277  BIN3     3'  GGAGGGTGCTGCTGCTCCG   33083      AA  AAG_
                                GGAG  GG    GCTGCTCCG
                                ||||  ||    |||||||||
                                CCTC  CC    CGACGAGGC
                                  __  ACGA
GAM277  CASP8    3'  GGGGACGGGGTCTTGCTC    37875    A  A  AA  _  _
                                GG GA GG  GG CT GCTC
                                || || ||  || || ||||
                                CC CT CC  CC GA CGAG
                                 C  G  __  A  A
GAM277  CCND1    3'  TCCGGAGAGGAGGGACTG    38224        A   A  _
                                TCCGGAGA GGA GG CTG
                                |||||||| ||| || |||
                                AGGCCTCT CCT CC GAC
                                     _   C  T
GAM277  CGA      5'  TCCGAAGAGGGATTTTAGCTTC 8823         A   AGGCT   C
           G                     TCCGGAGA GGA     GCT CG
                                |||||||| |||     ||| ||
                                AGGCTTCT CCT     CGA GC
                                    C   AAAAT   A
GAM277  EGLN3    5'  TCGGGAGAAGGGATCTGC    35211    C       AAGG
                                TC GGAGAAGG    CTGC
                                || ||||||||    ||||
                                AG CCTCTTCC    GACG
                                 C       CTA_
GAM277  GNA11    3'  TCCGTGGAAGGAAGGTCCTGC  44051      GA       __
                                TCCG  GAAGGAAGG  CTGC
                                ||||  |||||||||  ||||
                                AGGC  CTTCCTTCC  GACG
                                  AC        AG
GAM277  HTR2C    5'  GAGGAAGGAAGCGTCCTCCGC  9286    GA       GCTG
                                G  GAAGGAAG    CTCCGC
                                |  ||||||||    ||||||
                                C  CTTCCTTC    GAGGCG
                                 TC       GCAG
GAM277  IL1RAPL2 5'  TCCGAAGAGGGAAGGGCGC   32642         A     C
                                TCCGGAGA GGAAGG TGC
                                |||||||| |||||| |||
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                                AGGCTTCT CCTTCC GCG
                                    C     C
GAM277  KEL     5'  CCTGGAGAAGGGGCACTTCTGC 7678    _      AA  T  _ C
                                CC GGAGAAGG  GGC GCT C GC
                                || ||||||||  ||| ||| | ||
                                GG CCTCTTCC  CCG TGA G CG
                                 A       __  _  A A
GAM277  MAPK1   3'  TCCGGAGACGGAAGCACTTGC  15654        A   _  _
                                TCCGGAGA GGAAG GCT GC
                                |||||||| ||||| ||| ||
                                AGGCCTCT CCTTC TGA CG
                                    G    G  A
GAM277  MAPK1   3'  TCAGGAGAGGGAGGAACCACTG 15653   C   ___    G_
          C                      TC GGAGA   AGGAA  GCTGC
                                || |||||   |||||  |||||
                                AG CCTCT   TCCTT  TGACG
                                 T    CCC    GG
GAM277  NEFH    3'  GAAGAAGGAGGCCCCG      34346        A   GCT
                                GGAGAAGGA GGCT   CCG
                                |||||||||  ||||   |||
                                CTTCTTCCT CCGG   GGC
                                    _   ___
GAM277  NRXN2   5'  TCCGAGGAGGATGCTCCG    31491     GAGA   A  C
                                TCCG   AGGA GG TGCTCCG
                                ||||   |||| || |||||||
                                AGGC   TCCT CC ACGAGGC
                                  ____   _ T
GAM277  NRXN3   3'  TCCGGAGAAGGAAGTTTGC   39944          ______
                                TCCGGAGAAGGAAG     GC
                                ||||||||||||||     ||
                                AGGCCTCTTCCTTC     CG
                                       AAAIII
GAM277  NTSR1   3'  GGGGAGGAAGGCCCCTC     14888    A  A      G
                                GG GA GGAAGGCT CTC
                                || || |||||||| |||
                                CC CT CCTTCCGG GAG
                                 C  _       G
GAM277  NTSR1   3'  CCCGGGTGGGGGCTGCTC    14879      AGAA  AA
                                TCCGG   GG  GGCTGCTC
                                |||||   ||  ||||||||
                                GGGCC   CC  CCGACGAG
                                  CA__  C_
GAM277  PPM1D   5'  CCCGGAGAAGGGGGGGCGC   18836         AA_  T
                                TCCGGAGAAGG   GGC GC
                                ||||||||||   ||| ||
                                GGGCCTCTTCC   CCG CG
                                      CCC   _
GAM277  PTPN6   5'  TCCGGAGAGGAAGGGGGC    15917       A     CT
                                TCCGGAGA GGAAGG  GC
                                |||||||| ||||||  ||
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                                AGGCCTCT CCTTCC  CG
                                    _     CC
GAM277  RPP30    5'  CGGAGAAACTTACTTGCTTTGC 26935        GAAG  _  CC
                                CGGAGAAG   GCT GCT  GC
                                ||||||||   ||| |||  ||
                                GCCTCTTT   TGA CGA  CG
                                    GAA_  A   AA
GAM277  TGM1     3'  TCCTGGGGAGCTGCTC      7417      _ AGAA   AG
                                TCC GG   GGA  GCTGCTC
                                ||| ||   |||  |||||||
                                AGG CC   CCT  CGACGAG
                                  A ____  __
GAM277  TNFSF8   3'  CCTGGAGAAGGAGGACTGC   10329    _       A
                                CC GGAGAAGGA GGCTGC
                                || |||||||| ||||||
                                GG CCTCTTCCT CTGACG
                                 A        C
GAM277  UTF1     3'  CCTGGAGAGGGGAGACTGC   18712    _    A  A
                                CC GGAGA GG AGGCTGC
                                || ||||| || |||||||
                                GG CCTCT CC TCTGACG
                                 A    C  C
GAM278  ABCC3    3'  CACCACGGCCACCAGTGCCCC  33414      T   G  ___
                                CACC CGGC GCC   GCCCC
                                |||| |||| |||   |||||
                                GTGG GCCG TGG   CGGGG
                                  T   G   TCA
GAM278  ALK      5'  CACCGCTGCCGCCCC       43832      TCG  G
                                CACC   GC GCCGCCCC
                                ||||   || ||||||||
                                GTGG   CG CGGCGGGG
                                  ___  A
GAM278  ARF4L    5'  CACCGCAGCCGCCCC       43070      TCG
                                CACC   GCGGCCGCCCC
                                ||||   ||||||||||
                                GTGG   CGTCGGCGGGG
                                  ___
GAM278  BACE     3'  CCTCTTTCCAGCCGCCCC    39957      GG__
                                CCTC   CGGCCGCCCC
                                ||||   ||||||||||
                                GGAG   GTCGGCGGGG
                                  AAAG
GAM278  BAX      3'  CAGCCCAACAGCCGCTCC    39869    C         _
                                CA CTCGGCGGCCGC CC
                                || ||||||||||| ||
                                GT GGGTTGTCGGCG GG
                                 C          A
GAM278  CAPN7    5'  CACCCGGCCGCCCC        30709      TCGG
                                CACC   CGGCCGCCCC
                                ||||   ||||||||||
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                                GTGG   GCCGGCGGGG
                                 ____
GAM278  CAPS    3'  ACCTCGGCGGGGGCATCC    19759         CC __
                                ACCTCGGCGG  GC  CC
                                ||||||||||  ||  ||
                                TGGAGCCGCC  CG  GG
                                      CC  TA
GAM278  CDK9    3'  CACTCAGCGGGCTGCTCC    10388     C     _ C _
                                CAC TCGGCGG C GC CC
                                ||| ||||||| | || ||
                                GTG AGTCGCC G CG GG
                                  _     C A  A
GAM278  CDS1    5'  CACCTCGCAGCCGCGCCC    10394       G     _
                                CACCTCG CGGCCGC CCC
                                ||||||| ||||||| |||
                                GTGGAGC GTCGGCG GGG
                                   _     C
GAM278  CENPB   5'  CACCCCGTACTTGCGCTCC   43011       _ GGC  _
                                CACCTCG GC   CGC CC
                                ||||||| ||   ||| ||
                                GTGGGGC TG   GCG GG
                                    A  AAC   A
GAM278  CLCN4   5'  CCTCGCGCTGGCCGCCCC    12281      _ _
                                CCTCG GC GGCCGCCCC
                                ||||| || |||||||||
                                GGAGC CG CCGGCGGGG
                                   G  A
GAM278  DNMT3B  3'  CACCTCAGGCTACCCC      27869       GC   CG
                                CACCTCG  GGC  CCCC
                                |||||||  |||  ||||
                                GTGGAGT  CCG  GGGG
                                    __  AT
GAM278  DYRK2   5'  CGCCTCCCGGCCGCCCC     27037   A   GG
                                C CCTC  CGGCCGCCCC
                                | ||||  ||||||||||
                                G GGAG  GCCGGCGGGG
                                 C   G_
GAM278  ELK1    5'  CACCTAGAAGCCGCCCC     23406      C  C
                                CACCT GG GGCCGCCCC
                                ||||| || |||||||||
                                GTGGA TC TCGGCGGGG
                                   _ T
GAM278  EN2     5'  CCTCGCGGCCGCCGCCCC    10940     __  G
                                CCTC  GGC GCCGCCCC
                                ||||  ||| ||||||||
                                GGAG  CCG CGGCGGGG
                                  CG   G
GAM278  EN2     5'  CACCACGAGCCGCCCC      10929     T  GC
                                CACC CG  GGCCGCCCC
                                |||| ||  |||||||||
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                                GTGG GC  TCGGCGGGG
                                  T __
GAM278  EN2     5'  CACCCGGCGACAGCCCC     10930     T     C
                                CACC CGGCGGC GCCCC
                                |||| ||||||| |||||
                                GTGG GCCGCTG CGGGG
                                  _      T
GAM278  ESRRA   5'  CACCGCGCCGCGTCCC     20825     TCG   G   __
                                CACC   GCG CCGC  CCC
                                ||||   ||| ||||  |||
                                GTGG   CGC GGCG  GGG
                                  ___  _   CA
GAM278  FBXL7   5'  CGCCTCCTTCGGCTGCCCC   29400   A   GG_   C
                                C CCTC   CGGC GCCCC
                                | ||||   |||| |||||
                                G GGAG   GCCG CGGGG
                                 C   GAA   A
GAM278  FZD10   5'  CCTCAGCGCCGCCGCTCC    28449       __    _
                                CCTCGGCG  GCCGC CC
                                ||||||||  ||||| ||
                                GGAGTCGC  CGGCG GG
                                    GG    A
GAM278  GATA6   5'  CAGCTCGACAGGTTGCCCC   23537    C      CC_
                                CA CTCGGCGG   GCCCC
                                || ||||||||   |||||
                                GT GAGCTGTC   CGGGG
                                 C       CAA
GAM278  GMDS    3'  ACCTCGGCGGGGCGGCCCC   11298       __  C
                                ACCTCGGC  GGC GCCCC
                                ||||||||  ||| |||||
                                TGGAGCCG  CCG CGGGG
                                    CC   C
GAM278  GNA11   5'  CCTGCCCGCCGCCGCCCC    44039    __ G  G
                                CCT  C GC GCCGCCCC
                                |||  | || ||||||||
                                GGA  G CG CGGCGGGG
                                  CG G  G
GAM278  GPR30   5'  CACTTCCGAGTGCGCCCC    11305    C_   CG  C
                                CAC  TCGG  GC GCCCC
                                |||  ||||  || |||||
                                GTG  GGCT  CG CGGGG
                                  AA   CA  _
GAM278  GRIN2A  5'  CTCAGCAGTGGCCGCTCC    9109      ___    _
                                CTCGGC   GGCCGC CC
                                ||||||   |||||| ||
                                GAGTCG   CCGGCG GG
                                   TCA     A
GAM278  GTF2I   5'  CGCCGCATGGCCGCCCC     37434   A  T  GC
                                C CC CG  GGCCGCCCC
                                | || ||  |||||||||
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                                G GG GT  CCGGCGGGG
                                 C  C  A_
GAM278  HDAC4    5'  CCCCGGCGGGCGAAGCCGCC  25749        _______
                                CCTCGGCG     GCCGCC
                                ||||||||     ||||||
                                GGGGCCGC     CGGCGG
                                     CCGCTT
GAM278  HMGA2    5'  CGCCTCGACCGCCCC       18508   A    GCG
                                C CCTCG   GCCGCCCC
                                | |||||   ||||||||
                                G GGAGC   TGGCGGGG
                                 C    ___
GAM278  HOXB5    3'  CACCTCAACTGCTGCCCC    13444         G  C
                                CACCTCGGC GC GCCCC
                                ||||||||| || |||||
                                GTGGAGTTG CG CGGGG
                                      A  A
GAM278  HR       5'  CACCCCAAAGCCGTTCC     32909         C    CC
                                CACCTCGG GGCCG  CC
                                |||||||| |||||  ||
                                GTGGGGTT TCGGC  GG
                                     _    AA
GAM278  IL27     3'  CACCCTGCAAGCCCC       42105       CG   CC
                                CACCT  GCGG  GCCCC
                                |||||  ||||  |||||
                                GTGGG  CGTT  CGGGG
                                   A_   __
GAM278  INPPL1   5'  CCCCGCGCCATCCGCCCC    11461      _  GG_
                                CCTCG GC   CCGCCCC
                                ||||| ||   |||||||
                                GGGGC CG   GGCGGGG
                                   G  GTA
GAM278  KCNC1    5'  CCCCTGGCGGCCGCTCCG    22487      _       _  CIII
                                CCTC GGCGGCCGC CC    G
                                |||| |||||||| ||    |
                                GGGG CCGCCGGCG GG    C
                                   A        A  IIIC
GAM278  LDB1     5'  CCTCAACAATGGCTGCTCC   19334        ___   C  _
                                CCTCGGC   GGC GC CC
                                |||||||   ||| || ||
                                GGAGTTG   CCG CG GG
                                     TTA   A  A
GAM278  LHX3     5'  CACCCCGCAATAGCCCC     31017        G   CC
                                CACCTCG CGG  GCCCC
                                ||||||| |||  |||||
                                GTGGGGC GTT  CGGGG
                                     _  AT
GAM278  LIF      3'  CACCCTTGGACAGGCCCC    14137       C__    CC
                                CACCT   GGCGG  GCCCC
                                |||||   |||||  |||||
```

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                                GTGGG  CTGTC  CGGGG
                                  AAC   __
GAM278  LRPAP1   3'  CACCCGTGCCAGCCCC     14233     T  GCG  _
                                CACC CG   GCC GCCCC
                                |||| ||   ||| |||||
                                GTGG GC   CGG CGGGG
                                  _ A__   T
GAM278  MAP3K5   5'  CCCGGCGGCGGCTCGCTCC   25437    __     _  _
                                CCT  CGGCGGC CGC CC
                                |||  ||||||| ||| ||
                                GGG  GCCGCCG GCG GG
                                 CC      A   A
GAM278  MAP3K8   5'  CACCCCGCCGCCCC       23301       GGCG
                                CACCTC    GCCGCCCC
                                ||||||    ||||||||
                                GTGGGG    CGGCGGGG
                                  ____
GAM278  MDFI     3'  CACCCCAGCCCTGCCCC     24611        GG  _
                                CACCTCGGC  CC GCCCC
                                |||||||||  || |||||
                                GTGGGGTCG  GG CGGGG
                                     __ A
GAM278  MGAM     5'  ACCTCTTGCAGCCGCTCC    43649      G_      _
                                ACCTC  GCGGCCGC CC
                                |||||  |||||||| ||
                                TGGAG  CGTCGGCG GG
                                  AA       A
GAM278  MOCS1    3'  CACCCCGGTGGGGCCCC     45121        C  CC
                                CACCTCGG GG  GCCCC
                                |||||||| ||  |||||
                                GTGGGGCC CC  CGGGG
                                    A  C_
GAM278  MUCDHL   5'  ACCTCAGCGACCTTCGCCCC  34926          ___
                                ACCTCGGCGGCC   GCCCC
                                ||||||||||||   |||||
                                TGGAGTCGCTGG   CGGGG
                                     AAG
GAM278  NDUFA8   5'  CCTCAGCCGCGTCGCCCC    30591       G  __
                                CCTCGGC GC  CGCCCC
                                |||||||  ||  ||||||
                                GGAGTCG CG  GCGGGG
                                   G  CA
GAM278  NLGN2    3'  CCTCGGCAGGGTCCGCCCC   44751         ___
                                CCTCGGCGG   CCGCCCC
                                |||||||||   |||||||
                                GGAGCCGTC   GGCGGGG
                                     CCA
GAM278  NT5M     3'  CACCTCAGTCGCCGGGTTCC  33644        CG   C___
                                CACCTCGG  GCCG   CC
                                ||||||||  ||||   ||
```

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                                GTGGAGTC CGGC   GG
                                    AG   CCAA
GAM278  NTRK2   5' CACCTCGAGGCCGGGCTCC  26144       C   __ _
                                CACCTCGG GGCC  GC CC
                                |||||||| ||||  || ||
                                GTGGAGCT CCGG  CG GG
                                    _   CC  A
GAM278  OPRD1   5' CCGCGCCCCGGCCGCCCC   9511    T  G__
                                CC CG   CGGCCGCCCC
                                || ||   ||||||||||
                                GG GC   GCCGGCGGGG
                                 C  GGG
GAM278  PHLDA3  5' CTCCGCGCCCACCGCCCC   29612    G  ___
                                CTC GCG   GCCGCCCC
                                ||| |||   ||||||||
                                GAG CGC   TGGCGGGG
                                  G   GGG
GAM278  PKIA    5' CTCGACGATCGCTGCCCC   27740      ___ C
                                CTCGGCG   GC GCCCC
                                |||||||   || |||||
                                GAGCTGC   CG CGGGG
                                    TAG  A
GAM278  PLA2G10 5' CACCCCGGCTGTCACGCCCC  18670       GGC__
                                CACCTCGGC    CGCCCC
                                |||||||||    ||||||
                                GTGGGGCCG    GCGGGG
                                     ACAGT
GAM278  PVT1    3' CACCTCGGGAGAAGGCTCC   42307      C  CC_ _
                                CACCTCGG GG   GC CC
                                |||||||| ||   || ||
                                GTGGAGCC TC   CG GG
                                    C  TTC  A
GAM278  RCN1    5' CACCGCGCGCCATCGTCCC   16200    TCG  _   ____
                                CACC   GCG GCCG   CCC
                                ||||   ||| ||||   |||
                                GTGG   CGC CGGT   GGG
                                  ___   G   AGCA
GAM278  REST    5' CCTCGGCGGCGCTCGCTCC   24708       ___  _
                                CCTCGGCGGC   CGC CC
                                ||||||||||   ||| ||
                                GGAGCCGCCG   GCG GG
                                     CGA   A
GAM278  SLC4A2  5' CACCCCGGGGCGCGCCCC   16771      C  _
                                CACCTCGG GGC CGCCCC
                                |||||||| ||| ||||||
                                GTGGGGCC CCG GCGGGG
                                    _  C
GAM278  STIM1   5' CACCCGCGAGCCTGCCCC   41123     CG  _  _
                                CACCT  GCG GCC GCCCC
                                |||||  ||| ||| |||||
```

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                                GTGGG  CGC CGG CGGGG
                                  __  T   A
GAM278  SURF4    3'  CACCCCGAACCAGTCC     37652        CG   CC
                                CACCTCGG  GCCG  CC
                                ||||||||  ||||  ||
                                GTGGGGCT  TGGT  GG
                                    __    CA
GAM278  TCF3     3'  CACCTTGGCCGCCCC      43316      CGGC
                                CACCT   GGCCGCCCC
                                |||||   |||||||||
                                GTGGA   CCGGCGGGG
                                  A___
GAM278  TFRC     5'  CACCGGAGCGGCCGCTCC    17428     TC       _
                                CACC  GGCGGCCGC CC
                                ||||  |||||||||  ||
                                GTGG  TCGCCGGCG GG
                                  CC        A
GAM278  TRRAP    5'  ACCTCGGCGGCCCGGCTCC   18587           __ _
                                ACCTCGGCGGCC  GC CC
                                ||||||||||||  || ||
                                TGGAGCCGCCGG  CG GG
                                      GC  A
GAM278  UROS     5'  CACCCGCGCTGGGCCCC     7506      T _ _ CC
                                CACC CG GC GG  GCCCC
                                ||||  ||  ||  ||  |||||
                                GTGG GC CG CC  CGGGG
                                  _  G  A  __
GAM278  VDR      3'  CACCCGAGACTGCCCC      7513      T   C   C
                                CACC CGG GGC GCCCC
                                ||||  |||  |||  |||||
                                GTGG GCT CTG CGGGG
                                  _   _   A
GAM278  WBSCR1   3'  CCTGCTGCCGGCCGCCCC    35268     CG_ _
                                CCT   GC GGCCGCCCC
                                |||   ||  |||||||||
                                GGA   CG CCGGCGGGG
                                  CGA  G
GAM278  WBSCR5   5'  CCTCAACACGGCCGCCCC    37125      __
                                CCTCG  GCGGCCGCCCC
                                |||||  ||||||||||
                                GGAGT  TGCCGGCGGGG
                                   TG
GAM278  WBSCR5   5'  CCTCACCACGGCCGCCCC    37126      __
                                CCTCG  GCGGCCGCCCC
                                |||||  ||||||||||
                                GGAGT  TGCCGGCGGGG
                                   GG
GAM278  WHSC1    3'  CCTCTTGGCGACCAGGCCCC  39361      __      __
                                CCTC  GGCGGCC  GCCCC
                                ||||  |||||||  |||||
```

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                                GGAG  CCGCTGG  CGGGG
                                  AA      TC
GAM278  WNT2     5'  CGCCTCGCCGCGCCCC     18105   A    G  GC
                                C CCTCG CG  CGCCCC
                                | ||||| ||  ||||||
                                G GGAGC GC  GCGGGG
                                 C    G  __
GAM278  ANK1     3'  CCCCGGGGCCTGCCTGGCCGG 33853    G   A   GC   CC
                                CC CCG GGT  GCC  GGCCGG
                                || ||| |||  |||  ||||||
                                GG GGC CCG  CGG  CCGGCC
                                 _  C   GA   A_
GAM278  AXUD1    5'  CGCGACCCGCGTCCCGGCCGG 37486     C  GG    C
                                CGC GA  TGCG CCCGGCCGG
                                ||| ||  |||| |||||||||
                                GCG CT  GCGC GGGCCGGCC
                                 _ GG    A
GAM278  BTG3     5'  CCGCCGCCGCTCTTCGGCCGGA 27715       AGGT  GCCC
                                CCGCCG   GC   CGGCCGGA
                                ||||||   ||   ||||||||
                                GGCGGC   CG   GCCGGCCT
                                   GG__  AGAA
GAM278  COMT     3'  GCCGAGGTGTGCTTTGTCCGGC 28692         C  C_______  GGCC
          G                     GCCGAGGTG GC      CC   G
                                |||||||| ||       ||   |
                                CGGCTCCAC CG      GG   C
                                     A  AAACIIIA  CCGG
GAM278  DXYS155E 3'  CCTTGGGGGCACCGGCCGG   22951    GA_  T    CC
                                CC   GG GCGCC  GGCCGG
                                ||   || |||||  ||||||
                                GG   CC CGTGG  CCGGCC
                                 AAC  C    __
GAM278  EFNB1    5'  CCCCCGAAGCCTCGGCCGG   20711    G    GTGC   C
                                CC CCGAG    GCC CGGCCGG
                                || |||||    ||| |||||||
                                GG GGCTT    CGG GCCGGCC
                                 G    _____   A
GAM278  EPIM     5'  CCGAGCTGCCTCCGGCCGG   12740      G   GCC
                                CCGAG TGC   CCGGCCGG
                                ||||| |||   ||||||||
                                GGCTC ACG   GGCCGGCC
                                   G   GA_
GAM278  GNA11    5'  CCCCCGGCCCGGCCCTGGCCGG 44033    G  GA   G  _   C
          A                      CC CC  GGT CG CCC GGCCGGA
                                 || ||  ||| || ||| |||||||
                                 GG GG  CCG GC GGG CCGGCCT
                                  G  __  G  C   A
GAM278  IMPDH1   5'  CCGGGGCCCCCGGCTGG      9406      A  TGC       C
                                CCG GG   GCCCCGGC GG
                                ||| ||   |||||||| ||
```

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                                GGC CC   CGGGGCCG CC
                                  _ ___       A
GAM278  INHBB    3'  CCGCCGAGCTGCGCTCCC    13548        G    _
                                CCGCCGAG TGCGC CCC
                                |||||||| ||||| |||
                                GGCGGCTC ACGCG GGG
                                     G    A
GAM278  LBX1     5'  CGGGGTCCCGGCCGG      27282    A  GCGC
                                CG GGT    CCCGGCCGG
                                || |||    |||||||||
                                GC CCA    GGGCCGGCC
                                 C  ____
GAM278  LBX1     5'  CCGCCGGGCAGCTCGGCCGGA  27280       A   C  CC
                                CCGCCG GGTG GC  CGGCCGGA
                                |||||| |||| ||  ||||||||
                                GGCGGC CCGT CG  GCCGGCCT
                                   _   _ A_
GAM278  MARK1    5'  GCCGGGGTCTAGACCGGCCGG  33009     A   GCGCC
                                GCCG GGT    CCGGCCGG
                                |||| |||    ||||||||
                                CGGC CCA    GGCCGGCC
                                  C   GATCT
GAM278  MEN1     5'  CCGATGGGGTGCGCCCCA    39169     ___
                                CCGA   GGTGCGCCCCG
                                ||||   ||||||||||
                                GGCT   CCACGCGGGGT
                                  ACC
GAM278  MNT      5'  GCCGGGGGCGCGCCGG      33716     A  T   CCCG
                                GCCG GG GCGC    GCCGG
                                |||| || ||||    |||||
                                CGGC CC CGCG    CGGCC
                                  C  _   ____
GAM278  MPHOSPH9  3'  GCAGAGGTGCGCAAAACATGGA 35567    C       CCC   C_
                                GC GAGGTGCGC   GGC  GGA
                                || |||||||||   |||  |||
                                CG CTCCACGCG   TTG  CCT
                                 T       TT_   TA
GAM278  OCLN     5'  CCCCGGGGTGCGTTCGG     14900    G   A     CCC
                                CC CCG GGTGCG   CGG
                                || ||| ||||||   |||
                                GG GGC CCACGC   GCC
                                 _  C     AA_
GAM278  P3       5'  GCCAGGCCCGGCCG       33380     G   TGCGC
                                GCC AGG    CCCGGCCG
                                ||| |||    ||||||||
                                CGG TCC    GGGCCGGC
                                  _  _____
GAM278  PRKCABP   3'  CCGCCGAGGTGTGATGGGGACT 29670          CGCCCC_   C
            GGA                   CCGCCGAGGTG      GGC GGA
                                ||||||||||       ||| |||
```

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                                GGCGGCTCCAC      CTG CCT
                                      ACTACCC   A
GAM278  RAB18    5'  CCGCCCGGGTGCGCCTCTCCGG 34572      GA       CCGG
              A                    CCGCC  GGTGCGCC    CCGGA
                                   |||||  ||||||||    |||||
                                   GGCGG  CCACGCGG    GGCCT
                                     GC       AGA_
GAM278  RUNX1    3'  CCTCGAGGTGCGTCGCCTCGG  12018    GC       ___   C
                                   CC  CGAGGTGC   GCC CGG
                                   ||  ||||||||   ||| |||
                                   GG  GCTCCACG   CGG GCC
                                    A_       CAG   A
GAM278  SLC6A8   5'  CGTCGGGGCCCGGCCGG     24764    C  A  T  GCC
                                   CG CG GG GC   CCGGCCGG
                                   || || || ||   ||||||||
                                   GC GC CC CG   GGCCGGCC
                                    A  _  _  ___
GAM278  SLC6A8   5'  CCGCGCCCCCCGCCCCGGCCGG 24756      C AGGTG
                                   CCGC G    CGCCCCGGCCGG
                                   ||||  |    ||||||||||||
                                   GGCG C    GCGGGGCCGGCC
                                     _ GGGGG
GAM278  TEAD3    5'  CGCGGGGGCGCTCCGGCCGG   17371     C A  T    C
                                   CGC G GG GCGC CCGGCCGG
                                   ||| | || |||| ||||||||
                                   GCG C CC CGCG GGCCGGCC
                                    _ C  _    A
GAM279  ACADM    3'  AACCTATGTAGTTTTCTAGGT  6146       CG ATCCTTT
                                   AACC  T      TTTTCTAGGT
                                   ||||  |      ||||||||||
                                   TTGG  A      AAAAGATCCA
                                     AT CATC___
GAM279  EDNRA    3'  CGATCTTTTTCTCTTAGGT    41993     T   C       _
                                   CG ATC TTTTTTTCT AGGT
                                   || ||| ||||||||| ||||
                                   GC TAG AAAAAGAGA TCCA
                                    _  _        A
GAM279  HAP1     3'  CCTGTCCTCCAGCCTGGGT    19497     GTA     TTT   A
                                   CC   TCCTTT   TCT GGT
                                   ||   ||||||   ||| |||
                                   GG   AGGAGG   GGA CCA
                                    AC_     TC_   C
GAM279  MBD1     3'  ACCAGCAAGTTTTTTCTGGGT  31918     C   TCCT       A
                                   ACC GTA    TTTTTTCT GGT
                                   ||| |||    |||||||| |||
                                   TGG CGT    AAAAAAGA CCA
                                     T   TC__       C
GAM279  OTOR     3'  AACCTACAGACTTTTTTTTTTC 33553      CG  TC      ___   A
              TGGGT                    AACC  TA  CTTTTTT   TCT GGT
                                   ||||  ||  |||||||   ||| |||
```

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                                TTGG  GT  GAAAAAA   AGA CCA
                                  AT  CT      AAA   C
GAM279  POLQ     3'  ATCTCTGTTCTTTCCAGG    27319     _ _
                                ATC CT TTTTTTCTAGG
                                ||| || ||||||||||
                                TAG GA AAGAAAGGTCC
                                  A  C
GAM279  ADAMTS4  3'  CCCAGAAAGGGCAGCCGG    23001            G A
                                CCCAGAAAGGGCAG C GG
                                |||||||||||||| | ||
                                GGGTCTTTCCCGTC G CC
                                         _ G
GAM279  ADARB1   3'  TCCCTGGAACCCGGCAGGTCAG 31884     AGAAA   A_
                                TCCC    GGGC  GGCAGGTCAG
                                ||||    ||||  ||||||||||
                                AGGG    CTTG  CCGTCCAGTC
                                  AC___   GG
GAM279  ALDH3B1  3'  CAGAGAGGGCAGGAATGG    45060     A      CA_
                                CAGA AGGGCAGG   GG
                                |||| ||||||||   ||
                                GTCT TCCCGTCC   CC
                                  C       TTA
GAM279  ARHGEF6  3'  TCTAAGGAAGGGCAGCTGG   42805    CC  A      G A
                                TC  AG AAGGGCAG C GG
                                ||  || |||||||| | ||
                                AG  TC TTCCCGTC G CC
                                 AT  C       _ A
GAM279  ATP8B2   3'  TCCCAGGCAGGGCAGGGGCAG  42215       AA      CA  T
                                TCCCAG  AGGGCAGG  GG CAG
                                ||||||  ||||||||  || |||
                                AGGGTC  TCCCGTCC  CC GTC
                                   CG       __  _
GAM279  CLCN7    3'  TCCAGGGCAGGGCAGCCC    10522     CAGAA      _   G
                                TCC    AGGGCAGG CAG TC
                                |||    |||||||| ||| ||
                                AGG    TCCCGTCC GTC GG
                                 ______       C   G
GAM279  CRYBB3   3'  CCAGGGAAGGGTGGACAGGTC  19836     A_    CA
                                CCAG  AAGGG  GGCAGGTC
                                ||||  |||||  ||||||||
                                GGTC  TTCCC  CTGTCCAG
                                  CC    AC
GAM279  CTLA1    5'  TCTCAGGAAGGCTGCCCAGGTC 37902    C   AA    AGG_
           AG                    TC CAG  AGGGC    CAGGTCAG
                                || |||  |||||   ||||||||
                                AG GTC  TTCCG    GTCCAGTC
                                 A  C_    ACGG
GAM279  DUSP4    5'  TCCCGGGTGGACAGGTC     38427      AGAAA   CA
                                TCCC    GGG  GGCAGGTC
                                ||||    |||  ||||||||
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                                AGGG    CCC  CTGTCCAG
                                  _____  AC
GAM279  DUSP5    3'  TCCCAAGAGGGCAGGGG    20662       AA       CA
                                TCCCAG  AGGGCAGG  GG
                                ||||||  ||||||||  ||
                                AGGGTT  TCCCGTCC  CC
                                   C_       __
GAM279  ELK1     3'  CCCCAGAAGGGGTGGTGG    23408        A   CA  CA
                                TCCCAGAA GGG  GG  GG
                                |||||||| |||  ||  ||
                                GGGGTCTT CCC  CC  CC
                                     C   A_  A_
GAM279  EPB72    3'  TCTCAGAAAAGGTTTTCAGTCA 19903    C        CAGGCA
           G                     TC CAGAAAGGG     GGTCAG
                                || |||||||||     ||||||
                                AG GTCTTTTCC     TCAGTC
                                 A        AAAAG_
GAM279  GDI1     3'  CAGAAAGGGTGGGTCAA     41011          CAGGCA
                                CAGAAAGGG     GGTCAG
                                |||||||||     ||||||
                                GTCTTTCCC     CCAGTT
                                     AC_____
GAM279  GNAI2    3'  TCTCAGACAAGGGCAGGC    42653    C   _
                                TC CAGA AAGGGCAGGC
                                || |||| ||||||||||
                                AG GTCT TTCCCGTCCG
                                 A   G
GAM279  JTB      5'  TCCCAGAGGTTCCAGGTCA   27446        AA  GCAGG
                                TCCCAGA  GG    CAGGTCA
                                |||||||  ||    |||||||
                                AGGGTCT  CC    GTCCAGT
                                   __  AAG__
GAM279  LMNA     5'  TCCCGGAAAGGGCGCGG     24531      A       AG  A
                                TCCC GAAAGGGC  GC GG
                                |||| ||||||||  || ||
                                AGGG CTTTCCCG  CG CC
                                  C       __  _
GAM279  MDM2     3'  CCCGGGGAGGGCAGAGCTTGCA 27806     AGAA      _  AG T
           G                     CCC    AGGGCAG GC  G CAG
                                |||    ||||||| ||  | |||
                                GGG    TCCCGTC CG  C GTC
                                  CCCC      T  AA _
GAM279  MGAT1    3'  CAGAAAGGAGGGGTCA      14425         GC   CA
                                CAGAAAGG  AGG  GGTCA
                                ||||||||  |||  |||||
                                GTCTTTCC  TCC  CCAGT
                                     __   __
GAM279  PACE     3'  GAGGGGGGCATGACAGGTCAG  15034    AA_    _
                                GA   GGGCA GGCAGGTCAG
                                ||   ||||| ||||||||||
```

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                                CT   CCCGT CTGTCCAGTC
                                 CCC    A
GAM279  PAFAH1B1  3'  TCCCAGGCAAGGCACAGG    7723        AA    AG
                                TCCCAG  AGGGC  GCAGG
                                ||||||  |||||  |||||
                                AGGGTC  TTCCG  TGTCC
                                   CG    __
GAM279  PFKM      3'  CCATGAGGGGCAGGCGCACAG  41177     GAAA      AGGT
                                CCA   GGGCAGGC   CAG
                                |||   ||||||||   |||
                                GGT   CCCGTCCG   GTC
                                  ACTC      CGT_
GAM279  POU5F1    3'  TCCTAGAAGGGCAGGCAG    15475     C    A
                                TCC AGAA GGGCAGGCAG
                                ||| |||| ||||||||||
                                AGG TCTT CCCGTCCGTC
                                  A   _
GAM279  POU5F1    3'  TCCTAGAAGGGCAGGCA     45552     C    A
                                TCC AGAA GGGCAGGCA
                                ||| |||| |||||||||
                                AGG TCTT CCCGTCCGT
                                  A   _
GAM279  PTGS1     3'  TCCTGAAAAGGGCAGTGCCTGG 38744     CA        _ A_
                                TCC  GAAAGGGCAG GC  GG
                                |||  ||||||||| ||  ||
                                AGG  TTTTCCCGTC CG  CC
                                  AC         A  GA
GAM279  RECQL5    3'  TCCCAGAAGAGGGTGGAG    20172         _    CA  C
                                TCCCAGAA AGGG  GG AG
                                |||||||| ||||  || ||
                                AGGGTCTT TCCC  CC TC
                                    C    A_  _
GAM279  SHC1      3'  TCCCAGAAAGGGAGGCAGGGCA 16708           C      T
          G                      TCCCAGAAAGGG AGGCAGG CAG
                                ||||||||||| ||||||| |||
                                AGGGTCTTTCCC TCCGTCC GTC
                                       _      C
GAM279  SLC7A5    3'  TCCCAGAGCAGGAGGT      18556        AAGG    C
                                TCCCAGA    GCAGG AGGT
                                |||||||    ||||| ||||
                                AGGGTCT    CGTCC TCCA
                                     ____    _
GAM279  SOX12     3'  CCAGGAGGGGGCAGGC      28031      AA   CA
                                CCAG  AGGG  GGCAGGT
                                ||||  ||||  |||||||
                                GGTC  TCCC  CCGTCCG
                                  C_   __
GAM279  SOX13     3'  CCCCAGGGAGACAGGTC     25011      GAAA  C
                                TCCCA    GGG AGGCAGGTC
                                |||||    ||| |||||||||
```

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                                GGGGT   CCC TCTGTCCAG
                                  _____  _
GAM279  SPS2    3'  CCTAGAAAGGGCAGCCGG    29302    C        G A
                                CC AGAAAGGGCAG C GG
                                || |||||||||| | ||
                                GG TCTTTCCCGTC G CC
                                 A         _ G
GAM279  TPTE    3'  TCCCAGAAGGGGAAGGGG    30025        A   C   CA
                                TCCCAGAA GGG AGG  GG
                                |||||||| ||| |||  ||
                                AGGGTCTT CCC TCC  CC
                                     C   T  __
GAM279  TXNIP   3'  TCTCAGAAAAGGGTGGAGCTCA 27001    C       CA  C  G
          G                      TC CAGAAAGGG  GG AG TCAG
                                || |||||||||  || || ||||
                                AG GTCTTTTCC  CC TC AGTC
                                 A        CA  _  G
GAM279  ZNF261  3'  TCCTAGAGAAGGCAGGGAATGG 22993     C   A       CA__
                                TCC AGA AGGGCAGG    GG
                                ||| ||| ||||||||    ||
                                AGG TCT TTCCGTCC    CC
                                  A   C       CTTA
GAM280  APXL    3'  AGGGAGAAAGATGG        11616    C   AAAAC
                                AG GGA     GGAGGATGG
                                || |||     |||||||||
                                TC CCT     CTTTCTACC
                                 _   ______
GAM280  ARHGEF1  3'  AGCGAAGGCACTTGGGGGTGG  21734       AAA  __  A  A
                                AGCGGA   AC  GG GG TGG
                                ||||||   ||  || || |||
                                TCGCTT   TG  CC CC ACC
                                    CCG  AA  _  C
GAM280  ASIC4   5'  AAGCGGGAAGAGGACAG     33061       AAAAAC
                                AAGCGG     GGAGGATGG
                                ||||||     |||||||||
                                TTCGCC     TCTCCTGTC
                                    CT_____
GAM280  ATP2B4   5'  AGAGGAGGAAGAGGATGG    43194    C   AAAAC
                                AG GGA     GGAGGATGG
                                || |||     |||||||||
                                TC CCT     TCTCCTACC
                                 T   CCT__
GAM280  AXUD1   3'  AAGGGGGAAGATGGAA      37483     C  AAAAAC
                                AAG GG     GGAGGATGGAA
                                ||| ||     ||||||||||
                                TTC CC     CCTTCTACCTT
                                  _  _______
GAM280  B4GALT6  5'  AGCGGACGGAATGAATGG    40845       AAAA   __
                                AGCGGA   CGGA  GGATGG
                                ||||||   ||||  ||||||
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```
                                TCGCCT   GCCT  CTTACC
                                   ____   TA
GAM280  B4GALT6  5' AGCGGAAAAGAGGAAATGG   40844       AAC    __
                                AGCGGAAA  GGAGGA  TGG
                                ||||||||  ||||||  |||
                                TCGCCTTT  TCTCCT  ACC
                                   ___    TT
GAM280  B4GALT6  3' AGCAGGGAGGACGG      40843     AAAAAC
                                AGCGG     GGAGGATGG
                                |||||     |||||||||
                                TCGTC     CCTCCTGCC
                                   ______
GAM280  BASP1    3' AGAGGAAGAATGGAGGATTGG 44012   C   A  C     _
                                AG GGAA AA GGAGGAT GG
                                || |||| || ||||||| ||
                                TC CCTT TT CCTCCTA CC
                                 T   C  A      A
GAM280  BGN      3' AGAGGAAGGACGGGGAAAG   11812   C   AA   A  T
                                AG GGAA  ACGG GGA GG
                                || ||||  |||| ||| ||
                                TC CCTT  TGCC CCT TC
                                 T   CC   _  T
GAM280  CALM2    3' AAGGGAAGAAAACATGGAGG  11948    C   __   __
                                AAG GGAA  AAAC  GGAGG
                                ||| ||||  ||||  |||||
                                TTC CCTT  TTTG  CCTCC
                                  _   CT   TA
GAM280  CCND2    3' AGGGGAAAGACGGAGGGG   12044   C    A     AT
                                AG GGAAA ACGGAGG  GG
                                || ||||| |||||||  ||
                                TC CCTTT TGCCTCC  CC
                                 C    C     __
GAM280  CD53     3' AAGGGAAAGGATGG       8153     C  AAAACG
                                AAG GGA     GAGGATGG
                                ||| |||     ||||||||
                                TTC CCT     TTCCTACC
                                  _  ______
GAM280  COG2     5' AAGCGAGAAAACGCAGGAGG  28877      GA    G   T
                                AAGCG  AAAACG AGGA GG
                                |||||  |||||| |||| ||
                                TTCGC  TTTTGC TCCT CC
                                   TC     G   _
GAM280  COL5A3   3' ACGGAGGAGTGAGGA      31847      AAAAC  _ T
                                GCGGA    GGAG GA GGA
                                |||||    |||| || |||
                                TGCCT    CCTC CT CCT
                                   _____   A  _
GAM280  CRY1     5' AGTGGAAAGATGAATGGA    19830   C   AAAC  _
                                AG GGAA    GGA GGATGGA
                                || ||||    ||| |||||||
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                                TC CCTT   TCT CTTACCT
                                 A  _____  A
GAM280  DTNB    3' GCGGTGGAAAGATGGA     37605     AAAAAC
                                GCGG     GGAGGATGGA
                                ||||     ||||||||||
                                CGCC     CTTTCTACCT
                                  AC_____
GAM280  DYSF    3' GGAGAAGGAAATGATGGAAG  18581     AAAAC   __
                                GGA    GGAG  GATGGAAG
                                |||    ||||  ||||||||
                                CCT    CCTT  CTACCTTC
                                 CTT__   TA
GAM280  FAAH    3' GCAGGACGGAGGGGGTGG    11052     AAAA     A__
                                GCGG   ACGGAGG   TGG
                                ||||   |||||||   |||
                                CGTC   TGCCTCC   ACC
                                  C___     CCC
GAM280  FCAR    3' AAGCGGAAAGTGTGGTGGGG  39331        AAC_ A  AT
                                AAGCGGAAA   GG GG  GG
                                |||||||||   || ||  ||
                                TTCGCCTTT   CC CC  CC
                                     CACA  A  __
GAM280  FGF2    3' AGGGAGAAAGGATGGAA    12827    C   AAAAC
                                AG GGA    GGAGGATGGAA
                                || |||    ||||||||||
                                TC CCT    TTTCCTACCTT
                                 _  C_____
GAM280  FOXD2    5' GCAGAAAAAAATGGAA     20965        CGGAG
                                GCGGAAAAA    GATGGAA
                                |||||||||    |||||||
                                CGTCTTTTT    TTACCTT
                                     _____
GAM280  GDI1    3' AGCAGAAGAATTAGGGGTGG  41010       A  C__  A  A
                                AGCGGAA AA   GG GG TGG
                                ||||||| ||   || || |||
                                TCGTCTT TT   CC CC ACC
                                    C  AAT  _  _
GAM280  GPRK6    3' GCTGAGGGACGGAGGACACTGG 13270    G  AAA      ___
                                GC GA   ACGGAGGA   TGG
                                || ||   ||||||||   |||
                                CG CT   TGCCTCCT   ACC
                                 A  CCC       GTG
GAM280  GRF2    3' AAGAGGGGAGAGATGGAA    23672     C  AAAAAC   _
                                AAG GG     GGAG GATGGAA
                                ||| ||     |||| |||||||
                                TTC CC     CCTC CTACCTT
                                  T  _______   T
GAM280  HOXB3    3' GGAACAAGGGGTGGAAG     13440     AAAC  A  A
                                GGAA    GG GG TGGAAG
                                ||||    || || ||||||
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                                CCTT    CC CC ACCTTC
                                  GTT_  _  _
GAM280  ID1      5'  AAGCGAAAAAAATGAGGTGGAA 43114          CG    A
              G                   AAGCGGAAAAA  GAGG TGGAAG
                                  ||||||||||  |||| ||||||
                                  TTCGCTTTTTT  CTCC ACCTTC
                                        TA   _
GAM280  JMJ      3'  AAGCGGTGAGATGGAGATGG   22481       AAAAAC    G
                                  AAGCGG     GGAG ATGG
                                  ||||||     |||| ||||
                                  TTCGCC     CCTC TACC
                                     ACTCTA   _
GAM280  KLF8     5'  GCTGGAAAATGAGGAGG     28535    _     ACG    T
                                  GC GGAAAA   GAGGA GG
                                  || ||||||   ||||| ||
                                  CG CCTTTT   CTCCT CC
                                   A     A__    _
GAM280  KLHL3    3'  AGGGGAGGGGAGGATGG     44637    C   AAAAC
                                  AG GGA     GGAGGATGG
                                  || |||     |||||||||
                                  TC CCT     CCTCCTACC
                                   C   CC___
GAM280  LAMC2    3'  GGAAAGATGGATGGAAG     33115      AAAC   _
                                  GGAA    GGA GGATGGAAG
                                  ||||    ||| |||||||||
                                  CCTT    TCT CCTACCTTC
                                     _____   A
GAM280  LAMC2    3'  GGAAGGATGAATGGA       33116      AAAC   _
                                  GGAA    GGA GGATGGA
                                  ||||    ||| |||||||
                                  CCTT    CCT CTTACCT
                                     _____   A
GAM280  LETM1    3'  GCTGGGCAGGAGGATGGA    29504    _ AAAAAC
                                  GC GG      GGAGGATGGA
                                  || ||      ||||||||||
                                  CG CC      CCTCCTACCT
                                   A  CGT___
GAM280  MAPRE2   3'  AAGCGGAAAGTGGGGTGG    30688         AAC  A  A
                                  AAGCGGAAA   GG GG TGG
                                  |||||||||   || || |||
                                  TTCGCCTTT   CC CC ACC
                                        CA_  _  _
GAM280  MMP19    3'  AGGGAGGGAGAACATGGGA   35578    C   AAAAC      ___
                                  AG GGA     GGAGGAT   GGA
                                  || |||     |||||||   |||
                                  TC CCT     CCTCTTG   CCT
                                   _  C_____       TAC
GAM280  MUC3B    3'  AGGGGAGGGAGATGGAA     45335    C   AAAAC  AG
                                  AG GGA     GG  GATGGAA
                                  || |||     ||  |||||||
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                                TC CCT    CC  CTACCTT
                                 C  _____  CT
GAM280  NF2     5'  AGCGGAAAGGGGAGTTGG   7063        AAC   GA
                                AGCGGAAA  GGAG  TGG
                                ||||||||  ||||  |||
                                TCGCCTTT  CCTC  ACC
                                    CC_   A_
GAM280  NPR3    3'  GCAGAAAAAAAAAAGTGG   9481         CG   A
                                GCGGAAAAA  GAGG TGG
                                |||||||||  |||| |||
                                CGTCTTTTT  TTTC ACC
                                     TT   _
GAM280  OPA3    3'  AGGTGAAGGATGATGGA    36068    CG  AAAC  G
                                AG  GAA   GGA GATGGA
                                ||  |||   ||| ||||||
                                TC  CTT   CCT CTACCT
                                 CA  ____  A
GAM280  PCTK1   3'  AAGCAGGGAAGATG       37460       AAAAAC
                                AAGCGG    GGAGGATG
                                ||||||    ||||||||
                                TTCGTC    CCTTCTAC
                                          _______
GAM280  PDE4A   3'  GGACAGAGGGATGGAAG    26260    AAAA    _
                                GGA   CGGAGG ATGGAAG
                                |||   |||||| |||||||
                                CCT   GTCTCC TACCTTC
                                 ____     C
GAM280  PDGFB   3'  AAGAGGAAAATGCAGGGTGGA  15164    C    A_  A  A
                                AAG GGAAAA  CGG GG TGGA
                                ||| ||||||  ||| || ||||
                                TTC CCTTTT  GTC CC ACCT
                                  T     AC  _ _
GAM280  PIK4CB  3'  AAGCGGGTGAGAGAACATGGAA 15310       AAAAAC   G
          G                      AAGCGG    GGAG ATGGAAG
                                ||||||    |||| |||||||
                                TTCGCC    TCTT TACCTTC
                                   CACTC_   G
GAM280  PKM2    3'  AGTGGGGGAAAATGGAA    15330   C  AAAAAC
                                AG GG     GGAGGATGGAA
                                || ||     ||||||||||
                                TC CC     CCTTTTACCTT
                                 A  C_____
GAM280  POU2AF1 3'  GGAGGGGAAGAATGGAA    26371    AAAAC
                                GGA    GGAGGATGGAA
                                |||    ||||||||||
                                CCT    CTTCTTACCTT
                                  CCC__
GAM280  POU2AF1 3'  AGGGGAAGAATGGAAGGATGG  26363   C   A  C  _
                                AG GGAA AA GGA GGATGG
                                || |||| || ||| ||||||
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                                TC CCTT TT CCT CCTACC
                                 C   C A  T
GAM280  PPP2R2B  3' GGAAAAAAAAATGGTGGA   21333       CG  _  A
                                GGAAAAA  GA GG TGGA
                                |||||||  || || ||||
                                CCTTTTT  TT CC ACCT
                                    TT  A  _
GAM280  PPP2R4   3' AAGGGAAAAGCAATGGAA   41321    C    AAC  AG
                                AAG GGAAA   GG  GATGGAA
                                ||| |||||   ||  |||||||
                                TTC CCTTT   TC  TTACCTT
                                  _    ___  G_
GAM280  RAB6A    5' AGCGGAAGGGCGGGCACCGA  16098       AAA  AGG  G
                                AGCGGAA   CGG   AT GA
                                |||||||   |||   || ||
                                TCGCCTT   GCC   TG CT
                                    CCC   CG_  G
GAM280  RABL2A   3' AAGAGGAAAAAAGATGG    30194    C    AACG
                                AAG GGAAA   GAGGATGG
                                ||| |||||   ||||||||
                                TTC CCTTT   TTTCTACC
                                  T   _____
GAM280  RABL2B   3' AAGAGGAAAAAAGATGG    28200    C    AACG
                                AAG GGAAA   GAGGATGG
                                ||| |||||   ||||||||
                                TTC CCTTT   TTTCTACC
                                  T   _____
GAM280  RAD52    3' AAGTGGGAAAACGGCAGACAG  39552    C  A     A
                                AAG GG AAAACGG GGATGG
                                ||| || ||||||| ||||||
                                TTC CC TTTTGCC TCTGTC
                                  A  C      G
GAM280  RAP1GDS1 3' AAGCGGAAGAAGCCGCTGGATG 34506       AAA__  GA
           GA                   AAGCGGAA    CG  GGATGGA
                                ||||||||    ||  |||||||
                                TTCGCCTT    GC  CCTACCT
                                    CTTCG  GA
GAM280  RELA     3' AAGCTGGAGGATGGGGATGG   35035     _  AAAAC  A
                                AAGC GGA    GG GGATGG
                                |||| |||    || ||||||
                                TTCG CCT    CC CCTACC
                                  A  CCTA_ _
GAM280  RERE     3' AAGCCGAGAAGGTGG      29019     G  AAAAC    A
                                AAGC GA    GGAGG TGG
                                |||| ||    ||||| |||
                                TTCG CT    CTTCC ACC
                                  G  _____   _
GAM280  RNF26    5' AAGTGGGTAAGACGGAAGTGGA 36751    C  AAAA_     A
                                AAG GG    ACGGAGG TGGA
                                ||| ||    ||||||| ||||
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                                TTC CC    TGCCTTC ACCT
                                  A  CATTC      _
GAM280  RTN3    3'  AAGGGAAAGGATGG       43956    C   AAAACG
                                AAG GGA     GAGGATGG
                                ||| |||     ||||||||
                                TTC CCT     TTCCTACC
                                  _  _______
GAM280  SCNN1B  5'  AGCGGGGACACGGAGGATG   7332       AAAA
                                AGCGG   ACGGAGGATG
                                |||||   ||||||||||
                                TCGCC   TGCCTCCTAC
                                   CCTG
GAM280  SEPN1   5'  AAGCGAAAGAGCGGGGCGG   42421        AAA  A  A
                                AAGCGGAA   CGG GG TGG
                                ||||||||   ||| || |||
                                TTCGCTTT   GCC CC GCC
                                     CTC  _ _
GAM280  SFTPA2  3'  AAGGGGAAAGTGGAGCCGG   27961    C    AAC   GA
                                AAG GGAAA   GGAG  TGG
                                ||| |||||   ||||  |||
                                TTC CCTTT   CCTC  GCC
                                  C    CA_   G_
GAM280  SLC17A4 3'  AGTGGAAGAGTGGAGAACA   24255    C   AAAC
                                AG GGAA    GGAGGATG
                                || ||||    ||||||||
                                TC CCTT    CCTCTTGT
                                  A    CTCA
GAM280  SLC9A1  5'  AAGGGGGAGGACGGA      43227     C  AAAAAC
                                AAG GG     GGAGGATGGA
                                ||| ||     ||||||||||
                                TTC CC     CCTCCTGCCT
                                  _  _______
GAM280  TBL1X   3'  AGTGGAAAGACAGGGGGAGGG  24871    C    A   A_  T
                                AG GGAAA ACGG  GGA GG
                                || ||||| ||||  ||| ||
                                TC CCTTT TGTC  CCT CC
                                  A    C   CC  C
GAM280  TIMELESS 5' AAGTGGAGAAACAGGAGACAG  19395    C  A    AG
                                AAG GGA AAACGG  GATGG
                                ||| ||| ||||||  |||||
                                TTC CCT TTTGTC  CTGTC
                                  A  C     CT
GAM280  TNFRSF10B 3'  GGAAGTGGGAGAGGATGGAAG  19288     AAAC_
                                GGAA    GGAGGATGGAAG
                                ||||    ||||||||||||
                                CCTT    TCTCCTACCTTC
                                   CACCC
GAM280  TPM2    5'  GCGAGGAGGACGGA       17643     AAAAAC
                                GCGG     GGAGGATGGA
                                ||||     ||||||||||
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                              CGCT     CCTCCTGCCT
                                       _______
GAM280  TRH      3'  GGAGGGGATGGAAG       28291     AAAAC  A
                              GGA     GG GGATGGAAG
                              |||     || |||||||||
                              CCT     CC CCTACCTTC
                                       ______ _
GAM280  VARS2    5'  AAGTGGAAAAACTGGAGG    26659     C      _
                              AAG GGAAAAAC GGAGG
                              ||| |||||||| |||||
                              TTC CCTTTTTG CCTCC
                                A       A
GAM280  ZNF144   3'  AAGTGGAAGGAGTGGA      28333     C   AAAC   GA
                              AAG GGAA    GGAG  TGGA
                              ||| ||||    ||||  ||||
                              TTC CCTT    CCTC  ACCT
                                A   _____   __
GAM280  ARHGAP6  3'  TCTCCACGCCTTCCGGGGG   30229    C  T      ATTCTCC
                              TC CC CGCCTTCC      GG
                              || || ||||||||      ||
                              AG GG GCGGAAGG      CC
                               A  T       CCC_____
GAM280  ASK      5'  CTCGCGCCTCGCTCTGG     27476      _   CATT   C
                              CTCGC CTTC    CTC GG
                              ||||| ||||    ||| ||
                              GAGCG GGAG    GAG CC
                                 C    C___   A
GAM280  BACH2    5'  TCCCCGCGTCTTCCCG      34809      T  C    ATTCTC
                              TCCCC CG CTTCC     CG
                              ||||| || |||||     ||
                              AGGGG GC GAAGG     GC
                                 C  A    _______
GAM280  BAT4     5'  CCCTTCGCCTTCCTCAACGTGG 37689     C       ATTCTCC
           C                   CCC TCGCCTTCC      GGC
                              ||| |||||||||      |||
                              GGG AGCGGAAGG      CCG
                                A        AGTTGCA
GAM280  CA11     3'  TCCCCTCGCCTTGTGGGGAGGC 10238          CCATTCTCC
                              TCCCCTCGCCTT       GGC
                              ||||||||||||       |||
                              AGGGGAGCGGAA       CCG
                                     CACCCCT__
GAM280  CDKN2A   5'  CCTCTTTCTTCCTCCGG     38471     GC_    ATTC
                              CCTC   CTTCC    TCCGG
                              ||||   |||||    |||||
                              GGAG   GAAGG    AGGCC
                                AAA    _____
GAM280  CPNE6    5'  CCTCTCTCCGGCTCTCTGGC   25733     GC    CA    C
                              CCTC  CTTC  TTCTC GGC
                              ||||  ||||  ||||| |||
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                                GGAG  GAGG  GAGAG CCG
                                  A_   CC    A
GAM280  CSF2RB   3'  TCCCCTTGCCTGTCTAGG    7571       C   TCCAT   CC
                                TCCCCT GCCT    TCT  GG
                                |||||| ||||    |||  ||
                                AGGGGA CGGA    AGA  CC
                                   A   C_____   T_
GAM280  GABRG2   5'  CTCGCCTCTTGCCTCTTGG   9049        CCA_   CC
                                CTCGCCTT   TTCT  GG
                                ||||||||   ||||  ||
                                GAGCGGAG   GAGA  CC
                                    AACG   A_
GAM280  GPR65    5'  CCTTTCCTTCCATATTTCTTCC 40734     CG      ___   _
           GG                     CCT  CCTTCCAT   TCT CCGG
                                |||  ||||||||   ||| ||||
                                GGA  GGAAGGTA   AGA GGCC
                                  AA       TAA   A
GAM280  KCNH2    3'  TCCTCTCCCCTTCCACGG    6949     C   G     TTCTC
                                TCC CTC CCTTCCA    CGG
                                ||| ||| |||||||    |||
                                AGG GAG GGAAGGT    GCC
                                  A   G     _____
GAM280  KCNK3    3'  CCCCTTTGCCTTTTGCTCTCTG 13899      C_    CCA    C
           G                     CCCCT  GCCTT   TTCTC GG
                                |||||  |||||   ||||| ||
                                GGGGA  CGGAA   GAGAG CC
                                   AA    AAC    A
GAM280  MN1      3'  TCCCTTCCCTTTCCATTC    14593     C  G   _
                                TCCC TC CCTT CCATTC
                                |||| || |||| ||||||
                                AGGG AG GGAA GGTAAG
                                  A  _   A
GAM280  OLFM1    5'  TCTCCTCGCCTCCTAATGG   26782    C       CATTCTCC
                                TC CCTCGCCTTC       GG
                                || ||||||||||       ||
                                AG GGAGCGGAGG       CC
                                 A        ATTA____
GAM280  PDXK     5'  TCCCCTCGGCTGCGACTCTGGC 18969        C  TCCATT   C
                                TCCCCTCG CT     CTC GGC
                                |||||||| ||     ||| |||
                                AGGGGAGC GA     GAG CCG
                                    C  CGCT__   A
GAM280  RAP1GA1  3'  TCCCCTTGTGCTTCTGTGG   16170      C__  CTTCCA   CC
                                TCCCCT   GC     TTCT  GG
                                ||||||   ||     ||||  ||
                                AGGGGA   CG     AAGA  CC
                                   ACA  _______   CA
GAM280  RPIP8    5'  TCCCCCTGCCTTTGCGCCCGG  27452      TC    CCATTC
                                TCCCC  GCCTT     TCCGG
                                |||||  |||||     |||||
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                                AGGGG  CGGAA     GGGCC
                                  GA    ACGC__
GAM280  TRIM9    5'  CCTCTCGCCTTTCGAGG     31558    C       CCAT  TCC
                                CC CTCGCCTT    TC   GG
                                || ||||||||    ||   ||
                                GG GAGCGGAA    AG   CC
                                 A       _____  CT_
GAM281  ABL2     5'  CCCGCGCCCCCGCCGACCCCTG 28724     A    T      _ ATTA
          G                      CCC CGCC CCCGCCG C    GG
                                ||| |||| ||||||| |    ||
                                GGG GCGG GGGCGGC G    CC
                                  C    _      T GGGA
GAM281  AKAP13   3'  CCCACGCCTCCCCTGCGC    28477           GC_
                                CCCACGCCTCCC   CGC
                                ||||||||||||   |||
                                GGGTGCGGAGGG   GCG
                                       GAC
GAM281  ALDH3B1  3'  CCCATGCCTCCCACCTCGG    45061     C         GCATTA
                                CCCA GCCTCCCGCC     GG
                                |||| ||||||||||     ||
                                GGGT CGGAGGGTGG     CC
                                  A         AG_____
GAM281  APTX     3'  CCATACTCTGCATTAGG     32807     CG _  CCCGCC
                                CCA  C CT     GCATTAGG
                                |||  | ||     ||||||||
                                GGT  G GA     CGTAATCC
                                  AT A  _______
GAM281  CDS1     5'  CCCGGGCCTCCCGCACCAGG   10395     AC      GCC
                                CCC  GCCTCCC   GCATTAGG
                                |||  |||||||   ||||||||
                                GGG  CGGAGGG   CGTGGTCC
                                  CC      ___
GAM281  CHRNA4   5'  CATGCCTCCCGCGCCTCGC    8846     C        _____
                                CA GCCTCCCGC    CGC
                                || |||||||||    |||
                                GT CGGAGGGCG    GCG
                                 A        CGGA
GAM281  DRD1     5'  CCCGCGCCTCCCCGCAGG     9006      A       GC    TTA
                                CCC CGCCTCCC  CGCA   GG
                                ||| ||||||||  ||||   ||
                                GGG GCGGAGGG  GCGT   CC
                                  C       __   ____
GAM281  DSCR3    5'  CCCACGCCTTCCTCCTTCCGGC 25821          C  G  GCATTA
                                CCCACGCCT CC CC     GGC
                                ||||||||| || ||     |||
                                GGGTGCGGA GG GG     CCG
                                      A  A  AAGG__
GAM281  DVL1     3'  CCCTGCCTCCCGTCCTGGC    40405     AC       _ __
                                CCC  GCCTCCCG CC  GC
                                |||  |||||||| ||  ||
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                                GGG  CGGAGGGC GG  CG
                                  A_       A  AC
GAM281  FBN1    5'  CCCGCCGCCTCTTGCCGC    42049     A_     CC
                                CCC  CGCCTC  GCCGC
                                |||  ||||||  |||||
                                GGG  GCGGAG  CGGCG
                                  CG     AA
GAM281  GCS1    5'  CCCGCCTCTCGCCCTGG     26697    A     C   GCATTA
                                CC CGCCTC CGCC     GG
                                || |||||| ||||     ||
                                GG GCGGAG GCGG     CC
                                 _     A   GA____
GAM281  HDAC1   5'  CGCCCTCCCGCCCGCGG     22441     _      _ ATTA
                                CGCC TCCCGCC GC    GG
                                |||| ||||||| ||    ||
                                GCGG AGGGCGG CG    CC
                                  G      G  ____
GAM281  HDAC4   5'  CCCGCGCCCCCGCCCCGG    25750     A   T     GCATTA
                                CCC CGCC CCCGCC     GG
                                ||| |||| ||||||     ||
                                GGG GCGG GGGCGG     CC
                                  C    _     GG____
GAM281  HIRA    5'  CCCGCGCCACCCGCCCTCCGGC 17738     A   T     GCATTA
                                CCC CGCC CCCGCC     GGC
                                ||| |||| ||||||     |||
                                GGG GCGG GGGCGG     CCG
                                  C   T     GAGG__
GAM281  KCNF1   5'  CCCACGCCGTCCGCGAGG    13827        TCCCG   ATT
                                CCCACGCC    CCGC   AGG
                                ||||||||    ||||  |||
                                GGGTGCGG    GGCG   TCC
                                     CA___    C__
GAM281  KCNK3   3'  CGCCCCTCCTGCTGCCTGC    13903       _ _  C  ATTAG
                                CGCCTC CC GC GC     GC
                                |||||| || || ||     ||
                                GCGGGG GG CG CG     CG
                                   A  A  A  GA___
GAM281  MAD2L2  5'  CGCCTCCCGCTCAACCCGGGC  26802          _  CA TA
                                CGCCTCCCGC CG  T  GGC
                                |||||||||| ||  |  |||
                                GCGGAGGGCG GT  G  CCG
                                      A  TG GC
GAM281  MADH6   3'  CCCGCCCCTCCCGCCGGGG   24594     ACG        CATTA
                                CCC   CCTCCCGCCG    GG
                                |||   ||||||||||    ||
                                GGG   GGAGGGCGGC    CC
                                  CGG         C____
GAM281  MAFK    5'  CCCGCGCCGCCCGCCGCCACCG 14315     A   T       ATTAG
            C                    CCC CGCC CCCGCCGC    GC
                                |||| |||| ||||||||    ||
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                                GGG GCGG GGGCGGCG    CG
                                  C   C      GTGG_
GAM281  MYO1D   5' CCGCTCCTCCCGCCGCGG   43491   ACG       ATTA
                                CC  CCTCCCGCCGC   GG
                                ||  ||||||||||   ||
                                GG  GGAGGGCGGCG   CC
                                 CGA       ____
GAM281  NGB     5' CCCGTGCCTCCGCCCGGC   34583    AC    C  __
                                CCC  GCCTCC GCC  GC
                                |||  |||||| |||  ||
                                GGG  CGGAGG CGG  CG
                                  CA    _  GC
GAM281  NMB     5' CCCACCCTCCCGCTAG     43946     G      CGCAT
                                CCCAC CCTCCCGC    TAG
                                ||||| ||||||||    |||
                                GGGTG GGAGGGCG    ATC
                                  _     _____
GAM281  PSCD3   3' CCACGCCTTCCGCGGAGGGGC  20126       C   CGCATTA
                                CCACGCCT CCGC      GGC
                                |||||||| ||||      |||
                                GGTGCGGA GGCG      CCG
                                    A   CCTCC__
GAM281  SLC6A8  5' CCCGCGCCCCCCCGCCCCGG   24754    A       GCATTA
                                CCC CGCCTCCCGCC     GG
                                ||| ||||||||||     ||
                                GGG GCGGGGGGCGG    CC
                                  C         GG____
GAM281  SMURF1  3' CGCCTCCCGCGGGTTAGGC   45193        C CA
                                CGCCTCCCGC G  TTAGGC
                                |||||||||| |  ||||||
                                GCGGAGGGCG C  AATCCG
                                      _ CC
GAM281  SULT1C1 3' GCCAGGCACTGCATTAGG   9841    TCC  C
                                GCC  CGC GCATTAGG
                                |||  ||| ||||||||
                                CGG  GTG CGTAATCC
                                  TCC  A
GAM281  TNFRSF7 3' CCCGCCCTCCTGCAGCGCAGGC 10303   A  _  C  C  AT
                                CC CGCC TCC GC GC  TAGGC
                                || |||| ||| || ||  |||||
                                GG GCGG AGG CG CG  GTCCG
                                 _   G  A  T  C_
GAM281  ACP1    5' GGCTCGCGGCTCCGCGGCGCC  28241    CA  AGAC  G_
                                GGC  GC   GG  CCGCGGCGCC
                                |||  ||   ||  ||||||||||
                                CCG  CG   CC  GGCGCCGCGG
                                  AG  ____  GA
GAM281  ADRA2B  3' GGCCAGCAGAGGGTCACAG   8649         C  C
                                GGCCAGCAGA GGG CGCGG
                                |||||||||| ||| |||||
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                                CCGGTCGTCT CCC GTGTC
                                      _  A
GAM281  AF3P21   5'  GGTGGCAAGGGCTGCGGCGCC  32402    CCA   AC   C
                                GG  GCAG  GGGC GCGGCGCC
                                ||  ||||  |||| ||||||||
                                CC  CGTT  CCCG CGCCGCGG
                                 AC_   __   A
GAM281  AMPD3    5'  GCCCGGGCCGCGGCGC     7898     AGCAGA
                                GCC     CGGGCCGCGGCGC
                                |||     ||||||||||||
                                CGG     GCCCGGCGCCGCG
                                 _______
GAM281  AREG     5'  GGCGGCGGGCGCGGCGC     11663     CA  AGAC   C
                                GGC  GC   GGGC GCGGCGC
                                |||  ||   |||| |||||||
                                CCG  CG   CCCG CGCCGCG
                                  C_ _____   _
GAM281  CEP2     5'  GGCGGCAGAGCGCGGCGC    28442     CA    CGG  C
                                GGC  GCAGA  GC GCGGCGC
                                |||  |||||  || |||||||
                                CCG  CGTCT  CG CGCCGCG
                                  C_   ___ _
GAM281  CHAC     5'  GGCGGCTTCAGCTGCGGCGCC  37814     CA  AGACG  C
                                GGC  GC    GGC GCGGCGCC
                                |||  ||    ||| ||||||||
                                CCG  CG    TCG CGCCGCGG
                                  C_  AAG__  A
GAM281  CLDN3    5'  GGCCTGGCGGGAGCTGCGGCGC 10569      A_  AGAC   C
           C                     GGCC  GC   GGGC GCGGCGCC
                                ||||  ||   |||| ||||||||
                                CCGG  CG   CTCG CGCCGCGG
                                  AC  CC__   A
GAM281  DIA1     3'  GGGCAGACGGGGCTGC     28792    CCA       CC  G
                                GG  GCAGACGGG  GC GC
                                ||  |||||||||  || ||
                                CC  CGTCTGCCC  CG CG
                                 ___       __ A
GAM281  F8A      5'  AGCTGGCGGGCGGGCCGGGGC  29104     CA  AGA     C
                                GGC  GC   CGGGCCG GGC
                                |||  ||   ||||||| |||
                                TCG  CG   GCCCGGC CCG
                                  AC  CCC      C
GAM281  FBXL7    5'  GGCCGGCGGGCGCAGCGC    29408     A  AGAC   C
                                GGCC GC    GGGC GCGGCGC
                                ||||  ||   |||| |||||||
                                CCGG CG    CCCG CGTCGCG
                                  C _____   _
GAM281  FGF2     5'  ACCCGCCGGGCCGCGGCG    12826     A  AGA
                                GCC GC   CGGGCCGCGGCG
                                |||  ||  ||||||||||||
```

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                                TGG CG   GCCCGGCGCCGC
                                  G ___
GAM281  FGFR3   5' GGCGGGGGCCGCGGCG     6616     CAGCAGAC
                                GGC      GGGCCGCGGCG
                                |||      ||||||||||
                                CCG      CCCGGCGCCGC
                                  CC_______
GAM281  FTH1    5' GGCGGTGGCTGCGCGGCGC   42791    CAGCAGACG  __
                                GGC      GGC  CGCGGCGC
                                |||      |||  ||||||||
                                CCG      CCG  GCGCCGCG
                                  CCA_______  AC
GAM281  GNA15   3' GGCCAGCAGCGGGCCGTCCG  40905        A     __
                                GGCCAGCAG CGGGCCG  CG
                                |||||||| |||||||  ||
                                CCGGTCGTC GCCCGGC  GC
                                     _     AG
GAM281  HCN4    5' GGCCGGGGGCAGGAGCGCGGCG 24228     A___   AC   C
           CC                     GGCC   GCAG  GGGC GCGGCGCC
                                |||| |||| |||| ||||||||
                                CCGG   CGTC  CTCG CGCCGCGG
                                  CCCC   __   _
GAM281  ICMT    5' GACTAGCGGGCGGCGGCGCC  29652    C  AGAC   C
                                GGC AGC   GGGC GCGGCGCC
                                ||| |||   |||| ||||||||
                                CTG TCG   CCCG CGCCGCGG
                                  A _____   C
GAM281  IGFBP5  5' GCCAGCGGTGCGCGGCGC   8270       AGAC  GC
                                GCCAGC   GG  CGCGGCGC
                                ||||||   ||  ||||||||
                                CGGTCG   CC  GCGCCGCG
                                   _____ AC
GAM281  JAG2    3' GGCCGGCAGGTGGGCAGCGCC 13729     A   AC   CGC
                                GGCC GCAG  GGGC   GGCGCC
                                |||| ||||  ||||   ||||||
                                CCGG CGTC  CCCG   TCGCGG
                                  C   CA   ___
GAM281  JPH3    5' GGCGCGGGCGGCCGCGGCGCC 34021    CA  AGACG
                                GGC  GC    GGCCGCGGCGCC
                                |||  ||    ||||||||||||
                                CCG  CG    CCGGCGCCGCGG
                                  __  CCCG_
GAM281  KCNK7   3' GGCCGCGGGCGGCAGGGTGC  37862     A  AGAC   C __  C
                                GGCC GC   GGGC GC  GG GC
                                |||| ||   |||| ||  || ||
                                CCGG CG   CCCG CG  CC CG
                                  _ _____   C  TC  A
GAM281  KCNQ2   3' GGCCGCGGGCGGGTCCACTGGC 41510     A  AGA   _   _
                                GGCC GC   CGGG CCGC GGC
                                |||| ||   |||| |||| |||
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                                CCGG CG   GCCC GGTG CCG
                                  _ CCC   A   A
GAM281  LMO2    5'  GGCCCCGGGTCGCGGCGC   24545     AGCAGA   C
                                GGCC     CGGG CGCGGCGC
                                ||||     |||| ||||||||
                                CCGG     GCCC GCGCCGCG
                                  G_____   A
GAM281  MAML1   3'  GCCAGCAGATGGGCTGGGGCC  31283        C   CGC  C
                                GCCAGCAGA GGGC   GG GCC
                                ||||||||| ||||   || |||
                                CGGTCGTCT CCCG   CC CGG
                                     A   AC_ _
GAM281  MAP2K2  5'  GGCCGGCGGCGGCGGCGC    36209     A  AGACG   C
                                GGCC GC    GGC GCGGCGC
                                |||| ||    ||| |||||||
                                CCGG CG    CCG CGCCGCG
                                  C _____  C
GAM281  MASP2   3'  GGCCAGCAGGCTGGCTCTGGC  40176        ACG   CGC
                                GGCCAGCAG   GGC   GGC
                                |||||||||   |||   |||
                                CCGGTCGTC   CCG   CCG
                                     CGA   AGA
GAM281  PABPC1  5'  GGCCGCGGGCGGGCG       15025     A  AGAC    C C
                                GGCC GC    GGGC G GGCG
                                |||| ||    |||| | ||||
                                CCGG CG    CCCG C CCGC
                                  _ _____   _ _
GAM281  PAM     5'  GGCTGGCGGTTGGGCAGCGGCG 39884     CA  AGAC    C
          CC                    GGC  GC    GGGC GCGGCGCC
                                |||  ||    |||| ||||||||
                                CCG  CG    CCCG CGCCGCGG
                                  AC  CCAA    T
GAM281  PCTK1   3'  GGCCAATGGGTGGGTTGACAGG 37475       CA_________
          CC                    GGCCAG        GACGGGCC
                                ||||||        ||||||||
                                CCGGTT        CTGTCCGG
                                   ACCCACCCAA
GAM281  PCTK1   5'  GGCCGGCGCGGCGGCG      37476     A  AGACGG  C
                                GGCC GC     GC GCGGCG
                                |||| ||     || ||||||
                                CCGG CG     CG CGCCGC
                                  C _______ C
GAM281  POU3F1  3'  GGCCGCGCGGGCGGGCTGCGCG 40375     A_  AGA    C   G
          CC                    GGCC  GC   CGGGC GCG CGCC
                                ||||  ||   ||||| ||| ||||
                                CCGG  CG   GCCCG CGC GCGG
                                  CG  CCC    A  _
GAM281  PPARG   5'  GGCCACGGCGGCGTGGCGC   39816      G AGA   GC  C
                                GGCCA C   CGG  CG GGCGC
                                ||||| |   |||  || |||||
```

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                                CCGGT G   GCC  GC CCGCG
                                   _ CC_   __  A
GAM281   RCN1     5'  GGCCCGCAGAACCCGCGGCGCC 16203      A     CG G
                                GGCC GCAGA  G CCGCGGCGCC
                                |||| |||||  | ||||||||||
                                CCGG CGTCT  T GGCGCCGCGG
                                  G    __ G
GAM281   RENT1    3'  GGCCAGCAGGGGGCGC      16256          AC    C
                                GGCCAGCAG  GGGC GC
                                |||||||||  |||| ||
                                CCGGTCGTC  CCCG CG
                                     C_   _
GAM281   RHCG     3'  AGCCAGCAGGTGGGGGTGC   32240          AC   CCGC  C
                                GGCCAGCAG  GGG   GG GC
                                |||||||||  |||   || ||
                                TCGGTCGTC  CCC   CC CG
                                     CA   _____  A
GAM281   RRAS2    5'  GGTCAGCGCGGTAGCGCGGCGC 29309    C    AGA   GC_
                                GG CAGC   CGG   CGCGGCGC
                                || ||||   |||   ||||||||
                                CC GTCG   GCC   GCGCCGCG
                                 A   C__   ATC
GAM281   SIAH1    3'  GGTTGGCAGACAGATGGGTGCC 16713    CCA        CCGC  C
                                GG   GCAGACGGG   GG GCC
                                ||   |||||||||   || |||
                                CC   CGTCTGTCT   CC CGG
                                 AAC        AC__  A
GAM281   SLC2A1   3'  GGCCAGCAGAACGGGTGGC   27140          _    CCGC
                                GGCCAGCAGA CGGG   GGC
                                |||||||||| ||||   |||
                                CCGGTCGTCT GCCC   CCG
                                     T   A___
GAM281   SLC6A8   5'  GGCCGGGCCGGGGTCGCGGCGC 24775      A_  AGAC   C
            C                    GGCC  GC   GGG CGCGGCGCC
                                |||| ||   ||| |||||||||
                                CCGG  CG   CCC GCGCCGCGG
                                  CC  GC__   A
GAM281   TCFL4    5'  GGCCAGCGGGCGGGCC      41829         AGAC   C C   G
                                GGCCAGC   GGGC G GGC C
                                |||||||   |||| | ||| |
                                CCGGTCG   CCCG C CCG G
                                   ____   _ _  G
GAM281   WEE1     5'  GCCTAGTCGCAGCCGCGGCG   18095     AGC  A  _
                                GCC   AG CG GGCCGCGGCG
                                |||   || || ||||||||||
                                CGG   TC GC TCGGCGCCGC
                                  A__  A  G
GAM281   XCL1     3'  GGCTGGAGACGGACAGGGTGCC 16492     CAGC       CGC  C
                                GGC   AGACGGGC   GG GCC
                                |||   ||||||||   || |||
```

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                                CCG   TCTGCCTG   CC CGG
                                  ACC_       TC_ A
GAM281  ZFP103   5' GGTCAGGAGGGCGCGGCGC   24962    C   CA  C    C
                                GG CAG  GA GGGC GCGGCGC
                                || |||  || |||| |||||||
                                CC GTC  CT CCCG CGCCGCG
                                 A   __ _   _
GAM281  ZFP103   5' GGCCGGCTGGCGGGCGGCGCC  24960     A  AGA    CGC
                                GGCC GC   CGGGC   GGCGCC
                                |||| ||   |||||   ||||||
                                CCGG CG   GCCCG   CCGCGG
                                  C  ACC    ___
GAM282  PP       3'  TGAGTATATTGGATTAGTCACA 34443         CA ____
                                TGAGTATAT  GA    TCATA
                                |||||||||  ||    |||||
                                ACTCATATA  CT    AGTGT
                                      AC  AATC
GAM282  SLC21A3  5'  GAGTGTGCATGTCATATTATAA 39572      ATAT  GA
                                GAGT    CA  TCATATTATAA
                                ||||    ||  ||||||||||
                                CTCA    GT  AGTATAATATT
                                  CAC_  AC
GAM282  ADAR     3'  GTTAAGCCAACAGGATTT    31907      CTTTGA
                                GTTA     AACAGGATTT
                                ||||     |||||||||
                                CAAT     TTGTCCTAAA
                                  TCGG__
GAM282  PLAUR    5'  TGATTATTTGGCTAACAGGATT 15372   A    C    A__
           T                     A GTTA TTTG   AACAGGATTT
                                | |||| ||||   ||||||||||
                                A TAAT AAAC   TTGTCCTAAA
                                 C    _    CGA
GAM283  CUGBP1   3'  TCAAAGGTGAGAGTTCAAGCAT 27278         A     ATGAC
                                TTAAAGGT AGAGTT     GCAT
                                |||||||| ||||||     ||||
                                AGTTTCCA TCTCAA     CGTA
                                      C     GTT__
GAM283  PCK1     3'  TAAAGGTAAGGAACAATG    40945          _  TT
                                TAAAGGTAAG AG  ATG
                                |||||||||| ||  |||
                                ATTTCCATTC TT  TAC
                                      C  GT
GAM283  AIPL1    3'  AAACTGATTTAAACAGATTACT 40815     G   CTCCTC
                                AAA TGA     CAGATTACT
                                ||| |||     |||||||||
                                TTT ACT     GTCTAATGA
                                  G   AAATTT
GAM283  BAZ2A    3'  GTGACTCCCCACCTCCCT    30311         T   GA TA
                                GTGACTCC CCA  T  CT
                                |||||||| |||  |  ||
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                                CACTGAGG GGT  A  GA
                                    _  GG GG
GAM283  GFI1    3'  AAATGATTCCTCCAAGATT   23548       C     _
                                AAGTGA TCCTCCA GATT
                                |||||| ||||||| ||||
                                TTTACT AGGAGGT CTAA
                                   A      T
GAM283  HDAC4   3'  AAAGTGGCCCTCCAGAACC   25736       A T      TT
                                AAAGTG C CCTCCAGA  ACT
                                |||||| | ||||||||  |||
                                TTTCAC G GGAGGTCT  TGG
                                   C _      __
GAM283  KCNA5   3'  AAGTATTCCTCCAATATCA   40680      AC       _
                                AAGTG  TCCTCCAG ATTA
                                |||||  |||||||| ||||
                                TTCAT  AGGAGGTT TAGT
                                   A_       A
GAM283  KCNJ16  3'  AAAGTGACTCTTTACT      33012          CTCCAGA
                                AAAGTGACTC      TTACT
                                ||||||||||      |||||
                                TTTCACTGAG      AATGA
                                     A_______
GAM283  KIAA0857 3'  GTGACTCCCCCTCTCTCA    42475          AGA  A
                                GTGACTCCTCC   TT CTCA
                                ||||||||||   || ||||
                                CACTGAGGGGG   AG GAGT
                                     ___  A
GAM283  MTMR8   3'  AAATGGTTTTAAAGATTACTCA 31746      ACTCCTCC
                                AAGTG       AGATTACTCA
                                |||||       ||||||||||
                                TTTAC       TCTAATGAGT
                                   CAAAATT_
GAM283  OCM     3'  AAGTGACTCTCTCGTGACCTC  26188         _  CA   TA
                                AAGTGACTC CTC  GAT  CTC
                                ||||||||| |||  |||  |||
                                TTCACTGAG GAG  CTG  GAG
                                     A   CA  __
GAM283  PDGFRB  3'  AGGGATTCCTCCAAAGCCTCA  42331    T  C       TTA
                                AG GA TCCTCCAGA   CTCA
                                || || |||||||||   ||||
                                TC CT AGGAGGTTT   GAGT
                                 C  A        CG_
GAM283  SSA1    3'  AAGTGACTTCCCTGCTAAAGCT 17119        _  CCAGATTA
           C                     AAGTGACT CCT       CTC
                                ||||||||| |||       |||
                                TTCACTGA GGG       GAG
                                     A   ACGATTTC
GAM283  STAT3   3'  AAAGTGCCCAGATTGCTC    40229       ACTCC       A
                                AAAGTG    TCCAGATT CTC
                                ||||||    |||||||| |||
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                                TTTCAC    GGGTCTAA GAG
                                ______      C
GAM283  TGFBR2   5'  AAAGTGACTTCTCAATGTAAAC 17466        C  CAGATT_
           T                    AAAGTGACT CTC      ACT
                                ||||||||| |||      |||
                                TTTCACTGA GAG      TGA
                                    A   TTACATT
GAM284  FGF2     3'  ACACAAATCAAAATACCA    12824           G
                                GCACAAATCAAAA TATTA
                                |||||||||||||| |||||
                                TGTGTTTAGTTTT ATGGT
                                          _
GAM284  IL13RA1  3'  AGCACAAACCAAAGACAC    11438           AG
                                AGCACAAATCAAA  TAT
                                |||||||||||||  |||
                                TCGTGTTTGGTTT  GTG
                                    CT
GAM284  IMPA1    3'  CAGCACAATCAAATCAGTA    24390        A   __
                                CAGCACAA TCAAA  AGTA
                                |||||||| |||||  ||||
                                GTCGTGTT AGTTT  TCAT
                                   _    AG
GAM284  KIAA0442 3'  AGCACATTTTAAGAAGTATTAA 31787       AATCAA_
           T                    AGCACA      AAGTATTAAT
                                ||||||      ||||||||||
                                TCGTGT      TTCATAATTA
                                   AAAATTC
GAM284  KLHL3    3'  CAGCACAAACTAGAAAATA    44640         CA_
                                CAGCACAAAT   AAAGTA
                                ||||||||||   ||||||
                                GTCGTGTTTG   TTTTAT
                                    ATC
GAM284  MMP10    3'  CAGTGCAATTCAAAAGCA     14550     CA  A
                                CAG  CAA TCAAAAGTA
                                |||  ||| |||||||||
                                GTC  GTT AGTTTTCGT
                                  AC   A
GAM284  SDHC     3'  CAGCACAAATCAAAGCCCAATA 42976           A  A
                                CAGCACAAATCAAA GT TTAATA
                                |||||||||||||| || ||||||
                                GTCGTGTTTAGTTT CG GGTTAT
                                          _ _
GAM284  SLC14A2  5'  CAGTAAAATCAAAAGCA     28395     CAC
                                CAG   AAATCAAAAGTA
                                |||   ||||||||||||
                                GTC   TTTAGTTTTCGT
                                  AT_
GAM284  CNGB3    3'  TGTAGGTTCCGGAAATTGTGG  33312     TAT  G  A
                                TGTA   TT CG AAATTGTGG
                                ||||   || || |||||||||
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                                ACAT   AA GC TTTAACACC
                                  CC_  G  C
GAM284  CYBB     3'  TGTGTATTTACGGAAAATAAGG 44104     A       _     TGT
                                TGT TATTTGCG AAAAT   GG
                                ||| |||||||| |||||   ||
                                ACA ATAAATGC TTTTA   CC
                                  C       C    TT_
GAM285  BIN3     3'  GAATTCTTGTGGGACAGTTC   33080      C  C    _  TT
                                GAAT TC TGTGG AC  GGTTC
                                |||| || ||||| ||  |||||
                                CTTA AG ACACC TG  TCAAG
                                  _ A    C __
GAM285  EFNA1    5'  CGGGTCTCCTATGGGTCTGGGT 20699    AA        A_  T
              TC                  CG  TCTCCTGTGG  CT GGTTC
                                ||  ||||||||||  || |||||
                                GC  AGAGGATACC  GA CCAAG
                                 CC         CA  C
GAM285  HCS      3'  GAATCTTGCTTGGTT       33230       CC  TGGA
                                GAATCT  TG    CTTGGTT
                                ||||||  ||    |||||||
                                CTTAGA  AC    GAACCAA
                                   __  _____
GAM285  Nrap     3'  ATCTCCTGGGTTCAGTTC    40187        T  AC TG
                                ATCTCCTG GG  T  GTTC
                                |||||||| ||  |  ||||
                                TAGAGGAC CC  A  CAAG
                                    _  A_ GT
GAM285  PLA2G2D  3'  GAGCTCCTTCTTGGTT     29633    AT    GTGGA
                                GA  CTCCT    CTTGGTT
                                ||  |||||    |||||||
                                CT  GAGGA    GAACCAA
                                 C_    A____
GAM285  RELN     3'  CTTTTATAGCTTGGTTC     45355    CC    A
                                CT  TGTGG CTTGGTTC
                                ||  ||||| ||||||||
                                GA  ATATC GAACCAAG
                                 AA    _
GAM285  RREB1    5'  CGAGTCTCCTGGGGACGTG    16396     A     T   T
                                CGA TCTCCTG GGAC TG
                                ||| ||||||| |||| ||
                                GCT AGAGGAC CCTG AC
                                  C      C   C
GAM285  SNCAIP   3'  GAATGTCCTGTGGGTAGGGT   45504      C       ACTT
                                GAAT TCCTGTGG    GGT
                                |||| ||||||||    |||
                                CTTA AGGACACC    CCA
                                  C       CATC
GAM285  ADAM19   3'  GCAGGGGTTTGGGGAGAGGT   37768          TGT  CCC
                                GCAGGGGTTTG   GA   GGT
                                ||||||||||   ||   |||
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                                CGTCCCCAAAC  CT  CCA
                                     CC_  CT_
GAM285  CAPN10   3'  GCAGGGGTTGGTGGGG     35771        T T  ACCC
                                GCAGGGGTT G GTG   GG
                                ||||||||| | |||   ||
                                CGTCCCCAA C CAC   CC
                                    _ _  C___
GAM285  CORO2A   3'  AGGGGACTTGTGGTTTGGT   38059     _    TGACCC
                                AGGGG TTTGTG    GGT
                                ||||| ||||||    |||
                                TCCCC GAACAC    CCA
                                   T    CAAA__
GAM285  DEDD     3'  GCAGGGGTGTGATTGG     37428       TTGT   CCC
                                GCAGGGGT   GTGA  GG
                                ||||||||   ||||  ||
                                CGTCCCCA   CACT  CC
                                    _____   AA_
GAM285  DRD1     5'  GCAGGGGTTCGGCTCCCGGT  9007         T  GA
                                GCAGGGGTTTG GT  CCCGGT
                                |||||||||| ||  ||||||
                                CGTCCCCAAGC CG  GGGCCA
                                     _  A_
GAM285  GPRC5B   3'  GCGGGGATTGAGGTTGGTCTGG 32175   A   T  T_  GACCC_
           T                    GC GGGG TTG  GT    GGT
                                || |||| |||  ||    |||
                                CG CCCC AAC  CA    CCA
                                 _   T  TC  ACCAGA
GAM285  SLC22A2  3'  GCAGGGATTTCTACTTTTGGT  40524        G  GACCC
                                GCAGGGGTTT TGT    GGT
                                |||||||||| |||    |||
                                CGTCCCTAAA ATG    CCA
                                     G  AAAA_
GAM285  TYRO3    3'  GCATGCCTTTGTGTGACCCGGT 26654    GGGG
                                GCA   TTTGTGTGACCCGGT
                                |||   ||||||||||||||
                                CGT   AAACACACTGGGCCA
                                  ACGG
GAM286  EPB49    5'  AGCCACCCAGAGTCCTGCTCGT 12721         ATAG_  TT
                                AGCCGCCCAGA    GT  TCGT
                                ||||||||||    ||  ||||
                                TCGGTGGGTCT    CG  AGCA
                                     CAGGA  __
GAM286  FHL1     3'  AAGCTTCCAGAAGTATTCG   11090     CGC    ATA  T
                                AAGC  CCAGA  GGT TTCG
                                ||||  |||||  ||| ||||
                                TTCG  GGTCT  TCA AAGC
                                  AA_    ___  T
GAM286  IGFBP5   5'  GCCCCCGGAGATTTT      8271     G  A  ATA
                                GCC CCC GA  GGTTTT
                                ||| ||| ||  ||||||
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```
                                CGG GGG CT   CTAAAA
                                  _  C  ___
GAM286  NPEPPS   3'  AAACCAGAACAGGGTAGGTTTT 26714       CC_  AA      C
            TGT                   AAGCCG   CAG  TAGGTTTT GT
                                |||||||  |||  |||||||| ||
                                TTTGGGT   GTC  ATCCAAAA CA
                                   CTT   CC       A
GAM286  F2RL3    3'  TGTGTAGAGATGGGATCCCCCT 19535    A        A  A  G
                                TG TGTAGAGATG GA TT TTCT
                                || |||||||||| || || ||||
                                AC ACATCTCTAC CT AG GGGA
                                  _        C  _  G
GAM287  ALDOC    3'  GTATGGTATGTACTCAAGGC  23158      _   _  A_
                                GTGTG TGTG GC  AAGGC
                                ||||| |||| ||  |||||
                                CATAC ATAC TG  TTCCG
                                   C    A  AG
GAM287  B4GALT1  3'  GCACAGTAGGTGCAGAGGC   11283        T   TG CAA
                                GCACAGTG GTG  G   AGGC
                                |||||||| |||  |   ||||
                                CGTGTCAT CAC  C   TCCG
                                     C   GT ___
GAM287  CALM1    3'  GTGTGTGTGGACAGAAGG    27861          _  _
                                GTGTGTGTGG CA AAGG
                                |||||||||| || ||||
                                CACACACACC GT TTCC
                                      T  C
GAM287  DIA1     3'  CCTTATAGTGTGTGTGGGGGG  28785    GCAC        CAAA
                                CC    AGTGTGTGTGG    GG
                                ||    ||||||||||    ||
                                GG    TCACACACACC    CC
                                 AATA         CC__
GAM287  DRD2     3'  GCGTCAGAGTGTGGCAGAGGC  9016     A_  TGT      A
                                GC  CAG   GTGTGGCA AGGC
                                ||  |||   |||||||| ||||
                                CG  GTC   CACACCGT TCCG
                                 CA  T__       C
GAM287  FGFR3    3'  CCGTGGTGCAAAGGCAGAGGC  6613     CACA    TGT    A
                                CCG    GTGTG   GGCA AGGC
                                |||    |||||   |||| ||||
                                GGC    CACGT   CCGT TCCG
                                  AC__     TT_    C
GAM287  FGFRL1   3'  CCGTGCATGTGTGTGTCAAGGC 34903     CACA       GCA
                                CCG    GTGTGTGTG   AAGGC
                                |||    |||||||||   |||||
                                GGC    TACACACAC   TTCCG
                                  ACG_        AG_
GAM287  FGFRL1   3'  GTGTGTGTGTCCAGGGGC    34916         G_  AA
                                GTGTGTGTG  CA  GGC
                                |||||||||  ||  |||
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                                CACACACAC  GT  CCG
                                     AG  CC
GAM287  FGFRL1   3'  CCGTGTGTGTGTGTGTCCAG 34905     CACA       GCAA_
          GC                   CCG   GTGTGTGTG    AGGC
                               |||   |||||||||    ||||
                               GGC   CACACACAC    TCCG
                                ACA_       ACAGG
GAM287  GFRA2    3'  GCAAGGTGTGTGTGTGTGCCTT 11266     CA       _______  AAAG
          G                    GCA  GTGTGTGTG    GC   G
                               |||  |||||||||     ||   |
                               CGT  CACACACAC     CG   C
                                TC       ACAIII  GAAA
GAM287  GNA11    3'  CCACACGTGGCAAGGG      44029       AGTGTGT      A
                               CCGCAC      GTGGCAA GG
                               ||||||      ||||||| ||
                               GGTGTG      CACCGTT CC
                                  ________      C
GAM287  GOT2     3'  CACAGTGTGAGATGAGAGGC   45234         T_   CAA
                               CACAGTGTG  GTGG   AGGC
                               |||||||||  ||||   ||||
                               GTGTCACAC  TACT   TCCG
                                     TC   C__
GAM287  HAGH     5'  CCGCACAGTGGATCCCTGGAGG 23709          TG G__   CAA
          C                    CCGCACAGTG  T   TGG   AGGC
                               ||||||||||  |   |||   ||||
                               GGCGTGTCAC  A   ACC   TCCG
                                     CT GGG  ___
GAM287  OXTR     3'  GCGTGTGTGTGTGTGCCTTG   9526     ACA       ____  AAAG
                               GC   GTGTGTGTG    GC   G
                               ||   |||||||||    ||   |
                               CG   CACACACAC    CG   C
                                CA_       AIII  GAAA
GAM287  PLXNB2   3'  GCTGGTGCGTGGGCGGAGGC   29647    ACA      T   AA
                               GC   GTGTGTG GGC  AGGC
                               ||   ||||||| |||  ||||
                               CG   CACGCAC CCG  TCCG
                                AC_      _   CC
GAM287  PTER     3'  GCATGGTGTGCCTATCTGAAGG 36217     CA     G  GCA_
                               GCA  GTGTGT TG    AAGG
                               |||  |||||| ||    ||||
                               CGT  CACACG AT    TTCC
                                 AC     G  AGAC
GAM287  RABIF    3'  GTATAATGTGGCAAAGGC     16126      _
                               GTGTG TGTGGCAAAGGC
                               ||||| ||||||||||||
                               CATAT ACACCGTTTCCG
                                  T
GAM287  RARA     3'  CAGTGTGTGTGTGTGCCTTG   9703           _______  AAAG
                               CAGTGTGTGTG     GC   G
                               ||||||||||      ||   |
```

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                                GTCACACACAC     CG    C
                                      ACAIII  GAAA
GAM287  VAPB     3'  GTATGTGTGTGCAGGGAGG   21875         _   A__
                                GTGTGTGTG GCA   AGG
                                ||||||||| |||   |||
                                CATACACAC CGT   TCC
                                     A   CCC
GAM287  VDAC2    3'  GCACAGTTTTCATAAAGG    17934        GTG    GCA
                                GCACAGT   TGTG   AAGG
                                |||||||   ||||   ||||
                                CGTGTCA   GTAT   TTCC
                                   AAA    ___
GAM287  WDR4     3'  GCAGTGTGTGCCAAGG      38020     CAGT      G   A
                                GCA    GTGTGTG CAA GG
                                |||    ||||||| ||| ||
                                CGT    CACACAC GTT CC
                                  ____      G   _
GAM287  CYP7B1   5'  CGGCGCGCGCTAGGCCGCGGTG 22075    A       TT   CA  A___
            GGC                   CG CGCGCGCT  GTT  GC    GGC
                                || ||||||||  |||  ||    |||
                                GC GCGCGCGA  CGG  CG    CCG
                                 C       TC   __  CCAC
GAM287  F8A      5'  CGACGCGCCGCCGCAGCTGGC  29106         _   TTGTT    A
                                CGACGCGC GCT     CAGC GGC
                                |||||||| |||     |||| |||
                                GCTGCGCG CGG     GTCG CCG
                                     G   C____    A
GAM287  LMO1     5'  GCGCGCTTTGGCGGGGC     14181          TTCA  A_
                                GCGCGCTTTG    GC  GGC
                                ||||||||||    ||  |||
                                CGCGCGAAAC    CG  CCG
                                      ____  CC
GAM287  NFATC2   5'  GCGCGCCTGGCGCAGCGGG   29587        T  T    A
                                GCGCGCTT GT CAGC GG
                                |||||||| || |||| ||
                                CGCGCGGA CG GTCG CC
                                     C  C    C
GAM287  PAX2     3'  CGGCGCGCACCAGCAG      19623    A      TTTGTT
                                CG CGCGCGC     CAGCAG
                                || |||||||     ||||||
                                GC GCGCGTG     GTCGTC
                                 C      _______
GAM287  PEX10    3'  GACCGTGGGTCAGCAGG     15219     G  CGCTT  T_
                                GAC CG    TG  TCAGCAGG
                                ||| ||    ||  ||||||||
                                CTG GC    AC  AGTCGTCC
                                  _ ______  CC
GAM288  MHC2TA   3'  ACGTGCACACACGTGCA     6978       T  T    A
                                ACGT GC CGCAC TGCG
                                |||| || ||||| ||||
```

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                                TGCA CG GTGTG ACGT
                                  _ T    C
GAM288  MAP1B   3'  GCATGGCCAGTCTACACTCA  36741     A   TAACC
                                GCGT GCCA    TTACACTCA
                                |||| ||||    |||||||||
                                CGTA CGGT    GATGTGAGT
                                  C   CA___
GAM289  ACO1    3'  AGGAGACACCTCCG       13580      CCCC      C
                                AGGAG   ACGCCTCC G
                                |||||   |||||||| |
                                TCCTC   TGTGGAGG C
                                  ____      A
GAM289  AMFR    3'  AGCAGAAGTTTCTCCCTCTTCC 39933       _____  CACG
          T                      AGCAGGAG    CCC   CCT
                                |||||||    |||   |||
                                TCGTCTTC    GGG   GGA
                                    AAAGA   AGAA
GAM289  ANG     5'  GGACAGGAGCTTTGCTCTC   10082   A     CCCAC  _
                                A GCAGGAGC    GC CTC
                                | ||||||||    || |||
                                C TGTCCTCG    CG GAG
                                 C      AAA__  A
GAM289  ARNT2   3'  AGCAGGAGCCTCACTCT    31351        C  GC
                                AGCAGGAGCC CAC  CT
                                |||||||||| |||  ||
                                TCGTCCTCGG GTG  GA
                                    A  A_
GAM289  CDA     5'  AAACAGGAGCTCCGGCCAGCC  12143        C  AC   TC
                                AAGCAGGAGC CC  GCC  CC
                                |||||||||| ||  |||  ||
                                TTTGTCCTCG GG  CGG  GG
                                    A  C_  TC
GAM289  COL9A2  3'  GCAGGGCCCGGGCCTCCCGA  12338     A   CAC
                                GCAGG GCCC   GCCTCCCGA
                                ||||| ||||   |||||||||
                                CGTCC CGGG   CGGAGGGCT
                                  _   CC_
GAM289  DRD1    5'  AGCAGGGCCCCGCGCCTCCC   9005      A    A
                                AGCAGG GCCCC CGCCTCCC
                                |||||| ||||| ||||||||
                                TCGTCC CGGGG GCGGAGGG
                                  _    C
GAM289  DUSP4   5'  AGCCAGGAACTGCCTCCCG   10813    _    CCCAC
                                AGC AGGAGC    GCCTCCCG
                                ||| ||||||    ||||||||
                                TCG TCCTTG    CGGAGGGC
                                 G     A_____
GAM289  EGFL4   5'  GCAGCAGCCCCCCGACCCG   41572     G     A  CCT
                                GCAG AGCCCC CG   CCCG
                                |||| |||||| ||   ||||
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                                CGTC TCGGGG GC   GGGC
                                  G     G  T__
GAM289  EMP1     5'  GAAGGACCCGCCTCCCG     10894      CC  A
                                GGAG  CC CGCCTCCCG
                                ||||  || |||||||||
                                CTTC  GG GCGGAGGGC
                                  CT  _
GAM289  FOLH1    5'  AGCAGAGCCGGCCTCCCG    20988       G    CCAC
                                AGCAG AGCC    GCCTCCCG
                                ||||| ||||    ||||||||
                                TCGTC TCGG    CGGAGGGC
                                   _    C___
GAM289  FXYD6    3'  AGTAGAAGCCCTGGGCCT    35113     C       CAC
                                AG AGGAGCCC   GCCT
                                || ||||||||   ||||
                                TC TCTTCGGG   CGGA
                                 A       ACC
GAM289  HMGCL    3'  AGCAAGGGCCCCACGGCC    6789        A       _
                                AGCAGG GCCCCACG CC
                                |||||| |||||||| ||
                                TCGTTC CGGGGTGC GG
                                   C       C
GAM289  IL2RB    3'  AAGTGGGAGCCTCCCAA     9376      CA     CCACGCC
                                AAG  GGAGCC      TCCCGA
                                |||  ||||||      ||||||
                                TTC  CCTCGG      AGGGTT
                                  AC     ________
GAM289  IRTA2    3'  AAGCAGGAGTTCCCCCTTAC  36334         __    AC_
                                AAGCAGGAG  CCCC   GC
                                |||||||||  ||||   ||
                                TTCGTCCTC  GGGG   TG
                                     AA    GAA
GAM289  KIF3C    3'  GCAGGAGCTCCTCCTCC     13953         C  ACG
                                GCAGGAGC CC   CCTCC
                                |||||||| ||   |||||
                                CGTCCTCG GG   GGAGG
                                     A  A__
GAM289  MAPK8IP1 3'  GCAGGAGCCACAGCGCCCGA  24156         C  C  CT
                                GCAGGAGCC CA GC  CCCGA
                                ||||||||| || ||  |||||
                                CGTCCTCGG GT CG  GGGCT
                                     T  _  C_
GAM289  MCM4     5'  GCCGGGCCCGCCTCCCG     41594    A  A    CAC
                                GC GG GCCC   GCCTCCCG
                                || || ||||   ||||||||
                                CG CC CGGG   CGGAGGGC
                                 G  _   ____
GAM289  MECP2    3'  GCAGGAGCCAAACCTC      22590          CCAC
                                GCAGGAGCC    GCCTC
                                |||||||||    |||||
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                                CGTCCTCGG   TGGAG
                                    TT__
GAM289  MNT     3'  AAGCAGCAGCCCTAGCTCT   33698      G    CAC  _
                                AAGCAG AGCCC   GC CT
                                |||||| |||||   || ||
                                TTCGTC TCGGG   CG GA
                                   G    AT_  A
GAM289  MUC4    3'  AAGGAGGAGTTCCCGTCT    39653    C    CC  A  C
                                AAG AGGAG  CC CG CT
                                ||| |||||  || || ||
                                TTC TCCTC  GG GC GA
                                  C    AA  _  A
GAM289  NAPB    3'  AGCAGGAAGCCTGCTCT     43166      _  CCAC  _
                                AGCAGGA GCC    GC CT
                                ||||||| |||    || ||
                                TCGTCCT CGG    CG GA
                                    T   A___  A
GAM289  NFATC4  5'  GCAGGAGCCCCCAGGTCCCG  21245         A  CC
                                GCAGGAGCCCC CG  TCCCG
                                |||||||||| ||  |||||
                                CGTCCTCGGGG GT  AGGGC
                                      _  CC
GAM289  PCTK3   3'  AAGCAGGAGCCACCTC      43773         CCAC
                                AAGCAGGAGCC    GCCTC
                                ||||||||||    |||||
                                TTCGTCCTCGG    TGGAG
                                      ____
GAM289  PLD2    3'  GCAGAGCCCCCTTCTCC     15380     G     ACGC
                                GCAG AGCCCC    CTCC
                                |||| ||||||    ||||
                                CGTC TCGGGG    GAGG
                                  _     GAA_
GAM289  POLR2J  3'  AGCAGAGCCCCCTC       26356      G     ACGC
                                AGCAG AGCCCC    CTC
                                ||||| ||||||    |||
                                TCGTC TCGGGG    GAG
                                  _     ____
GAM289  POU3F2  3'  AGGGGGAGCCCCGCGCTCT   24665    CA      A  _
                                AG  GGAGCCCC CGC CT
                                ||  |||||||| ||| ||
                                TC  CCTCGGGG GCG GA
                                 CC       C   A
GAM289  RDBP    5'  AACCGGGGGCCCCACGGTCTCC 16229     A_  A      C_
                                AGC  GG GCCCCACG  CTCC
                                |||  || ||||||||  ||||
                                TTG  CC CGGGGTGC  GAGG
                                  GC  C       CA
GAM289  SDC1    3'  GCGGCGGCCCCACGGCAGCCT  16506    A  A_     ____
                                GC GG  GCCCCAC    GCCT
                                || ||  |||||||    ||||
```

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                                CG CC  CGGGGTG   CGGA
                                 _ GC      CCGT
GAM289  SLC2A8   3' GCAGTGAGCCTCCTAGCCCC  31029     _    _ AC
                                GCAG GAGCC CC  GCCTC
                                |||| ||||| ||  |||||
                                CGTC CTCGG GG  CGGGG
                                  A    A  AT
GAM289  TCIRG1   5' GCAGGAGGCCTCCCG      25840       CCCCAC
                                GCAGGAG     GCCTCCCG
                                |||||||     ||||||||
                                CGTCCTC     CGGAGGGC
                                      _______
GAM289  TMEPAI   3' AAGCAGGAGCCCTTGGTGGACC 33586          CACGCCT_
           C                     AAGCAGGAGCCC       CCC
                                ||||||||||||       |||
                                TTCGTCCTCGGG       GGG
                                      AACCACCT
GAM289  YES1     3' AAGCAGGAGCCTCACTGTCC  24114         C  GCC
                                AAGCAGGAGCC CAC   TCC
                                |||||||||||| |||   |||
                                TTCGTCCTCGG GTG   AGG
                                      A  AC_
GAM289  ADRB3    3' TGAGAGAGGCCACTGCTTG   6180        G    TCC
                                TGAGAGAGG CCGCT   GCTTG
                                ||||||||| |||||   |||||
                                ACTCTCTCC GGTGA   CGAAC
                                      _   ____
GAM289  CD4      3' TGAGAGAAGGGCTAGGCTTGA 8329         CC   TCC
                                TGAGAGAGGG  GCT   GCTTGA
                                ||||||||||  |||   ||||||
                                ACTCTCTTCC  CGA   CGAACT
                                      __  TC_
GAM289  DLX2     3' GAGAGAGGGGCCCGTTTG    20590        CC  TT   C
                                GAGAGAGGG  GC  CCG TTG
                                |||||||||  ||  ||| |||
                                CTCTCTCCC  CG  GGC AAC
                                      __ __  A
GAM289  HTR4     3' TGAGGAGGGTCGTTCCTTTGA 9304      A    C  C   GC
                                TGAG GAGGG CG TTCC  TTGA
                                |||| ||||| || ||||  ||||
                                ACTC CTCCC GC AAGG  AACT
                                  _    A  _   A_
GAM289  MASP1    3' TGGGAGAGGCATTTTGCTTG  40117    A     G CGCTTCC
                                TG GAGAGG C      GCTTG
                                || |||||| |      |||||
                                AC CTCTCC G      CGAAC
                                 C     _ TAAAA__
GAM290  FBXL11   3' GGGAAGATCGGTTTCCTGTTG 29434         ATG  G_
                                GGGAAGATCG   TT  GTTG
                                ||||||||||   ||  ||||
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                                CCCTTCTAGC  AG  CAAC
                                     CAA  GA
GAM290  MUC4    3'  TAAGGGAAGTTCTAGGTT   39673        A  GATGTT
                                TAAGGGAAG TC    GGTT
                                ||||||||| ||    ||||
                                ATTCCCTTC AG    CCAA
                                     A  AT____
GAM290  TRPM1   5'  AGGGGGGATATGCTGGTTG   14539    AA  CG
                                AGGG  GAT  ATGTTGGTTG
                                ||||  |||  ||||||||||
                                TCCC  CTA  TACGACCAAC
                                  CC  __
GAM290  D10S170 3'  GCTTATACTGGGTGAAAT   24134       GA  AG
                                GCTTATAC  GGT  AGT
                                ||||||||  |||  |||
                                CGAATATG  CCA  TTA
                                     AC  CT
GAM290  GABRP   3'  TCTTTATATGAGGTAAA    30561   GC   C
                                TC  TTATA GAGGTAGA
                                ||  ||||| ||||||||
                                AG  AATAT CTCCATTT
                                 A_   A
GAM291  ELF3    3'  TCAGTGTTCTGAGTTCATGTCC 20757        CA  G_
          T                      TCGGTGTTC  GAG  CATGTCCT
                                 |||||||||  |||  ||||||||
                                 AGTCACAAG  CTC  GTACAGGA
                                      A_  AA
GAM291  PTP4A2  5'  TCGGTGTCCAGGAGTCT    38643       T   A  CAT  C
                                TCGGTGT CCAG GG  GTC T
                                ||||||| |||| ||  ||| |
                                AGCCACA GGTC CT  CAG A
                                   _   _ ___  A
GAM291  ACCN2   5'  GCGGGTCCTGGGGCGCTG   33448    T     ACA
                                GCG GTCCTGGG  GTTG
                                ||| ||||||||  ||||
                                CGC CAGGACCC  CGAC
                                  C      CG_
GAM291  EDAR    3'  GCTTGTCCTGGGAGGACAG   35308   G       ___
                                GC TGTCCTGGGA  CAG
                                || ||||||||||  |||
                                CG ACAGGACCCT  GTC
                                 A        CCT
GAM291  EHD3    3'  CAGCCTGTCCTGGGAGGCTGCA 31108     G       CA
                                CAGC TGTCCTGGGA  GTTGCA
                                |||| ||||||||||  ||||||
                                GTCG ACAGGACCCT  CGACGT
                                  G        C_
GAM291  EMS1    3'  CAGCGGTGTCCTGGAGCTG   23424      _      GAC
                                CAGCG TGTCCTGG  AGTTG
                                ||||| ||||||||  |||||
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                                GTCGC ACAGGACC   TCGAC
                                  C      ___
GAM291  HBZ      3'  CAGCCTGTCCTGGGGGTC    23731      G       ACA
                                CAGC TGTCCTGGG   GTT
                                |||| |||||||||   |||
                                GTCG ACAGGACCC   CAG
                                  G       C__
GAM291  JAG2     3'  ACGCGTGGACAGTTGC      13699       CCTG
                                GCGTGT   GGACAGTTGC
                                ||||||   ||||||||||
                                TGCGCA   CCTGTCAACG
                                         _____
GAM291  PCTK3    5'  GCGTGTCCTGGGGGCCGC    43779          ACA
                                GCGTGTCCTGGG   GTTGC
                                ||||||||||||   |||||
                                CGCACAGGACCC   CGGCG
                                       C__
GAM291  SH3BP4   3'  GTGTCCTGGTTCTTGCA     30962         GACAG
                                GTGTCCTGG    TTGCA
                                |||||||||    |||||
                                CACAGGACC    AACGT
                                     AAG__
GAM291  SLC24A1  3'  CAGCGTGTGTTTGGGGCAG   21816        CC_   A
                                CAGCGTGT   TGGG CAG
                                ||||||||   |||| |||
                                GTCGCACA   ACCC GTC
                                     CAA   C
GAM291  SLC2A8   3'  CAGGGTGTCCTGGGCAGT    31028    C       A
                                CAG GTGTCCTGGG CAGT
                                ||| ||||||||||| ||||
                                GTC CACAGGACCC GTCA
                                  C       _
GAM292  HOXD3    3'  CCCTTGGTCCGCAG       27895         ATGTCGC
                                CCTTTGGTCC      GCGG
                                ||||||||||      ||||
                                GGGAACCAGG      CGTC
                                        ________
GAM292  ACHE     5'  AGGCGGCGTCTGAGGCGG    8560      A       A _
                                AGGC GGCGTCTGA GG GG
                                |||| ||||||||| || ||
                                TCCG CCGCAGACT CC CC
                                  _       _ G
GAM292  ADAM10   5'  AGGGAGAAGCTGAAGGGGCTTG 9966     C   C T
                                AGG AGG G CTGAAGGGGCTTG
                                ||| ||| | ||||||||||||
                                TCC TCT C GACTTCCCCGAAC
                                  C   T _
GAM292  AEGL1    3'  AGGCAGGTGTTGGACTTG    10059       C  CTGAAG
                                AGGCAGG GT     GGGCTTG
                                |||||||  ||     |||||||
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                                TCCGTCC CA     CCTGAAC
                                   A  A_____
GAM292  ALDH3B1  3'  AGGCAGGCGCTGCTTTGA    45058         T   AAGG
                                AGGCAGGCG CTG    GG
                                ||||||||| |||    ||
                                TCCGTCCGC GAC    CT
                                     _   GAAA
GAM292  AQP1     3'  AGCGGGTCAGGGGCTTG     7545      A  C   TGA
                                GGC GG GTC   AGGGGCTTG
                                ||| || |||   |||||||||
                                TCG CC CAG   TCCCCGAAC
                                  _ _  ____
GAM292  AVPR2    5'  GGCAGGTGTTCTGAGGGCCTG  6288        C  _    AG
                                GGCAGG GT CTGA  GGGCTTG
                                |||||| || ||||  |||||||
                                CCGTCC CA GACT  CCCGGAC
                                   A  A   __
GAM292  CHRM1    5'  AGGCAGCGTCTGGGGTTG    45422       G    GAA    C
                                AGGCAG CGTCT   GGGG TTG
                                |||||| |||||   |||| |||
                                TCCGTC GCAGA   CCCC AAC
                                  _    ____   _
GAM292  CYP4A11  3'  AGGCAGGAGTTTGGGAGGTGG  8933         C  C  A_  _
                                AGGCAGG GT TG  AGG GG
                                ||||||| || ||  ||| ||
                                TCCGTCC CA AC  TCC CC
                                    T  A  CC   A
GAM292  FAT2     3'  GGCAGGCGTCTGCAGTGG    11078          A  _
                                GGCAGGCGTCTG AG GG
                                ||||||||||| || ||
                                CCGTCCGCAGAC TC CC
                                       G  A
GAM292  FZD10    5'  GGCGCGTCTGGAGCGG      28455     AG      A  G
                                GGC  GCGTCTG AG GG
                                |||  ||||||| || ||
                                CCG  CGCAGAC TC CC
                                  __      C  G
GAM292  G6PD     5'  GGCGGGCGCCTGGGCTG     7609      A     GAAG    T
                                GGC GGCGTCT    GGGCT G
                                ||| |||||||    ||||| |
                                CCG CCGCGGA    CCCGA C
                                  C      ____    _
GAM292  GAS11    3'  GGCAGTGTCTGAGGCCCA    11217       GC     AGG
                                GGCAG  GTCTGA   GGCTTG
                                |||||  ||||||   ||||||
                                CCGTC  CAGACT   CCGGGT
                                   A_     ___
GAM292  GRAF     3'  AGGTTGGGCGTTTGGACCGTTG 31436     CA_    CTGAAG    __
            A                    AGG   GGCGT     GGGCT  TGA
                                |||   |||||     |||||  |||
```

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                                TCC  CCGCA    CCTGG  ACT
                                  AAC    AA____    CA
GAM292  GRB10    5'  AGGCAGGCGTTTGGAGAGG   23646         C  A
                                AGGCAGGCGT TG AGGGG
                                |||||||||| || |||||
                                TCCGTCCGCA AC TCTCC
                                      A  C
GAM292  HTR1D    3'  GGTGGGCGTCTAAAGCCGG   9263    CA        __
                                GG  GGCGTCTGAAG  GG
                                ||  ||||||||||  ||
                                CC  CCGCAGATTTC  CC
                                 AC         GG
GAM292  IGSF8    3'  AGGCCAGAGGGAGGGGCTTG   38079     A  CGTCT  A
                                AGGC GG    GA GGGGCTTG
                                |||| ||    || ||||||||
                                TCCG TC    CT CCCCGAAC
                                  G  TCC__  _
GAM292  KNSL1    5'  AGGGGCGGAGGGGCTT     21176    CA   TCT  A
                                AGG  GGCG   GA GGGGCTT
                                |||  ||||   || |||||||
                                TCC  CCGC   CT CCCCGAA
                                 __   ___ _
GAM292  MAT1A    3'  AGCCAGGCGTCTGGGGA     44900    G        AA
                                AG CAGGCGTCTG  GGGG
                                || ||||||||||  ||||
                                TC GTCCGCAGAC  CCCT
                                 G        __
GAM292  MBD3     3'  GGCAGGCGTCTGTGGCTTG   19419          AAGG
                                GGCAGGCGTCTG   GGCTTG
                                ||||||||||||   ||||||
                                CCGTCCGCAGAC   CCGAAC
                                      A___
GAM292  MSF      3'  GGCAGCTGCCAGGGGGCTTG  44736      GC   TGAA
                                GGCAG  GTC   GGGGCTTG
                                |||||  |||   ||||||||
                                CCGTC  CGG   CCCCGAAC
                                   GA   TC__
GAM292  MUC1     5'  AGGCAGGCGCTGGCTGCTTGA  43770        T   AAGGG
                                AGGCAGGCG CTG    GCTTGA
                                |||||||| |||    ||||||
                                TCCGTCCGC GAC    CGAACT
                                     _  CGA__
GAM292  PEX14    3'  AGGGGGCTGGGGAGGGGCTTG  41869    CA   GTCT  A
                                AGG  GGC   GA GGGGCTTG
                                |||  |||   || ||||||||
                                TCC  CCG   CT CCCCGAAC
                                  C_  ACCC  _
GAM292  PKD2L1   5'  AGGTGGGGGTTTGAAGAGG   32017    CA  C  C
                                AGG  GG GT TGAAGGGG
                                |||  || || ||||||||
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                                TCC  CC CA ACTTCTCC
                                  AC  C  A
GAM292  PRX2     3'  AGGGAGGCGTCTGGGTCCTG   32228     C       GAA   G
                                AGG AGGCGTCT   GGG CTTG
                                ||| ||||||||   ||| ||||
                                TCC TCCGCAGA   CCC GGAC
                                  C       ___   A
GAM292  SLC22A12 3'  GGCAGGTGGCTGAGGCCTG   40333       CGT    AGG
                                GGCAGG   CTGA   GGCTTG
                                ||||||   ||||   ||||||
                                CCGTCC   GACT   CCGGAC
                                   ACC   ___
GAM292  SLC38A3  3'  AGGAGGGAATGAGGGGCTTG   27756     C   CGTC   A
                                AGG AGG    TGA GGGGCTTG
                                ||| |||    ||| ||||||||
                                TCC TCC    ACT CCCCGAAC
                                  _  CTT_  _
GAM292  TIMM23   3'  AGGCAGGCGGCTGGGAGGTGG  26749         T   A_  _
                                AGGCAGGCG CTG  AGG GG
                                ||||||||| |||  ||| ||
                                TCCGTCCGC GAC  TCC CC
                                     C   CC   A
GAM293  COL4A4   3'  GGGAAGGAGAAAGG        6403           CACC
                                GGGGAGGAGGG    AGG
                                ||||||||||    |||
                                CCCTTCCTCTT    TCC
                                       ____
GAM293  GNAS     3'  CTCCACGGGGGGCACCAGG    38660      _    AGGAG
                                TTCC CGGGG    GGCACCAGG
                                |||| |||||    |||||||||
                                GAGG GCCCC    CCGTGGTCC
                                  T    _____
GAM293  KRTHB6   5'  GGGGAAGAGAGGAGGT      14035          CACC
                                GGGGAGGAGGG    AGGT
                                ||||||||||    ||||
                                CCCCTTCTCTC    TCCA
                                      C___
GAM293  PSD      5'  TTCCCGGGGGGAGGACCAGGT  15795         A    GC
                                TTCCCGGGG GGAGG  ACCAGGT
                                ||||||||| |||||  |||||||
                                AAGGGCCCC CCTCC  TGGTCCA
                                       _    __
GAM293  ADAM11   3'  GGGTGCCAGGCTTGGAGGGAGG 34657     CA      CCC
           AG                    GGG  CCAGGTT   GGGGAGGAG
                                |||  |||||||   |||||||||
                                CCC  GGTCCGA   TCCCTCCTC
                                  AC      ACC
GAM293  ADAMTS5  5'  GCGCTGCCCGCGGGGAGG    28180    ACCAG   C
                                GC    GTTC CGGGGAGG
                                ||    |||| ||||||||
```

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                                CG    CGGG GCCCCTCC
                                 CGA__   C
GAM293  ARVCF    3'  GGGCACTGTGTTCCCAGGG   11706      CAG
                                GGGCAC  GTTCCCGGGG
                                ||||||  ||||||||||
                                CCCGTG  CAAGGGTCCC
                                   ACA
GAM293  BAT2     3'  GGGACCAGGGGAAGGGGGAGGA 21580    C     TTCCC
           G                     GGG ACCAGG    GGGGAGGAG
                                ||| ||||||    |||||||||
                                CCC TGGTCC    CCCCTCCTC
                                  _     CCTTC
GAM293  BLTR2    5'  GGTGCTAGGTTCCAGGAG    33371    _ ACC      CG
                                GG GC   AGGTTCC  GGGAG
                                || ||   |||||||  |||||
                                CC CG   TCCAAGG  TCCTC
                                 A  A__      __
GAM293  BTG2     3'  GGGACTGGCTGTGGGGAGGAG  27619     C  CA   CCC
                                GGG AC  GGTT   GGGGAGGAG
                                ||| ||  ||||   |||||||||
                                CCC TG  CCGA   CCCCTCCTC
                                  _ A_   CA_
GAM293  CACNG6   5'  GGGTCGGGAAGGGGGAGGAG   36699     CACCA  TTCCC
                                GGG    GG    GGGGAGGAG
                                |||    ||    |||||||||
                                CCC    CC    CCCCTCCTC
                                  AG____  CTTC_
GAM293  CAPON    5'  GGCGCCCCTGCCCGGGGAGG   41925     A  AGGTT
                                GGC CC    CCCGGGGAGG
                                ||| ||    ||||||||||
                                CCG GG    GGGCCCCTCC
                                  C  GGAC_
GAM293  CLN6     3'  GGGTCCTAGGTAGGGGGAG   32827     CA  _   TCCC
                                GGG  CC AGGT   GGGGAG
                                |||  || ||||   ||||||
                                CCC  GG TCCA   CCCCTC
                                  A_  A   TC__
GAM293  CSK      5'  GGTGCAAGGAGAGGGGAGGAG  20471    _  CC   TTCCC
                                GG GCA  AGG    GGGGAGGAG
                                || |||  |||    |||||||||
                                CC CGT  TCC    CCCCTCCTC
                                 A   __   TCT__
GAM293  CTSD     3'  GGCGCTGGTAGGGCCGGGGAGG 12532     ACCA   TC__
                                GGC    GGT   CCGGGGAGG
                                |||    |||   |||||||||
                                CCG    CCA   GGCCCCTCC
                                  CGA_   TCCC
GAM293  CYFIP2   5'  GGCTGCTGGTCGGGGAGG    43912     ACCA   TCC
                                GGC    GGT   CGGGGAGG
                                |||    |||   ||||||||
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                                CCG   CCA  GCCCCTCC
                                  ACGA  ___
GAM293  DRPLA   3' GGGTTGGGCATGGGGGAGGAG 12593    CACCA  TCCC
                                GGG   GGT   GGGGAGGAG
                                |||   |||   |||||||||
                                CCC   CCG   CCCCTCCTC
                                  AAC__  TAC_
GAM293  EPS15   5' GGGCTCGGGGCGGGGAGGA  12745    ACCA TTCC
                                GGGC  GG  CGGGGAGGA
                                ||||  ||  |||||||||
                                CCCG  CC  GCCCCTCCT
                                  AG__ CC__
GAM293  FBXL11  3' GGGACCATGGATGGGGAGGAG 29435    C  _ TTCCC
                                GGG ACCA GG   GGGGAGGAG
                                ||| |||| ||   |||||||||
                                CCC TGGT CC   CCCCTCCTC
                                  _   A  TA___
GAM293  FUT6    3' GGGTGCCAGTTCCCAGGG   6653    CA   G
                                GGG  CCAG TTCCCGGGG
                                |||  |||| |||||||||
                                CCC  GGTC AAGGGTCCC
                                  AC   _
GAM293  FXR2    3' GGGTACAGGATGGGAGGA   22168    CAC   TTCCCG
                                GGG  CAGG    GGGAGGA
                                |||  ||||    |||||||
                                CCC  GTCC    CCCTCCT
                                  AT_   TA____
GAM293  GALGT   3' GGGCATCAGGTTCTGAAAAG  11188     C     CC GG
                                GGGCA CAGGTTC  G  GAG
                                ||||| |||||||  |  |||
                                CCCGT GTCCAAG  C  TTC
                                   A     A_ TT
GAM293  GGT2    5' GGTTGTCAGGTTCCTTGGAG  43927   GCAC     CGG
                                GG   CAGGTTCC  GGAG
                                ||   ||||||||  ||||
                                CC   GTCCAAGG  CCTC
                                 AACA      AA_
GAM293  GRN     3' GGGTCCACTGAAACGGGGAGG 13294    CA  GGTTCC
                                GGG  CCA    CGGGGAGG
                                |||  |||    ||||||||
                                CCC  GGT    GCCCCTCC
                                  A_  GACTTT
GAM293  HBA1    3' GGGTGCAGGAAGGGGAGGA  8152    CAC   TTCCC
                                GGG  CAGG   GGGGAGGA
                                |||  ||||   ||||||||
                                CCC  GTCC   CCCCTCCT
                                  AC_   TT___
GAM293  HIP12   3' GGGCACCAGGTGGAGG    42403         TCCCGG
                                GGGCACCAGGT    GGAGG
                                ||||||||||    |||||
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                                CCCGTGGTCCA     CCTCC
                                       _______
GAM293  HLX1     5'  GGGCGCGCGGGGAGG       34990      ACCAG  TCC
                                GGGC    GT   CGGGGAGG
                                ||||    ||   ||||||||
                                CCCG    CG   GCCCCTCC
                                  ______ C__
GAM293  IMMP2L   5'  GGGCGCCGGCTCGGCGGGGAGG 37181      A  A    C_
           AG                     GGGC CC GGTTC  CGGGGAGGAG
                                ||||  ||  |||||  ||||||||||
                                CCCG GG CCGAG  GCCCCTCCTC
                                  C  _    CC
GAM293  JUND     3'  GGGCACACTCGGGGAGG     23807       CAGGTTCC
                                GGGCAC      CGGGGAGG
                                ||||||      ||||||||
                                CCCGTG      GCCCCTCC
                                   TGA_____
GAM293  LENG4    3'  GGACTCTTTCTGGGGAGGA   35887      ACCAGG   CC
                                GGGC     TTC  GGGGAGGA
                                ||||     |||  ||||||||
                                CCTG     AAG  CCCCTCCT
                                  AGA___   A_
GAM293  MAML1    3'  GGGCCTTGGGAGGGAGGA    31294      ACCA  TTCCC
                                GGGC   GG    GGGGAGGA
                                ||||   ||    ||||||||
                                CCCG   CC    TCCCTCCT
                                  GAAC  _____
GAM293  MGAT5    5'  GGTTACCAGGGGTGGGGAGGAG 14476    GC     TTCCC
                                GG  ACCAGG    GGGGAGGAG
                                ||  ||||||    |||||||||
                                CC  TGGTCC    CCCCTCCTC
                                 AA     CCA__
GAM293  NAGA     5'  GGGTCCGGGTTCCCGCCCTGGG 7041      CA  A      ____
                                GGG  CC GGTTCCCG    GGG
                                |||  || ||||||||    |||
                                CCC  GG CCAAGGGC    CCC
                                  A_  C       GGGA
GAM293  NPC2     5'  GGGCGGGCCCGGGGAGGA    26964      ACCA  TT
                                GGGC   GG  CCCGGGGAGGA
                                ||||   ||  ||||||||||
                                CCCG   CC  GGGCCCCTCCT
                                  _____  C_
GAM293  NRXN1    5'  GGGCTCCAGGTTCTCGAG    22050      A       C
                                GGGC CCAGGTTC CGGG
                                |||| |||||||| ||||
                                CCCG GGTCCAAG GCTC
                                  A       A
GAM293  PACSIN1  3'  GGGCGGCAGTGGGGAGGA    45158      ACCA   TCCC
                                GGGC   GGT   GGGGAGGA
                                ||||   |||   ||||||||
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                                CCCG   CCG   CCCCTCCT
                                  ____  TCA_
GAM293  PAFAH1B1  5'  GGGCCCGGGGAGGGGGAGG   7714      A  A  TTCCC
                                GGGC CC GG    GGGGAGG
                                |||| || ||    |||||||
                                CCCG GG CC    CCCCTCC
                                  _  C  CTC__
GAM293  PAFAH1B1  5'  GGGCCCGGGCCCGGGGAGG   7713      A  A  TT
                                GGGC CC GG  CCCGGGGAGG
                                |||| || ||  ||||||||||
                                CCCG GG CC  GGGCCCCTCC
                                  _  C  __
GAM293  PEX14     3'  GGGCCCAGGGAGGGAGG     41873     A    TTCCC
                                GGGC CCAGG    GGGGAGG
                                |||| |||||    |||||||
                                CCCG GGTCC    TCCCTCC
                                  _    C____
GAM293  PIK3CD    3'  GGGCCCAGGGCTGGGAGGA   22730     A    TTCCCG
                                GGGC CCAGG     GGGAGGA
                                |||| |||||     |||||||
                                CCCG GGTCC     CCCTCCT
                                  _    CGA___
GAM293  PLD2      3'  GGGCCCTGGGACAGGGAGG   15382     A  A  TTCC
                                GGGC CC GG   CGGGGAGG
                                |||| || ||   ||||||||
                                CCCG GG CC   GTCCCTCC
                                  _  A  CT__
GAM293  PRKCL1    5'  GGGCGTGGCGGGGAGG     41703     ACCA  TTCC
                                GGGC   GG   CGGGGAGG
                                ||||   ||   ||||||||
                                CCCG   CC   GCCCCTCC
                                  CA__  ____
GAM293  SHANK2    3'  GGGTGCCAAGGTTTGGGAG   29464     CA  _   CCCG
                                GGG  CCA GGTT   GGGAG
                                |||  ||| ||||   |||||
                                CCC  GGT CCAA   CCCTC
                                  AC   T   A___
GAM293  SLC21A9   3'  GGCTGCTGGAGTTGGGGAGGAG 28567     ACCA  TTCCC
                                GGC   GG    GGGGAGGAG
                                |||   ||    |||||||||
                                CCG   CC    CCCCTCCTC
                                  ACGA  TCAA_
GAM293  SRC       3'  GGGTGCCGACTTGGGGAGGAG  24037     CA  A GT CCC
                                GGG  CC G  T   GGGGAGGAG
                                |||  || |  |   |||||||||
                                CCC  GG C  A   CCCCTCCTC
                                  AC  _ TG A__
GAM293  SRD5A1    5'  GGGCGGCGGCGCGGGGGGAGGA 9832      ACCA   TCCC
            G                    GGGC   GGT   GGGGAGGAG
                                ||||   |||   |||||||||
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                              CCCG   CCG   CCCCTCCTC
                                CCG_  CGCC
GAM293  TEAD3   5' GGGGGTCGTGGGGAGG    17377    CACCA   CCC
                              GGG    GGTT  GGGGAGG
                              |||    ||||  |||||||
                              CCC    CCAG  CCCCTCC
                               ______   CA_
GAM293  TEM5    3' GGTGCTGGTGTTTAAAAGGAG 37240   _ ACCA  TCCCG
                              GG GC   GGT   GGGAGGAG
                              || ||   |||   ||||||||
                              CC CG   CCA   TTTTCCTC
                               A  A___  CAAA_
GAM293  TEM6    3' GGGTCCAGGGAGGGAGG    35557    CA   TTCCC
                              GGG  CCAGG   GGGGAGG
                              |||  |||||   |||||||
                              CCC  GGTCC   TCCCTCC
                                A_   C____
GAM293  TIRAP   5' AGGCATTGGTGAAGGGGGAGGA 38089     CCA  TCCC
           G                   GGGCA  GGT   GGGGAGGAG
                              |||||  |||   |||||||||
                              TCCGT  CCA   CCCCTCCTC
                                AA_  CTTC
GAM293  TXNRD2  3' GGCACCAGGAGCCTGGGGGGG 26976       TT  C   A
                              GGCACCAGG  CC GGGG GG
                              |||||||||  || |||| ||
                              CCGTGGTCC  GG CCCC CC
                                   TC  A   C
GAM293  UBE2I   5' GGGCACCAGGCTTCTGAAG   17817         CCCGG
                              GGGCACCAGGTT   GGAG
                              ||||||||||||   ||||
                              CCCGTGGTCCGA   CTTC
                                    AGA__
GAM293  UMPK    5' GGGCTGGGTTTCCCGAAGGAG 29776     ACCA  _   _
                              GGGC   GGTT CCCGG GGAG
                              ||||   |||| ||||| ||||
                              CCCG   CCAA GGGCT CCTC
                                AC__   A    T
GAM293  VIPR2   3' GAGCGCCAGCTCTGGGGAGGAG 18015     A   G   CC
                              GGGC CCAG TTC  GGGGAGGAG
                              |||| |||| |||  |||||||||
                              CTCG GGTC GAG  CCCCTCCTC
                                C   _  A_
GAM293  WNT8B   3' GGGCTGCTAGGAGAGGGGAGGA 40587     ACC_  TTCCC
           G                   GGGC   AGG   GGGGAGGAG
                              ||||   |||   |||||||||
                              CCCG   TCC   CCCCTCCTC
                                ACGA  TCT__
GAM293  ZIC3    5' GGGTGTTGGCGGGGGGAGGAG 18254    CACCA   TCCC
                              GGG    GGT   GGGGAGGAG
                              |||    |||   |||||||||
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                              CCC    CCG   CCCCTCCTC
                                ACAA_  CC__
GAM293  ZNF236   3' GGGCCAGGTTCCCAGAG    28864     AC
                              GGGC CAGGTTCCCGGGG
                              |||| ||||||||||||
                              CCCG GTCCAAGGGTCTC
                                 __
GAM293  ZNF278   5' GGGCACGCGCACGCGGGGAGGA 36803      CAG TCC
           G                   GGGCAC  GT  CGGGGAGGAG
                              |||||| ||  ||||||||||
                              CCCGTG  CG  GCCCCTCCTC
                                 CG_ TGC
GAM294  GGT1     5' TGTTGGCCACGAAAGACAGG  23574        TGTG_
                              TGTTGGCCGCG   TAGG
                              ||||||||||    ||||
                              ACAACCGGTGC   GTCC
                                    TTTCT
GAM294  GGT2     5' TGTTGGCCACGAAAGACAGG  43929        TGTG_
                              TGTTGGCCGCG   TAGG
                              ||||||||||    ||||
                              ACAACCGGTGC   GTCC
                                    TTTCT
GAM294  PMP2     3' TAAAATGTTGGCTGGAGTAGAG 15423         CGCGT  T
           G                   TAAAATGTTGGC   GTG AGG
                              ||||||||||    ||| |||
                              ATTTTACAACCG   CAT TCC
                                    ACCT_  C
GAM294  SLC21A9  3' AAATCTTGGCAATGTGTAGG  28555    G   CGC
                              AAAT TTGGC  GTGTGTAGG
                              |||| |||||  |||||||||
                              TTTA AACCG  TACACATCC
                                G   T__
GAM294  WISP2    3' ATATAGGCTGTGTGTGTAGG  19309    T  CGC
                              ATGT GGC  GTGTGTAGG
                              |||| |||  |||||||||
                              TATA CCG  CACACATCC
                                T  ACA
GAM294  ZNF36    3' ATGTTGGCCAAAGTAGG    45289       CGTGT
                              ATGTTGGCCG   GTAGG
                              |||||||||    |||||
                              TACAACCGGT   CATCC
                                   TT___
GAM294  BCS1L    5' TGCAAATACGCAACAAATATGT 20252        T   _  CC
           TCA                   TGCAAATACGC ACGAA ATG  CA
                              |||||||||| ||||| |||  ||
                              ACGTTTATGCG TGTTT TAC  GT
                                    T   A  AA
GAM294  CLCN4    3' CAAATACAAAGATGCCC    12277       CTAC  A
                              CAAATACG   GA ATGCCC
                              ||||||||   || ||||||
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                                GTTTATGT    TT TACGGG
                                     ____  C
GAM294  DHFR     3'  TACAGGTGTGCGCCACAATGCC 8997      AATA__       AA
            CA                    TGCA     CGCTACGA  TGCCCA
                                  ||||     ||||||||  ||||||
                                  ATGT     GCGGTGTT  ACGGGT
                                    CCACAC       __
GAM294  ITCH     3'  TGCAAATAAGTTCTTGCCC   36457        CG__  ACGAAA
                                  TGCAAATA   CT     TGCCC
                                  ||||||||   ||     |||||
                                  ACGTTTAT   GA     ACGGG
                                       TCAA _______
GAM294  PDX1     3'  CAAATATTCCAAAATGCTCA   18487       CGCTA       C
                                  CAAATA    CGAAATGC CA
                                  ||||||    |||||||| ||
                                  GTTTAT    GTTTTACG GT
                                     AAG__       A
GAM294  PTTG1IP  3'  TACAAATACAAATGCC      20289          CTACGA
                                  TGCAAATACG     AATGCC
                                  ||||||||||     ||||||
                                  ATGTTTATGT     TTACGG
                                         _______
GAM295  AQP2     5'  CGGGGCTGGCCCAGCTG     7932     CA    C TATA
                                  CG  GCTG G    CCCAGCTG
                                  ||  |||| |    ||||||||
                                  GC  CGAC C    GGGTCGAC
                                   CC    _ _____
GAM295  CD5      3'  GCACTCGCCCAGCT       30545     G  G  TATA
                                  GCA CT CG    CCCAGCT
                                  ||| || ||    |||||||
                                  CGT GA GC    GGGTCGA
                                    _  _  _____
GAM295  CENTD2   5'  GCGGGCTGCGTATGCCCA    31596    A_       A
                                  GC  GCTGCGTAT CCCA
                                  ||  |||||||| ||||
                                  CG  CGACGCATA GGGT
                                   CC        C
GAM295  GPR30    3'  CGCAGTTGTCCCCAGCTGT   11306      C  CGTATA
                                  CGCAG TG     CCCAGCTGT
                                  ||||| ||     |||||||||
                                  GCGTC AC     GGGTCGACA
                                     A  AG_____
GAM295  IL2RA    3'  ACGCAGACAATGTCCAGTTGT  7668        CT   TATAC    C
                                  ACGCAG  GCG    CCAG TGT
                                  ||||||  |||    |||| |||
                                  TGCGTC  TGT    GGTC ACA
                                     __   TACA_    A
GAM295  LIMK1    3'  CAGCTGCTCCAGCTG       32527        GTATAC
                                  CAGCTGC     CCAGCTG
                                  |||||||     |||||||
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                                GTCGACG     GGTCGAC
                                   A_____
GAM295  STAT5B   5'  CGCGGCTGCTCCGGCCCAGCTG 29718     A    GTATA
             T                    CGC GCTGC     CCCAGCTGT
                                  ||| |||||     |||||||||
                                  GCG CGACG     GGGTCGACA
                                    C     AGGCC
GAM295  DLEC1    3'  GCACCTCGGTGGGCCCAGCTG  28827     G  G   AGA
                                  GCA CT GGT   CCCAGCTG
                                  ||| || |||   ||||||||
                                  CGT GA CCA   GGGTCGAC
                                    G  G   CCC
GAM295  ENDOGL1  3'  GCCTGTAGTCCCAGCTG     23015     GG    A
                                  GCT  GTAG CCCAGCTG
                                  |||  |||| ||||||||
                                  CGG  CATC GGGTCGAC
                                    A_   A
GAM295  FXYD1    5'  GCCGGGGTGAGGCCCAGCTG   34861       TA __
                                  GCTGGG  GA  CCCAGCTG
                                  ||||||  ||  ||||||||
                                  CGGCCC  CT  GGGTCGAC
                                     CA  CC
GAM295  RPA2     3'  AACTAGGTCCAGCT       16375         AGAC
                                  AGCTGGGT    CCAGCT
                                  ||||||||    ||||||
                                  TTGATCCA    GGTCGA
                                        _____
GAM295  RXRA     3'  GCCTGGGAGGGGCCCAGCTG   16427    AG    T  A__
                                  GC  CTGGG AG   CCCAGCTG
                                  ||  ||||| ||   ||||||||
                                  CG  GACCC TC   GGGTCGAC
                                    __    _  CCC
GAM295  STAR     3'  GCAGCTGGGCACAG       7390           GACC
                                  GCAGCTGGGTA    CAG
                                  ||||||||||    |||
                                  CGTCGACCCGT    GTC
                                        _____
GAM295  UBE2I    5'  CACGTGGCAGGCCCAGCT    17813     AGCTG    A
                                  CGC    GGTAG CCCAGCT
                                  |||    ||||| |||||||
                                  GTG    CCGTC GGGTCGA
                                    CA___     C
GAM295  VCY      3'  GCAGCTGGGCCTAAACT     21711          AGACCC
                                  GCAGCTGGGT     AGCT
                                  ||||||||||     ||||
                                  CGTCGACCCG     TTGA
                                        GAT___
GAM296  ACVRL1   3'  GTATTTTTGGCTGGGTGGGC   6167       CCCA   A   T_
                                  GTATT   GCTG GGT  GC
                                  |||||   |||| |||  ||
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                                CATAA   CGAC CCA  CG
                                  AAAC   _  CC
GAM296  ARHGAP6  5'  TGGGTTCCCAGCTCCAGCC   30232    TA      GAGGTT
                                TGG  TTCCCAGCT    GCC
                                |||  |||||||||    |||
                                ACC  AAGGGTCGA    CGG
                                  C_       GGT___
GAM296  CIT      3'  TGGTTTTTCTGGCTGAGAT   43062    A_  CCA
                                TGGT  TTC   GCTGAGGT
                                ||||  |||   ||||||||
                                ACCA  AAG   CGACTCTA
                                  AA   AC_
GAM296  LDHB     5'  TGGGTTCCTTTTTGGTTGCCT  14125    TA   CAGCTGA
                                TGG  TTCC     GGTTGCCT
                                |||  ||||     ||||||||
                                ACC  AAGG     CCAACGGA
                                  C_   AAAAA__
GAM296  POU2AF1  3'  TGGTACTTCTGGCTGAGGCT   26379       CCCA
                                TGGTATT    GCTGAGGTT
                                |||||||    |||||||||
                                ACCATGA    CGACTCCGA
                                    AGAC
GAM296  PPP1R2   3'  TGGTATTCCTAGCTGAAAT   26423        C
                                TGGTATTCC AGCTGAGGT
                                ||||||||| |||||||||
                                ACCATAAGG TCGACTTTA
                                     A
GAM296  SLC25A19 3'  TGGTGTCCCAGCTGGGT    34710     AT       A
                                TGGT  TCCCAGCTG GGT
                                ||||  ||||||||| |||
                                ACCA  AGGGTCGAC CCA
                                  C_       _
GAM296  SNRPN    5'  TGGTGTCTCAGCTAAGAATGCC 35610     AT  C      GT
           T                     TGGT  TC CAGCTGAG  TGCCT
                                ||||  || ||||||||  |||||
                                ACCA  AG GTCGATTC  ACGGA
                                  C_ A       TT
GAM296  TRPM8    3'  TGGTAATCGCTAGAGGTTGCCT 35863      T  CCA  _
                                TGGTA TC   GCT GAGGTTGCCT
                                ||||| ||   ||| ||||||||||
                                ACCAT AG   CGA CTCCAACGGA
                                   T ___   T
GAM296  TSG      3'  GGTATTCCTAAAAAGTTGC    34006        CAGCT
                                GGTATTCC    GAGGTTGC
                                ||||||||    ||||||||
                                CCATAAGG    TTTCAACG
                                     ATT__
GAM296  HTR2C    3'  TGCAAATGCCACCTG      9293     TTCCGG   A
                                TGC     AAAT CCACCTG
                                |||     |||| |||||||
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                                ACG     TTTA GGTGGAC
                                 _______   C
GAM296  PSCD3   3'  GCCTTGGGGATACCACCTG   20127     CC  AA
                                GCTT  GG  ATACCACCTG
                                ||||  ||  ||||||||||
                                CGGA  CC  TATGGTGGAC
                                  A_  CC
GAM296  SOS2    3'  ATGCTACTGATCACCTGA    42851      TCCG  AATAC
                                ATGCT   GA    CACCTGA
                                |||||   ||    |||||||
                                TACGA   CT    GTGGACT
                                  TGA_  A____
GAM297  AGTR1   5'  GAGGGCCGGCTGCGCTG     28913     T  G  C
                                GAG GC CG GCTGCGCTG
                                ||| || || |||||||||
                                CTC CG GC CGACGCGAC
                                 C  _  _
GAM297  APP     5'  GAGTGCGCTGCTGTGCGA    7917        GC   C  T
                                GAGTGCGC  GCTG GC GA
                                ||||||||  |||| || ||
                                CTCACGCG  CGAC CG CT
                                    A_    A  _
GAM297  CHRM1   5'  GAGCTGCGCCCTGTGCTG    45424     GC   G  C
                                GAGT  GCGC CTG GCTG
                                ||||  |||| ||| ||||
                                CTCG  CGCG GAC CGAC
                                  A_    G  A
GAM297  CML66   5'  GAGGCGGCCCGCGCTG      42817     T  C  G
                                GAG GCG GC CTGCGCTG
                                ||| ||| || ||||||||
                                CTC CGC CG GGCGCGAC
                                 _  _  _
GAM297  ETF1    3'  GTAGGCTGCTGCGCTGAC    21833     C  GC
                                GTG GC  GCTGCGCTGAC
                                ||| ||  ||||||||||
                                CAT CG  CGACGCGACTG
                                 C  A_
GAM297  EXTL1   3'  GAGTGCGGCGCGACGCTGAC  20867       C   T
                                GAGTGCG GCGC GCGCTGAC
                                ||||||| |||| ||||||||
                                CTCACGC CGCG TGCGACTG
                                   _   C
GAM297  EXTL3   3'  ATGTGCACGCTGCTGA     11025     C       GC
                                GTG GCGCGCTGC  TGA
                                ||| |||||||||  |||
                                TAC CGTGCGACG  ACT
                                 A       __
GAM297  GPR30   5'  GAGTGCGCCCCCTACTGGC   11310        GC___   C
                                GAGTGCGC    GCTG GC
                                ||||||||    |||| ||
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                                CTCACGCG    TGAC CG
                                    GGGGA   _
GAM297  GSPT1   5'  GAGTGGGCAACGCTGA     13310      C   CGCT
                                GAGTG GCG   GCGCTGA
                                ||||| |||   |||||||
                                CTCAC CGT   TGCGACT
                                  C  ____
GAM297  HMX1    5'  GAGTGCGCGCCGACAGCTGA  33211         GCT  _
                                GAGTGCGCGC  GC GCTGA
                                ||||||||||  || |||||
                                CTCACGCGCG  TG CGACT
                                    GC_  T
GAM297  HNRPDL  5'  GACTGCGCCCGGCGCTG    24173    G    G  CT
                                GA TGCGC CG  GCGCTG
                                || ||||| ||  ||||||
                                CT ACGCG GC  CGCGAC
                                 G    G  __
GAM297  KCNF1   5'  GTGCCACCCGTGCGCTGA   13838     _  G  C
                                GTGC GC CG TGCGCTGA
                                |||| || || ||||||||
                                CACG TG GC ACGCGACT
                                  G  G  _
GAM297  LAMP1   5'  AGTGCGCGCGAGACGGCGCTG  24503          ___ T
                                AGTGCGCGCG  C GCGCTG
                                ||||||||||  | ||||||
                                TCACGCGCGC  G CGCGAC
                                    TCT C
GAM297  LMNA    5'  GAGTGCGCCGGCCGGCTG    24530        GC   C
                                GAGTGCGC  GCTG GCTG
                                ||||||||  |||| ||||
                                CTCACGCG  CGGC CGAC
                                    GC   _
GAM297  MOX2    5'  GAGGCGCGCGCGAGGTGGC   42516    T      ____  C
                                GAG GCGCGCGC   TG GC
                                ||| ||||||||   || ||
                                CTC CGCGCGCG   AC CG
                                  _      CTCC  _
GAM297  PFKL    3'  GAGCCCTGGCGCTGCGCTG   15235     GCGC
                                GAGT   GCGCTGCGCTG
                                ||||   ||||||||||
                                CTCG   CGCGACGCGAC
                                  GGAC
GAM297  PPFIA3  3'  GCGCGCGCACTCCCGCTG   41422         G_
                                GTGCGCGCGCT  CGCTG
                                ||||||||||  |||||
                                CGCGCGCGTGA  GCGAC
                                    GG
GAM297  SCNN1B  5'  GGTGCGCGCCAAGCTGGC   7339    A      ___   C
                                G GTGCGCGC   GCTG GC
                                | ||||||||   |||| ||
```

```
                                C CACGCGCG   CGAC CG
                                _       GTT    _
GAM297   SIAH2    5'  GCGCGCGCGGACGTGAC     22865         CT   C
                                GTGCGCGCG  GCG TGAC
                                |||||||||  ||| ||||
                                CGCGCGCGC  TGC ACTG
                                     C_   _
GAM297   SOX12    3'  GCGTGCGCGCCCCGCTGAC    28041     C      G
                                GTG GCGCGCT CGCTGAC
                                ||| ||||||| |||||||
                                CGC CGCGCGG GCGACTG
                                  A      G
GAM297   VEGF     5'  GAGCGCGCGCGCTGGAGC     17953            C_
                                GAGTGCGCGCGCTG  GC
                                ||||||||||||||  ||
                                CTCGCGCGCGCGAC  CG
                                         CT
GAM297   WWOX     3'  GAGTGCGCGTCCTCCCCGC    39119         CG__  G
                                GAGTGCGCG    CT CGC
                                |||||||||    || |||
                                CTCACGCGC    GG GCG
                                     AGGA  G
GAM297   LRRC2    3'  TCTTAGTCACAAAAGCTGCTT  36001     C      CCT
                                TCT AGTCGCG   AGCTGCTT
                                ||| |||||||   ||||||||
                                AGA TCAGTGT   TCGACGAA
                                  A      TT_
GAM297   MPP6     5'  TCTCTCCTGCTGTTTAGCTGCT 32397       AGTC  GCC_
           T                     TCTCTC    GC    TAGCTGCTT
                                ||||||    ||    |||||||||
                                AGAGAG    CG    ATCGACGAA
                                   GA__  ACAA
GAM298   BTG2     3'  GCTCAACAGTCCAGCTCA     27618         C   AAAACCA
                                GCTCAACAG CCG       TCA
                                ||||||||| |||       |||
                                CGAGTTGTC GGT       AGT
                                     A   CG_____
GAM298   CYFIP1   3'  GCTCATAAAAGACCATCA     42458       ACAGCCC   A
                                GCTCA       GAA ACCATCA
                                |||||       ||| |||||||
                                CGAGT       TTT TGGTAGT
                                   AT_____   C
GAM298   FGF23    3'  CAGCTTAAAACCATCAG      33949      CCG
                                CAGC   AAAACCATCAG
                                ||||   ||||||||||
                                GTCG   TTTTGGTAGTC
                                  AA_
GAM298   KCNS2    3'  GCTCAGTGACCCAATACCATCA 42832       ACA      AA
           G                     GCTCA   GCCCGA  ACCATCAG
                                |||||   ||||||  ||||||||
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                                CGAGT   TGGGTT  TGGTAGTC
                                  CAC     A_
GAM298  SLC17A5  5'  GCCCGACAGCCCGAAGCCC   29687     A       AA
                                GCTC ACAGCCCGAA  CC
                                |||| ||||||||||  ||
                                CGGG TGTCGGGCTT  GG
                                  C        CG
GAM298  YWHAH    3'  GCTCAAAGCAACCATC      18195      C  CCGAA
                                GCTCAA AGC    AACCATC
                                |||||| |||    |||||||
                                CGAGTT TCG    TTGGTAG
                                  _  _____
GAM299  APOB     3'  TGAATTTTTTCTGTGCTATG  7543         _  C  _
                                TGAATTTTT CTG GC ATG
                                ||||||||| ||| || |||
                                ACTTAAAAA GAC CG TAC
                                     A  A  A
GAM299  ZNF83    5'  TCCGGGTTTGCGCGCATGTGCG 32894     AATT  C      C
                                TCTG   TTT TGCGCATG GCG
                                ||||   ||| |||||||| |||
                                AGGC   AAA GCGCGTAC CGC
                                  CC__  C      A
GAM300  ABH      3'  GTTCCAAGGCAACAGTG     40741      _   TCCTA
                                GTTCCA GGCA    AGTG
                                |||||| ||||    ||||
                                CAAGGT CCGT    TCAC
                                   T   TG___
GAM300  BCL2L2   3'  GCAAGTTCCAGGTCGTTTCATG 19742          CATCCTAA
                                GCAAGTTCCAGG      GTG
                                ||||||||||||      |||
                                CGTTCAAGGTCC      TAC
                                      AGCAAAG_
GAM300  GNB5     3'  GTTCCAGGCATCACAGTGC   32110          CTA
                                GTTCCAGGCATC  AGTGC
                                ||||||||||||  |||||
                                CAAGGTCCGTAG  TCACG
                                      TG_
GAM300  IER3     3'  GCAGTTCCAGGTGTCCT     19353     A      CA
                                GCA GTTCCAGG  TCCT
                                ||| ||||||||  ||||
                                CGT CAAGGTCC  AGGA
                                  _       AC
GAM300  LCP2     3'  AGTTCAGTCCTAAGTG      24519      C  GCA
                                AGTTC AG   TCCTAAGTG
                                ||||| ||   |||||||||
                                TCAAG TC   AGGATTCAC
                                  _ ____
GAM300  MYC      5'  AAGTTCCAGTGCAAAGTGC   14705        _  TCCT
                                AAGTTCCAG GCA   AAGTGC
                                ||||||||| |||   ||||||
```

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                                TTCAAGGTC CGT    TTCACG
                                    A  _____
GAM300  RPE      3'  GCAAGCTCTAGTCTGTGCTTAA 41640        C  GCATCC__
              GTG                    GCAAGTTC AG       TAAGTG
                                ||||||||  ||       ||||||
                                CGTTCGAG TC       ATTCAC
                                    A  AGACACGA
GAM301  CSNK2A2  3'  GAGTCTGTGGTCAGCTAGTT   12485     A   C    T
                                GAGT CTG GGTT AGCTAGTT
                                ||||  |||  ||||  ||||||||
                                CTCA GAC CCAG TCGATCAA
                                  _   A    _
GAM302  TGFA     3'  TCTGTGACTGGGCAGGTTG    17446        C__   AC
                                TCTGTGAC   GCG  GTTG
                                ||||||||   |||  ||||
                                AGACACTG   CGT  CAAC
                                    ACC   C_
GAM303  ATP5B    5'  ATTGGTGCACCAGAATCCAG   40646        T    C  ___
                                ATTGGTG CACCG GG   CAG
                                |||||||  |||||  ||   |||
                                TAACCAC GTGGT CT   GTC
                                   _    _  TAG
GAM303  CAPZA1   5'  TGGAATCACCGCGGCGGC    43723     T         A
                                TGG GTCACCGCGGC GC
                                |||  ||||||||||  ||
                                ACC TAGTGGCGCCG CG
                                  T         C
GAM303  FACL3    3'  TAATTGGTGCACTATTGC     20881         T   CGCG
                                TAATTGGTG CAC    GC
                                |||||||||  |||    ||
                                ATTAACCAC GTG    CG
                                    _   ATAA
GAM303  HTR2C    5'  AGCGGTCGCCGCGGCGGC     9277       _  A      A
                                GGTG TC CCGCGGC GC
                                ||||  ||  |||||||  ||
                                TCGC AG GGCGCCG CG
                                  C  C      C
GAM303  IL13RA1  3'  AGTTTCCACCGCGGTGGC     11440     G_        CA
                                GGT  TCACCGCGG  GC
                                |||  |||||||||  ||
                                TCA  GGTGGCGCC  CG
                                  AA        AC
GAM303  SCG3     3'  ATTGGTGCATTTTACAGAG    29879         CACC_   C
                                ATTGGTGT    GCGG AG
                                ||||||||    ||||  ||
                                TAACCACG    TGTC TC
                                    TAAAA   _
GAM303  SCG3     3'  ATTGGTGCGTTTTACAGAG    29880         CACC_   C
                                ATTGGTGT    GCGG AG
                                ||||||||    ||||  ||
```

```
                                TAACCACG    TGTC TC
                                    CAAAA   _
GAM303  SCG3    3'  ATTGGTGTGTTTTACAGAGC  29881       CACC_   C
                                ATTGGTGT    GCGG AGC
                                ||||||||    |||| |||
                                TAACCACA    TGTC TCG
                                    CAAAA   _
GAM303  SSX1    5'  TGGTTGCGATTGCGGCAGC   24835    _ CACC
                                TGGT GT   GCGGCAGC
                                |||| ||   ||||||||
                                ACCA CG   CGCCGTCG
                                  A  CTAA
GAM303  UTY     5'  TAATTGTGTCACGGGC     28316      G    C C
                                TAATTG TGTCAC G GGC
                                |||||| |||||| | |||
                                ATTAAC ACAGTG C CCG
                                  _    _ _
GAM304  CLCN4   5'  CCCGCGGCCGCCCACCTGG   12280      A  A
                                CTCGCG CC CCCACCTGG
                                |||||| || |||||||||
                                GGGCGC GG GGGTGGACC
                                   C  C
GAM305  DSC3    3'  TTTAAAAAGTCAAGGCCATC  35952       _ TG  GTTA
                                TTTAAAAA T  GG   GCCATC
                                |||||||| |  ||   ||||||
                                AAATTTTT A  TC   CGGTAG
                                    C GT  ____
GAM305  EGF     3'  TTTAAAAAATAAGGCCATC   12653       T   GTTA
                                TTTAAAAA TGGG   GCCATC
                                |||||||| ||||   ||||||
                                AAATTTTT ATTC   CGGTAG
                                    T   ____
GAM305  FCRH3   5'  TTTAGAAGTTGGGGCTCATC  38116    A  A      AGC
                                TTTA AA TTGGGGTT  CATC
                                |||| || ||||||||  ||||
                                AAAT TT AACCCCGA  GTAG
                                  C  C      ___
GAM305  GYG     3'  TTTAAGAACTGATACAGCCATC 19972     A    GGT
                                TTTAA AATTGG  TAGCCATC
                                ||||| ||||||  ||||||||
                                AAATT TTGACT  GTCGGTAG
                                   C     AT_
GAM305  IL6     3'  TTTAAAAATATGTATAAGTTAG 8279         TG____
            CCAT                TTTAAAAAT     GGGTTAGCCAT
                                |||||||||     ||||||||||
                                AAATTTTTA     TTCAATCGGTA
                                    TACATA
GAM305  LBR     3'  TTTAGAAGTTGAGGTTAAGCC  40433     A  A      _
                                TTTA AA TTGGGGTTA GCC
                                |||| || ||||||||| |||
```

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                                AAAT TT AACTCCAAT CGG
                                  C  C        T
GAM305  MLLT2    3'  TTTAAAAGCACTTTAGCCATC  25517        ATTGGGG
                                TTTAAAA      TTAGCCATC
                                |||||||      |||||||||
                                AAATTTT      AATCGGTAG
                                    CGTGA__
GAM305  RAB1A    3'  TCTGAAAATGAAGTTAGCTGTC 43190     A    T       CA
                                TTT AAAAT GGGGTTAGC  TC
                                ||| ||||| |||||||||  ||
                                AGA TTTTA CTTCAATCG  AG
                                  C    _       AC
GAM306  CALCR    3'  CTTCTTTTCGATCCCCCC    11945      CGCC
                                CTTCT   CGATCCCCCC
                                |||||   ||||||||||
                                GAAGA   GCTAGGGGGG
                                   AAA_
GAM306  DSCR1    3'  TTCTGCCACCCCGAT      20641     C   CGATCC
                                TTCT GCC     CCCCGAT
                                |||| |||     |||||||
                                AAGA CGG     GGGGCTA
                                  _   T_____
GAM306  RAF1     5'  CTTCTCGCCCGCTCCTCC    44333          A   C
                                CTTCTCGCCCG TCC CC
                                |||||||||||| ||| ||
                                GAAGAGCGGGC AGG GG
                                       G   A
GAM306  S100A5   5'  CTTCTGCCTTTATTTCCCTGAT 16443      C   CG_  CC   C
           CT                    CTTCT GCC   AT  CCC GATCT
                                |||||| |||   ||  ||| |||||
                                GAAGA CGG   TA  GGG CTAGA
                                  _  AAA  AA   A
GAM306  TCF19    5'  CTGCTTGCCTGCGCCCCGATCT 45556    T  C   CGATCC
                                CT CT GCC     CCCCGATCT
                                || || |||     |||||||||
                                GA GA CGG     GGGGCTAGA
                                 C  A   ACGC__
GAM307  CNTNAP2  3'  GTCATGGTTATGGAGGCTGC   30489     T     _____
                                GTC ATGGTT     GGCTGC
                                ||| ||||||     ||||||
                                CAG TACCAA     CCGACG
                                  _      TACCT
GAM307  COL17A1  3'  GCTAGGTTGGCTGTGCTG    39081   T   T       C
                                G CTA GGTTGGCTG GCTG
                                | ||| ||||||||| ||||
                                C GAT CCAACCGAC CGAC
                                 _   _        A
GAM307  ICA1     3'  GTCTTTGGTTGGCCAGAGC    22468      A        C_
                                GTCT TGGTTGGCTG  GC
                                |||| ||||||||||  ||
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```
                                CAGA ACCAACCGGT  CG
                                  A        CT
GAM307  MBP     3'  GTCCATGGTACTTGCTG     44891         TG   GC
                                GTCTATGGT  GCT  GCTG
                                |||||||||  |||  ||||
                                CAGGTACCA  TGA  CGAC
                                     __   A_
GAM307  NGFR    5'  CTGATGGGGCTGCGCTGC    14776    _    TT
                                CT ATGG  GGCTGCGCTGC
                                || ||||  ||||||||||
                                GA TACC  CCGACGCGACG
                                 C   __
GAM307  NR2E1   5'  GTCAGTCGCGCGCTGCGCTGC 17579     TAT    ___
                                GTC   GGTTG   GCTGCGCTGC
                                |||   |||||   ||||||||||
                                CAG   TCAGC   CGACGCGACG
                                  ___    GCG
GAM307  SPTB    3'  GCCTGTTTCCTCTGCGCTG   7379      ATGG  GG
                                GTCT    TT  CTGCGCTG
                                ||||    ||  ||||||||
                                CGGA    AG  GACGCGAC
                                  CAA_  GA
GAM307  ATSV    3'  TGGGGAGGGCCCTAAAACC   20230     C   CCTA   _
                                TGG GGA    GGCC TAAAACC
                                ||| |||    |||| |||||||
                                ACC CCT    CCGG ATTTTGG
                                  _  C___    G
GAM307  DTNB    3'  TGGGGGTTTTACACATAAAACC 37609     C  ACC  G  C
          C                      TGG GG   TA GC TAAAACCC
                                ||| ||   || || ||||||||
                                ACC CC   AT TG ATTTTGGG
                                  C  AAA  G  T
GAM307  FAH     3'  TGGCGGACCAGGCCTACAGCCC 6593          T      AAA
                                TGGCGGACC AGGCCTA   CCC
                                ||||||||| |||||||   |||
                                ACCGCCTGG TCCGGAT   GGG
                                     _      GTC
GAM307  LTA     3'  GGATCTAGGCCCCACC      8240      C       AAA
                                GGA CTAGGCCT   ACC
                                ||| ||||||||   |||
                                CCT GATCCGGG   TGG
                                  A       G__
GAM307  MLANA   3'  TAGCGGACCTACTAAAA     24300           GGC
                                TGGCGGACCTA   CTAAAA
                                ||||||||||   ||||||
                                ATCGCCTGGAT   GATTTT
                                          ___
GAM307  ST5     3'  GGACTAGGCCTAAGACCC    24046     C       A
                                GGAC TAGGCCTAA ACCC
                                |||| ||||||||| ||||
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```
                                CCTG ATCCGGATT TGGG
                                  _       C
GAM307  VANGL2   3'  TGGGGGTCTCTCCAAAACC   43465    C  AC  AGG  T
                                TGG GG  CT   CC AAAACC
                                ||| ||  ||   || ||||||
                                ACC CC  GA   GG TTTTGG
                                  _ CA  GA_  _
GAM308  CYP4F3   3'  TCTGTGGAGTTTGCAGGG    9456           GTTT G
                                TCTGTGGAGTTTG   C AGGG
                                ||||||||||||   | ||||
                                AGACACCTCAAAC   G TCCC
                                          _____ _
GAM308  DLG5     5'  TCTGGGAGGTTTTGGGGG    44468     T   __    TTTCGA
                                TCTG GGAG  TTTGG     GGG
                                |||| ||||  |||||     |||
                                AGAC CCTC  AAACC     CCC
                                  _   CA    _______
GAM308  MOV10L1  3'  TGGGGGTCACTCGAGGG    33297    AGTTT   __
                                TGG    GGTT  TCGAGGG
                                |||    ||||  |||||||
                                ACC    CCAG  AGCTCCC
                                  C____   TG
GAM308  SECTM1   3'  TCTGTGGGTTTGATGAGGG   16544       A      TTC
                                TCTGTGG GTTTGGT   GAGGG
                                ||||||| |||||||   |||||
                                AGACACC CAAACTA   CTCCC
                                        _     ____
GAM309  MAPK4    3'  TAAGGCGTGTGGTGTGAG    15665       AC   C   AC
                                TAAGGTGT  GTG GTGT  GAG
                                ||||||||  ||| ||||  |||
                                ATTCCGCA  CAC CACA  CTC
                                          __  _   __
GAM309  NPR1     5'  AGTGTGCGTGCGTGTTAGAGA  44575      A       AC
                                GGTGT CGTGCGTGT  GAGA
                                ||||| |||||||||  ||||
                                TCACA GCACGCACA  CTCT
                                   C        AT
GAM309  SH3GL1   3'  AAGGAGTGCGTGTGTGAG    16663     TGTAC      AC
                                AAGG    GTGCGTGT  GAG
                                ||||    ||||||||  |||
                                TTCC    CACGCACA  CTC
                                  T____       CA
GAM309  UBE2G2   3'  GGTGTGTGCGCGCCTGTGCGAG 42125      A__    G   A
                                GGTGT   CGTGC TGT CGAG
                                |||||   ||||| ||| ||||
                                CCACA   GCGCG ACA GCTC
                                   CAC    G   C
GAM310  FGF20    3'  TTGGTTTTTTTTCTCAATA   33387     G_       TT
                                TTGG  TTTTTTCTC  TA
                                ||||  |||||||||  ||
```

```
                                AACC  AAAAAAGAG  AT
                                  AA        TT
GAM310  GPC4     3'  TTGGGCTTTTTCTTTTAA    11089           C
                                TTGGGTTTTTTCT TTTAA
                                |||||||||||| |||||
                                AACCCGAAAAAGA AAATT

                                        _
GAM310  MTAP     3'  GGGTTTTTTTTTTCCCCCTTAA 14675        _____
             AAT                  GGGTTTT    TTCTCTTTAAAAT
                                |||||||    ||||||||||||
                                CCCAAAA    AGGGGGAATTTTA
                                   AAAAA
GAM310  PCDHA11  5'  TTGGGTTTCTTCCCCCAAATAT 36582             TA
                                TTGGGTTTTTTCTCTT  AAATAT
                                |||||||||||||||  ||||||
                                AACCCAAAGAAGGGGG  TTTATA

                                       __
GAM310  SIGLEC6  3'  GGTTTTCCTTAAAATA     40932      TTTC
                                GGTTT   TCTTTAAAATA
                                |||||   ||||||||||
                                CCAAA   AGGAATTTTAT

                                      _____
GAM311  ADCY8    5'  TCCCGGAGGGGGTGTGGG    10016    G    A   GT
                                TC CGGAG GGGG  TGGG
                                || ||||| ||||  ||||
                                AG GCCTC CCCC  ACCC
                                 G    _   AC
GAM311  AGL      5'  TCGGGGGGAGGGGACGGGG   8492     C  A     TT
                                TCG GG GAGGGGG  GGG
                                ||| || |||||||  |||
                                AGC CC CTCCCCT  CCC
                                  C  C      GC
GAM311  ATP2A3   3'  TCGTGGGGAGGGGGCAAGG   23199    C  A      T
                                TCG GG GAGGGGGT GGG
                                ||| || ||||||||| |||
                                AGC CC CTCCCCCG TCC
                                  A  C      T
GAM311  B4GALT6  5'  TCGGGGGAGGGGAGGCG    40854    C  A    GTT
                                TCG GG GAGGGG   GGGCG
                                ||| || ||||||   |||||
                                AGC CC CTCCCC   TCCGC
                                  _  C    ___
GAM311  BACE2    5'  TCGCGGGAGGGGAGAAGGCG  39996      A     TT
                                TCGCGG GAGGGGG  GGGCG
                                |||||| |||||||  |||||
                                AGCGCC CTCCCCT  TCCGC
                                   _      CT
GAM311  C5R1     3'  GGGGGAGGCTGGGTGAA    11921    AGA       C
                                GG   GGGGGTTGGG GAA
                                ||   |||||||||| |||
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                                CC   CCTCCGACCC CTT
                                 C__         A
GAM311  CDC25B   5'  GCGGGGAGGGCGGGGGGCGA  34851      A    _  TT
                                GCGG GAGGG GG  GGGCGA
                                |||| ||||| ||  ||||||
                                CGCC CTCCC CC  CCCGCT
                                  C    G  C_
GAM311  CDKN2B   3'  GGTGGAGTTGGGCGA       38549    AGAG
                                GG    GGGGTTGGGCGA
                                ||    ||||||||||||
                                CC    CCTCAACCCGCT
                                 A___
GAM311  DMPK     3'  TCGCGAGGGTCGGGGGGTGGGG  20623        AGA__     T
                                TCGCGG     GGGGGT GGG
                                ||||||     |||||| |||
                                AGCGCT     CCCCCA CCC
                                    CCCAG      C
GAM311  DYSF     5'  TCGCTGGAGAGGGCTGGCTGGG 18584      _       __
            CGA                    TCGC GGAGAGGG  GGTTGGGCGA
                                |||| ||||||||  ||||||||||
                                AGCG CCTCTCCC  CCGACCCGCT
                                  A       GA
GAM311  EGR3     5'  TCGTGGGGGGGGTGGGG     40559     C  AGA     T
                                TCG GG   GGGGGT GGG
                                ||| ||   |||||| |||
                                AGC CC   CCCCCA CCC
                                  A  C__      C
GAM311  EGR3     5'  TCGGGGGGAGGGGGGAGG    40558     C  A      TT
                                TCG GG GAGGGGG  GG
                                ||| || |||||||  ||
                                AGC CC CTCCCCC  CC
                                  C  C       CT
GAM311  EMS1     3'  TCCGGGGGGGGGGCTGGG     23427     G   AGA
                                TC CGG   GGGGGGTTGGG
                                || |||   ||||||||||
                                AG GCC   CCCCCGACCC
                                 _   CC_
GAM311  GNB1     3'  GCGGGGGGCGGGGCG       13206      AGAG    T
                                GCGG    GGGGT GGGCG
                                ||||    ||||| |||||
                                CGCC    CCCCG CCCGC
                                   _____     C
GAM311  GTF2IRD1 5'  CGCGGGGAGGGGGGCGCGGG   32254       A      _
                                CGCGG GAGGGGGT TGGG
                                ||||| |||||||| ||||
                                GCGCC CTCCCCCG GCCC
                                   C       C
GAM311  IREB2    5'  TCCGGGGAGGGGGGCCAGCG   42454    G   A       TG G
                                TC CGG GAGGGGGT  G CG
                                || ||| ||||||||  | ||
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                                AG GCC CTCCCCCG  C GC
                                 _  C       GT _
GAM311  LY95    5'  TCGTGGGAGGGGACACCTGGA  22102     C  A     ___
                                TCG GG GAGGGGG   TTGGG
                                ||| || |||||||   |||||
                                AGC CC CTCCCCT   GACCT
                                  A _      GTG
GAM311  MYO1D   5'  CGGGAGGGGCCGGGGCGA    43494     A     GTT
                                CGG GAGGGG   GGGCGA
                                ||| ||||||   ||||||
                                GCC CTCCCC   CCCGCT
                                  _     GGC
GAM311  NEURL   5'  TCGCGGGTGGGGGCGAGG    20103       AGA     T
                                TCGCGG   GGGGGT GGG
                                ||||||   |||||| |||
                                AGCGCC   CCCCCG TCC
                                    CA_     C
GAM311  OPHN1   3'  TCGGGGGAGGGGGGAGG     14972     C  A     TT
                                TCG GG GAGGGGG  GG
                                ||| || |||||||  ||
                                AGC CC CTCCCCC  CC
                                  _ C      CT
GAM311  PRKCM   5'  CGGGAGGGGAGGGCGA      15639     A      TT
                                CGG GAGGGGG  GGGCGA
                                ||| |||||||  ||||||
                                GCC CTCCCCT  CCCGCT
                                  _     __
GAM311  RAB3B   5'  CGCGGAGGGGGCCGGGGCG   16080       GA       _
                                CGCGGA  GGGGGTTGGG CG
                                ||||||  |||||||||| ||
                                GCGCCT  CCCCCGGCCC GC
                                   __        C
GAM311  RAD21   5'  TCGGGGGAGGGGGTGGGG    26529     C  A      T
                                TCG GG GAGGGGGT GGG
                                ||| || |||||||| |||
                                AGC CC CTCCCCCA CCC
                                  _ C       C
GAM311  SFN     3'  GCGGAGAGCAGGGGTGGGG   43968        __    T
                                GCGGAGAG  GGGGT GGG
                                ||||||||  ||||| |||
                                CGCCTCTC  CCCCA CCC
                                     GT    C
GAM311  SLC22A1LS 5'  TCGCAGAGAGTGGGGGTGGG  28258          _   T
                                TCGCGGAGAG GGGG TGGG
                                |||||||||| |||| ||||
                                AGCGTCTCTC CCCC ACCC
                                      A   C
GAM311  TEAD3   5'  TCGTGGGGAGGGGGCTGG    17380     C  A
                                TCG GG GAGGGGGTTGG
                                ||| || ||||||||||
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                                AGC CC CTCCCCCGACC
                                  A  C
GAM311  WT1     5'  TCGCGGCGAGGAGACGGCG   35968      A     TTG
                                TCGCGG GAGGGGG  GGCG
                                |||||| |||||||  ||||
                                AGCGCC CTCCTCT  CCGC
                                   G     G__
GAM312  CYP8B1  3'  TCTTGGGGCTGCAGAGGG   20510    C__  CGACC
                                TCT  GGC   GCAGAGGG
                                |||  |||   ||||||||
                                AGA  CCG   CGTCTCCC
                                  ACC  A____
GAM312  TERT    3'  CTCTCGGCCTGGCTGTGGG   17394       GACC  AGA
                                CTCTCGGCC   GC  GGG
                                |||||||||   ||  |||
                                GAGAGCCGG   CG  CCC
                                     AC__  ACA
GAM312  ZNF133  5'  ACTCTCGGCTGGGCGCAG   18319       CGAC
                                ACTCTCGGC   CGCAG
                                |||||||||   |||||
                                TGAGAGCCG   GCGTC
                                     ACCC
GAM313  BACH2   3'  AAGAAGAGGAGAGGTCACT   34767       AAAAAAA
                                AAGAAGAG     GTCATT
                                ||||||||     ||||||
                                TTCTTCTC     CAGTGA
                                     CTCTC__
GAM313  BTG2    3'  TAAAGAAGAGAAGAGAGACA  27620   C       AAAA  T
                                A AAGAAGAGAA   AG CA
                                | ||||||||||   || ||
                                A TTCTTCTCTT   TC GT
                                 T       CTC_  T
GAM313  C11orf8 3'  GAGAAAACAGAAGTCATT    11480       A__
                                GAGAAAA  AAGTCATT
                                |||||||  ||||||||
                                CTCTTTT  TTCAGTAA
                                    GTC
GAM313  DDB2    3'  CACTGAGAGGAGAAAAGTCATT 6459     A_  A    AAA
                                CAC  AGA GAGAAA  AGTCATT
                                |||  ||| ||||||  |||||||
                                GTG  TCT CTCTTT  TCAGTAA
                                  AC  C    ____
GAM313  ESR2    5'  CAAGAAGAGGCACAAAGGTCAT 11010       AAA_  A
           T                     CAAGAAGAG   AAA GTCATT
                                |||||||||   ||| ||||||
                                GTTCTTCTC   TTT CAGTAA
                                     CGTG  C
GAM313  EVI2B   3'  AAAGAAAAAAGAGTCATT    27091         _
                                AGAGAAAAAA AGTCATT
                                |||||||||| |||||||
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                                TTTCTTTTTT TCAGTAA
                                      C
GAM313  GARP    3' AGAGAGACTGAAAGTCAT   24303    A   AAA
                                AGA GAGA  AAAGTCAT
                                ||| ||||  ||||||||
                                TCT CTCT  TTTCAGTA
                                  _   GAC
GAM313  HRH2    5' TGAAGAAGAGAGAAAAGC   35292   C       AA
                                A AAGAAGAGA  AAAAGT
                                | |||||||||  ||||||
                                A TTCTTCTCT  TTTTCG
                                 C       C_
GAM313  IGF2R   3' ACAATGCGAGAAAAGTCATT  9332     GAA     AAA
                                ACAA  GAGAAA  AGTCATT
                                ||||  ||||||  |||||||
                                TGTT  CTCTTT  TCAGTAA
                                  ACG    ___
GAM313  ISL1    3' AGAGAGAGAAAACAGTCATT  13593    _      AA
                                AGA AGAGAAAA  AGTCATT
                                ||| ||||||||  |||||||
                                TCT TCTCTTTT  TCAGTAA
                                  C       G_
GAM313  MEN1    3' AAAGGAAAAGAAGTCATT    39138     A    A
                                GAAG GAAAA AAGTCATT
                                |||| ||||| ||||||||
                                TTTC CTTTT TTCAGTAA
                                  _    C
GAM313  MPDZ    3' CAAGAAGAAAAGAAAAAT    19255          A
                                CAAGAAGAGAA AAAAGT
                                |||||||||| ||||||
                                GTTCTTCTTTT TTTTTA
                                       C
GAM313  NUP50   3' CAAAGAAGAGAAGAAAAA   28405   C       _
                                A AAGAAGAGAA AAAAA
                                | |||||||||| |||||
                                G TTCTTCTCTT TTTTT
                                 T        C
GAM313  PAG     3' GAGAGATCGCTCAAAGTCATT 32954    A   AAA___
                                GA GAGA     AAAGTCATT
                                || ||||     |||||||||
                                CT CTCT     TTTCAGTAA
                                  _   AGCGAG
GAM313  PCDH11X 3' CAAGAAGAGGGTGCCCAGTCAT 37323         AAAAAA_
          T                     CAAGAAGAG      AGTCATT
                                |||||||||      |||||||
                                GTTCTTCTC      TCAGTAA
                                      CCACGGG
GAM313  PCDH11Y 3' CAAGAAGAGGGTGCCCAGTCAT 37335         AAAAAA_
          T                     CAAGAAGAG      AGTCATT
                                |||||||||      |||||||
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                                GTTCTTCTC      TCAGTAA
                                     CCACGGG
GAM313  PIP5K1B  5'  CAGGAAGAGAAAAGGCC    18665    A       AAA
                                CA GAAGAGAAAA   GTC
                                || ||||||||||   |||
                                GT CTTCTCTTTT   CGG
                                 C        C__
GAM313  SET      3'  CACAAGAGGGAAAAAAAA    16560       A_
                                CACAAGA  GAGAAAAAA
                                |||||||  |||||||||
                                GTGTTCT  CTTTTTTTT
                                    CC
GAM313  SH3BP2   3'  CACAGGAAGAGAAGAAGCAT   16624     A      AAA   T
                                CACA GAAGAGAA   AAG CAT
                                |||| ||||||||   ||| |||
                                GTGT CTTCTCTT   TTC GTA
                                  C       C__   _
GAM313  SLC20A1  5'  AGAAGAGAAAGGACGCAAGT   40448         AA____
                                AGAAGAGAAA     AAGT
                                ||||||||||     ||||
                                TCTTCTCTTT     TTCA
                                     CCTGCG
GAM313  SOCS4    5'  TAAAGAAAACAAAAAAAAGTCA 38922    C      _
          TT                    A AAGAAGA GAAAAAAAGTCATT
                                | ||||||| ||||||||||||||
                                A TTCTTTT TTTTTTTTCAGTAA
                                 T      G
GAM313  SPAP1    3'  AGAAGAGAAGCCACT       39862         AAAAA
                                AGAAGAGA    AGTCATT
                                ||||||||    |||||||
                                TCTTCTCT    TCGGTGA
                                     _____
GAM313  SREBF1   3'  CACAGGAGGAAAAAAGCCACT  45369      AGAA   A
                                CACA    GAG AAAAAAGTCATT
                                ||||    ||| ||||||||||||
                                GTGT    CTC TTTTTTCGGTGA
                                  C___   C
GAM313  TM4SF4   3'  CAAGAAGAGAAGAAGT      21455          AAA
                                CAAGAAGAGAA   AAGT
                                ||||||||||   ||||
                                GTTCTTCTCTT   TTCA
                                     C__
GAM313  WNT5B    3'  AGAGGGAGAGAAAAAGCC    37211     A_   A
                                AGA  GAGA AAAAAGTC
                                |||  |||| ||||||||
                                TCT  CTCT TTTTTCGG
                                  CC    C
GAM314  CLASP1   3'  TAGCAGTTGCAGTGGGCT    42246    A     ATA
                                TA CAGTTG   GGTGGGCT
                                || ||||||   ||||||||
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                                AT GTCAAC   TCACCCGA
                                 C     G__
GAM314  EPHA8    3'  ACAGCCGGGGTGGGCT      33888        ATA
                                ACAGTTG   GGTGGGCT
                                |||||||   ||||||||
                                TGTCGGC   CCACCCGA
                                    C__
GAM314  FBLN1    3'  CAAACAGTTGAGCAACTGGGCT 27047   T       _  G
                                A AACAGTTGA TAG TGGGCT
                                | |||||||||| ||| ||||||
                                G TTGTCAACT GTT ACCCGA
                                 T       C  G
GAM314  GALC     3'  CATAACAGGTTGAAGTGG    6671         _   TA
                                CATAACAG TTGA  GGTGG
                                |||||||| ||||  |||||
                                GTATTGTC AACT  TCACC
                                     C   __
GAM314  MYO10    3'  AGCAAAGACAGGTGGGCT    29568     T__
                                AGT   GATAGGTGGGCT
                                |||   ||||||||||||
                                TCG   CTGTCCACCCGA
                                  TTT
GAM314  NGFR     3'  CAAAATGAGGGGGGTGGGCT   14774     T_  TA__
                                CAG  TGA    GGTGGGCT
                                |||  |||    ||||||||
                                GTT  ACT    CCACCCGA
                                  TT   CCCC
GAM314  TEM8     3'  CAAAACAGTTGTGATGGGCT   38174    T      ATA
                                CA AACAGTTG   GGTGGGCT
                                || ||||||||   ||||||||
                                GT TTGTCAAC   CTACCCGA
                                 T      A__
GAM314  TNFSF5   3'  CAGTTAACAGGGGGTGGGCT   6322         ___
                                CAGTTGATA   GGTGGGCT
                                |||||||||   ||||||||
                                GTCAATTGT   CCACCCGA
                                     CCC
GAM314  TSG      3'  ATAACAGTTGATCATAA     34000          AG
                                ATAACAGTTGAT  GTGG
                                ||||||||||||  ||||
                                TATTGTCAACTA  TATT
                                      G_
GAM315  MGAM     3'  TGTTTGCCTTTTCTTTGCT   43659       ACAATGTAC
                                TGTTTG       TCTTTGCT
                                ||||||       ||||||||
                                ACAAAC       AGAAACGA
                                   GGAAA____
GAM315  RP42     3'  TGTTTGAAAATCTTTGCT    33996        C  TGTAC
                                TGTTTGA AA    TCTTTGCT
                                ||||||| ||    ||||||||
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                                ACAAACT TT    AGAAACGA
                                   T _____
GAM316  NID     3'  GGAGGCCGGAGGTGAGGGACTG 14797    C    C____
              T                   GG GGCCG    GAGGGACTGT
                                  || |||||    ||||||||||
                                  CC CCGGC    CTCCCTGACA
                                   T    CTCCA
GAM317  DSCR3   3'  TCTTGGCAAATAGCATT    25830    _  CGCTT
                                  TCT GGC    GTAGCATT
                                  ||| |||    ||||||||
                                  AGA CCG    TATCGTAA
                                    A  TT___
GAM317  E2F3    3'  TCAGGCACATAGCATT     12633    T  C  TT
                                  TC GGC GC  GTAGCATT
                                  || ||| ||  ||||||||
                                  AG CCG TG  TATCGTAA
                                   T  _  __
GAM317  EXTL3   5'  TCTGACTTGTGTAGCATT    11039      CGCT
                                  TCTGGC   TGTAGCATT
                                  ||||||   |||||||||
                                  AGACTG   ACATCGTAA
                                     AAC_
GAM317  FANCC   3'  TCTGACTGCAGCAT      43282      CGCT
                                  TCTGGC   TGTAGCAT
                                  ||||||   ||||||||
                                  AGACTG   ACGTCGTA
                                     ____
GAM317  FMR2    3'  TCTAGAGTGTAGCATT     12984     CCGCT
                                  TCTGG    TGTAGCATT
                                  |||||    |||||||||
                                  AGATC    ACATCGTAA
                                    TC___
GAM317  HADHSC  3'  TCTGACCAAAGAGCATT    23719       CTTGT
                                  TCTGGCCG    AGCATT
                                  ||||||||    ||||||
                                  AGACTGGT    TCGTAA
                                       TTC__
GAM317  NPTX2   3'  TCAGGCTGCGATAGCATT   45209    T  C  TT
                                  TC GGC GC  GTAGCATT
                                  || ||| ||  ||||||||
                                  AG CCG CG  TATCGTAA
                                   T  A  C_
GAM317  SCN7A   5'  CCTGGCCATGTTGGCATT   16481       CT  A_
                                  TCTGGCCG  TGT  GCATT
                                  ||||||||  |||  |||||
                                  GGACCGGT  ACA  CGTAA
                                       __  AC
GAM317  SUFU    3'  TCTGCTTGTCGCAGCATT    32097     G CGC
                                  TCTG C   TTGTAGCATT
                                  |||| |   ||||||||||
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                                AGAC G   AGCGTCGTAA
                                  _ AAC
GAM318  ABR     3'  GAAGTGGAGATTCCCAAACGG  9911        AACC    TC
                                GAAGTGGA   CTCAG  ACGG
                                ||||||||   |||||  ||||
                                CTTCACCT   GGGTT  TGCC
                                    CTAA   __
GAM318  CDH10   3'  GAAGTGGAGACAGCATGG   27487       AACCCT  T  C
                                GAAGTGGA    CAG CA GG
                                ||||||||    ||| || ||
                                CTTCACCT    GTC GT CC
                                    CT____  _  A
GAM318  DAG1    3'  GAAGACCCCTTGGTCGTGGG  20520     TGGAAA   CA   AC
                                GAAG    CCCT  GTC  GGG
                                ||||    ||||  |||  |||
                                CTTC    GGGA  CAG  CCC
                                  TG____   AC   CA
GAM318  DCTN1   3'  GTGAAGTCCTCAATCAAGGG  35702     AAC       C
                                GTGGA   CCTCAGTCA GGG
                                |||||   ||||||||| |||
                                CACTT   GGAGTTAGT CCC
                                  CA_       T
GAM318  DLG5    5'  GAGGTGAGGTCCTCATCACAGG 44458   A   AAAC    G
                                GA GTGG   CCTCA TCACGGG
                                || ||||   ||||| |||||||
                                CT CACT   GGAGT AGTGTCC
                                 C   CCA_   _
GAM318  GNL1    5'  GAAGGGAAACCCAAGCGG    45563     T      TC  TCA
                                GAAG GGAAACCC  AG   CGG
                                |||| ||||||||  ||   |||
                                CTTC CCTTTGGG  TC   GCC
                                  _      T_ ___
GAM318  LDLR    3'  GAAGTGGAAGCACTAGG     8025        AACCCTC  T  _
                                GAAGTGGA      AG CAC GGG
                                ||||||||      || ||| |||
                                CTTCACCT      TC GTG TCC
                                    ________  _   A
GAM318  RP1     3'  GAAGTGGAAAATTCTTAGAGG  26553        CC_  C  TCAC
                                GAAGTGGAAA   CT AG   GGG
                                ||||||||||   || ||   |||
                                CTTCACCTTT   GA TC   TCC
                                     TAA  A  _____
GAM318  KCNMB1  3'  TATGGCACTTTATATCCTA   19982      T       T
                                TATGGC ACTTTGTGT CCTA
                                |||||| ||||||||| ||||
                                ATACCG TGAAATATA GGAT
                                  _       _
GAM318  MNT     3'  TGGCTTCTATGCTCCT      33728      AC
                                TGGCT  TTTGTGTTCCT
                                |||||  ||||||||||
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                                ACCGA  AGATACGAGGA
                                   __
GAM318  PCDH15   3' GCTACTTTGTAGTTTTTAAAA 37506        _  CC
                                GCTACTTTGT GTT  TAAAA
                                |||||||||| |||  |||||
                                CGATGAAACA CAA  ATTTT
                                      T   AA
GAM318  PRKCM    3' TATGGCAGTTTACATTTCTAA 15646      TAC   TG  C
                                TATGGC   TTTG  TT CTAA
                                ||||||   ||||  || ||||
                                ATACCG   AAAT  AA GATT
                                   TC_   GT  A
GAM318  SCML1    3' TATGGCTATTCTCTTTCTG   27561       ____   G
                                TATGGCTA   CTTT TG
                                ||||||||   |||| ||
                                ATACCGAT   GAAA AC
                                     AAGA   G
GAM318  SPOCK    3' TGGTTCACCCTGTTCCTA    41744    C_    TG
                                TGG  TACTT  TGTTCCTA
                                |||  |||||  ||||||||
                                ACC  GTGGG  ACAAGGAT
                                  AA    __
GAM319  ACTN1    3' GGAATATAACTTTGTGCTTG  9935     CCAAC   CC
                                GGA    AAC  TGTGCTTG
                                |||    |||  ||||||||
                                CCT    TTG  ACACGAAC
                                  TATA_  AA
GAM319  GAC1     5' TAAGGGTCAGCAACCCTG    26795     AC  A
                                TGAGG  CA CAACCCTG
                                |||||  ||  ||||||||
                                ATTCC  GT GTTGGGAC
                                   CA  C
GAM319  LZTS1    3' TGGGGCCAGGCTCTGTGCTTG 34279    A  A   ACAACC
                                TG GG CCA     CTGTGCTTG
                                || || |||     |||||||||
                                AC CC GGT     GACACGAAC
                                 C  _   CCGA__
GAM319  PIK3CD   3' AGGACCAATGTGCT       22723        CAACCC
                                AGGACCAA     TGTGCT
                                ||||||||     ||||||
                                TCCTGGTT     ACACGA
                                   _______
GAM319  SUOX     5' TGAGGACCACAGCTCTGTGC  7840         A  ACC
                                TGAGGACCA CA   CTGTGC
                                ||||||||| ||   ||||||
                                ACTCCTGGT GT   GACACG
                                      _ CGA
GAM319  AKAP2    3' TTTGTCCTTTTGGATCCA    28504        CCA_   G
                                TTTGTCCT   GATC CA
                                ||||||||   |||| ||
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                                AAACAGGA   CTAG GT
                                    AAAC   _
GAM319  CD4     3'  TTTGTCCTCTGGTAACAGAT  8330        _______
                                TTTGTCCTC     CAGAT
                                |||||||||     |||||
                                AAACAGGAG     GTCTA
                                    ACCATT
GAM320  DPYSL3  3'  CCTAGTCAATGAGGTATATGCT 10764     AT    _ C_
          T                      CCTA  TCGAT AG  ATATGCTT
                                ||||  ||||| ||  ||||||||
                                GGAT  AGTTA TC  TATACGAA
                                  C_    C  CA
GAM320  FZD3    3'  ACCCTTGTTTAAATATGCT   32626      AA  CG TAGC
                                ACCCT  TT  A   ATATGCT
                                |||||  ||  |   |||||||
                                TGGGA  AA  T   TATACGA
                                   AC  AT _____
GAM320  RAI2    5'  CCTAATTCTCAGCTTATATG  34745       GA   __
                                CCTAATTC  TAGC  ATATG
                                ||||||||  ||||  |||||
                                GGATTAAG  GTCG  TATAC
                                    A_   AA
GAM321  GTF2H1  3'  GCAGCGCCATTGTCT      23689       TGCGA  C
                                GCAGCGT    CAT GTCT
                                |||||||    ||| ||||
                                CGTCGCG    GTA CAGA
                                    _____  A
GAM322  CD74    3'  TGGGTGTAGGGTTATC     20340    C   TTTCTGA
                                TGG GTGT     GGTTATC
                                ||| ||||     |||||||
                                ACC CACA     CCAATAG
                                  _   TC_____
GAM322  EDAR    3'  TGGGGTGTTTTCTAAATGTT  35313    C        _
                                TGG GTGTTTTCTGAG GTT
                                ||| |||||||||||| |||
                                ACC CACAAAAGATTT CAA
                                  C         A
GAM322  ETV5    3'  TGGTGGTTTTCTGCCCCTCCC 20857    CGT      AGGTTA
                                TGG   GTTTTCTG    TCCC
                                |||   ||||||||    ||||
                                ACC   CAAAAGAC    AGGG
                                  AC_      GGGG__
GAM322  FUT9    3'  GTGTTTTCTATATATCCC    42733        AGGT
                                GTGTTTTCTG   TATCCC
                                ||||||||||   ||||||
                                CACAAAAGAT   ATAGGG
                                    AT__
GAM322  HPSE    3'  TGGGTGTTTTCTAAAATTTATC 27421    C          _
          C                      TGG GTGTTTTCTGAGGTT ATCC
                                ||| |||||||||||||| ||||
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```
                                ACC CACAAAAGATTTTAA TAGG
                                  _          A
GAM322  P3      5' GTGCTGTTGGGTTGTCC    33384      TTC  A   A
                                GTGTT  TG GGTT TCC
                                |||||  || |||| |||
                                CACGA  AC CCAA AGG
                                   CA_ _   C
GAM322  DBN1    5' TCGGAGCCTCTGCAGCGTC   38942       TC __ _
                                TCGGAGC  CT  AG GTC
                                |||||||  ||  || |||
                                AGCCTCG  GA  TC CAG
                                    GA  CG  G
GAM322  IHPK3   5' TCAGAGCTTCCTCCAAGATC  38373       _  ___
                                TCGGAGCT CCT   AGGTC
                                |||||||| |||  |||||
                                AGTCTCGA GGA   TCTAG
                                     A   GGT
GAM322  L1CAM   3' GGAGCTCCTGAAAGCCGGCCA 35802        __    AGA
                                GGAGCTCCT  AGGTC  CCA
                                |||||||||  |||||  |||
                                CCTCGAGGA  TTCGG  GGT
                                     CT    CC_
GAM322  MECP2   3' TCGGAGCTTCGTGGGAACC   22612       CCTA  TCA
                                TCGGAGCT   GG   GACC
                                ||||||||   ||  ||||
                                AGCCTCGA   CC   TTGG
                                     AGCA  C__
GAM323  ALOX15  3' CCTCTAGAGTAAAATGTGTT  10075     ATGCGT
                                CCTT     TAAAATGTGTT
                                ||||     ||||||||||
                                GGAG     ATTTTACACAA
                                  ATCTC_
GAM323  CTLA4   5' CCTGAAGCTTTGAAATGTGTT 23328     TAT  G  A
                                CCT   GC TT AAATGTGTT
                                |||   || || |||||||||
                                GGA   CG AA TTTACACAA
                                  CTT  A  C
GAM323  FBXL2   3' CCTTTAGTAAAAATGTGTT   29120     A  C  T
                                CCTT TG GT AAAATGTGTT
                                |||| || || ||||||||||
                                GGAA AT CA TTTTACACAA
                                  _ _  T
GAM323  NEDD4L  3' ACCCTGTCTCAAATGTGT    31615     TATGC  A_
                                ACCCT    GTT  AAATGTGT
                                |||||    |||  ||||||||
                                TGGGA    CAG  TTTACACA
                                  ______  AG
GAM324  PA2G4   3' CGCCATGTTGGTTAGGC     43417    T      ATC
                                CG CCATGTTG   AGGT
                                || ||||||||   ||||
```

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                                GC GGTACAAC   TCCG
                                 _      CAA
GAM324  RASD1    3'  GTCCATGTTGACACC      32012          TCAGGT
                                GTCCATGTTGA     CATC
                                ||||||||||     ||||
                                CAGGTACAACT     GTGG
                                       _______
GAM324  EIF2C1   5'  TCTCGCTGCTCGGGATCCCGG  29185            __
                                TCTCGCTGCTCGGG  CTCGG
                                ||||||||||||||  |||||
                                AGAGCGACGAGCCC  GGGCC
                                          TA
GAM324  FLII     5'  TCTCGCTGCCGGGCCGCGC    12899         T    T  _
                                TCTCGCTGC CGGGC CG GT
                                |||||||| ||||| || ||
                                AGAGCGACG GCCCG GC CG
                                      _    _ G
GAM324  TBX6     5'  TCTCGCTGCTTAGGGCCCCCGG 38862          C_    __
             T                   TCTCGCTGCT  GGGCT  CGGT
                                ||||||||||  |||||  ||||
                                AGAGCGACGA  CCCGG  GCCA
                                      AT    GG
GAM325  CKTSF1B1 3'  TGCTGGGTGCACCTGGAT    30093     CTAACC  A
                                TGC     TG TACCTGGAT
                                |||     || |||||||||
                                ACG     AC GTGGACCTA
                                  ACCC__  _
GAM325  GOLGA4   5'  TAACTCAAGCTGGATCT     41057     CT  TAC
                                TAAC  GA   CTGGATCT
                                ||||  ||   ||||||||
                                ATTG  TT   GACCTAGA
                                  AG  C__
GAM325  RAI14    3'  TGCCGACAACTCTGGATCT    31807     TAACCT   _ _
                                TGCC     GATA C CTGGATCT
                                ||||     |||| | ||||||||
                                ACGG     CTGT G GACCTAGA
                                  _______   T A
GAM325  TRIM14   3'  CCTTGGCAACATCTGGATCTA  37699     AACCT   C
                                CCT    GATA CTGGATCTA
                                |||    |||| |||||||||
                                GGA    TTGT GACCTAGAT
                                  ACCG_   A
GAM325  BF       5'  AAGCTGGGCCTGGGGCAGGA   11809     G     C  TCA  T
                                AAG TGGGCC GG   GC GGA
                                ||| |||||| ||   || |||
                                TTC ACCCGG CC   CG CCT
                                  G     A  C__  T
GAM325  CISH     5'  GGAGTGGGGACTCGGCTGGACG 40359    A     CCCGG  A
                                A GGTGGG    TC GCTGGACG
                                | ||||||    || ||||||||
```

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                                C TCACCC    AG CGACCTGC
                                 C     CTG__ C
GAM325  COL6A2   3'  GGAGGGCCCAGCCCGGCTGGGC 38443    T       A_    A
              G                   GG GGGCCCGGTC  GCTGG CG
                                  || ||||||||||  ||||| ||
                                  CC CCCGGGTCGG  CGACC GC
                                   T        GC    C
GAM325  CTSD     3'  GGAGGGCCCGGGAGGAC     12531    T      TCAGCT
                                  GG GGGCCCGG     GGAC
                                  || ||||||||     ||||
                                  CC CCCGGGCC     CCTG
                                   T       CT____
GAM325  DGAT1    3'  AGGTGGGCTCTGGCAGCGGG   42071        CC_  T   T
                                  AGGTGGGC   GG CAGC GG
                                  ||||||||   || |||| ||
                                  TCCACCCG   CC GTCG CC
                                       AGA  _    C
GAM325  EPHA8    3'  GGTGGGCCTGGTGCTGG     33900        C   CA
                                  GGTGGGCC GGT  GCTGG
                                  |||||||| |||  |||||
                                  CCACCCGG CCA  CGACC
                                       A   __
GAM325  ESRRB    5'  AAGGTGGGCCTGGCCTAGACA  42626          C   CAG
                                  AAGGTGGGCC GGT   CTGGACG
                                  |||||||||| |||   |||||||
                                  TTCCACCCGG CCG   GATCTGT
                                       A   ___
GAM325  FAT2     3'  AGGTGGGCCCGTTCCTCTG    11070          G  AG
                                  AGGTGGGCCCG TC  CTG
                                  |||||||||| ||  |||
                                  TCCACCCGGGC AG  GAC
                                       A  GA
GAM325  FZD10    3'  GGTGGGCCCTGGGGA       28459          _  TCAGCT
                                  GGTGGGCCC GG     GGA
                                  ||||||||| ||     |||
                                  CCACCCGGG CC     CCT
                                       A  _______
GAM325  G6PC     3'  AAGGAGGGCCCGGTGCGG    6656      T       CA  T
                                  AAGG GGGCCCGGT  GC GG
                                  |||| |||||||||  || ||
                                  TTCC CCCGGGCCA  CG CC
                                    T        __  _
GAM325  LENG4    5'  AAGGTGGGTGGGCTGG      35875        CCC  TCA
                                  AAGGTGGG   GG   GCTGG
                                  ||||||||   ||   |||||
                                  TTCCACCC   CC   CGACC
                                       A__  ___
GAM325  OAS3     3'  AGGGGGCATTCTCAGCTGG   26178     T   CCGG
                                  AGG GGGC    TCAGCTGG
                                  ||| ||||    ||||||||
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                                TCC CCCG    AGTCGACC
                                  _    TAAG
GAM325  S100A10   5'  AGCTGGGCGAGCTGGAC     40386    G    CCGGTC
                                AG TGGGC     AGCTGGAC
                                || |||||     ||||||||
                                TC ACCCG     TCGACCTG
                                 G    C_____
GAM325  SLC7A8    3'  GGTGGGCAAGCTGGC       29295        CCGGTC     A
                                GGTGGGC     AGCTGG C
                                |||||||     |||||| |
                                CCACCCG     TCGACC G
                                    T_____      C
GAM325  WHN       3'  AAGGTGAGCCCGATGTGGGCG  18751             CAGC   A
                                AAGGTGGGCCCGGT    TGG CG
                                ||||||||||||||    ||| ||
                                TTCCACTCGGGCTA    ACC GC
                                        C___   C
GAM325  WHSC1L1   3'  AGGTGGGCCTCGTTAGACTG   35710          _ GTCA
                                AGGTGGGCC CG    GCTG
                                |||||||| ||    ||||
                                TCCACCCGG GC    TGAC
                                     A  AATC
GAM326  ACR       3'  TATGTTTATTTATTTATT    9920            T
                                TATGTTTATTT TTTATT
                                |||||||||| ||||||
                                ATACAAATAAA AAATAA
                                      T
GAM327  EHF       3'  CATGTGGTTATGCAGAGATTAT 29113          TATTTGTT
              A                  CATGTGGTT       ATTATA
                                 |||||||||       ||||||
                                 GTACACCAA       TAATAT
                                      TACGTCTC
GAM327  EMX2      3'  ATGCGGTTTGTTTTTGTT    44677          A__
                                ATGTGGTTT   TTTGTT
                                |||||||||   ||||||
                                TACGCCAAA   AAACAA
                                     CAA
GAM327  PTER      3'  TGTGGCCTTTGTTATTATAA   36218        TA
                                TGTGGTT  TTTGTTATTATAA
                                |||||||  ||||||||||||
                                ACACCGG  AAACAATAATATT
                                    __
GAM327  SHANK2    3'  CATGTGGTTTGCTTGTCA    29452          A
                                CATGTGGTTT TTTGTTA
                                |||||||||| |||||||
                                GTACACCAAA GAACAGT
                                      C
GAM327  SLC1A1    3'  CAGGTGGTTTAGATGCATTATA 20031    T       TT   T
              A                  CA GTGGTTTA  TGT ATTATAA
                                 || ||||||||  ||| |||||||
```

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                                GT CACCAAAT  ACG TAATATT
                                 C       CT  _
GAM327  ZNF36    3' ATGGGGTTCTCTTGTTAT    45288     T    A
                                ATG GGTTT TTTGTTAT
                                ||| ||||| ||||||||
                                TAC CCAAG GAACAATA
                                  C    A
GAM328  ATP7B    5' TCGGCGCGGCGCGGCTCGG   6279        GAC  A   TAG
                                TCGGCGC   GG CGCG   CGG
                                |||||||   || ||||   |||
                                AGCCGCG   CC GCGC   GCC
                                    ____ _    CGA
GAM328  CLTCL1   5' TCGGCGGCGGCGGCGGCAGCGG 41887       _ A   A  C
            C                    TCGGCG CG CGG CG GTAGCGGC
                                ||||||| || ||| || ||||||||
                                AGCCGC GC GCC GC CGTCGCCG
                                   C  C  _ _
GAM328  DDEF2    5' TCGGCGCGAGGGCGCTGGC   19328         C  A   GTA
                                TCGGCGCGA GG CGC   GC
                                ||||||||| || |||   ||
                                AGCCGCGCT CC GCG   CG
                                     C  _   AC_
GAM328  HDGF     5' CCGGCGCGGTGGGTGCGC    21059        AC  AC
                                TCGGCGCG  GG  GCGT
                                ||||||||  ||  ||||
                                GGCCGCGC  CC  CGCG
                                     CA  CA
GAM328  JUP      5' TCGGCGCGGTCGGGCGGCGGC  13783        A_  AC   TA
                                TCGGCGCG  CGG  GCG  GCGGC
                                ||||||||  |||  |||  |||||
                                AGCCGCGC  GCC  CGC  CGCCG
                                     CA  __  __
GAM328  MECP2    5' TCGGCGCGGCGGCGGCGG    22613        A  A  CGTA
                                TCGGCGCG CGG CG    GCGG
                                |||||||| ||| ||    ||||
                                AGCCGCGC GCC GC    CGCC
                                     C  _ _____
GAM328  RNTRE    5' CGGCGCGGCGGCGGCGG     31254        A  A  CGTA
                                CGGCGCG CGG CG    GCGG
                                ||||||| ||| ||    ||||
                                GCCGCGC GCC GC    CGCC
                                    C  _ ____
GAM329  ACK1     5' TCGGGCTGCTGCAGCAGCC   25119    A   A  __
                                TC GGCT GC  CGGCAGCC
                                || |||| ||  ||||||||
                                AG CCGA CG  GTCGTCGG
                                 C   _ AC
GAM329  ACP1     5' GCTCAGGCTCGCGGCTCC    28239    T      A  C   AG
                                G CTCAGGCT GC GGC  CC
                                | |||||||| || |||  ||
```

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                                C GAGTCCGA CG CCG  GG
                                _       G  _   A_
GAM329  ACTR1B   3'  AGCTCAGGGAGGCAGCCC    43342    T     CTAGCC
                                AG CTCAGG     GGCAGCCC
                                || ||||||     ||||||||
                                TC GAGTCC     CCGTCGGG
                                 _     CT_____
GAM329  ADAMTS13 3'  GTTCCGGGCGAGGCAGCCCC   40042    CT A   TAGCC
                                GT  C GGC     GGCAGCCCC
                                ||  | |||     |||||||||
                                CA  G CCG     CCGTCGGGG
                                 AG C   CT___
GAM329  AIRE     5'  GTCCCGGGACACTGGCAGCCCC 7541       A  CTA  C
                                GTCTC GG   GC GGCAGCCCC
                                ||||| ||   || |||||||||
                                CAGGG CC   TG CCGTCGGGG
                                   C  TG_  A
GAM329  ALPI     3'  AGTCCCAGGCTCAGCC      11574          AGCCGG   _
                                AGTCTCAGGCT     CAGC C
                                ||||||||||      |||| |
                                TCAGGGTCCGA     GTCG G
                                       _______   A
GAM329  AQP2     3'  AGGCTCAGGCTCCTCCGGCAGC 7931     T      AG_
          C                      AG CTCAGGCT   CCGGCAGCC
                                || ||||||||   |||||||||
                                TC GAGTCCGA   GGCCGTCGG
                                 C       GGA
GAM329  BMP8     5'  GCCTCAGGCGCGGTCC      11879         TA  C  CAG
                                GTCTCAGGC  GC GG   CC
                                |||||||||  || ||   ||
                                CGGAGTCCG  CG CC   GG
                                     __  _  A__
GAM329  CALR     3'  AATCTCAGGCCTGTGGC     41768          AGCC
                                AGTCTCAGGCT    GGC
                                ||||||||||    |||
                                TTAGAGTCCGG    CCG
                                      ACA_
GAM329  CBFA2T2  3'  AGCTCAGGCTGGCTGCC     22965    T      AGCC   A
                                AG CTCAGGCT    GGC GCC
                                || ||||||||    ||| |||
                                TC GAGTCCGA    CCG CGG
                                 _       _____   A
GAM329  CD97     3'  AGCCTCAGGCAGTGGCCCC    38521          T  CC   AG
                                AGTCTCAGGC AG  GGC  CCC
                                |||||||||| ||  |||  |||
                                TCGGAGTCCG TC  CCG  GGG
                                      _ A_  ___
GAM329  ENAM     3'  AGTCTCAGAGCGGCAG      36672         GCT   C
                                AGTCTCAG   AGC GGCAG
                                ||||||||   ||| |||||
```

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                              TCAGAGTC  TCG CCGTC
                                   ___  _
GAM329  FASN    3'  AGTCTCCAAGTCGGCAGC   19928      AGGCT  C
                              AGTCTC    AG CGGCAGC
                              ||||||    || |||||||
                              TCAGAG    TC GCCGTCG
                                 GT___  A
GAM329  GAS7    3'  GCTCAGGCTTCCTGGCCC   25273  T     AG  GGCA
                              G CTCAGGCT  CC   GCCC
                              | ||||||||  ||   ||||
                              C GAGTCCGA  GG   CGGG
                               _      A_  AC__
GAM329  HARS    3'  ATCTCAGGCTGGGTCC     13337        AGCC  CAG
                              GTCTCAGGCT   GG  CC
                              ||||||||||   ||  ||
                              TAGAGTCCGA   CC  GG
                                   ____  CA_
GAM329  HD      3'  GCCTCAGGCTCAGCC      13352        AGCCGG
                              GTCTCAGGCT    CAGCC
                              ||||||||||    |||||
                              CGGAGTCCGA    GTCGG
                                   _______
GAM329  HIP12   5'  AGCCTCACGGTCCGGCAGCCCC 42390       _ CTAG
                              AGTCTCA GG   CCGGCAGCCCC
                              ||||||| ||   ||||||||||
                              TCGGAGT CC   GGCCGTCGGGG
                                 G  A___
GAM329  IL1RAPL2 5'  GTCTCAGATGCGTAGTTCC   32641       __ _  __
                              GTCTCAG  GC TAG  CC
                              |||||||  || |||  ||
                              CAGAGTC  CG ATC  GG
                                 TA  C   AA
GAM329  IL6R    5'  GCTCAGGCCCCGGGGGCAGCCC 8177   T     AGCC_
          C                    G CTCAGGCT    GGCAGCCCC
                              | ||||||||    |||||||||
                              C GAGTCCGG    CCGTCGGGG
                              _      GGCCC
GAM329  JRK     3'  AGCTCAAGCCTGGCAGCTCC  44495   T     AGCC    _
                              AG CTCAGGCT   GGCAGC CC
                              || ||||||||   |||||| ||
                              TC GAGTTCGG   CCGTCG GG
                               _      A___    A
GAM329  KRT13   3'  AGCCTTGGGTCCAGCAGCCCC  14008     CA  CTAG
                              AGTCT  GG   CCGGCAGCCCC
                              |||||  ||   ||||||||||
                              TCGGA  CC   GGTCGTCGGGG
                                A_  CA__
GAM329  LIF     3'  AGTCCCAGGCGTCTGCAGCC  14135        TAGCCG
                              AGTCTCAGGC    GCAGCC
                              ||||||||||    ||||||
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                                TCAGGGTCCG     CGTCGG
                                     CAGA__
GAM329  LRP8     5'  GCTCAGGCTGGGCGCGCGGCCC 37798   T      AGC  _  A
            C                    G CTCAGGCT   CG GC GCCCC
                                 | ||||||||   || || |||||
                                 C GAGTCCGA   GC CG CGGGG
                                 _      CCC  G  C
GAM329  LY64     3'  AGACTCCGGGGCCGGCAGTCCC 24566    T   A  CTA      _
                                 AG CTC GG   GCCGGCAG CCC
                                 || ||| ||   |||||||| |||
                                 TC GAG CC   CGGCCGTC GGG
                                  T   G  C__       A
GAM329  MECP2    3'  AGCCTCAGGCCCCACTGGCAGC 22571          A_  C
                                 AGTCTCAGGCT  GC GGCAGC
                                 ||||||||||  || ||||||
                                 TCGGAGTCCGG  TG CCGTCG
                                       GG  A
GAM329  MECP2    3'  TCCAGGCTGGAGCCAGCTCC   22611    T     __      AG
                                 TC CAGGCT  AGCCGGC  CC
                                 || ||||||  |||||||  ||
                                 AG GTCCGA  TCGGTCG  GG
                                  _     CC      A_
GAM329  MRPL49   3'  GTCTCAGGCCTTTGGCCCC   43027         AGCC   AG
                                 GTCTCAGGCT   GGC  CCC
                                 ||||||||||   |||  |||
                                 CAGAGTCCGG   CCG  GGG
                                       AAA_  __
GAM329  NFRKB    5'  GTCCAGGCGGGCAGTCCC    26099     T    TAGCC    _
                                 GTC CAGGC    GGCAG CCC
                                 ||| |||||    ||||| |||
                                 CAG GTCCG    CCGTC GGG
                                   _    C____    A
GAM329  NPAS1    3'  GTCCGGCGCCGGCAGC     40874      CA   TA
                                 GTCT  GGC  GCCGGCAGC
                                 ||||  |||  |||||||||
                                 CAGG  CCG  CGGCCGTCG
                                      __  __
GAM329  NR4A1    5'  AGTCTCAGCCTGGTCCCTGGTC 13414        G  AG_  GGCAG
            CC                     AGTCTCAG CT   CC    CCC
                                 |||||||| ||   ||    |||
                                 TCAGAGTC GA   GG    GGG
                                     G  CCA  GACCA
GAM329  OXTR     3'  AGCCTCAGGCTGCAGCCC    9519          AGCCG
                                 AGTCTCAGGCT    GCAGCCC
                                 ||||||||||    |||||||
                                 TCGGAGTCCGA    CGTCGGG
                                                _____
GAM329  PCDHGA1  3'  GTCTGGGGTTCTCTGGCAGCCC 36732      CA  CTAGCC
            C                    GTCT  GG     GGCAGCCCC
                                 ||||  ||     |||||||||
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                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA10 3' GTCTGGGGTTCTCTGGCAGCCC 36874    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA11 3' GTCTGGGGTTCTCTGGCAGCCC 36885    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA12 3' GTCTGGGGTTCTCTGGCAGCCC 36893    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA2  3' GTCTGGGGTTCTCTGGCAGCCC 36739    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA3  3' GTCTGGGGTTCTCTGGCAGCCC 33162    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA4  3' GTCTGGGGTTCTCTGGCAGCCC 36823    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA5  3' GTCTGGGGTTCTCTGGCAGCCC 36832    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA6  3' GTCTGGGGTTCTCTGGCAGCCC 36839    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA7  3' GTCTGGGGTTCTCTGGCAGCCC 33169    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA8  3' GTCTGGGGTTCTCTGGCAGCCC 36857    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
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                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGA9  3' GTCTGGGGTTCTCTGGCAGCCC 36865    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB1  3' GTCTGGGGTTCTCTGGCAGCCC 36901    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB2  3' GTCTGGGGTTCTCTGGCAGCCC 36910    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB3  3' GTCTGGGGTTCTCTGGCAGCCC 36919    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB4  3' GTCTGGGGTTCTCTGGCAGCCC 36928    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB5  3' GTCTGGGGTTCTCTGGCAGCCC 33174    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB6  3' GTCTGGGGTTCTCTGGCAGCCC 36943    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGB7  3' GTCTGGGGTTCTCTGGCAGCCC 36951    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGC3  3' GTCTGGGGTTCTCTGGCAGCCC 37051    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
                                CAGA CC    CCGTCGGGG
                                  CC AAGAGA
GAM329  PCDHGC4  3' GTCTGGGGTTCTCTGGCAGCCC 37073    CA CTAGCC
          C                      GTCT GG    GGCAGCCCC
                                 |||| ||    |||||||||
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                                CAGA  CC     CCGTCGGGG
                                  CC  AAGAGA
GAM329  PCDHGC5  3'  GTCTGGGGTTCTCTGGCAGCCC 37081      CA  CTAGCC
           C                     GTCT  GG     GGCAGCCCC
                                 ||||  ||     |||||||||
                                 CAGA  CC     CCGTCGGGG
                                   CC  AAGAGA
GAM329  PEX10    3'  GCTCGGGCGCCCCTGGCAGCCC 15221    T   A   TA  ___
           C                     G CTC GGC  GCC   GGCAGCCCC
                                 | ||| |||  |||   |||||||||
                                 C GAG CCG  CGG   CCGTCGGGG
                                  _  C  __  GGA
GAM329  PSEN2    5'  GTCTCAGGTTCCTTCAGCTCC  29812        CTAG  GG   _
                                 GTCTCAGG   CC  CAGC CC
                                 ||||||||   ||  |||| ||
                                 CAGAGTCC   GG  GTCG GG
                                      AA__  AA   A
GAM329  RAB3A    5'  GCTCAGGCCCCTGCAGTCC   16068   T      AG  G   _
                                 G CTCAGGCT  CC GCAG CC
                                 | ||||||||  || |||| ||
                                 C GAGTCCGG  GG CGTC GG
                                  _      __ A   A
GAM329  REV3L    5'  GTCCCAGGCTGCAGC       16268          AGCCG
                                 GTCTCAGGCT    GCAGC
                                 ||||||||||    |||||
                                 CAGGGTCCGA    CGTCG
                                               _____
GAM329  RNPEPL1  3'  AGTCCCAGGCTGGAGGCCC   32875          AGCC  CA
                                 AGTCTCAGGCT   GG  GCCC
                                 ||||||||||    ||  ||||
                                 TCAGGGTCCGA   CC  CGGG
                                       ____  TC
GAM329  SLC22A12 3'  ATCTCAGGCTGGCCCTGGACCC 40329          A  __  CA
           C                     GTCTCAGGCT GCC  GG  GCCCC
                                 ||||||||||| |||  ||  |||||
                                 TAGAGTCCGA CGG  CC  TGGGG
                                      C   GA  __
GAM329  SOX12    5'  GTCTCAGGCGGGCTCGGCGCGC 28055        TA  _   A_
           CCC                     GTCTCAGGC  GC CGGC  GCCCC
                                 |||||||||  || ||||  |||||
                                 CAGAGTCCG  CG GCCG  CGGGG
                                      CC  A   CG
GAM329  SUFU     3'  AGTCCCAGGCTGGCTGCAGCCC 32081          A  CG
           C                     AGTCTCAGGCT GC  GCAGCCCC
                                 |||||||||||  ||  ||||||||
                                 TCAGGGTCCGA CG  CGTCGGGG
                                       C  A_
GAM329  TIMP3    3'  AGTCTCAGTTACTAGTTCC   7442          __    __
                                 AGTCTCAG  GCTAG  CC
                                 ||||||||  |||||  ||
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                                TCAGAGTC  TGATC  GG
                                    AA    AA
GAM329  TNFAIP1  3'  GTCTCAGGCTGACGCATTCC  34481        AG CG  GC
                                GTCTCAGGCT  C  GCA  CC
                                ||||||||||  |  |||  ||
                                CAGAGTCCGA  G  CGT  GG
                                     CT __  AA
GAM329  TRPM1    5'  AGCTCAGGCTCTTTCAGCC   14538   T     AGCCGG
                                AG CTCAGGCT     CAGCC
                                || ||||||||     |||||
                                TC GAGTCCGA     GTCGG
                                 _      GAAA__
GAM329  WEE1     5'  AGTCTCAGGTTCGGGCTCC   18079       CTAGC  CA  _
                                AGTCTCAGG    CGG  GC CC
                                |||||||||    |||  || ||
                                TCAGAGTCC    GCC  CG GG
                                     AA___   __  A
GAM330  MASP1    3'  GATGAGCCGGTTGAGAAAG   40099       CCC__
                                GATGAGCCG    GAAGG
                                |||||||||    |||||
                                CTACTCGGC    CTTTC
                                     CAACT
GAM331  CLECSF5  3'  AGACTATCCAAAATTTTAAAAA 29924      CAGT
          TA                   AGATTA   AGATTTTAAAAATA
                               ||||||   ||||||||||||||
                               TCTGAT   TTTAAAATTTTTAT
                                  AGGT
GAM331  CUL3     3'  TTACAGTAGACAGGCAAA    18750         TTTA
                               TTACAGTAGAT   AAA
                               ||||||||||   |||
                               AATGTCATCTG   TTT
                                     TCCG
GAM331  IFNA10   3'  ATTACATAAATTTTAAAAATA  13479      G
                               ATTACA TAGATTTTAAAAATA
                               |||||| ||||||||||||||
                               TAATGT ATTTAAAATTTTTAT
                                  _
GAM331  IL13RA1  3'  AGGTCACAGTGAAGGTAAAAAT 11439   A     A  TTT
          A                    AG TTACAGT GA   TAAAAATA
                               || ||||||| ||   ||||||||
                               TC AGTGTCA CT   ATTTTTAT
                                C      _  TCC
GAM331  RUNX1    3'  GAATACAGTAGTTAAAAAT   12020   T     ATT
                               GA TACAGTAG   TTAAAAAT
                               || ||||||||   ||||||||
                               CT ATGTCATC   AATTTTTA
                                T      ____
GAM331  TEAD3    3'  ACAGCTGGATTTTAAAAAT   17368     A_
                               ACAGT  GATTTTAAAAAT
                               |||||  ||||||||||||
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                                TGTCG  CTAAAATTTTTA
                                  AC
GAM332  EFEMP1   3'  ATCTTTATTGACCTTTTCCATT 19951     CC_    AAGA
           T                     ATCT   TTGAT    TTTCCATTT
                                 ||||   |||||   |||||||||
                                 TAGA   AACTG    AAAGGTAAA
                                   AAT    GA__
GAM332  F8      3'  ATCTCCTGTTTTCCAT     6562         TGATAAGA
                                 ATCTCCT      TTTCCAT
                                 |||||||      |||||||
                                 TAGAGGA      AAAGGTA
                                    CA______
GAM332  GABRA5   3'  TCTCCTTGGTACCAT      41187        A  AGATTT
                                 TCTCCTTG TA     CCAT
                                 |||||||| ||     ||||
                                 AGAGGAAC AT     GGTA
                                     C  _______
GAM332  MN1     3'  TCTCCAGGATTTCCATT     14596      TTGATAA
                                 TCTCC      GATTTCCATT
                                 |||||      ||||||||||
                                 AGAGG      CTAAAGGTAA
                                   TC_____
GAM332  NEU3    3'  TCCCCTGGTTTCCAT      27409    T    ATAAGA
                                 TC CCTTG     TTTCCAT
                                 || |||||     |||||||
                                 AG GGGAC     AAAGGTA
                                  _    C_____
GAM332  RAD52    3'  ATCCTCTTGATAAGGTTC    39553     TC       A
                                 ATC  CTTGATAAG TTT
                                 |||  ||||||||| |||
                                 TAG  GAACTATTC AAG
                                   GA       C
GAM332  TCP10    3'  ATCTTCTGATAAGATTT     21425     CC
                                 ATCT  TTGATAAGATTT
                                 ||||  ||||||||||||
                                 TAGA  GACTATTCTAAA
                                   A_
GAM332  TEM5    3'  TCCCTCGGTTTCCATT     37245    T    ATAAGA
                                 TC CCTTG     TTTCCATT
                                 || |||||     ||||||||
                                 AG GGAGC     AAAGGTAA
                                  _    C_____
GAM333  PSG7    3'  CATGTTTTATTCTGCTAGAA   15806      ATT      C
                                 TATGT   TTTATTC GCTAGAA
                                 |||||   ||||||| |||||||
                                 GTACA   AAATAAG CGATCTT
                                    ___      A
GAM334  ABCD4    3'  CAAGCATATGGAGGCTCT    33742         T   A
                                 TAAGTGTAT GGA GCTCT
                                 ||||||||| ||| |||||
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                                GTTCGTATA CCT CGAGA
                                     _  C
GAM334  ADAM19   3'  AAGCCACAGGAAGCTCT    37759     G  T
                                AAGT TAT GGAAGCTCT
                                |||| ||| |||||||||
                                TTCG GTG CCTTCGAGA
                                  _  T
GAM334  ADAM19   3'  AAGCAATGGGAAGCTCT    37758     T  T
                                AAGTG AT GGAAGCTCT
                                ||||| || |||||||||
                                TTCGT TA CCTTCGAGA
                                   _ C
GAM334  CLASP1   5'  TAACTGTAGAAGCTCT     42244    G  ATT
                                TAA TGT  GGAAGCTCT
                                ||| |||  |||||||||
                                ATT ACA  TCTTCGAGA
                                  G  ___
GAM334  DHCR7    3'  CAAGTGCTGGGCTC       10683      AT  AA
                                TAAGTGT  TGG  GCTC
                                |||||||  |||  ||||
                                GTTCACG  ACC  CGAG
                                     __  __
GAM334  FBXL11   3'  AAGTGCAAAAAGCTCT     29421      TT
                                AAGTGTA  GGAAGCTCT
                                |||||||  |||||||||
                                TTCACGT  TTTTCGAGA
                                     __
GAM334  IL1RAP   3'  AGTGACCATGGAAGCTCT   13496     TAT_
                                AGTG   TGGAAGCTCT
                                ||||   ||||||||||
                                TCAC   ACCTTCGAGA
                                  TGGT
GAM334  IL1RN    3'  CAAGTGCCAGAAGCTCT    8212       AT
                                TAAGTGT  TGGAAGCTCT
                                |||||||  ||||||||||
                                GTTCACG  GTCTTCGAGA
                                     __
GAM334  ILK      3'  CAAGTGACAAAGCTCT     21123      TATTG
                                TAAGTG   GAAGCTCT
                                ||||||   ||||||||
                                GTTCAC   TTTCGAGA
                                   TG___
GAM334  IRAK4    3'  TAAGTGTATGTCCAAAGCT  41461       __ G
                                TAAGTGTA  TT GAAGCT
                                ||||||||  || ||||||
                                ATTCACAT  AG TTTCGA
                                     AC  G
GAM334  LCN1     3'  TAACTGCTGAAGCTCT     42022    G  ATTG
                                TAA TGT   GAAGCTCT
                                ||| |||   ||||||||
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                                ATT ACG    CTTCGAGA
                                  G   A___
GAM334   MAML1    3'  AAATATACAGTTGGAAGCTCT  31276        ___
                                AAGTGTAT   TGGAAGCTCT
                                ||||||||   ||||||||||
                                TTTATATG   ACCTTCGAGA
                                    TCA
GAM334   NDUFA7   3'  AAGTGATACCTGAGCTCT    22669      _  TG  A
                                AAGTG TAT  GA GCTCT
                                ||||| |||  || |||||
                                TTCAC ATG  CT CGAGA
                                   T   GA  _
GAM334   PRSS7    3'  TAAGTGTATGGTATATGCT   15756         T  AA___
                                TAAGTGTAT GG    GCT
                                ||||||||| ||    |||
                                ATTCACATA CC    CGA
                                     _  ATATA
GAM334   RAB27A   3'  TAAATGCTCATGAGCTCT    21363        A   GA
                                TAAGTGT TTG  AGCTCT
                                ||||||| |||  ||||||
                                ATTTACG AGT  TCGAGA
                                    _   AC
GAM334   TSN      3'  CAAGTGTATATGGCTGGTTCT  21491         _  AAGC_
                                TAAGTGTAT TGG    TCT
                                ||||||||| |||    |||
                                GTTCACATA ACC    AGA
                                     T   GACCA
GAM335   ABCB11   3'  TCAAAGTGTCACTTACTC    19046      ACA      T
                                TCAAA   TCACTTA CTC
                                |||||   ||||||| |||
                                AGTTT   AGTGAAT GAG
                                   CAC      _
GAM335   AMPH     3'  TCAAGTACAAGAGTCTCCACAG 11603     A_   TCACTTA
                                TCAA  ACA      TCTCCACAG
                                ||||  |||      |||||||||
                                AGTT  TGT      AGAGGTGTC
                                   CA   TCTC___
GAM335   BCL2L11  3'  TCAAGGATTCAGCCTCCACAG  39789     AACA   CTTA
                                TCAA    TCA    TCTCCACAG
                                ||||    |||    |||||||||
                                AGTT    AGT    GGAGGTGTC
                                   CCTA   C___
GAM335   BCLG     3'  CACCACTTATCTTTACAG    39828          CC
                                CATCACTTATCT  ACAG
                                ||||||||||||  ||||
                                GTGGTGAATAGA  TGTC
                                      AA
GAM335   ELF3     3'  CCAAAACATCAGCTTCTCTCCA 20751          _  A
              CAG                    TCAAAACATCA CTT TCTCCACAG
                                ||||||||||| ||| |||||||||
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                                GGTTTTGTAGT GAA AGAGGTGTC
                                      C   G
GAM335  NRXN1    3'  AAAACGTCACTTATCACAG   39835      A       TCC
                                AAAAC TCACTTATC   ACAG
                                ||||| |||||||||   ||||
                                TTTTG AGTGAATAG   TGTC
                                   C       ___
GAM335  RAB1A    3'  TCAAAACAATACTTATCACCAT 43188        TC      T __
            ACAG                    TCAAAACA  ACTTATC CC  ACAG
                                ||||||||  |||||||  ||  ||||
                                AGTTTTGT  TGAATAG GG  TGTC
                                     TA      T  TA
GAM335  TFDP1    3'  TCAAAACACACATCCACA    28287        T   TTATC
                                TCAAAACA CAC    TCCACA
                                |||||||| |||    ||||||
                                AGTTTTGT GTG    AGGTGT
                                     _   T_____
GAM335  TLR4     3'  TCAAACATCACTTGTTCT    17565      A      A_
                                TCAAA CATCACTT  TCT
                                ||||| ||||||||  |||
                                AGTTT GTAGTGAA  AGA
                                   _       CA
GAM335  UMPK     3'  TCAAAGGCATTTCATCTCCA   29777      A_   CAC
                                TCAAA  CAT   TTATCTCCA
                                |||||  |||   |||||||||
                                AGTTT  GTA   AGTAGAGGT
                                   CC   A__
GAM336  CBFA2T3  3'  TGTAGTTTTTTTGTTTTT    23274         GATG
                                TGTAGTTTTT    GTTTTT
                                ||||||||||    ||||||
                                ACATCAAAAA    CAAAAA
                                      AA__
GAM336  CENTD1   3'  TCCTGCAGTTTTGTGCTTTTT  40145          T A  G
                                TCCTGTAGTTTT G TG TTTTT
                                |||||||||||| | || |||||
                                AGGACGTCAAAA C AC AAAAA
                                      _ _  G
GAM336  NT5E     3'  CCTGTAAAGATGGTTTT     14859        TTTTT
                                CCTGTAG    GATGGTTTT
                                |||||||    |||||||||
                                GGACATT    CTACCAAAA
                                     T_____
GAM336  PCDH11X  3'  TGAGATTTTGATGGTTTTT   37312    T  T
                                TG AG TTTTGATGGTTTTT
                                || || ||||||||||||||
                                AC TC AAAACTACCAAAAA
                                 _ T
GAM336  PCDH11Y  3'  TGAGATTTTGATGGTTTTT   37353    T  T
                                TG AG TTTTGATGGTTTTT
                                || || ||||||||||||||
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                                AC TC AAAACTACCAAAAA
                                 _ T
GAM336  TRPC5    5'  ATCCTGAGCCAAGTGGTTTTT  29765       T    TTTGA
                                ATCCTG AGTT     TGGTTTTT
                                |||||| ||||     ||||||||
                                TAGGAC TCGG     ACCAAAAA
                                   _    TTC__
GAM336  CLECSF5  3'  ACAAGATCATCCTGGTTGCTGG 29923         AAA__   A
                                ACAAGATCA     GTT CTGG
                                |||||||||     ||| ||||
                                TGTTCTAGT     CAA GACC
                                     AGGAC   C
GAM336  PTMA     3'  TACACAAAAAAGTTACTGG    15875         TCAA
                                TACACAAGA    AAGTTACTGG
                                |||||||||    ||||||||||
                                ATGTGTTTT    TTCAATGACC
                                             _____
GAM337  ATP7A    3'  TGAGTTCAAAAGCATGAATATC 6267        A    A   A
           T                     TGAGTT AAAA TAT GAATATCT
                                |||||| |||| ||| ||||||||
                                ACTCAA TTTT GTA CTTATAGA
                                   G    C   _
GAM337  BCRP2    3'  TGAGTTAAATGAATATAG    41655         A_
                                TGAGTTAAA  AATATAG
                                |||||||||  |||||||
                                ACTCAATTT  TTATATC
                                     AC
GAM337  MEIS2    3'  TGAGGTAAACACATAGAATATC 33547      T    AA
           T                     TGAG TAAA  ATATAGAATATCT
                                |||| ||||  ||||||||||||||
                                ACTC ATTT  TGTATCTTATAGA
                                  C    G_
GAM338  DMRT1    5'  GAGGGATGAACCCGACGGAC   34982         _    TCCA
                                GAGGGATGG CTCG    AC
                                ||||||||| ||||    ||
                                CTCCCTACT GGGC    TG
                                     T    TGCC
GAM338  HEM1     5'  TGAGAGATGGTTCCA       23743          CTCG
                                TGAGGGATGG    TCCA
                                ||||||||||    ||||
                                ACTCTCTACC    AGGT
                                     A___
GAM338  KIR3DL2  3'  TGAGGGAAGGTGGAACAGCAA  27556        T  CTCGTC  A
                                TGAGGGA GG     CA CAA
                                ||||||| ||     || |||
                                ACTCCCT CC     GT GTT
                                   T  ACCTT_  C
GAM338  PPP2R2B  5'  TGGGGAGATGCCCAACA     21342    A    T  CTC
                                TG GGGA GG   GTCCAACA
                                || |||| ||   ||||||||
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                                AC CCCT CT   CGGGTTGT
                                 _   _ A__
GAM338  ZNF215   3'  GAGGGATATCTGACAAA     29917       GGCTC   CA
                                GAGGGAT    GTC  ACAAA
                                |||||||    |||  |||||
                                CTCCCTA    TAG  TGTTT
                                    _____  AC
GAM338  BRCA1    3'  TAATACCTGCCTCAGA      28641         CCTCT
                                TAATACCTGT    CTCAGA
                                ||||||||||    ||||||
                                ATTATGGACG    GAGTCT
                                      _____
GAM338  CBFA2T2  3'  CCTCATTCTCTCTCAGAT    22971     _  C
                                CCT GT CTCTCTCAGAT
                                ||| || ||||||||||
                                GGA TA GAGAGAGTCTA
                                  G  A
GAM338  CNTNAP2  3'  TAATACCTGTAAACCAG     30491         CCTCT T
                                TAATACCTGT    C CAG
                                ||||||||||    | |||
                                ATTATGGACA    G GTC
                                     TTT__ _
GAM338  LUZP1    3'  TAATATCTGCCCCCAGGCAGAT 37964       C       TCT
                                TAATA CTGTCCTC   CAGAT
                                ||||| ||||||||   |||||
                                ATTAT GACGGGGGG   GTCTA
                                   A       TCC
GAM338  ZNF10    3'  TAATAATTCCTTCTCAGAT    31741      CCTG    C
                                TAATA    TCCT TCTCAGAT
                                |||||    |||| ||||||||
                                ATTAT    AGGA AGAGTCTA
                                   TA__    _
GAM339  EGLN1    5'  TTTAAAACATTTTTCATACA   35183        TTT
                                TTTAAGAT   ATTTTTCATACA
                                ||||||||   ||||||||||||
                                AAATTTTG   TAAAAAGTATGT
                                      ___
GAM340  DNMT2    3'  GCTTATTTCACTTCGCATAAT  20628     CAGC    AA
                                GCT    TCGCT  TGCATAAT
                                |||    |||||  ||||||||
                                CGA    AGTGA  GCGTATTA
                                  ATAA    A_
GAM340  SLC12A6  3'  GCTCAGCTTGTTAATTCTAAT  23080        CGC    GCA
                                GCTCAGCT   TAAT   TAAT
                                ||||||||   ||||   ||||
                                CGAGTCGA   ATTA   ATTA
                                     ACA   AG_
GAM341  ADAM19   3'  ATGCACTTCCTTGCTC      37761       TATT
                                ATGTA    CTTCCTTGCTC
                                |||||    ||||||||||
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                                TACGT   GAAGGAACGAG
                                  ____
GAM341  ALDH8A1  3' CTATGTACTCTTCTTGTTCC  35452       AT   C  C
                                TTATGTAT  TCTTC TTG TCC
                                ||||||||  ||||| ||| |||
                                GATACATG  AGAAG AAC AGG
                                   __   _  A
GAM341  CDKN1B   3' TCATGTATATCTTCCTTGCT  19804        T
                                TTATGTATAT CTTCCTTGCT
                                |||||||||| ||||||||||
                                AGTACATATA GAAGGAACGA
                                   _
GAM341  DNMT3B   3' TTATCTAAGCTCCTTGCT   27884     G  TATTC
                                TTAT TA    TTCCTTGCT
                                |||| ||    |||||||||
                                AATA AT    GAGGAACGA
                                  G  TC___
GAM341  FZD10    3' TTATGTATTTCTCTTTTGCT  28464       A    CC
                                TTATGTAT TTCTT  TTGCT
                                |||||||| |||||  |||||
                                AATACATA AAGAG  AACGA
                                   _    AA
GAM341  HMG20A   3' ATGAGAATTCTTCCTTGCT   32864    TAT
                                ATG   ATTCTTCCTTGCT
                                |||   ||||||||||||
                                TAC   TAAGAAGGAACGA
                                  TCT
GAM341  MEF2C    5' TTATGTATTTTTTCCTTCCTT  14411       A___
                                TTATGTAT   TTCTTCCTT
                                ||||||||   |||||||||
                                AATACATA   AGGAAGGAA
                                   AAAA
GAM341  ADCY6    5' AGGAGGATGGCTTAAGGCTA  34163       A  C  CCT
                                GGGAGGAT GCT AA   GTTA
                                |||||||| ||| ||   ||||
                                TCCTCCTA CGA TT   CGAT
                                   C  A  C__
GAM341  CASP10   3' GGGAGGATCGCTTGAGCCCA  37389       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
                                CCCTCCTA CGA   GGGT
                                   G  ACTC
GAM341  CASP10   3' GGGAGGACAGCTTGAGCCTG  37388         CAA_
                                GGGAGGATAGCT   CCTG
                                ||||||||||||   ||||
                                CCCTCCTGTCGA   GGAC
                                      ACTC
GAM341  CST      5' GGGAGGATTGCTTGAGCCTG  22172       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
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                                CCCTCCTA CGA   GGAC
                                    A  ACTC
GAM341  CTF1    3'  GGAAGGATGGCTTGAGCCCA  10628       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
                                CCTTCCTA CGA   GGGT
                                    C  ACTC
GAM341  GRM6    3'  GGGAGGATTGCTTGAGCCCA  9172        A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
                                CCCTCCTA CGA   GGGT
                                    A  ACTC
GAM341  HUS1    3'  GGGAGGATGCCTTGAGCCAAG 45002       A  CAACCT
                                GGGAGGAT GCT    GTTAAG
                                |||||||| |||    ||||||
                                CCCTCCTA CGG    CGGTTC
                                    _  AACT__
GAM341  IL1R1   3'  GGAAGGATGGTTCATGTGT   9362        AGC  ACC
                                GGGAGGAT  TCA  TGT
                                ||||||||  |||  |||
                                CCTTCCTA  AGT  ACA
                                    CCA  AC_
GAM341  KMO     3'  GGGAGGATTGCTTGAGCCCA  18955       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
                                CCCTCCTA CGA   GGGT
                                    A  ACTC
GAM341  LZTS1   3'  GGGAGGATGGCTGGTGGCCA  34273       A  CAACCT
                                GGGAGGAT GCT    GTTA
                                |||||||| |||    ||||
                                CCCTCCTA CGA    CGGT
                                    C  CCAC__
GAM341  NEU3    5'  GGGAGGATGCCTTGAGCCCA  27405       _______
                                GGGAGGAT    AGCTCA
                                ||||||||    ||||||
                                CCCTCCTA    TCGGGT
                                    CGGAAC
GAM341  PCDHB16 3'  GGGAGGATGGCTTGAGCCCA  34143       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
                                CCCTCCTA CGA   GGGT
                                    C  ACTC
GAM341  RGS9    5'  GGGAGGATCGCTTGAGCCCA  19264       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
                                CCCTCCTA CGA   GGGT
                                    G  ACTC
GAM341  RPP30   3'  GGGAGGATGGCTTGATCCTA  26937       A  CAA_
                                GGGAGGAT GCT   CCTG
                                |||||||| |||   ||||
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                                CCCTCCTA CGA    GGAT
                                     C   ACTA
GAM341  SHOX     3'  GGGAGGATTGCTTGAGCCCA  27823        A   CAA_
                                GGGAGGAT GCT    CCTG
                                |||||||| |||    ||||
                                CCCTCCTA CGA    GGGT
                                     A   ACTC
GAM341  WBSCR5   5'  GGGAGGATCGCTTGAGATCAAG 30503        A   CAACCT
                                GGGAGGAT GCT     GTTAAG
                                |||||||| |||     ||||||
                                CCCTCCTA CGA     TAGTTC
                                     G   ACTC__
GAM341  ZNF74    5'  GGGAGAATAGTTTGAACCCG   18301         CTC_
                                GGGAGGATAG    AACCTG
                                ||||||||||    ||||||
                                CCCTCTTATC    TTGGGC
                                      AAAC
GAM342  COL5A1   3'  TGGGTCGGGCGAGCTGGGGGGC 6422     A   A  AG  CACAGA_
           TGG                    TG GTCG GC  GC      CTGG
                                || |||| ||  ||      ||||
                                AC CAGC CG  CG      GACC
                                 C   C  CT  ACCCCCC
GAM342  FABP3    3'  TGAGTCGAGGGGGTAGCCGATTG 43431        CA__   ACA  C
           G                     TGAGTCGAG   GGCC   GA TGG
                                |||||||||   ||||  || |||
                                ACTCAGCTC   TCGG   CT ACC
                                     CCCA   ___  A
GAM342  HDAC4    3'  TGAGTCGAGTGGTTTACACAG  25785        CA  C___
                                TGAGTCGAG  GG   CACAG
                                |||||||||  ||   |||||
                                ACTCAGCTC  CC   GTGTC
                                     A_  AAAT
GAM342  LZTR1    3'  GAGCAGGGTTGCAGACTGG   27638       CCA_
                                GAGCAGG   CAGACTGG
                                |||||||   ||||||||
                                CTCGTCC   GTCTGACC
                                    CAAC
GAM342  GABRA6   3'  ACATGCTTACAGAAGCTGCGT  9046     TCA  C   TATTC
                                AC   CT ACA    GGCTGCGT
                                ||   || |||    ||||||||
                                TG   GA TGT    TCGACGCA
                                 TAC  A   CT___
GAM342  GABRB3   3'  TCACATATATATACAATTGCGT 34876        TCG_  ___
                                TCACATAT    GC   TGCGT
                                ||||||||    ||   |||||
                                AGTGTATA    TG   ACGCA
                                     TATA  TTA
GAM342  WBSCR1   3'  CACTCACAAGCTGG       36725        TATTC    C
                                CACTCACA    GGCTG G
                                ||||||||    ||||| |
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                                GTGAGTGT    TCGAC C
                                   _____    A
GAM343  BCL7A   3'  TGCCTGGCGTGGCCGT     34222    A  GACG  C   A
                                TG CC   TG GCG GGCCGT
                                || ||   || ||| ||||||
                                AC GG   AC CGC CCGGCA
                                 _ ____ _  A
GAM343  KIP2    3'  GACCACAGCGGGGCTGTGG   26888     G   TGC   A   C
                                GACC ACG   GCG GGC GTGG
                                |||| |||   ||| ||| ||||
                                CTGG TGT   CGC CCG CACC
                                  _  ___  C   A
GAM343  TNFRSF8 3'  TGCCTGGGTGAGGCCGTG    10325    A  GAC  GCGC
                                TG CC   GT   GAGGCCGTG
                                || ||   ||   |||||||||
                                AC GG   CA   CTCCGGCAC
                                 _ ACC  ____
GAM344  ACADM   5'  TGGCTCCCGTTCCGGCCA    6150        CCG   GGTT
                                TGGCTCCCG   CCGG   CTA
                                |||||||||   ||||   |||
                                ACCGAGGGC   GGCC   GGT
                                     AA_   ____
GAM344  C4orf1  5'  TGGCTTCGCCGCCACAAGCT   40494      CC      _
                                TGGCT  CGCCGCCG GGGTT
                                |||||  |||||||| |||||
                                ACCGA  GCGGCGGT TTCGA
                                   A_      G
GAM344  CDC2L2  5'  GCTCCCGCTGCTCCTTCT    37940       C  CGGGG
                                GCTCCCGC GC     TTCT
                                |||||||| ||    ||||
                                CGAGGGCG CG     AAGA
                                     A  AGG__
GAM344  FBN1    5'  GGCTCCCGCCGCCTCTTGC    42055          GGG_
                                GGCTCCCGCCGCC    GT
                                ||||||||||||    ||
                                CCGAGGGCGGCGG    CG
                                       AGAA
GAM344  HMGA2   5'  TGCCTCCCGCCGCCGCTA    18532    G        GGGTT
                                TG CTCCCGCCGCCG    CTA
                                || ||||||||||||    |||
                                AC GAGGGCGGCGGC    GAT
                                 G          _____
GAM344  NRG1    5'  TGGGTCCCGCCGCTGGCGGC   30351     C       C  _
                                TGG TCCCGCCGC GG GGT
                                ||| ||||||||| || |||
                                ACC AGGGCGGCG CC CCG
                                  C       A  G
GAM344  NRXN2   5'  GCTCCCGCCGCCGCATCCC    39831          GG
                                GCTCCCGCCGCCG  GTTCT
                                ||||||||||||  |||||
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                                CGAGGGCGGCGGC TAGGG
                                      G_
GAM344  ODC1     5' TGGCTCCCGCCCGCCGGAG  14924        _
                                TGGCTCCCGCC GCCGGGG
                                |||||||||| |||||||
                                ACCGAGGGCGG CGGCCTC
                                      G
GAM344  PIK3R2   3' TGGCTCCCGCCGCCGCAGC  22752           G
                                TGGCTCCCGCCGCCG GGT
                                |||||||||||||| |||
                                ACCGAGGGCGGCGGC TCG
                                      G
GAM344  PRSS11   3' TGGCTCCCGTGGGGCTTCT  15767        CCGCC    _
                                TGGCTCCCG    GGGGTT CT
                                |||||||||    |||||| ||
                                ACCGAGGGC    CCCCGA GA
                                     A____    A
GAM344  PSCD4    3' GCTCCCGGGGTTCT       30126       GCCGCC
                                GCTCCC     GGGGTTCT
                                ||||||     ||||||||
                                CGAGGG     CCCCAAGA
                                _______
GAM344  SEPN1    3' TGGCTCCCGCAGTCCT      42439         CGCCGG
                                TGGCTCCCGC     GGTTCT
                                ||||||||||     ||||||
                                ACCGAGGGCG     TCAGGA
                                _______
GAM344  SLC11A3  3' TGGCTTTTGGCTTCTAGGTTCT 31051      CCC_ CGCCG
           A                     TGGCT   GC    GGGTTCTA
                                |||||   ||    ||||||||
                                ACCGA   CG    TCCAAGAT
                                   AAAC  AAGA_
GAM345  AKT1     3' GGAAAGGTTAAGCGTCGAA   23139         A  AA
                                GGAAAGGTTAA CG  GGA
                                |||||||||| ||  |||
                                CCTTTCCAATT GC  CTT
                                      C  AG
GAM345  AR       5' GGAGAGGAGGAGGACAAA    6234     A  TTAAAC  A
                                GGA AGG     GA GGACAAA
                                ||| |||     || |||||||
                                CCT TCC     CT CCTGTTT
                                  C  TC____  _
GAM345  ATP6V1A1 3' GGAAAGGGTACACCTAGGACAA 11780       T  A  GA
           AG                     GGAAAGG TA AC  AGGACAAAG
                                ||||||| || ||  |||||||||
                                CCTTTCC AT TG  TCCTGTTTC
                                    C  G  GA
GAM345  CD44     3' GGAAAGGTTGGCGATCAGG   8300         AAA  __
                                GGAAAGGTT   CGA  AGG
                                |||||||||   |||  |||
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                                CCTTTCCAA  GCT  TCC
                                     CC_  AG
GAM345  CDK4    3'  GGAAAGGCTCCACGGGGCA  38141       AA  AA  A
                                GGAAAGGTT  ACG  GG CA
                                |||||||||  |||  || ||
                                CCTTTCCGA  TGC  CC GT
                                     GG  C_  _
GAM345  CSNK1E  5'  GGAAAAACGAAGGGCAAAG  12473   TT      A
                                GG  AAACGAAGG CAAAG
                                ||  ||||||||| |||||
                                CC  TTTGCTTCC GTTTC
                                 TT       C
GAM345  DRP2    3'  GGAAAGGTTGGGTGAAGG   12583       AAAC
                                GGAAAGGTT   GAAGG
                                |||||||||   |||||
                                CCTTTCCAA   CTTCC
                                     CCCA
GAM345  ELK1    3'  GGGAGGTTGGCAGACAAA   23412   AA   AAACGAA
                                GG  AGGTT     GGACAAA
                                ||  |||||     |||||||
                                CC  TCCAA     TCTGTTT
                                 C_   CCG____
GAM345  GJA5    3'  GGAAAGGTTGCAACATCACCAA 23583       A_  _____
           GG                     GGAAAGGTT  AACG    AAGG
                                |||||||||  ||||    ||||
                                CCTTTCCAA  TTGT    TTCC
                                     CG   AGTGG
GAM345  HD      3'  GGAAGCGGGGGAGGGACAAAG  13354     A_  TTAAAC  A
                                GGAA  GG     GA GGACAAAG
                                ||||  ||     || ||||||||
                                CCTT  CC     CT CCTGTTTC
                                  CG  CC____  C
GAM345  HFE     3'  GGAAAAGTTGAACGGGTCCA  40008       A   AA  A_
                                GGAAAGGTT AACG  GG  CA
                                |||||||||  ||||  ||  ||
                                CCTTTTCAA TTGC  CC  GT
                                     C   __  AG
GAM345  HOXC13  3'  GGAAAGGTGACTGGACA    40668       TAAAC  A_
                                GGAAAGGT   GA  GGACA
                                ||||||||   ||  |||||
                                CCTTTCCA   CT  CCTGT
                                     _____  GA
GAM345  IL1F8   5'  GGAGAGGTGAGAAAGACA   30894    A   TAAAC
                                GGA AGGT   GAAGGACA
                                |||  ||||   ||||||||
                                CCT TCCA   CTTTCTGT
                                  C   CT___
GAM345  KIR2DL4 3'  GGAAAGGTGGAACAGCAC   13960       TA  GA  G
                                GGAAAGGT  AAC  AG AC
                                ||||||||  |||  || ||
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                                CCTTTCCA  TTG  TC TG
                                    CC  __  G
GAM345  KIR2DL5  3'  GGAAAGGTGAAACAGCATGAGG 33922        T    A____
                                GGAAAGGT AAACG    AGG
                                |||||||| |||||    |||
                                CCTTTCCA TTTGT    TCC
                                    C    CGTAC
GAM345  MECP2    3'  GGAAAGGTTTGGGCGGGA    22595        AAA_  AA
                                GGAAAGGTT   CG  GGA
                                |||||||||   ||  |||
                                CCTTTCCAA   GC  CCT
                                     ACCC  __
GAM345  NOVA1    3'  GGAAAGTTCATGAGGACAAAG  27061       G   AAC  A
                                GGAAAG TTA   GA GGACAAAG
                                |||||| |||   || ||||||||
                                CCTTTC AGT   CT CCTGTTTC
                                   A   A__  _
GAM345  NT5C2    3'  GGAAAAGTTGGACCTTGGA    29232        AA  GAA
                                GGAAAGGTT  AC   GGA
                                |||||||||  ||   |||
                                CCTTTTCAA  TG   CCT
                                     CC  GAA
GAM345  PCSK2    3'  GGAGAGGCTGAAGACAAA    15129     A    AAAC    G
                                GGA AGGTT    GAAG ACAAA
                                ||| |||||    |||| |||||
                                CCT TCCGA    CTTC TGTTT
                                  C    _____   _
GAM345  PDGFRA   3'  GGAAAGTTAAATTAAGG     26287       G    CG
                                GGAAAG TTAAA  AAGG
                                |||||| |||||  ||||
                                CCTTTC AATTT  TTCC
                                   _    AA
GAM345  PLA2G2D  3'  GGAGGGGGTGAGGAAGGACAA  29634     AA_   TAAAC
                                GGA   GGT    GAAGGACAA
                                |||   |||    |||||||||
                                CCT   CCA    CTTCCTGTT
                                  CCC   CTC__
GAM345  RING1    3'  GGGGGTACTGGGGGACAAAG   16335    AAA   TAA  GAA_
                                GG   GGT   AC   GGACAAAG
                                ||   |||   ||   ||||||||
                                CC   CCA   TG   CCTGTTTC
                                 C__   ___  ACCC
GAM345  SCN4A    3'  GGAAAGGTGAGAAAGAGAC   7324         TAAAC   _
                                GGAAAGGT    GAAG GAC
                                ||||||||    |||| |||
                                CCTTTCCA    TTTC CTG
                                    CTC__    T
GAM345  SKI      3'  GGGAAGGTTGTGGACAAA    16734    A     AAACGAA
                                GG AAGGTT      GGACAAA
                                || ||||||      |||||||
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                                CC TTCCAA      CCTGTTT
                                 C     CA_____
GAM345  SOX12    3'  GGAGGGGTGTCAGAGGGACAAA 28044     AA   TAAAC  A
              G                   GGA  GGT    GA GGACAAAG
                                  |||  |||    || ||||||||
                                  CCT  CCA    CT CCTGTTTC
                                    CC   CAGT_  C
GAM345  TCF3     3'  GGCAAAGGAGTGAAGGACA    43323    _    TTAAAC
                                  GG AAAGG     GAAGGACA
                                  || |||||     ||||||||
                                  CC TTTCC     CTTCCTGT
                                   G    TCA___
GAM346  BSN      3'  CCCTATTGCTTCTAAGTCAACA 18398     AC_   C   __  G
              T                    CCC   TGCT CTA  TC AACAT
                                  |||   |||| |||  || |||||
                                  GGG   ACGA GAT  AG TTGTA
                                    ATA    A   TC  _
GAM346  DMD      3'  CTGCTCCTTCTTCATC      19683         A  GAA
                                  CTGCTCCT TC   CATC
                                  |||||||| ||   ||||
                                  GACGAGGA AG   GTAG
                                       _ AA_
GAM346  ID4      3'  TCCCACTGTTGCCTATTAA    11388         CT_    CG
                                  TCCCACTG   CCTAT  A
                                  ||||||||   |||||  |
                                  AGGGTGAC   GGATA  T
                                       AAC     AT
GAM346  P2RY6    3'  TCCCACTGCCTGGAGCATC    19992          CCTATC  A
                                  TCCCACTGCT     GA CATC
                                  ||||||||||     || ||||
                                  AGGGTGACGG     CT GTAG
                                        AC_____  C
GAM346  SLC22A2  5'  CCCCACTGTTCTCCGATATC   40521         __    __
                                  TCCCACTG  CTCC  TATC
                                  ||||||||  ||||  ||||
                                  GGGGTGAC  GAGG  ATAG
                                       AA    CT
GAM346  SMOH     3'  CACTGCTCCTATCCCACTCC   24808           GA  A
                                  CACTGCTCCTATC  AC TCC
                                  ||||||||||||  || |||
                                  GTGACGAGGATAG  TG AGG
                                         GG  _
GAM346  VDR      3'  TCCCACTGACTTTAACAT     7528          _  CCTATCG
                                  TCCCACTG CT      AACAT
                                  |||||||| ||      |||||
                                  AGGGTGAC GA      TTGTA
                                       T  AA_____
GAM347  BRS3     3'  CACACAGCTTAGAGTCGGATAC 11901      TG      A   A
                                  CACG  GCTTAGA TCG ATAC
                                  ||||  ||||||| ||| ||||
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                                GTGT  CGAATCT AGC TATG
                                  GT      C   C
GAM347  NR3C1    3'  GTGGCTTAGTAAATA      6754          AATC
                                GTGGCTTAG    GAATA
                                |||||||||    |||||
                                CACCGAATC    TTTAT
                                     A___
GAM348  KPNA1    3'  TAAGGATTAATGCAAATCTG   44318     A         AG
                                TGA GATTAATGCGG  GTCTG
                                ||| ||||||||||  |||||
                                ATT CTAATTACGTT  TAGAC
                                  C         __
GAM348  MASP1    3'  TGAAGATTGATGTTGGGC    40108        A   CGGA
                                TGAAGATT ATG    GGT
                                |||||||| |||    |||
                                ACTTCTAA TAC    CCG
                                     C   AAC_
GAM348  MGAM     3'  ATGAAGATTAATGTGGTC    43650           CGGA
                                ATGAAGATTAATG    GGTC
                                ||||||||||||    ||||
                                TACTTCTAATTAC    CCAG
                                       A___
GAM348  TAPBP    3'  ATGAGCATTGAGAGGAGGTCTG 17297      A ATTAATGC
                                ATGA G       GGAGGTCTG
                                |||| |       |||||||||
                                TACT C       CCTCCAGAC
                                  _ GTAACTCT
GAM348  ADCY2    3'  TTCAGGTTGGGGCCTGAGA   42149      A  A_   CCAA
                                TTCAG TT  GGCC    GAGG
                                ||||| ||  ||||    ||||
                                AAGTC AA  CCGG    CTCT
                                   C  CC    A___
GAM348  CNTNAP2  3'  TTCAGATTAAACTAAGAGG   30499          CCC
                                TTCAGATTAGGC   AAGAGG
                                ||||||||||||   ||||||
                                AAGTCTAATTTG   TTCTCC
                                       A__
GAM348  PXF      3'  TTCAGATCTGGGCTCTTCCA   16015        A_   C___
                                TTCAGATT  GGC    CCA
                                ||||||||  |||    |||
                                AAGTCTAG  CCG    GGT
                                     AC   AGAA
GAM348  TEM6     3'  TCCAGGGCTTCGAGAGGCAT   35560      ATTA   CCCA
                                TTCAG    GGC    AGAGGCAT
                                |||||    |||    ||||||||
                                AGGTC    CCG    TCTCCGTA
                                   _____   AAGC
GAM349  NBEA     3'  CCAGGTGCTGGGAAGTTAT    45432     A_   TAT
                                TCA  TGT   TGGGAAGTTAT
                                |||  |||   ||||||||||
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                                GGT  ACG   ACCCTTCAATA
                                  CC  ___
GAM350  KNSL1    5'  GGGGCTTGGCGCCGACAG    21180      A       TAT C   A
                                GGGG TTGGCGCT   G ACA G
                                |||| ||||||||   | ||| |
                                CCCC AACCGCGG   C TGT C
                                  G       ___ _   C
GAM350  KRTHA5   3'  GGGGATTGGGCTACAA      14025         C   TATGC
                                GGGGATTGG GCT    ACAA
                                ||||||||| |||    ||||
                                CCCCTAACC CGA    TGTT
                                      _  _____
GAM350  PLA2G2A  5'  GGGGTAGGTGAGGCACAAGG   7153       ATT  CGCTTAT
                                GGGG   GG     GCACAAGG
                                ||||   ||     ||||||||
                                CCCC   CC     CGTGTTCC
                                  AT_  ACTC___
GAM350  SLC1A2   5'  GGGGATGGCGCTTGGC      41601       T      AT
                                GGGGAT GGCGCTT  GC
                                |||||| |||||||  ||
                                CCCCTA CCGCGAA  CG
                                   _      C_
GAM350  SLC22A1  3'  GGGGTAGGCAAGTATGAG    16855      ATT   CT   CACA
                                GGGG   GGCG  TATG   AG
                                ||||   ||||  ||||   ||
                                CCCC   CCGT  ATAC   TC
                                  AT_   TC   _____
GAM351  GNRH1    5'  ACTAAAATAGTCTATACTTTT  9073         ACCA
                                ACTAAAATA    TTTATACTTTT
                                |||||||||    ||||||||||||
                                TGATTTTAT    AGATATGAAAA
                                     C___
GAM351  SRRM1    3'  TAAAATATTCATTTATACTTTT 25190        AC
                                TAAAATA  CATTTATACTTTT
                                |||||||  ||||||||||||
                                ATTTTAT  GTAAATATGAAAA
                                   AA
GAM351  INMT     3'  TAGATTTATTTCATTTATCTA  27681            CT
                                TAGATTTATTTTATT  TTTA
                                ||||||||||||||  ||||
                                ATCTAAATAAAGTAA  AGAT
                                        AT
GAM351  PTH      3'  GAATTTTATTCTTTTATAA   7223     TTT
                                GA   ATTTTATTCTTTTATAA
                                ||   ||||||||||||||||
                                CT   TAAAATAAGAAAATATT
                                  ___
GAM352  DAG1     3'  AATAAAAAAGTCCCCAAAGTCT 20515          T TT    A
              C                   GATAAAAAAGT T  CGAA TCTC
                                ||||||||||| |  |||| ||||
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```
                                TTATTTTTTCA G  GTTT AGAG
                                      _ GG   C
GAM352  CASP8   3'  TAACTTTAGCTCTTATAAAAAA 37877      CG     CG
                                TAACT  AGCTCT  ATAAAAAA
                                |||||  ||||||  ||||||||
                                ATTGA  TCGAGA  TATTTTTT
                                   AA     A_
GAM352  WIG1    3'  AACTTGAGCAAGATAAAAA   45383     C    TCTC
                                AACT GAGC   GATAAAAA
                                |||| ||||   ||||||||
                                TTGA CTCG   CTATTTTT
                                  A   TT__
GAM353  COL4A6  3'  AGCTTTCCGATCAAGAC    37972         AA  TC
                                AGCTTTTCGA  TC  GAT
                                ||||||||||  ||  |||
                                TCGAAAGGCT  AG  CTG
                                      __  TT
GAM353  FER     5'  AGCTCTTCGGGAGTCTAGA   23492        AAA_  C
                                AGCTTTTCG   TCT GA
                                |||||||||   ||| ||
                                TCGAGAAGC   AGA CT
                                     CCTC   T
GAM353  IGFBP3  3'  AAGGTTTTCCTATTCTCGATAA 8263     C    GAAA
          A                      AAG TTTTC   TCTCGATAAA
                                 ||| |||||   ||||||||||
                                 TTC AAAAG   AGAGCTATTT
                                   C    GATA
GAM354  CASP8   3'  TAACTTTAGCTCTTATAAAAAA 37878      CG     CG
          G                      TAACT  AGCTCT  ATAAAAAAG
                                 |||||  ||||||  |||||||||
                                 ATTGA  TCGAGA  TATTTTTTC
                                    AA     A_
GAM354  SUOX    5'  ACTTAAACAGGGATAAAAAAG  7837     CG   TCTC
                                ACT  AGC   GATAAAAAAG
                                |||  |||   ||||||||||
                                TGA  TTG   CTATTTTTTC
                                  AT   TCC_
GAM355  DMD     3'  AGCTTTTCCTCTTGAGCT    19677        GAAA   C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                     G___   A
GAM355  DMD     3'  AGCTTTTCCTCTTGAGCT    19677        GAAA   C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                     G___   A
GAM355  DMD     3'  AGCTTTTCCTCTTGAGCT    19677        GAAA   C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
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```
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19702      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19702      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
                                TCGAAAAG   AGA CTCGA
                                   G___   A
GAM355  DMD    3' AGCTTTTCCTCTTGAGCT   19677      GAAA  C
                                AGCTTTTC   TCT GAGCT
                                ||||||||   ||| |||||
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```
                                TCGAAAAG   AGA CTCGA
                                   G___  A
GAM355  FZD8    3' CTCCAAATCTCGGGTTCT   36611    G      AGC
                                TTC AAATCTCG  TCT
                                ||| ||||||||  |||
                                GAG TTTAGAGC  AGA
                                  G       CCA
GAM355  PROS1   5' AAGCTTTTCGGAGCT      44610         AAATCTC
                                AAGCTTTTCG     GAGCT
                                ||||||||||     |||||
                                TTCGAAAAGC     CTCGA
                                      _______
GAM355  PTPN2   3' TTTTCAAATTGAGCTCT    15916        ATCTC
                                TTTTCGAA   GAGCTCT
                                ||||||||   |||||||
                                AAAAGTTT   CTCGAGA
                                   AA___
GAM356  CASP8   3' TAACTTTAGCTCTTATAAAAAA 37883     CG    CG
          G                     TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  CASP8   3' TAACTTTAGCTCTTATAAAAAA 37878     CG    CG
          G                     TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  CASP8   3' TAACTTTAGCTCTTATAAAAAA 37878     CG    CG
          G                     TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  CASP8   3' TAACTTTAGCTCTTATAAAAAA 37878     CG    CG
          G                     TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  SUOX    5' ACTTAAACAGGGATAAAAAAG 7837     CG   TCTC
                                ACT  AGC   GATAAAAAAG
                                |||  |||   ||||||||||
                                TGA  TTG   CTATTTTTTC
                                  AT   TCC_
GAM356  CASP8   3' TAACTTTAGCTCTTATAAAAAA 37878     CG    CG
          G                     TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  CASP8   3' TAACTTTAGCTCTTATAAAAAA 37878     CG    CG
          G                     TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
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```
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 37878      CG     CG
            G                    TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  CASP8    3'  TAACTTTAGCTCTTATAAAAAA 37878      CG     CG
            G                    TAACT  AGCTCT  ATAAAAAAG
                                |||||  ||||||  |||||||||
                                ATTGA  TCGAGA  TATTTTTTC
                                  AA     A_
GAM356  SUOX     5'  ACTTAAACAGGGATAAAAAAG  7837     CG   TCTC
                                ACT  AGC    GATAAAAAAG
                                |||  |||    ||||||||||
                                TGA  TTG    CTATTTTTTC
                                  AT   TCC_
GAM357  DIO3     3'  GGAGATTGTTCATGTGGCTGAG 10693         GAACC
            G                    GGGGATTGT    GTGGCTGAGG
                                |||||||||    ||||||||||
                                CCTCTAACA    CACCGACTCC
                                     AGTA_
GAM357  GMDS     3'  GGGGATTGTAGCCGGA      11301          AA   TGGCT
                                GGGGATTGTG  CCG    GA
                                ||||||||||  |||    ||
                                CCCCTAACAT  GGC    CT
                                     C_  ______
GAM357  MBNL     3'  GGATGTCTTGTGGCTGAGG    34315      T  GAACC
                                GGAT GT    GTGGCTGAGG
                                ||||  ||    ||||||||||
                                CCTA CA    CACCGACTCC
                                  _  GAA__
GAM357  RARA     3'  GGGGGTGCTGGTGGCTGAG    9712       ATT   AACC
                                GGGG   GTG    GTGGCTGAG
                                ||||   |||    |||||||||
                                CCCC   CAC    CACCGACTC
                                  ___   GAC_
GAM357  AMFR     3'  TGGGACAGAAAGGGGTGAC    39937           AAAGCGT
                                TGGGACAGGAA      GTGAT
                                ||||||||||       |||||
                                ACCCTGTCTTT      CACTG
                                     CCC_____
GAM357  CHD4     3'  TGGGACAAGAGAAAGTGA     10461          A   GCGT
                                TGGGACAGGA AAA    GTGA
                                |||||||||| |||    ||||
                                ACCCTGTTCT TTT    CACT
                                     C  _____
GAM357  COL19A1  3'  TGAGGCAGGAAAAAGTAT    12385      A         CG
                                TGGG CAGGAAAAAG  T
                                |||| ||||||||||  |
```

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                                ACTC GTCCTTTTTC  A
                                  C        AT
GAM357  DCLRE1C  5'  TGGGACAGGAAGTAGGCGC   35418          AA  C
                                TGGGACAGGAA  AG GTGT
                                ||||||||||  || ||||
                                ACCCTGTCCTT  TC CGCG
                                      CA  _
GAM357  DGCR2    3'  TGGGATGGAAAAAATGGGT   23101      CA      CGT
                                TGGGA  GGAAAAAG   GT
                                |||||  ||||||||   ||
                                ACCCT  CCTTTTTT   CA
                                   A_       ACC
GAM357  DISC1    3'  TGGCACAGGAAAAAGAGACAT  33055     G         ___
                                TGG ACAGGAAAAAG   CGT
                                ||| ||||||||||   |||
                                ACC TGTCCTTTTTC   GTA
                                  G         TCT
GAM357  DLST     3'  GGGACAGGGAGAAGACTGGT   12574        AAA  _ GT
                                GGGACAGG   AAG C  GT
                                ||||||||   ||| |  ||
                                CCCTGTCC   TTC G  CA
                                     CTC   T AC
GAM357  EGR2     3'  GGGACAGGAAAGGGTGGTAGTG 7582           AAGC_ _
                                GGGACAGGAAA    GT GTG
                                ||||||||||    || |||
                                CCCTGTCCTTT    CA CAC
                                      CCCAC  T
GAM357  FACL4    5'  TGGGACGAGGAGGAGCGC    35688       _   AAA
                                TGGGAC AGGA   AGCGT
                                ||||||| ||||   |||||
                                ACCCTG TCCT   TCGCG
                                   C   CC_
GAM357  FACL6    3'  TGGGACAGGAAAAGGCTCAGT  31610          A  GT_
                                TGGGACAGGAAAA GC   GT
                                |||||||||||| ||   ||
                                ACCCTGTCCTTTT CG   CA
                                       C  AGT
GAM357  FCGR3A   3'  TGGGACAGAAAAAGTGT     8190           AGC
                                TGGGACAGGAAAA   GTGT
                                ||||||||||||   ||||
                                ACCCTGTCTTTTT   CACA
                                                ___
GAM357  GNAZ     3'  TGGGACAGGAAGGCCCAGATC  13188          AAA  G  T
                                TGGGACAGGAA   GC TG GATC
                                ||||||||||   || || ||||
                                ACCCTGTCCTT   CG GT CTAG
                                      C__  G  _
GAM357  HLA-A    3'  TGGAACAGGAAAGATGAT    44860          AAGCGT
                                TGGGACAGGAAA     GTGAT
                                ||||||||||||     |||||
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                                ACCTTGTCCTTT     TACTA
                                      C_____
GAM357  HLA-C    3'  TGGAACAGGAAAGATGAT    45135          AAGCGT
                                TGGGACAGGAAA     GTGAT
                                ||||||||||||     |||||
                                ACCTTGTCCTTT     TACTA
                                      C_____
GAM357  HLA-G    3'  TGGAACAGGAAAGGTGAT    13403          AAGCGT
                                TGGGACAGGAAA     GTGAT
                                ||||||||||||     |||||
                                ACCTTGTCCTTT     CACTA
                                      C_____
GAM357  MYLK     5'  TGGGACAGGAAAGGCGT     38168          AA
                                TGGGACAGGAAA  GCGT
                                ||||||||||||  ||||
                                ACCCTGTCCTTT  CGCA
                                      C_
GAM357  NGFR     3'  GGACAGGAAGTGTG        14780          AAAGC
                                GGACAGGAA    GTGTG
                                |||||||||    |||||
                                CCTGTCCTT    CACAC
                                      _____
GAM357  PRKCG    3'  TGGGACAGGGGGGTGGTGA   15630          AAAAAGC  _
                                TGGGACAGG      GTG TGA
                                |||||||||      ||| |||
                                ACCCTGTCC      CAC ACT
                                     CC_____   C
GAM357  RBP5     3'  GGACAGGAGAGAGCGGAGAT  36462          AAA   TGT
                                GGACAGGA   AGCG   GAT
                                ||||||||   ||||   |||
                                CCTGTCCT   TCGC   CTA
                                    CTC    CT_
GAM357  SELP     3'  TGGGACAGGAAGGGGTG     16552          AAAGC
                                TGGGACAGGAA    GTG
                                ||||||||||     |||
                                ACCCTGTCCTT    CAC
                                      CCC__
GAM357  SELPLG   3'  GGGACAGGAAAAAGGAGAGAAT 40675            CGTGT
          C                      GGGACAGGAAAAAG    GATC
                                 ||||||||||||||    ||||
                                 CCCTGTCCTTTTTC    TTAG
                                       CTCTC
GAM357  TAC3     3'  TGGGACAGGGAAAGAGGT    29921          _  A  C
                                TGGGACAGG AAA AG GT
                                ||||||||| ||| || ||
                                ACCCTGTCC TTT TC CA
                                     C   C  _
GAM357  TCF12    3'  TGGGACAGGGGCAGATG     17346          AAAAA  T
                                TGGGACAGG    GCG GTG
                                |||||||||    ||| |||
```

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                                ACCCTGTCC    CGT TAC
                                     C____   C
GAM357  TCF21    3'  TGGGACAGAGAGAGGAGCAT  17351       _ AAA_
                                TGGGACAG GA   AGCGT
                                |||||||| ||   |||||
                                ACCCTGTC CT   TCGTA
                                     T  CTCC
GAM357  TIMP3    3'  TGGGGCATGGAAGGGTAGTGT  7472     A _   AAAGC
                                TGGG CA GGAA    GTGT
                                |||| || ||||    ||||
                                ACCC GT CCTT    CACA
                                  C A   CCCAT
GAM357  TYRO3    3'  TGGGACAGAAGAGGCTGT    26655        AAAA  G
                                TGGGACAGGA   GC TGT
                                ||||||||||   || |||
                                ACCCTGTCTT   CG ACA
                                      CTC_ _
GAM358  NEUROD1  3'  TTTGCACTTTGCAGCAGTAGTA 14760     A  CTA_
                                TTTG CGC   CAGCAGTAGTA
                                |||| |||   ||||||||||
                                AAAC GTG   GTCGTCATCAT
                                  _  AAAC
GAM359  NCAM2    3'  TTAATGGTGAACCTATAACAGT 21227      TTTAAC    C
                                TTAATG     GCCTA AACAGT
                                ||||||     ||||| ||||||
                                AATTAC     TGGAT TTGTCA
                                   CACT__    A
GAM360  ARL4     3'  TCCCACAACTGTGTTCT     25068        A  GAC
                                TCCCGCGG TG   GTTCT
                                |||||||| ||   |||||
                                AGGGTGTT AC   CAAGA
                                     G  A__
GAM360  CDH11    3'  TCTCACGGACATCTTCT     38035    C      GACG
                                TC CGCGGATG    TTCT
                                || ||||||||    ||||
                                AG GTGCCTGT    AAGA
                                 A       AG__
GAM360  CHC1     3'  TCCCATGGACACCTGTTCT    10427      C    GAC
                                TCCCG GGATG   GTTCT
                                ||||| |||||   |||||
                                AGGGT CCTGT   CAAGA
                                   A    GGA
GAM360  DUSP4    5'  TCCCGCGGGAGAGCCTCT    38426        AT   CG
                                TCCCGCGG  GGA  TTCT
                                ||||||||  |||  ||||
                                AGGGCGCC  TCT  GAGA
                                     C_   CG
GAM360  MASP1    3'  TCCTGCGGGGTGGATTCT    12434     C   A_   CG
                                TCC GCGG  TGGA  TTCT
                                |||  ||||  ||||  ||||
```

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                                AGG CGCC  ACCT  AAGA
                                  A   CC   __
GAM360  NFATC1   3'  TCTCCATCAGCGACGTTCT   26081   _  _  ATG
                                TC CCG CGG   GACGTTCT
                                || ||| |||   ||||||||
                                AG GGT GTC   CTGCAAGA
                                 A  A  G__
GAM360  PDE4D    5'  TCCCGCAGATGTGCCATT    43899         GA_
                                TCCCGCGGATG   CGTT
                                ||||||||||   ||||
                                AGGGCGTCTAC   GTAA
                                      ACG
GAM360  PRKY     3'  CCTTAAAGTGGACGTTCT    15694    GC  _
                                CC  GGA TGGACGTTCT
                                ||  ||| ||||||||||
                                GG  TTT ACCTGCAAGA
                                 AA   C
GAM360  USP11    5'  CCCGCAGTGGACGTTCT     21630       A
                                CCCGCGG TGGACGTTCT
                                ||||||| ||||||||||
                                GGGCGTC ACCTGCAAGA
                                   _
GAM360  WNT11    3'  TCCCGCAGAACATTCT      21542        TGG
                                TCCCGCGGA   ACGTTCT
                                |||||||||   |||||||
                                AGGGCGTCT   TGTAAGA
                                    ___
GAM360  FE65L2   3'  GGTCTGGGGAGCAGCAAGAG   39322    GATCC   TGC TG
                                GGT    GGA   G  GCAAGAG
                                |||    |||   |  |||||||
                                CCA    CCT   C  CGTTCTC
                                  GACC_   ___ GT
GAM360  HOXD4    5'  GGTGGGCTGGGATGGTGGCAAG 31178     ATCC_    C
                                GGTG    GGATG GTGGCAAG
                                ||||    ||||| ||||||||
                                CCAC    CCTAC CACCGTTC
                                  CCGAC    _
GAM360  MAP3K7   5'  GGCGATCCGTGGCGGG      17272        GAT   T
                                GGTGATCCG   GCG GG
                                |||||||||   ||| ||
                                CCGCTAGGC   CGC CC
                                     AC_  _
GAM360  PODXL    3'  GGTGTCCTGGTGGCAAGA    23981     A  GGA  C
                                GGTG TCC   TG GTGGCAAGA
                                |||| |||   || |||||||||
                                CCAC AGG   AC CACCGTTCT
                                  _  ___ _
GAM360  PTMA     5'  GGTGATCCGATGCAGGG     15874        G    T
                                GGTGATCCG ATGCG GG
                                ||||||||| ||||| ||
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                                CCACTAGGC TACGT CC
                                    _    C
GAM360  TBX2    3'  GGTGGCCTGCGTGGCA     25630     AT CGGA
                                GGTG  C   TGCGTGGCA
                                ||||  |   |||||||||
                                CCAC  G   ACGCACCGT
                                  CG ____
GAM361  LAMC1   3'  AGCAGTATAATAATCCCTGTGT 14077       G       AA
                                AGCAGTA TAATAATTTT  TGT
                                ||||||| ||||||||||  |||
                                TCGTCAT ATTATTAGGG  ACA
                                    _       AC
GAM361  NOVA1   3'  AACAGTAGTTAATTTAGTGT   27057       AA    TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                    __     TC_
GAM361  TRIM    3'  TAGTAATGCATTTTAATG    32299       A_
                                TAGTAAT  ATTTTAATG
                                |||||||  |||||||||
                                ATCATTA  TAAAATTAC
                                   CG
GAM362  LAMC1   3'  AGCAGTATAATAATCCCTGTGT 14077       G       AA
                                AGCAGTA TAATAATTTT  TGT
                                ||||||| ||||||||||  |||
                                TCGTCAT ATTATTAGGG  ACA
                                    _       AC
GAM362  NOVA1   3'  AACAGTAGTTAATTTAGTGT   14816       AA    TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                    __     TC_
GAM362  NOVA1   3'  AACAGTAGTTAATTTAGTGT   27057       AA    TAA
                                AGCAGTAGT  TAATTT   TGT
                                |||||||||  ||||||   |||
                                TTGTCATCA  ATTAAA   ACA
                                    __     TC_
GAM362  TRIM    3'  TAGTAATGCATTTTAATG    32299       A_
                                TAGTAAT  ATTTTAATG
                                |||||||  |||||||||
                                ATCATTA  TAAAATTAC
                                   CG
GAM363  ADAMTS5 3'  TGCTTTCCAGTTGGGAAAAA  28187       C___
                                TGCTTTCCGG   GAAAAA
                                ||||||||||   ||||||
                                ACGAAAGGTC   CTTTTT
                                     AACC
GAM363  BMPR1A  3'  ATGCTTTCCGTGACAAAAA   20253        __
                                ATGCTTTCCG  GCGAAAA
                                ||||||||||  |||||||
```

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                                TACGAAAGGC  TGTTTTT
                                      AC
GAM363  FMN2     5'  AAATGCTTTCTGAAAA      44284          CGGC
                                AAATGCTTTC    GAAAA
                                ||||||||||    |||||
                                TTTACGAAAG    CTTTT
                                      A___
GAM363  MPP1     3'  AAAACGCTTTCTCCAAAA     14620           CGG
                                AAAATGCTTTC   CGAAA
                                ||||||||||||  |||||
                                TTTTGCGAAAG   GTTTT
                                      AG_
GAM363  PSEN1    3'  AATGCTTTCTTGAAAA      28735          CGGC
                                AATGCTTTC    GAAAA
                                |||||||||    |||||
                                TTACGAAAG    CTTTT
                                      AA__
GAM363  TCF20    3'  CTTTCCAGACTAAAAATA    42534         _ GA
                                CTTTCCGG C  AAAAATA
                                |||||||| |  |||||||
                                GAAAGGTC G  TTTTTAT
                                     T A_
GAM363  VHL      3'  AAAATGCTTCCTACAAAAA   8101          T  G
                                AAAATGCTT CC GCGAAAA
                                ||||||||| || |||||||
                                TTTTACGAA GG TGTTTTT
                                      _  A
GAM364  ADH1B    3'  CATCATCTAAATAATCAT    43740         TACT
                                TATCATCTA    ATAATCAT
                                |||||||||    ||||||||
                                GTAGTAGAT    TATTAGTA
                                      T___
GAM364  ID4      3'  CCCCGTTATAATCATCT     11376     ATAC
                                TCT    TATAATCATCT
                                |||    ||||||||||||
                                GGG    ATATTAGTAGA
                                  GCA_
GAM364  KCNJ15   3'  TCATTTGTACACAAATCATCT  13879     CTA   TAT
                                TCAT   TAC   AATCATCT
                                ||||   |||   ||||||||
                                AGTA   ATG   TTAGTAGA
                                   AAC   TGT
GAM364  OPCML    3'  ATCATCTATATTGAAATC    14947         CTAT
                                ATCATCTATA    AATC
                                ||||||||||    ||||
                                TAGTAGATAT    TTAG
                                      AACT
GAM364  P2RY1    3'  TATCATCTATGCTTATAAGACA 15011          A _    T_
             C                   TATCATCTAT CT ATAA  CAT
                                ||||||||||| || ||||  |||
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                                ATAGTAGATA GA TATT  GTG
                                      C  A    CT
GAM365  DIAPH2   3'  AAATCTAAATAAACGTA     28664            C
                                AAATCTGAATAAAC GTA
                                |||||||||||||| |||
                                TTTAGATTTATTTG CAT
                                                _
GAM365  SULT2A1  3'  TAAAATCTGTCACTGTAGCTA  43473         AATAA  C
                                TAAAATCTG    AC GTAGCTA
                                |||||||||    || |||||||
                                ATTTTAGAC    TG CATCGAT
                                     AG___  A
GAM365  TOX      3'  TAAAATCTGAATGGTCCA    31273           AAA
                                TAAAATCTGAAT   CCG
                                ||||||||||||   |||
                                ATTTTAGACTTA   GGT
                                       CCA
GAM366  BACE     3'  TAAGAAAAGAAGAATAC     29046      TTTTC
                                TAAG    AAGAAGAATAC
                                ||||    ||||||||||||
                                ATTC    TTCTTCTTATG
                                  TT___
GAM366  SRR      3'  TACAAGTTTTCAAGAACC     34968             AGAAT
                                TATAAGTTTTCAAGA    ACC
                                ||||||||||||||    |||
                                ATGTTCAAAAGTTCT    TGG
                                                _____
GAM366  ZNF36    3'  TATAAGTTTCTCAAGGGAA   45295         _     AA
                                TATAAGTT TTCAAG  GAA
                                |||||||| ||||||  |||
                                ATATTCAA GAGTTC  CTT
                                     A     C_
GAM366  CALD1    3'  TCACAGCATGGGTTTCTT    37628       C  TTATA
                                TCATA GT    GGTTTCTT
                                ||||| ||    ||||||||
                                AGTGT CG    CCAAAGAA
                                   _  TAC__
GAM366  NAT2     3'  GTTTAGGATTTTCTTCAA    6144        TAGG
                                GTTTA    TTTCTTCAA
                                |||||    |||||||||
                                CAAAT    AAAGAAGTT
                                   CCTA
GAM366  PHGDH    3'  TCACAGTGGGTGGGTTTCTTCA 42035       C  TTATA
                                TCATA GT    GGTTTCTTCA
                                ||||| ||    ||||||||||
                                AGTGT CA    CCAAAGAAGT
                                   _  CCCAC
GAM367  ATP8A2   3'  TAGGAAGCAAAGTGCACTAA   45266          A_   G
                                TAGGAAGCAGA  GTA TAG
                                ||||||||||  ||| |||
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                                ATCCTTCGTTT  CGT ATT
                                      CA   G
GAM367  BCL9    3'  GGAAGCAGAGGGTCACCAGCG  20243        AGTAG  G
                                GGAAGCAGA    TA CAGCG
                                |||||||||    || |||||
                                CCTTCGTCT    GT GTCGC
                                     CCCA_  G
GAM367  CCND1   3'  GGAAGTCAACGGTAGCAGCG  38211      _  AAGTA
                                GGAAG CAG    GTAGCAGCG
                                ||||| |||    |||||||||
                                CCTTC GTT    CATCGTCGC
                                  A   GC___
GAM367  CKB     3'  TAGGAAGCAGCAGGGC      12257        GAA   TA
                                TAGGAAGCA   GTAG  GC
                                |||||||||   ||||  ||
                                ATCCTTCGT   CGTC  CG
                                     ___    C_
GAM367  CRAT    3'  GGAAGCAGGGTACAG       19665        AAGTA   G
                                GGAAGCAG    GTA CAG
                                ||||||||    ||| |||
                                CCTTCGTC    CAT GTC
                                     C____  _
GAM367  EGFL4   3'  GGAAGCAGACGGTGACCTTGGC 41574         A_  AG AGCA
          G                      GGAAGCAGA  GT  T   GCG
                                |||||||||  ||  |   |||
                                CCTTCGTCT  CA  G   CGC
                                     GC  CT GAAC
GAM367  IBSP    5'  AGGAAGCAGGCTCAAGGCAG  41802        AAG   TA
                                AGGAAGCAG   TAG  GCAG
                                |||||||||   |||  ||||
                                TCCTTCGTC   GTT  CGTC
                                     CGA   C_
GAM367  MSI1    3'  GGGGGCAGGCAGTAGC      14649    AA   AA
                                GG  GCAG  GTAGTAGC
                                ||  ||||  ||||||||
                                CC  CGTC  CGTCATCG
                                 CC    __
GAM367  PKD1    3'  TAGGGGCAGGGTGGCGGC    7142      AA   AAGTA  A  A
                                TAGG  GCAG    GT GC GC
                                ||||  ||||    || || ||
                                ATCC  CGTC    CA CG CG
                                  C_   C____  C  C
GAM367  TCTA    3'  GGAGTAGCAGAACCCAGT    35282     __      G_
                                GGA  AGCAGAA  TAGT
                                |||  |||||||  ||||
                                CCT  TCGTCTT  GTCA
                                  CA      GG
GAM367  TIMM17B 3'  AGGAAGTAGCTCCCATGGTGGC 25178       C  AA___  A  A
          AG                      AGGAAG AG    GT GT GCAG
                                ||||||  ||    || || ||||
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                                TCCTTC TC     TA CA CGTC
                                   A  GAGGG  C  C
GAM367  UGDH     3'  GGAAGCAGAGCTTGCAG     17885         A  AGTA
                                GGAAGCAGA GT    GCAG
                                ||||||||| ||    ||||
                                CCTTCGTCT CG    CGTC
                                     _  AA__
GAM368  CAPON    5'  TACCCGCGGCGGACCCGC    41935    G    T TTCAA
                                TG CTGC G     CGGACCCGC
                                || |||| |     |||||||||
                                AT GGCG C     GCCTGGGCG
                                 G    C _____
GAM368  DAZL     5'  GGCTGCTGTGAGGTCCGC    42779         TCAAC  AC
                                GGCTGCTGT     GG  CCGC
                                |||||||||     ||  ||||
                                CCGACGACA     CC  GGCG
                                     CT___  A_
GAM368  FOXO1A   3'  TGGTGGCTGTTCAATGAA    12893     CT       C
                                TGG  GCTGTTCAA GGA
                                |||  ||||||||| |||
                                ACC  CGACAAGTT CTT
                                  AC        A
GAM368  G6PD     5'  TGGGCTGAGCGGACCCGC    7613      CT    TTCAA
                                TGG  GCTG     CGGACCCGC
                                |||  ||||     |||||||||
                                ACC  CGAC     GCCTGGGCG
                                  __    TC___
GAM368  OSBP     5'  TGGCTGCTGTTTCCG       14990           CAACGGAC
                                TGGCTGCTGTT       CCG
                                ||||||||||        |||
                                ACCGACGACAA       GGC
                                      A_______
GAM368  PIG3     5'  TGGTCTGCCGCGGACCCGC   22199     _     TTCAA
                                TGG CTGCTG     CGGACCCGC
                                ||| ||||||     |||||||||
                                ACC GACGGC     GCCTGGGCG
                                  A     _____
GAM368  PTEN     5'  TGGTTGCAGCGACTGGGCCTGC 7221      C   T  TCAAC  A  C
                                TGG TGC GT     GG CC GC
                                ||| ||| ||     || || ||
                                ACC ACG CG     CC GG CG
                                  A   T  CTGAC  _  A
GAM368  PTPN11   5'  GGCTCCGCGACGGACCCGC   15920      G    TCA
                                GGCT CTGT   ACGGACCCGC
                                |||| ||||   ||||||||||
                                CCGA GGCG   TGCCTGGGCG
                                  _    C__
GAM368  STAU     5'  TGGCTGCTGCTCCGGACTCG  32700           AA    C
                                TGGCTGCTGTTC  CGGAC CG
                                ||||||||||||  ||||| ||
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                                ACCGACGACGAG  GCCTG GC
                                      __     A
GAM368  STAU     5'  TGGCTGCTGCTCCGGACTCG   32700          AA    C
                                TGGCTGCTGTTC  CGGAC CG
                                ||||||||||||  |||||| ||
                                ACCGACGACGAG  GCCTG GC
                                      __     A
GAM368  AKAP1    3'  TGTAAGCTGTACAAGTAG    40228     TGC       C
                                TGT   CTGTACAAG AG
                                |||   ||||||||| ||
                                ACA   GACATGTTC TC
                                  TTC        A
GAM368  ATRX     5'  GACCTGTTGTCCACAAGCAG  39608     _    _ TGT
                                GAC TGTTG CC   ACAAGCAG
                                ||| ||||| ||   ||||||||
                                CTG ACAAC GG   TGTTCGTC
                                  G    A ___
GAM368  B3GALT2  5'  CGTTGTTGCCTGGCAG      19110    AC       TACAA
                                CG  TGTTGCCTG    GCAG
                                ||  |||||||||    ||||
                                GC  ACAACGGAC    CGTC
                                 A_       _____
GAM368  MYO1D    3'  ACCTCTGCCTGTGCAGGCAGC  43485     G       A  A
                                ACT TTGCCTGT CA GCAGC
                                ||| |||||||| || |||||
                                TGG GACGGACA GT CGTCG
                                  A       C  C
GAM368  RNTRE    5'  CCGACTGCTAGGCTGTGGGCAG 31252          C_    ACAA
            C                    CCGACTGTTG  CTGT    GCAGC
                                ||||||||||  ||||    |||||
                                GGCTGACGAT  GACA    CGTCG
                                      CC    CC__
GAM369  DPYD     3'  TTTTACTTAATAAAGTT     41297         T
                                TTTTACTT AATAAAGTT
                                |||||||| |||||||||
                                AAAATGAA TTATTTCAA
                                      _
GAM369  IGF1     3'  TTTTACTTTAAAAAAGCT    8365           T
                                TTTTACTTTAA AAAGTT
                                |||||||||||| ||||||
                                AAAATGAAATT TTTCGA
                                       T
GAM369  NPM1     3'  TTTTACTTTATTAAAATACTGA 14824          A     TA__
            GTTT                   TTTTACTTTA TAAAGT    AGTTT
                                |||||||||| ||||||    |||||
                                AAAATGAAAT ATTTTA    TCAAA
                                      A     TGAC
GAM369  XCL1     3'  TTTTACTTGAATAAAGTT    16494         T
                                TTTTACTT AATAAAGTT
                                |||||||| |||||||||
```

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                                AAAATGAA TTATTTCAA
                                    C
GAM370  AQP5     5'  GGGCCCGCCGCTCTCCGTC   11635      G      CT
                                GGGCC CGCCGCTC  CGTC
                                ||||| ||||||||  ||||
                                CCCGG GCGGCGAG  GCAG
                                  _       AG
GAM370  ARHGAP6  3'  GGGCCGCGTCCTCTTGCATAGC 30223        CCGC    GTCT___
          C                      GGGCCGCG   TCCTC      GCC
                                 ||||||||   |||||      |||
                                 CCCGGCGC   AGGAG      CGG
                                      _____   AACGTAT
GAM370  BCL10    5'  GGGCTGCGCCGCCCCGCC    19407     C      T  T
                                GGGC GCGCCGC CC CGTC
                                |||| ||||||| || ||||
                                CCCG CGCGGCG GG GCGG
                                  A      _ _
GAM370  CDH23    5'  GGGCCGCCTGCTCTGGCC    38076       GCC    CTC
                                GGGCCGC   GCTC   GTC
                                |||||||   ||||   |||
                                CCCGGCG   CGAG   CGG
                                    GA_   AC_
GAM370  CLDN14   5'  GGGTCACGCCGCTCCTCAGGTG 40323     C          TC
          CC                      GGG CGCGCCGCTCCTCG  TGCC
                                  ||| ||||||||||||||  ||||
                                  CCC GTGCGGCGAGGAGT  ACGG
                                    A           CC
GAM370  DXYS155E 3'  GGGCCGCGCTCTCCTTGGGGGC 22960        CG    CGTCT
                                GGGCCGCGC  CTCCT    GC
                                |||||||||  |||||    ||
                                CCCGGCGCG  GAGGA    CG
                                     A_    ACCCC
GAM370  ECGF1    5'  GGGCCGCACGTCGTCTGC    12640        CGCTCC
                                GGGCCGCGC     TCGTCTGC
                                |||||||||     ||||||||
                                CCCGGCGTG     AGCAGACG
                                     C_____
GAM370  EML1     5'  GGGCCGCGCCCGCTCCCCGGCC 40722          _      TCT
                                GGGCCGCGCC GCTCCTCG   GCC
                                |||||||||| ||||||||   |||
                                CCCGGCGCGG CGAGGGGC   CGG
                                      G      ___
GAM370  ESRRA    5'  GGGCCGCGCCGCCCCACCGCGC 20835            _   CT
          C                      GGGCCGCGCCGCTCC TCGT  GCC
                                 |||||||||||||| ||||  |||
                                 CCCGGCGCGGCGGGG GGCG  CGG
                                       T   __
GAM370  FXR2     5'  GGGCCGGGCCGCTCCCCGTC   22165       C
                                GGGCCG GCCGCTCCTCGTC
                                |||||| ||||||||||||
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                                CCCGGC CGGCGAGGGGCAG
                                   C
GAM370  GATM    5'  GGGCCGCGTCGCTCGTGC    11228       C    CTCGTC
                                GGGCCGCG CGCTC     TGC
                                |||||||| |||||     |||
                                CCCGGCGC GCGAG     ACG
                                     A    C_____
GAM370  HSPG2   5'  GGCCCGCGCCGCTCTCTCGC  24365    G        _
                                GG CCGCGCCGCTC CTCGT
                                || |||||||||| |||||
                                CC GGCGCGGCGAG GAGCG
                                 G         A
GAM370  KCNA6   5'  GGGCCGCGCTCTCCCGGT    13817        CG    C
                                GGGCCGCGC  CTCCT GT
                                |||||||||  ||||| ||
                                CCCGGCGCG  GAGGG CA
                                     A_    C
GAM370  KNS2    5'  GGGCCGCGCTCTCTCGCGCTG 24474        CG   C   _
                                GGGCCGCGC  CTC TCGT CTG
                                |||||||||  ||| |||| |||
                                CCCGGCGCG  GAG AGCG GAC
                                     A_  _    C
GAM370  LUZP1   5'  GGGTTCCGCCGCTCAGCTGCC 37963    CCG       CTC T
                                GGG   CGCCGCTC   G CTGCC
                                |||   ||||||||   | |||||
                                CCC   GCGGCGAG   C GACGG
                                  AAG       T__ _
GAM370  MID2    5'  GGGCGCTGGGCTCTCGTCTGCC 29221     C  GCC    C
                                GGGC GC   GCTC TCGTCTGCC
                                |||| ||   |||| |||||||||
                                CCCG CG   CGAG AGCAGACGG
                                  _  ACC    _
GAM370  MYO1D   3'  GGGCTGTTCCGCTCCTGCC   43502     CGCG       C
                                GGGC    CCGCTCCT GTC
                                ||||    |||||||| |||
                                CCCG    GGCGAGGA CGG
                                  ACAA       _
GAM370  NRXN2   5'  GGCCGCGCCGCTGCTGC     39832          CCTC T
                                GGCCGCGCCGCT    G CTGC
                                ||||||||||||    | ||||
                                CCGGCGCGGCGA    C GACG
                                                _____ _
GAM370  NT5M    5'  GGGCCGCGCCGTGCTG      33653          CTCCTC T
                                GGGCCGCGCCG     G CTG
                                ||||||||||||     | |||
                                CCCGGCGCGGC     C GAC
                                       A_____ _
GAM370  PITX1   3'  GGGCCGCGCCCCTTGCTCTGCC 15327          GCT   C _
                                GGGCCGCGCC   CCT G TCTGCC
                                ||||||||||   ||| | ||||||
```

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                                CCCGGCGCGG  GGA C AGACGG
                                      ___   A G
GAM370  RANBP9   5'  GGGCCGCGGCGCTGCTGC   24254       C   CCTC T
                                GGGCCGCG CGCT   G CTGC
                                |||||||| ||||   | ||||
                                CCCGGCGC GCGA   C GACG
                                     C   ____ _
GAM370  SGT      3'  GCGCCGTGGGCTCGTCTGCC  16615      CTC_
                                GCGCCG   CTCGTCTGCC
                                ||||||   ||||||||||
                                CGCGGC   GAGCAGACGG
                                   ACCC
GAM370  TFRC     5'  GGGCCGCGACCGCTTTCCCGC  17431       _   C_
                                GGGCCGCG CCGCT  CTCGT
                                |||||||| |||||  |||||
                                CCCGGCGC GGCGA  GGGCG
                                     T    AA
GAM370  WNT7A    5'  GGGCTGTGCTGATCCCGCGGGC 21529     CGC  CGC   T   CT
            C                    GGGC   GC   TCC CGT  GCC
                                ||||   ||   ||| |||  |||
                                CCCG   CG   AGG GCG  CGG
                                  ACA  ACT   _   CC
GAM371  ARHGAP6  3'  TCCTATGTAAAAATATGGCTTC 30228     TTACCGCTC
            T                    TCCT       ATATGGCTTCT
                                ||||       ||||||||||
                                AGGA       TATACCGAAGA
                                  TACATTTT_
GAM371  CDC2L2   5'  CTTTTAACTGTGCTGGCTTCT  37938     ACC   CATA
                                CTTT   GCT   TGGCTTCT
                                ||||   |||   ||||||||
                                GAAA   TGA   ACCGAAGA
                                  AT_   CACG
GAM371  COL19A1  3'  TCCTTTGTTTTGATGGTGGCTT 12382      ACCGCTCATA
            CT                   TCCTTT        TGGCTTCT
                                ||||||        ||||||||
                                AGGAAA        ACCGAAGA
                                   CAAAACTACC
GAM371  LFG      3'  TCCTTTACAGCTTGTGACACCT 44148       C   CATA   T
                                TCCTTTAC GCT   TGGC TCT
                                |||||||| |||   |||| |||
                                AGGAAATG CGA   ACTG GGA
                                     T   AC__   T
GAM371  MAPK10   5'  CCACAGCTTGTATGGTTTCT  39978     C   CA   C
                                TTAC GCT  TATGG TTCT
                                |||| |||  ||||| ||||
                                GGTG CGA  ATACC AAGA
                                  T   AC    A
GAM371  PDGFRB   5'  TCCTTGCTGCTGATGGCTTCT  42342     TACC   CAT
                                TCCTT   GCT   ATGGCTTCT
                                |||||   |||   |||||||||
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                                AGGAA   CGA   TACCGAAGA
                                  CGA_  C__
GAM371  GCS1    3'  GAGCCAGAGTGGCATGA    26699    A      CCTA
                                GA CCAGAGTG   TATGA
                                || ||||||||   |||||
                                CT GGTCTCAC   GTACT
                                 C      C___
GAM371  PBP     3'  ACCAGAGTGACATACTGA    15017        _ C  A
                                ACCAGAGTG C TAT TGA
                                ||||||||| | ||| |||
                                TGGTCTCAC G ATG ACT
                                     T T  _
GAM371  POLQ    3'  GAACCAAAGTGCTAAGTG    27320         C  TA
                                GAACCAGAGTGC TA  TG
                                |||||||||||| ||  ||
                                CTTGGTTTCACG AT  AC
                                      _  TC
GAM372  GNAO1   3'  GGGGCTGCGCCGCGAGG    44941    A  CCTC
                                GG GT   GCGCCGCGAGG
                                || ||   ||||||||||
                                CC CG   CGCGGCGCTCC
                                 C  A___
GAM372  PAX2    5'  CGGAGAGCGCCGCGGGGCG   19622      TCCTC      A
                                TGGAG    GCGCCGCG GGCG
                                |||||    |||||||| ||||
                                GCCTC    CGCGGCGC CCGC
                                   T_____      C
GAM373  KAL1    3'  TGATTAGCAGCTTATTTCA   6875     AC       CG
                                TGA  AGCAGCTTGT  CG
                                |||  ||||||||||  ||
                                ACT  TCGTCGAATA  GT
                                  AA        AA
GAM373  PROC    3'  GAACAGCAGGCCGGTGTGCT   7189         CTT   C___
                                GAACAGCAG   GTCG   GCT
                                |||||||||   ||||   |||
                                CTTGTCGTC   CGGC   CGA
                                     ___   CACA
GAM373  KCNA6   5'  GCGGTTCCGGCCGCCACA    13815       _
                                GCGGTTC GGCCGCCACG
                                ||||||| ||||||||||
                                CGCCAAG CCGGCGGTGT
                                    G
GAM373  RNF12   5'  GGTTCGGCCGCCGCCGCCGAGG 32037          A_  ACAA
          C                      GGTTCGGCCGCC  CGT   GC
                                ||||||||||||  |||   ||
                                CCAAGCCGGCGG  GCG   CG
                                       CG   GCTC
GAM373  SOX11   3'  GGTTCGGCCCTCCCAGGC    17031        G__  C
                                GGTTCGGCC   CCA GT
                                |||||||||   ||| ||
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                                CCAAGCCGG  GGT CG
                                     GAG  C
GAM374  GJB3    5'  GTGCCTTGTTTCTGTGCTGCTG 35837          AT__   C
              T                  GTGCCTTGTTTT   CTGC GT
                                 ||||||||||||   |||| ||
                                 CACGGAACAAAG   GACG CA
                                       ACAC   A
GAM375  CSK     3'  ACGTCTGCCTCGGGCGCAT   20456     A__
                                 GCGT  CCTCGGGCGCGT
                                 ||||  ||||||||||||
                                 TGCA  GGAGCCCGCGTA
                                   GAC
GAM375  MAPK12  5'  CGCGCGCCTCGGGCCGGC   16464     TA      GCGT
                                 CGCG  CCTCGGGC   TGGC
                                 ||||  ||||||||   ||||
                                 GCGC  GGAGCCCG   GCCG
                                   GC      ____
GAM375  ABCC5   3'  CTCCAGCCGCCCACCCG    25022         T  AG
                                 CTCCAGCCGC CCG  CG
                                 ||||||||||| |||  ||
                                 GAGGTCGGCG GGT  GC
                                       _  GG
GAM375  F8      3'  CCTCCAACTGCTCTATAAC   6564         C   CG_
                                 CCTCCAGC GCTC  AGC
                                 |||||||| ||||  |||
                                 GGAGGTTG CGAG  TTG
                                     A   ATA
GAM375  FMNL    5'  CCTCCAGCTCCTCCAC     25294        CG   GAGCGC
                                 CCTCCAGC  CTCC    AC
                                 ||||||||  ||||    ||
                                 GGAGGTCG  GAGG    TG
                                     AG   _______
GAM375  KCNA6   5'  CCTCCAGCCGCTCCGGAC   13811           AG
                                 CCTCCAGCCGCTCCG  C
                                 |||||||||||||||  |
                                 GGAGGTCGGCGAGGC  G
                                       CT
GAM375  KCNK4   5'  CTCCAGCCTTCCCCTTACCT  37830        G_   GAGCGC
                                 CTCCAGCC  CTCC    ACCT
                                 ||||||||  ||||    ||||
                                 GAGGTCGG  GGGG    TGGA
                                     AA   AA____
GAM375  KIFAP3  5'  CCTCCAGCTCCTCCCACAGC  31404        CG   GA  _
                                 CCTCCAGC  CTCC  GC GC
                                 ||||||||  ||||  || ||
                                 GGAGGTCG  GAGG  TG CG
                                     AG   G_  T
GAM375  KLK3    3'  CCTCCAGCTTCTGCTCAGTGC  11610        C___   CG  C
                                 CCTCCAGC   GCTC  AG GC
                                 ||||||||   ||||  || ||
```

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                                GGAGGTCG   CGAG  TC CG
                                    AAGA   __  A
GAM375  NCF4    5'  CCTCCAGCCACCCTGCG    8436          T  GA
                                CCTCCAGCCGC CC  GCG
                                |||||||||||  ||  |||
                                GGAGGTCGGTG GG  CGC
                                      _  A_
GAM375  NGFRAP1  5'  CCTCCAGCTTTCTCCCCTTACC 30776       CG_   GAGCGC
          T                     CCTCCAGC   CTCC     ACCT
                                ||||||||   ||||     ||||
                                GGAGGTCG   GAGG     TGGA
                                    AAA    GGAA__
GAM375  NPY2R   5'  CTCAGGCCAAGCGCGCC    9493      C  CCGCT      A
                                CTC AG     CCGAGCGC CC
                                ||| ||     |||||||| ||
                                GAG TC     GGTTCGCG GG
                                  _ C____       C
GAM375  NR2E1   5'  CTCCAGCCGCCCTCCAGC    17577          __  G
                                CTCCAGCCGC  TCC AGC
                                ||||||||||  ||| |||
                                GAGGTCGGCG  AGG TCG
                                     GG  _
GAM375  P2RY1   3'  CCCCAGTTGCTTCATACA    15005       CC   C  A
                                CTCCAG  GCT CG GCG
                                ||||||  ||| || |||
                                GGGGTC  CGA GT TGT
                                   AA   A  A
GAM375  PPP5C   3'  CCCCAGCTGCTCCAC       26485        C    GAGCGC
                                CTCCAGC GCTCC     AC
                                ||||||| |||||     ||
                                GGGGTCG CGAGG     TG
                                   A    _______
GAM375  RAB33A  5'  CTCCAGCCGCCGCCGCGC    21999          _  GA
                                CTCCAGCCGCT CC  GCGC
                                ||||||||||  ||  ||||
                                GAGGTCGGCGG GG  CGCG
                                      C  __
GAM375  SMARCD1  3'  CTCCAGCCCTAGGCGC      40084        G  CCGA
                                CTCCAGCC CT    GCGC
                                ||||||||  ||    ||||
                                GAGGTCGG GA    CGCG
                                     _  TC__
GAM375  TAC1    5'  CTCTGGTTCCTCCGAGCGCACG 30393     CAGCCG         _
          CT                      CTC     CTCCGAGCGCAC CT
                                  |||     ||||||||||||  ||
                                  GAG     GAGGCTCGCGTG GA
                                    ACCAAG          C
GAM375  UBTF    5'  CCTCCAGCTGTCCAGCCACCT  30609        CGC   G   G
                                CCTCCAGC   TCC AGC CACCT
                                ||||||||   ||| ||| |||||
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                                GGAGGTCG   AGG TCG GTGGA
                                    AC_  _  _
GAM376  ACP1    3'  TACTGTCAATCCACAAAAGGCC 28247    GCAC       T   A
                                TAC   CAATCCACG AGAG CC
                                |||   ||||||||| |||| ||
                                ATG   GTTAGGTGT TTTC GG
                                  ACA_       _   C
GAM376  EMS1    3'  CGTCCCAATCCAGAGAC    39739    CA      CGTA
                                CG  CCAATCCA   GAGAC
                                ||  ||||||||   |||||
                                GC  GGTTAGGT   CTCTG
                                 AG       ____
GAM376  NKX3A   3'  GCCACCAACAGTAGAGAC    26113    _     CCAC
                                GC ACCAAT   GTAGAGAC
                                || ||||||   ||||||||
                                CG TGGTTG   CATCTCTG
                                 G     T___
GAM376  TPM1    3'  GCACCAATCCACACCTGA    7485            TA_
                                GCACCAATCCACG   GA
                                ||||||||||||   ||
                                CGTGGTTAGGTGT   CT
                                       GGA
GAM376  WASF3   3'  TACCACTATTTGGGTGTAGAGA 27391    G   CAATCCAC_
          CC                      TAC CAC       GTAGAGACC
                                ||| |||       |||||||||
                                ATG GTG       CATCTCTGG
                                  _  ATAAACCCA
GAM376  BIN3    3'  CGTTCCCGAGGTACCAGTC   33077    _ AGCAGC
                                CGT CC     GGTACCAGTC
                                ||| ||     ||||||||||
                                GCA GG     CCATGGTCAG
                                  A  GCT___
GAM376  EPHB2   3'  TCATTTTCAGCACACCAGT   32678    CGTC    GCGG
                                TCA   CAGCA   TACCAGT
                                |||   |||||   |||||||
                                AGT   GTCGT   GTGGTCA
                                  AAAA   _____
GAM376  FRK     5'  TCAGTCCAGCAGCTGGGT    13014    C       __
                                TCA GTCCAGCAGC  GGT
                                ||| ||||||||||  |||
                                AGT CAGGTCGTCG  CCA
                                  _        AC
GAM376  HS3ST4  5'  CGCCTCCAGCAGCGCGCGGGTC 43867    __      _ ACCA
                                CGT  CCAGCAGCG GT   GTC
                                |||  ||||||||| ||   |||
                                GCG  GGTCGTCGC CG   CAG
                                  GA       G  CC__
GAM376  RAB36   3'  GCCCAGCAAACCTGGTC    22242         CGGT   A_
                                GTCCAGCAG   ACC  GTC
                                |||||||||   |||  |||
```

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                                CGGGTCGTT   TGG  CAG
                                     ____   AC
GAM376  TH1L    3'  TCACGTCCAGCTGGGAGTGCTC 32310          AGC_  AC_
            AGTC                  TCACGTCCAGC   GGT   CAGTC
                                  ||||||||||   |||  |||||
                                  AGTGCAGGTCG   TCA   GTCAG
                                       ACCC   CGA
GAM377  ABCC3   3'  GGCCAGGAGGAAATCTCAG   33424          C   C
                                  GGCCAGGAGG AATC CAG
                                  |||||||||| |||| |||
                                  CCGGTCCTCC TTAG GTC
                                       T   A
GAM377  ABCF1   3'  GGCCAGAGGCAGTCTTCAGAGG 9907        G    A  C_
            AG                    GGCCAG AGGCA TC  CAGAGGAG
                                  |||||| ||||| ||  ||||||||
                                  CCGGTC TCCGT AG  GTCTCCTC
                                     _    C  AA
GAM377  ADCY8   5'  GGCCAGAAGCATCCCTCCCGGA 10011       G    A___   A
            GG                    GGCCAG AGGCA   TCCC GAGG
                                  |||||| |||||   |||| ||||
                                  CCGGTC TTCGT   AGGG CTCC
                                     _    AGGG   C
GAM377  AKT1    3'  GGCCAGGAGGCGTGGAGG    23140          AATCCCA
                                  GGCCAGGAGGC     GAGG
                                  ||||||||||      ||||
                                  CCGGTCCTCCG     CTCC
                                       CAC____
GAM377  ALDH3A1  3'  GGTCAGCAGGTCAGCAGAGGAG 8666    C  G  _  ATCC
                                  GG CAG AGG CA   CAGAGGAG
                                  || ||| ||| ||   ||||||||
                                  CC GTC TCC GT   GTCTCCTC
                                   A  G  A  C___
GAM377  BLAME   3'  GGCTGGAGGCAATTCCTTGG  33492    CA       C  AGA
                                  GGC  GGAGGCAAT CC   GG
                                  |||  |||||||| ||   ||
                                  CCG  CCTCCGTTA GG   CC
                                    A_       A  AA_
GAM377  CHRNB4   3'  GGGAAGGCCTCTCAGAGGAG  8871    CCA     AA  C
                                  GG   GGAGGC  TC CAGAGGAG
                                  ||   ||||||  || ||||||||
                                  CC   CTTCCG  AG GTCTCCTC
                                   ___     G_  A
GAM377  DLEC1   3'  GGCCTGGGGACCAGAGGA   28832     A  A  CAATC
                                  GGCC GG GG    CCAGAGGA
                                  |||| || ||    ||||||||
                                  CCGG CC CC    GGTCTCCT
                                    A  _  T____
GAM377  EFNB1   3'  GGCCAGGAGGCAGTGTGGA   20722          ATCCCAGA
                                  GGCCAGGAGGCA      GGA
                                  ||||||||||||      |||
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                                CCGGTCCTCCGT       CCT
                                      CACA____
GAM377  GAMT     3'  GGCCAGGAAGGCACGGAGGAG  6682         _   ATCCCA
                                GGCCAGGA GGCA     GAGGAG
                                |||||||| ||||     ||||||
                                CCGGTCCT CCGT     CTCCTC
                                     T   GC____
GAM377  KCNH3    3'  GACCGGGAGGTCAGAGGA    42086     A    CAATCC
                                GGCC GGAGG     CAGAGGA
                                |||| |||||     |||||||
                                CTGG CCTCC     GTCTCCT
                                  C    A_____
GAM377  KHK      3'  GGCTGGTGGGCAGGGCAGAGGA 27055     CA  A_   ATCC
           G                     GGC  GG  GGCA    CAGAGGAG
                                |||  ||  ||||    ||||||||
                                CCG  CC  CCGT    GTCTCCTC
                                  A_  AC    CCC_
GAM377  LDB1     5'  GGCCAGGAGAGGTACGGGGGAG 19341          CAATCCCAGA
                                GGCCAGGAGG         GGAG
                                ||||||||||         ||||
                                CCGGTCCTCT         CCTC
                                      CCATGCCC__
GAM377  MEN1     3'  GGCAGGAGGCGGCAGGGGA   39189     C      AATCC   A
                                GGC AGGAGGC     CAG GGA
                                ||| |||||||     ||| |||
                                CCG TCCTCCG     GTC CCT
                                  _      CC___   C
GAM377  MLLT7    5'  GGCCAGGAGGCACATTCC     25530           A__
                                GGCCAGGAGGCA   TCC
                                ||||||||||||   |||
                                CCGGTCCTCCGT   AGG
                                      GTA
GAM377  MUC5B    3'  GGCCGGGGGGCTCCGCAGAGGA 42498      A  A   AA   _
           G                     GGCC GG GGC  TCC CAGAGGAG
                                |||| || |||  ||| ||||||||
                                CCGG CC CCG  AGG GTCTCCTC
                                  C  C   __   C
GAM377  NCOA3    3'  GGTAGGGGGCAGAAGAGG    27218    CC   A   ATCCC
                                GG  AGG GGCA     AGAGG
                                ||  ||| ||||     |||||
                                CC  TCC CCGT     TCTCC
                                 A_   C    CT___
GAM377  NPTX1    3'  GGCCAGGAGGCTGCAGGG     14840          AATCC   A
                                GGCCAGGAGGC     CAG GG
                                ||||||||||     ||| ||
                                CCGGTCCTCCG     GTC CC
                                      AC___   _
GAM377  NUCB1    3'  GGCCAAGAGGTCCAGGAGGAG  26158          CAA   CA
                                GGCCAGGAGG   TCC  GAGGAG
                                |||||||||   |||  ||||||
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                                CCGGTTCTCC   AGG  CTCCTC
                                     ___   TC
GAM377  ODF2     5'  GCTCAGGGGGACCCAGAGG   14929   _    A  CAAT
                                GC CAGG GG    CCCAGAGG
                                || |||| ||    ||||||||
                                CG GTCC CC    GGGTCTCC
                                 A    _ CT__
GAM377  OVOL1    3'  AGCTGGGAGGCAATCCTGG   21268     CA         CAGA
                                GGC  GGAGGCAATCC    GG
                                |||  ||||||||||    ||
                                TCG  CCTCCGTTAGG    CC
                                  AC         A___
GAM377  PHKG2    3'  GGCCAGAGCCCAGAGG      7132        G  GCAAT
                                GGCCAG AG    CCCAGAGG
                                ||||||  ||    ||||||||
                                CCGGTC TC    GGGTCTCC
                                  _  ______
GAM377  PIK3C2B  3'  GGCCAGGAGAATGGAGG     15293          CAATCCCA
                                GGCCAGGAGG       GAGG
                                ||||||||||       ||||
                                CCGGTCCTCT       CTCC
                                     TAC_____
GAM377  PPP2R5B  3'  GGCCAGGAGCAGAGG       26447         GCAATCC
                                GGCCAGGAG      CAGAGG
                                |||||||||      ||||||
                                CCGGTCCTC      GTCTCC
                                ________
GAM377  PPP4C    3'  GGCCAGAAGGGTTGGAGG     15534          CAATCCCA
                                GGCCAGGAGG       GAGG
                                ||||||||||       ||||
                                CCGGTCTTCC       CTCC
                                     CAAC____
GAM377  PSMB8    3'  GGCCAAGACCTCCCAGAGGAG  45547         GGCAA
                                GGCCAGGA    TCCCAGAGGAG
                                ||||||||    ||||||||||
                                CCGGTTCT    AGGGTCTCCTC
                                     GG___
GAM377  PTPN11   3'  GGCCTAGAGGGGCTCCTCTGGG 38756      A    CAA___   CAGA
                                GGCC GGAGG     TCC    GG
                                |||| |||||     |||    ||
                                CCGG TCTCC     AGG    CC
                                  A    CCIIIG   AGAC
GAM377  PTPRN    3'  GGCTGGTGGGGCAGTGAGGAG  15982     CA__  A    ATCCCA
                                GGC    GG GGCA     GAGGAG
                                |||    || ||||     ||||||
                                CCG    CC CCGT     CTCCTC
                                  ACCA  _    CA____
GAM377  SHC1     3'  GGCCAGGAGGCACTGAGCAAGG 16702           ATCC_   A
            GAG                    GGCCAGGAGGCA    CAG GGAG
                                ||||||||||||    ||| ||||
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                                CCGGTCCTCCGT    GTT CCTC
                                      GACTC   C
GAM377  SLC29A1  3'  GGCAGGAGGCAGACAGGGAG  22416    C      ATCC   A
                                GGC AGGAGGCA   CAG GGAG
                                ||| ||||||||   ||| ||||
                                CCG TCCTCCGT   GTC CCTC
                                  _      CT__   _
GAM377  TCF20    3'  GGACAGGGGGCCCCAGAGGAG  42535    C   A   AAT
                                GG CAGG GGC   CCCAGAGGAG
                                || |||| |||   ||||||||||
                                CC GTCC CCG   GGGTCTCCTC
                                 T   C  ____
GAM377  TFAP2C   3'  GGCCAGGAGGGGTTCCCAG   17405         CAA
                                GGCCAGGAGG   TCCCAG
                                ||||||||||   ||||||
                                CCGGTCCTCC   AGGGTC
                                      CCA
GAM377  TLX1     3'  GGCCAGGAGGGTGGGGAGGAG  24341         CAATCCCA
                                GGCCAGGAGG       GAGGAG
                                ||||||||||       ||||||
                                CCGGTCCTCC       CTCCTC
                                      CACCC____
GAM377  USP21    3'  GGCTGGGAGACAAGGG      32444     CA      ATCCC  A
                                GGC  GGAGGCA    AG GG
                                |||  |||||||    || ||
                                CCG  CCTCTGT    TC CC
                                  AC      ______  _
GAM377  VAMP1    3'  GGCAAGGAGGAGCCCAGAGGAG 32576     C      CAAT
                                GGC AGGAGG    CCCAGAGGAG
                                ||| ||||||    ||||||||||
                                CCG TCCTCC    GGGTCTCCTC
                                  T     TC__
GAM377  VAT1     3'  GGTCAGGAAGCGGGGAGG    26852    C       AATCCCA
                                GG CAGGAGGC      GAGG
                                || ||||||||      ||||
                                CC GTCCTTCG      CTCC
                                 A       CCC_____
GAM377  CACNG8   5'  GGGCCACCACCGGG       43527     A       AAACC A
                                GGG CCACCACC     G GG
                                ||| ||||||||     | ||
                                CCC GGTGGTGG     C CC
                                  _       ______ _
GAM377  DLEC1    3'  AGGGACCACCACCTGCTTGGGG 28814           AAACCGA
                C                AGGGACCACCACC       GGGC
                                 ||||||||||||||      ||||
                                 TCCCTGGTGGTGG       CCCG
                                       ACGAAC_
GAM377  EPHA8    3'  AGGGACCACACACTAGAGTGAG 33890          _   CAAACC
                GG                 AGGGACCAC CAC     GAGGG
                                 |||||||||  |||      |||||
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                                TCCCTGGTG GTG     CTCCC
                                     T  ATCTCA
GAM377  G6PT1    5'  GGAACCACGGGGGCCGGGGG  11164        CACCAAA  A
                                GGGACCAC      CCG GGG
                                ||||||||      ||| |||
                                CCTTGGTG      GGC CCC
                                     CCCCC__  C
GAM377  GYG2     3'  GAGACCACCATCGAGAG     19390          CCAAAC
                                GGGACCACCA     CGAGGG
                                ||||||||||     ||||||
                                CTCTGGTGGT     GCTCTC
                                     A_____
GAM377  HMGN1    3'  AGGGACCACTGATAAGACATGG 22447         CACC  AC  A
                                AGGGACCAC    AA  CG GG
                                |||||||||    ||  || ||
                                TCCCTGGTG    TT  GT CC
                                     ACTA  CT  A
GAM377  LOH11CR2A 3'  GGGACCACTGTCACTTTTCTGA 31191         ___  CAAACC
           GGGC                    GGGACCAC   CAC     GAGGGC
                                |||||||  |||     ||||||
                                CCCTGGTG   GTG     CTCCCG
                                     ACA   AAAAGA
GAM377  MUS81    5'  GGGGCCGCCATGAGCCCGAGGG 36065     A  A   CCAAA
           C                     GGG CC CCA    CCGAGGGC
                                ||| || |||    ||||||||
                                CCC GG GGT    GGCTCCCG
                                  C  C   ACTCG
GAM377  OAS3     3'  GGCCATTGCCAAAGACTGAGGG 26182    A   CCA   __  C
           C                     GG CCA   CCAA  AC GAGGGC
                                || |||   ||||  || ||||||
                                CC GGT   GGTT  TG CTCCCG
                                 _  AAC    TC  A
GAM377  PCDHGA1  3'  AGGGGCTGGCACCAAACCA   36727     ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGA10 3'  AGGGGCTGGCACCAAACCA   36868     ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGA11 3'  AGGGGCTGGCACCAAACCA   36877     ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGA12 3'  AGGGGCTGGCACCAAACCA   19025     ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
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                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA2  3' AGGGGCTGGCACCAAACCA  33153    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA3  3' AGGGGCTGGCACCAAACCA  33157    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA4  3' AGGGGCTGGCACCAAACCA  33165    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA5  3' AGGGGCTGGCACCAAACCA  36826    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA6  3' AGGGGCTGGCACCAAACCA  33167    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA7  3' AGGGGCTGGCACCAAACCA  36842    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA8  3' AGGGGCTGGCACCAAACCA  36851    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGA9  3' AGGGGCTGGCACCAAACCA  36860    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGB1  3' AGGGGCTGGCACCAAACCA  36895    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
                              TCCC    GTGGTTTGGT
                                CGACC
GAM377  PCDHGB2  3' AGGGGCTGGCACCAAACCA  36904    ACCAC
                              AGGG    CACCAAACCG
                              ||||    ||||||||||
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                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGB3  3' AGGGGCTGGCACCAAACCA  36913    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGB4  3' AGGGGCTGGCACCAAACCA  36922    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGB5  3' AGGGGCTGGCACCAAACCA  36931    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGB6  3' AGGGGCTGGCACCAAACCA  33175    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGB7  3' AGGGGCTGGCACCAAACCA  33177    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGC3  3' AGGGGCTGGCACCAAACCA  37054    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGC4  3' AGGGGCTGGCACCAAACCA  37068    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PCDHGC5  3' AGGGGCTGGCACCAAACCA  37075    ACCAC
                                AGGG    CACCAAACCG
                                ||||    ||||||||||
                                TCCC    GTGGTTTGGT
                                  CGACC
GAM377  PHKA1    3' AGGGACCAGCTGTCAAAAGGC 15273      CCACCAAACC
                                AGGGACCA      GAGGGC
                                ||||||||      ||||||
                                TCCCTGGT      TTTCCG
                                    CGACAGT___
GAM377  PLIN     3' GGGACCACTTTGAAAGTGGC  15400      CACCAAACC  _
                                GGGACCAC      GAG GGC
                                ||||||||      ||| |||
```

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                                CCCTGGTG       TTC CCG
                                    AAACT____  A
GAM377  PPFIA3   3'  GGGAGGCCGACCGAGAGTCGGG 41425     CCA  _  AAAC__  A
          GGC                    GGGA  CC ACC     CG GGGC
                                ||||  || |||     || ||||
                                CCCT  GG TGG     GC CCCG
                                  CC_ C  CTCTCA  C
GAM377  RORC     3'  GGGACCACCCTCCAGGG     22813         ACCAAA  G
                                GGGACCACC     CC AGGG
                                |||||||||     || ||||
                                CCCTGGTGG     GG TCCC
                                    GA____ _
GAM377  VIPR1    3'  AGAGACCAGGGGGCCGGGGGC  21503        CCACCAAA  A
                                AGGGACCA      CCG GGGC
                                ||||||||      ||| ||||
                                TCTCTGGT      GGC CCCG
                                    CCCCC___  C
GAM377  ZNF7     5'  AGGGATCACTCGGACCGAGGGC 18260      C  CACCAA
                                AGGGA CAC     ACCGAGGGC
                                ||||| |||     |||||||||
                                TCCCT GTG     TGGCTCCCG
                                  A  AGCC__
GAM378  ATP1A2   3'  GGGACGTAGAGCTGGA     8707      T  AGC
                                GGG CG  AGAGCTGGA
                                ||| ||  |||||||||
                                CCC GC  TCTCGACCT
                                  T  A__
GAM378  CD86     3'  GGCATACGGAGCAGAGCTGGAG 27866     C____
                                GGT    GAGCAGAGCTGGAG
                                |||    ||||||||||||||
                                CCG    CTCGTCTCGACCTC
                                  TATGC
GAM378  ELL      3'  TCTGGGGGCACCAGCTGGA   27208     AA   CGA  AG
                                TCT  GGGT  GC  AGCTGGA
                                |||  ||||  ||  |||||||
                                AGA  CCCG  TG  TCGACCT
                                  CC   ___  G_
GAM378  GNAI2    3'  GGGTCCAGGCTGGA       42651      GAG  A
                                GGGTC  CAG GCTGGA
                                |||||  ||| ||||||
                                CCCAG  GTC CGACCT
                                   ___  _
GAM378  KCNA5    5'  TCTGGGGAGAGCTGG      40684     AA  TCGAGC
                                TCT  GGG     AGAGCTGG
                                |||  |||     ||||||||
                                AGA  CCC     TCTCGACC
                                  C_  _______
GAM378  KCNA6    3'  TCTAGGGCTTTAAGCTGGA   13821      A  CGAGCA
                                TCTA GGGT     GAGCTGGA
                                |||| ||||     ||||||||
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                                AGAT CCCG     TTCGACCT
                                  _   AAA___
GAM378  LASS1   3'  CCTAGAGGAGCAGAGTTGGAG  34596     A  TC      C
                                TCTA GGG  GAGCAGAG TGGAG
                                |||| |||  |||||||| |||||
                                GGAT CTC  CTCGTCTC ACCTC
                                  _  __       A
GAM378  LMO4    5'  GGGCTGGCGGAGCTGGAG    27660     CGA  A
                                GGGT   GC GAGCTGGAG
                                ||||   || |||||||||
                                CCCG   CG CTCGACCTC
                                  AC_  C
GAM378  MMP15   3'  CCTGGGGGCACAGGGAGCTGGA 14560     AA   CG  CA
          G                      TCT  GGGT  AG  GAGCTGGAG
                                ||| ||||  ||  |||||||||
                                GGA  CCCG  TC  CTCGACCTC
                                  CC   TG  C_
GAM378  NPC2    3'  AAGCAGCAGAGCTGGAG    26960     CG
                                GGGT  AGCAGAGCTGGAG
                                ||||  ||||||||||||||
                                TTCG  TCGTCTCGACCTC
                                  __
GAM378  SDC4    3'  CAAAGGTAATCAGAGCTGGAG  16518       CGAG
                                TAAGGGT   CAGAGCTGGAG
                                |||||||   ||||||||||
                                GTTTCCA   GTCTCGACCTC
                                    TTA_
GAM378  SIAT1   3'  AGGCCAGGCAGAGCTGGAG   16716      A
                                GGGTCG GCAGAGCTGGAG
                                |||||| ||||||||||||
                                TCCGGT CGTCTCGACCTC
                                   C
GAM379  ACATN   5'  TCCAAGGCTGTCGCGC     21843    G  A  AGCCAA
                                TC AA GCT     GTCGCGC
                                || || |||     |||||||
                                AG TT CGA     CAGCGCG
                                 G  C  _______
GAM379  CR1     3'  TCGAAAGCGGCCAGGCGCGGTG 8203        TA   A T   C
                                TCGAAAGC  GCCA G CGCG TG
                                ||||||||  |||| | |||| ||
                                AGCTTTCG  CGGT C GCGC AC
                                    C_   C _   C
GAM379  PODXL   5'  CCGGGGCTCCCGAGTCGCGCTG 23964    AAA  AG  A
                                TCG   GCT  CC AGTCGCGCTG
                                |||   |||  || ||||||||||
                                GGC   CGA  GG TCAGCGCGAC
                                  CC_   G_  C
GAM379  TUBA2   3'  GAAAGCAGCCACGC       38616       T   AAGTC
                                GAAAGC AGCC    GCGC
                                |||||| ||||    ||||
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                                CTTTCG TCGG    TGCG
                                  _  _____
GAM380  ENC1    3'  GAAGACAGCTGTAGGCATTGTT 18862         A  TC  __
          T                      GAAGGCAGCT TA  GCG  GTTT
                                 |||||||||| ||  |||  ||||
                                 CTTCTGTCGA AT  CGT  CAAA
                                       C  C_   AA
GAM380  GAD1    5'  GCGGGGGCAGCTAGTCGG    30290     AA      TATCG
                                 GCG  GGCAGCTA    CGG
                                 |||  ||||||||    |||
                                 CGC  CCGTCGAT    GCC
                                   CC       CA___
GAM380  SDHB    5'  AGGCGGCTTCCGGTTT      41311      A   ATA  G
                                 AGGC GCT   TC CGGTTT
                                 |||| |||   || ||||||
                                 TCCG CGA   AG GCCAAA
                                   C  ___  _
GAM380  TSC     5'  GCGGAGGGCGGCGCGCCGCGGT 32833     AA_   A  TATA
          TT                     GCG   GGC GC    TCGCGGTTT
                                 |||   ||| ||   |||||||||
                                 CGC   CCG CG    GGCGCCAAA
                                   CTC   C  CGC_
GAM381  EPHB2   3'  CTCGCCCTTGGTGTATTGCCTA 32668       _       C  AAT
          AG                     CTCGCC TTGGTGTAT GC   GG
                                 |||||| ||||||||| ||   ||
                                 GAGCGG AACCACATA CG   TC
                                    G        A  GAT
GAM381  LIF     3'  CTCCTCTTGGGAGCAATGG   14145     GC    TGTATC
                                 CTC  CTTGG     GCAATGG
                                 |||  |||||     |||||||
                                 GAG  GAACC     CGTTACC
                                   GA    CT____
GAM381  NUP62   3'  GCCTTGGTGGTTAGCATGG   29602         TATC   A
                                 GCCTTGGTG   GCA TGG
                                 |||||||||   ||| |||
                                 CGGAACCAC   CGT ACC
                                       CAAT  _
GAM381  PYGB    3'  CTCTCTTGGGCAATG      16048     GC    TGTATC
                                 CTC  CTTGG     GCAATG
                                 |||  |||||     ||||||
                                 GAG  GAACC     CGTTAC
                                   A_   _______
GAM382  ADCY8   5'  CCCCAGGGTCCCAGCCTGATCT 9998          ATTAACA_
          AT                     CCCCAGGGTC       ATCTAT
                                 ||||||||||       ||||||
                                 GGGGTCCCAG       TAGATA
                                       GGTCGGAC
GAM382  BBS4    3'  GGGTCATTCATTCTAT      37497         AA  A
                                 GGGTCATT  CA TCTAT
                                 ||||||||  || |||||
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                                CCCAGTAA  GT AGATA
                                   __ A
GAM382  DLEC1    3'  TCCCCAGGTCCCCAAGTCT   28838        G  ATTAA  _
                                TCCCCAGG TC    CAA TCT
                                |||||||| ||    ||| |||
                                AGGGGTCC AG    GTT AGA
                                   _ GG___   C
GAM382  IL17     3'  TCCTCAGGGCCATTATCT    13533     C        ACAA
                                TCC CAGGGTCATTA   TCT
                                ||| ||||||||||    |||
                                AGG GTCCCGGTAAT   AGA
                                  A        ____
GAM382  MAFF     3'  CCCAGGGTCATTCGGTCCCA  29512          AACAA
                                CCCAGGGTCATT    TCTA
                                ||||||||||||    ||||
                                GGGTCCCAGTAA    GGGT
                                      GCCA_
GAM382  NEK4     3'  TCCTTAAGGTTATTAACAAT  17193     CC    C
                                TCC  AGGGT ATTAACAAT
                                |||  ||||| |||||||||
                                AGG  TTCCA TAATTGTTA
                                  AA    A
GAM382  VSX1     3'  CCCTAGGTCACTCATCT     31096     A      TAACA
                                CCC GGGTCAT    ATCT
                                ||| |||||||    ||||
                                GGG TCCAGTG    TAGA
                                  A      AG___
GAM382  ABCG1    3'  CCAATGTCTTCTCACAATT   22252       _  CAG
                                CCAATG CT   TCACAATT
                                |||||| ||   ||||||||
                                GGTTAC GA   AGTGTTAA
                                   A  AG_
GAM382  HKE4     3'  AGTAACCATTGCTCCCAGGCTA 28092        A    A___ TC
           CA                     AGTAACCA TGCTC    G  ACA
                                |||||||| |||||   |  |||
                                TCATTGGT ACGAG    C  TGT
                                     A    GGTC GA
GAM382  RAB27A   5'  AGTTACCAATGCTTCAACAATT 21357     A       _  GTC
                                AGT ACCAATGCT CA   ACAATT
                                ||| ||||||||| ||   ||||||
                                TCA TGGTTACGA GT   TGTTAA
                                  A        A ___
GAM383  ADAM10   5'  CCCGCCCATACCCG       9967       GGTCCA
                                TCCGC     CCATACCCG
                                |||||     |||||||||
                                GGGCG     GGTATGGGC
                                   _______
GAM383  ADARB1   3'  CCTGCACCCCCCATCATGTCTG 31876    _  G   A    ACCC___
           CC                     CC GCG TCC CCAT      GCC
                                || ||| ||| ||||      |||
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                                GG CGT GGG GGTA      CGG
                                 A  G  _   GTACAGA
GAM383  BARX1   5'  TCCGCGGCCCACTCGTGCGCC  34628          CATACC
                                TCCGCGGTCCAC     CGCC
                                ||||||||||||     ||||
                                AGGCGCCGGGTG     GCGG
                                       AGCAC_
GAM383  BMP8    5'  CGCCGCCGTACCCGCC     11877     G   CACCA
                                CGC GTC    TACCCGCC
                                ||| |||    ||||||||
                                GCG CGG    ATGGGCGG
                                  G  C____
GAM383  CABC1   5'  TCCGCGGTCACCTTCTAGCCGC 33690         C  A__  C
              C                  TCCGCGGTC ACC   TA CCGCC
                                ||||||||| |||   || |||||
                                AGGCGCCAG TGG   AT GGCGG
                                      _  AAG  C
GAM383  G6PD    5'  CCGGCTGCCTGCCATACCCGC  7598     _ G   CA
                                CCG C GTC  CCATACCCGC
                                ||| | |||  ||||||||||
                                GGC G CGG  GGTATGGGCG
                                  C A   AC
GAM383  GPC5    5'  TCCTGGTCCCCTTTACCCGCC  20920     GC    A  A_
                                TCC  GGTCC CC  TACCCGCC
                                |||  ||||| ||  ||||||||
                                AGG  CCAGG GG  ATGGGCGG
                                  A_    _ AA
GAM383  HYAL3   5'  GCGCGTCACAACACCCGCC   18646    _   C  C
                                GCG GTC AC ATACCCGCC
                                ||| ||| || |||||||||
                                CGC CAG TG TGTGGGCGG
                                  G  _ T
GAM383  IGF2R   3'  TCCGCGCTGTACCCGCC    9342        GTCCACCA
                                TCCGCG       TACCCGCC
                                ||||||       ||||||||
                                AGGCGC       ATGGGCGG
                                   GAC_____
GAM383  LHX2    3'  TCCTCGGTCCACACCGC     21983     G      CATAC
                                TCC CGGTCCAC     CCGC
                                ||| ||||||||     ||||
                                AGG GCCAGGTG     GGCG
                                  A       T____
GAM383  NTSR1   5'  TCCGCGGCTCTGTCCGGCGCC  14895         CCA__  ATACC
                                TCCGCGGT    CC    CGCC
                                ||||||||    ||    ||||
                                AGGCGCCG    GG    GCGG
                                     AGACA  CC___
GAM383  RAB4A   5'  CCCGCGGTCCGCCGGCGC    21346          A  ATACC
                                TCCGCGGTCC CC    CGC
                                |||||||||| ||    |||
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                                GGGCGCCAGG GG    GCG
                                     C  CC___
GAM383  TJP1    5'  TCCGCGGCGCTGGCCCGCC   17546       CCACCATA
                                TCCGCGGT      CCCGCC
                                ||||||||      ||||||
                                AGGCGCCG      GGGCGG
                                    CGACC___
GAM383  WASF3   5'  TCCGCGGTCCCGCCGC     27392         ACCATAC
                                TCCGCGGTCC     CCGC
                                ||||||||||     ||||
                                AGGCGCCAGG     GGCG
                                     GC_____
GAM383  AGTR1   5'  GGGGTCCTGGCTGTCAGGCGC  28917     C  GC  GC
                                GGGG CC  GGC  GTCAGGCGC
                                |||| ||  |||  |||||||||
                                CCCC GG  CCG  CAGTCCGCG
                                  A  A_  A_
GAM383  ATP8B2  5'  GGGAGCCCCAGCCGTCGGGCGC 42209       G   G   A
                                GGGGGCCC CGGC CGTC GGCGC
                                |||||||| |||| |||| |||||
                                CCCTCGGG GTCG GCAG CCGCG
                                    _   _   C
GAM383  CDH23   5'  GGGGGCTCGGACTGGGCG   38077      C  C   GCGTCA
                                GGGGGC CG GGC    GGCG
                                |||||| || |||    ||||
                                CCCCCG GC CTG    CCGC
                                   A  _  AC____
GAM383  CPNE7   5'  GGGGGCCCGGCTGGGCGC   30870        _ __
                                GGGGGCCCG C  GGCGC
                                ||||||||| |  |||||
                                CCCCCGGGC G  CCGCG
                                     C AC
GAM383  GATA6   5'  GGGGCCCGCGACCCCAGGCGC  23539          GCG
                                GGGGCCCGCGGC   TCAGGCGC
                                ||||||||||||   ||||||||
                                CCCCGGGCGCTG   GGTCCGCG
                                       G__
GAM383  LHX5    5'  GGGGGCCCAGCGGCCAATGGGC 35321       _    G  TCA
            GC                   GGGGGCCC GCGGC CG   GGCGC
                                |||||||| ||||| ||   |||||
                                CCCCCGGG CGCCG GT   CCGCG
                                    T    _  TAC
GAM383  PKD2L1  5'  GGGGGCCCGGTACCCCAGGTGC 32021       GC  CG G    C
                                GGGGGCCC  GG  C TCAGG GC
                                ||||||||  ||  | ||||| ||
                                CCCCCGGG  CC  G GGTCC CG
                                    __  AT G    A
GAM383  PRKCM   5'  GGGGGCTGGCGGCGCGGC    15645      CC     GTCA
                                GGGGGC  GCGGCGC   GGC
                                ||||||  |||||||   |||
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                                CCCCCG CGCCGCG  CCG
                                   AC     ____
GAM383  PTPN11   5' GGGGGCTCCGCGGAGGCG   38757      _    CGCGTC
                                GGGGGC CCGCGG    AGGCG
                                |||||| ||||||     |||||
                                CCCCCG GGCGCC    TCCGC
                                   A    _______
GAM383  STAT5B   5' GGGGCCCGCGGGGGC      29722         CGCGTCA
                                GGGGCCCGCGG     GGC
                                ||||||||||      |||
                                CCCCGGGCGCC     CCG
                                      C_______
GAM383  TLX1     5' GGGGGCCCGGGCGGCGGCG   24345       C   C  CA
                                GGGGGCCCG GGCG GT  GGCG
                                ||||||||| |||| ||  ||||
                                CCCCCGGGC CCGC CG  CCGC

                                   _   _  __
GAM384  CKTSF1B1 3' ACATGCTGGGTGCACCTGGA  30077        CC   G
                                ACATGCTGGG  TACC TGGA
                                ||||||||||  |||| ||||
                                TGTACGACCC  GTGG ACCT
                                      AC   _
GAM384  CML66    5' CATGCTGGGCTATGTAG    42815         C  CC
                                CATGCTGGGC TA  GTGG
                                |||||||||| ||  ||||
                                GTACGACCCG AT  CATC
                                      _ A_
GAM384  COL19A1  3' ATGCTGGGTGTTTGGGCTC   12371       CCTACCG  A
                                ATGCTGGG     TGG CTC
                                ||||||||     ||| |||
                                TACGACCC     ACC GAG
                                     ACAA___  C
GAM384  COL9A3   3' ATGCTGGGCTTACAGG     12342        C  CGT
                                ATGCTGGGC TAC   GG
                                ||||||||| |||   ||
                                TACGACCCG ATG   CC
                                     A  T__
GAM384  EGFR     3' ACAGTTGGGCCTGGATGAACTC 23395    TGC     ACC
                                ACA  TGGGCCT  GTGGACTC
                                |||  |||||||  ||||||||
                                TGT  ACCCGGA  TACTTGAG
                                  CA_     CC_
GAM384  EN2      3' ACATGTTTCAGAACTGTGGACT 10926     C__  GC  ACC
           C                     ACATG  TGG  CT  GTGGACTC
                                |||||  |||  ||  ||||||||
                                TGTAC  GTC  GA  CACCTGAG
                                   AAA  TT  ___
GAM384  FXYD7    3' TGCTGGGCCGGGATGGACTC  35131       TACC
                                TGCTGGGCC   GTGGACTC
                                |||||||||   ||||||||
```

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                                ACGACCCGG   TACCTGAG
                                    CCC_
GAM384  HRH1    3'  ACATGCTGGGATTATAGGCT  9249         CCTACCGT  A
                                ACATGCTGGG      GG CT
                                ||||||||||      || ||
                                TGTACGACCC      CC GA
                                    TAATAT__  _
GAM384  IL17E   5'  ACATGCTGGGCACTGCACACTC 35571         CT  C   G
                                ACATGCTGGGC  AC GTG ACTC
                                ||||||||||  || ||| ||||
                                TGTACGACCCG  TG CGT TGAG
                                    __ A   G
GAM384  MAP3K14  3'  TGCTGGGCCTGAAGGGGCTC  19546        ACCGT  A
                                TGCTGGGCCT    GG CTC
                                |||||||||     || |||
                                ACGACCCGGA    CC GAG
                                    CTTCC  _
GAM384  MSX1    5'  TGCTGGGCCTGGCCT      14672         ACCGT  A
                                TGCTGGGCCT    GG CT
                                |||||||||     || ||
                                ACGACCCGGA    CC GA
                                    _____  G
GAM384  NEU3    5'  GCTGGGCCTGGTGGCT     27403         ACC    A
                                GCTGGGCCT   GTGG CT
                                |||||||||   |||| ||
                                CGACCCGGA   CACC GA
                                    C__   _
GAM384  SNCAIP   5'  TGCTGGGCTCAGAGCT     45505        CTAC  T  A
                                TGCTGGGC    CG GG CT
                                ||||||||    || || ||
                                ACGACCCG    GT TC GA
                                    A___  C  _
GAM384  VCY     3'  CAGCTGGGCCTAAAC      21709    T       CCGTG
                                CA GCTGGGCCTA    GAC
                                || ||||||||||    |||
                                GT CGACCCGGAT    TTG
                                _       _____
GAM384  WBP2    3'  ACGCTGGGCAGCACTGTGGGCT 43808         C_  C   A
            C                    ATGCTGGGC  TAC GTGG CTC
                                |||||||||  ||| |||| |||
                                TGCGACCCG  GTG CACC GAG
                                    TC   A   C
GAM384  BCL11B   5'  GAGCCGCCGCCGCGCCGCT   35648     G      G  GAA
                                GAGC CGCCGCCG GT   CGCT
                                |||| |||||||| ||   ||||
                                CTCG GCGGCGGC CG   GCGA
                                  _      G ___
GAM384  GUCY1A2  5'  GCCGCCGCCGCCTCTGCTG   9220     G      GGTGAAC
                                GC CGCCGCCG      GCTG
                                || ||||||||      ||||
```

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                                CG GCGGCGGC      CGAC
                                 _       GGAGA__
GAM384  RAB26    5'  GAGCGCGCCGGTCGGGCCCCG  30747          C_    GAA
                                GAGCGCGCCG  CGGGT   CG
                                ||||||||||  |||||   ||
                                CTCGCGCGGC  GCCCG   GC
                                      CA    GG_
GAM384  RENT1    5'  GAGCCCGCCGCCGCGC      16251      G       GGTGAA
                                GAGC CGCCGCCG     CGC
                                ||||  ||||||||      |||
                                CTCG GCGGCGGC     GCG
                                  G       _______
GAM384  ZIC1     5'  GCGCGCCGCGCGGCGCT     18237          _   GTGAA
                                GCGCGCCGC CGG    CGCT
                                |||||||||  |||    ||||
                                CGCGCGGCG GCC    GCGA
                                      C  ______
GAM385  ABCB1    5'  GCGCTCCTTGGAACGGCC    9573      A  ____
                                GCG TC   GGAACGGCC
                                |||  ||   |||||||||
                                CGC AG   CCTTGCCGG
                                  G  GAA
GAM385  ADCY7    3'  TCAGAGCAAGAACGGC      9990         ATC
                                TCAGGGCG   GGAACGGC
                                ||||||||   ||||||||
                                AGTCTCGT   TCTTGCCG
                                           ___
GAM385  ADRA2B   3'  CCAGGGCGATACTCTGGCC   8646          CGGAAC
                                TCAGGGCGAT     GGCC
                                ||||||||||     ||||
                                GGTCCCGCTA     CCGG
                                      TGAGA_
GAM385  ARHC     5'  CCAGGGCAGGCGGCGGCC    23167        AT   AA
                                TCAGGGCG  CGG  CGGCC
                                ||||||||  |||  |||||
                                GGTCCCGT  GCC  GCCGG
                                     CC   __
GAM385  CALCB    5'  TCAGGGCAGCGCGAGCGGCC  44714         AT  _  A
                                TCAGGGCG  CG GA CGGCC
                                ||||||||  || ||  |||||
                                AGTCCCGT  GC CT GCCGG
                                     C_  G  C
GAM385  CLCN6    3'  TCAGGGCAGGCGGC       10510        ATC  AA
                                TCAGGGCG   GG  CGGC
                                ||||||||   ||  ||||
                                AGTCCCGT   CC  GCCG
                                           ___  __
GAM385  COMT     3'  TCAGGGCGCAGGCCTCGGCC  28694        ATC  AA_
                                TCAGGGCG   GG   CGGCC
                                ||||||||   ||   |||||
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                                AGTCCCGC  CC  GCCGG
                                    GT_ GGA
GAM385  CRHR1   3' CCAGGGCAGCAAATGGCC   20437      AT   AC
                                TCAGGGCG CGGA GGCC
                                |||||||| |||| ||||
                                GGTCCCGT GTTT CCGG
                                    C_   A_
GAM385  CYP3A4  3' TCAGGCGATCCACCCGGC   32715     G   GGAA
                                TCAGG CGATC   CGGC
                                ||||| |||||   ||||
                                AGTCC GCTAG   GCCG
                                  _   GTGG
GAM385  FNTB    3' AGAGGCAGCAAATGGCC    12999   _  AT   AC
                                AG GGCG CGGA GGCC
                                || |||| |||| ||||
                                TC CCGT GTTT CCGG
                                 T  C_   A_
GAM385  HDAC4   3' TCAGAGCAAAGAGTGGCC   25784      TC  AC
                                TCAGGGCGA GGA GGCC
                                ||||||||| ||| ||||
                                AGTCTCGTT TCT CCGG
                                    __  CA
GAM385  HIC1    5' CAGGGCGAGAGGCGGC     44562      TC AA
                                CAGGGCGA GG CGGC
                                |||||||| || ||||
                                GTCCCGCT CC GCCG
                                    CT __
GAM385  HIP12   3' TCAGGGCAGTTGCAGAGGCC 42407      AT__  AC
                                TCAGGGCG  CGGA GGCC
                                ||||||||  |||| ||||
                                AGTCCCGT  GTCT CCGG
                                    CAAC  __
GAM385  HTR4    3' TCAGGGCAGACACGCCAGCGGC 9302      _ _ GAA_
          C                      TCAGGGC GAT CG   CGGCC
                                ||||||| ||| ||   |||||
                                AGTCCCG CTG GC   GCCGG
                                    T  T GGTC
GAM385  IL6R    5' TCAGAGCGGCGGACGG     8186       AT  A
                                TCAGGGCG CGGA CGG
                                |||||||| |||| |||
                                AGTCTCGC GCCT GCC
                                    C_   _
GAM385  LASS1   3' TCAGGGCAATGCCCCGCGGCC 34617       CGGAA_
                                TCAGGGCGAT    CGGCC
                                ||||||||||    |||||
                                AGTCCCGTTA    GCCGG
                                     CGGGGC
GAM385  LGALS3BP 3' AGGGCGACATCTGGTGGCC  42927      C___ AAC
                                AGGGCGAT  GG  GGCC
                                ||||||||  ||  ||||
```

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                                TCCCGCTG   CC  CCGG
                                    TAGA  A__
GAM385  LGR6    5'  TCAGGGCATCGACTGAGGC   44481      G    AAC_
                                TCAGGGC ATCGG   GGC
                                ||||||| |||||   |||
                                AGTCCCG TAGCT   CCG
                                    _    GACT
GAM385  LUM     5'  TCAGGACGGAACTGGC     14272      GATC   _
                                TCAGGGC   GGAAC GGC
                                |||||||   ||||| |||
                                AGTCCTG   CCTTG CCG
                                    ____    A
GAM385  MASP1   3'  GAGGAGTCGGGGAACGGC   12433    C  _  __
                                GGG GA TC  GGAACGGC
                                ||| || ||  ||||||||
                                CTC CT AG  CCTTGCCG
                                  _  C  CC
GAM385  MTMR3   3'  TCAGGGCAGGCTTTGGCC   34398      ATC  AAC_
                                TCAGGGCG   GG   GGCC
                                ||||||||   ||   ||||
                                AGTCCCGT   CC   CCGG
                                    ___  GAAA
GAM385  MUCDHL  3'  TCAGGGCGGGACGG       34945      ATC   A
                                TCAGGGCG   GGA CGG
                                ||||||||   ||| |||
                                AGTCCCGC   CCT GCC
                                    ___   _
GAM385  NPTX1   3'  TCAGGGCAGAGGATGGC    14842      ATC   AC
                                TCAGGGCG   GGA  GGC
                                ||||||||   |||  |||
                                AGTCCCGT   CCT  CCG
                                    CT_   A_
GAM385  PFKL    5'  TCAGGACGCCGATGGCC    15239      A   AAC
                                TCAGGGCG TCGG   GGCC
                                |||||||| ||||   ||||
                                AGTCCTGC GGCT   CCGG
                                    _    A__
GAM385  POLS    3'  TCAGAGCAGGACAACGGCC   28125      ATC   __
                                TCAGGGCG   GGA  ACGGCC
                                |||||||   |||  ||||||
                                AGTCTCGT   CCT  TGCCGG
                                    ___   GT
GAM385  POLS    3'  TCAGGGCGACCTGGC       28126      GGAAC
                                TCAGGGCGATC    GGC
                                ||||||||||     |||
                                AGTCCCGCTGG    CCG
                                    A____
GAM385  RAB7L1  3'  TCAGGCGATCCACCTGCC    19436      G    GGA  G_
                                TCAGG CGATC   AC  GCC
                                ||||| |||||   ||  |||
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                                AGTCC GCTAG  TG  CGG
                                  _    G__  GA
GAM385  RAD17   5'  TCAGGGCGCGCGGC      39412       AT  GAA
                                TCAGGGCG  CG  CGGC
                                ||||||||  ||  ||||
                                AGTCCCGC  GC  GCCG
                                    __  ____
GAM385  SEPX1   3'  CCAGGGCGGCTGGCAGGGGCGG 32267       ATC  AA____
          CC                    TCAGGGCG  GG    CGGCC
                                ||||||||  ||    |||||
                                GGTCCCGC  CC    GCCGG
                                    CGA  GTCCCC
GAM385  SLC15A1  3'  TCAGGGCATCTGCGGGCC   22901      G  GGAAC
                                TCAGGGC ATC   GGCC
                                ||||||| |||   ||||
                                AGTCCCG TAG   CCGG
                                   _  ACGC_
GAM385  SLC25A11 3'  CCAGGGCGCAGTGGC     18676       AT  AAC
                                TCAGGGCG  CGG  GGC
                                ||||||||  |||  |||
                                GGTCCCGC  GTC  CCG
                                    __  A__
GAM385  SLC38A3  3'  CCAGGGCGCAGACCGTGGCC  27759       AT   AC__
                                TCAGGGCG  CGGA   GGCC
                                ||||||||  ||||   ||||
                                GGTCCCGC  GTCT   CCGG
                                    __   GGCA
GAM385  SPAG6   5'  TCGTGGCGACGACTCGGCC  29705   AG   T  AA
                                TC  GGCGA CGG  CGGCC
                                ||  ||||| |||  |||||
                                AG  CCGCT GCT  GCCGG
                                 CA    _  GA
GAM385  SWAP70   3'  TCAGAGCACCAATGG     43426       G   AAC
                                TCAGGGC ATCGG  GG
                                ||||||| |||||  ||
                                AGTCTCG TGGTT  CC
                                   _    A__
GAM385  TRPV2   5'  CCAGGGCGTGGCGGC     32025       ATC  AA
                                TCAGGGCG  GG  CGGC
                                ||||||||  ||  ||||
                                GGTCCCGC  CC  GCCG
                                    A__  __
GAM385  UGCG    5'  TCGGGGCGACCGCGGCC    17880   A      GAA
                                TC GGGCGATCG  CGGCC
                                || |||||||||  |||||
                                AG CCCGCTGGC  GCCGG
                                 C       ____
GAM386  ATF5    5'  GGTGAGCGCGGAGACGGGC  28938   _  TT   A
                                GG GGG  CGCG AGACGGGC
                                || |||  |||| ||||||||
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                                CC CTC  GCGC TCTGCCCG
                                 A  __   C
GAM386  CA3     5'  TGACGGGGGCGGAGGTGGG   23219       GTTC  A  AC
                                TGACGGGG   GCG AG  GGG
                                ||||||||   ||| ||  |||
                                ACTGCCCC   CGC TC  CCC
                                     _____  C  CA
GAM386  EN1     3'  GGGGGAGAAGAGGTGGGC    10921      TTCGC   C__
                                GGGGG   GAAGA  GGGC
                                |||||   |||||  ||||
                                CCCCC   CTTCT  CCCG
                                   T_____   CCA
GAM386  PAX5    3'  TGCTGGGGTCCTGGAGGG    32524    ACG     GCGAA  C
                                TG  GGGGTTC   GA GGG
                                ||  |||||||   || |||
                                AC  CCCCAGG   CT CCC
                                 GA_     AC___  _
GAM386  PPP2R5E  5'  GGAGGGGCGGGAGACGGG    26472     TTC  A_
                                GGGGG  GCG  AGACGGG
                                |||||  |||  |||||||
                                CCTCC  CGC  TCTGCCC
                                   C__  CC
GAM386  TRC8    5'  CGGGGGCTAAGGCGGG     28512       CGCG  A
                                CGGGGGTT   AAG CGGG
                                ||||||||   ||| ||||
                                GCCCCCGA   TTC GCCC
                                     _____  C
GAM386  BSCL2   5'  GTCGGGGGATGGCGGGCG   37219      AA   TGT
                                GTCGGGG  GTGGC  CG
                                |||||||  |||||  ||
                                CAGCCCC  TACCG  GC
                                    C_   CCC
GAM386  CDH1    3'  AGTTGGGGAGCTGGGCAGGT  20360    C   A __  T_
                                AGT GGGGA GT  GGC  GT
                                ||| ||||| ||  |||  ||
                                TCA CCCCT CG  CCG  CA
                                 A   _ AC  TC
GAM386  GJA5    3'  AGTCGGGGGGGTGGTGT     23578       AA  C
                                AGTCGGGG  GTGG TGT
                                ||||||||  |||| |||
                                TCAGCCCC  CACC ACA
                                    C_   _
GAM386  MAPK3   3'  GTCAGGGAGGTGGCAGGGGC  43846       A   TGTCGA
                                GTCGGGGA GTGGC    GC
                                |||||||| |||||    ||
                                CAGTCCCT CACCG    CG
                                    C   TCCC__
GAM386  MATK    5'  GTCGGGGAGTGGGGGAAAGC  40315       A  CTGTC
                                GTCGGGGA GTGG   GAGC
                                |||||||| ||||   ||||
```

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                                CAGCCCCT CACC    TTCG
                                     _   CCCT_
GAM386  RALB    3'  AGTCGGGGAGAGTGGGAAGCA  16144        _    CTGTC
                                AGTCGGGGA AGTGG    GAGCA
                                ||||||||| |||||    |||||
                                TCAGCCCCT TCACC    TTCGT
                                     C    C____
GAM386  STK10   3'  AGTCGGGGGGGATGGGGC    25613        AA   CT
                                AGTCGGGG  GTGG  GT
                                ||||||||  ||||  ||
                                TCAGCCCC  TACC  CG
                                     CC   C_
GAM386  TBX6    3'  AGTTGAGGGGGTGGGTGGGCA  38852    C   AA   C  TCGA
                                AGT GGGG  GTGG TG   GCA
                                ||| ||||  |||| ||   |||
                                TCA CTCC  CACC AC   CGT
                                  A   CC   C  C___
GAM387  E2F2    5'  CCGAGCAGAGAGCAGCGCTTA  19869    TTTTGA
                                CC     AGAGCAGCGCTTA
                                ||     |||||||||||||
                                GG     TCTCGTCGCGAAT
                                 CTCGTC
GAM387  EIF4E   3'  TTTTGAAGAGGCTT       12697         CAGC
                                TTTTGAAGAG   GCTT
                                ||||||||||   ||||
                                AAAACTTCTC   CGAA
                                     _____
GAM387  ZNF200  3'  TACCTTTTTAGGCAGC      18374        GA  A
                                TACCTTTT  AG GCAGC
                                ||||||||  || |||||
                                ATGGAAAA  TC CGTCG
                                     A_  _
GAM388  CNTN2   3'  AAGGGCACTGTTTAAAGTAGG  22907        TCTAC   TGA
                                AAGGGCACT    TGA   TAGG
                                |||||||||    |||   ||||
                                TTCCCGTGA    ATT   ATCC
                                     CAA__   TC_
GAM388  CYP3A43 3'  AAGTGCACTTTTAGAACAATAG 38396    G    C  CT  TG
          G                      AAG GCACTT TA  GA  ATAGG
                                ||| |||||| ||  ||  |||||
                                TTC CGTGAA AT  TT  TATCC
                                  A     A  C_  GT
GAM388  DPYSL2  3'  GGGTGTGGTTCCCTGTAT    10754    C   C_
                                GG TGTG  TCCCTGTAT
                                || ||||  |||||||||
                                CC ACAC  AGGGACATA
                                 C   CA
GAM388  ESR1    3'  GGCTGTGCTCAGAACTGTAT   6531          C___
                                GGCTGTGCTC   CTGTAT
                                ||||||||||   ||||||
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                                CCGACACGAG   GACATA
                                     TCTT
GAM388  FGF2    3'  TAGGCTGCTGCTGTAT     12842       GCTCC
                                TAGGCTGT    CTGTAT
                                ||||||||    ||||||
                                ATCCGACG    GACATA
                                    AC___
GAM388  FGF5    3'  AGGAGTGTGCTCCCTGTAT   37577    C_
                                AGG  TGTGCTCCCTGTAT
                                |||  ||||||||||||||
                                TCC  ACACGAGGGACATA
                                  TC
GAM388  LAD1    3'  TAGGCCTGGCCCTGTAT     24492      GTGCT
                                TAGGCT    CCCTGTAT
                                ||||||    ||||||||
                                ATCCGG    GGGACATA
                                   ACC__
GAM388  MGEA5   3'  AGACTCTCTCCCTGTAT     29210      GTG
                                AGGCT   CTCCCTGTAT
                                |||||   ||||||||||
                                TCTGA   GAGGGACATA
                                  GA_
GAM388  PCCA    3'  CAGGGGTGTTCCTGTAT     43415     CT   CTC
                                TAGG  GTG   CCTGTAT
                                ||||  |||   |||||||
                                GTCC  CAC   GGACATA
                                  C_   AA_
GAM388  RFX5    3'  AGGCTGCAGCTTGTAT      7791        _   CCC
                                AGGCTGT GCT   TGTAT
                                ||||||| |||   |||||
                                TCCGACG CGA   ACATA
                                   T  ____
GAM388  RNTRE   3'  AGACATTTCCCTGTAT      31246     T  GC
                                AGGC GT  TCCCTGTAT
                                |||| ||  |||||||||
                                TCTG TA  AGGGACATA
                                  _  A_
GAM388  SLA     3'  CAGATGTCTCCTTGTAT     27564     C   G   C
                                TAGG TGT CTCC TGTAT
                                |||| ||| |||| |||||
                                GTCT ACA GAGG ACATA
                                  _   _    A
GAM388  SLC7A5  3'  GGCCGCCGGCTCCCTGTAT   18551       __
                                GGCTGT  GCTCCCTGTAT
                                ||||||  ||||||||||||
                                CCGGCG  CGAGGGACATA
                                   GC
GAM388  TFRC    3'  CAGGTTATCTACCCTGTAT   17429     C   G  _
                                TAGG TGT CT CCCTGTAT
                                |||| ||| ||  ||||||||
```

```
                                GTCC ATA GA GGGACATA
                                  A  _ T
GAM388  VCX     5'  CAGGCTGCCTGGCCTCCCTGTA 42907       ___ _
           T                    TAGGCTGT  GC TCCCTGTAT
                                |||||||| || |||||||||
                                GTCCGACG  CG AGGGACATA
                                    GAC  G
GAM388  VCY     5'  CAGGCTGCCTGGCCTCCCTGT  21710       ___ _
                                TAGGCTGT  GC TCCCTGT
                                |||||||| || |||||||
                                GTCCGACG  CG AGGGACA
                                    GAC  G
GAM389  DLEC1   3'  TTTGCCATAGTAGACA     28854       CAG
                                TTTGTCA  TAGTAGACA
                                |||||||  |||||||||
                                AAACGGT  ATCATCTGT
                                   ___
GAM389  PLEK    3'  TTTGTCACAGAAGTGGACA   15391         T  A
                                TTTGTCACAG AGT GACA
                                |||||||||| ||| ||||
                                AAACAGTGTC TCA CTGT
                                     T  C
GAM389  TPS1    3'  GTCCAAGTAGTAGGTGACACG  41306    AC      ACA
                                GTC  AGTAGTAG  ACACG
                                |||  |||||||  |||||
                                CAG  TCATCATC  TGTGC
                                  GT      CAC
GAM389  C11orf8 3'  ACAATGGCATGGCCT      11477        TATGC
                                ACAATGGCA    TGGTTT
                                |||||||||    ||||||
                                TGTTACCGT    ACCGGA
                                    _____
GAM389  DGKE    3'  ACAATTAACCATGCTGGTTT  18887      _  A
                                ACAAT GGC TATGCTGGTTT
                                ||||| ||| ||||||||||
                                TGTTA TTG GTACGACCAAA
                                  A  _
GAM389  HIF1A   3'  TAACAATGTCATGTTCCAGGTT 11350       G  ATG  _
           TAA                   TAACAATG CAT  CT GGTTTAA
                                |||||||| |||  || |||||||
                                ATTGTTAC GTA  GG CCAAATT
                                    A  CAA  T
GAM389  SFTPA2  3'  TGGCACATGGTATGTGCTC   27966       C__ _
                                TGGCATATG  TG GTTT
                                |||||||||  || ||||
                                ACCGTGTAC  AC CGAG
                                     CAT  A
GAM389  SLC1A4  3'  AATGGCTTAGCTGGTTTAA   16738      A  T
                                AATGGC TA GCTGGTTTAA
                                ||||||  || ||||||||||
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                                TTACCG AT CGACCAAATT
                                   A  _
GAM389  ZNF236   3'  ACTGTGGCGTGTGGCTCA    28857    AA    ATA  C
                                AC  TGGC   TG TGGTTTA
                                ||  ||||   || |||||||
                                TG  ACCG   AC ACCGAGT
                                 AC    C__  _
GAM390  PAFAH1B1  3'  CGAGAGCAATATTATATACAT  7705              CTAG
                                CGAGAGCAATGTTATG    ACAT
                                ||||||||||||||||   ||||
                                GCTCTCGTTATAATAT    TGTA
                                          A___
GAM390  UBQLN1   3'  GAGACAATGTTACATTA     30278      G        GC
                                GAGA CAATGTTAT  TA
                                |||| |||||||||  ||
                                CTCT GTTACAATG  AT
                                  _        TA
GAM390  GFRA2    3'  TGCAAGGTGTGTGTGTG     11269       AA  A    A
                                TGCAA  TG TGTGT TG
                                |||||  || ||||| ||
                                ACGTT  AC ACACA AC
                                   CC  _    C
GAM391  ATP7A    5'  TTCCTGGTTTCTCTATCC    6270          C   _
                                TTCCTGGTT CTCT TCC
                                ||||||||| |||| |||
                                AAGGACCAA GAGA AGG
                                     A   T
GAM391  BAZ2A    5'  TTCCACCCTCTCCTCTTCC   30319      TGG__
                                TTCC    TTCCTCTTCC
                                ||||    ||||||||||
                                AAGG    GAGGAGAAGG
                                  TGGGA
GAM391  BCL11B   5'  TCTCTTTCCCTCTCTTCC    39757    _ GG  _
                                TC CT  TTC CTCTTCC
                                || ||  ||| |||||||
                                AG GA  GGG GAGAAGG
                                 A  AA   A
GAM391  CIT      3'  TCCCGACGGGCCTCTTCC    43056       TT__
                                TCCTGG   CCTCTTCC
                                ||||||   ||||||||
                                AGGGCT   GGAGAAGG
                                   GCCC
GAM391  CSF1R    5'  TCCTTGGGCTGATCCTCTTC  23315     __  ___
                                TCCT  GGT   TCCTCTTC
                                ||||  |||   ||||||||
                                AGGA  CCG   AGGAGAAG
                                  AC   ACT
GAM391  EDARADD  5'  CTCCTCCTTCGCTTCTTCC   38848      GG  _ _
                                TTCCT  TTC CT CTTCC
                                |||||  ||| || |||||
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                                GAGGA  AAG GA GAAGG
                                   GG   C  A
GAM391   EIF5A    3'  TCCCCTCTCCTCCTCTTCC   12702      GG__
                                TTCCT   TTCCTCTTCC
                                |||||   ||||||||||
                                AGGGG   GAGGAGAAGG
                                   AGAG
GAM391   GNB2     3'  CTCCTGCTCCTCCTCTTCC   23599      G __
                                TTCCTG T  TCCTCTTCC
                                ||||||  |  |||||||||
                                GAGGAC A  AGGAGAAGG
                                   G GG
GAM391   GRIA2    5'  TTCCTTTTCCTCCTCTTCC   9085       GG__
                                TTCCT   TTCCTCTTCC
                                |||||   ||||||||||
                                AAGGA   GAGGAGAAGG
                                   AAAG
GAM391   HIS1     5'  TTCCCACAGCTCCTCTTCC   26997      __
                                TTCCT  GGTTCCTCTTCC
                                |||||  ||||||||||||
                                AAGGG  TCGAGGAGAAGG
                                   TG
GAM391   ITGA6    3'  CTCCCAACACCCTTTTCC    6829       GG _   C
                                TTCCT  T TCCT TTCC
                                |||||  | |||| ||||
                                GAGGG  G GGGA AAGG
                                   TT T   A
GAM391   KRT4     3'  CTCCTGGTCATTTTCTTC    14004       CC__
                                TTCCTGGTT   TCTTC
                                |||||||||   |||||
                                GAGGACCAG   AGAAG
                                      TAAA
GAM391   LIMD1    3'  CTCCTGCCCCTCCTCTTCC   30630      G __
                                TTCCTG T  TCCTCTTCC
                                ||||||  |  |||||||||
                                GAGGAC G  AGGAGAAGG
                                   G GG
GAM391   PRX      3'  TTCCCCACTGCCCTCTTCC   34138      G T__
                                TTCCT G   TCCTCTTCC
                                |||||  |   |||||||||
                                AAGGG T   GGGAGAAGG
                                   G GAC
GAM391   PTGFRN   3'  TCCCAGTTCCCTTCTTCC    42598     TG   __
                                TCC  GTTCC  TCTTCC
                                |||  |||||  ||||||
                                AGG  CAAGG  AGAAGG
                                  GT    GA
GAM391   RAB13    3'  TCCCTTCCTCTCTCTTCC    16120      GG  _
                                TTCCT  TTC CTCTTCC
                                |||||  |||  |||||||
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                                AGGGA  GAG GAGAAGG
                                  AG   A
GAM391  SLC17A1  3'  CTCCTACCACCTTCTTCC    22903       GTT  _
                                TTCCTG   CCT CTTCC
                                ||||||   ||| |||||
                                GAGGAT   GGA GAAGG
                                   GGT   A
GAM391  SRC      3'  CTCCTGGTTCCTCTTCCG    24034             III
                                TTCCTGGTTCCTCTTCC   G
                                ||||||||||||||||   |
                                GAGGACCAAGGAGAAGG   C
                                          III
GAM391  TAF4B    3'  TTCCGATTCCACCTCTTCC    44553     T     ____
                                TTCC GGTTCC   TCTTCC
                                |||| ||||||   ||||||
                                AAGG CTAAGG   AGAAGG
                                  _     TGG
GAM391  TCF15    3'  CTCCTGGGGTCTTCTTCC    21421       T_  C
                                TTCCTGG  TC TCTTCC
                                |||||||  || ||||||
                                GAGGACC  AG AGAAGG
                                    CC  A
GAM391  TMEPAI   3'  TTCCTCTCACTCCTCTTC    33628      GG__
                                TTCCT    TTCCTCTTC
                                |||||    |||||||||
                                AAGGA    GAGGAGAAG
                                  GAGT
GAM391  VEGFB    3'  CTCCCAGTCTCCTCTTCC    17978     TG  _
                                TTCC  GT TCCTCTTCC
                                ||||  || |||||||||
                                GAGG  CA AGGAGAAGG
                                  GT  G
GAM392  APOD     3'  TCGTGGTTGATTGGTTT     11608     GT   CG
                                TCG  TGG  TGATTGGTTT
                                |||  |||  ||||||||||
                                AGC  ACC  ACTAACCAAA
                                  __   A_
GAM392  BRCA1    3'  GGTGGCGTTTAAATGGTTT    28637     T    GAT__
                                GGT GGCGT    TGGTTT
                                ||| |||||    ||||||
                                CCA CCGCA    ACCAAA
                                  _    AATTT
GAM393  DNAJB9   3'  TGAGGTATCAGTCAATCTCTAG 29562     AA    CGAT  _
          A                      TGA  TATC    TCA TCTCTAGA
                                 |||  ||||   ||| ||||||||
                                 ACT  ATAG    AGT AGAGATCT
                                   CC   TC__   T
GAM393  MAN1A1   3'  TGAAATACCCTCTCTTTAG   45100          GATTCA   C
                                TGAAATATCC     TCT TAG
                                ||||||||||     ||| |||
```

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                                ACTTTATGGG     AGA ATC
                                     AG____   A
GAM393  RBBP2    3'  TGAAGGCCATTCATCTTTAGA  22804     ATAT  G      C
                                TGAA   CC ATTCATCT TAGA
                                ||||   || |||||||| ||||
                                ACTT   GG TAAGTAGA ATCT
                                  CC__ _      A
GAM393  TRPM8    3'  TCCTTCAATAGGAGCCTGGTGA 35861       CAATTAT  _ C
          G                      TCTTTCAA     GTC GG GAG
                                ||||||||     ||| || |||
                                AGGAAGTT     CGG CC CTC
                                     ATCCT__  A  A
GAM394  BIN3     3'  CCAGAAGGTGGGCCAGGGCCGG 33073        AT   TT
                                CTAGAAGGTG  GTT  GGCCGG
                                ||||||||||  |||  ||||||
                                GGTCTTCCAC  CGG  CCGGCC
                                      C_   TC
GAM394  CAPS     3'  GGTTGATGTTTTACAGA     19763     _      GC
                                GGT GATGTTTTG  CGGA
                                ||| |||||||||  ||||
                                CCA CTACAAAAT  GTCT
                                  A       __
GAM394  CDK2     3'  CTAGAAGGTGAGTGTTTAAGG  12202         _    T_
                                CTAGAAGGTGA TGTTT  GG
                                |||||||||| |||||  ||
                                GATCTTCCACT ACAAA  CC
                                      C     TT
GAM394  CGB      5'  CCAGGAGGTGATAGGATGCTGG 8824      A      TTTTG  C
                                CTAG AGGTGATG    GC GG
                                |||| ||||||||    || ||
                                GGTC TCCACTAT    CG CC
                                  C       CCTA_  A
GAM394  EMP1     3'  CTGGAATGTGATGTTTTGCTTT 10893    A  G        GCC_
          GG                     CT GAA GTGATGTTTTG   GG
                                || ||| ||||||||||   ||
                                GA CTT CACTACAAAAC   CC
                                 C  A         GAAA
GAM394  F9       3'  TAAACATTGATGTTTTGGTTGG 6577      AGG        CC
          A                      TAGA   TGATGTTTTGG  GGA
                                ||||   ||||||||||  |||
                                ATTT   ACTACAAAACC  CCT
                                  GTA         AA
GAM394  IL6R     3'  GGAGGAGGCTTTGGCTGGA   8179     T_ T      C
                                GG  GA GTTTTGGC GGA
                                ||  || |||||||| |||
                                CC  CT CGAAACCG CCT
                                 TC  C       A
GAM394  PTMS     5'  GAGGGTGGCCGCGGCCGGA   15885    A   AT  TT
                                GA GGTG  GT  TGGCCGGA
                                || ||||  ||  ||||||||
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                                CT CCAC  CG  GCCGGCCT
                                 C   __  GC
GAM394  SOX10   5'  AGGTGACGCTGGTGGGCTGG  27995        TT__  C
                                AGGTGATGTT   GGC GG
                                ||||||||||   ||| ||
                                TCCACTGCGA   CCG CC
                                     CCAC   A
GAM394  SUFU    3'  CTAGAAGATGAGGCG      32084         TGTTTT  C
                                CTAGAAGGTGA    GGC G
                                ||||||||||     ||| |
                                GATCTTCTACT    CCG C
                                      _____  A
GAM394  TAL1    3'  CTAGAAGTGAGGCG       17283       G  TGTTTT  C
                                CTAGAAG TGA    GGC G
                                ||||||| |||    ||| |
                                GATCTTC ACT    CCG C
                                   _  _____  A
GAM394  CIAO1   3'  TGACGTTTTCTGGGGAGTC   22067   A  GC     TG
                                C ACG  TTCTGGGG  GGTT
                                | |||  ||||||||  ||||
                                A TGC  AAGACCCC  TCAG
                                 C  AA     __
GAM394  CSNK2A1  3'  GCTTCTGAAGTGTTTCA    12477        GG
                                GCTTCTGGGGT  GTTTCA
                                ||||||||||  ||||||
                                CGAAGACTTCA  CAAAGT
                                          __
GAM394  IGHMBP2  3'  GGCTGGGATGTGGGTTT    13493    TCT  __
                                GGCT  GGG  GTGGGTTT
                                ||||  |||  ||||||||
                                CCGA  CCC  CACCCAAA
                                  ___  TA
GAM394  MIR16   3'  GGCAGTTTCTGAACCCGTTTC  32496    ___    GTGG
                                GGC  TTCTGGG   GTTTC
                                |||  |||||||   |||||
                                CCG  AAGACTT   CAAAG
                                  TCA     GGG_
GAM394  PCDHB16  5'  CAACGGTGTCTTAAAGAGGTTT 34140      CT  GG  T
          CA                    CAACGG  TCT  GG GGGTTTCA
                                ||||||  |||  || ||||||||
                                GTTGCC  AGA  TT TCCAAAGT
                                   AC  AT  C
GAM394  SIL     3'  GGCTTTTCTTAAAGGTTTCA  16728    __  GGGGT
                                GGCT  TCT    GGGTTTCA
                                ||||  |||    ||||||||
                                CCGA  AGA    TCCAAAGT
                                  AA  ATT__
GAM394  SPANXC   5'  CGGCAGGCTTTTGTAGGTTT  35490    TT_  GGG
                                CGGC  CT   GTGGGTTT
                                ||||  ||   ||||||||
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                                GCCG  GA  CATCCAAA
                                  TCC  AAA
GAM394  XKRY    3'  GCTTCTGGATGATTTTCA   21704        G  GG
                                GCTTCTGGG TG  TTTCA
                                ||||||||| ||  |||||
                                CGAAGACCT AC  AAAGT
                                     _  TA
GAM395  ASTN    3'  TTCCAGATGAGGAGCCCTGGT  42960       CAAA   ____
                                TTCCAGAT   GAGGG   TGGT
                                ||||||||   |||||   ||||
                                AAGGTCTA   CTCCT   ACCA
                                     ____   CGGG
GAM395  CAMK4   3'  TTCCAGATCTGAAGGAAGC   11952        AAA   T
                                TTCCAGATC  GAGGG GGT
                                |||||||||  ||||| |||
                                AAGGTCTAG  CTTCC TCG
                                     A__    T
GAM395  COL4A6  3'  TTCCGATCAAGACGGT     37980     A    A  G
                                TTCC GATCAA GA GGT
                                |||| |||||| || |||
                                AAGG CTAGTT CT CCA
                                  _    _ G
GAM395  CYP1B1  3'  TTCCATGTCAAAAATAGGTGGT 6458       GA    _
                                TTCCA  TCAAAGA GGGTGGT
                                |||||  ||||||| |||||||
                                AAGGT  AGTTTTT TCCACCA
                                   AC      A
GAM395  DMXL1   3'  TTCTGAATCAGAAAAGGT   24295    CA   A
                                TTC  GATCA AGAGGGT
                                |||  ||||| |||||||
                                AAG  TTAGT TTTTCCA
                                  AC    C
GAM395  EGFL5   3'  TTCCAATCAAAGCTGT     44547      A    AGG
                                TTCCAG TCAAAG  GT
                                |||||| ||||||  ||
                                AAGGTT AGTTTC  CA
                                   _    GA_
GAM395  FCMD    3'  TTCCAGATAAAGGT       27528       CAAA
                                TTCCAGAT   GAGGGT
                                ||||||||   ||||||
                                AAGGTCTA   TTTCCA
                                     _____
GAM395  FCMD    3'  TTCCAGATTTAGCTCTGGT   27529       CAA  AGGG
                                TTCCAGAT  AG   TGGT
                                ||||||||  ||   ||||
                                AAGGTCTA  TC   ACCA
                                     AA_  GAG_
GAM395  FCRH1   3'  TTCCAGATTGAGTGACAG   38110       CAAA  _  TG
                                TTCCAGAT   GAG GG  G
                                ||||||||   ||| ||  |
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                                AAGGTCTA   CTC CT  C
                                   A___   A  GT
GAM395  GOSR1    3'  TTCCAGACCAGGGTG      22180        AAGA
                                TTCCAGATCA   GGGTG
                                ||||||||||   |||||
                                AAGGTCTGGT   CCCAC
                                     ____
GAM395  GPRC5C   3'  TTCCAGATCTGGGGCA     35133        AAAGA
                                TTCCAGATC    GGGTG
                                |||||||||    |||||
                                AAGGTCTAG    CCCGT
                                   AC___
GAM395  IGF1     3'  TTCCAGATAGGAATTGGT    8362        CAAAG   __
                                TTCCAGAT    AGGG  TGGT
                                ||||||||    ||||  ||||
                                AAGGTCTA    TCCT  ACCA
                                     _____   TA
GAM395  JPH3     3'  TTCTAGACAGAGAAAGCAGT  34031    C   T  A     TG
                                TTC AGA CA AGAGGG  GT
                                ||| ||| || ||||||  ||
                                AAG TCT GT TCTTTC  CA
                                  A  _ C     GT
GAM395  MHC2TA   3'  TTCCAGACTGGGGGC       6994        CAAAGA   T
                                TTCCAGAT     GGG GGT
                                ||||||||     ||| |||
                                AAGGTCTG     CCC CCG
                                   A_____  _
GAM395  PCDH11X  3'  TTCCAGATATGAGGAT      37320        CAAA
                                TTCCAGAT   GAGGGT
                                ||||||||   ||||||
                                AAGGTCTA   CTCCTA
                                   TA__
GAM395  PCDH11Y  3'  TTCCAGATATGAGGAT      37365        CAAA
                                TTCCAGAT   GAGGGT
                                ||||||||   ||||||
                                AAGGTCTA   CTCCTA
                                   TA__
GAM395  PDE6A    3'  TCCCAGGAAAGGGTGGT     7759        ATCAA
                                TTCCAG    AGAGGGTGGT
                                ||||||    ||||||||||
                                AGGGTC    TTTCCCACCA
                                  C____
GAM395  PPP1R12A 3'  TTCTAGATAAGAGGGCA     14730    C   CA
                                TTC AGAT  AAGAGGGTG
                                ||| ||||  |||||||||
                                AAG TCTA  TTCTCCCGT
                                  A   __
GAM395  PPP1R12B 5'  TTCCAGGTGAAAGCAGGT    36984       ATC   A
                                TTCCAG   AAAG GGGT
                                ||||||   |||| ||||
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                                AAGGTC   TTTC TCCA
                                   CAC    G
GAM395  PYGB    3'  TTCCAGACGAGGCTG       16053        CAAA    G
                                TTCCAGAT    GAGG TG
                                ||||||||    |||| ||
                                AAGGTCTG    CTCC AC
                                    _____    G
GAM395  RET     3'  TTCCAAATCGAGGGT       34156        AAA
                                TTCCAGATC   GAGGGT
                                |||||||||   ||||||
                                AAGGTTTAG   CTCCCA
                                     ___
GAM395  RPL10   3'  AGCTACAAGGAGGGTGGT    25667    AT_   A
                                AG   CAA GAGGGTGGT
                                ||   ||| |||||||||
                                TC   GTT CTCCCACCA
                                 GAT   C
GAM395  SEL1L   3'  TTCTAATCAAAGAGAAT     22853     CA
                                TTC  GATCAAAGAGGGT
                                |||  ||||||||||||
                                AAG  TTAGTTTCTCTTA
                                  A_
GAM395  SOX12   3'  TCCCGGATCAAAGGAT      28059     A    AA
                                TTCC GATCA  GAGGGT
                                |||| |||||  ||||||
                                AGGG CTAGT  TTCCTA
                                  C    __
GAM395  STK6    3'  TTCTAGATTGAGGGCAGC    18778     C   CAAA    TG
                                TTC AGAT    GAGGG  GT
                                ||| ||||    |||||  ||
                                AAG TCTA    CTCCC  CG
                                  A   A___     GT
GAM395  TACR1   3'  TTCCAGATGAAGGGA       31860        CAAA    TG
                                TTCCAGAT    GAGGG  G
                                ||||||||    |||||  |
                                AAGGTCTA    CTTCC  T
                                    _____    CT
GAM395  TBX6    5'  TTCCAGATCCAGGAT       38865        AAAG
                                TTCCAGATC    AGGGT
                                |||||||||    |||||
                                AAGGTCTAG    TCCTA
                                     G___
GAM395  TGFA    3'  TTCCAGATCAGGGT        17451         AAGA
                                TTCCAGATCA    GGGT
                                ||||||||||    ||||
                                AAGGTCTAGT    CCCA
                                     _____
GAM395  TMOD2   3'  TTCCGGATAGAGGGT       30971     A   CAA
                                TTCC GAT   AGAGGGT
                                |||| |||   |||||||
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                                AAGG CTA   TCTCCCA
                                  C  ___
GAM395  TRRAP    3'  TTCCAGACCGGAGAAT     18594        AAA
                                TTCCAGATC   GAGGGT
                                |||||||||  ||||||
                                AAGGTCTGG   CTCTTA
                                    C__
GAM395  VSNL1    3'  TTCCAGATCGATAGGAT     18042        AAAG
                                TTCCAGATC    AGGGT
                                |||||||||   |||||
                                AAGGTCTAG    TCCTA
                                    CTA_
GAM395  ZNF146   3'  CTCCAGATCTATGGTGGT    28351        AAAGAG
                                TTCCAGATC     GGTGGT
                                |||||||||     ||||||
                                GAGGTCTAG     CCACCA
                                    ATA___
GAM396  CCND1    5'  GGGGCTCTTCCTGGGCAGCT   38216    AA   C    _
                                GG  CTCT CCTGGG GGCT
                                ||  |||| |||||| ||||
                                CC  GAGA GGACCC TCGA
                                 CC   A    G
GAM396  GALGT    5'  GGAACTCCCGGGGCTTTT    11186        CCTG
                                GGAACTCTC   GGGGCTTTT
                                |||||||||   |||||||||
                                CCTTGAGGG   CCCCGAAAA
                                    ____
GAM396  KIF5A    5'  GGGACTCTTCTTGGGCT     22549    A    CC  GG
                                GG ACTCT  CT  GGGCT
                                || |||||  ||  |||||
                                CC TGAGA  GA  CCCGA
                                 C    A_  A_
GAM396  OGG1     3'  GGAACCCTTTCTGCGCTTT   32566        CC   GGG
                                GGAACTCT  CTG   GCTTT
                                ||||||||  |||   |||||
                                CCTTGGGA  GAC   CGAAA
                                    AA   G__
GAM396  PDE5A    5'  TCGGAGGCTCTCTGGTACTGCT 37906      ACT   C    GG__
          TTT                  TCGGA   CTC CTGG    GCTTTT
                               |||||   ||| ||||    ||||||
                               AGCCT   GAG GACC    CGAAAA
                                 CC_   A    ATGA
GAM396  PRKACA   3'  GGGGCTCCCCCTCTGTCTTTT  15587    AA       GGGGG
                                GG  CTCTCCCT    CTTTT
                                ||  ||||||||    |||||
                                CC  GAGGGGGA    GAAAA
                                 CC       GACA_
GAM396  SLC38A2  3'  GGAATTTTCCCTAGGCACTT   33276     CTC       G
                                GGAA   TCCCTGGG GCTT
                                ||||   |||||||| ||||
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                                CCTT  AGGGATCC TGAA
                                  AAA      G
GAM397  BAIAP3   3'  TCGGCTCTTTGCGGCTGCTGG  19459    A  C       ACC
                                TC GC TTTTGCGGTT  GCTGG
                                || || ||||||||||  |||||
                                AG CG GAAACGCCGA  CGACC
                                 C  A        ___
GAM397  MIR16    3'  TCAGCTTTCTGAATTGCTG   32498      C    C   ACC
                                TCAGC TTTTG GGTT  GCTG
                                ||||| ||||| ||||  ||||
                                AGTCG AAGAC TTAA  CGAC
                                  A    _   ___
GAM397  PROX1    3'  GCCTTTTGGGGTACTTTGG   15722        C  T  CGC
                                GCCTTTTG GG TAC  TGG
                                |||||||| || |||  |||
                                CGGAAAAC CC ATG  ACC
                                    _ C  AA_
GAM397  RXRA     3'  CTTTTGCACTCCCACCGCTGG  16425        G __
                                CTTTTGCG TT  ACCGCTGG
                                |||||||| ||  ||||||||
                                GAAAACGT AG  TGGCGACC
                                    G  GG
GAM397  ZNF268   5'  TCAGTTTTGTGTGCCTCGCTGG 41763     CC    CG_  AC
                                TCAG  TTTTG  GTT  CGCTGG
                                ||||  |||||  |||  ||||||
                                AGTC  AAAAC  CGG  GCGACC
                                  __   ACA  A_
GAM398  CHRNA3   3'  TGAGAAGTTTCTGTTGTTT   8840          AAACGA
                                TGAGAGGTTTC    TTGTTT
                                ||||||||||     ||||||
                                ACTCTTCAAAG    AACAAA
                                      AC____
GAM398  FBXW1B   3'  TGGAGGTTTATTGTT      37997    A     CAAACG
                                TG GAGGTTT     ATTGTT
                                || |||||||     ||||||
                                AC CTCCAAA     TAACAA
                                 _     _______
GAM398  LFNG     3'  TGGGAGGTTCCAGATGCT    45221    A       AAC  T
                                TG GAGGTTTCA  GAT GTT
                                || |||||||||  ||| |||
                                AC CTCCAAGGT  CTA CGA
                                 C       ___  _
GAM398  NSF      3'  TGAGAGGTTTGTAAATTACTT  41785         CAAAC
                                TGAGAGGTTT    GATTGTTT
                                ||||||||||    ||||||||
                                ACTCTCCAAA    TTAATGAA
                                      CAT__
GAM398  CACNA1C  5'  CAAATTTTTGCCTTTT     8745           AA
                                CAAATTTTTGC  CTTTT
                                ||||||||||  |||||
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                                GTTTAAAAACG  GAAAA
                                    __
GAM398  COL19A1   3'  TCTAGATTTCTGCAACATCCTC 12383    CAA        TT
            A                    TC   ATTTTTGCAAC  TTCTCA
                                 ||   ||||||||||  ||||||
                                 AG   TAAAGACGTTG  AGGAGT
                                  ATC         T_
GAM398  EIF2C1    3'  TCCAAATTTTGGCAATACACTC 29182         T    CTTTT
            A                    TCCAAATTTT GCAA    CTCA
                                 ||||||||||  ||||    ||||
                                 AGGTTTAAAA CGTT    GAGT
                                       C    ATGT_
GAM398  LMO4      3'  TCCAAATTTTTTTTCTTTT   27661          GCAA
                                 TCCAAATTTTT    CTTTT
                                 ||||||||||    |||||
                                 AGGTTTAAAAA    GAAAA
                                       AAA_
GAM398  PCDHAC1   3'  AATTTTTGCCCTTGTTTCTCA  36615         AACT_
                                 AATTTTTGC     TTTCTCA
                                 |||||||||     |||||||
                                 TTAAAAACG     AAAGAGT
                                       GGAAC
GAM398  WIF1      3'  TCCAAATTCTTGTGACTT    41171           CA
                                 TCCAAATTTTTG  ACTT
                                 ||||||||||||  ||||
                                 AGGTTTAAGAAC  TGAA
                                       AC
GAM398  ZNF141    3'  ATTTCTATAACTTTTCTC    18345        C
                                 ATTTTTG AACTTTTCTC
                                 ||||||| ||||||||||
                                 TAAAGAT TTGAAAAGAG
                                     A
GAM398  ZNF146    3'  TCCAATATTTACAACTTAATTT 28358       ATT        _____
              TTCT                  TCCAA   TTTGCAACTT    TTCT
                                 |||||   ||||||||||    ||||
                                 AGGTT   AAATGTTGAA    AAGA
                                    AT_        TTAAA
GAM399  ABCD4     3'  CCTTGGGTGTTTGACATA    33743    C  ___
                                 CC TGG   TTTGACATA
                                 || |||   |||||||||
                                 GG ACC   AAACTGTAT
                                  A   CAC
GAM399  ITK       3'  TCTCCTAGCTCAGTACATA   24446    C       __
                                 TC CCTGGTTTG  ACATA
                                 || |||||||||  |||||
                                 AG GGATCGAGT  TGTAT
                                  A        CA
GAM399  MYOG      3'  CCCCCTGAGCTGGGGCATA   40421        GT   A__
                                 TCCCCTG  TTG   CATA
                                 |||||||  |||   ||||
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                                GGGGGAC  GAC   GTAT
                                    TC   CCC
GAM399  NPTX1    3'  CCTCCTGGTCCCCAACAT    14834    _      __
                                CC CCTGGTTT  GACAT
                                || ||||||||  |||||
                                GG GGACCAGG  TTGTA
                                 A       GG
GAM399  UCP2     5'  TCCCCTTGGTTTTCCATA    17848       _    GA
                                TCCCCT GGTTT  CATA
                                |||||| |||||  ||||
                                AGGGGA CCAAA  GTAT
                                   A     AG
GAM399  ATP2B3   3'  GCGTGTGACTTCGTGTGAGTC  34973      A       C  TT
                                GCGT TGATTTCG GT  GGTT
                                |||| |||||||| ||  ||||
                                CGCA ACTGAAGC CA  TCAG
                                  C       A  C_
GAM399  MAP3K5   3'  TATGGTCACATTTTGGTTT   25445      ATT       _
                                TATG   TCGCGTTT GGTTT
                                ||||   |||||||| |||||
                                ATAC   AGTGTAAA CCAAA
                                  C__       A
GAM399  RBMX     3'  GCATGTGATTTCAGGTTT    42809      A       C
                                GCGT TGATTTCG GTTT
                                |||| |||||||| ||||
                                CGTA ACTAAAGT CAAA
                                  C       C
GAM400  RANBP2L1 3'  TTCCAGTTGGTATGGTACC   37030          CCCGATAAC
                                TTCCAGTTGG        GTACT
                                ||||||||||        |||||
                                AAGGTCAACC        CATGG
                                     ATAC_____
GAM401  DPYSL3   3'  GAATGGAAAGGTGGAACCAGG  10768     AT     A    A  T
                                GAA  GAAAGG TGGAA CA GG
                                |||  |||||| ||||| || ||
                                CTT  CTTTCC ACCTT GT CC
                                  AC     _     G  _
GAM401  LLGL1    3'  TGAGGGGGAAGGATGGTGTGTG 42511     AATGA       AAACA
           G                     TGA     AAGGATGG     TGG
                                |||     ||||||||     |||
                                ACT     TTCCTACC     ACC
                                  CCCCC       ACAC_
GAM401  PABPN1   3'  TGAAGGGGGCAGGGAAACATGG 21611      A__  AT_
                                TGAA   GG   GGAAACATGG
                                ||||   ||   ||||||||||
                                ACTT   CC   CCTTTGTACC
                                  CCC  GTC
GAM401  PCDH9    5'  TGACAGGAGATGGAAACATGG  44411     A    __
                                TGA AGGA  TGGAAACATGG
                                ||| ||||  ||||||||||
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                                ACT TCCT  ACCTTTGTACC
                                  G   CT
GAM401  PMP22    3'  TGAAAGGGAAGGGGCGACATGG 7163        AT___  AA
                                TGAAAGG    GG  ACATGG
                                |||||||    ||  ||||||
                                ACTTTCC    CC  TGTACC
                                    CTTCC  GC
GAM401  POLR2F   3'  TGAGAATGAAAATTGGGCATGG 35034    _      GA   AAA
                                TGA AATGAAAG  TGG   CATGG
                                ||| ||||||||  |||   |||||
                                ACT TTACTTTT  ACC   GTACC
                                  C       A_   C__
GAM401  PSMB2    3'  GAAAGGAAGCCAAGCATGG   15817       TGGA  _
                                GAAAGGA    AA CATGG
                                |||||||    || |||||
                                CTTTCCT    TT GTACC
                                    TCGG  C
GAM401  SLC38A2  3'  TGAAATGGAAGGGTTGACATG  33278       A    ATG  AA
                                TGAAATG AAGG   GA  CATG
                                ||||||| ||||   ||  ||||
                                ACTTTAC TTCC   CT  GTAC
                                    C    CAA  __
GAM401  SLC7A6   3'  TGAAAGGAGGATGACATG    19598        T   A_
                                TGAAAGGA GGA  ACATG
                                |||||||| |||  |||||
                                ACTTTCCT CCT  TGTAC
                                     _   AC
GAM401  SPN      3'  TGCCGGGTGGAAACATGG    17090    AAA  A
                                TG   GG TGGAAACATGG
                                ||   || ||||||||||
                                AC   CC ACCTTTGTACC
                                 GG_  C
GAM401  STATH    3'  ATGAAAGATGAGAATATGG   17164       G   GA  C
                                ATGAAAG ATG  AA ATGG
                                ||||||| |||  || ||||
                                TACTTTC TAC  TT TACC
                                    _   TC  A
GAM401  ZNF261   3'  TGATGTGAAAGATGGATATGG  22994     AA     G     AAC
                                TGA  TGAAAG ATGGA   ATGG
                                |||  |||||| |||||   ||||
                                ACT  ACTTTC TACCT   TACC
                                  AC     _     A__
GAM402  ABCB10   3'  CATAGTCTCTGAGTTTTTTTTC 28988        AT__
           T                    CATAGTCTT    TTTTTTTTCT
                                |||||||||    ||||||||||
                                GTATCAGAG    AAAAAAAAGA
                                     ACTC
GAM402  ADH4     3'  TACCAGGTCTTATTCATTCT   8575       TA       T
                                TACCA  GTCTTATTT TTTT
                                |||||  ||||||||| ||||
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                                ATGGT  CAGAATAAG AAGA
                                  C_       T
GAM402  C11orf8  3'  CCTGTTTCTTATTTTTTTTTCT 11479    ATAG
                                CC   TCTTATTTTTTTTTCT
                                ||   ||||||||||||||||
                                GG   AGAATAAAAAAAAAGA
                                 ACAA
GAM402  FOG2     3'  ACAGCTTATTTTTTTTTCT   28966     T
                                ATAG CTTATTTTTTTTTCT
                                |||| ||||||||||||||
                                TGTC GAATAAAAAAAAAGA
                                  _
GAM402  ITGB2    3'  AGTTTTATTTTTTTTTCT    6834     C
                                AGT TTATTTTTTTTTCT
                                ||| ||||||||||||||
                                TCA AATAAAAAAAAAGA
                                  A
GAM402  RGS5     3'  CATAGTCTTGTCTTATATTTCT 18831        A   TT_
                                CATAGTCTT TTTT   TTTCT
                                ||||||||| ||||   |||||
                                GTATCAGAA AGAA   AAAGA
                                     C   TAT
GAM402  SERPINE2 3'  TACCATAAAACATTTTTTTTTC 44006       TCT
          T                      TACCATAG   TATTTTTTTTTCT
                                 ||||||||   ||||||||||||
                                 ATGGTATT   GTAAAAAAAAAGA
                                     TT_
GAM402  SLC4A10  3'  CATAGTCTTATTCATTTTT   35191          T
                                CATAGTCTTATTT TTTTT
                                |||||||||||| |||||
                                GTATCAGAATAAG AAAAA
                                       T
GAM402  SMT3H1   3'  TACTTAGTCTTACTTTTTT   41002    CA
                                TAC  TAGTCTTATTTTTTT
                                |||  ||||||||||||||
                                ATG  ATCAGAATGAAAAAA
                                  A_
GAM402  VDR      3'  ACCATGCCCGGCTATTTTTTTT 7509      A   ___
          T                      ACCAT GTCT   TATTTTTTTTT
                                 |||||  ||||   ||||||||||
                                 TGGTA CGGG   ATAAAAAAAAA
                                   _   CCG
GAM402  WIF1     3'  TACCACAGTGTAATTTTTTTTT 41168        CTT
                                TACCATAGT   ATTTTTTTTT
                                |||||||||   ||||||||||
                                ATGGTGTCA   TAAAAAAAAA
                                     CAT
GAM402  ZNF85    3'  CCATAGTCTTCACATTTTT   18314         ATTT
                                CCATAGTCTT   TTTTT
                                ||||||||||   |||||
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                                GGTATCAGAA    AAAAA
                                      GTGT
GAM402  AMT      3'  ACAAGACATTGTGTGAGC    7904       AA        T
                                ACAA  ACATTGTGTG AGT
                                ||||  |||||||||| |||
                                TGTT  TGTAACACAC TCG
                                  C_        _
GAM402  EPS8     3'  AACATTGTTGCTTTGTT     20807        G   AG
                                AACATTGT TGT  TGTT
                                |||||||| |||  ||||
                                TTGTAACA ACG  ACAA
                                     _   AA
GAM402  GPC4     3'  ACAAAAACTTTGCCCGAGTGTT 11080         A    G  T
                                ACAAAAAC TTGT TG AGTGTT
                                |||||||| |||| || ||||||
                                TGTTTTTG AACG GC TCACAA
                                     A    G  _
GAM402  IL1A     3'  AACATTATATGTTAGTGTT    41674           _
                                AACATTGTGTGT AGTGTT
                                |||||||||||| ||||||
                                TTGTAATATACA TCACAA
                                       A
GAM402  NRCAM    5'  AAACGTTGTGTGCAAGTT    22685      A        T
                                AAAC TTGTGTGTAG GTT
                                |||| |||||||||| |||
                                TTTG AACACACGTT CAA
                                  C         _
GAM402  NRXN1    3'  AAAACACTGTGGATGTTA    39834           TGTA
                                AAAACATTGTG    GTGTTA
                                ||||||||||    ||||||
                                TTTTGTGACAC    TACAAT
                                       C___
GAM403  AMACR    3'  CAATACAGGTGAAACTT     42857      TAG   A
                                CAAT   GCA GTGAAACTT
                                ||||   ||| |||||||||
                                GTTA   TGT CACTTTGAA
                                  ___   C
GAM403  RDX      3'  TATCCAATAAGGTAATTAAA  16237         T   C  G
                                TATCCAAT AGG AA TGAA
                                |||||||| ||| || ||||
                                ATAGGTTA TCC TT ATTT
                                     T   A  A
GAM403  MADH4    3'  CAGTTTCCAAAATATTCAGTTT 23818      C     TTTA
                                CAGT TCCAAA    GTTTAGTTT
                                |||| ||||||    |||||||||
                                GTCA AGGTTT    TAAGTCAAA
                                  A     TA__
GAM403  PCNA     3'  CAGTTCTCAAAGAGCTTAGTTT 15118      _   C   TTT
                                CAGT CTC AAA   AGTTTAGTTT
                                |||| ||| |||   ||||||||||
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                                GTCA GAG TTT   TCGAATCAAA
                                  A  _  C__
GAM403  RDX     3'  ATCTCCAAATTTAGCTGTTT  16235            TA
                                GTCTCCAAATTTAGTT  GTTT
                                |||||||||||||||  ||||
                                TAGAGGTTTAAATCGA  CAAA
                                                  __
GAM404  AVP     5'  GAGGACAGGGGCTGCACCA   7936        TATCC
                                GAGGACG    CTGCACCA
                                |||||||    ||||||||
                                CTCCTGT    GACGTGGT
                                    CCCC_
GAM404  DAAM2   3'  GATGGCTTTGGTCCCTGCATCA 45175   _ ACGTA_      C
                                GA GG     TCCCTGCA CA
                                || ||     |||||||| ||
                                CT CC     AGGGACGT GT
                                 A  GAAACC       A
GAM404  FE65L2  3'  TCGAGGGGTTGCCCCTGCACC  39324       ACGTA
                                TCGAGG    TCCCTGCACC
                                ||||||    ||||||||||
                                AGCTCC    GGGGACGTGG
                                   CCAAC
GAM404  MCM6    5'  TGCCGAGGATTCGCCTGCGCCA 25407         CGTA  _    A
                                TGTCGAGGA   TC CCTGC CCA
                                |||||||||   || ||||| |||
                                ACGGCTCCT   AG GGACG GGT
                                      A___  C    C
GAM404  ADRA2A  3'  AGGGACAGTCACCAGTTGC   8625     A  _      G
                                AGG AC GTCACCAG TGC
                                ||| || |||||||| |||
                                TCC TG CAGTGGTC ACG
                                  C  T       A
GAM404  FZD1    3'  AGGAGCGCTGTGCGGTTG    18609     A   CACCAG
                                AGGA CGT     GTGCGGTTG
                                |||| |||     |||||||||
                                TCCT GCG     CACGCCAAC
                                  C   A_____
GAM404  GYS1    5'  GGAATGCACCAGGTAGGGT   44790     C T       C
                                GGAA G CACCAGGTG GGT
                                |||| | |||||||| |||
                                CCTT C GTGGTCCAT CCA
                                  A _       C
GAM404  RGS16   3'  AGGAGTGTTACGAGGTACAA  16317     AC  C  C
                                AGGA  GT AC AGGTGCGG
                                ||||  || || ||||||||
                                TCCT  CA TG TCCATGTT
                                  CA  A  C
GAM404  WBSCR1  3'  GGGACTCACCAGGCTGTGC   35271    A  G      T_______
                                GG AC TCACCAGG      GC
                                || || ||||||||      ||
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                                CC TG AGTGGTCC      CG
                                 C  _       GACAIII
GAM405  ADCY2    3'  TTCTTCAAGGCCTTCTGTC   42150     C       _ _
                                TTC TTAAGGCCT C GTC
                                ||| ||||||||| | |||
                                AAG AGTTCCGGA G CAG
                                  A        A A
GAM406  ANKH     3'  AGGTGATTTTATTCTTCCATT  38311        A     AG
                                AGGTGATT TATTTT  TATT
                                |||||||| ||||||  ||||
                                TCCACTAA ATAAGA  GTAA
                                     A     AG
GAM406  PCSK2    3'  AGCGAGACATATTTTAGTATTA 15122      T_
                                GGTGA  TATATTTTAGTATTA
                                |||||  ||||||||||||||
                                TCGCT  GTATAAAATCATAAT
                                   CT
GAM407  BCAT1    5'  CCCGAGGCGGCGGCGAG     42379     T  ACAA  A_
                                CCCG AG   CG  GGCGGG
                                |||| ||   ||  ||||||
                                GGGC TC   GC  CCGCTC
                                  _  C___  CG
GAM407  EMP3     3'  CAGCCGAGCGAGGCGGG     10902    C   T  ACAA
                                CA CCG AG   CGAGGCGGG
                                || ||| ||   |||||||||
                                GT GGC TC   GCTCCGCCC
                                 C  _  _____
GAM407  MASP1    3'  CACCCGTAGTGGAAAGGGG   40096        ACAAC   C
                                CACCCGTAG    GAGG GG
                                |||||||||    |||| ||
                                GTGGGCATC    TTCC CC
                                     ACCT_   _
GAM407  PPFIA3   3'  CCCGCAGATGACCCGGGGGAC  41416        CA  GA  C
                                CCCGTAGA  AC  GG GGGAC
                                ||||||||  ||  || |||||
                                GGGCGTCT  TG  CC CCCTG
                                     AC  GG  _
GAM407  SNX9     3'  CACCTGTGGGAGACGGGA    32149     C  AGACAAC
                                CACC GT      GAGGCGGGA
                                |||| ||      |||||||||
                                GTGG CA      CTCTGCCCT
                                  A  CC_____
GAM407  ST5      3'  CACCCGTAGATGGGAAGGAGGG 24041         CAAC   C
           A                     CACCCGTAGA   GAGG GGGA
                                 ||||||||||   |||| ||||
                                 GTGGGCATCT   TTCC CCCT
                                      ACCC   T
GAM407  TLL1     5'  CACCCGGAGGCTCCTCGGCGGG 29734       T  ACAACGA
           AC                     CACCCG AG      GGCGGGAC
                                  ||||||  ||      ||||||||
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                                GTGGGC TC      CCGCCCTG
                                   C  CGAGGAG
GAM407  ZNF26    5'  CCCGAAGACAGGTGCGGGAC   43798      T     ACGAG
                                CCCG AGACA     GCGGGAC
                                |||| |||||     |||||||
                                GGGC TCTGT     CGCCCTG
                                  T     CCA__
GAM407  ADORA3   3'  ACTAGAGCCTTTTGTCA     8615           GC
                                ACTAGAGCCTT  TGTTA
                                ||||||||||  |||||
                                TGATCTCGGAA  ACAGT
                                       A_
GAM407  FANCF    3'  TAGGCCTTGCTATGGT      35535     A        TAAC
                                TAG GCCTTGCTGT    GGT
                                ||| ||||||||||    |||
                                ATC CGGAACGATA    CCA
                                  _       _____
GAM407  NDRG3    3'  GCTCTTGCTATGTGGTA     36747     _       TAAC
                                GC CTTGCTGT    GGTA
                                || ||||||||    ||||
                                CG GAACGATA    CCAT
                                 A       CA__
GAM407  SHANK2   3'  CAGGGCCTTGCTGGGGT     29451     A        TTAAC
                                TAG GCCTTGCTG     GGT
                                ||| |||||||||     |||
                                GTC CGGAACGAC     CCA
                                  C        C_____
GAM407  WFDC1    3'  CAGGGCCTTGCTCCCAGGATGG 34522     A       G   AC__
           TA                     TAG GCCTTGCT TTA    GGTA
                                ||| |||||||| |||    ||||
                                GTC CGGAACGA GGT    CCAT
                                  C       G   CCTA
GAM408  ADAMTS1  3'  GAAGGAACACCCAAACCA    28113     TTTTT
                                GA     ACACCCAAACCA
                                ||     ||||||||||||
                                CT     TGTGGGTTTGGT
                                 TCCT_
GAM408  COG4     3'  TCAGATCTCCCCCAAGCCA    31723          ACA     A
                                TCAGATTTTT   CCCAA CCA
                                |||||||||   ||||| |||
                                AGTCTAGAGG   GGGTT GGT
                                      ____     C
GAM408  DUSP6    3'  TATCAGATTTTTTTTTCCAAAC 42328            ACAC
                                TATCAGATTTTT    CCAAAC
                                ||||||||||||    ||||||
                                ATAGTCTAAAAA    GGTTTG
                                       AAAA
GAM408  NOS1     3'  TAGCAGACACCCAAAC      8377     T    TTTTTA
                                TA CAGA     CACCCAAAC
                                || ||||     |||||||||
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                                AT GTCT     GTGGGTTTG
                                 C  _______
GAM408  SIRT1    3'  CAGATTTTGAGTACTTCAAACC 29253         ___  ACC
              A                   CAGATTTT   TAC   CAAACCA
                                  ||||||||   |||   |||||||
                                  GTCTAAAA   ATG   GTTTGGT
                                      CTC   AA_
GAM408  XK       3'  TCAGGTTACCCAAAC       34368      A  TTTAC
                                  TCAG TT    ACCCAAAC
                                  |||| ||    ||||||||
                                  AGTC AA    TGGGTTTG
                                    C  _____
GAM408  IL21R    3'  ACGTTTATTGAGGGTCTGC   34752         A   AC__
                                  GCGTTTATT AGG    GC
                                  |||||||| |||    ||
                                  TGCAAATAA TCC    CG
                                       C   CAGA
GAM409  CLC      3'  GTCTGGTCTGGTCTGTCCCT   29900       TG  A__
                                  GTCTG  CT   TTGTCCCT
                                  |||||  ||   ||||||||
                                  CAGAC  GA   GACAGGGA
                                     CA  CCA
GAM409  HAL      5'  GGTGTGGTCAGCTGCTGTCCCT 13332    C  A   TGT   A
                                  GG GT GTC   GCT TTGTCCCT
                                  || || |||   ||| ||||||||
                                  CC CA CAG   CGA GACAGGGA
                                   A  C   T__   C
GAM410  ABP1     3'  GGAATGTCCTCTGAGTG     41791     CC  CAGA
                                  GGA  TG    CTCTGAGTG
                                  |||  ||    |||||||||
                                  CCT  AC    GAGACTCAC
                                    T_  AG__
GAM410  ENO2     5'  TCGGGACTGCAGACTCAGACGG 12716    A   C       T  __
              TG                    TC GGAC TGCAGACTC GA  GTG
                                  || |||| ||||||||| ||  |||
                                  AG CCTG ACGTCTGAG CT  CAC
                                   C   _       T  GC
GAM410  LIG3     3'  GGCCAGCAGCTGAGTGA     30359    A  T    ACT
                                  GG CC GCAG   CTGAGTGA
                                  || || ||||   ||||||||
                                  CC GG CGTC   GACTCACT
                                   _  T   ____
GAM410  LUM      5'  GGCTGCCAGATTCTGAGTGA   14271    AC   _   C
                                  GG  CTGC AGA TCTGAGTGA
                                  ||  |||| ||| |||||||||
                                  CC  GACG TCT AGACTCACT
                                    __   G   A
GAM410  NRBP     3'  TCAGGGCCTGGCCCGAGTG   30162       A   CAGAC
                                  TCAGG CCTG    TCTGAGTG
                                  ||||| ||||    ||||||||
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                                AGTCC GGAC    GGGCTCAC
                                  C   C____
GAM410  TCF1    3'  TCAGGACCTCAGACTCCTCAGG 8092         G      GA___
            GTG                   TCAGGACCT CAGACTCT    GTG
                                  ||||||||| ||||||||    |||
                                  AGTCCTGGA GTCTGAGG    CAC
                                      _       AGTCC
GAM410  TRIM14  3'  TCAGGACCTCAGACTCC     37705         G
                                  TCAGGACCT CAGACTCT
                                  ||||||||| ||||||||
                                  AGTCCTGGA GTCTGAGG
                                      _
GAM410  UFD1L   3'  TCAGGTTCTTCTGAGT      43824       AC  GCAGAC
                                  TCAGG  CT     TCTGAGT
                                  |||||  ||     |||||||
                                  AGTCC  GA     AGACTCA
                                    AA  _______
GAM410  ZNF278  3'  CAGGATCTAGATCTGAGTG   36786       C  GC   C
                                  CAGGA CT  AGA TCTGAGTG
                                  ||||| ||  ||| ||||||||
                                  GTCCT GA  TCT AGACTCAC
                                    A  __  _
GAM410  ADRA2A  3'  TGGCCCTGGAGGGAGAGAGGG  8643         AAAATGCC
                                  TGGCCCTG       GGAGAGGG
                                  ||||||||       ||||||||
                                  ACCGGGAC       TCTCTCCC
                                       CTCCC___
GAM410  ARHGDIB  3'  TGGCCCTGATGGAGGATCAGAG 10129         AAA  CC  ___
            GG                    TGGCCCTGA   TG  GGA   GAGGG
                                  |||||||||   ||  |||   |||||
                                  ACCGGGACT   AC  CCT   CTCCC
                                       ___  CT   AGT
GAM410  BMP1    3'  GGTCCTGGGGCCTGGGGGAGAG 25990    C    AAAAT  ____
            GG                    GG CCTG    GCC    GGAGAGGG
                                  || ||||    |||    ||||||||
                                  CC GGAC    CGG    CCTCTCCC
                                   A   CC___   ACCC
GAM410  CAPN1   3'  TGGCCTCTGAAGTGGGGAGAGG 23256      _    AA  CC
            G                     TGGCC CTGAA  TG  GGAGAGGG
                                  ||||| |||||  ||  ||||||||
                                  ACCGG GACTT  AC  CCTCTCCC
                                    A    C_  C_
GAM410  CD79A   3'  TGGCCCTGACAGATCAGGGAGG 34649         AAATGCC_   _
            AGGG                    TGGCCCTGA       GGAG AGGG
                                  |||||||||       |||| ||||
                                  ACCGGGACT       CCTC TCCC
                                       GTCTAGTC    C
GAM410  CREBL2  3'  TGGCCTGAGAGAAGAG      10589       C   AAATGCC
                                  TGGCC TGA      GGAGAG
                                  ||||| |||      ||||||
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                                ACCGG ACT      CTTCTC
                                  _  CT_____
GAM410  DLX2    3'  TGGCCCCGGGAGTGAGCAGGG  20597        AAAATGCCG  _
                                TGGCCCTG       GAG AGGG
                                ||||||||       ||| ||||
                                ACCGGGGC       CTC TCCC
                                    CCTCA____  G
GAM410  EGLN2   5'  GCCCTGGAAAGAGAGG     38827       A  ATGCC
                                GCCCTG AA    GGAGAGG
                                |||||| ||    |||||||
                                CGGGAC TT    TCTCTCC
                                  C  _____
GAM410  EPHB3   3'  GGCCCTGAGGGGCTTGGGGAGG 20788        AAAT  C_  A
          G                      GGCCCTGA   GC  GG GAGGG
                                 ||||||||   ||  || |||||
                                 CCGGGACT   CG  CC CTCCC
                                    CCC_  AA  C
GAM410  GPR56   3'  TGGCCCTGAAGGTCTGCCCTGG 25002         AA__   GGAGA
          G                      TGGCCCTGAA   TGCC    GGG
                                 ||||||||||   ||||    |||
                                 ACCGGGACTT   ACGG    CCC
                                      CCAG    GA___
GAM410  HM13    3'  TGGCCCTGAGAGGCTCGG    43112         AAAT  _
                                TGGCCCTGA   GC CGG
                                |||||||||   || |||
                                ACCGGGACT   CG GCC
                                     CTC_  A
GAM410  IHPK1   3'  TGGCCCTAGGCTCAAAGGAGAG 45498        AAAATGCC
          GG                     TGGCCCTG       GGAGAGGG
                                 ||||||||       ||||||||
                                 ACCGGGAT       CCTCTCCC
                                    CCGAGTTT
GAM410  KCNJ4   3'  GGTTCTGAGAGCAAAGAGGG  22540    CC   AAAT  C
                                GG  CTGA   GC GGAGAGGG
                                ||  ||||   || ||||||||
                                CC  GACT   CG TTTCTCCC
                                 AA   CT__  _
GAM410  LAG3    5'  GGCCTTGGAGAGAGGG     14045     C  AAAATGCC
                                GGCC TG       GGAGAGGG
                                |||| ||       ||||||||
                                CCGG AC       TCTCTCCC
                                  A  C________
GAM410  LIG3    3'  TGGCCTGAGGGAGAG      30360      C   AAATGCC
                                TGGCC TGA      GGAGAG
                                ||||| |||      ||||||
                                ACCGG ACT      CCTCTC
                                  _  C_______
GAM410  MASP1   3'  TGGCCTTGCAAGATGAGG    40116      CTGAAAA   C  _
                                TGGCC      TGC GGA GAGG
                                |||||      ||| ||| ||||
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                                ACCGG      ACG TCT CTCC
                                  A______  T  A
GAM410  MVK      3'  TGGCCCTGAGAGACAGG     41342         AAATGCC  G
                                TGGCCCTGA      GGA AGG
                                |||||||||      ||| |||
                                ACCGGGACT      TCT TCC
                                    C_______   G
GAM410  MYO15A   5'  TGGCCCTGGGTGGCGTGGGGAG 32186         AAAAT  C_  A
          GG                      TGGCCCTG    GC  GG GAGGG
                                |||||||||    ||  || |||||
                                ACCGGGAC    CG  CC CTCCC
                                    CCAC_  CA  C
GAM410  NIPSNAP1 3'  TGGCCCTGCAGAATGAGG    18875         AAAATGC   __
                                TGGCCCTG      CGGA  GAGG
                                |||||||||      ||||  ||||
                                ACCGGGAC      GTCT  CTCC
                                    ________   TA
GAM410  NT5E     3'  TAGCCTCTTGCTGGAGAGG    14865      _  GAAAA   C
                                TGGCC CT    TGC GGAGAGG
                                ||||| ||    ||| |||||||
                                ATCGG GA    ACG CCTCTCC
                                  A  ______  A
GAM410  NTSR1    3'  GGTCCTGTGGTTGGAGAGGG   14892    C   AAAA  CC_
                                GG CCTG    TG   GGAGAGGG
                                || ||||    ||   ||||||||
                                CC GGAC    AC   CCTCTCCC
                                 A   _____  CAA
GAM410  PDE4A    3'  TGGCTCCTGGAGAAGGGGGGAG 26280      _   AAAATGCC  A
          GG                      TGGC CCTG       GG GAGGG
                                |||| ||||       || |||||
                                ACCG GGAC       CC CTCCC
                                  A   CTCTTCCC  _
GAM410  PLA2G5   3'  TGGCCCTGGGGGTCCGCCAA   9579         AAAA__
                                TGGCCCTG     TGCCGG
                                ||||||||     ||||||
                                ACCGGGAC     GCGGTT
                                    CCCCAG
GAM410  PLEK     3'  GGCCCTGAGGCTGGAGAGGG   15389        AAAT  C
                                GGCCCTGA    GC GGAGAGGG
                                ||||||||    || ||||||||
                                CCGGGACT    CG CCTCTCCC
                                    C___  A
GAM410  PML      3'  TGGCCCTGGTGTAGTGGGAGGG 37744         AAAATGCC  A
                                TGGCCCTG       GG GAGGG
                                ||||||||       || |||||
                                ACCGGGAC       CC CTCCC
                                    CACATCA_  _
GAM410  PTPRF    3'  TGGCCCTGAGGTGCATGGG    39039         AAA   CGGAGA
                                TGGCCCTGA   TGC     GG
                                |||||||||   |||     ||
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                                ACCGGGACT  ACG    CC
                                     CC_  TAC___
GAM410  SCA2    5'  TGGCCCCGGGGCCGGGAGG  16480       AAAAT   A
                                TGGCCCTG   GCCGG GAGG
                                ||||||||   ||||| ||||
                                ACCGGGGC   CGGCC CTCC
                                     CC___   _
GAM410  SLC17A5  3'  TGACCCTGAAGCCAGGGAGGG  29692        AAT   A
                                TGGCCCTGAA  GCCGG GAGGG
                                ||||||||||  ||||| |||||
                                ACTGGGACTT  CGGTC CTCCC
                                      ___   C
GAM410  SLC9A5   3'  TGGCCCTGAGATGCTGG    21394        AA   C
                                TGGCCCTGA  ATGC GG
                                |||||||||  |||| ||
                                ACCGGGACT  TACG CC
                                     C_   A
GAM410  TNFAIP2  3'  GGCCTTGGGGGATGAAGAGGG  26640    C  AAAATGCC
                                GGCC TG      GGAGAGGG
                                |||| ||      ||||||||
                                CCGG AC      CTTCTCCC
                                  A  CCCCTA__
GAM410  ZNF236   3'  TGGCCCGAGAGAGAG      28869      T  AAATGCC
                                TGGCCC GA     GGAGAG
                                |||||| ||     ||||||
                                ACCGGG CT     TCTCTC
                                   _  C_______
GAM411  BCL11B   3'  TAAAGTGCGGGTCAACAGAAT  39754    _   TAAA
                                TAAA TGC   TCAACAGAAT
                                |||| |||   ||||||||||
                                ATTT ACG   AGTTGTCTTA
                                  C  CCC_
GAM411  GCMB     3'  TCTAAATGCTAAACAAAA    21910          ATCA
                                TCTAAATGCTAA   ACAGAA
                                ||||||||||||   ||||||
                                AGATTTACGATT   TGTTTT
                                       _____
GAM411  GPM6A    3'  TAAGTGCTAAACAACAAA    23613    A     T
                                TAA TGCTAAA CAACAGA
                                ||| ||||||| |||||||
                                ATT ACGATTT GTTGTTT
                                  C      _
GAM411  POLS     3'  AACGGAATCAACAGAAT     28117     CTA
                                AATG   AATCAACAGAAT
                                ||||   ||||||||||||
                                TTGC   TTAGTTGTCTTA
                                  C__
GAM411  VIPR2    3'  TCTAAATGCTGGAGTTTAAATC 18029         ________
                                TCTAAATGCT      AAATC
                                ||||||||||      |||||
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                                AGATTTACGA      TTTAG
                                     CCTCAAA
GAM412  IL8     3'  TTATAACTATTCAATCAATGAT 45395        _ C       A
              TCA                    TTATAAT AT CAATTAAT ATTCA
                                |||||||| || |||||||| |||||
                                AATATTG TA GTTAGTTA TAAGT
                                    A  A       C
GAM413  B4GALT7  3'  TAAGAATCCAGCATTCTA    28549        AT  _
                                TAAGAATT  CAG ATTCTA
                                |||||||||  ||| ||||||
                                ATTCTTAG  GTC TAAGAT
                                     __   G
GAM414  CLN5    3'  ACATATTAAACGTGAATTG   27076          TGCA
                                ACATATTAAAC   GGATTG
                                ||||||||||    ||||||
                                TGTATAATTTG   CTTAAC
                                      CA__
GAM414  GAN     3'  ACATATTAAACATGATTG    35136          TGCAG
                                ACATATTAAAC    GATTG
                                ||||||||||     |||||
                                TGTATAATTTG    CTAAC
                                      TA___
GAM414  UBE4A   3'  TCAGCATATTAAGCTGCACAAT 21976     A       A    G
              TG                   TCA CATATTAA CTGCA GATTG
                                ||| |||||||| ||||| |||||
                                AGT GTATAATT GACGT TTAAC
                                  C       C    G
GAM414  CCND3   3'  TATCATGCATTAAATTTTAGAG 12065          A   GAAATT
                                TATCATGCAT TAAA     GAG
                                |||||||||| ||||     |||
                                ATAGTACGTA ATTT     CTC
                                      _   AAAAT_
GAM414  DVL3    3'  TCATGCATGGGTGAAGTTG   20689        ATAAA  A
                                TCATGCAT    GAA TTG
                                ||||||||    ||| |||
                                AGTACGTA    CTT AAC
                                     CCCA_  C
GAM414  KHK     3'  ACAGATGAAGAAATTGAG    27051     T  A
                                GCA AT AAGAAATTGAG
                                ||| || ||||||||||
                                TGT TA TTCTTTAACTC
                                  C  C
GAM414  MAS1    3'  TCATGCATATGGGATGA     14366          AAA  AAT
                                TCATGCATAT   GA   TGA
                                ||||||||||   ||   |||
                                AGTACGTATA   CT   ACT
                                      CC_  ___
GAM415  KL      3'  TCTCTAGCATCCAATTT     22006        GTAGT
                                TTTCTAG    TCCAATTT
                                |||||||    ||||||||
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                                AGAGATC    AGGTTAAA
                                   GT___
GAM415  MITF     5'  TTTCTATAATTCCAATTT    6996       AG
                                TTTCT  GTAGTTCCAATTT
                                |||||  ||||||||||||||
                                AAAGA  TATTAAGGTTAAA
                                   __
GAM415  PRPSAP2  5'  TTCTTGGTTTTCCAATTT    15741     A   AG
                                TTCT GGT  TTCCAATTT
                                |||| |||  |||||||||
                                AAGA CCA  AAGGTTAAA
                                  A  A_
GAM415  RASGRP1  3'  TTTCCAGGTACCTAATTT    25083         GTT  _
                                TTTCTAGGTA   CC AATTT
                                ||||||||||   || |||||
                                AAAGGTCCAT   GG TTAAA
                                      ___  A
GAM415  STAU     3'  TTCCTAAATTGTCCAATTT    32702         A  T
                                TTTCTAGGT GT CCAATTT
                                ||||||||| || |||||||
                                AAGGATTTA CA GGTTAAA
                                     A  _
GAM416  CD28     3'  GAGCTCTGAGCCCTAAACCA   26020         CAAA  _
                                GAGTTCTGA    TC AAACCA
                                |||||||||    || ||||||
                                CTCGAGACT    GG TTTGGT
                                     CG__  A
GAM416  CDKN2C   5'  TTAGGGTCCTGACGATCA    38573     A       AA
                                TTAG GTTCTGAC  ATCA
                                |||| ||||||||  ||||
                                AATC CAGGACTG  TAGT
                                  C       C_
GAM416  COL15A1  3'  TTAGAGTCTGATAGCATCA    12360       T    CAA_
                                TTAGAGT CTGA    ATCA
                                ||||||| ||||    ||||
                                AATCTCA GACT    TAGT
                                    _   ATCG
GAM416  SLC29A1  3'  GAGTATATCAGGTCAAACCA   22414     TCTGA  AA
                                GAGT    CA  TCAAACCA
                                ||||    ||  ||||||||
                                CTCA    GT  AGTTTGGT
                                  TATA_  CC
GAM416  TBP      3'  TTAAAGTTTTCTCCCTCAAACC 42115        CTGACAAA
            A                    TTAGAGTT       TCAAACCA
                                 ||||||||       ||||||||
                                 AATTTCAA       AGTTTGGT
                                     AAGAGGG_
GAM416  UC28     3'  TTAGAGTTCTGGTATTACC    34696          ACAAATCAA
                                 TTAGAGTTCTG       ACC
                                 ||||||||||        |||
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                                AATCTCAAGAC       TGG
                                     CATAA____
GAM416  GAS11   3'  GTGGTTCTTGCTCATGG    11219       GCCTGACT
                                GTGGTTC      TTCATGG
                                |||||||      |||||||
                                CACCAAG      GAGTACC
                                   AAC_____
GAM416  MTCP1   5'  GGTGCTGACTTTTGTGG    30585    TC  C     CA
                                GGT  GC TGACTTT  TGG
                                |||  || |||||||  |||
                                CCA  CG ACTGAAA  ACC
                                  __ _     AC
GAM416  OSR1    3'  GGCGAACTGATTTTCATGGG  23037    TCGC   C
                                GGT   CTGA TTTCATGGG
                                |||   |||| |||||||||
                                CCG   GACT AAAGTACCC
                                  CTT_   A
GAM417  ABCC12  5'  TGAGAACTGTTTTCACCAA   37719   A       A _
                                C AGAACTGTT TC CCGA
                                | |||||||| || ||||
                                A TCTTGACAA AG GGTT
                                 C       A  T
GAM417  AP2B1   3'  GAGCTGTTATCCATCAC     10485    A       CGAGG
                                GA CTGTTATCC     CAC
                                || |||||||||     |||
                                CT GACAATAGG     GTG
                                 C       TA___
GAM417  CD34    3'  CAAGAACAGCCTCTGAGG    12112       T   A  CC
                                CAAGAAC GTT TC  GAGG
                                ||||||| ||| ||  ||||
                                GTTCTTG CGG AG  CTCC
                                   T  _ A_
GAM417  CHST6   3'  AAAACTGTTGTCCTTGCG    34672        A  _______
                                AGAACTGTT TCC     CG
                                ||||||||| |||     ||
                                TTTTGACAA AGG     GC
                                     C   AACIII
GAM417  EGFL5   5'  AGAACTGTTGCACG       44511        ATCCCGAG
                                AGAACTGTT      GCACG
                                |||||||||      |||||
                                TCTTGACAA      CGTGC
                                     _________
GAM417  FGF2    3'  AAGAATTGTTATCCATAG    12823      C       CG
                                AAGAA TGTTATCC  AG
                                ||||| ||||||||  ||
                                TTCTT ACAATAGG  TC
                                   A       TA
GAM417  PRDM2   3'  CAAGAACTGAGAGGCCG    31967        TTATCCC    A
                                CAAGAACTG      GAGGC CG
                                |||||||||      ||||| ||
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                                GTTCTTGAC      CTCCG GC
                                     T_______    _
GAM418  CLECSF12  5'  CCCCTGAATAGATATAG     44121      AGTT
                                CCTC    AATAGATATAG
                                ||||    ||||||||||
                                GGGG    TTATCTATATC
                                  AC__
GAM418  ELOVL4    3'  TACCTAGTTAATAAATA     35542       C
                                TACCT AGTTAATAGATA
                                ||||| ||||||||||
                                ATGGA TCAATTATTTAT
                                  _
GAM418  NRAS      3'  CTCAAATAGATATAG       14850      GTT
                                CTCA   AATAGATATAG
                                ||||   ||||||||||
                                GAGT   TTATCTATATC
                                  ___
GAM418  RPE65     3'  CCTCAGTTGATTAAACATAG  7265         AA_
                                CCTCAGTT   TAGATATAG
                                ||||||||   |||||||||
                                GGAGTCAA   ATTTGTATC
                                     CTA
GAM418  SYT1      3'  CTCAGTCAATTTACATAG    24852         AG
                                CTCAGTTAAT  ATATAG
                                ||||||||||  ||||||
                                GAGTCAGTTA  TGTATC
                                      AA
GAM418  CHST6     3'  CTGCCTGTGTTAACAAAC    34678          _ TT
                                CTGCCTGTGTTA C  AC
                                ||||||||||||  |  ||
                                GACGGACACAAT G  TG
                                       T TT
GAM418  DUSP4     5'  CATCTGTCTTTAGTTACTT   38410       C  GT_
                                CATCTG CT   GTTACTT
                                |||||| ||   |||||||
                                GTAGAC GA   CAATGAA
                                    A  AAT
GAM418  MAP3K7    3'  CAGCTGCCACTTACC       17269     T    TGTGTT
                                CA CTGCC     ACTTACC
                                || |||||     |||||||
                                GT GACGG     TGAATGG
                                 C    _______
GAM418  MTA1L1    3'  CACCTGTTATCTGTTTACTC  21881       C___    G
                                CATCTG    CTGT TTACTT
                                ||||||    |||| ||||||
                                GTGGAC    GACA AATGAG
                                    AATA   _
GAM418  NHLH1     3'  TCTGCCTGTGCCCAGGGCCTT  24658           ACTTAC
                                TCTGCCTGTGTT     CCTT
                                ||||||||||||     ||||
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                                AGACGGACACGG    GGAA
                                      GTCCC_
GAM419  ABP1    3'  GGCCGTTGTCCCGAGGCCAC  41793    ACA__  ACATG
                                GGCC   CCC   GAGGCCAC
                                ||||   |||   ||||||||
                                CCGG   GGG   CTCCGGTG
                                  CAACA  _____
GAM419  ANKRD3  3'  GGCCACACCCCAAACTGC   33969       A  TGGAG
                                GGCCACACCC CA   GC
                                |||||||||| ||   ||
                                CCGGTGTGGG GT   CG
                                     _ TTGA_
GAM419  APTX    5'  GGCCACACCCGGTGCCA    32810       ACAT  AG
                                GGCCACACCC   GG  GCCA
                                ||||||||||   ||  ||||
                                CCGGTGTGGG   CC  CGGT
                                     _____  A_
GAM419  ARF3    3'  GGCCACACTTGCATGGAG   11673       CCA
                                GGCCACAC   CATGGAG
                                ||||||||   |||||||
                                CCGGTGTG   GTACCTC
                                    AAC
GAM419  B3GAT1  3'  AGGCTGCAGTCCACCAGGG  38291    CA  C_   A   A
                                AGGC  CA  CCAC TGG GG
                                ||||  ||  |||| ||| ||
                                TCCG  GT  GGTG GTC CC
                                  AC  CA   _  _
GAM419  B4GALT1 3'  AGGCCAGTTCACACAGAGTCAC 11276      CACC       GC
                                AGGCCA   CACATGGAG  CAC
                                ||||||   |||||||||  |||
                                TCCGGT   GTGTGTCTC  GTG
                                   CAA_       A_
GAM419  B4GALT2 3'  GGCCACGACGGAGGCC    36142      ACCCAC
                                GGCCAC    ATGGAGGCC
                                ||||||    |||||||||
                                CCGGTG    TGCCTCCGG
                                   C_____
GAM419  BAALC   3'  AAGCCATGCCTGCTGCCA   36032      CA  CACA  GAG
                                AGGCCA  CC   TG   GCCA
                                ||||||  ||   ||   ||||
                                TTCGGT  GG   AC   CGGT
                                   AC  _____  GA_
GAM419  BIN1    3'  GGCCCCACCCACAGCAGCTGC  40300    A      _  AG
                                GGCC CACCCACA TGG  GC
                                |||| |||||||| |||  ||
                                CCGG GTGGGTGT GTC  CG
                                  G       C   GA
GAM419  CENTD2  5'  AGATCACACCCACCCGGGGC  31587    GC       A   A
                                AG  CACACCCAC TGG GGC
                                ||  ||||||||| ||| |||
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                                TC  GTGTGGGTG GCC CCG
                                 TA       G  _
GAM419  CERD4    3'  AGACCACTGTGGGGGTCA    28943       ACCCACA  A  C
                                AGGCCAC      TGG GG CA
                                |||||||      ||| || ||
                                TCTGGTG      ACC CC GT
                                   AC_____   C  A
GAM419  COL18A1  3'  AGGCCAGCCCCAGGCTGC    39052      CA   CAT  AG
                                AGGCCA  CCCA   GG  GC
                                ||||||  ||||   ||  ||
                                TCCGGT  GGGT   CC  CG
                                   CG    ___  GA
GAM419  CRHR2    3'  GGCCACACCATTGCCTGGCTGC 12442        CACA__  AG
                                GGCCACACC     TGG  GC
                                |||||||||     |||  ||
                                CCGGTGTGG     ACC  CG
                                     TAACGG   GA
GAM419  CYLN2    3'  AGCCACACCCGGGCGGCCAC   18044        ACAT  A
                                GGCCACACCC    GG GGCCAC
                                ||||||||||    || ||||||
                                TCGGTGTGGG    CC CCGGTG
                                     C___  G
GAM419  CYP8B1   3'  AGCTGCACAGTTCGGAGGCCA  20502     CA   CCACA
                                GGC  CAC    TGGAGGCCA
                                |||  |||    |||||||||
                                TCG  GTG    GCCTCCGGT
                                  AC   TCAA_
GAM419  DAAM2    3'  AGGCCTCACCCACAACCTCCCA 45172      A       TGGAGG
                                AGGCC CACCCACA     CCA
                                |||||  ||||||||     |||
                                TCCGG GTGGGTGT     GGT
                                   A       TGGAG_
GAM419  DBH      3'  AGGCCACACCCAGTGAGGC    8965          CATG
                                AGGCCACACCCA    GAGGC
                                ||||||||||||    |||||
                                TCCGGTGTGGGT    CTCCG
                                      CA__
GAM419  FUT5     3'  AGGTCACACCCACAGTGATGC  13018     C        TG  G
                                AGG CACACCCACA  GA GC
                                |||  ||||||||||  || ||
                                TCC GTGTGGGTGT  CT CG
                                  A         CA  A
GAM419  GGT2     5'  AGGCCAGCCTGGGGGCCA    43921       CA  CACA   A
                                AGGCCA  CC    TGG GGCCA
                                ||||||  ||    ||| |||||
                                TCCGGT  GG    ACC CCGGT
                                   C_  _____   C
GAM419  GYPE     3'  AGGCCACATCCTCATGCC    13329        C  A   GGAG
                                AGGCCACA CC CAT    GCC
                                |||||||| || |||    |||
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                                TCCGGTGT GG GTA    CGG
                                    A  A  ____
GAM419  GYS1    3'  GGCCACACCCAGTGCAGA    44791          CA  G
                                GGCCACACCCA  TG AGG
                                ||||||||||  || |||
                                CCGGTGTGGGT  AC TCT
                                     C_  G
GAM419  ICMT    3'  GGCCACGGTCACACAAAGCCAC 29655       ACC   TG   G
                                GGCCAC   CACA  GAG CCAC
                                ||||||   ||||  ||| ||||
                                CCGGTG   GTGT  TTC GGTG
                                   CCA   GT  _
GAM419  IGFBP4  3'  AGGGCACACCCATGCTCA    11393    C      CATGGAG  _
                                AGG CACACCCA      GC CA
                                ||| ||||||||      || ||
                                TCC GTGTGGGT      CG GT
                                  C       A_______  A
GAM419  IRAK4   3'  AGGTCTCATCTCCTAGAGGCCA 41458    CCA  CCCACA
            C                    AGG   CA     TGGAGGCCAC
                                |||   ||     ||||||||||
                                TCC   GT     ATCTCCGGTG
                                  AGA  AGAGG_
GAM419  JAG2    3'  AGGCCACACCATCAGCCA    13700         CACATGGA
                                AGGCCACACC       GGCCA
                                ||||||||||       |||||
                                TCCGGTGTGG       TCGGT
                                     TAG_____
GAM419  JAG2    3'  GGCCACACCAACACAGCCA    13728        C   GGA
                                GGCCACACC ACAT   GGCCA
                                |||||||||| ||||   |||||
                                CCGGTGTGG TGTG   TCGGT
                                     T   ___
GAM419  KIP2    3'  AGGCCACACCCATGTGACTGC  26886          CA   AG
                                AGGCCACACCCA  TGG  GC
                                ||||||||||||  |||  ||
                                TCCGGTGTGGGT  ACT  CG
                                      AC   GA
GAM419  KNS2    3'  GGCCACACTCGGCAGTCCCA   24473        CCACA  _  G_
                                GGCCACAC    TGG AG  CCA
                                ||||||||    ||| ||  |||
                                CCGGTGTG    GCC TC  GGT
                                    A____   G  AG
GAM419  KRT3    3'  AGGCCACACCTGGACAATCAC  38382         CACA   GGC_
                                AGGCCACACC   TGGA   CAC
                                ||||||||||   ||||   |||
                                TCCGGTGTGG   ACCT   GTG
                                     _____   GTTA
GAM419  LDLR    3'  AGCCACACCTGGGTGCAGGCCA 8021         CACA  G
            C                    GGCCACACC   TG AGGCCAC
                                |||||||||   || |||||||
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                                TCGGTGTGG   AC TCCGGTG
                                     ACCC  G
GAM419  LYL1    3'  AGGCCACTTCCAGAGG     24573       AC   CATG
                                AGGCCAC  CCA   GAGG
                                |||||||  |||   ||||
                                TCCGGTG  GGT   CTCC
                                   AA  ____
GAM419  MCM4    3'  AGACCACACCCATGTGGC    41592          CA  GA
                                AGGCCACACCCA  TG  GGC
                                ||||||||||||  ||  |||
                                TCTGGTGTGGGT  AC  CCG
                                      __  A_
GAM419  MECP2   3'  GGCTCACCCTGACCAGGTCAC  22601    CA    ACATGG   C
                                GGC  CACCC     AGG CAC
                                |||  |||||     ||| |||
                                CCG  GTGGG     TCC GTG
                                  A_    ACTGG_   A
GAM419  MEL     3'  AGGACACGAAGGAGTGGGGGCC 23866    C   ACCCACA   A
            A                    AGG CAC      TGG GGCCA
                                |||  |||      ||| |||||
                                TCC  GTG      ACC CCGGT
                                  T   CTTCCTC   C
GAM419  MGAT5   5'  AGGCCCCACCCACACCCA    14468      A       GGAGG
                                AGGCC CACCCACAT    CCA
                                |||||  |||||||||    |||
                                TCCGG GTGGGTGTG    GGT
                                   G       _____
GAM419  MYOM2   3'  GCCACACCCATGTGCCCAC    19559         CA  GAGG
                                GCCACACCCA  TG   CCAC
                                ||||||||||  ||   ||||
                                CGGTGTGGGT  AC   GGTG
                                      __  ACG_
GAM419  NID     3'  AGGCTGAGCTCATAAGGCCAC  14794     CACACCCA   G
                                AGGC       CATG AGGCCAC
                                ||||       |||| |||||||
                                TCCG       GTAT TCCGGTG
                                  ACTCGA__   _
GAM419  NUP62   3'  AAGCCACACCCATGAGGC    29598          CATG
                                AGGCCACACCCA   GAGGC
                                ||||||||||||   |||||
                                TTCGGTGTGGGT   CTCCG
                                      A___
GAM419  OCA2    3'  AGGACACACAGAGGAGGTCA  41189    C    CCACAT    C
                                AGG CACAC     GGAGG CA
                                |||  |||||     ||||| ||
                                TCC  GTGTG     CCTCC GT
                                  T    TCT___    A
GAM419  OTOF    3'  GGCCGGCCAGGAGGCCA     22060     ACAC   CAT
                                GGCC   CCA   GGAGGCCA
                                ||||   |||   ||||||||
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                                CCGG   GGT  CCTCCGGT
                                  CC__  ___
GAM419  P53AIP1  3' GGCCCACACCCATGAATTCAC 35233     _     CA   GGC
                                GGCC ACACCCA  TGGA  CAC
                                |||| |||||||  ||||  |||
                                CCGG TGTGGGT  ACTT  GTG
                                  G     __   AA_
GAM419  PML      3' GGTCACTACCCACGAGGCCAC 37735    C  _    ATG
                                GG CAC ACCCAC  GAGGCCAC
                                || ||| ||||||  ||||||||
                                CC GTG TGGGTG  CTCCGGTG
                                 A  A    ___
GAM419  POLR2E   3' AGGCCAGTGCCCTGGGCCA  40912      CA_  ACA  AG
                                AGGCCA  CCC  TGG  GCCA
                                ||||||  |||  |||  ||||
                                TCCGGT  GGG  ACC  CGGT
                                   CAC  ___  __
GAM419  PYGO2    3' GGCCACACCCCATGCCTGC  41952        A   GAG
                                GGCCACACCC CATG  GC
                                |||||||||| ||||  ||
                                CCGGTGTGGG GTAC  CG
                                      _  GGA
GAM419  RPH3AL   3' GGCCACACGCAGCTTCGGAGGC 28103       C  CA__
           C                    GGCCACAC CA   TGGAGGCC
                                |||||||| ||   ||||||||
                                CCGGTGTG GT   GCCTCCGG
                                    C  CGAA
GAM419  S100B    3' GGCCACACCGGCCA       26571        CACATGGA
                                GGCCACACC      GGCCA
                                |||||||||      |||||
                                CCGGTGTGG      CCGGT
                                       _________
GAM419  SERPINA3 3' GGCCACACATGCCATGGCCAC 41457       CCA_  GGA
                                GGCCACAC   CAT  GGCCAC
                                ||||||||   |||  ||||||
                                CCGGTGTG   GTA  CCGGTG
                                    TACG  ___
GAM419  SERPINF2 3' AGGCCACAGCCAGGC      9589        C  CATGGA
                                AGGCCACA CCA    GGC
                                |||||||| |||    |||
                                TCCGGTGT GGT    CCG
                                    C  _______
GAM419  SHOX     3' GGCTGAACTCGTGAAGCCAC  27822    CACACCC  A  _
                                GGC     AC TG GAGGCCAC
                                |||     || || ||||||||
                                CCG     TG GC CTTCGGTG
                                  ACT_____  A  A
GAM419  SLC13A3  3' AGCCACAGAGGCCTATGGGGGC 41298      C___  AC   A
           CAC                    GGCCACA   CC  ATGG GGCCAC
                                |||||||   ||  |||| ||||||
```

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                                TCGGTGT   GG  TACC CCGGTG
                                    CTCC  A_   C
GAM419  STIM1    3'  GGCCACACGCTGGCGGTCAC  41130       CCACA  A  C
                                GGCCACAC    TGG GG CAC
                                ||||||||    ||| || |||
                                CCGGTGTG    ACC CC GTG
                                    CG___   G  A
GAM419  TNFRSF14 3'  GGCCTGTCCTGCTGAGGCCAC  19233     ACA  CACATG
                                GGCC   CC    GAGGCCAC
                                ||||   ||    ||||||||
                                CCGG   GG    CTCCGGTG
                                  ACA  ACGA__
GAM419  UBE2G2   3'  GGCCTGCACCCACAGACC    42123     A_      TGGA
                                GGCC  CACCCACA   GGCC
                                ||||  ||||||||   ||||
                                CCGG  GTGGGTGT   CTGG
                                  AC      _____
GAM419  USP6     5'  AGGCCACACCTGGA       45024         CACA
                                AGGCCACACC   TGGA
                                ||||||||||   ||||
                                TCCGGTGTGG   ACCT
                                           _____
GAM419  WDR4     5'  GGCCACACCCGTGTGGC     38022         ACA  GA
                                GGCCACACCC   TG  GGC
                                ||||||||||   ||  |||
                                CCGGTGTGGG   AC  CCG
                                     C__  A_
GAM419  WHSC1    3'  AGCCACACCCACGGC       39350         ATGGA  C
                                GGCCACACCCAC    GG C
                                ||||||||||||    || |
                                TCGGTGTGGGTG    CC G
                                      _____  A
GAM419  WWP2     3'  GGCCACATCCACGGGGGC    41453       C   AT  A
                                GGCCACA CCAC  GG GGC
                                |||||||  ||||  || |||
                                CCGGTGT GGTG  CC CCG
                                    A   C_  _
GAM419  ZNF138   5'  AGGCCAGACCTGCAGCACC   44341       C  CACA  G  _
                                AGGCCA ACC    TG AG GCC
                                ||||||  |||    || || |||
                                TCCGGT TGG    AC TC TGG
                                   C   ____  G  G
GAM420  ADAM22   3'  ACAATTGTCCTTGTATGCTAA  34699         C  CTC
                                ACAATTGTTC TG   GTTAA
                                ||||||||||  ||   |||||
                                TGTTAACAGG AC   CGATT
                                     A  ATA
GAM420  ADAMTS13 3'  CACGCGGCACTGCTCGTT    40027     AATT  TC
                                CAC    GT  CTGCTCGTT
                                |||    ||  |||||||||
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                                GTG   CG  GACGAGCAA
                                  CGC_  T_
GAM421  HOXD4   3'  TTGGAGCTTTTCCACACCT   31185       CC   CTAA
                                TTGGAGCT  TCC   ATGCCT
                                ||||||||  |||   ||||||
                                AACCTCGA  AGG   TGTGGA
                                    AA  _____
GAM421  SURF4   3'  TTGGGTGTCCCTAAATG    37662     AGCTCC
                                TTGG    TCCCTAAATG
                                ||||    ||||||||||
                                AACC    AGGGATTTAC
                                  CAC___
GAM422  IGF1    3'  TGGTGTGCTTCTTGACGACTTG 8358    A  GA       TC__
           CT                     TG TG  CTTCTTGGCG   GCT
                                || ||  ||||||||||   |||
                                AC AC  GAAGAACTGC   CGA
                                 C  AC        TGAA
GAM422  KIP2    3'  TGGTGGACTTCTAGGCCCCTAC 26891    A       T   G  G
                                TG TGGACTTCT GGC TC CTAC
                                || |||||||| ||| || ||||
                                AC ACCTGAAGA CCG GG GATG
                                 C       T  _ _
GAM422  NXF2    5'  TGATGGACTTCCTGAGACACC  35188            CGT
                                TGATGGACTTCTTGG   CGCT
                                ||||||||||||||   ||||
                                ACTACCTGAAGGACT   GTGG
                                      CT_
GAM422  TRIM9   3'  TGGTGAATTTCTTGGCTCAC  31583    A   C      G
                                TG TGGA TTCTTGGC TCGC
                                || |||| |||||||| ||||
                                AC ACTT AAGAACCG AGTG
                                 C   A       _
GAM422  ATP1A2  3'  GTGCTTCCTTCCTGTCTGCC  8710        __  ATCA  _
                                GTGCTTC  TCC    TCT CC
                                |||||||  |||   ||| ||
                                CACGAAG  AGG    AGA GG
                                    GA   AC__   C
GAM422  CDC2L2  5'  TCGTGCTCTCTTTCTTTCAC  37944       T   CA  ATCTC
                                TCGTGCT CTC  TC    CAC
                                |||||||  |||  ||    |||
                                AGCACGA GAG  AG    GTG
                                    _   AA  AAA__
GAM422  DUSP4   3'  GTCTTCTCATCCCTTTGCC   38424    G     C   A   ___
                                GT CTTCTC ATC TCT   CC
                                || ||||||  ||| |||   ||
                                CA GAAGAG TAG GGA   GG
                                 _     _   _   AAC
GAM422  FCN2    3'  GTACTTCTCCGCCTC       31893          ATCA
                                GTGCTTCTCC    TCTC
                                ||||||||||    ||||
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                                CATGAAGAGG   GGAG
                                     C___
GAM422  FLRT3   3'  GTGTTCAGGCATCTCCAC   30006    C   TCCAT
                                GTG TTC    CATCTCCAC
                                ||| |||    |||||||||
                                CAC AAG    GTAGAGGTG
                                  _  TCC__
GAM422  GAB2    3'  GTGTCCTTGTCATCTCCAC   29381    C   CCA
                                GTG TTCT   TCATCTCCAC
                                ||| ||||   ||||||||||
                                CAC AGGA   AGTAGAGGTG
                                  _   AC_
GAM422  GALNT1  3'  GTACTTCTTCATAGTTCT    33840       C   CA_
                                GTGCTTCT CAT   TCT
                                |||||||| |||   |||
                                CATGAAGA GTA   AGA
                                     A   TCA
GAM422  HEPH    3'  TCTGCTTCTCCACCACC     31345    G
                                TC TGCTTCTCCATCATC
                                || ||||||||||||||
                                AG ACGAAGAGGTGGTGG
                                 _
GAM422  IL1A    3'  TCGTGCTTTGCCTTCATC    41676       CT  A
                                TCGTGCTT  CC TCATC
                                ||||||||  || |||||
                                AGCACGAA  GG AGTAG
                                     AC  A
GAM422  LZTR1   5'  CTTCCCATTGTCTCCAC     27636     T   CA
                                CTTC CCAT  TCTCCAC
                                |||| ||||  |||||||
                                GAAG GGTA  AGAGGTG
                                  _   AC
GAM422  MAPT    3'  GTGCTTCCTCCTCCCCTCTGCC 32591       _  A  AT   CA
                                GTGCTTC TCC TC  CTC  CC
                                ||||||| ||| ||  |||  ||
                                CACGAAG AGG AG  GAG  GG
                                     G   _  GG   AC
GAM422  MDM2    5'  TCGGCTTCTTGCTCCATC    27812    T   _____
                                TCG GCTTC    TCCATC
                                ||| |||||    ||||||
                                AGC CGAAG    AGGTAG
                                  _    AACG
GAM422  NFRKB   5'  GTGCTTCTTTAACATTATC   26100       C___   C
                                GTGCTTCT    CAT ATC
                                ||||||||    ||| |||
                                CACGAAGA    GTA TAG
                                     AATT   A
GAM422  RAP1GA1 3'  GTGCTTCTGTGGCCTCATC   16169       _____ A
                                GTGCTTCT    CC TCATC
                                ||||||||    || |||||
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                                CACGAAGA   GG AGTAG
                                     CACC  _
GAM422  SERPINH2  3'  TCTGCTTTTCCACCCCCAC   10299    G    C    CAT
                                TC TGCTT TCCAT   CTCCAC
                                || ||||| |||||   ||||||
                                AG ACGAA AGGTG   GGGGTG
                                 _    A    ___
GAM422  SUFU      3'  GCTTCTCCAGTCCCTGCC    32091         _ A  _
                                GCTTCTCCA TC TCT CC
                                ||||||||| || ||| ||
                                CGAAGAGGT AG GGA GG
                                     C  _  C
GAM422  YWHAB     5'  TCCTGCTTCTCTATCCACAGCC 18188    G      C   ATCT_
                                TC TGCTTCTC ATC    CC
                                || |||||||| |||    ||
                                AG ACGAAGAG TAG    GG
                                 G       A  GTGTC
GAM422  ZNF236    3'  GTGCTTCTTCATGTGCACC    28865       CCA    CTC
                                GTGCTTCT   TCAT   CACC
                                ||||||||   ||||   ||||
                                CACGAAGA   AGTA   GTGG
                                     ___    CAC
GAM423  ABCC1     5'  CCGGTTGCTGGCGCGGGCGGC  33399       CCTCCA    A
                                CCGGTTGT     CGGGC GC
                                ||||||||     ||||| ||
                                GGCCAACG     GCCCG CG
                                     ACCGC_    C
GAM423  ARHGEF6   3'  AACTGAAAGGCCTCTACGGGCA 42794     C  TTGT   C
           GC                    AGC GG    CCTC ACGGGCAGC
                                ||| ||    |||| |||||||||
                                TTG CT    GGAG TGCCCGTCG
                                  A  TTCC    A
GAM423  COL18A1   3'  AGCCAGCCTGTCCATGGGCAG  36130       GTCC   C
                                AGCCGGTT    TCCA GGGCAG
                                ||||||||    |||| ||||||
                                TCGGTCGG    AGGT CCCGTC
                                     AC__    A
GAM423  DDX3      5'  GCCCTCGCTCTTCCGCGGGTAG 35820     GG   TC  _  A   C
           C                     GCC  TTG  CT CC CGGG AGC
                                |||  |||  || || |||| |||
                                CGG  AGC  GA GG GCCC TCG
                                  G_   GA  A  C    A
GAM423  FOXF2     3'  AGCGGTTGTCCTTCTTCCAGC  11126     C       CCACGGG
                                AGC GGTTGTCCT      CAGC
                                ||| |||||||||      ||||
                                TCG CCAACAGGA      GTCG
                                  _       AGAAG__
GAM423  HR        5'  GCCGGTCGCGGCGCGGGC    32921         CCTCCA
                                GCCGGTTGT     CGGGC
                                |||||||||     |||||
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                                CGGCCAGCG     GCCCG
                                     CCGC__
GAM423  IGF1R    3'  AGCTGTCTCCCGCGGGCAG   9326        CT  A
                                GGTTGTC  CC CGGGCAG
                                |||||||  ||  |||||||
                                TCGACAG  GG GCCCGTC
                                   AG  C
GAM423  IGSF6    3'  AGCCAGTTGTCTTTTCAG    25197         CTCCA
                                AGCCGGTTGTC    CGG
                                ||||||||||     |||
                                TCGGTCAACAG    GTC
                                     AAAA_
GAM423  PACE4    3'  GCCTGCCCTCTGTGGGCAGC   15050    GGT      CAC
                                GCC   TGTCCTC   GGGCAGC
                                |||   |||||||   |||||||
                                CGG   ACGGGAG   CCCGTCG
                                 ___      ACA
GAM423  PRM1     5'  AGCAGGTGGAACTCTGTGGGCA 15716    C   TGTC   CAC
           GC                     AGC GGT    CTC   GGGCAGC
                                |||  |||    |||   |||||||
                                TCG CCA    GAG   CCCGTCG
                                  T   CCTT   ACA
GAM423  AKAP13   5'  CCATTGCTCGCCTCGGTCGCCG 28476    _   GCAC        A
                                CC TTGC    CGCCTCGGTC CCG
                                ||  ||||    |||||||||| |||
                                GG AACG    GCGGAGCCAG GGC
                                 T   A___         C
GAM423  CDH23    3'  CCTTGCGCCTGCTTAGCC    38074        ACC  C CG
                                CCTTGCGC   GC T  GTC
                                ||||||||   ||  |  |||
                                GGAACGCG   CG A  CGG
                                     GA_  _ AT
GAM423  PFKL     5'  CCTTGCGCGTCGCCGCCG    15231        AC   _
                                CCTTGCGC  CGCC TCG
                                ||||||||  ||||  |||
                                GGAACGCG  GCGG GGC
                                     CA    C
GAM423  RHEB2    5'  CTTCGCGCCGTGGCCCGCCG  24717    G   A   CCTC   A_
                                CTT CGC CCG    GGTC  CCG
                                |||  |||  |||    ||||  |||
                                GAA GCG GGC    CCGG  GGC
                                  _   C   A___    GC
GAM423  SECTM1   3'  TGCGAGGCCTCGGTCACCG   16545     CACC
                                TGCG    GCCTCGGTCACCG
                                ||||    ||||||||||||||
                                ACGC    CGGAGCCAGTGGC
                                  TC__
GAM423  SGT      5'  CTTGCGCACCGCGGTGCC    16612          CTC   CA
                                CTTGCGCACCGC   GGT  CC
                                ||||||||||||   |||  ||
```

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                                GAACGCGTGGCG  CCA  GG
                                      ____  C_
GAM423  SOX11    3'  CCTTGCGCGTCCCGGACTACCG 17014       ACCG  T  TC_
                                CCTTGCGC   CC CGG  ACCG
                                ||||||||   || |||  ||||
                                GGAACGCG   GG GCC  TGGC
                                    CA__  _  TGA
GAM424  PSEN1    3'  TCTCCACTGGCTGTTGCTGAGG 28741     GTTGCC  C
          CT                    TCTC    CTG TGCTGAGGCT
                                ||||     ||| ||||||||||
                                AGAG     GAC ACGACTCCGA
                                  GTGACC  A
GAM424  SLA2     3'  TCTCGTTGACTCTAGGG     37017       CCCT  G  A
                                TCTCGTTG   GCT CTG GG
                                ||||||||   ||| ||| ||
                                AGAGCAAC   TGA GAT CC
                                    _____  _  C
GAM424  TCF8     3'  TCGTTGCCTTCCAGAGGCT   36241       CTG  GCT
                                TCGTTGCC  CT  GAGGCT
                                ||||||||  ||  ||||||
                                AGCAACGG  GG  CTCCGA
                                    AA_  T__
GAM424  TNC      5'  GCTGGGTGCTGCTGGGGCT   13468     CCC      A
                                GTTG  TGCTGCTG GGCT
                                ||||  |||||||| ||||
                                CGAC  ACGACGAC CCGA
                                  CC_      C
GAM425  ACK1     5'  CTGCACCCCGGGCAGCCAAT  25113       CT_  A
                                CTGCACCTC  CA CCAAT
                                |||||||||  || |||||
                                GACGTGGGG  GT GGTTA
                                     CCC  C
GAM425  ANKRD3   3'  CTGCACCTCTTCCCCAA    33964       C  AA
                                CTGCACCTC TC  CCAA
                                ||||||||| ||  ||||
                                GACGTGGAG AG  GGTT
                                     A  G_
GAM425  CLC      3'  TACTGTACCTCCTCCCCA   29902     C      AA
                                TACTG ACCTCCTC  CCA
                                ||||| ||||||||  |||
                                ATGAC TGGAGGAG  GGT
                                  A       G_
GAM425  DYRK1A   3'  CTGTGACCTTCAACCAAT   38993    C_   CC
                                CTG  ACCT  TCAACCAAT
                                |||  ||||  |||||||||
                                GAC  TGGA  AGTTGGTTA
                                  AC   __
GAM425  FANCC    3'  CACTGCACCCAGCCAGGCCAAT 43268        CC  A_
                                TACTGCACCT  TCA  CCAAT
                                ||||||||||  |||  |||||
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                                GTGACGTGGG  GGT  GGTTA
                                      TC   CC
GAM425  MEN1     5'  TACTGAAGAGCCTCAACCAAT  39200      CACCT
                                TACTG    CCTCAACCAAT
                                |||||    ||||||||||
                                ATGAC    GGAGTTGGTTA
                                   TTCTC
GAM425  TEM8     3'  TACTGGCATTGCCAACCAAT   38190      _ CCTCC
                                TACTG CA    TCAACCAAT
                                ||||| ||    |||||||||
                                ATGAC GT    GGTTGGTTA
                                   C  AAC__
GAM426  LENG4    5'  CACGGTTATTAGGGCAGTGGT  35878     _        TAACA
                                CACG TTATTAGGGC    GGT
                                |||| ||||||||||    |||
                                GTGC AATAATCCCG    CCA
                                   C        TCA__
GAM426  SLC12A4  3'  CAGGCAAGCAGGGCTGGCAGGT 22888    C  TAT     AA
                                CA GT   TAGGGCT  CAGGT
                                || ||   |||||||  |||||
                                GT CG   GTCCCGA  GTCCA
                                 C  TTC      CC
GAM427  SUFU     3'  ATCTCGTTGACACAACTG    32082     C  CG    ACG
                                ATC CG  GACA   TAGCTG
                                ||| ||  ||||   ||||||
                                TAG GC  CTGT   GTTGAC
                                  A  AA   ____
GAM427  ZNF36    3'  TCTCATGGACTTTAGCTGCT   45297    C  C    AACG
                                TC CG GGAC    TAGCTGCT
                                || || ||||    ||||||||
                                AG GT CCTG    ATCGACGA
                                 A  A    AA__
GAM428  RABIF    3'  TAGTACATAAGCATCTTTTGT  16127         C  AATT    C
                                TAGTACATA AG    TCTTT GT
                                ||||||||| ||    ||||| ||
                                ATCATGTAT TC    AGAAA CA
                                      _ GT__     A
GAM428  TEC      3'  TGATACAGTTTCTTTC      17392   C     AA
                                A ATACAG  TTTCTTTC
                                | ||||||  ||||||||
                                A TATGTC  AAAGAAAG
                                 C     __
GAM429  CCNT2    3'  TTACAGAGTGAAAAGTGAATAC 38499      T  C  TT  _
           A                     TTACA AG TG  AA TGAATACA
                                ||||| || ||  || ||||||||
                                AATGT TC AC  TT ACTTATGT
                                   C  _  TT  C
GAM429  EIF4G2   3'  CATGCTGCTAATATAC      10874     A       GA
                                CAT GCTGTTAAT  ATAC
                                ||| |||||||||  ||||
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                                GTA CGACGATTA  TATG
                                  _      __
GAM430  MEF2D    5'  TCATGAACGGTCTGGGAACA  25422         CCTAG  TT
                                TCATGGACGG    CTG  AACG
                                ||||||||||    |||  ||||
                                AGTACTTGCC    GAC  TTGT
                                     A____   CC
GAM431  MYH11    3'  ATGCAATTATAGCTCAT    35638    A       A
                                ATG AATTATAGCT CGT
                                ||| |||||||||| |||
                                TAC TTAATATCGA GTA
                                  G       _
GAM432  COCH     3'  TCTCTTATTCAGTGTGATATTT 19861   GTTACC  A
                                TC     TCA TGTGATATTT
                                ||     ||| ||||||||||
                                AG     AGT ACACTATAAA
                                 AGAATA  C
GAM433  EHD3     3'  GCAAGTGAATTGCCTCAGG   31112       CGCA
                                GCAGGTGA   CCTCAGG
                                ||||||||   |||||||
                                CGTTCACT   GGAGTCC
                                     TAAC
GAM433  GNL1     5'  AGCAGGTGACGTCAG      45560         CACC
                                AGCAGGTGACG   TCAG
                                ||||||||||   ||||
                                TCGTCCACTGC   AGTC
                                              ____
GAM433  HD       3'  ACCAGCAGGTGACTATCAGG  13340          GCACC
                                ACCAGCAGGTGAC    TCAGG
                                ||||||||||||    |||||
                                TGGTCGTCCACTG    AGTCC
                                       AT___
GAM433  HIP12    3'  CCAACAGAACACTTCAG    42394       TGAC   C
                                CCAGCAGG   GCAC TCAG
                                ||||||||   |||| ||||
                                GGTTGTCT   TGTG AGTC
                                     ____   A
GAM433  MBD3     3'  CCAGTGGGCACCAACCTCAGG  19415    CA  GA  C
                                CCAG  GGT  CG ACCTCAGG
                                ||||  |||  || ||||||||
                                GGTC  CCG  GT TGGAGTCC
                                  AC  TG  _
GAM433  MDK      3'  ACTGGTGGGTCACATCTCGGG  14391   A   A__   C  A
                                GC GGTG   CGCA CTC GG
                                || ||||   |||| ||| ||
                                TG CCAC   GTGT GAG CC
                                 A   CCA   A  C
GAM433  OTP      3'  CCAGCAGGTGGCCGAG     36990        AC  ACCTC
                                CCAGCAGGTG  GC    AG
                                ||||||||||  ||    ||
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                                GGTCGTCCAC  CG    TC
                                      __  GC___
GAM433  SLC4A4   3'  CACTAGGTAAACCTCAGG    19062    GC     CGC
                                CA  AGGTGA   ACCTCAGG
                                ||  ||||||   ||||||||
                                GT  TCCATT   TGGAGTCC
                                 GA     ___
GAM433  ST5      3'  CAGCGGGGACCTCAG       24043      A  T  CGCA
                                CAGC GG GA    CCTCAG
                                |||| || ||    ||||||
                                GTCG CC CT    GGAGTC
                                  C  _ _____
GAM433  DGCR2    3'  GCCTGCTGCTCTGGAACCTGG  23095         CC   AT  TC
                                GCCTGCTGT  CTG  GT  GG
                                |||||||||  |||  ||  ||
                                CGGACGACG  GAC  TG  CC
                                      A_   CT  GA
GAM433  DNASE1L1 5'  CTTCTGTCCCTGTTGTTGGG  27493    G       A    C
                                CT CTGTCCCTG TGTT GG
                                || |||||||||  |||| ||
                                GA GACAGGGAC ACAA CC
                                 A        A   C
GAM433  FLG      5'  CTACTGTCTCTGACTGCAGA   43358         C     GTT
                                CTGCTGTC CTGAT   CGGA
                                |||||||| |||||   ||||
                                GATGACAG GACTG   GTCT
                                     A     AC_
GAM433  FMR2     3'  ACCTGCTGTTTCTATCATGGAC 12948         CC   A   TC
                                GCCTGCTGT  CTG TGT  GGAC
                                |||||||||  ||| |||  ||||
                                TGGACGACA  GAT GTA  CCTG
                                      AA   A   __
GAM433  GAS11    3'  ACTTGCTGTCCTTGGTGT    11208    C       C  A
                                GC TGCTGTCC TG TGT
                                || ||||||||  || |||
                                TG ACGACAGG AC ACA
                                 A       A  C
GAM433  HD       3'  CTGCTGTCCCTGACTGGTGG   13348           GTTC
                                CTGCTGTCCCTGAT    GG
                                ||||||||||||||    ||
                                GACGACAGGGACTG    CC
                                        ACCA
GAM433  IL11     3'  GCCTGCTGTTTCATGTCAGGAC 8480          CCCTG    C
                                GCCTGCTGT    ATGTT GGAC
                                |||||||||    ||||| ||||
                                CGGACGACA    TACAG CCTG
                                      AAG__     T
GAM433  MELK     5'  GCCTGCTGTCCTGAGAGA    31334          C   TGTTC
                                GCCTGCTGTCC TGA    GGA
                                |||||||||| |||    |||
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                                CGGACGACAGG ACT    TCT
                                      _  C____
GAM433  PSMD9   3'  GCTTGCTGCCCTCTGGTGGG  15845   C     _  A  TTC
                                GC TGCTGTCC CTG TG  GG
                                || |||||||| ||| ||  ||
                                CG ACGACGGG GAC AC  CC
                                 A      A  C ___
GAM433  SERPINF1 3'  CTGCTGTCCCTCGG      15215        TGATGT
                                CTGCTGTCCC    TCGG
                                ||||||||||    ||||
                                GACGACAGGG    AGCC
                                      _______
GAM433  UBTF    3'  TGCTGTCCCTGGAGGAGGAC  30619         ATGTTC
                                TGCTGTCCCTG    GGAC
                                ||||||||||    ||||
                                ACGACAGGGAC    CCTG
                                      CTCCT_
GAM433  VDR     3'  CTCTGTCCCTGAGGAATGGA  7518    G       TGTTC
                                CT CTGTCCCTGA    GGA
                                || ||||||||||    |||
                                GA GACAGGGACT    CCT
                                 _       CCTTA
GAM433  ZNF80   5'  TGTTCCTTCTGATGTTCGGA  28331    _ __
                                TGT CC  CTGATGTTCGGA
                                ||| ||  ||||||||||||
                                ACA GG  GACTACAAGCCT
                                  A  AA
GAM434  GLS     3'  TGTAATCCCCAGGAAGAAT  31381       G    TTC
                                TGTAATCC CAGGA  GAGT
                                |||||||| |||||  ||||
                                ACATTAGG GTCCT  CTTA
                                     G    T__
GAM435  CASP2   3'  TGAGATCGTGCCACTGCCC  37403       AG_ A_
                                TGAGGTCGT  GC  CCC
                                |||||||||  ||  |||
                                ACTCTAGCA  TG  GGG
                                      CGG  AC
GAM435  CHRNB4  5'  TGGGGTCACAGGGCACCC   8873    A      _
                                TG GGTCGTAGG CACCC
                                || |||||||| |||||
                                AC CCAGTGTCC GTGGG
                                 C       C
GAM435  COG6    5'  TGAGGCCGTTGGCAGCCC   43765       A  _
                                TGAGGTCGT GGCA CCC
                                ||||||||| |||| |||
                                ACTCCGGCA CCGT GGG
                                      A   C
GAM435  GRLF1   3'  TGGGTCGCAGCAGGTGCCC  44237   A      G ____
                                TG GGTCGTAG CA   CCC
                                || |||||||| ||   |||
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```
                                AC CCAGCGTC GT    GGG
                                 _       _ CCAC
GAM435  LZTS1    5'  TGAGGTCATAGCAAAGCCC   34276          G ___
                                TGAGGTCGTAG CA   CCC
                                |||||||||| ||   |||
                                ACTCCAGTATC GT   GGG
                                      _ TTC
GAM435  PDE6B    3'  TGAGATCGTGCCACGGCAC   7103          A____
                                TGAGGTCGT    GGCAC
                                |||||||||    |||||
                                ACTCTAGCA    CCGTG
                                     CGGTG
GAM435  PIAS3    3'  TGAGGCCAAAAGTAGGCA    25912        ____
                                TGAGGTC    GTAGGCA
                                |||||||    |||||||
                                ACTCCGG    CATCCGT
                                    TTTT
GAM435  RAD54B   3'  TGAGGTCGACAACTGCCC    39586        TA  A_
                                TGAGGTCG  GGC  CCC
                                ||||||||  |||  |||
                                ACTCCAGC  TTG  GGG
                                     TG   AC
GAM435  ELK1     3'  TCCTGGACCCCTGAGTATG   23416    A      C   T
                                TC TGGACCCC GAGT GTG
                                || |||||||| |||| |||
                                AG ACCTGGGG CTCA TAC
                                 G       A   _
GAM435  FCER1A   5'  TCATGGACTCCTGGTGC     12808        CC  GAGTT
                                TCATGGAC  CC    GTGT
                                ||||||||  ||    ||||
                                AGTACCTG  GG    CACG
                                     A_  AC___
GAM435  IGF1     3'  TCAGTGGACTTTTGTGTCT   8352     _    CCCCGAG
                                TCA TGGAC      TTGTGTCT
                                ||| |||||      ||||||||
                                AGT ACCTG      AACACAGA
                                  C    AA_____
GAM435  MAL      3'  CCATGGACCTCTGGAAAGATCT 35333        CCC_  TTGT
                                TCATGGACC   GAG   GTCT
                                |||||||||   |||   ||||
                                GGTACCTGG   CTT   TAGA
                                     AGAC   TC__
GAM435  SIP      3'  TCTGGATTTTTCCTGTGTGTCT 30848    A   CCC__  GA  T
           A                     TC TGGA    CC  GT GTGTCTA
                                || ||||    ||  || |||||||
                                AG ACCT    GG  CA CACAGAT
                                 _   AAAAA  A_  _
GAM436  ADAM19   3'  TGGGAGGAGCTCAGAGGCGGC  37782        _  G_  _
                                TGGGAGG GC  AG GGCGGC
                                ||||||| ||  || ||||||
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                                ACCCTCC CG  TC CCGCCG
                                    T  AG  T
GAM436  ALX4    3'  TGGGAGGCTGGGGGC      34953       G GA  C
                                TGGGAGG C  GGG GGC
                                ||||||| |  ||| |||
                                ACCCTCC G  CCC CCG
                                   _ A_  _
GAM436  ALX4    5'  TGGGGAGGCGAGGAGGC    34954     AG      C
                                TGGG  GGCGAGGG GGC
                                ||||  |||||||| |||
                                ACCC  CCGCTCCT CCG
                                  CT      _
GAM436  AP1M1   3'  TGGGAAGGCGCCACAGGC   37176         A___
                                TGGGAGGGCG   GGGC
                                ||||||||||   ||||
                                ACCCTTCCGC   TCCG
                                     GGTG
GAM436  ARHC    5'  TGGGAGGGGGTGCGGC     23177       CGA  _
                                TGGGAGGG  GG GCGGC
                                ||||||||  || |||||
                                ACCCTCCC  CC CGCCG
                                    ___ A
GAM436  ARNT2   3'  TGGGAGGGACACAAGGGC   31368        ___
                                TGGGAGGG  CGAGGGC
                                ||||||||  |||||||
                                ACCCTCCC  GTTCCCG
                                     TGT
GAM436  ATP1A1  5'  TGGGAGGGCGGCCGGCGGC  8701         AG_
                                TGGGAGGGCG  GGCGGC
                                ||||||||||  ||||||
                                ACCCTCCCGC  CCGCCG
                                     CGG
GAM436  ATP1A1  5'  GGGAGGGTGGGAGGGCGGC  8699        C__
                                GGGAGGG  GAGGGCGGC
                                |||||||  |||||||||
                                CCCTCCC  CTCCCGCCG
                                    ACC
GAM436  ATP5G2  3'  TGGGAGGTGGAGACGGC    23203       GC   G
                                TGGGAGG  GAGG CGGC
                                |||||||  |||| ||||
                                ACCCTCC  CTCT GCCG
                                    AC   _
GAM436  ATP7A   3'  TGGGAGGGAGAAGGAGGC   6268        C    C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCCC CTTCC CCG
                                     T    T
GAM436  BAP1    3'  TGGTGAGGGCCACACGGC   21648    _    GAGG
                                TGG GAGGGC   GCGGC
                                ||| ||||||   |||||
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                                ACC CTCCCG   TGCCG
                                  A     GTG_
GAM436  BARX2    3'  TGGGAGGGAGGGAGAC      18929        CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC CTG
                                     __    T
GAM436  BCL2L2   3'  TGGGAGAGGAGGGTGGC     19753        C    C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCTC CTCCC CCG
                                     _     A
GAM436  BMP1     3'  GGGAGGAGGCAGGGTGGC    25998        __ G   C
                                GGGAGG  GC AGGG GGC
                                ||||||  || |||| |||
                                CCCTCC  CG TCCC CCG
                                   TC  _    A
GAM436  C21orf2  3'  TGGGAGAACAGCGGC       22306        GAG
                                TGGGAGGGC   GGCGGC
                                |||||||||   ||||||
                                ACCCTCTTG   TCGCCG
                                     ___
GAM436  COL1A1   3'  TGGGAGCGCCAGATGGC     6382        G  G   GC
                                TGGGAG GC AGG  GGC
                                |||||| || |||  |||
                                ACCCTC CG TCT  CCG
                                   G  G   A_
GAM436  COL6A2   3'  GGGAGGGCCCAGCCCGGC    38444        GA  G_
                                GGGAGGGC  GG  CGGC
                                ||||||||  ||  ||||
                                CCCTCCCG  TC  GCCG
                                     GG  GG
GAM436  CYLN2    5'  TGGGAAGGCGGGAGGC      18071         A   C
                                TGGGAGGGCG GGG GGC
                                |||||||||| ||| |||
                                ACCCTTCCGC CCT CCG
                                     _  _
GAM436  CYLN2    5'  TGGGGGGCGAGGATGC      18072      A       CG
                                TGGG GGGCGAGGG  GC
                                ||||  |||||||||  ||
                                ACCC CCCGCTCCT  CG
                                  _       A_
GAM436  CYP11B1  3'  TGGGAGAGAAGAGGGGTGGC  41630        C_    C_
                                TGGGAGGG  GAGGG  GGC
                                ||||||||  |||||  |||
                                ACCCTCTC  CTCCC  CCG
                                     TT    CA
GAM436  CYP11B1  3'  TGGGAGGGATGGGGGC      41631        CGA   C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
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                                ACCCTCCC  CCC CCG
                                    TA_  _
GAM436  DNASE1   5'  GGGAGGGTGGGACTGGGC   23356      CGA  __
                                GGGAGGG  GGGC  GGC
                                |||||||  ||||  |||
                                CCCTCCC  CCTG  CCG
                                   AC_   AC
GAM436  DPYSL3   3'  TGGAAGGGGAAACAGGTGG   10781      C ___  C
                                TGGGAGGG GA  GGG GG
                                |||||||| ||  ||| ||
                                ACCTTCCC CT  TCC CC
                                    _ TTG  A
GAM436  EDNRA    5'  TGGGTGGCGCGGAGGGTGGC  42006     A _  _  C
                                TGGG GG GCG AGGG GGC
                                |||| || ||| |||| |||
                                ACCC CC CGC TCCC CCG
                                  A G  C   A
GAM436  EGR3     3'  TGGGAGGGCAGGGGGC     40563       G   C
                                TGGGAGGGC AGGG GGC
                                ||||||||| |||| |||
                                ACCCTCCCG TCCC CCG
                                    _   _
GAM436  EHD2     3'  TGGGAGGGGGGCCCGGC    31138       CGA  __
                                TGGGAGGG  GGGC  GGC
                                |||||||  ||||  |||
                                ACCCTCCC  CCCG  CCG
                                   ___   GG
GAM436  ELK1     3'  TGGGAGGGAGGGAAC      23417       CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC TTG
                                   __   _
GAM436  FAAH     5'  GGAGGGCGAGAAGGAGGCGGCG 11059        _____    III
                                GGAGGGCGAG   GGCGGC  G
                                ||||||||||   ||||||  |
                                CCTCCCGCTC   CCGCCG  C
                                     TTCCT    III
GAM436  FBXL4    5'  TGGGTGCGGGGGCGGC     29135     AGG  A
                                TGGG  GCG GGGCGGC
                                ||||  ||| |||||||
                                ACCC  CGC CCCGCCG
                                  A__  C
GAM436  FBXL7    3'  TGCGAGGGAAAGGGCGGC   29416    G   C
                                TG GAGGG GAGGGCGGC
                                || ||||| |||||||||
                                AC CTCCC TTCCCGCCG
                                 G   T
GAM436  FGFR1    3'  GGGAGGGCGTGTGGGTGGC  31947       A__  C
                                GGGAGGGCG  GGG GGC
                                |||||||||  ||| |||
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                                CCCTCCCGC   CCC CCG
                                     ACA   A
GAM436  FGFR1    3'  TGGGAGGGGATGAAGTGGC   31962        C__   GC
                                TGGGAGGG   GAGG  GGC
                                ||||||||   ||||  |||
                                ACCCTCCC   CTTC  CCG
                                     CTA    A_
GAM436  FMO1     3'  GGGAAGCGAGAGGGTGGC    12921       GC_    C
                                GGGAGG   GAGGG GGC
                                ||||||   ||||| |||
                                CCCTTC   CTCCC CCG
                                   GCT    A
GAM436  FOLR1    5'  TGGGAGAGGAGGTGGC      32503        C    GC
                                TGGGAGGG GAGG  GGC
                                |||||||| ||||  |||
                                ACCCTCTC CTCC  CCG
                                     _    A_
GAM436  FOXD2    5'  TGGGAGAGGTGAGATTGCGGC  20975       _ C   __
                                TGGGAG GG GAGG  GCGGC
                                |||||| || ||||  |||||
                                ACCCTC CC CTCT  CGCCG
                                   T  A    AA
GAM436  FOXG1B   3'  TGGGAGGGGGGGGC        23514        CGA   C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
                                ACCCTCCC   CCC CCG
                                     ____   _
GAM436  GATA3    5'  TGGGAGGTCGGGGGGC      13101        G  A   C
                                TGGGAGG CG GGG GGC
                                ||||||| || ||| |||
                                ACCCTCC GC CCC CCG
                                     A  _   _
GAM436  GFRA1    5'  TGGCGAGGGCGGGAGGCGG   23569     _      A_
                                TGG GAGGGCG  GGGCGG
                                ||| |||||||  ||||||
                                ACC CTCCCGC  TCCGCC
                                  G      CC
GAM436  GPC1     3'  TGGGAGGAGCGAACAGC     13263        _   GG
                                TGGGAGG GCGA  GCGGC
                                ||||||| ||||  |||||
                                ACCCTCC CGCT  TGTCG
                                     T   __
GAM436  GPR44    3'  TGGGAGGGAGCAGGGGC     21964        CGA   C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
                                ACCCTCCC   TCC CCG
                                     TCG   _
GAM436  GRB14    5'  GGGAGGGCGCGAGAGCGGC   21047         __
                                GGGAGGGC  GAGGGCGGC
                                ||||||||  |||||||||
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                                CCCTCCCG  CTCTCGCCG
                                    CG
GAM436  HDAC1    3'  TGGGTGGCAAGGTGGC     22445     AG     GC
                                TGGG  GGCGAGG  GGC
                                ||||  |||||||  |||
                                ACCC  CCGTTCC  CCG
                                  A_     A_
GAM436  HIC1     5'  TGGGCCCGAGGGCGGC     44572     AGGG
                                TGGG   CGAGGGCGGC
                                ||||   ||||||||||
                                ACCC   GCTCCCGCCG
                                  GG__
GAM436  HIC1     5'  TGGAAGGGCAGCGGC      44570       GAG
                                TGGGAGGGC   GGCGGC
                                |||||||||   ||||||
                                ACCTTCCCG   TCGCCG
                                     ___
GAM436  HPCA     3'  TGGGGTGGGAAGGGTGGC    13428     AG  C    C
                                TGGG  GG GAGGG GGC
                                ||||  || ||||| |||
                                ACCC  CC TTCCC CCG
                                  CA  C    A
GAM436  HPCAL1   3'  TGGGAGGATCATCACGGC    39551       _  AGG
                                TGGGAGGG CG   GCGGC
                                |||||||| ||   |||||
                                ACCCTCCT GT   TGCCG
                                    A  AG_
GAM436  HRMT1L1  3'  TGGGCAGCGGGGGGTGGC    42183     AG   A   C
                                TGGG  GGCG GGG GGC
                                ||||  |||| ||| |||
                                ACCC  TCGC CCC CCG
                                  G_   C   A
GAM436  HRY      3'  TAGGAGGAGGGGTGGC      24356       CGA   C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
                                ATCCTCCT   CCC CCG
                                    C__   A
GAM436  IDUA     3'  TGGGAGGGCAGCATGGGC    6814         A___
                                TGGGAGGGCG   GGGC
                                ||||||||||   ||||
                                ACCCTCCCGT   CCCG
                                     CGTA
GAM436  IGFBP1   5'  TGGGAGGGTGGCGGCGGC    8250        CGAG
                                TGGGAGGG   GGCGGC
                                ||||||||   ||||||
                                ACCCTCCC   CCGCCG
                                    ACCG
GAM436  IVD      3'  TGGGCAGGGTGGGAAAGC    13697     _   C__
                                TGGG AGGG   GAGGGC
                                |||| ||||   ||||||
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                                ACCC TCCC   CTTTCG
                                  G    ACC
GAM436  KCNK4    5'  TGGGAGGCCGAAAGAGAGC   37842       G     C _
                                TGGGAGG CGAGGG G GC
                                ||||||| |||||| | ||
                                ACCCTCC GCTTTC C CG
                                    G     T T
GAM436  LBX1     3'  TAGGAGCCCAGGGCGGC     27290       GG G
                                TGGGAG  C AGGGCGGC
                                ||||||  | ||||||||
                                ATCCTC  G TCCCGCCG
                                   GG _
GAM436  LEP      3'  TGGGAAGGGCATCCTGGTGGC  6922        _    AG__  C
                                TGGGA GGGCG   GG GGC
                                ||||| |||||   || |||
                                ACCCT CCCGT   CC CCG
                                   T    AGGA  A
GAM436  LMO1     3'  TGGCAGGAGAGCGGC       14186     G   GCG
                                TGG AGG   AGGGCGGC
                                ||| |||   ||||||||
                                ACC TCC   TCTCGCCG
                                  G   ___
GAM436  LTBP2    3'  TGGGAGGGTGGATGAGGGC   7696         C____
                                TGGGAGGG    GAGGGC
                                ||||||||    ||||||
                                ACCCTCCC    CTCCCG
                                     ACCTA
GAM436  M11S1    5'  TGAGGGGGCAAGGGTGGC    25332      A       C
                                TGGG GGGCGAGGG GGC
                                |||| ||||||||| |||
                                ACTC CCCGTTCCC CCG
                                  C       A
GAM436  MADH3    5'  GGGAGGGCGTGCGGGCGGC   25349        A__
                                GGGAGGGCG   GGGCGGC
                                |||||||||   |||||||
                                CCCTCCCGC   CCCGCCG
                                     ACG
GAM436  MAPT     5'  TGCGAGGGCGCGCGCGGC    32587    G      AGG
                                TG GAGGGCG   GCGGC
                                || |||||||   |||||
                                AC CTCCCGC   CGCCG
                                 G      GCG
GAM436  MATN1    5'  TGAGAGGGCGGGAGAGC     14369        A   C
                                TGGGAGGGCG GGG GGC
                                |||||||||| ||| |||
                                ACTCTCCCGC CCT TCG
                                      _  C
GAM436  MEF2B    5'  TGAGGAGGGCGGGGGTGG    25413    _      A   C
                                TG GGAGGGCG GGG GG
                                || |||||||| ||| ||
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                                AC CCTCCCGC CCC CC
                                 T       C   A
GAM436  MEOX1    3'  TAGGAGGAGGCATGGGTGGC  30402        __  A   C
                                TGGGAGG  GCG GGG GGC
                                |||||||  ||| ||| |||
                                ATCCTCC  CGT CCC CCG
                                    TC   A   A
GAM436  MLC1     3'  TGGGAGAGCAGCGGC      40156        GAG
                                TGGGAGGGC   GGCGGC
                                |||||||||   ||||||
                                ACCCTCTCG   TCGCCG
                                     ___
GAM436  MMP14    3'  TGGGGGAGCGAGAGGGC    22645     A       C
                                TGGG GGGCGAGGG GGC
                                |||| ||||||||| |||
                                ACCC CTCGCTCTC CCG
                                  C       _
GAM436  MMP25    5'  TGGAGAGGGCGGGGGGC    35394     _     A   C
                                TGG GAGGGCG GGG GGC
                                ||| ||||||| ||| |||
                                ACC CTCCCGC CCC CCG
                                  T     _  _
GAM436  NAV2     3'  TGGGAGGGTGGGTGGC     41152        CGA   C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
                                ACCCTCCC   CCC CCG
                                     A__   A
GAM436  NEK4     5'  AGGGGGCAGTGGGGGCGGC   17190     A    A___
                                GGG GGGCG   GGGCGGC
                                ||| |||||   |||||||
                                TCC CCCGT   CCCGCCG
                                  _    CACC
GAM436  NLGN3    3'  TGGGAGGGAGGGAGC      33289        CG   C
                                TGGGAGGG  AGGG GGC
                                ||||||||  |||| |||
                                ACCCTCCC  TCCC TCG
                                     __   _
GAM436  NPAS2    5'  TGGGAGACGAGGCGGC     14822        G    G
                                TGGGAGG CGAGG CGGC
                                ||||||| ||||| ||||
                                ACCCTCT GCTCC GCCG
                                     _    _
GAM436  NR2F2    5'  GGGAGGGCGCCCCGGGTGGC  34239         A___  C
                                GGGAGGGCG   GGG GGC
                                |||||||||   ||| |||
                                CCCTCCCGC   CCC CCG
                                     GGGG  A
GAM436  NTSR1    3'  TGGGAGGGACTCCCCACGGC  14897        _ GAGG_
                                TGGGAGGG C    GCGGC
                                |||||||| |    |||||
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                                ACCCTCCC G    TGCCG
                                     T AGGGG
GAM436  OTP      3'  TGGGAAGGGAAGAGGGGCGGC  37006        C__    _
                                TGGGAGGG   GAGGG CGGC
                                ||||||||   ||||| ||||
                                ACCCTTCC   CTCCC GCCG
                                     CTT    C
GAM436  P4HA1    5'  TGGGACGAGAGGGCGGC     9540       G  C
                                TGGGA GG GAGGGCGGC
                                ||||| || |||||||||
                                ACCCT CT CTCCCGCCG
                                   G  _
GAM436  PACE     3'  TGGGAGGGGTGCAAAAGGC   15042        C____
                                TGGGAGGG    GAGGGC
                                ||||||||    ||||||
                                ACCCTCCC    TTTCCG
                                     CACGT
GAM436  PACSIN1  3'  TGGGAGGGGAGGGGCGGC   45167        C    _
                                TGGGAGGG GAGGG CGGC
                                |||||||| ||||| ||||
                                ACCCTCCC CTCCC GCCG
                                     _    C
GAM436  PAK4     3'  TGGGAGGAGTGGGAGGC     25252        CGA  C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
                                ACCCTCCT   CCC CCG
                                     CA_  T
GAM436  PEX14    3'  TGGGAGGACGACGGGGC     41878         G  C
                                TGGGAGGGCGA GG GGC
                                |||||||||| || |||
                                ACCCTCCTGCT CC CCG
                                       G  _
GAM436  PFKFB3   5'  TGGCAGGAGAGCGGC      44441     G  GCG
                                TGG AGG   AGGGCGGC
                                ||| |||   ||||||||
                                ACC TCC   TCTCGCCG
                                  G  ___
GAM436  PTBP1    3'  GGGACAGGACGCGGGGGCGG  36723     __    A__
                                GGGA  GGGCG   GGGCGG
                                ||||  |||||   ||||||
                                CCCT  CCTGC   CCCGCC
                                   GT    GCC
GAM436  PTMS     3'  GGGAGAAAGAAGAGGGTGGC  15892       C___    C
                                GGGAGGG    GAGGG GGC
                                |||||||    ||||| |||
                                CCCTCTT    CTCCC CCG
                                     TCTT    A
GAM436  PTN      5'  TGGGAGGGATGAGAGGAGC   44393        C_    C
                                TGGGAGGG  GAGGG GGC
                                ||||||||  ||||| |||
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                                ACCCTCCC  CTCTC TCG
                                    TA    C
GAM436  PTPRA    5'  TGGCGAGGGGAAGCGGC    38918    _    C   G
                                TGG GAGGG GAGG CGGC
                                ||| ||||| |||| ||||
                                ACC CTCCC CTTC GCCG
                                  G    _   _
GAM436  QARS     3'  TGGGGTGGCGAGGGTAGC    22786     AG      CG
                                TGGG  GGCGAGGG  GC
                                ||||  |||||||  ||
                                ACCC  CCGCTCCC  CG
                                  CA      AT
GAM436  RAB6A    5'  TGGGAAGGGAAGGAGGGCGG   16109       C___
                                TGGGAGGG   GAGGGCGG
                                ||||||||   ||||||||
                                ACCCTTCC   CTCCCGCC
                                    CTTC
GAM436  RANBP3   3'  TGGGAAGGGTGTGGGTGGC   28772       CGA_  C
                                TGGGAGGG   GGG GGC
                                ||||||||   ||| |||
                                ACCCTTCC   CCC CCG
                                    CACA   A
GAM436  RFX1     3'  TGGGAGGGGGGCGGC      16300       CGA
                                TGGGAGGG   GGGCGGC
                                ||||||||   |||||||
                                ACCCTCCC   CCCGCCG
                                           ___
GAM436  RPH3AL   3'  TGGGGAGGCAGACGGC     28106     AG   GA
                                TGGG  GGC  GGGCGGC
                                ||||  |||  |||||||
                                ACCC  CCG  TCTGCCG
                                  CT   __
GAM436  RXRA     3'  TGGGAGGGGCCCAGCTGGC   16437       CGAG  _
                                TGGGAGGG   GGC GGC
                                ||||||||   ||| |||
                                ACCCTCCC   TCG CCG
                                    CGGG   A
GAM436  S100A4   3'  GGGAGGGCCCCAGCTGGC    16441       GAG  _
                                GGGAGGGC   GGC GGC
                                ||||||||   ||| |||
                                CCCTCCCG   TCG CCG
                                    GGG   A
GAM436  S100A5   3'  TGGGAGGGAGAGGAGGGC    16447       C    C
                                TGGGAGGG GAGGG GGC
                                |||||||| ||||| |||
                                ACCCTCCC CTCCT CCG
                                    T    C
GAM436  SAG      5'  TGGGAAGGGCCGGGTGGC    8077       _   GA   C
                                TGGGA GGGC  GGG GGC
                                ||||| ||||  ||| |||
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                                ACCCT CCCG  CCC CCG
                                  T   G_  A
GAM436  SEPN1   3'  TGAGGGGCAAGAGGGGCGGC  42438     A    ___
                                TGGG GGGCGA  GGGCGGC
                                |||| ||||||  |||||||
                                ACTC CCCGTT  CCCGCCG
                                  _    CTC
GAM436  SF1     5'  GGGCGGGCCGGGGGCGGC   21567    A   _ A
                                GGG GGGC G GGGCGGC
                                ||| |||| | |||||||
                                CCC CCCG C CCCGCCG
                                  G   G C
GAM436  SLC2A4  3'  TGGGAGGAGTCCAAGGTGG  9801        ___   GC
                                TGGGAGGG  CGAGG  GG
                                ||||||||  |||||  ||
                                ACCCTCCT  GTTCC  CC
                                     CAG   A_
GAM436  SLC39A4 5'  GGGCTGGCTGAGGGCGGC   32815    AG  _
                                GGG  GGC GAGGGCGGC
                                |||  ||| |||||||||
                                CCC  CCG CTCCCGCCG
                                  GA  A
GAM436  SNRPN   5'  GGGAAGACAGGGGGCGGC   35608       A_
                                GGGAGGGCG  GGGCGGC
                                |||||||||  |||||||
                                CCCTTCTGT  CCCGCCG
                                     CC
GAM436  SNX9    5'  GGCAAGGGCGAGGGCGGC   32157   _
                                GG GAGGGCGAGGGCGGC
                                || ||||||||||||||
                                CC TTCCCGCTCCCGCCG
                                 G
GAM436  SORCS2  3'  GGGGGGCCTGGAGGGTGG   34061    A   ___   C
                                GGG GGGC  GAGGG GG
                                ||| ||||  ||||| ||
                                CCC CCCG  CTCCC CC
                                  _   GAC   A
GAM436  STX1A   3'  TGGGAGGGCAGCCCAGC    21415       G  GG
                                TGGGAGGGC AG  CGGC
                                ||||||||| ||  ||||
                                ACCCTCCCG TC  GTCG
                                     _ GG
GAM436  SYN3    3'  TGTGAGGCGAGGGTGGC    18571   G   G    C
                                TG GAGG CGAGGG GGC
                                || |||| |||||| |||
                                AC CTCC GCTCCC CCG
                                 A   _    A
GAM436  TCF12   5'  TGGGAGGGGGAGGCGGC    17347       C   G
                                TGGGAGGG GAGG CGGC
                                |||||||| |||| ||||
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                                ACCCTCCC CTCC GCCG
                                    C   _
GAM436  THRA    5'  TGGGAGGGCTGGGGGC     17524        GA  C
                                TGGGAGGGC  GGG GGC
                                |||||||||  ||| |||
                                ACCCTCCCG  CCC CCG
                                    A_  _
GAM436  TRPV1   5'  TGGGAGGGTGGACAGGC    38804        CGA  _
                                TGGGAGGG  GGGC GGC
                                ||||||||  |||| |||
                                ACCCTCCC  CCTG CCG
                                    A__   T
GAM436  USP14   5'  TGGGCCTGACGAGGGCGGC  23119     AG_
                                TGGG  GGCGAGGGCGGC
                                ||||  ||||||||||||
                                ACCC  CTGCTCCCGCCG
                                  GGA
GAM436  WT1     5'  TGGGGGAGCGGACAGGC    35970     A   GA  _
                                TGGG GGGC  GGGC GGC
                                |||| ||||  |||| |||
                                ACCC CTCG  CCTG CCG
                                  C   __   T
GAM436  CD83    3'  CCTCATGCTATGTGGTCA   20135      AGAT      C
                                CCTCA   CTATGTGG CA
                                |||||   |||||||| ||
                                GGAGT   GATACACC GT
                                  AC__      A
GAM436  COCH    5'  CTCGAGATCCACCCGGCTGCG 19860     A      G   CA
                                CTC AGATCTAT TGGC  CG
                                ||| |||||||| ||||  ||
                                GAG TCTAGGTG GCCG  GC
                                  C       G   AC
GAM436  DBP     3'  CTCAAGATTTATTCAGGATCG 10666       C  GT_  CCA
                                CTCAAGAT TAT   GG   CG
                                |||||||| |||   ||   ||
                                GAGTTCTA ATA   CC   GC
                                    A   AGT  TA_
GAM436  FVT1    3'  CCTCAAGATTTCTTTATG    13028        __  A
                                CCTCAAGA  TCT TGTG
                                ||||||||  ||| ||||
                                GGAGTTCT  AGA ATAC
                                    AA   A
GAM436  IL1B    3'  CTTAGAACCAAATGTGGCC   8210     CAA   T_
                                CT   GATC  ATGTGGCC
                                ||   ||||  ||||||||
                                GA   TTGG  TACACCGG
                                 ATC    TT
GAM436  KCNK6   3'  CCTCAAGATCACCTGCTGTG  22078        TA____
                                CCTCAAGATC     TGTG
                                ||||||||||     ||||
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                                GGAGTTCTAG     ACAC
                                     TGGACG
GAM436  SULT1C1  3'  TACCTCAAGGTATTATGA    9842          ATCTA
                                TACCTCAAG    TGTGG
                                |||||||||    |||||
                                ATGGAGTTC    ATACT
                                     CATA_
GAM437  CD74     3'  TGTCAGGAACGGGGA      20341          CACCT
                                TGTCAGGGACGG    GGA
                                ||||||||||||    |||
                                ACAGTCCTTGCC    CCT
                                      _____
GAM437  CDH7     5'  TGTAGTAAGTACCTGGGGCCT  38003    C  GGAC  C     AA
                                TGT AG   GG ACCTGG  CCT
                                ||| ||   || ||||||  |||
                                ACA TC   TC TGGACC  GGA
                                  _ AT__ A     CC
GAM437  FCRH1    5'  GTCAGGGATGGTACCTAGAGAT 38108        C  C      A___
            GCCT                   GTCAGGGA GG ACCTGGA    CCT
                                ||||||||| || |||||||    |||
                                CAGTCCCT CC TGGATCT    GGA
                                     A  A      CTAC
GAM437  GRF2     3'  TCAGGGACCCTGGA       23677        GGCA
                                TCAGGGAC    CCTGGA
                                ||||||||    ||||||
                                AGTCCCTG    GGACCT
                                      _____
GAM437  GUCY1B3  3'  TGTTAGGAGAAAACTGGAACCT 9229     C   _  CG  ACC
                                TGT AGG GA  GC   TGGAACCT
                                ||| ||| ||  ||   ||||||||
                                ACA TCC CT  TG   ACCTTGGA
                                  A   T  TT  ___
GAM437  HTR1D    5'  TCAGGGTCCTGGAAC      9266        ACGGCA
                                TCAGGG     CCTGGAAC
                                ||||||     ||||||||
                                AGTCCC     GGACCTTG
                                   A_____
GAM437  KLRC1    5'  TGTCAGGGACTGTACTCT    28798          GGC  _
                                TGTCAGGGAC   AC CT
                                ||||||||||   || ||
                                ACAGTCCCTG   TG GA
                                      ACA  A
GAM437  PTPN7    3'  TGTCAGGGGCGGCGTGCCT   38721         A    A__
                                TGTCAGGG CGGC   CCT
                                |||||||| ||||   |||
                                ACAGTCCC GCCG   GGA
                                     C    CAC
GAM437  TRPC5    3'  GCAAAGTGGCACCTGG      29768   T    AC
                                G CAGGG  GGCACCTGG
                                | |||||  |||||||||
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                                C GTTTC  CCGTGGACC
                                 _    A_
GAM437  TTC3    5'  AGAAAAATACTTGGAACCT   17712     CG C  C
                                GGGA  G AC TGGAACCT
                                ||||  | || ||||||||
                                TCTT  T TG ACCTTGGA
                                  TT A  A
GAM437  GRIK3   3'  TCTCTGGCCTCACGGTCAAG  9100        G     AGA
                                TCTCTGGC TCACGG   CGGG
                                |||||||| ||||||   ||||
                                AGAGACCG AGTGCC   GTTC
                                     G     A__
GAM437  HNRPDL  5'  TCTCTGGCGTCCGGTCCAG   24180         A   AGA
                                TCTCTGGCGTC CGG   CGG
                                |||||||||| |||   |||
                                AGAGACCGCAG GCC   GTC
                                       _   AG_
GAM437  TNC     5'  CCTTTGTGCCCACGGAGGCGGG 13465    C _ G       A
                                TCT TG GC TCACGGAG CGGG
                                ||| || || |||||||| ||||
                                GGA AC CG GGTGCCTC GCCC
                                  A  A _       C
GAM438  ARHGAP6 3'  TGAGGTCGTGGGCGCCGCA   30230         A   A ____
                                TGAGGTCGT GGC CC    CA
                                ||||||||| ||| ||    ||
                                ACTCCAGCA CCG GG    GT
                                      C   C  CIII
GAM438  FSTL3   3'  GAGGCAGCAGGCACCTAGT   25219      C       C
                                GAGGT GTAGGCACC AGT
                                ||||| ||||||||| |||
                                CTCCG CGTCCGTGG TCA
                                   T       A
GAM438  KCNE1L  3'  TGGGGTGATACACCCAGTAATG 29378    A   CGTAG
                                TG GGT    GCACCCAGTAATG
                                || |||    ||||||||||||
                                AC CCA    TGTGGGTCATTAC
                                 C   CTA__
GAM438  XRCC2   3'  GGGTATATACCCAGTAATG   24094    TC   GGC
                                GG  GTA   ACCCAGTAATG
                                ||  |||   ||||||||||
                                CC  CAT   TGGGTCATTAC
                                 __   ATA
GAM438  HNRPF   3'  TGGGGCCGTGTGTCT      22460     ACC   GAG
                                TGG   GCC   GTGTGTCT
                                |||   |||   ||||||||
                                ACC   CGG   CACACAGA
                                  C__   ____
GAM438  TRIM    3'  TATGTGCTGCCGAGGTGAGC   32300      GACC       T
                                TATG    GCCGAGGTG GT
                                ||||    ||||||||| ||
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                                ATAC   CGGCTCCAC CG
                                  ACGA       T
GAM439  COL11A1  5' GCGTTCTTCGTGTCTCTAGCC 38760   TG  CG  GGA
                                GT  TC  CG   TTCTAGCC
                                ||  ||  ||   ||||||||
                                CG  AG  GC   GAGATCGG
                                 CA  AA  ACA
GAM439  GATA1    3' GTTGTCCAGAATTCTGGC    13078       GC      A
                                GTTGTCC  GGGATTCT GC
                                |||||||  |||||||| ||
                                CAACAGG  TCTTAAGA CG
                                    __       C
GAM439  GNAI1    3' GTTGCTGCAAGACTCTAG    13168      CC
                                GTTGT  GCGGGATTCTAG
                                |||||  ||||||||||||
                                CAACG  CGTTCTGAGATC
                                   A_
GAM439  RAB5A    3' TACATTGTTTATTATGGTTCTA 20013        CCGCG__  A
           GCC                    TACGTTGT      GG TTCTAGCC
                                ||||||||      || ||||||||
                                ATGTAACA      CC AAGATCGG
                                     AATAATA  _
GAM440  APBA1    3' TTCAGCTTGTCTCACTG     43093      ACTT  _
                                TTCA   GCT GTCTCACTG
                                ||||   ||| |||||||||
                                AAGT   CGA CAGAGTGAC
                                  ____  A
GAM440  CYP11A   3' TTCAACCTGCTGAGCAGGCTG 8940           TCTCA_
                                TTCAACTTGCTG     CTG
                                ||||||||||||     |||
                                AAGTTGGACGAC     GAC
                                       TCGTCC
GAM440  EGFL5    5' TTCAACTCATCACT       44546        CTGTC
                                TTCAACTTG    TCACT
                                |||||||||    |||||
                                AAGTTGAGT    AGTGA
                                      _____
GAM440  FXYD6    3' TTCAACCTCTCACT       35125       TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AAGTTGG    AGAGTGA
                                      _____
GAM440  HDC      3' CTCGGCCCTTTCTCACTG    13371     _  G__
                                CTTG CT   TCTCACTG
                                |||| ||   ||||||||
                                GAGC GG   AGAGTGAC
                                  C  GAA
GAM440  HGD      5' TTCACTGCGCTTCACTG     6782      AC    T TC
                                TTCA  TTGC G  TCACTG
                                ||||  |||| |  ||||||
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                              AAGT  GACG C  AGTGAC
                                __   _ GA
GAM440  HNRPK   3' CTCAACTTGTAGTACTG    36316       CT  CTC
                              TTCAACTTG  GT   ACTG
                              |||||||||  ||   ||||
                              GAGTTGAAC  CA   TGAC
                                   AT  ___
GAM440  HOXB5   3' CTCAGCTTGACCCCACTG   13445     A   CTG
                              TTCA CTTG   TCTCACTG
                              |||| ||||   ||||||||
                              GAGT GAAC   GGGGTGAC
                                C   T__
GAM440  JAG1    3' CTCAACTTGTTCCCTTACTG  6852        CTG   __
                              TTCAACTTG   TCTC  ACTG
                              |||||||||   ||||  ||||
                              GAGTTGAAC   AGGG  TGAC
                                   A__    AA
GAM440  KIF3B   3' TTCACTTTTCAACCTCACTG  22046     A  GCTG_
                              TTCA CTT    TCTCACTG
                              |||| |||    ||||||||
                              AAGT GAA    GGAGTGAC
                                _  AAGTT
GAM440  NOTCH2  3' TTCAAATATCTCACT      35916      CTTGC
                              TTCAA    TGTCTCACT
                              |||||    |||||||||
                              AAGTT    ATAGAGTGA
                                T____
GAM440  PCDHA1  3' TCCAACCTCTCACT       36400       TGCTG
                              TTCAACT    TCTCACT
                              |||||||    |||||||
                              AGGTTGG    AGAGTGA
                                   _____
GAM440  PCDHA10 3' TCCAACCTCTCACT       36567       TGCTG
                              TTCAACT    TCTCACT
                              |||||||    |||||||
                              AGGTTGG    AGAGTGA
                                   _____
GAM440  PCDHA11 3' TCCAACCTCTCACT       36580       TGCTG
                              TTCAACT    TCTCACT
                              |||||||    |||||||
                              AGGTTGG    AGAGTGA
                                   _____
GAM440  PCDHA12 3' TCCAACCTCTCACT       33135       TGCTG
                              TTCAACT    TCTCACT
                              |||||||    |||||||
                              AGGTTGG    AGAGTGA
                                   _____
GAM440  PCDHA13 3' TCCAACCTCTCACT       36607       TGCTG
                              TTCAACT    TCTCACT
                              |||||||    |||||||
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                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA2   3' TCCAACCTCTCACT      36469      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA3   3' TCCAACCTCTCACT      36478      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA4   3' TCCAACCTCTCACT      36491      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA5   3' TCCAACCTCTCACT      36500      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA6   3' TCCAACCTCTCACT      33146      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA7   3' TCCAACCTCTCACT      36522      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA8   3' TCCAACCTCTCACT      33149      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHA9   3' TCCAACCTCTCACT      36552      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHAC1  3' TCCAACCTCTCACT      36622      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
                                AGGTTGG    AGAGTGA
                                _______
GAM440  PCDHAC2  3' TCCAACCTCTCACT      36633      TGCTG
                                TTCAACT    TCTCACT
                                |||||||    |||||||
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                              AGGTTGG    AGAGTGA
                                   _____
GAM440  RFXAP    3'  TTCATTCAGCTCTCACTG    8059      ACTT  TG
                              TTCA   GC  TCTCACTG
                              ||||   ||  ||||||||
                              AAGT   CG  AGAGTGAC
                                AAGT  __
GAM440  RGL      3'  TTCAACCTGCATGAGGGCTG  31548         _  TCTCA
                              TTCAACTTGC TG    CTG
                              |||||||||| ||    |||
                              AAGTTGGACG AC    GAC
                                    T  TCCC_
GAM440  SCA1     3'  TTCTGTTGCTCTCACTG     7301     AAC   TG
                              TTC   TTGC  TCTCACTG
                              |||   ||||  ||||||||
                              AAG   AACG  AGAGTGAC
                                AC_   __
GAM440  STAC     3'  CTTGATTCTTGTCTCACTG   17134     C____
                              CTTG    TGTCTCACTG
                              ||||    ||||||||||
                              GAAC    ACAGAGTGAC
                                TAAGA
GAM440  MKKS     5'  TGTACTCCATCTTTAG      33111       CAGTGC
                              TGTACTCC     CTTTAG
                              ||||||||     ||||||
                              ACATGAGG     GAAATC
                                   TA____
GAM440  MLLT2    3'  AATTGCACTTCTGTCCTTTAG  25491        CCCA  G
                              AATTGTACT    GT CCTTTAG
                              |||||||||    || |||||||
                              TTAACGTGA    CA GGAAATC
                                   AGA_  _
GAM441  EPB41L2  3'  CTGGAATAGTGGTGTGGCATTA 11004         ATCTACAA
                              CTGGAATAGT       CATTA
                              ||||||||||       |||||
                              GACCTTATCA       GTAAT
                                    CCACACC_
GAM441  EXT2     5'  TCTGAGTAGCTCTATAACATTA 7590       AA    A   C
                              TCTGG  TAGT TCTA AACATTA
                              |||||  |||| |||| |||||||
                              AGACT  ATCG AGAT TTGTAAT
                                C_   _   A
GAM441  SLC14A2  3'  TCTGGAATGGTGACTACA    28401        A  AT
                              TCTGGAAT GT  CTACA
                              ||||||||  ||  |||||
                              AGACCTTA CA  GATGT
                                   C  CT
GAM442  ARHGEF6  3'  TGGATGTGTGCTGTTCTGT   42807      C____
                              TGGAT    TTGTTCTGT
                              |||||    |||||||||
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                                ACCTA    GACAAGACA
                                  CACAC
GAM442  CASP10   3'  AATTGGGTGTTCTGT      37380       ATCT
                                AATTGG   TGTTCTGT
                                ||||||   ||||||||
                                TTAACC   ACAAGACA
                                  C___
GAM442  DGKI     3'  TGGGCTATCATGTTCTGT    21788     ___   T
                                TGG  ATC TGTTCTGT
                                |||  ||| ||||||||
                                ACC  TAG ACAAGACA
                                  CGA  T
GAM442  DUSP4    3'  TAAGTTGGAGTGTTCTGT    38425     A    TCT
                                TAA TTGGA  TGTTCTGT
                                ||| |||||  ||||||||
                                ATT AACCT  ACAAGACA
                                  C    C__
GAM442  FLRT2    3'  AACTGTTTTGTTCTGT      29832      GATC
                                AATTG   TTGTTCTGT
                                |||||   |||||||||
                                TTGAC   AACAAGACA
                                  AA__
GAM442  RANBP2L1 3'  TAAATTGGAAACCAATGTTCTG 37025         T_ __
           T                     TAAATTGGA  CT  TGTTCTGT
                                |||||||||  ||  ||||||||
                                ATTTAACCT  GG  ACAAGACA
                                     TT  TT
GAM442  RIMS1    3'  TAGATTGCCTTGTTCTGT    43736      ___
                                TGGAT   CTTGTTCTGT
                                |||||   ||||||||||
                                ATCTA   GAACAAGACA
                                  ACG
GAM442  UBQLN2   3'  TAAATTGGACATCTG       30282         CTTGT
                                TAAATTGGAT    TCTG
                                ||||||||||    ||||
                                ATTTAACCTG    AGAC
                                     T_____
GAM442  UC28     5'  TAAATTGAATTGTAGCTCTGT  34693         CTT_
                                TAAATTGGAT   GTTCTGT
                                ||||||||||   |||||||
                                ATTTAACTTA   CGAGACA
                                     ACAT
GAM442  SP3      5'  TATTTGTTGATTCTGCAA    44382          _
                                TATTTGTTGAT TTGCAG
                                |||||||||| ||||||
                                ATAAACAACTA GACGTT
                                     A
GAM443  ARG2     3'  AATGTGTAAATGTTCTCATT   10121      A  TAGTT
                                AATGT TA    TGTTCTCATT
                                ||||| ||    ||||||||||
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                                TTACA AT    ACAAGAGTAA
                                  C  TT___
GAM443  CCRL1    3'  TGTATATAGTTCTGTGTCATT  32432          GTTC
                                TGTATATAGTTT   TCATT
                                ||||||||||||  |||||
                                ACATATATCAAG   AGTAA
                                      ACAC
GAM443  IL1RAP   3'  TGAGACATGGTTTGTTCT    13508    T_   A
                                TG  ATAT GTTTGTTCT
                                ||  |||| |||||||||
                                AC  TGTA CAAACAAGA
                                 TC   C
GAM443  MASP1    3'  TAATATATATATATATATGTTC 40106          GTT___
           TCATT                   TAATGTATATA     TGTTCTCATT
                                ||||||||||     ||||||||||
                                ATTATATATAT     ACAAGAGTAA
                                      ATATAT
GAM443  NPAT     3'  TAATTATAATTTCTGTTCTCAT 42616      G   TAG
           T                     TAAT TATA   TTTGTTCTCATT
                                |||| ||||  ||||||||||||
                                ATTA ATAT   AGACAAGAGTAA
                                  _   TAA
GAM443  NPEPPS   3'  TAATGTATATCAGTTTCTCT   26720         _    G
                                TAATGTATAT AGTTT TTCT
                                |||||||||| ||||| ||||
                                ATTACATATA TCAAA GAGA
                                      G   _
GAM443  USP9Y    3'  GTATATATACCTTTCTCATT   41958       GTTTG
                                GTATATA    TTCTCATT
                                |||||||    ||||||||
                                CATATAT    AAGAGTAA
                                    ATGGA
GAM443  WHSC1L1  3'  TAATGTATACAGTTTGGGCT   35714             TT
                                TAATGTATATAGTTTG  CT
                                ||||||||||||||||  ||
                                ATTACATATGTCAAAC  GA
                                          CC
GAM443  ITGA1    3'  TCATTTTATAAAATATGTCT   41858       AAAAT
                                TCATTT    TAAAATATGTCT
                                ||||||    ||||||||||||
                                AGTAAA    ATTTTATACAGA
                                   AT___
GAM444  AANAT    5'  AGCCCTGGGGGCCTGTCC    9898        AGAAA
                                AGCCCT    GCTTGTTT
                                ||||||    ||||||||
                                TCGGGA    CGGACAGG
                                   CCCC_
GAM444  CYB561   3'  CAGCCCCAGGGGGCTCTAGCCA 12541         AAA   GTTT
           C                     CAGCCCTAG   GCTT   TCAC
                                |||||||||  ||||   ||||
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                                GTCGGGGTC  CGAG   GGTG
                                     CCC   ATC_
GAM444  DBCCR1   3' CAGTTGCTAGAACGTTTTCA  31144    CC_    AGCT
                                CAG  CTAGAA   TGTTTTCA
                                |||  ||||||   ||||||||
                                GTC  GATCTT   GCAAAAGT
                                  AAC    ____
GAM444  GRM3     3' CAGCCTAGAAAGTTCTAGCAC 9149      C     C  GTTTT
                                CAGCC TAGAAAG TT    CAC
                                ||||| ||||||| ||    |||
                                GTCGG ATCTTTC AG    GTG
                                  _     A  ATC__
GAM444  MYCL2    3' CAAGTCTCTGAGCTTGTTTTCA 23898    CC  AGAA
           C                     CAG  CT   AGCTTGTTTTCAC
                                |||  ||   ||||||||||||
                                GTT  GA   TCGAACAAAAGTG
                                  CA  GAC_
GAM444  PAFAH1B1 3' GCACTGGAATGTCTGTTTTCAC 7709    C  A   AGC
                                GC CT GAA   TTGTTTTCAC
                                || || |||   ||||||||||
                                CG GA CTT   GACAAAAGTG
                                 T  C   ACA
GAM444  PRKCH    5' GCCCCGGGGGGCCTGCTTC   26509     AGAAA
                                GCCCT    GCTTGTTTT
                                |||||    |||||||||
                                CGGGG    CGGACGAAG
                                   CCCCC
GAM444  PRKCN    3' CAGCCTTATAAACTGTTTC   25158     C  GA    T
                                CAGCC TA  AAGCT GTTTT
                                ||||| ||  ||||| |||||
                                GTCGG AT  TTTGA CAAAG
                                   A  A_    _
GAM444  PTGS1    3' AACTTTAGAAAGCGAATTTT  38724    CC      TT
                                AGC  TAGAAAGC  GTTTT
                                |||  ||||||||  |||||
                                TTG  ATCTTTCG  TAAAA
                                  AA       CT
GAM444  PTTG1IP  3' CCTGGAAGGCTGGCAGGTTCAC 20285    A  A   T  T__
                                CCT GAA GCT GT   TTCAC
                                ||| ||| ||| ||   |||||
                                GGA CTT CGA CG   AAGTG
                                  C   C   C  TCC
GAM444  RP42     3' CAGCCCTAGTAAAAGTTTT   33984        _   CTT
                                CAGCCCTAG AAAG   GTTTT
                                ||||||||| ||||   |||||
                                GTCGGGATC TTTT   CAAAA
                                     A   ___
GAM444  SDC2     3' GCTTTAGAAAGCTAGGCT    42570    CC      T_
                                GC  TAGAAAGCT  GTT
                                ||  |||||||||  |||
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                                CG  ATCTTTCGA  CGA
                                 AA        TC
GAM444  SLC24A1  5'  CAGCTCTGGAAACTTGT     21817      C  A    G
                                CAGC CT GAAA CTTGT
                                |||| || |||| |||||
                                GTCG GA CTTT GAACA
                                  A  C   _
GAM444  SMARCD1  3'  CAGCCCTAGGCGCTTTCA    40082         AAA  TT
                                CAGCCCTAG   GC  GTTTTCA
                                |||||||||   ||  |||||||
                                GTCGGGATC   CG  CGAAAGT
                                     ___  __
GAM444  SOST     3'  CAGTCCTGCAGGCTTTCA    36100     C   AGAAA  TT
                                CAG CCT     GC  GTTTTCA
                                ||| |||     ||  |||||||
                                GTC GGA     CG  CGAAAGT
                                  A  _____  TC
GAM444  TCF2     3'  AGCTCTAGTCCTTGTTTTC   27018     C    AAAG
                                AGC CTAG    CTTGTTTTC
                                ||| ||||    |||||||||
                                TCG GATC    GAACAAAAG
                                  A   AG__
GAM444  TFRC     5'  AGTTCTAGAAGCCCGCACTCAC 17425    CC      A      T
                                AG  CTAGAA GCTTGT TTCAC
                                ||  |||||| |||||| |||||
                                TC  GATCTT CGGGCG GAGTG
                                 AA     _     T
GAM444  TUFT1    3'  AGCCCTAGAGAATTTTTC    33505         AAGCTTG
                                AGCCCTAGA      TTTTC
                                |||||||||      |||||
                                TCGGGATCT      AAAAG
                                     CTTA___
GAM444  USP6     5'  CCGGAGAGTCGTCCTCAC    45027    TA  A  C
                                C  GA AG TTGTTTTCAC
                                |  || || ||||||||||
                                G  CT TC AGCAGGAGTG
                                 GC  C  _
GAM444  USP9Y    3'  TAGATCTGACTTGTTTTCA   41960      AA__
                                TAGA    GCTTGTTTTCA
                                ||||    ||||||||||
                                ATCT    TGAACAAAAGT
                                  AGAC
GAM444  DLX4     3'  TGATGGTGGTCCACTTCTGCTT 39622       AAAGCA TG     A
                                TGATG      T  CTTCT CTT
                                |||||      |  ||||| |||
                                ACTAC      G  GAAGA GAA
                                   CACCA_ GT     C
GAM444  GOLGA4   5'  TGATGAAATGGCTGCTTC    41059         GCA
                                TGATGAAA   TTGCTTC
                                ||||||||   |||||||
```

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                                ACTACTTT  GACGAAG
                                    ACC
GAM444  MCF2    5' TGATGAAATACGAGCTGCTTC 23865       _ A__
                                TGATGAAA GC  TTGCTTC
                                |||||||| ||  |||||||
                                ACTACTTT TG  GACGAAG
                                    A  CTC
GAM444  PRKG1   3' TGGTGAAAGGCTTTGCTTC  26517   A    _ A
                                TG TGAAAG C TTGCTTC
                                || |||||| | |||||||
                                AC ACTTTC G AACGAAG
                                 C     C A
GAM445  DDX6    5' AAAATGAAGAGATAAATATAAG 20537        AATTG
                                AAAGTGAAGA    AAGTATAAG
                                ||||||||||    |||||||||
                                TTTTACTTCT    TTTATATTC
                                      CTA__
GAM445  PRKACB  3' AAAGGAAGAAATGGATGTA   15593    T      T  A
                                AAAG GAAGAAAT GA GTA
                                |||| |||||||| || |||
                                TTTC CTTCTTTA CT CAT
                                  _      C  A
GAM445  ERBB2IP 3' TCACATATTTTTAAAAGTGCTG 33101          T   AA
                                TCATATATTTTTAA AAGT  CTG
                                |||||||||||||| ||||  |||
                                AGTGTATAAAAATT TTCA  GAC
                                      _   C_
GAM445  PLN     3' TCATATATTTTTAAAAAATACT 15408          T    A
                                TCATATATTTTTAA AAGTA CT
                                |||||||||||||| ||||| ||
                                AGTATATAAAAATT TTTAT GA
                                       T   _
GAM446  ACP1    3' AGAGGTAGACTCGATTATCTAA 28231     C   CTAA  GC_
                                AGAGG AGAC   GG   TCTAA
                                ||||| ||||   ||   |||||
                                TCTCC TCTG   CT   AGATT
                                   A   AG__  AAT
GAM446  ACP5    5' AGAGGCTGGTGGGCTCTA    11511      AGACCTAA
                                AGAGGC       GGGCTCTA
                                ||||||       ||||||||
                                TCTCCG       CCCGAGAT
                                   ACCA_____
GAM446  ADAR    3' AGAGGCAGGCTCAGCTCC    31900       AC  AAG
                                AGAGGCAG  CT   GGCTCT
                                ||||||||  ||   ||||||
                                TCTCCGTC  GA   TCGAGG
                                    C_  G__
GAM446  ATP10C  3' AGAGGCAGACTCAGGAC     35975        CTA
                                AGAGGCAGAC   AGGGC
                                ||||||||||   |||||
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                                TCTCCGTCTG  TCCTG
                                     AG_
GAM446  BACH2   3' AGAGGCAGGTTTTAAAAG   34770       ACC_
                                AGAGGCAG   TAAGGG
                                ||||||||   ||||||
                                TCTCCGTC   ATTTTC
                                     CAAA
GAM446  BCL2    3' GAGGGCAGGAGGGCTCT    8521     _  ACCTA
                                GAGG CAG   AGGGCTCT
                                |||| |||   ||||||||
                                CTCC GTC   TCCCGAGA
                                  C  C____
GAM446  CASP10  3' AGAGGCAATCTAAGCTC    37381       AC  AG
                                AGAGGCAG  CTA  GGCTC
                                ||||||||  |||  |||||
                                TCTCCGTT  GAT  TCGAG
                                     A_  __
GAM446  CEP2    3' AGAGGCAAGCCCTCAGCTCT  28430      GA  AAG
                                AGAGGCA  CCT  GGCTCT
                                |||||||  |||  ||||||
                                TCTCCGT  GGG  TCGAGA
                                    TC  AG_
GAM446  CIT     3' GAGGCGGGCCTAAGAGTC    43050     AGA     C
                                GAGGC  CCTAAGGG TC
                                |||||  |||||||| ||
                                CTCCG  GGATTCTC AG
                                   CCC      _
GAM446  D12S2489E 3' AGAGGCAGCCTTGGGGATATCT 28882       A  AA  C__
                                AGAGGCAG CCT  GGG  TCT
                                |||||||| |||  |||  |||
                                TCTCCGTC GGA  CCC  AGA
                                     _  AC  TAT
GAM446  DPH2L1  3' GAGGTAGGCCTGACGCT    10728     C A  AAG  T
                                GAGG AG CCT  GGC CT
                                |||| || |||  ||| ||
                                CTCC TC GGA  CTG GA
                                  A C  ___  C
GAM446  FLOT2   3' AGATGGCACAAGGGCTCT    20979    _  GACC
                                AGA GGCA   TAAGGGCTCT
                                ||| ||||   ||||||||||
                                TCT CCGT   GTTCCCGAGA
                                  A  _____
GAM446  FN14    3' GAGGCAGAGACTGGCTCTA   32491       CCTAAG
                                GAGGCAGA    GGCTCTA
                                ||||||||    |||||||
                                CTCCGTCT    CCGAGAT
                                     CTGA__
GAM446  FPGS    3' GATGCGGACCCACCGGGCTCT  22429    G A    A_
                                GA GC GACCTA  GGGCTCT
                                || || ||||||  |||||||
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                                CT CG CTGGGT  CCCGAGA
                                 A  C     GG
GAM446  GPRK6    3'  AGAGGCAGACCTATCTGGG   13267          A__
                                AGAGGCAGACCTA   GGG
                                |||||||||||||   |||
                                TCTCCGTCTGGAT   CCC
                                      AGA
GAM446  HHIP     5'  AGGGCCAGCGCTGGGCTCTA  35403    A  _  AC  AA
                                AG GGC AG  CT  GGGCTCTA
                                || ||| ||  ||  ||||||||
                                TC CCG TC  GA  CCCGAGAT
                                 _  G  GC  __
GAM446  IL21R    3'  GAGGCAGACGCTGGAGGGCT  34754        _ A_
                                GAGGCAGAC CT  AGGGCT
                                |||||||| ||  ||||||
                                CTCCGTCTG GA  TCCCGA
                                      C  CC
GAM446  ITGB1    3'  AAAGGCAGATTTAGGATC    38040        CCTA   C
                                AGAGGCAGA   AGGG TC
                                |||||||||   |||| ||
                                TTTCCGTCT   TCCT AG
                                     AAA_   _
GAM446  ITPR3    3'  AGAGGCAGGTCCTGGGAGC   13684        A_  AA
                                AGAGGCAG  CCT  GGGC
                                ||||||||  |||  ||||
                                TCTCCGTC  GGA  CTCG
                                     CA   CC
GAM446  KLHL1    5'  AGAGGCAGGACTGGGACGCCAA 34076        AC  AA   T
           A                     AGAGGCAG  CT  GGGC CTAAA
                                ||||||||  ||  |||| |||||
                                TCTCCGTC  GA  CCTG GGTTT
                                     CT  C_   C
GAM446  KRT2A    3'  AGAGACAGGCTTCTA      7684        GACCTAAG   _
                                AGAGGCA      GGCT CTA
                                |||||||      |||| |||
                                TCTCTGT      CCGA GAT
                                     _________   A
GAM446  LALBA    3'  AGAGACAGATAAGCT      14058         CCTAA
                                AGAGGCAGA    GGGCT
                                |||||||||    |||||
                                TCTCTGTCT    TTCGA
                                     A____
GAM446  MADD     3'  AGAGACAGGCCGGGGC     39062        A  TAA
                                AGAGGCAG CC   GGGC
                                |||||||| ||   ||||
                                TCTCTGTC GG   CCCG
                                     C  C__
GAM446  MAPK3    3'  GAGGCAGGTCCAGGCCCCA   43842        A_  TAA
                                GAGGCAG  CC   GGGCTCTA
                                |||||||  ||   ||||||||
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                                CTCCGTC  GG   TCCGGGGT
                                    CA  ___
GAM446  MEN1    3'  GGCAGAGCCCTGGGTTCT    39188       _  AA   C
                                GGCAGA CCT  GGG TCT
                                |||||| |||  ||| |||
                                CCGTCT GGG  CCC AGA
                                   C   A_   A
GAM446  MPP2    5'  GAGGCAAGGGCTCT       40796       GACCTA
                                GAGGCA     AGGGCTCT
                                ||||||     ||||||||
                                CTCCGT     TCCCGAGA
                                    _______
GAM446  NELL2   3'  AGAGGCAGACTTGAGGTCTAA  26045         CTAA   C
                                AGAGGCAGAC    GGG TCTAA
                                ||||||||||    ||| |||||
                                TCTCCGTCTG    TCC AGATT
                                      AAC_  _
GAM446  OAS3    3'  AGACGGCAGAGAACAGGTTCTA 26177     _     CCTA   GC
                                AGA GGCAGA    AGG  TCTA
                                ||| ||||||    |||  ||||
                                TCT CCGTCT    TCC  AGAT
                                  G     CTTG   A_
GAM446  PPP1R11 3'  AGAGGAGACAGTCGGCTCTAA  45506      C    CTAAG
                                AGAGG AGAC     GGCTCTAA
                                ||||| ||||    ||||||||
                                TCTCC TCTG     CCGAGATT
                                   _    TCAG_
GAM446  PPT2    3'  AGGGGCAGGCCAAGAAC     39914    A    A  T
                                AG GGCAG CC AAGGGC
                                || ||||| || ||||||
                                TC CCGTC GG TTCTTG
                                 C    C  _
GAM446  PSCD4   3'  AGAGGCAGAGCTGGGACT    30119         C  AA
                                AGAGGCAGA CT  GGGCT
                                ||||||||| ||  |||||
                                TCTCCGTCT GA  CCTGA
                                      C  C_
GAM446  PSG4    3'  AGAGGCAGGCATGAGC      15796         ACC  A
                                AGAGGCAG   TA GGGC
                                ||||||||   || ||||
                                TCTCCGTC   GT CTCG
                                     C__  A
GAM446  PTPRN   3'  AGGCAGGAGAAGGCTCT     15978       ACCTA
                                AGGCAG     AGGGCTCT
                                ||||||     ||||||||
                                TCCGTC     TTCCGAGA
                                   CTC__
GAM446  PTPRN   3'  AGAGGCAGGCCCGGGGCT    15977         A   AA
                                AGAGGCAG CCT  GGGCT
                                |||||||| |||  |||||
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                                TCTCCGTC GGG  CCCGA
                                    C   C_
GAM446  S100A1   3'  AGAGGCAGGTCTGGGAGGG   26558       AC  A__
                                AGAGGCAG  CT   AGGG
                                ||||||||  ||   ||||
                                TCTCCGTC  GA   TCCC
                                    CA  CCC
GAM446  SEMA3F   5'  GAAGCAGGCTCCACTCTCTA  20059       AC_  AGGG
                                GAGGCAG   CTA   CTCTA
                                |||||||   |||   |||||
                                CTTCGTC   GGT   GAGAT
                                    CGA   GA__
GAM446  SKIV2L   5'  AGGGGCAGACCTGGACC    27968    A       AA
                                AG GGCAGACCT  GGGCT
                                || |||||||||  |||||
                                TC CCGTCTGGA  CCTGG
                                 C        __
GAM446  SLC7A6   3'  ACATGCCCTTGAGGGCTCT   19584    GA_  A_
                                GCA   CCT  AGGGCTCT
                                |||   |||  ||||||||
                                TGT   GGA  TCCCGAGA
                                  ACG   AC
GAM446  SPR      3'  GGAGCCACAGGGCTCT     17094    C  A  TA
                                GG AG CC  AGGGCTCT
                                || || ||  ||||||||
                                CC TC GG  TCCCGAGA
                                 _  _  TG
GAM446  TCP11    3'  AAGGTACCAGGGCTCT     33068     CAG   TA
                                GAGG   ACC  AGGGCTCT
                                ||||   |||  ||||||||
                                TTCC   TGG  TCCCGAGA
                                  A__   __
GAM446  TMEM1    3'  GAGGGAGGCCAGGGCTCT   17594     C  A  TA
                                GAGG AG CC  AGGGCTCT
                                |||| || ||  ||||||||
                                CTCC TC GG  TCCCGAGA
                                  C  C  __
GAM446  VHL      3'  AGAGGCAGAACCTCTA     8105          CCTAAG G
                                AGAGGCAGA     G CTCTA
                                |||||||||     | |||||
                                TCTCCGTCT     T GAGAT
                                      _______ G
GAM446  ADH4     3'  CCTGATGCTCTCTCTCTG    8573     AC      CTG
                                CCT  ATGCTCTC   CTTTG
                                |||  ||||||||   |||||
                                GGA  TACGAGAG   GAGAC
                                  C_       A__
GAM446  ADRB3    3'  CCTGCTGCTCTCAGCCT    6178     ACA     CT
                                CCT   TGCTCTC  GCTT
                                |||   |||||||  ||||
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                                GGA  ACGAGAG  CGGA
                                  CG_     T_
GAM446  BIN3    3'  CCCACTGTTCCTGCTTTG   33074      A  CTC
                                CCTAC TG  TCCTGCTTTG
                                |||||  ||  ||||||||||
                                GGGTG AC  AGGACGAAAC
                                  _ A__
GAM446  CCKAR   3'  ACATATCCTGCTTTG      8809       CTC
                                ACATG  TCCTGCTTTG
                                |||||  ||||||||||
                                TGTAT  AGGACGAAAC
                                  ___
GAM446  CORO1C  3'  CATGTGGCTACTGCTTTG   30722      CT_  C
                                CATG  CT CTGCTTTG
                                ||||  ||  ||||||||
                                GTAC  GA GACGAAAC
                                  ACC  T
GAM446  CSPG3   3'  CCTACATATTGCTTT      20485        CTCTCC
                                CCTACATG    TGCTTT
                                ||||||||    ||||||
                                GGATGTAT    ACGAAA
                                    A_____
GAM446  FGF1    3'  CTAGTGCTCTCCACCT     37569     CA       T
                                CTA  TGCTCTCC GCTT
                                |||  |||||||| ||||
                                GAT  ACGAGAGG TGGA
                                  C_      _
GAM446  FKRP    3'  CCTGGTGCTCTCCTCCT     35896     ACA       G
                                CCT  TGCTCTCCT CT
                                |||  ||||||||| ||
                                GGA  ACGAGAGGA GA
                                  CC_       G
GAM446  FLRT2   5'  CCTTGCCGCCCTGTTTTG   29846     ACA   C    C
                                CCT  TGCT TCCTG TTTG
                                |||  |||| ||||| ||||
                                GGA  ACGG GGGAC AAAC
                                  ___   C    A
GAM446  GP1BA   3'  CATTACCCCTTCTGCTTTG   6744     _    C_
                                CAT GCTCT  CTGCTTTG
                                ||| |||||  ||||||||
                                GTA TGGGG  GACGAAAC
                                  A    AA
GAM446  GUCY2C  5'  CCTTGTGCCCACTTGCTTTG  22440    ACA    TCC
                                CCT  TGCTC  TGCTTTG
                                |||  |||||  |||||||
                                GGA  ACGGG  ACGAAAC
                                  AC_    TGA
GAM446  JUN     3'  CCACCAATTCCTGCTTTG    13737     ATGCTC
                                CTAC    TCCTGCTTTG
                                ||||    ||||||||||
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                                GGTG     AGGACGAAAC
                                  GTTA__
GAM446  KISS1    3'  CCCGCATGCTCTGACTCCTTTG 13964    TA       C_  G
                                CC  CATGCTCT  CT CTTTG
                                ||  ||||||||  || |||||
                                GG  GTACGAGA  GA GAAAC
                                 GC       CT  G
GAM446  MAP2     3'  TACATGCTCTTCCCTTCCTG   36505          _   GC
                                TACATGCTCT CCT  TTTG
                                |||||||||| |||  ||||
                                ATGTACGAGA GGG  GGAC
                                      A   AA
GAM446  MYEOV    5'  CCCAAGCATACTTTCCTGCTTT 39873      __     C
           G                     CCTA  CATGCT TCCTGCTTTG
                                ||||  |||||| ||||||||||
                                GGGT  GTATGA AGGACGAAAC
                                  TC     A
GAM446  OGG1     5'  CCTGCATGCCTCGCCCTTTG   32559    A    T  _  G
                                CCT CATGC CTC CT CTTTG
                                ||| ||||| ||| || |||||
                                GGA GTACG GAG GG GAAAC
                                  C    _  C  _
GAM446  PCDHB12  3'  CATGCACATTTCCTGCTTTG   33183      TC___
                                CATGC    TCCTGCTTTG
                                |||||    ||||||||||
                                GTACG    AGGACGAAAC
                                   TGTAA
GAM446  PCDHGA12 5'  CCTAGCTATCTGCTTT     36890     CAT   CTC
                                CCTA   GCT   CTGCTTT
                                ||||   |||   |||||||
                                GGAT   CGA   GACGAAA
                                  ___   TA_
GAM446  PKD2     3'  CTGCATGCTCTTTTGCTT    41070    A      CC
                                CT CATGCTCT  TGCTT
                                || ||||||||  |||||
                                GA GTACGAGA  ACGAA
                                 C       AA
GAM446  PMP2     3'  CCTACCTTGCCCTTGCTTTG   15420      A_     CC
                                CCTAC  TGCTCT  TGCTTTG
                                |||||  ||||||  |||||||
                                GGATG  ACGGGA  ACGAAAC
                                   GA     __
GAM446  SGNE1    3'  CTACATACAGCTGCTTTG    16602        TCTC
                                CTACATGC    CTGCTTTG
                                ||||||||    ||||||||
                                GATGTATG    GACGAAAC
                                     TC__
GAM446  SLC22A2  5'  CCTATTAACCAGCCTGCTTTG 40522     CAT   CT
                                CCTA   GCT  CCTGCTTTG
                                ||||   |||  |||||||||
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                                GGAT   TGG  GGACGAAAC
                                  AAT   TC
GAM446  SNX9     3'  CTACATGCTCTTACATTCG   32152          CC  _
                                CTACATGCTCT  TGC TTTG
                                ||||||||||  ||| ||||
                                GATGTACGAGA  ATG AAGC
                                      __   T
GAM446  SORD     3'  CTACTTGCTGAACTTTG     16964      A    CTCCT
                                CTAC TGCT    GCTTTG
                                |||| ||||    ||||||
                                GATG ACGA    TGAAAC
                                  A   CT___
GAM446  SPAG6    3'  TACATGCCTGCTTC        29704        TCTC
                                TACATGC   CTGCTTT
                                |||||||   |||||||
                                ATGTACG   GACGAAG

                                    _____
GAM446  TIMP3    3'  CTGCAGCTCTCCCTCCT     7450     A  T      G
                                CT CA GCTCTCCT CTT
                                || || |||||||| |||
                                GA GT CGAGAGGG GGA
                                 C  _       A
GAM446  TMEPAI   3'  CCTCATGCTCTCCTCT      33598     A         G
                                CCT CATGCTCTCCT CT
                                ||| ||||||||||| ||
                                GGA GTACGAGAGGA GA
                                  _         _
GAM446  UBE2L3   3'  CCACAGAGTCCTGCTTTG    17824       TGCTC
                                CTACA    TCCTGCTTTG
                                |||||    ||||||||||
                                GGTGT    AGGACGAAAC
                                   CTC__
GAM447  FZD7     3'  TTAACTTTCCTTTATTATGAG  18637         AGACTC
                                TTAACTTTC     ATTATGAG
                                |||||||||     ||||||||
                                AATTGAAAG     TAATACTC
                                      GAAA__
GAM447  GALNT2   3'  TTTGACTTTCAGACCAT     21013     A        T
                                TTT ACTTTCAGAC CAT
                                ||| |||||||||| |||
                                AAA TGAAAGTCTG GTA
                                  C        _
GAM447  TEC      3'  ACTTTCTTCCATTATGAG     17381       AGAC
                                ACTTTC    TCATTATGAG
                                ||||||    ||||||||||
                                TGAAAG    GGTAATACTC
                                   AA__
GAM448  ACLY     3'  TGAGGTGGCAGCTGCCCAGAAT 42156     AA    AT    T
                                TGA  TGGT  AGTT CCCAGAAT
                                |||  ||||  |||| ||||||||
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                                ACT  ACCG  TCGA GGGTCTTA
                                  CC   __   C
GAM448  ARHGEF5  3'  TGAAAGGTTCCCAGA      24130      T   ATAGTT
                                TGAAA GGT     TCCCAGA
                                ||||| |||     |||||||
                                ACTTT CCA     AGGGTCT
                                  _  _______
GAM448  GNAO1    3'  TGAAATGGTGAGTTTTCC    44944        AT    C
                                TGAAATGGT  AGTTT CC
                                |||||||||  ||||| ||
                                ACTTTACCA  TCAAA GG
                                     C_    A
GAM448  MAP4K2   3'  GAATGGATGGCCCAGGCCCAG  21351     ___    A   TTT
                                GAA   ATGGT TAG   CCCAG
                                |||   ||||| |||   |||||
                                CTT   TACCG GTC   GGGTC
                                  ACC    G   C__
GAM448  PCLO     3'  TGAAATGGAAACCCAGA     45307       TATAGTTT
                                TGAAATGG       CCCAGA
                                ||||||||       ||||||
                                ACTTTACC       GGGTCT
                                     TTT_____
GAM448  PTEN     3'  GAGATGGTATATGGTCCAGA   7210     A      GTTTC
                                GA ATGGTATA    CCAGA
                                || ||||||||    |||||
                                CT TACCATAT    GGTCT
                                 C       ACCA_
GAM448  RAB18    3'  GAGATGGAATTTCCCAGA    34574    A   TAT
                                GA ATGG   AGTTTCCCAGA
                                || ||||   ||||||||||
                                CT TACC   TTAAAGGGTCT
                                 C   ___
GAM448  STK31    5'  TGAAATGGGCCTCGTCCCAG  37278       TATAGTT
                                TGAAATGG      TCCCAG
                                ||||||||      ||||||
                                ACTTTACC      AGGGTC
                                     CGGAGC_
GAM449  SEL1L    3'  CTCTGTAAAGGAAGTTTTT   22845    C  CT  T
                                CTC GTA  AA GAAGTTTTT
                                ||| |||  || |||||||||
                                GAG CAT  TT CTTCAAAAA
                                  A   __  C
GAM450  ADCY9    3'  GGGGTGGCGGAGCTGT     10023    A    CTCA
                                GG GTGGT   GGAGCTGT
                                || |||||   ||||||||
                                CC CACCG   CCTCGACA
                                 C    ____
GAM450  BAT1     3'  CATGGGGTGGGGGCTG      21587      A   TCTCA  A
                                TATGG GTGG    GG GCTG
                                ||||| ||||    || ||||
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                                GTACC CACC    CC CGAC
                                  C  _____ _
GAM450  CNGA3   3' ATGGAGGATAGGGGCTGT   10535      T  CTC  A
                                ATGGAG GGT  AGG GCTGT
                                |||||| |||  ||| |||||
                                TACCTC CTA  TCC CGACA
                                  _  ___  C
GAM450  FOXP2   3' TGGAGTGGTTATGAAGGTC   30939       CTCA  CT
                                TGGAGTGGT   GGAG  GTC
                                |||||||||   ||||  |||
                                ACCTCACCA   CTTC  CAG
                                     ATA_   __
GAM450  OSM     3' TGGGGACCCGGGAGCTGTC   33917    AGT  T   A
                                TGG   GG CTC GGAGCTGTC
                                |||   || ||| |||||||||
                                ACC   CC GGG CCTCGACAG
                                  ___ T   C
GAM450  STC1    3' GGGGTGGTCTCAGGGGAGC   17179    A      __
                                GG GTGGTCTCA  GGAGC
                                || |||||||||  |||||
                                CC CACCAGAGT  CCTCG
                                 C       CC
GAM450  CACNG7  3' TGCCCGAACCTGCTCT     36692       A  CAAC  CC
                                TGCCCGAG CCT   GT  CT
                                |||||||| |||   ||  ||
                                ACGGGCTT GGA   CG  GA
                                  _  _____ A_
GAM450  EPB72   5' TGCCCGAGACCGCAGTCC    19904         T  AC
                                TGCCCGAGACC CA  GTCC
                                |||||||||||  ||  ||||
                                ACGGGCTCTGG GT  CAGG
                                      C __
GAM450  GBAS    3' GCTTAAAACCTCAGTGTTTCT  11235    CC       AC  CC
                                GC  GAGACCTCA  GT  CT
                                ||  |||||||||  ||  ||
                                CG  TTTTGGAGT  CA  GA
                                 AA       CA  AA
GAM450  IGF1    3' GCTTGAGGTTTCAGAGTCCCTC 8343    CC   ACC   AC
            C                    GC  GAG   TCA  GTCCCTCC
                                ||  |||   |||  ||||||||
                                CG  CTC   AGT  CAGGGAGG
                                 AA   CAA   CT
GAM450  LFG     3' TGCCGAGGACCTGTCCCTC   44156     C  _   CAAC
                                TGCC GAG ACCT   GTCCCTC
                                |||| ||| ||||   |||||||
                                ACGG CTC TGGA   CAGGGAG
                                  _  C   _____
GAM450  NAB2    5' TGTCCAGGCTCTGTCCCTC   25565    C  G  AC   AAC
                                TG CC AG  CTC   GTCCCTC
                                || || ||  |||   |||||||
```

```
                                AC GG TC  GAG   CAGGGAG
                                 A  _  C_   A__
GAM450  PPP2R5E  5'  TGTCCGGTACGGGGTCCCTCC  26481    C   AG  CTCAAC
                                TG CCG  AC     GTCCCTCC
                                || |||  ||     ||||||||
                                AC GGC  TG     CAGGGAGG
                                 A   CA  CCC___
GAM450  PRX      3'  CCCTGAGACCTCAGCACC    34109     _       A  T
                                CCC GAGACCTCA CG CC
                                ||| ||||||||| || ||
                                GGG CTCTGGAGT GT GG
                                  A        C  _
GAM450  RAB7L1   3'  TGCCCAGACCCCTCCTTC    19439       G      AACG   C
                                TGCCC AGACCTC    TCC TC
                                ||||| |||||||    ||| ||
                                ACGGG TCTGGGG    AGG AG
                                  _      _____  A
GAM450  SUFU     3'  GCCTGAGACCTCGCACAAGCCT 32089     C       A_   TC
              CC                  GCC GAGACCTC  ACG  CCTCC
                                ||| ||||||||  |||  |||||
                                CGG CTCTGGAG  TGT  GGAGG
                                  A       CG   TC
GAM450  TNFAIP2  3'  TGCCCAGACCTCAGCC      26642       G       AC
                                TGCCC AGACCTCA  GTC
                                ||||| ||||||||  |||
                                ACGGG TCTGGAGT  CGG
                                  _      __
GAM450  WHSC1    3'  TGTCCGAGACCTGCAGCAGCAT 39394    C        _____  A
              CC                  TG CCGAGACCT    CA CGTCC
                                || |||||||||    || |||||
                                AC GGCTCTGGA    GT GTAGG
                                 A        CGTC  C
GAM450  WHSC1    3'  TGTCCGAGACCTTGGTC     39395    C        CAAC
                                TG CCGAGACCT    GTC
                                || |||||||||    |||
                                AC GGCTCTGGA    CAG
                                 A        AC__
GAM451  LAMC1    3'  CAGGAGTATATCGTCAAAACAC 14080    C  AC       CCT_
                                CA GA  ATATCGTC    CGC
                                || ||  ||||||||    |||
                                GT CT  TATAGCAG    GTG
                                 C  CA       TTTT
GAM451  MCOLN1   5'  CGACCTCGCTCCCTCGCG    33918     ACATA  _
                                CGA    TCG TCCCTCGCG
                                |||    ||| |||||||||
                                GCT    AGC AGGGAGCGC
                                  GG___   G
GAM451  S100B    3'  GAACGCAGGCCCTCGCG     26569      A  TC T
                                GAAC TA  G CCCTCGCG
                                |||| ||  | ||||||||
```

```
                              CTTG GT  C GGGAGCGC
                                C  C_ _
GAM451  SOX4     5'  CCACGCGCGCTCACACCCTCGC 16977      AACATA  GT_
           G                   CCACG     TC   CCCTCGCG
                               ||||||     ||  ||||||||
                               GGTGC     AG   GGGAGCGC
                                  GCGCG_  TGT
GAM452  GUCY1B3  3'  GTGGAACACTAAACAGATTT  9228     CA      TT_
                               GT  AACACTAA   GGTTT
                               ||  ||||||||   |||||
                               CA  TTGTGATT   CTAAA
                                CC       TGT
GAM452  TMPRSS3  3'  TACGTCAAGCACCAAATG    37064        A     T
                               TACGTCAA CACTAA TG
                               |||||||| |||||| ||
                               ATGCAGTT GTGGTT AC
                                    C     T
GAM453  CENTD1   5'  ACATCTTAAGGAAAGAAAAT  40134       TCCGT
                               ACATCTT    AAGAAAAT
                               |||||||    ||||||||
                               TGTAGAA    TTCTTTTA
                                   TTCCT
GAM453  CRK      3'  ACATCTGTAAGAAAA      40825       TTCC
                               ACATCT   GTAAGAAAA
                               ||||||   |||||||||
                               TGTAGA   CATTCTTTT
                                  ____
GAM453  FMR1     3'  TATAACATCTTAGAGTGAAG   12944          TCC  _
                               TATAACATCTT   GT AAG
                               ||||||||||   || |||
                               ATATTGTAGAA   CA TTC
                                     TCT  C
GAM453  SART2    3'  TATAACGGTTTTCCATATAAGG 30038       ATC      A___
              AAAAT                TATAAC   TTTCCGTA   GAAAAT
                               ||||||  ||||||||   ||||||
                               ATATTG   AAAGGTAT   CTTTTA
                                  CCA       ATTC
GAM454  CXCR6    3'  AATTTCATTTTTAAAATGC   27292
                               AATTTTATTTTTAAAATGT
                               ||||||||||||||||||
                               TTAAAGTAAAAATTTTACG

GAM455  CLECSF6  3'  TCATGTTCTCTCCATGT     43440      C  AGA
                               TCATG TC   CTCCGTGT
                               ||||| ||   ||||||||
                               AGTAC AG   GAGGTACA
                                  A  A__
GAM455  GNLY     5'  TCATCTCCCCCGTG       29806      G   AGA
                               TCAT CTC   CTCCGTG
                               |||| |||   |||||||
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                                AGTA GAG   GGGGCAC
                                  _  ___
GAM455  SLC17A2  3'  TCATGCTCAGTACCACAT    25183          _ TC
                                TCATGCTCAG AC  CGT
                                |||||||||| ||  |||
                                AGTACGAGTC TG  GTA
                                     A  GT
GAM455  SLC1A5   5'  TCTGCTCTGCCCCGTGT     24750    A    AGA
                                TC TGCTC   CTCCGTGT
                                || |||||   ||||||||
                                AG ACGAG   GGGGCACA
                                 _    AC_
GAM455  SNX9     3'  TGCTCAGAAACACCCTGTGT   32162        ____  C
                                TGCTCAGA   CTC GTGT
                                ||||||||   ||| ||||
                                ACGAGTCT   GGG CACA
                                     TTGT   A
GAM455  WNT2     5'  TCAGGTCAGACTCCGTGT    18109     TGC
                                TCA   TCAGACTCCGTGT
                                |||   ||||||||||||||
                                AGT   AGTCTGAGGCACA
                                  CC_
GAM456  ARHGEF12 3'  TCAAAATGAATTTCCGAT    31648    T   A
                                TC AAAT AATTTCCGAT
                                || |||| ||||||||||
                                AG TTTA TTAAAGGCTA
                                 T   C
GAM456  ITK      3'  CAAATAAAAAGTCCCTG     24440        TTTCCGA
                                TAAATAAA      TCCCTG
                                ||||||||      ||||||
                                GTTTATTT      AGGGAC
                                     TTC____
GAM456  PABPC4   3'  CAAATAAAACCAATTTCTGG   19219        TTT    CC
                                TAAATAAA   CCGAT  CTGG
                                ||||||||   |||||  ||||
                                GTTTATTT   GGTTA  GACC
                                     T__     AA
GAM457  BBS2     5'  GCTCTTTTTGCGGCTGCG    36639         A  A  A
                                GCTCTTTTT CG CT CG
                                ||||||||| || || ||
                                CGAGAAAAA GC GA GC
                                     C  C  C
GAM457  FGF13    3'  TCTCTTTACTGACTGGGG    37984         _   AC
                                TCTTTTTAC GACT  GGGG
                                ||||||||| ||||  ||||
                                AGAGAAATG CTGA  CCCC
                                     A   __
GAM457  HEXA     3'  GCTCTTTTGTGACCAGG     8014         TAC    C
                                GCTCTTTT   GACTA GG
                                ||||||||   ||||| ||
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                                CGAGAAAA  CTGGT CC
                                    CA_   _
GAM457  ITGA5    3'  GCTCTTTTTGGGGC      41498       ACGACTAC
                                GCTCTTTTT     GGGGC
                                |||||||||     |||||
                                CGAGAAAAA     CCCCG
                                ________
GAM457  SLC22A3  3'  GCTCATTTTACGATTACG    35051     T      C
                                GCTC TTTTACGA TACG
                                |||| |||||||| ||||
                                CGAG AAAATGCT ATGC
                                  T       A
GAM458  ADAMTS3  3'  TAGCACATTATTGCAG     30644       CGTT    A
                                TAGCACAT   TATTG CAG
                                ||||||||   ||||| |||
                                ATCGTGTA   ATAAC GTC
                                    ____   _
GAM458  AGM1     3'  GCCATTATTATTGACAGT    31815    A  CGT
                                GC CAT   TTATTGACAGT
                                || |||   ||||||||||
                                CG GTA   AATAACTGTCA
                                 _  AT_
GAM458  AKAP13   3'  GCACATCGTTCTGCAG      28483         AT  A
                                GCACATCGTTT  TG CAG
                                ||||||||||  || |||
                                CGTGTAGCAAG  AC GTC
                                    __ _
GAM458  APPBP2   3'  GCATGTGTTCACTGCAGT    26880    CATC      A
                                GCA   GTTTATTG CAGT
                                |||   |||||||| ||||
                                CGT   CAAGTGAC GTCA
                                  ACA_      _
GAM458  B4GALT6  3'  GCTGTCAATTATTGACAGT   40850    ACA   T
                                GC   TCG TTATTGACAGT
                                ||   ||| ||||||||||
                                CG   AGT AATAACTGTCA
                                 AC_   T
GAM458  BAZ2B    3'  TAGCACATCAGTGTAAACAGT  30324         TTTATT
                                TAGCACATCG     GACAGT
                                ||||||||||     ||||||
                                ATCGTGTAGT     TTGTCA
                                     CACAT_
GAM458  CALM2    3'  GCATATTTTTTTGACAGT    11950    CATCG   A
                                GCA    TTT TTGACAGT
                                |||    ||| ||||||||
                                CGT    AAA AACTGTCA
                                  ATA__   A
GAM458  GRINL1A  3'  AGCGATAATTATTGACAGT   42994    ACATCGT
                                AGC      TTATTGACAGT
                                |||      ||||||||||
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                              TCG      AATAACTGTCA
                                CTATT__
GAM458  HSPA6    3'  TAGCATAGCCCTGACAG     13463      CATC   TA
                              TAGCA   GTT  TTGACAG
                              |||||   |||  |||||||
                              ATCGT   CGG  GACTGTC
                                AT__  __
GAM458  LUM      3'  GCACATCATTTGACAGT     14269         TAT
                              GCACATCGTT   TGACAGT
                              ||||||||||   |||||||
                              CGTGTAGTAA   ACTGTCA
                                       ___
GAM458  LYPLA1   3'  CAGCATGTATTGACAG      26756      CATCGTT
                              TAGCA      TATTGACAG
                              |||||      |||||||||
                              GTCGT      ATAACTGTC
                                AC_____
GAM458  SIM2     3'  GCAGTCCATTGACAGT      22875     CATC
                              GCA   GTTTATTGACAGT
                              |||   ||||||||||||
                              CGT   CAGGTAACTGTCA
                                _____
GAM459  ARHGDIA  3'  CGAGGAGGCTGGGCCTG     20204         CAATT  A  G
                              CGAGGAGGCT    GG GC TG
                              ||||||||||    || || ||
                              GCTCCTCCGA    CC CG AC
                                    _____ _  G
GAM459  GUCY1A2  5'  CGGGGAGGCTCCGAGAGTGTG  9216     A      AATT   C
                              CG GGAGGCTC   GGAG GTG
                              || ||||||||   |||| |||
                              GC CCTCCGAG   TCTC CAC
                               C      GC__   A
GAM459  KCNS2    3'  CAAGGAGGCTTGACTGTGA   42820         CA   _
                              CGAGGAGGCT  ATTG GA
                              ||||||||||  |||| ||
                              GTTCCTCCGA  TGAC CT
                                    AC    A
GAM459  LIMD1    3'  AGGAGGCTCAGCCTGTGA    30627         A_  _
                              AGGAGGCTCA  TTG GA
                              ||||||||||  ||| ||
                              TCCTCCGAGT  GAC CT
                                    CG   A
GAM459  MBP      5'  CGGGGGGGCTCAGGTGGA    44887    A  A     AT
                              CG GG GGCTCA  TGGA
                              || || ||||||  ||||
                              GC CC CCGAGT  ACCT
                               C  C     CC
GAM459  NR3C2    3'  CGAAGAGGTTTCAGTGTGG   9469         C_  AT_
                              CGAGGAGG  TCA   TGG
                              ||||||||  |||   |||
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                                GCTTCTCC  AGT   ACC
                                     AA   CAC
GAM459  OAS3     3'  CGGGGAGGCCCAGAGTCTGTG  26180    A       ATTG   C__
                                CG GGAGGCTCA    GAG   GTG
                                || |||||||||    |||   |||
                                GC CCTCCGGGT    CTC   CAC
                                 C        ____   AGA
GAM459  PTPRN    3'  GAGGAGGCTGGGCGT       15979         CAATT  A
                                GAGGAGGCT     GG GCGT
                                |||||||||     || ||||
                                CTCCTCCGA     CC CGCA
                                      _____ _
GAM459  STAT4    3'  GAGGAGTGCCACGGGAGTGTGA 17146       _  T  ATT    C
                                GAGGAG GC CA   GGAG GTGA
                                |||||| || ||   |||| ||||
                                CTCCTC CG GT   CCTC CACT
                                    A  _  GC_    A
GAM459  UQCRFS1  5'  CGAGGAGGCGCGGGACGCGTGA 25635          TCAATT  _
                                CGAGGAGGC      GGA GCGTGA
                                |||||||||      ||| ||||||
                                GCTCCTCCG      CCT CGCACT
                                     CGC___    G
GAM460  TNFRSF6  3'  TATTGAACATTTTCGGGGGTGG 6224          CTA_  T   AC
           GGG                    TATTGAAC    TC GGG  GGGGG
                                |||||||||    || |||  |||||
                                ATAACTTG    AG CCC  CCCCC
                                     TAAA  C   CA
GAM461  CLCN4    3'  TGAAAAAGAAATAGCAACGGGA 12292    A      T    TG A_
                                A AAAAAGA ATAG  A  GGA
                                | ||||||| ||||  |  |||
                                A TTTTTCT TATC  T  CCT
                                 C      T    GT GC
GAM461  DACH     5'  TGAAAAGGAGGAGGTTTGAAGG 38882       AA  ATATAG
           AC                     TGAAAA  AG     TGAAGGAC
                                ||||||  ||     ||||||||
                                ACTTTT  TC     ACTTCCTG
                                    CC  CTCCAA
GAM461  FKBP1A   3'  GAGCAAAGGCAGTGAAGG    38278    AAA    ATA
                                GA   AAAG   TAGTGAAGG
                                ||   ||||   |||||||||
                                CT   TTTC   GTCACTTCC
                                 CG_    C__
GAM461  GAS7     3'  TGGGAAAAAAATAAAGAAGGA  25289    AA       TAGT
                                TG  AAAAAGATA    GAAGGA
                                ||  |||||||||    ||||||
                                AC  TTTTTTTAT    CTTCCT
                                 CC        TT__
GAM461  HOXD4    3'  AAAAAAGAAGAGAAGG      31163         TAT  T
                                AAAAAAGA   AG GAAGG
                                ||||||||   || |||||
```

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                                TTTTTTCT   TC CTTCC
                                    ___  T
GAM461  KLHL3    3'  TGAAAAAGGATACATGAGGA  44649       AA     G  A
                                TGAAAAA  GATATA TGA GGA
                                ||||||| ||||||| ||| |||
                                ACTTTTT  CTATGT ACT CCT
                                   C_     _  _
GAM461  KRT15    3'  TGAAATAAAAGACCGAGGGAC  14015      _      ATAG  A
                                TGAAA AAAAGAT    TGA GGAC
                                ||||| |||||||    ||| ||||
                                ACTTT TTTTCTG    GCT CCTG
                                   A      _____  C
GAM461  LHCGR    3'  TGAAAAAAAGATATGCAAAA  6932            A TG
                                TGAAAAAAAGATAT G  AAG
                                |||||||||||||| |  |||
                                ACTTTTTTTCTATA C  TTT
                                         _ GT
GAM461  MT1L     3'  GAAAAAAAGATGTAGCAAA   44946          A  TG
                                GAAAAAAAGAT TAG  AA
                                |||||||||| |||  ||
                                CTTTTTTTCTA ATC  TT
                                      C  GT
GAM461  NBS1     3'  TGAAAAAAAGATGCAATGA   42990          A
                                TGAAAAAAAGAT TAGTGA
                                |||||||||||| ||||||
                                ACTTTTTTTCTA GTTACT
                                      C
GAM461  NOTCH2   3'  TGAAAGAAAGATTGGTGAGCAG 35914      A     ATA   __
           G                     TGAAA AAAGAT   GTGA  AGG
                                |||||  ||||||   ||||  |||
                                ACTTT TTTCTA   CACT  TCC
                                   C     AC_    CG
GAM461  NUMA1    3'  AAGGCGCCAGTGAAGGAC    45239     ATA_
                                AAG    TAGTGAAGGAC
                                |||    ||||||||||
                                TTC    GTCACTTCCTG
                                  CGCG
GAM461  PIGN     3'  TGAAAAAAAAAAAAGTGAAGGA  29552          TAT
                                TGAAAAAAAGA   AGTGAAGGA
                                ||||||||||   |||||||||
                                ACTTTTTTTTT   TCACTTCCT
                                      T__
GAM461  PKHD1    3'  TGAAAGAAAGCATGTGCAGG   39808      A   A  A  A
                                TGAAA AAAG TAT GTG AGG
                                ||||| |||| ||| ||| |||
                                ACTTT TTTC GTA CAC TCC
                                   C   _  _  G
GAM461  POLA     3'  GAAAAAAATAGCAAGCGAGGG  32615        GATAT    A
                                GAAAAAAA    AGTGA GG
                                ||||||||    ||||| ||
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                                CTTTTTTT    TCGCT CC
                                    ATCGT    C
GAM461  PRSS16   3'  AAAAGATGGTGAGTGAAGG   25232       AT__
                                AAAAGAT   AGTGAAGG
                                |||||||   ||||||||
                                TTTTCTA   TCACTTCC
                                    CCAC
GAM461  SLC16A2  3'  TGGCAAAAAGATGATGAAAG  27162   AA      ATA
                                TG  AAAAAGAT   GTGAAGG
                                ||  ||||||||   |||||||
                                AC  TTTTTCTA   TACTTTC
                                 CG       C__
GAM461  ST7      3'  TAAAAGAAAGACGGTGGAGGA  30270      A     ATA   A
                                TGAAA AAAGAT   GTG AGGA
                                ||||| ||||||   ||| ||||
                                ATTTT TTTCTG   CAC TCCT
                                   C     C__   C
GAM461  TCF3     3'  AAAGGAGTGAAGGAC      43314      ATAT
                                AAAG   AGTGAAGGAC
                                ||||   ||||||||||
                                TTTC   TCACTTCCTG
                                  C___
GAM461  TPM1     3'  TGAACAAAAGACCACAGGGGGA 7488      A     _   TGAA
           C                     TGAA AAAAGAT ATAG   GGAC
                                ||||| ||||||| ||||   ||||
                                ACTT TTTTCTG TGTC   CCTG
                                  G      G   CC__
GAM461  UBE2B    3'  AAAAAAATACAAACAGGA    17788          TGA
                                AAAAAGATATAG   AGGA
                                ||||||||||||   ||||
                                TTTTTTTATGTT   TCCT
                                       TG_
GAM461  WT1      3'  AAAAAAAGAAGGGAAGG     35958         TAT  T
                                AAAAAAAGA   AG GAAGG
                                |||||||||   || |||||
                                TTTTTTTCT   TC CTTCC
                                     ___ C
GAM462  ANGPT2   3'  TAGGTGTTCTGTCTAATC    10089     A  _
                                TAG TGT TTGTCTAATT
                                ||| ||| ||||||||||
                                ATC ACA GACAGATTAG
                                  C   A
GAM462  CALU     3'  AATGTTTGTCTACATGTGT    10254          ATTTA
                                GATGTTTGTCTA    GT
                                ||||||||||||    ||
                                TTACAAACAGAT    CA
                                       GTACA
GAM462  TRIM9    5'  GATGTTTGTACTTTTAGTA   31569         _  AA
                                GATGTTTGT CT  TTTAGTA
                                |||||||| ||  |||||||
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                                CTACAAACA GA  AAATCAT
                                      T __
GAM462  TBL2     3'  TTTTTAATCCCCAGCTCATAT  37412        A   CA
                                TTTTTAAT CCCA  TCATAT
                                |||||||| ||||  ||||||
                                AAAAATTA GGGT  AGTATA
                                     G   CG
GAM463  COL1A2   3'  CAGAAGAAATGGAAGGATTCAG 6385        _    A___
          CTTT                    CAGAAGAA TGGAA   TTAGCTTT
                                |||||||| |||||   ||||||||
                                GTCTTCTT ACCTT   AGTCGAAA
                                     T    CCTA
GAM463  CPNE3    3'  CAGAAGAAGGGTTAG       19381        T  AAA
                                CAGAAGAA GG   TTAG
                                |||||||| ||   ||||
                                GTCTTCTT CC   AATC
                                     C  ___
GAM463  HD       3'  TACGGAAGAATGGTGATT    13359     A       AA
                                TAC GAAGAATGG  ATT
                                ||| |||||||||  |||
                                ATG CTTCTTACC  TAA
                                  C        AC
GAM463  KIF3B    3'  TACAGAATTCAGATTAGCTTT  22041       GAA   AA
                                TACAGAA   TGGA  TTAGCTTT
                                |||||||   ||||  ||||||||
                                ATGTCTT   GTCT  AATCGAAA
                                     AA_   __
GAM463  MMP19    3'  GAACATGGAGTTAGCTTT    35585     GA    AA
                                GAA  ATGGA  TTAGCTTT
                                |||  |||||  ||||||||
                                CTT  TACCT  AATCGAAA
                                  G_    C_
GAM463  PRELP    3'  CAGAAGAATAGATGGCTTT   15547          AATTA
                                CAGAAGAATGGA    GCTTT
                                ||||||||||||    |||||
                                GTCTTCTTATCT    CGAAA
                                       AC___
GAM463  SLC38A2  3'  GAAAAATAGGTTAGCTTT    33275        AAA
                                GAAGAATGG   TTAGCTTT
                                |||||||||   ||||||||
                                CTTTTTATC   AATCGAAA
                                     C__
GAM464  DSC3     3'  TTTACCAGTTGTCTGT      35953          CCCA
                                TTTACCGGTTG    TCTGT
                                ||||||||||    |||||
                                AAATGGTCAAC    AGACA
                                       ____
GAM465  CANX     3'  CTAAAATAATATCTAACTCT   44664          CGTT
                                CTAAAATAATATT    TTCT
                                ||||||||||||    ||||
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```
                                GATTTTATTATAG  GAGA
                                       ATT_
GAM466  HTR2C    3'  ATTGTAACACAACACTATATT  9279            T
                                ATTGTAACATAGTA CTATATT
                                |||||||||||||| |||||||
                                TAACATTGTGTTGT GATATAA
                                       _
GAM466  MCL1     3'  CAATATAGACACTTTCTT    34997          ATAAATC
                                TAATATAGACAT     TCTT
                                ||||||||||||     ||||
                                GTTATATCTGTG     AGAA
                                       AA_____
GAM467  PPM1D    3'  TATTAGATGAATATATACCCAT 18840         _   _
           ATAA                   TATTAGATGA TATAT TTCGTATAA
                                ||||||||||| ||||| |||||||||
                                ATAATCTACT ATATA GGGTATATT
                                       T   T
GAM467  KIF5C    3'  TAAAATATCCATCTATGTGGAT 21160        _   A  A
           T                    TAAAATATT ATCTA TGT GATT
                                ||||||||| ||||| ||| ||||
                                ATTTTATAG TAGAT ACA CTAA
                                     G   _  C
GAM467  PKP2     3'  TAAAACAACATTTAATGTAGAT 21318       T  C
           T                    TAAAATA TAT TAATGTAGATT
                                ||||||| ||| ||||||||||
                                ATTTTGT GTA ATTACATCTAA
                                    T  A
GAM467  SERPINE1 3'  AAATATTATCTAAGGTAG    8280           T
                                AAATATTATCTAA GTAG
                                |||||||||||| ||||
                                TTTATAATAGATT CATC
                                       C
GAM467  SIAH1    3'  TAAAATATTTCTAATGAACTGA 16714        A     TA__
           TT                    TAAAATATT TCTAATG   GATT
                                ||||||||| |||||||   ||||
                                ATTTTATAA AGATTAC   CTAA
                                     _     TTGA
GAM467  SPAG6    3'  AAAATATTATCTAAAGGTA   29699          T_
                                AAAATATTATCTAA  GTA
                                |||||||||||||  |||
                                TTTTATAATAGATT  CAT
                                       TC
GAM468  ANGPT2   5'  TGGGAAGAACAGTCCT     10090       TA  AA
                                TGGGAAGA  AG  TCCT
                                ||||||||  ||  ||||
                                ACCCTTCT  TC  AGGA
                                     TG  __
GAM468  ANXA9    3'  TGAGATGGGAAAATTAAG    18693    GA       _
                                TG  ATGGGAAGAT AAG
                                ||  |||||||||| |||
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                                AC  TACCCTTTTA TTC
                                 TC        A
GAM468  ASH1    3'  TGGGGTAGGAATAGGGATCCT  32978     AA     GATAA  A
                                TGG  TGGGAA    GA TCCT
                                |||  ||||||    || ||||
                                ACC  ATCCTT    CT AGGA
                                  CC     ATCC_  _
GAM468  CDH5    3'  GGAATGGGCTGCAGAGAATCCT 12188        AAGATA
                                GGAATGGG     AGAATCCT
                                ||||||||     ||||||||
                                CCTTACCC     TCTTAGGA
                                     GACGTC
GAM468  DMRT2   3'  TGGAATGGGGCGATAGCCT   27270        AA   AGAAT
                                TGGAATGGG  GATA    CCT
                                |||||||||  ||||    |||
                                ACCTTACCC  CTAT    GGA
                                     CG    C_____
GAM468  GABRE   3'  AAAATGGGGATAAGAATCCT   35071        AA
                                GGAATGGG  GATAAGAATCCT
                                ||||||||  ||||||||||||
                                TTTTACCC  CTATTCTTAGGA
                                          __
GAM468  IL2RA   5'  TGGGATGGGAAGATCGGTCC   7674      A        AAGAA
                                TGG ATGGGAAGAT    TCC
                                ||| ||||||||||    |||
                                ACC TACCCTTCTA    AGG
                                  C        GCC__
GAM468  MYO1A   5'  GGAATGGGGCATAAGAGTCCT  23920        AAG     A
                                GGAATGGG   ATAAGA TCCT
                                ||||||||   |||||| ||||
                                CCTTACCC   TATTCT AGGA
                                     CG_     C
GAM468  RARG    3'  TGGAATGGCAGGGTCTTCCT   9730         GA  ATAAGAA
                                TGGAATGG  AG      TCCT
                                ||||||||  ||      ||||
                                ACCTTACC  TC      AGGA
                                     G_  CCAGA__
GAM468  SF3B3   3'  GGAATGGGGGACTCAGGTTC   29680        AA   A_  AA
                                GGAATGGG  GAT  AG  TC
                                ||||||||  |||  ||  ||
                                CCTTACCC  CTG  TC  AG
                                     C_   AG  CA
GAM468  SIAT7D  3'  TGGGGTGGGAAGGAACCT    30834     AA      ATAA   T
                                TGG  TGGGAAG    GAA CCT
                                |||  |||||||    ||| |||
                                ACC  ACCCTTC    CTT GGA
                                  CC      _____   _
GAM468  SORBS1  3'  GGGATGGGAAGCTGATGGGATC 31709    A       ATAAGA__
            CTA                   GG ATGGGAAG       ATCCTA
                                  || ||||||||       ||||||
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                                CC TACCCTTC       TAGGAT
                                 C       GACTACCC
GAM468  XK      3'  GGAGTAAGATGGTAAGAATTCT 34364     A    AGA      C
              A                   GGA TGGGA   TAAGAAT CTA
                                  ||| |||||   ||||||| |||
                                  CCT ATTCT   ATTCTTA GAT
                                    C     ACC      A
GAM468  ZNF278   3'  GGAAGGGAGGATGACGAAC   36800     T   A   AA_
                                  GGAA GGGA GAT   GAAT
                                  |||| |||| |||   ||||
                                  CCTT CCCT CTA   CTTG
                                    _   C   CTG
GAM469  FOXO1A   3'  ATGCTTTTAATAACAGTA    12884      GA_
                                  ATGTT   AATAACAGTA
                                  |||||   ||||||||||
                                  TACGA   TTATTGTCAT
                                     AAA
GAM469  P53AIP1  3'  TATGCTAATGATAACAGTA   35235       A_
                                  TATGTTGA  ATAACAGTA
                                  ||||||||  |||||||||
                                  ATACGATT  TATTGTCAT
                                       AC
GAM469  PCMT1    3'  CATGCTGAAAATAACAGT    23939         _
                                  TATGTTGAAA TAACAGT
                                  |||||||||| |||||||
                                  GTACGACTTT ATTGTCA
                                        T
GAM469  SS18     3'  TATGTTGAGAACAGTA      24840        AAT
                                  TATGTTGA   AACAGTA
                                  ||||||||   |||||||
                                  ATACAACT   TTGTCAT
                                       C__
GAM469  TMOD2    3'  TATGTTGAATAGTCAGTA    30969         ATAA
                                  TATGTTGAA    CAGTA
                                  |||||||||    |||||
                                  ATACAACTT    GTCAT
                                        ATCA
GAM470  PCDH11X  3'  TAACTTTTTAATAATTAAAAG  37326              T
                                  TAATTTTTTAATAATTG AAG
                                  |||||||||||||||| |||
                                  ATTGAAAAATTATTAAT TTC
                                             T
GAM470  PCDH11Y  3'  TAACTTTTTAATAATTAAAAG  37348              T
                                  TAATTTTTTAATAATTG AAG
                                  |||||||||||||||| |||
                                  ATTGAAAAATTATTAAT TTC
                                             T
GAM471  PIGN     3'  TCTGACTCTTTTAAATTGTATT 29551       GTA
              T                    TTTGAT   TTTTAAATTGTATTT
                                   ||||||   |||||||||||||||
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                                AGACTG  AAAATTTAACATAAA
                                  AG_
GAM471  PPP3CA   3'  TTTGGTGTATCTTAAATC    9620      A
                                TTTG TGTATTTTAAATT
                                |||| ||||||||||||
                                AAAC ACATAGAATTTAG
                                  C
GAM472  SIGLEC6  3'  TATGTTATTATAGTTTCT    40933     __
                                TATG  ATTATAGTTTCT
                                ||||  ||||||||||||
                                ATAC  TAATATCAAAGA
                                  AA
GAM473  HAS2     3'  TTCCTTGAGTTTCCAAAATCCT 23722     A     ATATT_
           TT                    TTCC TTGAGT     AATCCTTT
                                |||| ||||||     ||||||||
                                AAGG AACTCA     TTAGGAAA
                                  _     AAGGTT
GAM474  ALEX2    3'  TATTGATGATACACAAA     31328     A       TTT
                                TATT GATGATACG   CAAA
                                |||| |||||||||   ||||
                                ATAA CTACTATGT   GTTT
                                  _       ____
GAM474  ALEX3    3'  TATTGATGATACACAAA     32483     A       TTT
                                TATT GATGATACG   CAAA
                                |||| |||||||||   ||||
                                ATAA CTACTATGT   GTTT
                                  _       ____
GAM474  DLEU2    3'  TCTATATATAAATGTTTCAAAT 25693      TAG    TAC
                                TCTAT   ATGA   GTTTCAAAT
                                |||||   ||||   |||||||||
                                AGATA   TATT   CAAAGTTTA
                                  TA_   TA_
GAM475  BTEB1    3'  TTTAAAATCTACCCAGTCT    10226           GT
                                TTTAAAATCTGCC  GTCT
                                ||||||||||||  ||||
                                AAATTTTAGATGG  CAGA
                                       GT
GAM475  DBY      3'  TCTAAAATCTGTTGTGTGCAAA 21662          CC__    C__
              TAGT                  TTTAAAATCTG    GTGT   TAGT
                                ||||||||||    ||||   ||||
                                AGATTTTAGAC    CACG   ATCA
                                      AACA    TTT
GAM475  KIF2     3'  TTTAAAACTGCTCAGTCT    21137       T   _  T
                                TTTAAAA CTGC CG GTCT
                                ||||||| |||| || ||||
                                AAATTTT GACG GT CAGA
                                   _    A  _
GAM476  VHL      3'  TCCATTAATACTATAATC    8118          AA  TT
                                TCCATTAATA  GT  TC
                                |||||||||  ||  ||
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                                AGGTAATTAT  TA  AG
                                      GA  TT
GAM477  ITGAL   3'  TCCTGAGTCCAGTTCTGGG   13623    GAAA      GTGTA
                                TCC   TCCAGTTT    GGG
                                |||   ||||||||    |||
                                AGG   AGGTCAAG    CCC
                                  ACTC      A____
GAM477  MN1     3'  CGGAGTCTAGTGTGTAGGG   14576    AAA  C   TT
                                CG   TC AGT  GTGTAGGG
                                ||   || |||  ||||||||
                                GC   AG TCA  CACATCCC
                                 CTC  A  __
GAM477  MPP1    3'  AAATCCAGATCAGTGGGGC   14621       TTT_  TA
                                AAATCCAG   GTG  GGGC
                                ||||||||   |||  ||||
                                TTTAGGTC   CAC  CCCG
                                     TAGT  __
GAM477  NAV2    3'  GAGACCCAGTCTGGAGGG    41141    A       TGT
                                GA ATCCAGTTTG   AGGG
                                || ||||||||||   ||||
                                CT TGGGTCAGAC   TCCC
                                 C        C__
GAM477  ZFX     5'  CGAGACCAGCCTGGGG     18214     AAT      TGTA
                                CGA   CCAGTTTG   GGG
                                |||   ||||||||   |||
                                GCT   GGTCGGAC   CCC
                                  CT_      ____
GAM478  FMR2    3'  AGTGTTTGGATGCATAAGTGTT 12952        CA  TTTTACC
          G                      AGTGTTTGG  GT      GTTG
                                |||||||||  ||      ||||
                                TCACAAACC  CG      CAAC
                                     TA  TATTCA_
GAM479  BCL11A  3'  GCTGTGATTGTCTGTTCTGATG 39713     TG      A   CA
                                GTT  GATTGTCT TTC  ATG
                                |||  |||||||| |||  |||
                                CGA  CTAACAGA AAG  TAC
                                  CA       C   AC
GAM479  GDF8    3'  GTTTGGATGGTTAAATG     23543        T  C  TTCC
                                GTTTGGAT GT TA    AATG
                                |||||||| || ||    ||||
                                CAAACCTA CA AT    TTAC
                                     C  _  ____
GAM479  KIF5C   3'  GTTTGGATGTCAAT       21159        T   TATTCC
                                GTTTGGAT GTC     AAT
                                |||||||| |||     |||
                                CAAACCTA CAG     TTA
                                     _  ______
GAM479  PDK1    3'  CATTTGGATTTTCCGATG    15201         GTCTA   A
                                CGTTTGGATT    TTCC ATG
                                ||||||||||    |||| |||
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                                GTAAACCTAA    AAGG TAC
                                      _____   C
GAM479  TM4SF2   3'  GTTTGGATGAGGTCCTCAATG  21449       T__   ATTC
                                GTTTGGAT  GTCT   CAATG
                                ||||||||  ||||   |||||
                                CAAACCTA  CAGG   GTTAC
                                    CTC   A___
GAM480  CDK5R2   5'  TAATCCTGAGCTCCGC     19477       ATGGG  _
                                TAATTCTGA    GC CCGC
                                |||||||||    || ||||
                                ATTAGGACT    CG GGCG
                                      _____  A
GAM480  CDKN1A   3'  TAATTCTAATGCCAGAGGC   38513       AT___
                                TAATTCTGA    GGGGC
                                |||||||||    |||||
                                ATTAAGATT    CTCCG
                                     ACGGT
GAM480  CSDA     3'  TTCTGAATGGTCATTAGCGGGC 18899        _________  CCCG
              C                  TTCTGAATGG      GG   CT
                                 ||||||||||      ||   ||
                                 AAGACTTACC      TC   GG
                                     AGTAAIII  GCCC
GAM480  HCS      3'  TTCTGAATGGCTGTTAGCGGGC 33237        _________  CCCG
              C                  TTCTGAATGG      GG   CT
                                 ||||||||||      ||   ||
                                 AAGACTTACC      TC   GG
                                     GACAAIII  GCCC
GAM480  HNRPF    3'  AATTCTGAATGGTTAG     22453          _____
                                AATTCTGAATGG    GG
                                ||||||||||||    ||
                                TTAAGACTTACC    TC
                                      AAIII
GAM480  IRTA2    3'  TAATCCTGAGCCTATGCT    36347       ATGGG  C__
                                TAATTCTGA    GCC  GCT
                                |||||||||    |||  |||
                                ATTAGGACT    CGG  CGA
                                     _____   ATA
GAM480  LMO2     5'  CAATTCTGCTCAAGGCCCG   24536       AA
                                TAATTCTG  TGGGGCCCG
                                ||||||||  |||||||||
                                GTTAAGAC  GTTCCGGGC
                                    GA
GAM480  RLN2     3'  TAATTCTGAAGGACTGCT    39590       AT   CC
                                TAATTCTGA  GGGGC  GCT
                                |||||||||  |||||  |||
                                ATTAAGACT  TCCTG  CGA
                                     __    A_
GAM480  SPAG6    3'  ATTCTGAATTCTACCCTCGCT  29700       GGG  __
                                ATTCTGAAT   GCCC  GCT
                                |||||||||   ||||  |||
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                                TAAGACTTA  TGGG  CGA
                                    AGA   AG
GAM480  TRIM9   3'  TAATTCTGGGGGAAGC     31578       AAT   CCC
                                TAATTCTG  GGGG  GC
                                ||||||||  ||||  ||
                                ATTAAGAC  CCCC  CG
                                   ___   TT_
GAM481  RYR3    3'  ACGTATTACTTTATTGCA    9770       _     A
                                GCGTGT ACTTTATT CA
                                |||||| |||||||| ||
                                TGCATA TGAAATAA GT
                                   A       C
GAM482  PIK3R1  3'  TCTTTTTTGTGAAAGAAA    42861          A
                                TCTTTTTTGTGAAA AAA
                                |||||||||||||| |||
                                AGAAAAAACACTTT TTT
                                        C
GAM482  RSN     3'  TCTTTTTTGTGATAAGAAAAT  16406        A  A
                                TCTTTTTTGTGA AA AAAAT
                                |||||||||||| || |||||
                                AGAAAAAACACT TT TTTTA
                                      A  C
GAM482  SCA1    5'  TCTTTCTCACGAAGAAAA    7291       TG   A
                                TCTTTTT  TGAA AAAA
                                |||||||  |||| ||||
                                AGAAAGA  GCTT TTTT
                                    GT   C
GAM482  TRAM    3'  TTTTTTGTGAAAGTAAAAAT  30708         A_
                                TTTTTTGTGAAA  AAAAAT
                                ||||||||||||  ||||||
                                AAAAAACACTTT  TTTTTA
                                      CA
GAM483  CYP1A1  3'  TCCCAATTGTCAAAGATT    7978    G  GC
                                TT TAG  GTCAAAGATT
                                || |||  ||||||||||
                                AG GTT  CAGTTTCTAA
                                 G   AA
GAM483  EMX2    5'  TTGCAGGCGTGGATT       44708        CAAA
                                TTGTAGGCGT   GATT
                                |||||||||    ||||
                                AACGTCCGCA   CTAA
                                      C___
GAM483  GGA1    3'  TGTAGGCGTCACCCCCCA    30053         AAGA
                                TGTAGGCGTCA   TTA
                                ||||||||||    |||
                                ACATCCGCAGT   GGT
                                      GGGG
GAM483  MEN1    3'  TGTCCTGAATCAAAGATTAA  39240    AGGC_
                                TGT    GTCAAAGATTAA
                                |||    ||||||||||||
```

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                                ACA    TAGTTTCTAATT
                                  GGACT
GAM483  MEN1    3'  TTGTAATATCAAAAGATTA   39258      GC    _
                                TTGTAG  GTCAAA GATTA
                                ||||||  |||||| |||||
                                AACATT  TAGTTT CTAAT
                                   A_     T
GAM483  PSEN1   5'  TTGCAGGCTCCCAGATTA    28744       G  AA
                                TTGTAGGC TC  AGATTA
                                |||||||| ||  ||||||
                                AACGTCCG AG  TCTAAT
                                     _ GG
GAM483  TJP1    5'  TTGTAGACAAAAGATT      17547        TC
                                TTGTAGGCG  AAAGATT
                                |||||||||  |||||||
                                AACATCTGT  TTTCTAA
                                           __
GAM483  TRIM14  3'  CTGTAGGCGTGATT        37700         CAAA
                                TTGTAGGCGT   GATT
                                ||||||||||   ||||
                                GACATCCGCA   CTAA
                                           ____
GAM483  TTN     3'  TTGAGGCACAAAGATT      39423    T    T
                                TTG AGGCG CAAAGATT
                                ||| ||||| ||||||||
                                AAC TCCGT GTTTCTAA
                                  _    _
GAM484  FMO5    3'  ACTATTGTAGGAACATTA    11141     C     CGTTA
                                ACTG TGTAGG    AACATTA
                                |||| ||||||    |||||||
                                TGAT ACATCC    TTGTAAT
                                  A    _____
GAM485  CASP8AP2 3'  TAAAATGCTACAAAACTAT   29065          ___
                                TAAAGTGCTAT   ACTAT
                                ||||||||||   |||||
                                ATTTTACGATG   TGATA
                                      TTT
GAM485  CNGB3   3'  CAAAGTGCTGTAACAGTGACCA 33303         AT_  TATA
          TCT                    TAAAGTGCT   AC   ACCATCT
                                |||||||||  ||   |||||||
                                GTTTCACGA  TG   TGGTAGA
                                     CAT  TCAC
GAM485  PITPNB  3'  AAGTGCTATATTTCCAAC    29624         CTA_
                                AAGTGCTATA   TAAC
                                ||||||||||   ||||
                                TTCACGATAT   GTTG
                                     AAAG
GAM485  SCD     3'  AAATGCTACAACCAT       22815         CTATA
                                AAGTGCTATA    ACCAT
                                ||||||||||    |||||
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                                TTTACGATGT    TGGTA
                                      _____
GAM485  SUV39H1  3'  AAGTGCTATCTACGGACTATCT 17220        A   A_  C
                                AAGTGCTAT CTAT  AC ATCT
                                ||||||||| ||||  || ||||
                                TTCACGATA GATG  TG TAGA
                                      _   CC  A
GAM485  TIMELESS 3'  AGTACTATATTCCAACCCTATC 19396        CTA   __
          T                      AGTGCTATA   TAACC  ATCT
                                ||||||||   |||||  ||||
                                TCATGATAT   GTTGG  TAGA
                                     AAG    GA
GAM485  VSX1     3'  TAAAGTGCCATTAAGGAACC   31097         ACTAT
                                TAAAGTGCTAT    AACC
                                ||||||||||    ||||
                                ATTTCACGGTA    TTGG
                                      ATTCC
GAM486  FLRT2    3'  GCAGGTGAGGCTGTAACA    29848    CAAC    CTT
                                GCA   GAGGC   TGTAACA
                                |||   |||||  |||||||
                                CGT   CTCCG   ACATTGT
                                  CCA_   ___
GAM486  JUND     3'  TGGCGTAACGAGACTTTA    23810     AC      C
                                TGGC  AACGAGGC TTTG
                                ||||  |||||||| ||||
                                ACCG  TTGCTCTG AAAT
                                  CA      _
GAM486  KRTHA5   3'  GGCAGCCGGCCTTTGTGACA   14024     CAACGA      A
                                GGCA     GGCCTTTGT ACA
                                ||||     ||||||||| |||
                                CCGT     CCGGAAACA TGT
                                  CGG___       C
GAM486  RANBP9   5'  GCCATGACCTTTGTA      24252    A  ACGA
                                GC CA   GGCCTTTGTA
                                || ||   ||||||||||
                                CG GT   CTGGAAACAT
                                 _ A___
GAM486  TM4SF2   3'  TGGCACAACAGGGCTTCACA   21453        G   C   TG
                                TGGCACAAC AGG CTT  TA
                                ||||||||| ||| |||  ||
                                ACCGTGTTG TCC GAA  GT
                                      _  C   GT
GAM486  ACK1     3'  GAGCAGCAGGAGCAGCGGGTCC 25115        CT  TTAACA  _
                                GAGCAGCAG  GT     GG CC
                                |||||||||  ||     || ||
                                CTCGTCGTC  CG     CC GG
                                      CT  TCGC__  A
GAM486  ADAM12   5'  GCAGCAGCTCTCGGGCC     18471         G  TAACA
                                GCAGCAGCT TT    GGCC
                                |||||||| ||    ||||
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                                CGTCGTCGA AG    CCGG
                                     G  C____
GAM486  ALPP    3'  GAGAGCAGCCAAGGGGCAGG  42869    C      TTTAA
                                GAG AGCAGCTG    CAGG
                                ||| ||||||||    ||||
                                CTC TCGTCGGT    GTCC
                                  _      TCCCC
GAM486  APTX    3'  AGCAGCAGCTCAGGC      32805         GTTTAA
                                AGCAGCAGCT    CAGGC
                                ||||||||||    |||||
                                TCGTCGTCGA    GTCCG
                                          _______
GAM486  BMP4    5'  GAGCAGCAGCGGCGTCTCAGGC 10192         T  TTAA
                                GAGCAGCAGC GT   CAGGC
                                |||||||||| ||   |||||
                                CTCGTCGTCG CG   GTCCG
                                     C  CAGA
GAM486  BSG     3'  GCAGCAGCTCCCGGGC     42694        G  TAACA
                                GCAGCAGCT TT    GGC
                                |||||||| ||    |||
                                CGTCGTCGA GG    CCG
                                     G  C____
GAM486  CDK6    3'  ACAGCAGCTGGAAGGCC     10382         TTTAAC
                                GCAGCAGCTG    AGGCC
                                |||||||||    |||||
                                TGTCGTCGAC    TCCGG
                                     CT____
GAM486  CLNS1A  5'  GCGGCAACACAGGCC      10527    A    TGTTTA
                                GC GCAGC    ACAGGCC
                                || |||||    |||||||
                                CG CGTTG    TGTCCGG
                                 C   _______
GAM486  COL9A2  3'  AGCAGCAGTCACCTAGTAGGTC 12336        CT TT  AC  _
          C                      AGCAGCAG  G  TA  AGG CC
                                |||||||  |  ||  ||| ||
                                TCGTCGTC  T  AT  TCC GG
                                     AG GG  CA   A
GAM486  DAZ     5'  GCAGCAGCTCCCGACAGGC   19851        G  TA
                                GCAGCAGCT TT  ACAGGC
                                |||||||| ||  ||||||
                                CGTCGTCGA GG  TGTCCG
                                     _ GC
GAM486  EGLN2   3'  GAGCAGCCAGCACAGGCC   38825       _  TGTTTA
                                GAGCAGC AGC    ACAGGCC
                                ||||||| |||    |||||||
                                CTCGTCG TCG    TGTCCGG
                                   G  _______
GAM486  ETS2    3'  AGCAGCTGGTCAGGATGGGC  23465        T  ACA__
                                AGCAGCTG TTA    GGC
                                |||||||| |||    |||
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                                TCGTCGAC AGT    CCG
                                    C   CCTAC
GAM486  FMR2    5'  GGCGGCAGCCGCTGCGGGC   12973   A  A       TAACA
                                G GC GCAGCTGTT    GGC
                                | || |||||||||    |||
                                C CG CGTCGGCGA    CCG
                                _ C       CGC__
GAM486  GRIN2A  5'  AGCAGCCACCGGGTTTAGCGG  9103       A  __    ACA
                                AGCAGC GCT  GTTTA  GG
                                |||||| |||  |||||  ||
                                TCGTCG TGG  CAAAT  CC
                                   G  CC    CG_
GAM486  HD      3'  CAGCAGCTGTGGTCCC      13343         TTAACA  _
                                CAGCAGCTGT    GG CCC
                                ||||||||||    || |||
                                GTCGTCGACA    CC GGG
                                      _______  A
GAM486  IL17BR  3'  GAGCAGCAGCCATCGTGGCAGG 33106           TAA_
            C                    GAGCAGCAGCTGTT   CAGGC
                                ||||||||||||||   |||||
                                CTCGTCGTCGGTAG   GTCCG
                                      CACC
GAM486  LGTN    5'  GCAGCAGCTGCCAGGCC    27886          TTAA
                                GCAGCAGCTGT   CAGGCC
                                ||||||||||   ||||||
                                CGTCGTCGACG   GTCCGG
                                      ____
GAM486  MAGEA9  3'  GCAGCTGCTGGATGGGGCCC  23849        TAACA_
                                GCAGCTGTT    GGCCC
                                |||||||||    |||||
                                CGTCGACGA    CCGGG
                                     CCTACC
GAM486  NOC4    3'  GAGCAGTGCTGTTCACAGCCC  25867      CA      A  G
                                GAGCAG  GCTGTTTA CAG CCC
                                ||||||  |||||||| ||| |||
                                CTCGTC  CGACAAGT GTC GGG
                                   A_      _  _
GAM486  NPAS2   5'  GCCGCAGCCGCGCGGGTCC   14818   A      TTAACA  _
                                GC GCAGCTGT    GG CC
                                || ||||||||    || ||
                                CG CGTCGGCG    CC GG
                                 G      CGC___  A
GAM486  PAX2    3'  AAGCAGCAGCCTGGTGGGC   19614         GTTTAACA
                                GAGCAGCAGCT      GGC
                                ||||||||||       |||
                                TTCGTCGTCGG      CCG
                                      ACCAC___
GAM486  PMM1    3'  AAGCAGCAGCTGTGGC     15415          TTAACA
                                GAGCAGCAGCTGT    GGC
                                ||||||||||||     |||
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                                TTCGTCGTCGACA     CCG
                                           _______
GAM486  POU4F1   3'  GAGAGCAGCCATAGGC      26386     C       TTAAC
                                GAG AGCAGCTGT     AGGC
                                ||| |||||||||     ||||
                                CTC TCGTCGGTA     TCCG
                                  _       ______
GAM486  PPIF     3'  ACAGCAGCAAACCAACAGGC  25057         TGT
                                GCAGCAGC   TTAACAGGC
                                ||||||||   |||||||||
                                TGTCGTCG   GGTTGTCCG
                                     TTT
GAM486  PPL      3'  GCAGCAGCCCCCCACGGGCCC  15493          G  TA  A
                                GCAGCAGCT TT  AC GGCCC
                                ||||||||| ||  || |||||
                                CGTCGTCGG GG  TG CCGGG
                                      G  __  C
GAM486  RAB36    3'  GCAGCAGTGGGCACAGGCCC  22241        C  TTTA
                                GCAGCAG TG    ACAGGCCC
                                ||||||| ||    ||||||||
                                CGTCGTC AC    TGTCCGGG
                                   _  CCG_
GAM486  RAB3A    5'  GCAGCAGCGGCTCAGGCC    16062         T   TAA
                                GCAGCAGC GTT   CAGGCC
                                |||||||| |||   ||||||
                                CGTCGTCG CGA   GTCCGG
                                     C   ___
GAM486  RXRA     3'  GCCGGCGGCTGACACAGGCCC 16426    A_  A    TTTA
                                GC  GC GCTG    ACAGGCCC
                                ||  || ||||    ||||||||
                                CG  CG CGAC    TGTCCGGG
                                 GC  C    TG__
GAM486  SNX6     3'  GAGCAGCAGATGAAGGGCC   34562         C  TTTAACA
                                GAGCAGCAG TG      GGCC
                                ||||||||| ||      ||||
                                CTCGTCGTC AC      CCGG
                                     T  TTC____
GAM486  SRGAP2   3'  GAGCAACAGAACAGGC      43981         CTGTTT
                                GAGCAGCAG     AACAGGC
                                |||||||||     |||||||
                                CTCGTTGTC     TTGTCCG
                                           _______
GAM486  STK10    3'  GAGCAGCCAGCTGCAGGCC   25619        _    TTTAA
                                GAGCAGC AGCTG    CAGGCC
                                ||||||| |||||    ||||||
                                CTCGTCG TCGAC    GTCCGG
                                   G    _____
GAM486  SURF5    3'  GCAGCAGCTGTCACACGGGCC 27581           TA  A
                                GCAGCAGCTGTT  AC GGCC
                                ||||||||||||  || ||||
```

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                                CGTCGTCGACAG  TG CCGG
                                      TG  C
GAM486  TAGLN2   3'  GCAGCAGCTGCCACAGGC    18684          TA
                                GCAGCAGCTGTT  ACAGGC
                                ||||||||||||  ||||||
                                CGTCGTCGACGG  TGTCCG
                                      __
GAM486  TAZ      3'  GAGAAGCAGCTGAGGC      31765     C       TTTAAC  _
                                GAG AGCAGCTG      AGG C
                                ||| ||||||||      ||| |
                                CTC TCGTCGAC      TCC G
                                  T       _______  A
GAM487  ADRA2A   3'  TGACCACTCCATTCATATTTA  8642    C         ATC
                                A ACCACTCCATT   TATTTA
                                | ||||||||||||  ||||||
                                A TGGTGAGGTAA   ATAAAT
                                 C          GT_
GAM487  AMPH     3'  TACACCATCTATTT        11601        CTCCATTA
                                TACACCA       TCTATTT
                                |||||||       |||||||
                                ATGTGGT       AGATAAA
                                      _________
GAM487  EPM2A    3'  CACTTCATCTATTTA       24966      CCA
                                CACT   TTATCTATTTA
                                ||||   ||||||||||
                                GTGA   AGTAGATAAAT
                                      ___
GAM487  MTA1L1   3'  CACCACCTGTTATCTGTTTAC  21880        CCA     A
                                CACCACT   TTATCT TTTAC
                                |||||||   |||||| |||||
                                GTGGTGG   AATAGA AAATG
                                     AC_     C
GAM487  NPM3     3'  CACACCACTTTATTTCAACCT  28116         CC   A  T
                                TACACCACT  ATT TC ATTT
                                |||||||||  ||| || ||||
                                GTGTGGTGA  TAA AG TGGA
                                      AA  _  T
GAM488  ECEL1    5'  GCGTGGCCGCCGGCCTCCT   22094    TCTT  _
                                GC    CC CCGGCCTCCT
                                ||    || ||||||||||
                                CG    GG GGCCGGAGGA
                                  CACC  C
GAM488  EYA4     5'  CCGCAGCTCTTTCCCCCTC   19906          C   GG
                                TCGCAGCTCTT CCC  CCTC
                                |||||||||||| |||  ||||
                                GGCGTCGAGAA GGG  GGAG
                                       A  __
GAM488  FBLN5    5'  TCGGGCACGTCGGCCTCCT   26754     CA  TCTTCCC
                                TCG  GC      CGGCCTCCT
                                |||  ||      |||||||||
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                                AGC  CG      GCCGGAGGA
                                  C_  TGCA___
GAM488  HCFC1    5'  GCTCTTCCCTTTCTTCTC    43396         CGGC  C
                                GCTCTTCCC    CT CTC
                                |||||||||    || |||
                                CGAGAAGGG    GA GAG
                                     AAA_  A
GAM488  HUNK     5'  TCGCAGCTCCTCCTCCCCAGGC 31083          ___      C   C
           TCTTC                  TCGCAGCTCT   TCCCCGG CTC TC
                                |||||||||   ||||||| ||| ||
                                AGCGTCGAGG   AGGGGTC GAG AG
                                     AGG      C   A
GAM488  IGFBP5   5'  GCAGCTCTTTCCTAGCTCT   8269          C  CG  _
                                GCAGCTCTT CC  GC CT
                                |||||||| ||  || ||
                                CGTCGAGAA GG  CG GA
                                     A  AT  A
GAM488  NCOA6IP  5'  GCAGCCTCCGCTTGGCTTC   36050      T    CCC_  C
                                GCAGC CTTC    GGC TC
                                ||||| ||||    ||| ||
                                CGTCG GAGG    CCG AG
                                   _    CGAA   A
GAM488  PSD      5'  TCGATGGCCGAGTCGGCCTCCT 15791     CA_   CTTCCC
           C                     TCG   GCT     CGGCCTCCTC
                                |||   |||     ||||||||||
                                AGC   CGG     GCCGGAGGAG
                                  TAC   CTCA__
GAM488  SYK      5'  CCGCGGCTCTTCCTCCTC    17235      A       CCGG
                                TCGC GCTCTTCC    CCTC
                                |||| ||||||||    ||||
                                GGCG CGAGAAGG    GGAG
                                  C       A___
GAM488  TACC1    5'  CCGCGTCCTCCTCGGCCTCCTC 26592      AGC     C
                                TCGC   TCTTCC CGGCCTCCTC
                                ||||   |||||| ||||||||||
                                GGCG   AGGAGG GCCGGAGGAG
                                  C__      A
GAM488  TRIM34   5'  GCAGCTCTCTCTGCTCCTC    38973         CCCCG  C
                                GCAGCTCTT    GC TCCTC
                                |||||||||    || |||||
                                CGTCGAGAG    CG AGGAG
                                     AGA__  _
GAM488  AGTR1    5'  TGCTAGCGGCGCGCCGG     28924     GAG   CAC
                                TGC   AGC   CGCGCCGG
                                |||   |||   ||||||||
                                ACG   TCG   GCGCGGCC
                                  A__   CC_
GAM488  ANP32A   5'  TGCAGAGGCTCCCGCGCCGGC  26708     _   A  CA
                                TGC GAG GC  CCGCGCCGGC
                                ||| ||| ||  ||||||||||
```

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                                ACG CTC CG  GGCGCGGCCG
                                  T  _  AG
GAM488  BCAS1    3'  GCGAGAGCCACCACGCCCGGC  18923                 _
                                GCGAGAGCCACCGCGCC GGC
                                ||||||||||||||||| |||
                                CGCTCTCGGTGGTGCGG CCG
                                          G
GAM488  C1orf6   5'  GCGGGCCGCAGCTGCGCCGGC  33529     AGA  ACC___
                                GCG  GCC     GCGCCGGC
                                |||  |||     ||||||||
                                CGC  CGG     CGCGGCCG
                                  C__  CGTCGA
GAM488  CDS1     5'  GAGCGGCCGCCGCGCCGG    10397     A_  A
                                GAG  GCC CCGCGCCGG
                                |||  ||| |||||||||
                                CTC  CGG GGCGCGGCC
                                  GC  C
GAM488  COG7     5'  TGCGAGAGCACCGAGG      42663         C   CGCC
                                TGCGAGAGC ACCG   GG
                                ||||||||| ||||   ||
                                ACGCTCTCG TGGC   CC
                                      _   T___
GAM488  CYLN2    3'  TGCGAGAGCTACCGAAAGC   18067         C   CGCC
                                TGCGAGAGC ACCG   GGC
                                ||||||||| ||||   |||
                                ACGCTCTCG TGGC   TCG
                                     A   TT__
GAM488  DSCAM    5'  GCGAGCGACGCGCCGGC     10804      AGCCAC
                                GCGAG     CGCGCCGGC
                                |||||     |||||||||
                                CGCTC     GCGCGGCCG
                                   GCT___
GAM488  EN1      5'  GCCCCGGCCGCCGCGCCGGC  10912    GAGA  A
                                GC   GCC CCGCGCCGGC
                                ||   ||| ||||||||||
                                CG   CGG GGCGCGGCCG
                                 GGGC  C
GAM488  ETS2     5'  GCGAGGGCGAGGGCGCCGGC  23468      A  CACC
                                GCGAG GC   GCGCCGGC
                                ||||| ||   ||||||||
                                CGCTC CG   CGCGGCCG
                                   C  CTCC
GAM488  GNB1     5'  TGCGGGCAGGTGCGCGCCGGC  13214     AGA  CAC__
                                TGCG  GC   CGCGCCGGC
                                ||||  ||   |||||||||
                                ACGC  CG   GCGCGGCCG
                                  C__  TCCAC
GAM488  HEXA     3'  TGCGAGCGCCAGCACCGGC   8015        A   CC
                                TGCGAG GCCA  GCGCCGGC
                                ||||||| ||||  ||||||||
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                                ACGCTC CGGT  CGTGGCCG
                                   G   __
GAM488  IHPK2    3'  TGCAGGAGCCACCACCTGGC  41591     A       GCC
                                TGCG GAGCCACCGC  GGC
                                |||| ||||||||||  |||
                                ACGT CTCGGTGGTG  CCG
                                  C        GA_
GAM488  IKBKB    3'  TGCAGACAAGGCGCCGGC    41813    G  GC  CC
                                TGC AGA  CA  GCGCCGGC
                                ||| |||  ||  ||||||||
                                ACG TCT  GT  CGCGGCCG
                                  _  __  TC
GAM488  IRS2     3'  TGCGAGAACTGCCACACACTGG 40717       ___    C   C
                                TGCGAGA   GCCAC GCGC GG
                                |||||||   ||||| |||| ||
                                ACGCTCT   CGGTG TGTG CC
                                     TGA    _   A
GAM488  JAG2     5'  GCTCCCAGCCGCCGCGCCGGC  13727   GAG_   A
                                GC   AGCC CCGCGCCGGC
                                ||   |||| ||||||||||
                                CG   TCGG GGCGCGGCCG
                                 AGGG   C
GAM488  JUND     5'  GCCTCCCCCGCCGCGCCGGC  23803   GAGAG  A
                                GC    CC CCGCGCCGGC
                                ||    || ||||||||||
                                CG    GG GGCGCGGCCG
                                 GAGGG  C
GAM488  LMO4     5'  TGCGAGAGGCGGCGG      27664       CCACC   C
                                TGCGAGAG    GCG CGG
                                ||||||||    ||| |||
                                ACGCTCTC    CGC GCC
                                     _____  C
GAM488  METTL1   3'  TGCAGGAGCTGCGCGTAGGGC  35708    A   CAC   CC_
                                TGCG GAGC   CGCG   GGC
                                |||| ||||   ||||   |||
                                ACGT CTCG   GCGC   CCG
                                  C   AC_   ATC
GAM488  NPY2R    5'  GCGAGAGCTGGCCCGGC    9496        CACC  G
                                GCGAGAGC    GC CCGGC
                                ||||||||    || |||||
                                CGCTCTCG    CG GGCCG
                                     AC__  _
GAM488  PABPN1   5'  TGGAGAGCTGCGCCGGC    21614    C    CACC
                                TG GAGAGC    GCGCCGGC
                                || ||||||    ||||||||
                                AC CTCTCG    CGCGGCCG
                                 _     A___
GAM488  PITPN    5'  CGCGGTCGCCGCGCCGGC    26334    AGA   ACC
                                TGCG   GCC   GCGCCGGC
                                ||||   |||   ||||||||
```

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                                GCGC  CGG  CGCGGCCG
                                  CAG  ___
GAM488  PML     3'  TGTGAGAGCCAGCACTCCGG  37747   C     C  G
                                TG GAGAGCCA CGC CCGG
                                || |||||||| ||| ||||
                                AC CTCTCGGT GTG GGCC
                                 A      C  A
GAM488  POLR2E  5'  TACGAGAGCGGCAGTTGGC   40924       CACC  CC_
                                TGCGAGAGC   GCG  GGC
                                |||||||||   |||  |||
                                ATGCTCTCG   CGT  CCG
                                     C___  CAA
GAM488  PPP3R1  5'  GCGGGGCCCGCGCCGGC    44078    AGA  AC
                                GCG  GCC  CGCGCCGGC
                                |||  |||  |||||||||
                                CGC  CGG  GCGCGGCCG
                                 CC_  __
GAM488  PTPN2   5'  GCAGAGCCTGCGCCGGC    15914    G    ACC
                                GC AGAGCC  GCGCCGGC
                                || ||||||  ||||||||
                                CG TCTCGG  CGCGGCCG
                                 _    A__
GAM488  S100B   3'  TGCAGGGCCACACCGG     26575    G A   CGC
                                TGC AG GCCAC  GCCGG
                                ||| || |||||  |||||
                                ACG TC CGGTG  TGGCC
                                 _ C    ___
GAM488  ST7     3'  TGCGAGAGCCTGGTGCCGGCGC 30274        A_______  CGC
          G                      TGCGAGAGCC      CCG  CG
                                ||||||||||      |||  ||
                                ACGCTCTCGG      GGC  GC
                                     ACCAIIIC  CGC
GAM488  TBX6    3'  TGCGTGAGCCACCACACCTGG  38863    A        _
                                TGCG GAGCCACCGCGCC GG
                                |||| ||||||||||||| ||
                                ACGC CTCGGTGGTGTGG CC
                                  A         A
GAM488  TLE1    5'  GCGGGGAGCGCGCTGGC    22921    A_  CACC   C
                                GCG  GAGC   GCGC GGC
                                |||  ||||   |||| |||
                                CGC  CTCG   CGCG CCG
                                 CC   ____   A
GAM488  TR2     3'  TGCGAGAGTCAGCCTTGGC   43638       C  CCGC  __
                                TGCGAGAG CA   GCC  GGC
                                |||||||| ||   |||  |||
                                ACGCTCTC GT   CGG  CCG
                                     A ____  AA
GAM489  ACADM   5'  GCGGGGTGGCAGCGGTCCCCGG 6148     AGC  _ _  GA
          C                     GCG  GTG C GCGG  TCCCCGGC
                                |||  ||| | ||||  ||||||||
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                                CGC   CAC G CGCC  AGGGGCCG
                                  CC_   C T   __
GAM489  AMPD3    5'  GCGCAGCGCTGCGGATCCCCGG 7899     _    GC   G
              C                   GCG AGCGT  GCGG ATCCCCGGC
                                  ||| |||||  |||| |||||||||
                                  CGC TCGCG  CGCC TAGGGGCCG
                                    G    A_   _
GAM489  ATBF1    5'  GCTGGCGTCCGGGTCCCCGGC  27848    GA   GCG   A
                                  GC  GCGT   CGGG TCCCCGGC
                                  ||  ||||   |||| ||||||||
                                  CG  CGCA   GCCC AGGGGCCG
                                   AC   G__   _
GAM489  CALU     3'  GAGGTATGAGGATCCCTGG   10258     C   CGC      C
                                  GAG GTG   GGGATCCC GG
                                  ||| |||   |||||||| ||
                                  CTC CAT   TCCTAGGG CC
                                    _  AC_      A
GAM489  FGFR1    5'  CGGGCGTGTGCCCGCGTCCCCG 31936    A    ____   GGA
              GC                    CG GCGTG   CGCG   TCCCCGGC
                                  || |||||   ||||  ||||||||
                                  GC CGCAC   GCGC   AGGGGCCG
                                   C    ACGG   ___
GAM489  FOXG1B   5'  GCGGGCGGCGCGGCGACCGG   23507    A   T    _ TCC
                                  GCG GCG GCGCGG GA   CCGG
                                  ||| ||| |||||| ||   ||||
                                  CGC CGC CGCGCC CT   GGCC
                                    C   _     G  ___
GAM489  HTR2C    5'  GACCGTGCGCCCCCCGG    9285    G     GGGA
                                  GA CGTGCGC   TCCCCGG
                                  || |||||||   |||||||
                                  CT GCACGCG   GGGGGCC
                                   G     _____
GAM489  KCNS2    5'  GCGAGTGTGTGCGCCCGG    42829      C   C   GGATC
                                  GCGAG GTG GCG    CCCGG
                                  ||||| ||| |||    |||||
                                  CGCTC CAC CGC    GGGCC
                                     A   A  ______
GAM489  MGAT3    5'  GCGGCCCCCGGGGTCCCCGGC  14461    T  G__   A
                                  GCG GC   CGGG TCCCCGGC
                                  ||| ||   |||| ||||||||
                                  CGC CG   GCCC AGGGGCCG
                                    _ GGG   C
GAM489  NAGLU    5'  GAGCGTGTGACCCCGG     7052        CGCGG  T
                                  GAGCGTG    GA CCCCGG
                                  |||||||    || ||||||
                                  CTCGCAC    CT GGGGCC
                                      A____  _
GAM489  NRIP1    5'  GCGGGCGGGCGTGGGGCCGG   40965    A   T   C   ATCC
                                  GCG GCG GCG GGG   CCGG
                                  ||| ||| ||| |||   ||||
```

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                                CGC CGC CGC CCC   GGCC
                                  C   C   A   C___
GAM489  PCDH7    5'  GCGGGCGGAGAATCCCCGG   37117    T   C
                                GCG GCG GGGATCCCCGG
                                ||| ||| ||||||||||
                                CGC CGC TCTTAGGGGCC
                                  C   C
GAM489  SLC25A13 5'  GCAGCGTGCGTTCCTG     30662    G      CGGGA   CC
                                GC AGCGTGCG    TCC  G
                                || ||||||||    |||  |
                                CG TCGCACGC    AGG  C
                                 _      A____   A_
GAM489  SLC6A3   3'  GCGAGGTGCGCTCCCG     9813       C     GGGATC
                                GCGAG GTGCGC     CCCG
                                ||||| ||||||     ||||
                                CGCTC CACGCG     GGGC
                                   _     A_____
GAM489  SMT3H1   5'  GCGAGCGGCGCGGGGAGGCGGC 40996        T      ATCCC
                                GCGAGCG GCGCGGG    CGGC
                                ||||||| |||||||    ||||
                                CGCTCGC CGCGCCC    GCCG
                                   _      CTCC_
GAM490  ACPP     3'  GTCTTCTTTCGTAAGAA    42490    G       C
                                GTC TTCTTTCGT GGGA
                                ||| ||||||||| ||||
                                CAG AAGAAAGCA TCTT
                                  _       T
GAM490  ADAM23   3'  GTTCCTTCGTCCATTAGGGA  19206          _____
                                GTTCTTTCGTC    GGGA
                                ||||||||||     ||||
                                CAAGGAAGCAG    CCCT
                                      GTAAT
GAM490  BACH2    3'  GTTCTTTTTTTAAAAGAAGA  34797        CGTC
                                GTTCTTT   GGGAGAAGA
                                |||||||   |||||||||
                                CAAGAAA   TTTTCTTCT
                                    AAAA
GAM490  BCL9     5'  GTCCTTTTTTATGAGGAGAA  20245        C__  C
                                GTTCTTT   GT GGGAGAA
                                |||||||   || |||||||
                                CAGGAAA   TA TCCTCTT
                                    AAA  C
GAM490  CBFA2T3  3'  GTCTTCTTTCGGAGAG     23267    G       TC
                                GTC TTCTTTCG  GGGAG
                                ||| ||||||||  |||||
                                CAG AAGAAAGC  CTCTC
                                  _      __
GAM490  ESR1     3'  GTTCTTTCTTCTCTAGAA    6533         G  GGG
                                GTTCTTTC TC   AGAA
                                |||||||| ||   ||||
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                                CAAGAAAG AG   TCTT
                                    A  AGA
GAM490  GAK     3'  GTTCCTTCGGGAGGAGAA    23533         TC
                                GTTCTTTCG  GGGAGAA
                                |||||||||  |||||||
                                CAAGGAAGC  TCCTCTT
                                     CC
GAM490  PSA     3'  GTTGTTCTTTCAAAAAAGAAGA 38455    C       TC
          A                      GT GTTCTTTCG  GGGAGAAGAA
                                || |||||||||  ||||||||||
                                CA CAAGAAAGT  TTTTCTTCTT
                                 A       T_
GAM490  ZNF76   3'  GTTCTTTAGGAGGAGA      18311        CGTC    A
                                GTTCTTT    GGGAG AGA
                                |||||||    ||||| |||
                                CAAGAAA    TCCTC TCT
                                    ____    C
GAM491  ADCY9   3'  GGCAGCGGGTGGGCGCC     10021      ACAGA   CA_   G
                                GGCAG    CGG   GGCG CC
                                |||||    |||   |||| ||
                                CCGTC    GCC   CCGC GG
                                   _____  CAC   _
GAM491  AF5Q31  5'  AGGCAGGCGGGGGCGG      30850       ACAGA   CA
                                AGGCAG    CGG  GGCGG
                                ||||||    |||  |||||
                                TCCGTC    GCC  CCGCC
                                   C____  C_
GAM491  AHSG    5'  GGCAGGCAGGCGTGCAGGTGG  11558      A   A  _    C
                                GGCAG CAG CG GCAGG GG
                                ||||| ||| || ||||| ||
                                CCGTC GTC GC CGTCC CC
                                  C   C  A    A
GAM491  AMN     3'  AGGTCGACGGTCAGGCGGCCG  36284     CAGACA    _
                                AGG     GACGG CAGGCGGCCG
                                |||     ||||| ||||||||||
                                TCC     CTGCC GTCCGCCGGC
                                  AG____     A
GAM491  APCS    5'  AGCAGACAACACAGTGGC    11604         A  G   GC
                                GGCAGACAG CG CAG  GGC
                                |||||||| || |||  |||
                                TCGTCTGTT GT GTC  CCG
                                    _ _  A_
GAM491  APOA4   3'  AGACAGACAGGTGGCAGG    7910          AC
                                AGGCAGACAG  GGCAGG
                                ||||||||||  ||||||
                                TCTGTCTGTC  CCGTCC
                                     CA
GAM491  ART1    3'  AGGCAGCAGGCGAGGC      20219       A  GAC  _
                                AGGCAG CA   GGC AGGC
                                ||||||  ||   ||| ||||
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                                TCCGTC GT   CCG TCCG
                                  _ ____  C
GAM491  ATP1A1   5' GGAGGGTGGGAGGGCGGCCG  8697    C  ACAGAC  CA
                                GG AG     GG  GGCGGCCG
                                || ||     ||  ||||||||
                                CC TC     CC  CCGCCGGC
                                 _  CCAC__  TC
GAM491  ATP2A3   3' GCAGACAGCGCGGCGGCCG   23196        A  G A
                                GCAGACAG CG C GGCGGCCG
                                |||||||| || | ||||||||
                                CGTCTGTC GC G CCGCCGGC
                                   _ _ _
GAM491  BARX1    5' GCAGGGGCCGGGCGGGCGGCCG 34626      ACAGAC   A
                                GCAG     GGC GGCGGCCG
                                ||||     ||| ||||||||
                                CGTC     CCG CCGCCGGC
                                  CCCGGC   C
GAM491  BLK      3' GGCGCAGGCGGGCGCGGCC   11847     AGA   A   CAG
                                GGC   CAG CGG   GCGGCC
                                |||   ||| |||   ||||||
                                CCG   GTC GCC   CGCCGG
                                 C__   C   CG_
GAM491  BMP7     5' GGCAGAGGGGGCAGGCGGCCG  11873       CAGAC
                                GGCAGA    GGCAGGCGGCCG
                                ||||||    ||||||||||||
                                CCGTCT    CCGTCCGCCGGC
                                   CCC__
GAM491  BMP8     5' GGCGGGACGGGCGGGCAGCCG  11883     A_   AGAC   A
                                GGC  GAC   GGC GGCGGCCG
                                |||  |||   ||| ||||||||
                                CCG  CTG   CCG CCGTCGGC
                                 CC   C___   C
GAM491  CEP2     5' AGGCGCGCAGACGGCAGAC   28431      AGA
                                AGGC   CAGACGGCAGGC
                                ||||   ||||||||||||
                                TCCG   GTCTGCCGTCTG
                                  CGC
GAM491  CHGA     5' GGCGGCTGGACTGGCGGCCG   10469     AGACA   GGCA
                                GGC    GAC   GGCGGCCG
                                |||    |||   ||||||||
                                CCG    CTG   CCGCCGGC
                                 CCGAC  A___
GAM491  CKB      5' GGCGGCGGGCGGGCGGCCG   12255     AGACAGAC   A
                                GGC       GGC GGCGGCCG
                                |||       ||| ||||||||
                                CCG       CCG CCGCCGGC
                                 CCGC____   C
GAM491  CLCN6    3' GGCAGCCTCAGGGCAGGCGGC  34717      A__   AC
                                GGCAG   CAG  GGCAGGCGGC
                                |||||   |||  ||||||||||
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                                CCGTC  GTC  CCGTCCGCCG
                                  GGA  __
GAM491  CSDA    5'  GGCGCAGGCGGCGGCGGCC   18898    AGA  A   A
                                GGC  CAG CGGC GGCGGCC
                                |||  ||| |||| |||||||
                                CCG  GTC GCCG CCGCCGG
                                 C__  C   _
GAM491  CSF1R   5'  GGCAGGCAGGTGCAGGGC   23311     A  ACG   CG
                                GGCAG CAG  GCAGG  GC
                                ||||| |||  |||||  ||
                                CCGTC GTC  CGTCC  CG
                                  C  CA_   __
GAM491  CSNK1E  5'  GGCTGGCAGGCGGGGCGGGCCG 12474    AGA  A  CA   _
                                GGC  CAG CGG  GGCGG CCG
                                |||  ||| |||  ||||| |||
                                CCG  GTC GCC  CCGCC GGC
                                 ACC  C  __   C
GAM491  CXCL1   5'  AGCAGGCGGGTCTGGCGGC   11321     ACAGA  CA__
                                GGCAG   CGG   GGCGGC
                                |||||   |||   ||||||
                                TCGTC   GCC   CCGCCG
                                  C____  CAGA
GAM491  CYLN2   3'  GGCAGGCAGGCTGGC      18058     GACAGAC    _
                                GGCA     GGCAGGC GGC
                                ||||     ||||||| |||
                                CCGT     CCGTCCG CCG
                                  _______     A
GAM491  DES     5'  GGCGGGCAGGCGGCCG     43570    AGACAGAC
                                GGC      GGCAGGCGGCCG
                                |||      ||||||||||||
                                CCG      CCGTCCGCCGGC
                                 C_______
GAM491  DES     5'  AGGCGGCGGGCAGGCGGCCG  43559    AGACAGAC
                                AGGC     GGCAGGCGGCCG
                                ||||     ||||||||||||
                                TCCG     CCGTCCGCCGGC
                                  CCGC____
GAM491  DLC1    5'  AGGCAGGCGGAGGCGGCC    25899     ACAGA  C    _
                                AGGCAG   CGG AGGCGGC C
                                ||||||   ||| ||||||| |
                                TCCGTC   GCC TCCGCCG G
                                  C____  _     A
GAM491  DYRK2   5'  AGGCGGCGGGAGCGGCGGCCG 27035    AGACAGAC  A
                                AGGC     GGC GGCGGCCG
                                ||||     ||| ||||||||
                                TCCG     TCG CCGCCGGC
                                  CCGCCC__  _
GAM491  E2F1    5'  GGTGACAGGCGGCGGCG    44490    CA   A   A
                                GG  GACAG CGGC GGCG
                                ||  ||||| |||| ||||
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                                CC  CTGTC GCCG CCGC
                                 A_    C   _
GAM491  EIF2C1   3'  AGGCAGACAGGCAGGCAG    29167        GAC
                                AGGCAGACA   GGCAGGCGG
                                |||||||||   |||||||||
                                TCCGTCTGT   CCGTCCGTC
                                      ___
GAM491  EIF2C1   3'  AGGCAGGCAGGCAGGCAGGCAG 29169       A   A _     _
           GCCG                    AGGCAG CAG C GGCAGGC GGCCG
                                |||||| ||| | ||||||| |||||
                                TCCGTC GTC G CCGTCCG CCGGC
                                   C   C T      T
GAM491  EIF2C1   3'  AGGCAGGCAGGCAGGCAG    29168       A  GAC
                                AGGCAG CA   GGCAGGCGG
                                ||||||| ||   |||||||||
                                TCCGTC GT   CCGTCCGTC
                                   C  ___
GAM491  EPS15    5'  AGGCGGAGGGAGCGGC      12742      A  CAGAC  CA
                                AGGC GA    GG  GGCGGC
                                |||| ||    ||  ||||||
                                TCCG CT    CC  TCGCCG
                                  C  _____  C_
GAM491  EVPL     5'  GGCAGGTGGGAGGCAGC     12766       ACAGAC  C
                                GGCAG     GG AGGCGGC
                                |||||     || |||||||
                                CCGTC     CC TCCGTCG
                                   CAC___  _
GAM491  FS       5'  GGCAGGCAGCGGGGC       35087       A   A   CAGGC
                                GGCAG CAG CGG     GGC
                                ||||| ||| |||     |||
                                CCGTC GTC GCC     CCG
                                   C  _  _____
GAM491  GAA      3'  GGCAGCCGGGAAGCGGC     6665        ACAGA   C     C
                                GGCAG     CGG AGGCGG C
                                |||||     ||| |||||| |
                                CCGTC     GCC TTCGCC G
                                   G____   C     A
GAM491  GDF2     5'  AGGAGACTGCAGGCGGCC    32120     CAGAC    G
                                AGG     AGAC GCAGGCGGCC
                                |||     |||| ||||||||||
                                TCC     TCTG CGTCCGCCGG
                                  _____   A
GAM491  GLUL     5'  AGGGGACAGACAGCGGCC    13151     CA      GGCA
                                AGG  GACAGAC    GGCGGCC
                                |||  |||||||    |||||||
                                TCC  CTGTCTG    TCGCCGG
                                  C_      _____
GAM491  GNAI1    5'  GGCAGACAGCAACGGGCGGC  13166         A    A
                                GGCAGACAG CGGC GGCGGC
                                ||||||||| |||| ||||||
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                                CCGTCTGTC GTTG CCGCCG
                                      _   C
GAM491  GRM4    3'  GGCAAGACAGACGGCAGACG  9161      _
                                GGCA GACAGACGGCAGGCG
                                |||| ||||||||||||||
                                CCGT CTGTCTGCCGTCTGC
                                  T
GAM491  GRM4    3'  GGCAGGCGGGCAGGCGG    9162      ACAGAC
                                GGCAG    GGCAGGCGG
                                |||||    |||||||||
                                CCGTC    CCGTCCGCC
                                  CGC___
GAM491  GTF2I   5'  GGCAGGCGGGCGGCCG     37442     GACAGAC  A
                                GGCA     GGC GGCGGCCG
                                ||||     ||| ||||||||
                                CCGT     CCG CCGCCGGC
                                  ________  C
GAM491  HDAC4   5'  GGCGGGCGGCGGCGGCC    25777     AGACAGA  A
                                GGC      CGGC GGCGGCC
                                |||      |||| |||||||
                                CCG      GCCG CCGCCGG
                                  CCC____  _
GAM491  HMX1    5'  GGCAGGCGGCGGCC       33213     GACAGAC  A
                                GGCA     GGC GGCGGCC
                                ||||     ||| |||||||
                                CCGT     CCG CCGCCGG
                                  ________ _
GAM491  IDS     5'  GGCGCAGACGGGCGGCCA   25961     AGA     CAG
                                GGC  CAGACGG  GCGGCCG
                                |||  |||||||  |||||||
                                CCG  GTCTGCC  CGCCGGT
                                  C__     ___
GAM491  IL13    3'  GGCAGACAGGAGCGGC     13526       ACGGCA
                                GGCAGACAG    GGCGGC
                                |||||||||    ||||||
                                CCGTCTGTC    TCGCCG
                                     C_____
GAM491  JUN     3'  GGCAGCCCGCAGGCGGCC   13744     ACAGA  G
                                GGCAG    CG CAGGCGGCC
                                |||||    || |||||||||
                                CCGTC    GC GTCCGCCGG
                                  GG___ _
GAM491  KIFC3   5'  GGGAAAGGGCGGGCGGCCG  24464   CA  C  AC  A
                                GG  GA AG  GGC GGCGGCCG
                                ||  || ||  ||| ||||||||
                                CC  CT TC  CCG CCGCCGGC
                                 __  T  __  C
GAM491  KRTHB6  3'  AGGCAGCGGGCGGCGGC    14029     ACAGAC  A
                                AGGCAG    GGC GGCGGC
                                ||||||    ||| ||||||
```

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                                TCCGTC     CCG CCGCCG
                                   GC____  _
GAM491  LAG3    5'  AGCAGACAGAGCAAAGTGGCCG 14041          CG   _ C
                                GGCAGACAGA  GCAG G GGCCG
                                ||||||||||  |||| | |||||
                                TCGTCTGTCT  CGTT C CCGGC
                                      __    T A
GAM491  LAMB1   5'  GGCTGAAGGGGCGGGCGGCCG  14067    A  C  AC   A
                                GGC GA AG  GGC GGCGGCCG
                                ||| || ||  ||| ||||||||
                                CCG CT TC  CCG CCGCCGGC
                                  A  _  C_   C
GAM491  LMO1    3'  AGGCAGGTGGGCAGGCGG    14175       ACAGAC
                                AGGCAG     GGCAGGCGG
                                ||||||     |||||||||
                                TCCGTC     CCGTCCGCC
                                   CAC___
GAM491  LMO1    3'  AGGCGGGCAGATGGACAGACG  14176     AGA    C  _
                                AGGC   CAGA GG CAGGCG
                                ||||   |||| || ||||||
                                TCCG   GTCT CC GTCTGC
                                  CCC    A  T
GAM491  MADH7   3'  GGCAGGCAGGGGAGAGGC    25369      A   AC  C   C
                                GGCAG CAG  GG AGG GGC
                                ||||| |||  || ||| |||
                                CCGTC GTC  CC TCT CCG
                                   C   C_  _   _
GAM491  MAP2K2  5'  AGGCCGGCGTCGGGGCGGCCG  36204     AGACAGA   CA
                                AGGC      CGG  GGCGGCCG
                                ||||      |||  ||||||||
                                TCCG      GCC  CCGCCGGC
                                  GCCGCA_   __
GAM491  MECP2   3'  GGCAGGCAGGGGGCC       22600      GACAGAC     C
                                GGCA      GGCAGG GGCC
                                ||||      |||||| ||||
                                CCGT      CCGTCC CCGG
                                  ________      C
GAM491  MGAT2   5'  GGCGGGCGGGCGGCGGCCG   14450     AGACAGAC   A
                                GGC       GGC GGCGGCCG
                                |||       ||| ||||||||
                                CCG       CCG CCGCCGGC
                                  CCCGC___  _
GAM491  MMP11   3'  AGGCAGACAGATGCAGG     25537          CG
                                AGGCAGACAGA  GCAGG
                                ||||||||||  |||||
                                TCCGTCTGTCT  CGTCC
                                      A_
GAM491  MSLN    5'  AGCAGACGGGAGTGGC      30173    A      C  GC
                                AG CAGACGG AG  GGC
                                || ||||||| ||  |||
```

```
                                TC GTCTGCC TC  CCG
                                 _      C  A_
GAM491  MUS81    3'  GGGGGACAGACGGGGGC     36066    CA       CA
                                GG  GACAGACGG  GGC
                                ||  |||||||||  |||
                                CC  CTGTCTGCC  CCG
                                 CC        C_
GAM491  MYO1F    3'  AGGCAGATAGGCGGGCG     44369       CAGAC   A
                                AGGCAGA     GGC GGCG
                                |||||||     ||| ||||
                                TCCGTCT     CCG CCGC
                                    AT___   C
GAM491  NLGN2    3'  GGCAGGCGGCGGGGGCCG    44758      ACAGA    A  C
                                GGCAG     CGGC GG GGCCG
                                |||||     |||| || |||||
                                CCGTC     GCCG CC CCGGC
                                   C_____    C  _
GAM491  NRG2     5'  GGCAGGCGGCAAGCGGGCCG   30368      ACAGA        _
                                GGCAG     CGGCAGGCGG CCG
                                |||||     |||||||||| |||
                                CCGTC     GCCGTTCGCC GGC
                                   C_____         C
GAM491  PACSIN1  3'  GGCGGCAGACGGCGGGCGG   45155     AGA       A
                                GGC   CAGACGGC GGCGG
                                |||   |||||||| |||||
                                CCG   GTCTGCCG CCGCC
                                  CC_       C
GAM491  PCTK3    3'  GGTGGACAGGCAGGAGCC    43785    CA    GAC     C
                                GG  GACA   GGCAGG GGCC
                                ||  ||||   |||||| ||||
                                CC  CTGT   CCGTCC TCGG
                                 AC    ___     _
GAM491  PDE4A    3'  AGGTAGAGACTCCCCAGGCGGC 26249     C   CA   GG__
                                AGG AGA  GAC    CAGGCGGC
                                ||| |||  |||    ||||||||
                                TCC TCT  CTG    GTCCGCCG
                                  A  __   AGGG
GAM491  PHKG2    5'  GGCAGGCAGAGGAGCCAG     7131        A    C  C  G
                                GGCAG CAGA GG AG CGG
                                ||||| |||| || || |||
                                CCGTC GTCT CC TC GTC
                                   C    _ _  G
GAM491  PITX3    5'  GGCAGGCAGGGGCCAGGGGCCG 22757       A   AC   _   C
                                GGCAG CAG  GGC AGG GGCCG
                                ||||| |||  ||| ||| |||||
                                CCGTC GTC  CCG TCC CCGGC
                                   C   C_   G   _
GAM491  POMZP3   5'  GGCGGGCGGGCGGCGGCCA   29243     AGACAGAC   A
                                GGC       GGC GGCGGCCG
                                |||       ||| ||||||||
```

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                                CCG       CCG CCGCCGGT
                                  CCCGC___  _
GAM491  PPP2R5A  5' GGCGCGCAGACGGTGGAAG   26440     AGA      CA  C
                                GGC   CAGACGG  GG GG
                                |||   |||||||  || ||
                                CCG   GTCTGCC  CC TC
                                  CGC      A_  T
GAM491  RGL      5' AGGCAGGCAGGAGGCATTACG  31538       A   AC    G_
                                AGGCAG CAG  GGCA  GCG
                                |||||| |||  ||||  |||
                                TCCGTC GTC  CCGT  TGC
                                   C   CT    AA
GAM491  RIMS1    5' GGCGGGCAGGCGGAGGCG    43735     AGA   A   C
                                GGC   CAG CGG AGGCG
                                |||   ||| ||| |||||
                                CCG   GTC GCC TCCGC
                                  CCC   C  _
GAM491  ROBO1    5' GGCAGGCGCGGCGGCGGC    39485      ACAGA    A
                                GGCAG    CGGC GGCGGC
                                |||||    |||| ||||||
                                CCGTC    GCCG CCGCCG
                                  CGC__   _
GAM491  RRP22    5' GGCAGACAGGTGGCGGGCG   27008         AC   A
                                GGCAGACAG  GGC GGCG
                                |||||||||  ||| ||||
                                CCGTCTGTC  CCG CCGC
                                     CA   C
GAM491  RRP22    5' GGCAGACAGGTGGCGGGCG   27008         AC   A
                                GGCAGACAG  GGC GGCG
                                |||||||||  ||| ||||
                                CCGTCTGTC  CCG CCGC
                                     CA   C
GAM491  RXRA     5' AGGCAGCGGGCGGCGGGCG   16411       ACAGA    A
                                AGGCAG    CGGC GGCG
                                ||||||    |||| ||||
                                TCCGTC    GCCG CCGC
                                   GCCC_   C
GAM491  SIX1     5' AGGCAGGGGGCGGCGGCC    25594       ACAGAC   A
                                AGGCAG     GGC GGCGGCC
                                ||||||     ||| |||||||
                                TCCGTC     CCG CCGCCGG
                                   CC_____  _
GAM491  SLC30A4  5' AGGCGGACGGCCGGCGGC    30008      AGACA     A
                                AGGC    GACGGC GGCGGC
                                ||||    |||||| ||||||
                                TCCG    CTGCCG CCGCCG
                                  C_____     G
GAM491  SLC39A1  5' GGCGGAGCAGGCGACC      30887     A  CAGACG
                                GGC GA     GCAGGCGGCC
                                ||| ||     ||||||||||
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                                CCG CT     CGTCCGCTGG
                                  C _______
GAM491  SMARCB1  5'  GGCAGAGGCGGGCGGCC     42313       CAGAC   A
                                GGCAGA     GGC GGCGGCC
                                ||||||     ||| |||||||
                                CCGTCT     CCG CCGCCGG
                                   ______  C
GAM491  SMTN     3'  AGGCAGGAGACGGTGCCC     39520       AC     CAG  GG
                                AGGCAG  AGACGG   GC  CC
                                ||||||  ||||||   ||  ||
                                TCCGTC  TCTGCC   CG  GG
                                   C_     A__  __
GAM491  SPARC    5'  AGGCAGGCAGGCGGCAGG    17065       A   A
                                AGGCAG CAG CGGCAGG
                                ||||||| ||| |||||||
                                TCCGTC GTC GCCGTCC
                                   C   C
GAM491  SPINT2   5'  GGCAGGCAGGGGGCGGGGC   41795       A   AC   A  C
                                GGCAG CAG  GGC GG GGC
                                ||||| |||  ||| || |||
                                CCGTC GTC  CCG CC CCG
                                   C   CC  _ _
GAM491  SQSTM1   3'  AGGCAGGGCAGGCGGTCC    19374       ACAGAC       _
                                AGGCAG     GGCAGGCGG CC
                                ||||||     ||||||||| ||
                                TCCGTC     CCGTCCGCC GG
                                   _______        A
GAM491  ST5      3'  AGGCAGGCAGGCAGGCAGGCCG 40119       A  GAC      _
                                AGGCAG CA   GGCAGGC GGCCG
                                |||||| ||   ||||||| |||||
                                TCCGTC GT   CCGTCCG CCGGC
                                   C ____      T
GAM491  SUV39H1  3'  GGCAGGTGGAGGCAGGCG    17224       ACA  C
                                GGCAG   GA GGCAGGCG
                                |||||   || ||||||||
                                CCGTC   CT CCGTCCGC
                                   CAC  _
GAM491  TAF15    5'  AGCCAGGCGGCGCGGCGGCCG  40183     AGA   A    A_
                                GGC   CAG CGGC  GGCGGCCG
                                |||   ||| ||||  ||||||||
                                TCG   GTC GCCG  CCGCCGGC
                                  ____  C    CG
GAM491  TBXA2R   5'  AGGCAGATGTGCGGGCGCC   9845        CAGACG  A   G
                                AGGCAGA     GC GGCG CC
                                |||||||     || |||| ||
                                TCCGTCT     CG CCGC GG
                                    ACA____  C   _
GAM491  TIMM23   3'  AGGCCAAGGCAGGCGGC     26750      AGA   AC
                                AGGC   CAG  GGCAGGCGGC
                                ||||   |||  ||||||||||
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                              TCCG  GTT  CCGTCCGCCG
                                ___  __
GAM491  VIPR1   3' GGCAGACAGAGGAGGC     21510        C  C
                              GGCAGACAGA GG AGGC
                              |||||||||| || ||||
                              CCGTCTGTCT CC TCCG
                                     _  _
GAM491  WHN     3' AGGTGAGCCCGATGTGGGCGGC 18752    CA  CAGA  CA__
           CG                   AGG  GA   CGG   GGCGGCCG
                              |||  ||   |||   ||||||||
                              TCC  CT   GCT   CCGCCGGC
                               A_  CGG_  ACAC
GAM491  YY1     5' GGCGGGCGAGGAGGCGGCCG  18177    AGACA  C  C
                              GGC    GA GG AGGCGGCCG
                              |||    || || |||||||||
                              CCG    CT CC TCCGCCGGC
                               CCCG_  _  _
GAM491  ZAP70   3' AGGCAGGCAATGCAAGGCC   43336      A  GACG   GC
                              AGGCAG CA   GCAG  GGCC
                              |||||| ||   ||||  ||||
                              TCCGTC GT   CGTT  CCGG
                                 C  TA__   __
GAM491  ZNF216  5' AGGTGGAGGGAGGACCGGCGGC 25650    CA  CA  C   A
           CG                   AGG  GA  GA GGC GGCGGCCG
                              |||  ||  || ||| ||||||||
                              TCC  CT  CT CTG CCGCCGGC
                               AC  CC  C   G
GAM491  ZNF42   5' AGGCAGACGGAGGCGAC    18288       AGAC  C
                              AGGCAGAC   GG AGGCGGC
                              ||||||||   || |||||||
                              TCCGTCTG   CC TCCGCTG
                                   _____  _
GAM491  BAP1    3' GCTGGACAGAGGCTCTTCTG  21644     CA  CCTCTC
                              GCTG  AC    CTCTTCTG
                              ||||  ||    ||||||||
                              CGAC  TG    GAGAAGAC
                                C_  TCTCC_
GAM491  BRCA1   3' GTTGCACATTCCTCTTCTG   28659   C   ACCCTC
                              G TGCA     TCCTCTTCTG
                              | ||||     ||||||||||
                              C ACGT     AGGAGAAGAC
                               A   GTA___
GAM491  CARPX   3' GCTGTATTTTCTCCTCTCTCT  33575     CAACCC      _
                              GCTG     TCTCCTCT TCT
                              ||||     |||||||| |||
                              CGAC     AGAGGAGA AGA
                                ATAAA_       G
GAM491  CIT     5' GCTGTGGTCTCTTCCAGCTCTG 43051     CAACC   _  TC
                              GCTG    CTCT CC  TTCTG
                              ||||    |||| ||  |||||
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                                CGAC    GAGA GG  GAGAC
                                  ACCA_   A  TC
GAM491  CYFIP2   3'  GCTGTGGCTTTCTCTCTCCTG  43910     CAACCC   C
                                GCTG     TCTC TCTTCTG
                                ||||     |||| |||||||
                                CGAC     AGAG AGAGGAC
                                  ACCGAA   _
GAM491  EFNB1    5'  GCTGCGCGCCCTCTCCCC    20721      AA_
                                GCTGC   CCCTCTCCTC
                                |||||   ||||||||||
                                CGACG   GGGAGAGGGG
                                  CGC
GAM491  FLG      5'  CTGCCTTCCTCTTCT      43359      AACC  C
                                CTGC    CT TCCTCTTCT
                                ||||    || |||||||||
                                GACG    GA AGGAGAAGA
                                  _____  _
GAM491  FMOD     3'  CTGGCCTTTCCTCTTCTG    12929     CAAC   C
                                CTG    CCT TCCTCTTCTG
                                |||    ||| ||||||||||
                                GAC    GGA AGGAGAAGAC
                                  C___   A
GAM491  GARP     3'  GCTCCAATTCTCTCTTCCG   24313     G   CCC    C
                                GCT CAA   TCTC TCTTCTG
                                ||| |||   |||| |||||||
                                CGA GTT   AGAG AGAAGGC
                                  G   A__   _
GAM491  GUCY1A3  5'  GCTGCGATCTCCTCCT     41837      AACCC
                                GCTGC    TCTCCTCTT
                                |||||    |||||||||
                                CGACG    AGAGGAGGA
                                  CT___
GAM491  HRH2     5'  GCTGTATCCCTCTCCATAGCTG 35290     CAA       TCTT
                                GCTG   CCCTCTCC    CTG
                                ||||   ||||||||    |||
                                CGAC   GGGAGAGG    GAC
                                  ATA       TATC
GAM491  KCNK1    5'  GCGCGGCCCGCCGCCTCTTCTG 13893    T  AA  _  T
                                GC GC  CCC TC CCTCTTCTG
                                || ||  ||| || |||||||||
                                CG CG  GGG GG GGAGAAGAC
                                 _  CC   C  C
GAM491  LASS2    3'  GCTGCAGCCTCCTCCCCCTCTG 42678       A  CT
                                GCTGCA CC  CTCCTCTTCTG
                                |||||| ||  ||||||||||
                                CGACGT GG  GAGGGGGAGAC
                                   C  AG
GAM491  MEN1     5'  GCGGCGGCTTCCCCTTCT    39187    T  AACC  C
                                GC GC    CT TCCTCTTCT
                                || ||    || |||||||||
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                                CG CG    GA AGGGGAAGA
                                 C  CC__  _
GAM491  NFATC3   5'  GCTGCAGCTCCTCCTC      21251        ACCCT
                                GCTGCA    CTCCTCTTC
                                ||||||    |||||||||
                                CGACGT    GAGGAGGAG
                                   C____
GAM491  NR1H2    3'  CTGCAACCCTTTCACCCCTTCT 43119          __  T
           G                     CTGCAACCC  TC CCTCTTCTG
                                |||||||||  || |||||||||
                                GACGTTGGG  AG GGGGAAGAC
                                     AA  T
GAM491  NUP98    3'  ACTGTCTCCTCTTC       32230      CAACCC
                                GCTG     TCTCCTCTTC
                                ||||     ||||||||||
                                TGAC     AGAGGAGAAG

                                _______
GAM491  P2RY1    3'  ACTGTCAACCTCTCCTTTTCTG 15002      _    C     C
                                GCTG CAACC TCTCCT TTCTG
                                |||| ||||| |||||| |||||
                                TGAC GTTGG AGAGGA AAGAC
                                  A    _     A
GAM491  PATE     3'  TGCAATCCTCTTCT       39646       CCCTC
                                TGCAA    TCCTCTTCT
                                |||||    |||||||||
                                ACGTT    AGGAGAAGA

                                ______
GAM491  PDE4B    3'  GCTTCAGCCCTCTCCACC    15149     G  A      T
                                GCT CA CCCTCTCC CT
                                ||| || |||||||| ||
                                CGA GT GGGAGAGG GG
                                  A  C       T
GAM491  PHB      5'  GCTGGACCCTCTCACACCTG   15265      CA      CTCT
                                GCTG  ACCCTCTC    TCTG
                                ||||  ||||||||    ||||
                                CGAC  TGGGAGAG    GGAC
                                  C_       TGT_
GAM491  PPP1R12B 5'  GCTGCTGGCCCTCCCCAGCTTC 36957       AA_       T_
           TG                    GCTGC   CCCTCTCC  CTTCTG
                                |||||   ||||||||  ||||||
                                CGACG   GGGAGGGG  GAAGAC
                                   ACC       TC
GAM491  PTGS1    3'  GCTGCAGCCTCCTCCGTTCTG  38738       A  CT    TC
                                GCTGCA CC  CTCC  TTCTG
                                ||||||  ||  ||||  |||||
                                CGACGT GG  GAGG  AAGAC
                                   C  AG   C_
GAM491  PTN      5'  GCTGCTCTCCCCGCCTTCTG   44388       AACC     _
                                GCTGC    CTCTCC TCTTCTG
                                |||||    |||||| |||||||
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                                CGACG    GAGGGG GGAAGAC
                                  A___     C
GAM491  RANBP9   5'  GCTGCAACTCCTTCTCCT    24253        _  _
                                GCTGCAAC CCT CTCCT
                                |||||||| ||| |||||
                                CGACGTTG GGA GAGGA
                                    A   A
GAM491  RNTRE    3'  GCTGCAACTTCTCCTGCTCTG  31256        CC     C
                                GCTGCAAC  TCTCCT TTCTG
                                |||||||| ||||||| |||||
                                CGACGTTG  AGAGGA GAGAC
                                    A_     C
GAM491  SPAP1    3'  GCTGTTGATCTTCCCTTCTG   39865      CAACCC   C
                                GCTG     TCT CTCTTCTG
                                ||||     ||| ||||||||
                                CGAC     AGA GGGAAGAC
                                  AACT__   A
GAM491  SYNGR1   3'  GCTGGGGTCCTCTCCATCACTG 21761      CAAC      _ TT
                                GCTG   CCTCTCC TC  CTG
                                ||||   ||||||| ||  |||
                                CGAC   GGAGAGG AG  GAC
                                  CCCA      T  T_
GAM491  TACC1    3'  CCGGCCCTTTTTCTCTTCTG   26593     CAA   CTC_
                                CTG   CCCT    CTCTTCTG
                                |||   ||||    ||||||||
                                GGC   GGGA    GAGAAGAC
                                  C__    AAAA
GAM491  TCF2     3'  ACTGCAACTTTTTCTTCTG    27016        CCTCTCC
                                GCTGCAAC      TCTTCTG
                                ||||||||      |||||||
                                TGACGTTG      AGAAGAC
                                    AAAA___
GAM491  TDRD1    5'  GCTCCAATTCCCTTCT      36331     G   CCCTC   T
                                GCT CAA     TCC CTTCT
                                ||| |||     ||| |||||
                                CGA GTT     AGG GAAGA
                                  G   A____   _
GAM491  TNXB     5'  GCTGGTGTGTCCTCTTCTG    37158      CAACCCTC
                                GCTG       TCCTCTTCTG
                                ||||       ||||||||||
                                CGAC       AGGAGAAGAC
                                  CACAC___
GAM491  TXK      3'  GCTTTTGTCTCCTCTTCTG    17766     GCAACCC
                                GCT      TCTCCTCTTCTG
                                |||      ||||||||||||
                                CGA      AGAGGAGAAGAC
                                  AAAC___
GAM491  VPS26    3'  GCTGCAACCATCTTTAACCTG  22210         C   CCTCT
                                GCTGCAACC TCT     TCTG
                                ||||||||| |||     ||||
```

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                                CGACGTTGG AGA    GGAC
                                     T  AATT_
GAM491  ZIC3    5'  GCTGCAACTTTCCGTCACTG  18249       CCTC  _ TT
                                GCTGCAAC   TCC TC  CTG
                                ||||||||   ||| ||  |||
                                CGACGTTG   AGG AG  GAC
                                     AA__  C  T_
GAM492  MECP2   3'  TGCCGACTACGTTCCG    22617        A   GA
                                TGCCGACTG CGTT  CG
                                ||||||||| ||||  ||
                                ACGGCTGAT GCAA  GC
                                     _   G_
GAM493  APG5L   3'  GTGTCTGATACTGTAAGCCTT  22133       C  CCTCC
                                GTGTCTGA ACT    CCTT
                                |||||||| |||    ||||
                                CACAGACT TGA    GGAA
                                     A  CATTC
GAM493  BSN     3'  TGTGTCTGTTGCTCTCTACTTT 18424       ACA  C  CC  _
            CC                    TGTGTCTG  CTC TC  CTT CC
                                ||||||||  ||| ||  ||| ||
                                ACACAGAC  GAG AG  GAA GG
                                     AAC  _ AT  A
GAM493  CABC1   3'  TGTGTCTGGCATTCCCTGTTCC 33692       A  C   CCCC
                                TGTGTCTG CA TCCT   TTCC
                                |||||||| || ||||   ||||
                                ACACAGAC GT AGGG   AAGG
                                     C  A   AC__
GAM493  CASR    3'  TGTGTCTATTATCCCTTC    7552        ACACTCCTC
                                TGTGTCTG       CCCTTC
                                ||||||||       ||||||
                                ACACAGAT       GGGAAG
                                     AATA_____
GAM493  CLOCK   3'  TGTCCTCTCCTCCCTTTC    22221      GACA      C
                                TGTCT   CTCCTCCC TTC
                                |||||   |||||||| |||
                                ACAGG   GAGGAGGG AAG
                                   A___       A
GAM493  ETV5    3'  TGTTCTGACTGCCCCCCTT   20859    G    ACTC
                                TGT TCTGAC   CTCCCCTT
                                ||| ||||||   ||||||||
                                ACA AGACTG   GGGGGGAA
                                  _     AC__
GAM493  FLG     5'  TGTGTCTGACTCTTCTGAATGT 43367        A  C  CCCCT
            CC                    TGTGTCTGAC CT CT    TCC
                                ||||||||||| || ||    |||
                                ACACAGACTG GA GA    AGG
                                     A  A  CTTAC
GAM493  HDAC4   3'  TGTGTCTGAACTTCTGCC    25792        C  C  C
                                TGTGTCTGA ACT CT CC
                                |||||||| ||| || ||
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                                ACACAGACT TGA GA GG
                                     _  A  C
GAM493  KL      3'  TGTATCTGCCATCTTCTTTTCC 22007        A  C  C  CCC
                                TGTGTCTG CA TC TC   TTCC
                                |||||||| || || ||   ||||
                                ACATAGAC GT AG AG   AAGG
                                     G  _  A  AA_
GAM493  KLK3    3'  TGTGTCTGCTGATTTCTTTTCC 11614        ACACTCC  CCC
                                TGTGTCTG      TC   TTCC
                                ||||||||      ||   ||||
                                ACACAGAC      AG   AAGG
                                     GACTAA_  AA_
GAM493  MECP2   3'  TGTGTCTGGTTATTACCCTCTT 22623        ACACTCCT  _
                                TGTGTCTG       CCC CTT
                                ||||||||       ||| |||
                                ACACAGAC       GGG GAA
                                     CAATAAT_  A
GAM493  MOCS1   3'  TGTGTCTGGCTTCCTGCC    45129        ACAC    C
                                TGTGTCTG    TCCT CC
                                ||||||||    |||| ||
                                ACACAGAC    AGGA GG
                                     CGA_    C
GAM493  NT5E    3'  GTCCTGTTCTTCCCCTTCC    14864      GACAC  C
                                GTCT    TC TCCCCTTCC
                                ||||    || |||||||||
                                CAGG    AG AGGGGAAGG
                                  ACA__  A
GAM493  PCLO    3'  TGTGTCTGTGCTGCTTCC    45313        ACA  C  C
                                TGTGTCTG   CT CT CC
                                ||||||||   || || ||
                                ACACAGAC   GA GA GG
                                     AC_  C  A
GAM493  PMX1    5'  TGTGCCTGACGTTTCACAGACC 35529          _____  TCC
           CCCTT                TGTGTCTGAC    AC   TCCCCTT
                                ||||||||||    ||   |||||||
                                ACACGGACTG    TG   GGGGGAA
                                      CAAAG  TCT
GAM493  PRG3    5'  TGTGTCTAGTATAGCCCCTTCC 37254        ACACTCCT
                                TGTGTCTG       CCCCTTCC
                                ||||||||       ||||||||
                                ACACAGAT       GGGGAAGG
                                     CATATC__
GAM493  PTGFRN  3'  TGTCCCCATCCTCCCCTTCC   42606      GA  C
                                TGTCT  CA TCCTCCCCTTCC
                                |||||  || ||||||||||||
                                ACAGG  GT AGGAGGGGAAGG
                                  G_  _
GAM493  SPARC   3'  TGTGTCTGTTACTTCCCTT    17070        AC   CCTC
                                TGTGTCTG  ACT   CCCTT
                                ||||||||  |||   |||||
```

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                                ACACAGAC  TGA   GGGAA
                                    AA  A___
GAM493  STAT6   3'  TGTGTCTGTATGTTCCTGCC  17161       ACAC_   C
                                TGTGTCTG    TCCT CC
                                ||||||||    |||| ||
                                ACACAGAC    AGGA GG
                                    ATACA   C
GAM493  TCF19   3'  TGTATTTCCATCTCTCCCCTTC 45550     CTGA  C  _
          C                      TGTGT   CA TC CTCCCCTTCC
                                |||||   || || ||||||||||
                                ACATA   GT AG GAGGGGAAGG
                                  AAG_  _  A
GAM494  MMP19   5'  ACCCGGCCTGAGACTGTCAT  35576       AC    _
                                ACCCGGCCT  GACTG CGT
                                |||||||||  ||||| |||
                                TGGGCCGGA  CTGAC GTA
                                     CT    A
GAM494  SECTM1  3'  CCCGGCCTGCGCTTGCCCCCT  16537       A  A  GC  G
                                CCCGGCCT CG CT  GT CTCT
                                |||||||| || ||  || ||||
                                GGGCCGGA GC GA  CG GGGA
                                    C  _  A_  G
GAM494  SLC26A4 3'  CCTGGCCTACATTCACTC    7761    C     ACTGCG
                                CC GGCCTACG     TGCTC
                                || ||||||||     |||||
                                GG CCGGATGT     GTGAG
                                 A      AA____
GAM494  TNFRSF6B 3'  CGGCTGGCACTGCGTGTTCT  32352    CTACG     C
                                CGGC    ACTGCGTG TCT
                                ||||    |||||||| |||
                                GCCG    TGACGCAC AGA
                                  ACCG_      A
GAM494  ARCN1   3'  GCCAGTGCCTGCAGCC     11656     T     T
                                GCCA GTGCCTGC GGCC
                                |||| |||||||| ||||
                                CGGT CACGGACG TCGG
                                  _      _
GAM494  AVP     5'  GCTGCCTCTGCTGGCTGCCTA  7938    CA  GC     C
                                GC  TGT  CTGCTGGC GCCTA
                                ||  |||  |||||||| |||||
                                CG  ACG  GACGACCG CGGAT
                                 __  GA      A
GAM494  FGFR4   3'  CCTATGTGCCTGCACAGCCT  35652   _       TG  C
                                CC ATGTGCCTGC  GC GCCT
                                || ||||||||||  || ||||
                                GG TACACGGACG  TG CGGA
                                 A        __ T
GAM494  HOXC5   3'  CGCCAGCCTTTGGCTGTCT   33245     TGT   GC   CGC
                                CGCCA   GCCT  TGGC   CT
                                |||||   ||||  ||||   ||
```

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                                GCGGT  CGGA ACCG  GA
                                  ___  A_   ACA
GAM494  RAD51L3  3'  CGCCATGCGCCGGCCGCCT  39467        TGCT
                                CGCCATGTGCC  GGCCGCCT
                                ||||||||||  ||||||||
                                GCGGTACGCGG  CCGGCGGA
                                     ____
GAM494  RAGE     5'  TGTGTCCCTGTCACCC    30605    _ TG  GC
                                TGTG CC  CTG  CGCCT
                                |||| ||  |||  |||||
                                ACAC GG  GAC  GTGGG
                                  A __  A_
GAM495  ABCC5    5'  CAGCCGCTCAACCACGC    25021      G    C
                                CAGCCGC TCAACC CGT
                                ||||||| |||||| |||
                                GTCGGCG AGTTGG GCG
                                   _    T
GAM495  AMPD3    5'  CAGCCGCGTGCAGCCCCCGT  7894        _ A_
                                CAGCCGCGT CA  CCCCGT
                                ||||||||| ||  ||||||
                                GTCGGCGCA GT  GGGGCA
                                     C  CG
GAM495  BTEB1    5'  GCCTCGCGGTCCCGTGGCC   10215    G  CAAC
                                GCC CGT   CCCGTGGCC
                                ||| |||   |||||||||
                                CGG GCG   GGGCACCGG
                                  A  CCA_
GAM495  CDC34    3'  CAGCAGCGCCCCCGTGGC    20350    C   CAA
                                CAGC GCGT  CCCCGTGGC
                                |||| ||||  |||||||||
                                GTCG CGCG  GGGGCACCG
                                  T  ___
GAM495  CDKN2B   3'  GCGTCAGTCCCCCGTGGC    38546     A__
                                GCGTCA  CCCCGTGGC
                                ||||||  |||||||||
                                CGCAGT  GGGGCACCG
                                   CAG
GAM495  CELSR3   3'  CAGCCACTCTCCCCCGTGG   10826      G  AA
                                CAGCCGC TC  CCCCGTGG
                                ||||||| ||  ||||||||
                                GTCGGTG AG  GGGGCACC
                                   _  AG
GAM495  CHS1     5'  GCCGCGTCGACGCGGCC    6348       AACCC
                                GCCGCGTC   CGTGGCC
                                ||||||||   |||||||
                                CGGCGCAG   GCGCCGG
                                    CT___
GAM495  CSK      3'  GCCGCCCGCTCCGTGGCC   20461     G  AACC
                                GCCGC TC   CCGTGGCC
                                ||||| ||   ||||||||
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                                CGGCG GG   GGCACCGG
                                  _ CGA_
GAM495  FANCG   5' GCCCCACAGTCCGTGGC    21557    G  T  ACC
                                GCC CG CA  CCGTGGC
                                ||| || ||  |||||||
                                CGG GT GT  GGCACCG
                                  G  _  CA_
GAM495  FRZB    5' CAGCCGCGCAGTGGAC     11153       T  ACCCC  _
                                CAGCCGCG CA   GTGG C
                                |||||||| ||    |||| |
                                GTCGGCGC GT   CACC G
                                    _ _____   T
GAM495  GGA3    3' CAACTCATCACTCCGTGGCC  39782    CG    A C
                                CAGC  CGTCA C CCGTGGCC
                                ||||  ||||| | ||||||||
                                GTTG  GTAGT G GGCACCGG
                                  A_    _ A
GAM495  HIC1    5' CAGTGCGTGTTGACCGCGGCC  44564    CC   CAACC
                                CAG  GCGT   CCGTGGCC
                                |||  ||||   ||||||||
                                GTC  CGCA   GGCGCCGG
                                  A_   CAACT
GAM495  HS3ST3A1 5' GCCGTGCGCCCCTGTGGCC  25806    C  CAA   _
                                GCCG GT  CCCC GTGGCC
                                |||| ||  |||| ||||||
                                CGGC CG  GGGG CACCGG
                                  A  C__   A
GAM495  JAG2    3' CAGGTGCGTCAACAGC     13704    CC     CCCGT
                                CAG  GCGTCAAC   GGC
                                |||  ||||||||   |||
                                GTC  CGCAGTTG   TCG
                                  CA     _____
GAM495  MMP14   3' CAGCCCACCCTGTGGC     22632     G GTCA   C
                                CAGCC C   ACCC GTGGC
                                |||||  |   |||| |||||
                                GTCGG G   TGGG CACCG
                                  _ _____   A
GAM495  MXI1    5' CAGCCGCGCCAGCCGCGCC   39013        ACC   G
                                CAGCCGCGTCA  CCGTG CC
                                ||||||||||  ||||| ||
                                GTCGGCGCGGT  GGCGC GG
                                     C__   _
GAM495  NAP1L4  5' GCTGCGCCGCCGTGGCC    25573   C   AACC
                                GC GCGTC   CCGTGGCC
                                || |||||   ||||||||
                                CG CGCGG   GGCACCGG
                                 A   C___
GAM495  NDUFA8  5' CAGCCGCGTCGCCCCCGT   30590        AA
                                CAGCCGCGTC  CCCCGT
                                ||||||||||  ||||||
```

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                                GTCGGCGCAG  GGGGCA
                                      CG
GAM495  PIGA     3'  AGTCCAGGCACCCCGTGGCC  33829    _  C  CA
                                AG CCG GT  ACCCCGTGGCC
                                || ||| ||  ||||||||||
                                TC GGT CG  TGGGGCACCGG
                                 A  C  __
GAM495  PITPN    5'  GCCGCTCTCCCCGTGGCC    26339      G  AA
                                GCCGC TC  CCCCGTGGCC
                                ||||| ||  ||||||||||
                                CGGCG AG  GGGGCACCGG
                                   _ A_
GAM495  PITX1    3'  GCCCGCTGTCGCTCCGTGGCC  15324     _ _  AACC
                                GCC GC GTC   CCGTGGCC
                                ||| || |||   ||||||||
                                CGG CG CAG   GGCACCGG
                                  G  A  CGA_
GAM495  POU4F1   5'  CAGCCGCGGCGGTCGCGGC   26381        TCAACCC
                                CAGCCGCG     CGTGGC
                                ||||||||     ||||||
                                GTCGGCGC     GCGCCG
                                     CGCCA__
GAM495  RFC4     5'  CAGTCGCCTCAGTTCCCGC   16285    C  G  AC_
                                CAG CGC TCA  CCCGT
                                ||| ||| |||  |||||
                                GTC GCG AGT  GGGCG
                                  A  G  CAA
GAM495  RNGTT    5'  AGCCGCCTCCCCGTGG     19162      G CAA
                                AGCCGC T  CCCCGTGG
                                |||||| |  ||||||||
                                TCGGCG A  GGGGCACC
                                   G ___
GAM495  SHOX     5'  CCGCGTTCTCTCCGTGGCC   7808       CAACC
                                CCGCGT    CCGTGGCC
                                ||||||    ||||||||
                                GGCGCA    GGCACCGG
                                    AGAGA
GAM495  SURF6    3'  ACCGTCTTCTGTCCCGTGGC  27584     CG_  AAC
                                GCCG  TC  CCCGTGGC
                                ||||  ||  ||||||||
                                TGGC  AG  GGGCACCG
                                  AGA  ACA
GAM495  TJP1     5'  CAGCAGCACCCGTGGC     17535     C  TCAAC
                                CAGC GCG    CCCGTGGC
                                |||| |||    ||||||||
                                GTCG CGT    GGGCACCG
                                  T  _____
GAM495  ZNF2     5'  GCCGGCTTCCCGTGGC      34381     C  CAAC
                                GCCG GT   CCCGTGGC
                                |||| ||   ||||||||
```

```
                                CGGC CG   GGGCACCG
                                  _ AA__
GAM495  ZYX     5'  GCCGCGTCTCGGGTGGCC   18434       AACCCC
                                GCCGCGTC    GTGGCC
                                ||||||||    ||||||
                                CGGCGCAG    CACCGG
                                    AGCC__
GAM495  AR      5'  CGGGGGCGGGGGGGGCGG    6231        AAC
                                CGGGGGC  GGGGGCGG
                                |||||||  ||||||||
                                GCCCCCG  CCCCCGCC
                                   CC_
GAM495  ATP11A  3'  CGGGGGCAGCGTGGGCAGGGCT 44175       A  G    C
                                CGGGGGCA CG GGGCGG GCT
                                |||||||| || |||||| |||
                                GCCCCCGT GC CCCGTC CGA
                                    C  A    C
GAM495  ATRN    3'  GGGGGCAGGGGGCGCCTTCT  40277       AC     G GC
                                GGGGGCA  GGGGGCG C  TCT
                                |||||||  ||||||| |  |||
                                CCCCCGT  CCCCCGC G  AGA
                                   __     _ GA
GAM495  CNN1    5'  CGGGGGCAGTGGCGGCACT   10539       ACGGG
                                CGGGGGCA   GGCGGCGCT
                                ||||||||   |||||||||
                                GCCCCCGT   CCGCCGTGA
                                    CA___
GAM495  CSRP1   5'  CAGGGGCGGCAGGCGCTC    19838       AACGGG  _
                                CGGGGGC    GGC GGCGCTC
                                |||||||    ||| |||||||
                                GTCCCCG    CCG CCGCGAG
                                   _______  T
GAM495  CUL3    5'  CGGCGGCGGCGGGGGGCGGC   18732    G  AA
                                CGG GGC  CGGGGGCGGC
                                ||| |||  ||||||||||
                                GCC CCG  GCCCCCGCCG
                                  G  CC
GAM495  CUL3    5'  CGGGGGCGGCGGCGGCGGC   18733       AA  G
                                CGGGGGC  CGG GGCGGC
                                |||||||  ||| ||||||
                                GCCCCCG  GCC CCGCCG
                                   CC  G
GAM495  DLG4    3'  GGGGGCAGGTGGGGGCGG    10708       AC_
                                GGGGGCA  GGGGGCGG
                                |||||||  ||||||||
                                CCCCCGT  CCCCCGCC
                                   CCA
GAM495  DUSP1   5'  CGGGGCCAAGGGCAGGGCGGCG 20655      G  C __
            CT                    CGGGG CAA GG  GGGCGGCGCT
                                |||||| ||| ||  ||||||||||
```

```
                                GCCCC GTT CC  CCCGCCGCGA
                                   G   C  GT
GAM495  FMNL    5'  GGGGGCGGCGGCGGTGGCGCT  25310       AA   G  C
                                GGGGGC  CGG GG GGCGCT
                                ||||||  ||| || ||||||
                                CCCCCG  GCC CC CCGCGA
                                   CC   G  A
GAM495  FMNL    5'  GGGGCAGCGGGAGGCGCT    25308       A    GC
                                GGGGCA CGGGG  GGCGCT
                                |||||| |||||  ||||||
                                CCCCGT GCCCT  CCGCGA
                                   C    __
GAM495  HCN2    3'  CAGGGGCGATGGGGGTGG    10165       AAC    C
                                CGGGGGC   GGGGG GG
                                |||||||   ||||| ||
                                GTCCCCG   CCCCC CC
                                    CTA    A
GAM495  HNF3G   5'  CGGGGGAACGGAGCGCTC    43646       C    GGGC
                                CGGGGG AACGG   GGCGCTC
                                |||||| |||||   |||||||
                                GCCCCC TTGCC   TCGCGAG
                                  _   _____
GAM495  HR      5'  CGGGGCGGCGGGGGCGCTCT  32917      GCAA  _  C
                                CGGGG   CGG GGG GGCGCTCT
                                |||||   ||| ||| ||||||||
                                GCCCC   GCC CCC CCGCGAGA
                                  _____  G  _
GAM495  ICMT    3'  GGGGCAGCAGAGTGGTGCTCT  29657       A    GC  C
                                GGGGCA CGGGG  GG GCTCT
                                |||||| |||||  || |||||
                                CCCCGT GTCTC  CC CGAGA
                                   C    A_ A
GAM495  IL2RB   5'  GGGGCGGTGGCAGCGCGCGCTC 9392       AAC  G   _
           T                     GGGGC   GG GGCG GCGCTCT
                                 |||||   || |||| |||||||
                                 CCCCG   CC TCGC CGCGAGA
                                   CCA  G   G
GAM495  KCNK4   3'  CAGGGGCAGTGGCAGCCTGCTC 32488        ACGGG    __
           T                     CGGGGGCA    GGCGGC  GCTCT
                                 ||||||||    ||||||  |||||
                                 GTCCCCGT    CCGTCG  CGAGA
                                    CA___     GA
GAM495  KIF3B   5'  CGGCGGCGGCGGGGGGCGGC   22033    G  AA
                                CGG GGC  CGGGGGCGGC
                                ||| |||  ||||||||||
                                GCC CCG  GCCCCCGCCG
                                  G  CC
GAM495  LASS1   3'  GGGGGCACGGGGGGCGCG    34613       A      G
                                GGGGGCA CGGGGGCG CG
                                ||||||| |||||||| ||
```

```
                                CCCCCGT GCCCCCGC GC
                                    _      _
GAM495  MAP4K5   5' CGGGGGCGGCGGAGGCGCG   27303       AA      G
                                CGGGGGC  CGGGGGCG CG
                                |||||||  |||||||| ||
                                GCCCCCG  GCCTCCGC GC
                                   CC       _
GAM495  NEK4     5' GGGGGCAGTGGGGGCGGC    17192       AC
                                GGGGGCA  GGGGGCGGC
                                |||||||  |||||||||
                                CCCCCGT  CCCCCGCCG
                                   CA
GAM495  NXF3     3' GGGGGTAACAGGGGTGGACA  35184      C       C _
                                GGGGG AACGGGGG GG CG
                                |||||  |||||||| || ||
                                CCCCC TTGTCCCC CC GT
                                  A       A  T
GAM495  PPP2R5A  5' CGGGGGCACGGGGGTGCG    26435       A     CG
                                CGGGGGCA CGGGGG  GCG
                                |||||||| ||||||  |||
                                GCCCCCGT GCCCCC  CGC
                                   _     A_
GAM495  RAB26    5' GGAGGCAGCGGGGGTGC     30749       A     CG
                                GGGGGCA CGGGGG  GC
                                |||||||  ||||||  ||
                                CCTCCGT GCCCCC  CG
                                   C     A_
GAM495  SF1      5' CGGGGGCGGCGGGGCCGGGGCC 21561       AA    G  C
                                CGGGGGC  CGGGG CGG GCT
                                |||||||  ||||| ||| |||
                                GCCCCCG  GCCCC GCC CGG
                                   CC    G  C
GAM495  SFRP5    3' CAGGGGCGGTGGGGAGAAC   16590       AAC    CG
                                CGGGGGC   GGGGG  GC
                                |||||||   |||||  ||
                                GTCCCCG   CCCCT  TG
                                   CCA    CT
GAM495  SLC2A1   5' GGGCGTGCGAGCGGCGCTCT  27142     AACGG
                                GGGC    GGGCGGCGCTCT
                                ||||    ||||||||||||
                                CCCG    CTCGCCGCGAGA
                                  CACG_
GAM495  SLC9A3R2 5' CGGGGGCGGCGGCGGCGCT   41526       AAC  G
                                CGGGGGC   GG GGCGGCGCT
                                |||||||   || |||||||||
                                GCCCCCG   CC CCGCCGCGA
                                   ___ G
GAM495  SPON2    5' CGGGGGCGGCGGGGGCTGCCGC 29713       AA      G _
            T                    CGGGGGC  CGGGGGC GC GCT
                                |||||||  ||||||| || |||
```

```
                                GCCCCCG  GCCCCCG CG CGA
                                   CC      A  G
GAM495  TGFB1    5'  CGGGGGCGGCGGCGGCTCGTCT 8538        AAC  G     GC_
                                CGGGGGC   GG GGCGGC   TCT
                                |||||||   || ||||||   |||
                                GCCCCCG   CC CCGCCG   AGA
                                   ___  G     AGC
GAM495  USP11    3'  GGGGAGCAGACTGGTGCT    21633     _  ACGGG  _ C
                                GGGG GCA    GGC GG GCT
                                |||| |||    ||| || |||
                                CCCC CGT    CTG CC CGA
                                  T  _____  A  A
GAM495  VGF      3'  CGGGGGCGCGCGGGGGCGG   17989       AA_
                                CGGGGGC   CGGGGGCGG
                                |||||||   |||||||||
                                GCCCCCG   GCCCCCGCC
                                   CGC
GAM496  PIGR     3'  GAGTGACAGAAATGGTGCGG   43705       TT_   A
                                GAGTGACG   GTGG TGCGG
                                ||||||||   |||| |||||
                                CTCACTGT   TACC ACGCC
                                    CTT   _
GAM497  F13A1    3'  TTTCTGGCTTTGCCAAAAATAA 44985         __
           AAA                    TTTCTGGCTTT  TAAAAATAAAAA
                                ||||||||||  ||||||||||||
                                AAAGACCGAAA  GTTTTTATTTTT
                                      CG
GAM497  KCNA5    3'  TTCCTGGGATAAAAATAAA    40686       CTTT
                                TTTCTGG    TAAAAATAAA
                                |||||||    ||||||||||
                                AAGGACC    ATTTTTATTT
                                   CT__
GAM497  PDE1A    3'  TCTGGCTTTTGTCTCAAAAA   22709        AAAAA
                                TCTGGCTTTT    TAAAAA
                                ||||||||||    ||||||
                                AGACCGAAAA    GTTTTT
                                      CAGA_
GAM497  PLAG1    3'  TTCTGGCCACTAGAGAATGAAA 15364       T  AA_  A
           AC                     TTCTGGCT TTA   AAT AAAAC
                                ||||||| |||   ||| |||||
                                AAGACCGG GAT   TTA TTTTG
                                    T  CTC  C
GAM497  RPP30    3'  TTTCTAGCTCCAAATGAAAAC  26942         TAA   A
                                TTTCTGGCTTT   AAAT AAAAC
                                ||||||||||   |||| |||||
                                AAAGATCGAGG   TTTA TTTTG
                                      ___   C
GAM497  ZNFN1A3  3'  TGGCTTTTAAATTCCATAAAA  41200         A___
                                TGGCTTTTAAA    ATAAAA
                                ||||||||||    ||||||
```

```
                                ACCGAAAATTT   TATTTT
                                      AAGG
GAM497  RBP1    3'  GAACACAGGTCACTTTATT   16182     _  TTTATG
                                GAAC CAG     CACTTTATT
                                |||| |||     |||||||||
                                CTTG GTC     GTGAAATAA
                                  T  CA____
GAM498  SURF6   3'  TAATTCTTCCATCCCACTTT  27590          A_
                                TAATTCTTTCAT  CGTTTT
                                ||||||||||||  ||||||
                                ATTAAGAAGGTA  GTGAAA
                                      GG
GAM499  BRCA1   3'  TGAAACCTTGAATGTAT    28650   A      TTT
                                A AAGCCTTG   TGTAT
                                | ||||||||   |||||
                                A TTTGGAAC   ACATA
                                 C       TT_
GAM499  CEACAM6 3'  AGTCTTGTTTTGACATC     14731    C       T
                                AG CTTGTTTTG ATATT
                                || |||||||| |||||
                                TC GAACAAAAC TGTAG
                                 A       _
GAM499  G6PC    3'  AAGTCTTGCTTTTGTATAT   6657     C      _
                                AAG CTTGTTTT GTATAT
                                ||| |||||||| ||||||
                                TTC GAACGAAA CATATA
                                  A       A
GAM499  MSH3    3'  CAAAAGCTTGGGAATTATATTC 14630       C   TTTTG
            T                    CAAAAGC TTG     TATATTCT
                                ||||||| |||     ||||||||
                                GTTTTCG AAC     ATATAAGA
                                    _  CCTTA
GAM499  SMCY    3'  CTTGTTTTTCCCTATTCT    21638        GTA_
                                CTTGTTTT    TATTCT
                                ||||||||    ||||||
                                GAACAAAA    ATAAGA
                                     AGGG
GAM499  U2AF1   3'  CAGAAACCCATCTTTGTAT   41866    A     TG
                                CA AAGCCT  TTTTGTAT
                                || ||||||  ||||||||
                                GT TTTGGG  GAAACATA
                                 C     TA
GAM499  UBE2V1  3'  TGAAAGCCCTGTTTAAAACTTC 17837   A         TGTATA
            T                    C AAAGCCTTGTTT     TTCT
                                | ||||||||||||     ||||
                                A TTTCGGGACAAA     AAGA
                                 C          TTTTG_
GAM499  ZNF257  3'  AAAGGCCTTGTCACATTC    37909    A      TTGT
                                AAA GCCTTGTT    ATATTC
                                ||| ||||||||    ||||||
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                                TTT CGGAACAG    TGTAAG
                                  C      ____
GAM499  B29     3'  TTCAACACATGCTTTATAGA  36713          A  GTAC
                                TTCAACACAT CTT    AGA
                                |||||||||| |||    |||
                                AAGTTGTGTA GAA    TCT
                                      C  ATA_
GAM499  RBMX    3'  AACACACACTTAAATG     42808          TACA
                                AACACATACTTG    GATG
                                ||||||||||||    ||||
                                TTGTGTGTGAAT    TTAC
                                          ____
GAM499  RING1   3'  TCCAACACCTCGTATAGATG  16336        ATA     C
                                TTCAACAC   CTTGTA AGATG
                                ||||||||   |||||| |||||
                                AGGTTGTG   GAGCAT TCTAC
                                    ___     A
GAM499  SERPINB13 3'  TCAATACATACTACAACAGATG 29623     C      TGT
            A                    TCAA ACATACT   ACAGATGA
                                 |||| |||||||   ||||||||
                                 AGTT TGTATGA   TGTCTACT
                                   A      TGT
GAM499  TEAD2   3'  TTCAACACACTGCTTGTGCAGC 18771         A_    A  A
            G                    TTCAACACAT  CTTGT CAG TG
                                 ||||||||||  ||||| ||| ||
                                 AAGTTGTGTG  GAACA GTC GC
                                      AC    C  _
GAM499  TTC3    3'  TTCAACACACTGGTGGATG   17723         ACT  TACA
                                TTCAACACAT   TG   GATG
                                ||||||||||   ||   ||||
                                AAGTTGTGTG   AC   CTAC
                                     ____  CAC_
GAM500  ALOX15  3'  GATTTATATAATTGTGGCTA  10076        GGTT   A
                                GATTTATA    TTGT GCTA
                                ||||||||    |||| ||||
                                CTAAATAT    AACA CGAT
                                    ATT_    C
GAM500  F8A     3'  ATGGATTTAGGGCTGTG     29105         TA   T
                                ATGGATTTA  GGTT TG
                                |||||||||  |||| ||
                                TACCTAAAT  CCGA AC
                                     C_    C
GAM500  FRK     3'  ATGGCTTTACCATCATTGTAG  13011      A    AGGTT
                                ATGG TTTAT     TTGTAG
                                |||| |||||     ||||||
                                TACC AAATG     AACATC
                                  G     GTAGT
GAM500  MAPRE2  3'  TGAATGACAGTTTTGTGGCT   30694      TTATA      A
                                TGGAT     GGTTTTGT GCT
                                |||||     |||||||| |||
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                                ACTTA    TCAAAACA CGA
                                   CTG__      C
GAM500  MEOX1    3'  TGGATTTAAAAGGAGTAGCT  30403       T_  TTTT
                                TGGATTTA  AGG   GTAGCT
                                ||||||||  |||   ||||||
                                ACCTAAAT  TCC   CATCGA
                                     TT   T___
GAM500  NQO1     3'  TGGATTTATTGGTTTATCTCT  9479        A    T  AG
                                TGGATTTAT GGTTT GT  CT
                                ||||||||| ||||| ||  ||
                                ACCTAAATA CCAAA TA  GA
                                     A    _  GA
GAM500  PMP2     3'  ATAGATTAGAATTTTGTAG   15419       TATA
                                ATGGATT   GGTTTTGTAG
                                |||||||   ||||||||||
                                TATCTAA   TTAAAACATC
                                    TC__
GAM500  SERPINB5 3'  GATTTATAGGTTGCT      15280         TTGTA
                                GATTTATAGGTT    GCT
                                ||||||||||||    |||
                                CTAAATATCCAA    CGA
                                          _____
GAM500  ZNF253   3'  ATAGGTTTATAGGTTTTG   34331     A
                                ATGG TTTATAGGTTTTG
                                |||| ||||||||||||
                                TATC AAATATCCAAAAC
                                  C
GAM500  CD28     3'  CTTTTTGTTTTCTACCC    26019     CCA
                                CTTTT  TTTTCTACCT
                                |||||  ||||||||||
                                GAAAA  AAAAGATGGG
                                   AC_
GAM500  CDK7     3'  TTTTCCATTATTTGCCTTT   12211       TTCTA
                                TTTTCCATT    CCTTT
                                |||||||||    |||||
                                AAAAGGTAA    GGAAA
                                     TAAAC
GAM500  CDKN2C   5'  CTTCTCCAGAAGAGCCTTTG  38561       TTTTCTA
                                CTTTTCCA     CCTTTG
                                ||||||||     ||||||
                                GAAGAGGT     GGAAAC
                                    CTTCTC_
GAM500  HDAC7A   3'  TTTTCCATTTTCTTCCTT    32480         A
                                TTTTCCATTTTCT CCTT
                                |||||||||||| ||||
                                AAAAGGTAAAAGA GGAA
                                       A
GAM500  PPARBP   3'  CTTTTTCATTTTCTGCCC    21928     C     A
                                CTTTT CATTTTCT CCT
                                ||||| |||||||| |||
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                                GAAAA GTAAAAGA GGG
                                   A       C
GAM500  UBL3     3'  CTTTTCCATTTTTTCCTC    28266          CTA
                                CTTTTCCATTTT   CCTT
                                ||||||||||||  ||||
                                GAAAAGGTAAAA   GGAG
                                      AA_
GAM500  ZNF146   3'  CTTTTCCATATTTCTGTTTTTA 28354        _    ACC
           ATC                    CTTTTCCAT TTTCT   TTTGATC
                                |||||||||  |||||  |||||||
                                GAAAAGGTA AAAGA   AAATTAG
                                      T    CAA
GAM501  CDH11    3'  TGGCAATATCAAAGGCT     38037        ATAAG   A
                                TGGCAATAT    TAAA GCT
                                |||||||||    |||| |||
                                ACCGTTATA    GTTT CGA
                                     _____   C
GAM501  DNAH9    5'  TGGCAGACTGTGTAAAAGCT   21671      ATATATAA
                                TGGCA       GTAAAAGCT
                                |||||       |||||||||
                                ACCGT       CATTTTCGA
                                   CTGACA__
GAM501  DNAJB9   3'  TGGCAATATTTCGTTAAGT    29563        A____
                                TGGCAATAT    TAAGT
                                |||||||||    |||||
                                ACCGTTATA    ATTCA
                                      AAGCA
GAM501  GJA1     5'  GCTGATACCTCGTAAAAGCT   6730     AAT   AA_
                                GC   ATAT   GTAAAAGCT
                                ||   ||||   |||||||||
                                CG   TATG   CATTTTCGA
                                 AC_    GAG
GAM501  MAPRE1   3'  GCTACAAGGTAAAAGCTC    29524    AATA    _
                                GC    TATAAG TAAAAGCTC
                                ||    |||||| |||||||||
                                CG    ATGTTC ATTTTCGAG
                                 _____     C
GAM501  PAX3     3'  TGGCAACAGAGTGAGAGCT   30327        TATA   AAA
                                TGGCAATA    AGT   AGCT
                                ||||||||    |||   ||||
                                ACCGTTGT    TCA   TCGA
                                     C___   CTC
GAM501  PUM1     3'  TGGAAATATACACAAGGCTC  31241     C       AGTAAAA
                                TGG AATATATA      GCTC
                                ||| ||||||||      ||||
                                ACC TTATATGT      CGAG
                                  T       GTTC___
GAM501  SOS2     3'  TGGCAAATAAAAGCT       42854       TATATAA
                                TGGCAA      GTAAAAGCT
                                ||||||      |||||||||
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                                ACCGTT      TATTTTCGA
                                       _______
GAM501  WFS1    3'  TGGCAACATGCACTGGAAGCTC 25644         A  AGTAA
              C                  TGGCAATAT TA     AAGCTCC
                                 ||||||||| ||     |||||||
                                 ACCGTTGTA GT     TTCGAGG
                                       C  GACC_
GAM501  MAF     3'  TAATGTACAGCTCTCACACAAA 23838         T     G   T
                                 TAATGTAC AGCTCT TAT CAAA
                                 |||||||| |||||| ||| ||||
                                 ATTACATG TCGAGA GTG GTTT
                                       _     _  T
GAM501  TDO2    3'  TAATGTACTGCATAAAATATT  24904         A  TCT__
                                 TAATGTACT GC     GTATT
                                 ||||||||| ||     |||||
                                 ATTACATGA CG     TATAA
                                       _  TATTT
GAM502  COG5    3'  AGCAGTCTTTTGGAGTAT    26812     G       AA
                                 AGC AGTCTTTT  AGTAT
                                 ||| ||||||||  |||||
                                 TCG TCAGAAAA  TCATA
                                   _       CC
GAM502  HOXA7   3'  AGTGAGTCTCTTAAAGACGCTT 45214    C           T TA
                                 AG GAGTCTTTTAAAG A  CTT
                                 || |||||||||||| |  |||
                                 TC CTCAGAGAATTTC T  GAA
                                  A           _ GC
GAM503  APM1    3'  GAACATAGCATATGAT      22012          ACA
                                 GAATATAGCA   ATGAT
                                 ||||||||||   |||||
                                 CTTGTATCGT   TACTA
                                       A__
GAM503  CDKN2A  3'  TAAGAATATATAAAAAATGAT  38477          GCAAC
                                 TAAGAATATA     AATGAT
                                 ||||||||||     ||||||
                                 ATTCTTATAT     TTACTA
                                       ATTTT
GAM503  EGFL5   5'  AGCAGCACCACAACAATGAT   44513    AA_   A
                                 AG   TAT GCAACAATGAT
                                 ||   ||| ||||||||||
                                 TC   GTG TGTTGTTACTA
                                  GTC   G
GAM503  FGF9    5'  CAAGAATAAACAATAATGAT   12864         T    C
                                 TAAGAATA AGCAA AATGAT
                                 |||||||| ||||| ||||||
                                 GTTCTTAT TTGTT TTACTA
                                       _    A
GAM503  PTGIS   3'  AAAATATAGCAAATAAT     9666           CA
                                 AGAATATAGCAA  ATGAT
                                 ||||||||||||  |||||
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                                TTTTATATCGTT  TATTA
                                      __
GAM504  MS4A7    3'  CAAAAGCTTTTTTTTTTTTAG  34527          GCGAC
                                CAAAAGCTTTTTT    TTTTAG
                                ||||||||||||    ||||||
                                GTTTTCGAAAAAA    AAAATC
                                      AA___
GAM504  SCP2     3'  CAAAAGCTTTTTTGTTTAC   16484          CG_
                                CAAAAGCTTTTTTG  AC
                                ||||||||||||||  ||
                                GTTTTCGAAAAAAC  TG
                                      AAA
GAM504  SLC7A8   3'  CAGAAGCTTTTTGGCTTCT   29280    A      T  GA
                                CA AAGCTTTTT GC  CT
                                || |||||||| ||  ||
                                GT TTCGAAAAA CG  GA
                                 C       C  AA
GAM504  CRIM1    3'  AAAGTTACCACTATAGTATACA 32366         _  ATCGAAT
           GTC                    AAAGTTACCAC ATA      GTC
                                ||||||||||| |||      |||
                                TTTCAATGGTG TAT      CAG
                                      A  CATATGT
GAM504  SDC2     3'  AAAGTTACCATTAGAATTGTC  42558         CATAATC  _
                                AAAGTTACCA      GAAT GTC
                                ||||||||||      |||| |||
                                TTTCAATGGT      CTTA CAG
                                      AAT____   A
GAM504  VDR      3'  AAAGTTTTACATTTACAAATGT 7507       ACC   AAT
           C                     AAAGTT  ACAT  CGAATGTC
                                ||||||  ||||  ||||||||
                                TTTCAA  TGTA  GTTTACAG
                                   AA_   AAT
GAM505  TP73     5'  TCCCGGCTGGCCTGGCGCGGG  24071     ATTA __  C
                                TCTC   GC  GCC GGCGCGGG
                                ||||   ||  ||| ||||||||
                                AGGG   CG  CGG CCGCGCCC
                                  C___  AC  A
GAM506  PTP4A2   3'  TCTATATTAATGGAATCTATTG 38644         A   ATA
           T                     TCTATATTAAT GGAG  GTTGT
                                ||||||||||| ||||  |||||
                                AGATATAATTA CCTT  TAACA
                                      _   AGA
GAM507  DCN      3'  AATACAGAGCTAGTGTTTGG  39442       TA  A   CA
                                AATACAGA  CTA TGTTT  GG
                                ||||||||  ||| |||||  ||
                                TTATGTCT  GAT ACAAA  CC
                                     C_  C   __
GAM507  DLEC1    3'  CAGGTCCAGTTTCAGGG    28820    ATA  AT
                                CAG  CTA  GTTTCAGGG
                                |||  |||  |||||||||
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                                GTC   GGT  CAAAGTCCC
                                  CA_  __
GAM507  DVL3     3'  AATACAGATCTAAAGTCTGGG  20666          A   T   CA
                                AATACAGAT CTAA GTTT  GGG
                                ||||||||| |||| ||||  |||
                                TTATGTCTA GATT CAGA  CCC
                                      _   T   __
GAM507  HUS1     3'  GATGGGTATGTTTCAGGG    45001     ACTA
                                GAT   ATGTTTCAGGG
                                |||   ||||||||||
                                CTA   TACAAAGTCCC
                                  CCCA
GAM507  LAPTM5   3'  GAACAGATGTGCCTGATTTCAG 27604   T     ACTAA  _
             GG                   A ACAGAT    TG TTTCAGGG
                                | ||||||    || ||||||||
                                C TGTCTA    AC AAAGTCCC
                                 T     CACGG  T
GAM507  TERF1    3'  GATACTAAATGTGGCAGGG   32742         _  TT
                                GATACTAA TGT  CAGGG
                                |||||||| |||  |||||
                                CTATGATT ACA  GTCCC
                                     T  CC
GAM507  BACH1    5'  TGCTTCTAATTATCATCAAC   10153          C      T
                                TGCTTCTAAT TATTATT GC
                                |||||||||| ||||||| ||
                                ACGAAGATTA ATAGTAG TG
                                      _      T
GAM507  CLASP1   3'  TGTTTCTAATCCTGTTTTTCTG 42252    C       A__  A
             CAA                    TG TTCTAATCT   TT TTTGCAA
                                || |||||||||   || |||||||
                                AC AAGATTAGG   AA AGACGTT
                                 A        ACA  A
GAM507  CLCN4    3'  GCTGGGTTTTCTGTTATTTGCA 12287     TCTAA_  A
                                GCT     TCT TTATTTGCA
                                |||     ||| |||||||||
                                CGA     AGA AATAAACGT
                                  CCCAAA  C
GAM507  GPR17    3'  CTTCTGGGTCATTTGCA     23619       AATCTA
                                CTTCT     TTATTTGCA
                                |||||     |||||||||
                                GAAGA     AGTAAACGT
                                   CCC___
GAM507  NCKAP1   3'  TGCTTCTAATACTAAGCA    30260          _  TTATTT
                                TGCTTCTAAT CTA     GCA
                                |||||||||| |||     |||
                                ACGAAGATTA GAT     CGT
                                      T  T_____
GAM507  SPS2     3'  TGCTTCTAATTTTTTTCATTTT 29305          CTA__     _
             GCAA                    TGCTTCTAAT    TTATTT GCAA
                                ||||||||||    |||||| ||||
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                                ACGAAGATTA    AGTAAA CGTT
                                      AAAAA     A
GAM507  TEM7R   3'  TTCTGATCCCTTTGCAAC   37271     A   ATTA
                                TTCT ATCT   TTTGCAAC
                                |||| ||||   ||||||||
                                AAGA TAGG   AAACGTTG
                                  C   G___
GAM508  GSBS    3'  GGTTGACTCCCCCAGCTCA   45000       GCG_
                                GGTTGACT   CAGCTCA
                                ||||||||   |||||||
                                CCAACTGA   GTCGAGT
                                     GGGG
GAM508  INHBA   3'  TTGGTTGATTCAAGCTCAC   13539       CTG  C
                                TTGGTTGA   CG AGCTCAC
                                ||||||||   || |||||||
                                AACCAACT   GT TCGAGTG
                                     AA_  _
GAM508  ITGA5   3'  TTGGTTGATGAGCTCA     41504       C  CGC
                                TTGGTTGA TG   AGCTCA
                                |||||||| ||   ||||||
                                AACCAACT AC   TCGAGT
                                      _  ___
GAM508  MYCL2   5'  TTGCTTGCTCACGCAGCT   23914    G   AC
                                TTG TTG  TGCGCAGCT
                                ||| |||  |||||||||
                                AAC AAC  GTGCGTCGA
                                  G   GA
GAM508  PRKY    3'  TTGGTTGACTGCAGCCTCC   15715         _  AG
                                TTGGTTGACTGC GC  CT
                                ||||||||||||| ||  ||
                                AACCAACTGACG CG  GG
                                       T  GA
GAM508  SLC26A4 3'  TGGTGATCAGTGCAGCTCA   7767      T  CTGC_
                                TGGT GA    GCAGCTCA
                                |||| ||    ||||||||
                                ACCA CT    CGTCGAGT
                                  _  AGTCA
GAM508  SLC9A6  3'  TTAGTTGACTCAAGCT     26835       G  C
                                TTGGTTGACT CG AGCT
                                |||||||||| || ||||
                                AATCAACTGA GT TCGA
                                      _  _
GAM508  SPTB    3'  GGCGGGGCTGCGCAGCTCA   7381     TGA_
                                GGT   CTGCGCAGCTCA
                                |||   ||||||||||||
                                CCG   GACGCGTCGAGT
                                  CCCC
GAM509  DUSP6   3'  TTAGAAAAGAGCACAATTTTC 42330       T   A TG
                                TTAGAAAA AGC A  ATTTTC
                                |||||||| ||| |  ||||||
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                                AATCTTTT TCG T  TAAAAG
                                     C   _ GT
GAM509  EDAR     3'  AAAGATATGACTGATTTTCCC  35298     A   GCAA
                                GAA ATA    TGATTTTCCC
                                ||| |||    ||||||||||
                                TTT TAT    ACTAAAAGGG
                                  C   ACTG
GAM509  ESRRBL1  3'  TTAAAAAATGCTTATTTTCCC  32845         A  AATG
                                TTAGAAAAT GC    ATTTTCCC
                                ||||||||| ||    ||||||||
                                AATTTTTTA CG    TAAAAGGG
                                     _  AA__
GAM509  GCNT2    5'  TAGAAAATAGCTTCTGTTTTCC 11251          AA_  A
                                TAGAAAATAGC   TG TTTTCC
                                ||||||||||   || ||||||
                                ATCTTTTATCG   AC AAAAGG
                                      AAG  _
GAM509  GPR30    5'  TTAGAAAGAAGCGTGATTCTC  11320        AT   AA
                                TTAGAAA  AGC  TGATTTTC
                                |||||||  |||  ||||||||
                                AATCTTT  TCG  ACTAAGAG
                                     CT   C_
GAM509  HLCS     3'  AGAAAATATCTGAATTTTCCC  7633         GCAA  _
                                AGAAAATA    TGA TTTTCCC
                                ||||||||    ||| |||||||
                                TCTTTTAT    ACT AAAAGGG
                                     AG__   T
GAM509  KCNAB1   3'  AGAAAATAGAATGGATTTTC  41399         C   _
                                AGAAAATAG AATG ATTTTC
                                ||||||||| |||| ||||||
                                TCTTTTATC TTAC TAAAAG
                                     _   C
GAM509  KCNJ1    5'  TTAGAGAATGCAATGAT     6893       A  A
                                TTAGA AAT GCAATGAT
                                ||||| ||| ||||||||
                                AATCT TTA CGTTACTA
                                   C  _
GAM509  LARGE    3'  TAGAGGCAGCTGATTTTCC   39513     AAA   AA
                                TAGA   TAGC  TGATTTTCC
                                ||||   ||||  |||||||||
                                ATCT   GTCG  ACTAAAAGG
                                   CC_   __
GAM509  NKX3A    3'  GAAAATACCACTTGATTTTCCC 26112       G  A_
                                GAAAATA CA  TGATTTTCCC
                                ||||||| ||  ||||||||||
                                CTTTTAT GT  ACTAAAAGGG
                                     G  GA
GAM509  NR4A2    3'  TTAGGAAATAGCAACAGTTTT  26174      A        GA
                                TTAG AAATAGCAAT  TTTT
                                |||| ||||||||||  ||||
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                                AATC TTTATCGTTG  AAAA
                                  C        TC
GAM509  PIG8    3'  GAAAATAGCTTTTTC      22187         AATGA
                                GAAAATAGC    TTTTC
                                |||||||||    |||||
                                CTTTTATCG    AAAAG
                                     A____
GAM509  PIGA    3'  GAAAATAGCCTTTTCC     33831         AATGA
                                GAAAATAGC    TTTTCC
                                |||||||||    ||||||
                                CTTTTATCG    AAAAGG
                                     G____
GAM509  PIK3C2B 3'  TTAGAAAATACAATTC     15297         G   GATTT
                                TTAGAAAATA CAAT    TC
                                |||||||||| ||||    ||
                                AATCTTTTAT GTTA    AG
                                     _  _____
GAM509  PKNOX1  3'  TTAGAAAATGGCAGCGCTATTC 21314         A  A  ATT
          C                      TTAGAAAAT GCA TG   TTCC
                                |||||||| ||| ||   ||||
                                AATCTTTTA CGT GC   AAGG
                                     C  C  GAT
GAM509  PNN     3'  TAGAAAATAGCAAATGATTTT  43402          _
                                TAGAAAATAGCAA TGATTTT
                                |||||||||||| |||||||
                                ATCTTTTATCGTT ACTAAAA
                                       T
GAM509  RU2     3'  AGAAAATAGTACATGCTTTCC  32289        CA_  A
                                AGAAAATAG   ATG TTTTCC
                                |||||||||   ||| ||||||
                                TCTTTTATC   TAC GAAAGG
                                     ATG  _
GAM509  RXRB    3'  AAAAATAGCAGATCGGTTCC   35038         AT   __
                                GAAAATAGCA  GATT  TTCC
                                ||||||||||  ||||  ||||
                                TTTTTATCGT  CTAG  AAGG
                                     __   CC
GAM509  SCA1    3'  TTAGAAAATAGAATATGAATTC 7299          CA_   T
                                TTAGAAAATAG   ATGA TTT
                                ||||||||||   |||| |||
                                AATCTTTTATC   TACT AAG
                                      TTA    T
GAM509  SUFU    3'  GAAAACAGTAGCACCCCTCCC  32088        CAATGA
                                GAAAATAG     TTTTCCC
                                ||||||||     |||||||
                                CTTTTGTC     GGGAGGG
                                    ATCGTG
GAM509  TBX3    3'  TAGGAAATAGCACTTTCC    32438     A      ATGA
                                TAG AAATAGCA    TTTTCC
                                ||| ||||||||    ||||||
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                                ATC TTTATCGT   GAAAGG
                                  C      ____
GAM510  IRAK4   3' GCTAAGTGTTGATATGGTGG  41459     A__  CT
                                GCTAA  TTG  TATGGTGG
                                |||||  |||  ||||||||
                                CGATT  AAC  ATACCACC
                                   CAC  T_
GAM510  PCDH9   5' TTAAAGCTGAATTCTTTGG   44414      A  G  A
                                TTAAAGCT AATT CTT TGG
                                |||||||| |||| ||| |||
                                AATTTCGA TTAA GAA ACC
                                     C   _  _
GAM511  ENPP3   3' TCTTTATTAATTGTGCAT    22713        A_
                                TCTTTGTTAATT  GCGT
                                ||||||||||||  ||||
                                AGAAATAATTAA  CGTA
                                      CA
GAM512  CABC1   3' TATCTGTTCATGTTTCTG    33689        _ CC
                                TATCTGTTCA GT  CTG
                                |||||||||| ||  |||
                                ATAGACAAGT CA  GAC
                                     A  AA
GAM512  CIT     3' TGTTCAGTGCTACAGACT    43064       CC   CA
                                TGTTCAGT  CTGC  ACT
                                ||||||||  ||||  |||
                                ACAAGTCA  GATG  TGA
                                     C_   TC
GAM512  COG5    3' TATGTGTTTAACTGCCAACTA  26813    C   CAGTCC
                                TAT TGTT     CTGCCAACTA
                                ||| ||||     ||||||||||
                                ATA ACAA     GACGGTTGAT
                                  C   ATT___
GAM512  DNMT2   3' TATCTGTTCAAGTCCCTGC   20631        _
                                TATCTGTTCA GTCCCTGC
                                |||||||||| ||||||||
                                ATAGACAAGT CAGGGACG
                                     T
GAM512  FBXL7   3' CATCTGTCTCTGCCAGCT    29395       CAGTCC    A
                                TATCTGTT     CTGCCA CT
                                ||||||||     |||||| ||
                                GTAGACAG     GACGGT GA
                                     A_____     C
GAM512  FGF2    3' TATCTGTTCATAGTTAACT   12843        GTCCCTGCC
                                TATCTGTTCA       AACT
                                ||||||||||       ||||
                                ATAGACAAGT       TTGA
                                      ATCAA____
GAM512  MAP1B   3' TGTTCAGCGACTTAACTA    25400       CC  GCC
                                TGTTCAGT  CT   AACTA
                                ||||||||  ||   |||||
```

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                                ACAAGTCG  GA   TTGAT
                                    CT  A__
GAM512  PTPN18   3'  TATCTGTCTAGTAATCTGACTA 30771       TC   CC_  CCA
                                TATCTGT  AGT   CTG   ACTA
                                |||||||  |||   |||   ||||
                                ATAGACA  TCA   GAC   TGAT
                                    GA   TTA  ____
GAM512  PTPRM    3'  TATCTGTTAGTCCTGGAAAGCT 15973        C    C  CC  _
          A                      TATCTGTT AGTCC TG  AA CTA
                                |||||||| ||||| ||  || |||
                                ATAGACAA TCAGG AC  TT GAT
                                    _    _  CT  C
GAM512  RARB     3'  TATCTTTTCAGTCCAAAAACTA 32061      G      CTGCC
                                TATCT TTCAGTCC     AACTA
                                ||||| ||||||||     |||||
                                ATAGA AAGTCAGG     TTGAT
                                   A       TTT__
GAM512  TNFRSF6  3'  TATCTGCTTCAGTTTATAACTA 6223         _   CCCTGCC
                                TATCTGTT CAGT      AACTA
                                |||||||| ||||      |||||
                                ATAGACGA GTCA      TTGAT
                                    A   AATA___
GAM512  ZNF36    3'  CTGTTCAGCAGCTAACT     45292         CCCT  C
                                CTGTTCAGT   GC AACT
                                |||||||||   || ||||
                                GACAAGTCG   CG TTGA
                                     T___  A
GAM513  ADAM12   5'  TTAAAAAAGTTTCCCCCCGTGT 18482        A    GTG
                                TTGAAAAA TTTTT   TCCGTGT
                                |||||||| |||||   |||||||
                                AATTTTTT AAAGG   GGGCACA
                                    C    G__
GAM513  RRAS2    3'  TTAAAAAAAGAGCATGTCTGTG 29312        TTTTT    C
          T                      TTGAAAAAA    GTGTC GTGT
                                |||||||||    ||||| ||||
                                AATTTTTTTT    TACAG CACA
                                     CTCG_    A
GAM514  HNF3A    3'  TCTTGAGGGCAATTCCT     40732    A   AC  AA
                                TC TGA  GG  CGATTCCT
                                || |||  ||  ||||||||
                                AG ACT  CC  GTTAAGGA
                                 A   __  C_
GAM514  CCRL1    3'  ACTTGTGTAGATTTGTATAAG  32428       T    AGA
                                ACTTGT GTAGG   TTGTATAAG
                                ||||||  |||||  |||||||||
                                TGAACA CATCT   AACATATTC
                                   _    A__
GAM514  COL4A5   3'  ACTTGATGTAGGAATATAA    37895      T     GATT
                                ACTTG TGTAGGA    GTATAA
                                |||||  |||||||    ||||||
```

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                                TGAAC ACATCCT    TATATT
                                  T     ____
GAM514  TXNRD1   3'  ACTTGTTTTGGGAATATAT   17769       GTA  A  T
                                ACTTGTT   GG GA TGTAT
                                |||||||   || || |||||
                                TGAACAA   CC CT ATATA
                                   AA_  _  T
GAM514  ZNF253   3'  ACTTGTTATAGGTTTATA    34330          AGA
                                ACTTGTTGTAGG   TTGTA
                                ||||||||||||   |||||
                                TGAACAATATCC   AATAT
                                      A__
GAM515  CELSR1   3'  CGTTCTGTTAAAAACCTCC   30651      C       G
                                CGTTC GTTAGAAAC TTT
                                ||||| ||||||||| |||
                                GCAAG CAATTTTTG AGG
                                   A        G
GAM515  DNAJB9   3'  ATTTCGTTAAGTTTTCAA    29558     C     AAAC
                                GTT CGTTAG    GTTTTCAA
                                ||| ||||||    ||||||||
                                TAA GCAATT    CAAAAGTT
                                  A     ____
GAM515  EHD2     3'  GTTCCGTTCAGAGGCCCCTCCC 31137        _    AACG_  TT
          A                      GTTCCGT TAGA     TT  CA
                                |||||||  ||||    ||  ||
                                CAAGGCA GTCT     GA  GT
                                   A    CCGGG  GG
GAM515  GRB10    3'  GTTCCTTAGGGAACACTTCA  23665      G    AAACGT
                                GTTCC TTAG      TTTCA
                                |||||  ||||     |||||
                                CAAGG AATC      GAAGT
                                  _    CCTTGT
GAM515  KERA     3'  GTTTTGTTAGAAAGCATTCAA  28155     CC       C  T
                                GTT  GTTAGAAA GT TTCAA
                                |||  |||||||| || |||||
                                CAA  CAATCTTT CG AAGTT
                                  AA       _  T
GAM515  ZHX1     3'  GCCCCAAAACGTTTTCAA    28517      GTTA
                                GTTCC    GAAACGTTTTCAA
                                |||||    ||||||||||||||
                                CGGGG    TTTTGCAAAAGTT
                                         _____
GAM516  DBN1     5'  CCCCGCCCTCGCTTTCCTTTG  38927        ___ AC_
                                CCCCGCC   G   TCCTTTG
                                |||||||   |   |||||||
                                GGGGCGG   C   AGGAAAC
                                   GAG GAA
GAM516  FHL2     5'  ACCCCGCCGTGTCATTTG    11103         AC  C
                                ACCCCGCCG  TC TTTG
                                |||||||||  || ||||
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                                TGGGGCGGC  AG AAAC
                                     AC  T
GAM516  MMP11    3'  TACCCCTCCCCATTTG      25539       G  GACT  _
                                TACCCC CC    CC TTTG
                                |||||| ||    || ||||
                                ATGGGG GG    GG AAAC
                                   A _____  T
GAM516  POU5F1   3'  CCCCTGCCCCCACCCTTTG    15469      _  G__  T
                                CCCC GCC   AC CCTTTG
                                |||| |||   || ||||||
                                GGGG CGG   TG GGAAAC
                                  A  GGG  _
GAM516  RANBP3   3'  CCCCGCTTCATTCCCTTTG    28754       __  AC
                                CCCCGC  CG  TCCTTTG
                                ||||||  ||  |||||||
                                GGGGCG  GT  GGGAAAC
                                   AA  AA
GAM516  TGIF     5'  CCCCTCTCCGCTCCTTTG     17497      G__  A
                                CCCC   CCG CTCCTTTG
                                ||||   ||| ||||||||
                                GGGG   GGC GAGGAAAC
                                  AGA  _
GAM516  TRPC5    5'  TACCTTGGCTTCCCCTTTG    29770      CC_  CGA
                                TACC   GC   CTCCTTTG
                                ||||   ||   ||||||||
                                ATGG   CG   GGGGAAAC
                                  AAC  AA_
GAM517  BTK      5'  CGCAGCAGACACTGGCCC     6295          ___
                                CGCAGCAGATA   GCCC
                                ||||||||||   ||||
                                GCGTCGTCTGT   CGGG
                                      GAC
GAM517  DLG5     5'  CCCGCAGCAGCTGCCC      44453    G       ATA
                                CC CGCAGCAG   GCCC
                                || ||||||||   ||||
                                GG GCGTCGTC   CGGG
                                 _      GA_
GAM517  FBXW1B   5'  CCGCGCAGCAGCGAACGGCCC  37988          ATA___
                                CCGCGCAGCAG     GCCC
                                ||||||||||      ||||
                                GGCGCGTCGTC     CGGG
                                      GCTTGC
GAM517  GALR1    5'  CCGCGCAGGTGGAAAGACCC   11198        CA_  T  _
                                CCGCGCAG   GA AG CCC
                                ||||||||   || || |||
                                GGCGCGTC   CT TC GGG
                                     CAC  T  T
GAM517  GRB10    5'  CCGCGCAGTCGGAGCACCC    23651        CA_  TA
                                CCGCGCAG   GA  GCCC
                                ||||||||   ||  ||||
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                                GGCGCGTC  CT  TGGG
                                    AGC  CG
GAM517  GTF2IRD1  5'  CCGCGCAACACCACCC     32252         GATA
                                CCGCGCAGCA   GCCC
                                ||||||||||   ||||
                                GGCGCGTTGT   TGGG
                                     GG__
GAM517  HIP12     3'  CCACGCAGCTGGAGGGCC    42395         A_  TA
                                CCGCGCAGC  GA  GCC
                                |||||||||  ||  |||
                                GGTGCGTCG  CT  CGG
                                     AC  CC
GAM517  HS3ST3A1  5'  CCGCGCAGGATCCCTGCC    25804         CA  A___
                                CCGCGCAG  GAT   GCC
                                ||||||||  |||   |||
                                GGCGCGTC  CTA   CGG
                                    __  GGGA
GAM517  JAK2      5'  CCGCAGCAGCCCTCAGCCC   22475     _    AGA
                                CCGC GCAGC   TAGCCC
                                ||||  |||||  ||||||
                                GGCG CGTCG   GTCGGG
                                  T    GGA
GAM517  KCNA7     5'  CGCGCGTAAAAATAGCCC    36651      AGC_
                                CGCGC   AGATAGCCC
                                |||||   |||||||||
                                GCGCG   TTTATCGGG
                                  CATT
GAM517  LENG4     3'  CCGCACAGCAGCGCACCC    35880         ATA
                                CCGCGCAGCAG  GCCC
                                ||||||||||   ||||
                                GGCGTGTCGTC  TGGG
                                      GCG
GAM517  MADD      5'  CCGCGAGGACAGCCC       39064      C  CA
                                CCGCG AG  GATAGCCC
                                |||||  ||  ||||||||
                                GGCGC TC  CTGTCGGG
                                  _  __
GAM517  MOG       5'  CCCGCAGAAACAGCCC      14609    G    C
                                CC CGCAG AGATAGCCC
                                ||  |||||  |||||||||
                                GG GCGTC TTTGTCGGG
                                  _    _
GAM517  PDE9A     3'  CCGCGCAGCTCGGCCAGCCC  15163         AGA__
                                CCGCGCAGC    TAGCCC
                                |||||||||    ||||||
                                GGCGCGTCG    GTCGGG
                                     AGCCG
GAM517  POLR2I    5'  CGCGCAGCCCGCGCAGCCC   26355         AGA__
                                CGCGCAGC    TAGCCC
                                ||||||||    ||||||
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                                GCGCGTCG    GTCGGG
                                    GGCGC
GAM517  PROC    5'  CCGCCATGACAGCCC      7188      G  GCA
                                CCGC CA   GATAGCCC
                                |||| ||   ||||||||
                                GGCG GT   CTGTCGGG
                                  _  A__
GAM517  RAB4A   5'  CCGCGCAGGCGCAGGGCCC   21347       ___   ATA
                                CCGCGCA   GCAG   GCCC
                                |||||||   ||||   ||||
                                GGCGCGT   CGTC   CGGG
                                    CCG    C__
GAM517  RAP1GA1  3'  CCTGCAGAGACAGCCC     16165    GC    C
                                CC  GCAG AGATAGCCC
                                ||  |||| |||||||||
                                GG  CGTC TCTGTCGGG
                                 A_   _
GAM517  SDC1    3'  CCACCAGACAGATAGTCC    16502     G  _     _
                                CCGC CAG CAGATAG CC
                                |||| ||| ||||||| ||
                                GGTG GTC GTCTATC GG
                                  _  T      A
GAM517  SIRT3   5'  CCGCGCAGTCCGAGGAGTCC  29261        CA_  T_  _
                                CCGCGCAG   GA  AG CC
                                ||||||||   ||  || ||
                                GGCGCGTC   CT  TC GG
                                    AGG  CC  A
GAM517  TNFRSF4  3'  CCGCCCAGCAGACCC      17762     G     ATA
                                CCGC CAGCAG   GCCC
                                |||| ||||||   ||||
                                GGCG GTCGTC   TGGG
                                  G     ___
GAM517  TRIM9   5'  CCGCGCAGCACTGGCCC     31557         GATA
                                CCGCGCAGCA    GCCC
                                ||||||||||    ||||
                                GGCGCGTCGT    CGGG
                                     GAC_
GAM517  UCP1    5'  CCGGGCAGCAAACCC       34835     C      ATA
                                CCG GCAGCAG   GCCC
                                ||| |||||||   ||||
                                GGC CGTCGTT   TGGG
                                  C      ___
GAM518  BUB3    3'  AAAGACCCTTCTCTGTA     21799     C   GTGCGG
                                AAA ACCC     TCTCTGTA
                                ||| ||||     ||||||||
                                TTT TGGG     AGAGACAT
                                  C   A_____
GAM518  CACNG3  5'  ACCCAGAGAGGTCTCTGT    27228      TGC_
                                ACCCG    GGTCTCTGT
                                |||||    |||||||||
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                                TGGGT   CCAGAGACA
                                  CTCT
GAM518  FCMD    3'  CCCTACAAAATCTCTGTAT   27515    G   __
                                CCC TGCG  GTCTCTGTAT
                                ||| ||||  ||||||||||
                                GGG ATGT  TAGAGACATA
                                  _   TT
GAM518  KCNA6   3'  AACACCAGTGCCTCTGT    13801      C   GGT
                                AACACC GTGC   CTCTGT
                                |||||| ||||   ||||||
                                TTGTGG CACG   GAGACA
                                   T   ___
GAM518  MDS1    5'  ACACACTCACTCTCTGTA    22557     CCGTG  G
                                ACAC    CG TCTCTGTA
                                ||||    || ||||||||
                                TGTG    GT AGAGACAT
                                  TGA__  G
GAM518  NEBL    3'  ACACCAGATCATCTCTGTAT   26896     CGTG  G
                                ACACC   CG TCTCTGTAT
                                |||||   || |||||||||
                                TGTGG   GT AGAGACATA
                                   TCTA  _
GAM518  RFNG    3'  AAACATCTCTGTGGTCCCAGT  44765     CCCG  C    T
                                AAACA   TG GGTCTC GT
                                |||||   || |||||| ||
                                TTTGT   AC CCAGGG CA
                                   AGAG  A    T
GAM518  SIL     3'  ACACCCTGTCCCTGTA     16724      GTGCG
                                ACACCC    GTCTCTGTA
                                ||||||    |||||||||
                                TGTGGG    CAGGGACAT
                                   A____
GAM518  TBXA2R  5'  GAACCCCTGGGCACATTTCTGT 9852   C   G  C   C____
            AT                    A ACCC TG GGT    TCTGTAT
                                | |||| || |||    |||||||
                                C TGGG AC CCG    AGACATA
                                 T   G  _   TGTAA
GAM518  TNXB    5'  CCACTGCTGTTGGTTTCTGT   37151    _  ____   C
                                CCG TGC   GGT TCTGT
                                ||| |||   ||| |||||
                                GGT ACG   CCA AGACA
                                  G   ACAA   A
GAM518  VSNL1   5'  AAACGCTTAAGCCGTCTCTGT  18034     ACCCGT  G
                                AAAC     GC GTCTCTGT
                                ||||     || ||||||||
                                TTTG     CG CAGAGACA
                                  CGAATT  G
GAM519  APPL    3'  TTCAAATCCAATTCTAAAGT   29016     T   TG A
                                TTCAA ATC  A TCTAAAGT
                                ||||| |||  | ||||||||
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                                AAGTT TAG  T AGATTTCA
                                  _  GT A
GAM519  PCDHB4   3'  TTCAGATAAATTTATTACTG  33198            A
                                TTCGGATAAATTTATTA TG
                                |||||||||||||||| ||
                                AAGTCTATTTAAATAAT AC
                                      G
GAM519  TCP11    3'  AGAAGTTTATTAATGAATG   33069    TAAA
                                GGA   TTTATTAATGAATG
                                |||   ||||||||||||||
                                TCT   AAATAATTACTTAC
                                  TC__
GAM520  DAZL     3'  TTGAATCTGTTTTGC      42783          CCTCCA
                                TTGAATCTGTT     TGC
                                ||||||||||     |||
                                AACTTAGACAA     ACG
                                      A_____
GAM520  FBXL5    5'  TTCAATCTGCTCATGCATT   37950    G       CTCC
                                TT AATCTGTTC   ATGCATT
                                || |||||||||   |||||||
                                AA TTAGACGAG   TACGTAA
                                 G       _____
GAM520  MAP2     3'  TTGAATCTTTCTTCCCATT   36507        G  C  ATG
                                TTGAATCT TTC TCC  CATT
                                |||||||| ||| |||  ||||
                                AACTTAGA AAG AGG  GTAA
                                     _  A  ___
GAM520  IL4      5'  CGATTTGCAGTGACAATGT   8233          TTT
                                CGATTTGCAGT  CAGTGT
                                ||||||||||  ||||||
                                GCTAAACGTCA  GTTACA
                                      CT_
GAM520  PMX1     3'  TAGCCATGGCGCTTTTCAGTGT 35517       ATT  AG
                                TAGCCG  TGC  TTTTCAGTGT
                                ||||||  |||  ||||||||||
                                ATCGGT  GCG  AAAAGTCACA
                                   ACC  __
GAM521  MMP25    3'  TTCGTTTTTATTGTCCTGAGT  35395      G    CAA
                                TTCGT TTTATT  TTCTGAGT
                                ||||| ||||||  ||||||||
                                AAGCA AAATAA  AGGACTCA
                                   A     C__
GAM521  NR1I2    5'  TGTCTAAGTAATTCTGAGT   19332       TTC
                                TGTTTA  AATTCTGAGT
                                ||||||  ||||||||||
                                ACAGAT  TTAAGACTCA
                                   TCA
GAM521  TOX      3'  TGTCTGTTTAATTCTGAGT   31274      A  C
                                TGTTT TT AATTCTGAGT
                                ||||| || ||||||||||
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                                ACAGA AA TTAAGACTCA
                                  C  A
GAM521  TYROBP   3'  TTCATGTTTATTTTAGGAGAGT 17777          CAATTCT
           A                     TTCGTGTTTATT      GAGTA
                                 ||||||||||||      |||||
                                 AAGTACAAATAA      CTCAT
                                       AATCCT_
GAM521  COG7     3'  TCAGTAATTCACACTCCGCATG 42660     C    G    A TT  C
           GT                     TCAG AATT ACAC T  TA GGT
                                 |||| |||| |||| |  || |||
                                 AGTC TTAA TGTG G  GT CCA
                                   A    G    A GC  A
GAM522  BVES     3'  CAGCATAAGTTTGGCCC     42926          TATTT
                                 CAGCATAAGTT    TGGTCT
                                 ||||||||||     ||||||
                                 GTCGTATTCAA    ACCGGG
                                        _____
GAM522  GPR87    5'  TTCAGCATAGGTTATTCCTGGT 35799         A   TA
                                 TTCAGCATA GTT  TTTTGGT
                                 |||||||| |||  |||||||
                                 AAGTCGTAT CAA  AGGACCA
                                      C   TA
GAM522  MAD2L1   3'  TTCAGTAAGTATCATTTTGGT  14313      CA    _
                                 TTCAG  TAAGT TTATTTTGGT
                                 |||||  ||||| ||||||||||
                                 AAGTC  ATTCA AGTAAAACCA
                                    __    T
GAM522  PDGFRA   3'  TTCAGCACAGGTTTATGCCT   26290         A     TTTG
                                 TTCAGCATA GTTTAT    GTCT
                                 |||||||| ||||||    ||||
                                 AAGTCGTGT CAAATA    CGGA
                                      C     _____
GAM522  ANK1     3'  TCTCCTCCTGTGTGCATGGCAG 33875      T       CG  C
           A                     TCTC CTCCTGTGT  AT GCAGA
                                 |||| |||||||||  || |||||
                                 AGAG GAGGACACA  TA CGTCT
                                   _       CG  C
GAM522  ASTN     3'  TCTCTCTCTGTGAGCA      42952         C    TCGATC
                                 TCTCTCTC TGTG     GCA
                                 |||||||| ||||     |||
                                 AGAGAGAG ACAC     CGT
                                      _   T_____
GAM522  CISH     3'  TCTCTCCTCTCATGTGCAG   30028         ___    CGATC
                                 TCTCTCCT   GTGT    GCAG
                                 ||||||||   ||||    ||||
                                 AGAGAGGA   TACA    CGTC
                                      GAG   ______
GAM522  CLECSF5  3'  TCTCTCTCTTATGCACCAAGCA 29930         C__  TG    TC
           GA                    TCTCTCTC   TG  TCGA  GCAGA
                                 ||||||||   ||  ||||  |||||
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                                AGAGAGAG  AC  GGTT  CGTCT
                                    AAT  GT   __
GAM522  F2RL2    5'  CTCTCCTGTGCCGTGCAG    19910          ATC
                                CTCTCCTGTGTCG  GCAG
                                ||||||||||||  ||||
                                GAGAGGACACGGC  CGTC
                                      A__
GAM522  LY95     5'  TCCTTTTCCTGTGCGCTCG   22101    CTC     T  A
                                TCT  TCCTGTG CG TCG
                                |||  ||||||| || |||
                                AGG  AGGACAC GC AGC
                                  AAA      _ G
GAM522  PCTK1    5'  TCTCCTCCTGTTCGCCGCAG  37480     T     G  A
                                TCTC CTCCTGT TCG TCGCAG
                                |||| ||||||| ||| ||||||
                                AGAG GAGGACA AGC GGCGTC
                                  _     _  _
GAM522  WHSC1    3'  TCGCTCTCCTGTGTTTCTCG  39384    T        CGA
                                TC CTCTCCTGTGT  TCG
                                || ||||||||||  |||
                                AG GAGAGGACACA  AGC
                                 C         AAG
GAM523  GRB10    3'  TACCACAGTGACACCTTTT   23666       G__
                                TACCACAG  TACCTTTT
                                ||||||||  ||||||||
                                ATGGTGTC  GTGGAAAA
                                    ACT
GAM523  TPM1     3'  ACCACAGGGGGACCTTTT    7481        T__
                                ACCACAGG  ACCTTTT
                                ||||||||  |||||||
                                TGGTGTCC  TGGAAAA
                                    CCC
GAM524  PPEF2    3'  GAAGATTGTGAGGTGGGG    26402        ATA  TTC
                                GAAGATTGT  AG  GGGG
                                |||||||||  ||  ||||
                                CTTCTAACA  TC  CCCC
                                    C__  CA_
GAM524  PPP1R2   3'  TAGAAGATTGTGTGCG     26422         ATAA  T
                                TAGAAGATTGT   GT CG
                                ||||||||||   || ||
                                ATCTTCTAACA   CA GC
                                      ____  C
GAM524  FGFRL1   3'  TCCAGGCAGCATATCTGT    34917      TCTA
                                TCCAG   CATATCTGT
                                |||||   |||||||||
                                AGGTC   GTATAGACA
                                  CGTC
GAM524  FGFRL1   3'  CATGTCCAGACAGCATATCTGT 34902    GA    TCTA
                                CA  TCCAG   CATATCTGT
                                ||  |||||   |||||||||
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                                GT  AGGTC    GTATAGACA
                                 AC     TGTC
GAM524  MAP3K7IP1 3'  CACAGGTCCAGTCTGCAC    25921       A       A
                                TACAG TCCAGTCT CAT
                                ||||| |||||||| |||
                                GTGTC AGGTCAGA GTG
                                   C       C
GAM524  PMCHL1    3'  GATCCAGTCTCCTG        36668          ACATA
                                GATCCAGTCT    TCTG
                                ||||||||||    ||||
                                CTAGGTCAGA    GGAC
                                      _____
GAM524  SERPINB13 3'  GATTTGCCACAATATCTGT    29622     CCA T    _
                                GAT   G CTACA TATCTGT
                                |||   | ||||| |||||||
                                CTA   C GGTGT ATAGACA
                                  AA_ _    T
GAM525  FLT1      3'  CAATTTTCAGTGCTATTTTAAT 12906        G   T     C
              G                  CAATTTTT AGT CTATTT AATG
                                 |||||||| ||| |||||| ||||
                                 GTTAAAAG TCA GATAAA TTAC
                                      _  C     A
GAM525  NFE2L3    3'  CAATTCTTGAAGCAGTTTCAAT 20183          _  TCTA
              G                  CAATTTTTGA GT    TTTCAATG
                                 |||||||||| ||    ||||||||
                                 GTTAAGAACT CG    AAAGTTAC
                                       T  TC__
GAM526  AGL       5'  AATGCTGTATTACA        8485          TTAA
                                AATGCTGTAT    TACA
                                ||||||||||    ||||
                                TTACGACATA    ATGT
                                      _____
GAM526  CAV1      3'  TGCTGTATTAGCAACT      11998         TAATA
                                TGCTGTATT     CAACT
                                |||||||||     |||||
                                ACGACATAA     GTTGA
                                      TC____
GAM526  CLCA2     3'  CAATGCATTTTAATACA     27222       TGTA
                                TAATGC    TTTAATACA
                                ||||||    |||||||||
                                GTTACG    AAATTATGT
                                   TA__
GAM526  GABRR1    3'  TAATGCTGTGTATTCAATA   13040         __
                                TAATGCTGT  ATTTAATA
                                |||||||||  ||||||||
                                ATTACGACA  TAAGTTAT
                                      CA
GAM526  PTTG1IP   3'  CAATGCTATTTAATACAA    20280         AT
                                TAATGCTGT  TTAATACAA
                                |||||||||  |||||||||
```

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                                GTTACGATA  AATTATGTT
                                          __
GAM526  XK      3'  AATGCTGTATTTGACAA     34356          AAT
                                AATGCTGTATTT   ACAA
                                ||||||||||||  ||||
                                TTACGACATAAA   TGTT
                                      C__
GAM527  DEFA4    3'  TGAAGCTAACACCACCGATGA  12563   A   AT_      C
                                A GAGT   CGCCACCGA GA
                                | ||||  ||||||||| ||
                                A TTCG   GTGGTGGCT CT
                                 C   ATT       A
GAM527  HNF3A    3'  TAAGAGTATTGCCACAGA    40731        C    C
                                TAAGAGTAT GCCAC GA
                                ||||||||| ||||| ||
                                ATTCTCATA CGGTG CT
                                      A    T
GAM527  XRCC4    5'  AGAGTATCAGCTACTTCCGCCG 35425       _  C  CGA  A
                                AGAGTATC GC AC   CG CG
                                |||||||| || ||   || ||
                                TCTCATAG CG TG   GC GC
                                     T  A  AAG  G
GAM527  GPR30    5'  CTGCCGTCCAGATGTTGGTGGC 11308       GTC  C  C
                                CTGCCGTC   GT GT GGTGGC
                                ||||||||   || || ||||||
                                GACGGCAG   TA CA CCACCG
                                     GTC  _  A
GAM528  AAAS     3'  CAAAAGGAAAACTTATTT    31825     T
                                CAAA GGAAAATTTGTTT
                                |||| ||||||||||||
                                GTTT CCTTTTGAATAAA
                                  T
GAM528  FGFR1    3'  CAAATGGAATGTTCTAT     31929        AATT
                                CAAATGGAA    TGTTTTAT
                                |||||||||   ||||||||
                                GTTTACCTT    ACAAGATA
                                          ____
GAM528  HOXD4    3'  CAAATAGAAAATTTGTCCT   31167
                                CAAATGGAAAATTTGTTTT
                                ||||||||||||||||||
                                GTTTATCTTTTAAACAGGA

GAM528  NYX      5'  CAAATGGACAGTTTGGATCTA  35443       AAA   TTTT
                                CAAATGGA   TTTG   ATCTA
                                ||||||||   ||||   |||||
                                GTTTACCT   AAAC   TAGAT
                                     GTC   C___
GAM528  OTOR     3'  GAAAATCCTCTTTTATCT    33554       G_
                                GAAAATTT  TTTTATCT
                                ||||||||  ||||||||
```

```
                                CTTTTAGG  AAAATAGA
                                    AG
GAM528  RP2     3'  AAATGGGTAAAAGGTCTTATCT 27928       AA  TTT
             A                   AAATGG  AA   GTTTTATCTA
                                 ||||||  ||   ||||||||||
                                 TTTACC  TT   CAGAATAGAT
                                    CA  TTC
GAM528  CD1A    3'  CAAAATTTTTACAAAGAGA   43405           TTT
                                 TAAAATTTTTACA   GAGA
                                 ||||||||||||   ||||
                                 GTTTTAAAAATGT   CTCT
                                       TT_
GAM529  ASPH    3'  TGATTTTAATCCTAAA      37143       GTTATG
                                 TGATTT     TGATCCTAAA
                                 ||||||     ||||||||||
                                 ACTAAA     ATTAGGATTT

                                  _______
GAM529  HIP2    3'  TTTGTATTGGTCCTAAAAA   23773      TATG  A
                                 TTTGT    TG TCCTAAAAA
                                 |||||    || |||||||||
                                 AAACA    AC AGGATTTTT
                                    TA__  C
GAM529  IL12B   3'  TATCATTGTGATCCTAAAAA   13520       _
                                 TGTTAT GTGATCCTAAAAA
                                 |||||| ||||||||||||
                                 ATAGTA CACTAGGATTTTT
                                    A
GAM529  RAG1    3'  TGATTAGTTGTGAATCCTAAAA 7789       T  TA    _
             A                   TGATT GT  TGTGA TCCTAAAAA
                                 ||||| ||  ||||| |||||||||
                                 ACTAA CA  ACACT AGGATTTTT
                                    T  __     T
GAM529  HSPA9B  3'  TTACATGCAGCTGAAAAATGA  19977       ACA    CATGC
                                 TTACAT   AGCTG    GATGA
                                 ||||||   |||||    |||||
                                 AATGTA   TCGAC    TTACT
                                    CG_    TTT__
GAM529  SHMT1   3'  TACAAGCTGTGGACATG     20024         CAT  G
                                 TACAAGCTG   GC ATG
                                 |||||||||   || |||
                                 ATGTTCGAC   TG TAC
                                       ACC  _
GAM529  TIA1    3'  CACAAGCTGAAGATGA      35134         CATGC
                                 TACAAGCTG    GATGA
                                 |||||||||    |||||
                                 GTGTTCGAC    CTACT
                                       TT___
GAM530  ADAM19  3'  CCCGAAGGTCAGGACTGCTGAG 37766        ACCTT  __    A
             GGT                    TCCGAAG    GGA  GCTGA GGT
                                 |||||||    |||  ||||| |||
```

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                                GGGCTTC    CCT  CGACT CCA
                                    CAGT_   GA    C
GAM530  DRD3    3'  TCCGGAACTCGATATTGAAGGT 38017     AA  C    AGC
                                TCCG  GA CTTGG   TGAAGGT
                                ||||  || |||||   |||||||
                                AGGC  CT GAGCT   ACTTCCA
                                  __  T    ATA
GAM530  GPR85   5'  TCCGAAGAGTTTTGTTTGTGGA 33263        CC_   GAGC  A
           GGT                    TCCGAAGA   TTG    TG AGGT
                                ||||||||   |||    || ||||
                                AGGCTTCT   AAC    AC TCCA
                                    CAA   AAAC  C
GAM530  MECP2   3'  CCCGGAGCGGGAGCTGGGGGT  22583     A  ACCTT      AA
                                TCCG AG    GGAGCTG  GGT
                                |||| ||    |||||||  |||
                                GGGC TC    CCTCGAC  CCA
                                  C  GC___      CC
GAM530  NPC2    3'  GAAGCAGCAGAGCTGGAGGT   26962     ACCTT      A
                                GAAG    GGAGCTG AGGT
                                ||||    ||||||| ||||
                                CTTC    TCTCGAC TCCA
                                  GTCG_      C
GAM530  RAB6A   5'  GAAGAGAAGCTGAGGGT     16104      CCTT       A
                                GAAGA   GGAGCTGA GGT
                                |||||   |||||||| |||
                                CTTCT   CTTCGACT CCA
                                   ____       C
GAM530  TNFAIP2 5'  GAGGCCTTGGAAGAAGGT    26637    A A      CT
                                GA G CCTTGGAG  GAAGGT
                                || | ||||||||  ||||||
                                CT C GGAACCTT  CTTCCA
                                 _ C       __
GAM530  TNXB    5'  TCTGAGAGAAGCTGAGGG    37160    C  A  CCTT       A
                                TC GA GA   GGAGCTGA GG
                                || || ||   |||||||| ||
                                AG CT CT   CTTCGACT CC
                                 A  _ ____       C
GAM530  CIT     3'  CGGTGGCAAAGACCTGATGATG 43046    A   CTACT
                                TG TGGT    GACCTGATGATG
                                || ||||    ||||||||||||
                                GC ACCG    CTGGACTACTAC
                                 C   TTT__
GAM531  ATP2B1  3'  TGTTGAAGTCCAAAGACAAGAA 11748    A       ATTTTC
                                TG TTGAAGTC     ACAAGAA
                                || ||||||||     |||||||
                                AC AACTTCAG     TGTTCTT
                                 _       GTTTC_
GAM531  BSN     3'  ATTGAGAAACTTCACAAGAA   18392       A TCAT
                                ATTGA G    TTTCACAAGAA
                                ||||| |    ||||||||||
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                                TAACT C   GAAGTGTTCTT
                                  _ TTT_
GAM531  FXYD6   3'  GATTGAAGTCTCAGAAG    35117        ATTT  C
                                GATTGAAGTC   TCA AAG
                                ||||||||||   ||| |||
                                CTAACTTCAG   AGT TTC
                                     ____  C
GAM531  HD      3'  TGGGTGAAGTCATTTTTAC   13367    AT        C
                                TG  TGAAGTCATTTT AC
                                ||  ||||||||||| ||
                                AC  ACTTCAGTAAAA TG
                                 CC          A
GAM531  HPS3    3'  TGATTGAGGTCATAAATTAAGA 37042       A    TTTCAC
           A                     TGATTGA GTCAT     AAGAA
                                |||||||  |||||     |||||
                                ACTAACT  CAGTA     TTCTT
                                    C    TTTAA_
GAM531  INHBA   3'  TGATTCAAGCTCACAAG    13538      G   CATTT
                                TGATT AAGT    TCACAAG
                                |||||  ||||    |||||||
                                ACTAA TTCG    AGTGTTC
                                  G   _____
GAM531  LANCL1  3'  TGATTGAAAACTTTCACAAGAA 25859        TC
                                TGATTGAAG  ATTTTCACAAGAA
                                |||||||||  ||||||||||||
                                ACTAACTTT  TGAAAGTGTTCTT
                                     __
GAM532  CNTNAP2 3'  TTTACATGCTGTTGC      30501       TTC
                                TTTGCGT   GCTGTTGC
                                |||||||   ||||||||
                                AAATGTA   CGACAACG
                                     ___
GAM532  FZD1    3'  TTTCAATTTCTGTTTACGTTTT 18621        GC   _  CTG
           GC                    TTTCAATTT  GTTT CG   TTGC
                                |||||||||  |||| ||   ||||
                                AAAGTTAAA  CAAA GC   AACG
                                     GA    T  AA_
GAM532  MEIS2   3'  TTTCACATTTGTGTTCTTGTTG 33549     _    C   CGC
           C                     TTTCA ATTTG GTTT   TGTTGC
                                |||||  ||||| ||||   ||||||
                                AAAGT  TAAAC CAAG   ACAACG
                                  G    A   A__
GAM532  PCDHB7  3'  TTTCAATTTTGTTTTCCGC   33206        GCG_
                                TTTCAATTT    TTTCGC
                                |||||||||    ||||||
                                AAAGTTAAA    AAGGCG
                                     ACAA
GAM533  APOL1   3'  CCTGTATCCAACTGTTCTA   18935        T_  C_
                                CCTGTATCC  CT  TCTA
                                |||||||||  ||  ||||
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                                GGACATAGG  GA  AGAT
                                     TT  CA
GAM533  CHRNA1   3'  CCTGCCCTTCTCTGCTCT    6341       AT   C    A
                                CCTGT  CCT TCTCT CTCT
                                |||||  ||| ||||| ||||
                                GGACG  GGA AGAGA GAGA
                                  __  _    C
GAM533  DISC1    3'  CACCTGTAATCTCAGCACT   33027       TCC   TC
                                CACCTGTA   TCTC  TACT
                                ||||||||   ||||  ||||
                                GTGGACAT   AGAG  GTGA
                                     T__   TC
GAM533  DSCR3    3'  CACCTGTAATCTCAGCACT   25817       TCC   TC
                                CACCTGTA   TCTC  TACT
                                ||||||||   ||||  ||||
                                GTGGACAT   AGAG  GTGA
                                     T__   TC
GAM533  EPHB2    3'  CCTGTATCCCTTTTACTCT   32666       T  CTC
                                CCTGTATCC CT   TACTCT
                                |||||||||  ||   ||||||
                                GGACATAGG GA   ATGAGA
                                     _ AA_
GAM533  FGA      3'  TGTATTTTCTCTCCACTTCT   34841      CC       _
                                TGTAT  TCTCTCTACT CT
                                |||||  ||||||||||  ||
                                ACATA  AGAGAGGTGA GA
                                   AA        A
GAM533  HCS      3'  CACCTGTAATCCTAGAACT   33222       _   CTCT
                                CACCTGTA TCCT    CT
                                ||||||||  ||||    ||
                                GTGGACAT AGGA    GA
                                     T    TCTT
GAM533  MTR      3'  CACCTGTAGTCCCAGCTACTCT 7012        _   CTCT
                                CACCTGTA TCCT    CTACTCT
                                ||||||||  ||||    |||||||
                                GTGGACAT AGGG    GATGAGA
                                     C    TC__
GAM533  POP2     3'  CTGTGTCCTCTCTCACC     35256      A       T
                                CTGT TCCTCTCTC ACT
                                ||||  |||||||||  |||
                                GACA AGGAGAGAG TGG
                                  C       _
GAM533  PRX      5'  CCTGTGTCCTCTCCCCTTTCT  34112      A        AC
                                CCTGT TCCTCTCTCT  TCT
                                |||||  ||||||||||  |||
                                GGACA AGGAGAGGGG  AGA
                                   C         AA
GAM533  PTPN18   3'  CACCTGTAATCTCAGCACT   30764       TCC   TC
                                CACCTGTA   TCTC  TACT
                                ||||||||   ||||  ||||
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                                GTGGACAT  AGAG  GTGA
                                   T__   TC
GAM533  PXF     3'  ACCTGTATTTTTTCCATCTCT  16005       _____  _
                                ACCTGTA    TCC TCTCT
                                |||||||    ||| |||||
                                TGGACAT    AGG AGAGA
                                   AAAAA   T
GAM533  RARB    3'  CACTTGTATCTGTTAACCACTC 32058    C     CTCTCT
          TA                     CAC TGTATC     CTACTCTA
                                ||| ||||||     ||||||||
                                GTG ACATAG     GGTGAGAT
                                  A     ACAATT
GAM533  SLC20A2  3'  CACCTGTGCATTCTCTACTCT  27568       ATCCTC
                                CACCTGT     TCTCTACTCT
                                |||||||     ||||||||||
                                GTGGACA     AGAGATGAGA
                                   CGTA__
GAM533  ST14    3'  CACCAGTGTCCTCCCCTTCTA  35059     T  A     T  AC
                                CACC GT TCCTCTC CT  TCTA
                                |||| || ||||||| ||  ||||
                                GTGG CA AGGAGGG GA  AGAT
                                  T  C     _ __
GAM533  TK2     3'  CACTTGTGTCTCTCTCT    21445    C   ATC
                                CAC TGT   CTCTCTCT
                                ||| |||   ||||||||
                                GTG ACA   GAGAGAGA
                                  A   CA_
GAM533  VBP1    3'  CTGTCTTCTCTACCTCTA    17928     ATC  C     _
                                CTGT   CT TCTCTAC TCTA
                                ||||   || ||||||| ||||
                                GACA   GA AGAGATG AGAT
                                  ___  _     G
GAM533  WASF3   3'  CTGTGTTCTCTCCATCCT    27384     ATCC      CT
                                CTGT    TCTCTCTA  CT
                                ||||    ||||||||  ||
                                GACA    AGAGAGGT  GA
                                  CA__       AG
GAM533  XYLB    3'  ACCTGTATCATCTTTTCT    23019        C   C_
                                ACCTGTATC TCT  TCT
                                ||||||||| |||  |||
                                TGGACATAG AGA  AGA
                                   T   AA
GAM534  BMP6    3'  GAGGTGTAGAAATGGTATG   11864       A   ATA
                                GAGGTGTA AAG   TATG
                                |||||||| |||   ||||
                                CTCCACAT TTT   ATAC
                                   C   ACC
GAM534  CDH5    3'  GAGGTGTAAAGACACATGGCTC 12186         A
          G                     GAGGTGTAAA GATATATGGCTCG
                                |||||||||| ||||||||||||
```

```
                                CTCCACATTT CTGTGTACCGAGC
                                          _
GAM534  COL4A1   3'  GGTTGGAAGATATGGCT    12306    GTAA    TA
                                GGT   AAGATA  TGGCT
                                |||   ||||||  |||||
                                CCA   TTCTAT  ACCGA
                                  ACC_    __
GAM534  DMRT2    3'  GAGGGTGAAAGATATCCATACT 27261     T  A     ATG_
                                GAGG GT AAAGATAT   GCT
                                |||| || ||||||||   |||
                                CTCC CA TTTCTATA   TGA
                                  _ C      GGTA
GAM534  SHC1     3'  GAGCTGTAAAAGGGCT     16699    G     ATATAT
                                GAG TGTAAAAG    GGCT
                                ||| ||||||||    ||||
                                CTC ACATTTTC    CCGA
                                  G     _______
GAM535  ATP2B3   3'  GTAGCTGACTTGGTGA     34976       GTCAA  AT
                                GTAGCTGAC   GG  TGA
                                |||||||||   ||  |||
                                CATCGACTG   CC  ACT
                                     AA___  __
GAM535  COL6A1   3'  AAGTAACTGTTAGGTGAGGATT 12326       ACGTCA_
          G                      AAGTAGCTG     AGGATTG
                                |||||||||     |||||||
                                TTCATTGAC     TCCTAAC
                                     AATCCAC
GAM535  FGF23    5'  AAGTAGCTGGTGTGAGGAT   33947       AC  CA
                                AAGTAGCTG  GT  AGGAT
                                |||||||||  ||  |||||
                                TTCATCGAC  CA  TCCTA
                                     CA  C_
GAM535  LFG      3'  GCGGCACAGGGATTGA     44139    T A  T  A
                                GC G CG CA GGATTGA
                                || | || || |||||||
                                CG C GT GT CCTAACT
                                 _ C  _  C
GAM535  PCSK2    3'  AGTGGTGACTTTTGGGATTGAC 15123    AGC   GTCAA
                                AGT   TGAC    GGATTGAC
                                |||   ||||    ||||||||
                                TCA   ACTG    CCTAACTG
                                  CC_   AAAAC
GAM535  PIAS3    3'  AGTAGCTGGGGGTTGGGAC    25908       AC  CAA
                                AGTAGCTG  GT   GGAT
                                ||||||||  ||   ||||
                                TCATCGAC  CA   CCTG
                                     CC  AC_
GAM535  RAD1     3'  AGTAGCTGGCATTACAGG    39343       A   CA_
                                AGTAGCTG CGT   AGG
                                |||||||| |||   |||
```

```
                                TCATCGAC GTA   TCC
                                    C   ATG
GAM535  SLBP    3'  AAGTAGCTGACTCTCAATTGG  27194          G_   __
                                AAGTAGCTGAC  TCAA  GG
                                ||||||||||  ||||  ||
                                TTCATCGACTG  AGTT  CC
                                      AG    AA
GAM535  CDKN1A  5'  CATCCTCGCGGACACGCA    38503        G    AGC   A
                                CATCCTCG CGGA   TAC CA
                                ||||||||  ||||   |||  ||
                                GTAGGAGC GCCT   GTG GT
                                    _    ___   C
GAM535  CLASP1  3'  CATCTCAGCAGGCTGTACAA  42236      C      AA   AC
                                CATC TCGGCGG  GCT  ACAA
                                ||||  |||||||  |||  ||||
                                GTAG AGTCGTC  CGA  TGTT
                                  _      __   CA
GAM535  FUT6    5'  CCAGGGAGCTATGCAA      6651       C   A    CA
                                TCGG GGA GCTA  CAA
                                ||||  |||  ||||  |||
                                GGTC CCT CGAT  GTT
                                  _   _    AC
GAM535  GAS11   3'  CATTCTCTCCCCAGCTACACA  11211     C   GGCGGA
                                CAT CTC      AGCTACACA
                                |||  |||      |||||||||
                                GTA GAG      TCGATGTGT
                                  A   AGGGG_
GAM535  MYO1E   3'  ACCCTTGGCACGTACA      22651       C   GGAA  _
                                ATCCT GGC    GC TACA
                                |||||  |||    ||  ||||
                                TGGGA CCG    TG ATGT
                                   A   ____   C
GAM535  PCOLN3  3'  CAGCCTCAGCATGGGCTGCAC  15748    T       GAA   A
                                CA CCTCGGCG   GCT CAC
                                ||  ||||||||   |||  |||
                                GT GGAGTCGT   CGA GTG
                                 C       ACC   C
GAM535  PTPRM   3'  TCCTGGAAAGCTACA       15974      C  CG
                                TCCT GG  GAAGCTACA
                                ||||  ||  |||||||||
                                AGGA CC  TTTCGATGT
                                  _  __
GAM535  UBE4A   3'  TCAACAGAAGTTGCACAA    21975          CTA
                                TCGGCGGAAG   CACAA
                                ||||||||||   |||||
                                AGTTGTCTTC   GTGTT
                                      AAC
GAM535  USP9Y   3'  TCCTCTTGGCTACACAAA    41962       GGCGGAA
                                TCCTC      GCTACACAAA
                                |||||      ||||||||||
```

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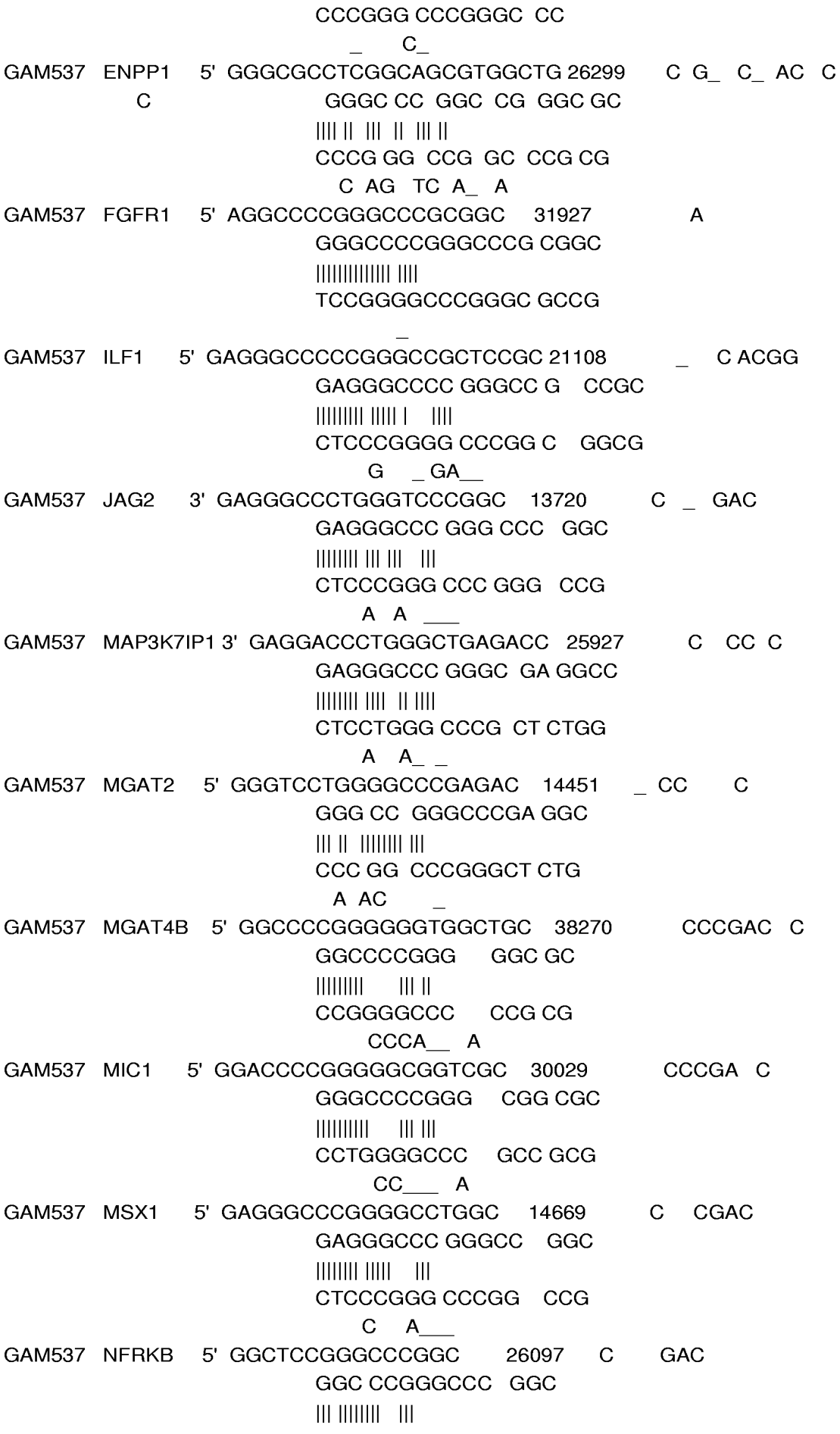
                                AGGAG     CGATGTGTTT
                                  AAC____
GAM536  CHD2    3' CAAGACATGGGATTCG     10440     TC   GGAG   CC
                                CAAG  ACGT   GGGA  CG
                                ||||  ||||   ||||  ||
                                GTTC  TGTA   CCCT  GC
                                  __   ____   AA
GAM536  ENG     3' GTCGAGTGGAGGACTGGCT   6505     AC    GG   CC
                                GTC  GTGGA  GGAC  GCT
                                |||  |||||  ||||  |||
                                CAG  CACCT  CCTG  CGA
                                  CT    __   AC
GAM536  GRLF1   3' CAAGTCACTGCAGCTGGCCTGC 44222        _ TG AGG  A  C
            T                    CAAGTCAC G  G   GG CC GCT
                                ||||||||  |  |   || || |||
                                GTTCAGTG C  C   CC GG CGA
                                    A GT GA_  _  A
GAM537  ADORA2A  3' GGGCCTGCCCAGCAAAGATG  8604       _    AT
                                GGGCC GCCCG  CGAAGATG
                                |||||  |||||  ||||||||
                                CCCGG CGGGT  GTTTCTAC
                                  A    C_
GAM537  PRSS15   3' GACCGAGCTGCTCGCTCG    21994        C  C  A
                                GACCGGGC GC CG TCG
                                |||||||  ||  ||  |||
                                CTGGCTCG CG GC AGC
                                    A  A  G
GAM537  ACP1    5' GAGGGCCCGGGCGC       28236        C   CCGACG
                                GAGGGCCC GGGC     GC
                                ||||||||  ||||     ||
                                CTCCCGGG CCCG     CG
                                  _   _______
GAM537  ALPI    3' GAGGGCCCATGGGCTCTGGGTT 11578        C_   CCGAC  CC
            GC                    GAGGGCCC  GGGC    GG  GC
                                ||||||||  ||||    ||  ||
                                CTCCCGGG  CCCG    CC  CG
                                    TA    AGAC_  AA
GAM537  CTRL    3' GGGCCCCGGCCTCGGC     12524        G  CGA
                                GGGCCCCGG CC   CGGC
                                |||||||||  ||   ||||
                                CCCGGGGCC GG   GCCG
                                    _  A__
GAM537  DRD2    5' GGCCCCGGACGGCG       9018         GCCCG    C
                                GGCCCCGG    ACGGC G
                                ||||||||    |||||  |
                                CCGGGGCC    TGCCG C
                                  _____     A
GAM537  EEF1A2   3' GGGCCCGGGCCCGGGG     41521       C      AC
                                GGGCCC GGGCCCG  GG
                                ||||||  |||||||  ||
```


CCCGGG CCCGGGC CC
_ C_
GAM537 ENPP1 5' GGGCGCCTCGGCAGCGTGGCTG 26299 C G_ C_ AC C
C GGGC CC GGC CG GGC GC
|||| || ||| || ||| ||
CCCG GG CCG GC CCG CG
C AG TC A_ A
GAM537 FGFR1 5' AGGCCCCGGGCCCGCGGC 31927 A
GGGCCCCGGGCCCG CGGC
|||||||||||||| ||||
TCCGGGGCCCGGGC GCCG
_
GAM537 ILF1 5' GAGGGCCCCCGGGCCGCTCCGC 21108 _ C ACGG
GAGGGCCCC GGGCC G CCGC
||||||||| ||||| | ||||
CTCCCGGGG CCCGG C GGCG
G _ GA__
GAM537 JAG2 3' GAGGGCCCTGGGTCCCGGC 13720 C _ GAC
GAGGGCCC GGG CCC GGC
|||||||| ||| ||| |||
CTCCCGGG CCC GGG CCG
A A ___
GAM537 MAP3K7IP1 3' GAGGACCCTGGGCTGAGACC 25927 C CC C
GAGGGCCC GGGC GA GGCC
|||||||| |||| || ||||
CTCCTGGG CCCG CT CTGG
A A_ _
GAM537 MGAT2 5' GGGTCCTGGGGCCCGAGAC 14451 _ CC C
GGG CC GGGCCCGA GGC
||| || |||||||| |||
CCC GG CCCGGGCT CTG
A AC _
GAM537 MGAT4B 5' GGCCCCGGGGGGGTGGCTGC 38270 CCCGAC C
GGCCCCGGG GGC GC
||||||||| ||| ||
CCGGGGCCC CCG CG
CCCA__ A
GAM537 MIC1 5' GGACCCCGGGGGGCGGTCGC 30029 CCCGA C
GGGCCCCGGG CGG CGC
|||||||||| ||| |||
CCTGGGGCCC GCC GCG
CC___ A
GAM537 MSX1 5' GAGGGCCCGGGGCCTGGC 14669 C CGAC
GAGGGCCC GGGCC GGC
|||||||| ||||| |||
CTCCCGGG CCCGG CCG
C A___
GAM537 NFRKB 5' GGCTCCGGGCCCGGC 26097 C GAC
GGC CCGGGCCC GGC
||| |||||||| |||

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                                CCG GGCCCGGG  CCG
                                  A     ___
GAM537  PRX     3'  GAGGGCCCTGGGCTGGGG   34119       C   CCGAC
                                GAGGGCCC GGGC    GG
                                |||||||| ||||    ||
                                CTCCCGGG CCCG    CC
                                    A   ACC__
GAM537  RBL2    5'  GAGGGCCCGGGCCCGCAGC  24705       C     A
                                GAGGGCCC GGGCCCG CGGC
                                |||||||| ||||||| ||||
                                CTCCCGGG CCCGGGC GTCG
                                    _     _
GAM537  RNF4    3'  GAGGGCCCTGGGTCCAGCG  16353       C  C  A
                                GAGGGCCC GGG CCG CG
                                |||||||| ||| ||| ||
                                CTCCCGGG CCC GGT GC
                                    A  A  C
GAM537  SOX2    5'  GGGCCCGGCCCGCCGGCGGCCG 45476      CG    A___
          C                      GGGCCC  GGCCCG   CGGCCGC
                                |||||| ||||||   |||||||
                                CCCGGG  CCGGGC   GCCGGCG
                                   __    GGCC
GAM537  SP3     5'  GGGCCCCGGCTGCGGCGGCCGC 44378       GCC  A
                                GGGCCCCGG  CG CGGCCGC
                                |||||||||  || |||||||
                                CCCGGGGCC  GC GCCGGCG
                                     GAC  C
GAM537  WNT2    5'  GAGCGCCTCGTCACGGCCG  18106    G  C  GGCCCG
                                GAG GCC CG    ACGGCCG
                                ||| ||| ||    |||||||
                                CTC CGG GC    TGCCGGC
                                  G  A  AG____
GAM537  WNT6    5'  GAGGGCCCGGGCTTCAGTGC  27181       C   CCGACG
                                GAGGGCCC GGGC    GC
                                |||||||| ||||    ||
                                CTCCCGGG CCCG    CG
                                   _   AAGTCA
GAM538  ADAM21  3'  CAAGAGACTAAAGTGTACTAAT 19209       C  ACA  A____
          GCATG                 CAGGAGAC AAA  TAC   CATG
                                |||||||| |||  |||   ||||
                                GTTCTCTG TTT  ATG   GTAC
                                    A  CAC  ATTAC
GAM538  AKAP13  5'  CAGGAACTGCTACACATG   28474      ACCAAAACA
                                CAGGAG       TACACATG
                                ||||||       ||||||||
                                GTCCTT       ATGTGTAC
                                   GACG_____
GAM538  AKAP13  3'  CAGGAACTGCTACACATG   28474      ACCAAAACA
                                CAGGAG       TACACATG
                                ||||||       ||||||||
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                                GTCCTT       ATGTGTAC
                                   GACG_____
GAM538  CLN2    3'  CAGGGAATCAAAACATTCAC  7554      AG C      A
                                CAGG  A CAAAACAT CAC
                                ||||  | |||||||| |||
                                GTCC  T GTTTTGTA GTG
                                  CT A       A
GAM538  GGT2    5'  GGCAGCCCTGGTGTACACATG  43926    _  A  AAAACA
                                GG AG CC     TACACATG
                                || || ||     ||||||||
                                CC TC GG     ATGTGTAC
                                 G  _  GACCAC
GAM538  GNAI3   3'  AGATTAAAAATGTACACATGA  27094    GACC   CA
                                GGA   AAAA  TACACATGA
                                |||   ||||  |||||||||
                                TCT   TTTT  ATGTGTACT
                                  AAT_   AC
GAM538  MX2     3'  CAGGAGACTGGACATACA    14694       CAAA
                                CAGGAGAC   ACATACA
                                ||||||||   |||||||
                                GTCCTCTG   TGTATGT
                                    ACC_
GAM538  PTTG1IP  3'  CAGGAGACCGCAATGGCCACGT 20281         AAAACATA   A
          G                     CAGGAGACC       CAC TG
                                |||||||||       ||| ||
                                GTCCTCTGG       GTG AC
                                    CGTTACCG   C
GAM538  SORCS1   3'  AGAGGTCAGAGAGCACACATGA 38097     AC  AAACA
                                GGAG  CA    TACACATGA
                                ||||  ||    |||||||||
                                TCTC  GT    GTGTGTACT
                                  CA  CTCTC
GAM538  UGCG    3'  AGATACCAAAACATACATGTGA 17863    G          CA
                                GGA ACCAAAACATACA  TGA
                                ||| ||||||||||||  |||
                                TCT TGGTTTTGTATGT  ACT
                                  A          AC
GAM538  ZNF134   3'  GAGACCAAGAATATCCATGA   18326       AAC   CA
                                GAGACCAA   ATA  CATGA
                                ||||||||   |||  |||||
                                CTCTGGTT   TAT  GTACT
                                    CT_   AG
GAM538  ZNF261   3'  CAGAAGACCAGGGCCCCATG   22989        AAACATACA
                                CAGGAGACCA       CATG
                                ||||||||||       ||||
                                GTCTTCTGGT       GTAC
                                    CCCGGG___
GAM538  CAST    3'  TGTAGAATGTGCAAAAA    11984       TTT
                                TGTAGAA   TGTGCAAAAA
                                |||||||   ||||||||||
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                                ACATCTT  ACACGTTTTT
                                   ___
GAM538  CLN5    5'  GATATGTAGCTTGTG      27081        AAT
                                GATATGTAG  TTTGTG
                                |||||||||  ||||||
                                CTATACATC  GAACAC
                                   ___
GAM538  SEL1L   3'  GATGTGTTCTTTGTGCAAAAA  22847    A  AGAA
                                GAT TGT   TTTTGTGCAAAAA
                                ||| |||   ||||||||||||
                                CTA ACA   GAAACACGTTTTT
                                  C  A___
GAM539  PRKAB1  3'  TGGAGAAATCCGGCAGCAG   26507    A    A  TAAT
                                TGGA AAATCC GC   GCAG
                                |||| |||||| ||   ||||
                                ACCT TTTAGG CG   CGTC
                                  C    C  T___
GAM539  RAG1    3'  GAAAAATCCATGACAGCAGAT  7786         GCTAAT
                                GAAAAATCCA    GCAGAT
                                ||||||||||    ||||||
                                CTTTTTAGGT    CGTCTA
                                     ACTGT_
GAM539  SLC6A12 5'  GGAAATCCAGGCCTTGGCAGAT 16800    AA    _  AAT
                                GGAA  ATCCAG CT   GCAGAT
                                ||||  |||||| ||   ||||||
                                CCTT  TAGGTC GG   CGTCTA
                                  __    C  AAC
GAM539  SMARCA2 3'  TGGAAAAATGTATATGCAG   16896       CCAGCTA
                                TGGAAAAAT     ATGCAG
                                |||||||||     ||||||
                                ACCTTTTTA     TACGTC
                                     CATA___
GAM540  ADRB1   3'  CTCCTCGTTCCCCTGGG    8656     C      GA
                                CTCC CGTTCCCC  GGG
                                |||| ||||||||  |||
                                GAGG GCAAGGGG  CCC
                                  A      A_
GAM540  AXIN1   3'  CCCGTGCCCCGAGGCG     41373     T      GTCC
                                CCCGT CCCCGAGG   CG
                                ||||| ||||||||   ||
                                GGGCA GGGGCTCC   GC
                                  C      _____
GAM540  BARHL1  3'  CTCCCCTTCTCTCCCTGG    33463      G_  _  GA
                                CTCCCC  TTC CCC  GG
                                ||||||  ||| |||  ||
                                GAGGGG  GAG GGG  CC
                                   AA  A  A_
GAM540  CIAO1   5'  CTCCCCGTTCCGCCGGAGGACC 43683          _  AG  T  C
            TGG                 CTCCCCGTTCC CCG  GG CC GG
                                |||||||||| |||  || || ||
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                                GAGGGGCAAGG GGC  CC GG CC
                                      C   CT  T  A
GAM540  DRD4    3'  CTCCTTGGTCCCTGAGGCCTGG 9024      CCGT   C   GT  C
                                CTCC   TCCC GAGG  CC GG
                                ||||   |||| ||||  || ||
                                GAGG   AGGG CTCC  GG CC
                                  AACC   A   __  A
GAM540  FOXE1   3'  CCGTTCCCTAGAACAGCGG   20939       CG  GG CC
                                CCGTTCCC  AG  T  CGG
                                ||||||||  ||  |  |||
                                GGCAAGGG  TC  G  GCC
                                    A_  TT TC
GAM540  HBZ     3'  CCTGTCCTGGGGGTCCCG    23732    C   CCCGA
                                CC GTTC    GGGTCCCG
                                || ||||    ||||||||
                                GG CAGG    CCCAGGGC
                                 A   ACC__
GAM540  HDAC5   3'  CCCGTTCCCTCCTCA      40163        CGAGGG  _
                                CCCGTTCCC    TCC CG
                                |||||||||     ||| ||
                                GGGCAAGGG    AGG GT
                                     _______  A
GAM540  LASS1   3'  CCTGGTCTCCTGGGGGTCCCGG 34597    CC  TC  CGA
                                CC  GT  CC   GGGTCCCGG
                                ||  ||  ||   |||||||||
                                GG  CA  GG   CCCAGGGCC
                                 AC  GA  ACC
GAM540  MADH1   5'  CTCTCCGCTCCCCGAGCCTCGG 25339    C         GGT  _
                                CTC CCGTTCCCCGAG   CC CGG
                                ||| ||||||||||||   || |||
                                GAG GGCGAGGGGCTC   GG GCC
                                  A          ___  A
GAM540  MEN1    5'  GTCCCCCACAATTCCGG    39252        AG   C
                                GTTCCCCG  GGT CCGG
                                ||||||||  ||| ||||
                                CAGGGGGT  TTA GGCC
                                     G_   A
GAM540  MGAT2   5'  CTCATCCCGGGCCCCGGGGGTC 14446    __   TT    A    C
           CTGG                   CTC  CCCG  CCCCG GGGTCC GG
                                ||||  ||||  ||||| |||||| ||
                                GAG  GGGC  GGGGC CCCAGG CC
                                  TA   CC    C     A
GAM540  MPL     3'  CTGCCTGTGGAGAAAGGGTCCT 23880    C  C  TCCCC      C
           GG                    CT CC GT    GAGGGTCC GG
                                || || ||    |||||||| ||
                                GA GG CA    TTCCCAGG CC
                                 C  A  CCTCT       A
GAM540  PDE1B   3'  CTCCCCGCTCCCTGGCAGCCAC 9563           CGAG   _ _
           CTGG                   CTCCCCGTTCCC   GGTC CC GG
                                ||||||||||||   |||| || ||
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                                GAGGGGCGAGGG   TCGG GG CC
                                      ACCG   T  A
GAM540  PIK3C2B  3'  CTCCTCTTCCCCCTCCG    15291     CCG    GAGGG  C
                                CTCC  TTCCCC   TCC G
                                ||||  ||||||   ||| |
                                GAGG  AGGGGG   AGG C
                                  AGA    _____  A
GAM540  PLSCR1   5'  TCCCGGTTCCCCGCGCTGG   34412     C      AG__
                                TCCC GTTCCCCG   GG
                                |||| ||||||||   ||
                                AGGG CAAGGGGC   CC
                                  C      GCGA
GAM540  RNPEPL1  3'  CTCCCCATTCTCCCTGCCTGG  32879         _  GAGGGT  C
                                CTCCCCGTTC CCC    CC GG
                                |||||||||| |||     || ||
                                GAGGGGTAAG GGG    GG CC
                                      A  AC____  A
GAM540  SIRT4    3'  TCCCTGTTCCAGGTTCTG    29262     C    CCG  G  CC
                                TCCC GTTCC  AGG TC  G
                                |||| |||||  ||| ||  |
                                AGGG CAAGG  TCC AG  C
                                  A    ___  A  A_
GAM540  TRPV3    3'  CTCCTTTTCCCCGAAGGGTTCC 45440     CCG      _   C
          GG                    CTCC  TTCCCCGA GGGT CCGG
                                ||||  |||||||| |||| ||||
                                GAGG  AAGGGGCT CCCA GGCC
                                  AA_      T   A
GAM540  WRN      5'  CTCCCCTTCCCTCCC      8139       G    CGAGGG
                                CTCCCC TTCCC     TCCC
                                |||||| |||||     ||||
                                GAGGGG AAGGG     AGGG
                                   _   _______
GAM540  ACCN2    3'  AGGTCCCTTGCCCCGTTC    33430       GG  TC
                                GGGTCCC  GC  CCCGTTC
                                |||||||  ||  |||||||
                                TCCAGGG  CG  GGGCAAG
                                   AA  __
GAM540  CLDN5    3'  GGGCCCCGGGCTCTGCATCC   17609          CC
                                GGGTCCCGGGCTC  CGTTC
                                ||||||||||||  |||||
                                CCCGGGGCCCGAG  GTAGG
                                      AC
GAM540  IL27     3'  GAGGGCCCTGGACCCTCTGTTC 42106       C     CCC
                                GAGGGTCC GGGCTC   GTTC
                                |||||||| ||||||   ||||
                                CTCCCGGG CCTGGG   CAAG
                                   A     AGA
GAM540  MGEA5    5'  AAGGGTCCTGTCCTCGTTC   29209       CGGGC  C
                                GAGGGTCC    TCC CGTTC
                                ||||||||    ||| |||||
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                                TTCCCAGG    AGG GCAAG
                                    AC___   A
GAM540  RGS3    5'  GAGGGTCCTGGGCCAGCCC   39125       C    C_
                                GAGGGTCC GGGCT  CCC
                                |||||||| |||||  |||
                                CTCCCAGG CCCGG  GGG
                                    A    TC
GAM540  SCTR    5'  AGGGTCCCGGGCTCCGGCC   16487           __
                                AGGGTCCCGGGCTCC  CC
                                |||||||||||||||  ||
                                TCCCAGGGCCCGAGG  GG
                                         CC
GAM540  SLC19A1 3'  GAGGGTCCCGGCTCCCACC   16847         G    CGTT
                                GAGGGTCCCGG CTCCC   CC
                                |||||||||| |||||   ||
                                CTCCCAGGGCC GAGGG   GG
                                    _    T___
GAM540  ST14    3'  GAGGCTCCGAAGCTCCGTTCCC 35062     G  CG    CC
                                GAGG TCC  GGCTCC  GTTCCC
                                |||| |||  ||||||  ||||||
                                CTCC AGG  TCGAGG  CAAGGG
                                  G  CT    __
GAM540  ST5     3'  GAGGGTCCCAGGCTGGGCCTTC 24045          C__  CG
          TC                    GAGGGTCCCGGGCT   CC  TTC
                                |||||||||||||  ||  |||
                                CTCCCAGGGTCCGA   GG  GAG
                                      CCC  AA
GAM540  XPR1    3'  GAGGGTCCTTGCAATGCCTGTT 21851       CGG  TC__  C
          C                     GAGGGTCC   GC    CC GTTC
                                ||||||||   ||    || ||||
                                CTCCCAGG   CG    GG CAAG
                                    AA_  TTAC  A
GAM541  ACHE    3'  GAGGAGGAAGGGAGCACTA   31863    A   G     T
                                GAG AGGA AGGGAGC CTA
                                ||| |||| ||||||| |||
                                CTC TCCT TCCCTCG GAT
                                  C   _     T
GAM541  ACTR1B  3'  GAGAGGGAGGTGGGGCCCT   43345     A   AG  A
                                GAGA GGAG  GG GCTCT
                                |||| ||||  || |||||
                                CTCT CCTC  CC CGGGA
                                  C   CA  C
GAM541  AP2A1   3'  GAGGGAGGGGGACTCCCCCTA  39104    AA   A  AG   AT
                                GAG  GGAG GGG  CTCT  CTA
                                |||  |||| |||  ||||  |||
                                CTC  CCTC CCC  GAGG  GAT
                                  __   _  CT   GG
GAM541  AP2B1   3'  GAGGGGGTGAGGGGACAGCATC 10486    AA  A    AG TC
          T                     GAG  GG GAGGG  C  TATCT
                                |||  || |||||  |  |||||
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                                CTC  CC CTCCC  G  GTAGA
                                  CC  A    CT TC
GAM541  AXL     3'  GAGAAGGGGAGGGACCTGTCT  34885       A     G  CTA
                                GAGAAGG GAGGGA CT   TCT
                                ||||||| |||||| ||   |||
                                CTCTTCC CTCCCT GA   AGA
                                    C     G  C__
GAM541  BAZ2A   3'  GAGAAGAGAGGGAGTTCC    30308       G       C
                                GAGAAG AGAGGGAG TCT
                                |||||| |||||||| |||
                                CTCTTC TCTCCCTC AGG
                                    _       A
GAM541  BIRC7   3'  GAGAGGGGCAGGGAGCCCACTC 40252      A  AG        TA
           T                     GAGA GG  AGGGAGCTC  TCT
                                |||| ||  |||||||||  |||
                                CTCT CC  TCCCTCGGG  AGA
                                  C  CG        TG
GAM541  CBFA2T3  3'  GATGGGAGGGAGCACGTCT   23264    A  A       TCTA
                                GA GG GAGGGAGC    TCT
                                || || ||||||||    |||
                                CT CC CTCCCTCG    AGA
                                 A  _       TGC_
GAM541  CEACAM1  3'  GAAGGGAGGGGAAGTTCT    11832       A    __  C
                                GAAGG GAGGG  AG TCT
                                ||||| |||||  || |||
                                CTTCC CTCCC  TC AGA
                                   _    CT  A
GAM541  CENTD2   5'  GAGGTGGAGAGGGAGGCT    40130     AA        _
                                GAG  GGAGAGGGAG CT
                                |||  |||||||||| ||
                                CTC  CCTCTCCCTC GA
                                  CA         C
GAM541  CLTC    5'  GAGAAGGGGAGGGGGGAGGCT  22150        A    A____
                                GAGAAGG GAGGG     GCT
                                ||||||| |||||     |||
                                CTCTTCC CTCCC     CGA
                                    C     CCCTC
GAM541  CSF3R   3'  GGGAGGAGAGGGAGATGCT   8908    A  A        CT_
                                G GA GGAGAGGGAG   CT
                                | || ||||||||||   ||
                                C CT CCTCTCCCTC   GA
                                 C  _         TAC
GAM541  CXCR4   3'  GAATGGAGAGATTATCTA    18443     _      GAGC
                                GAA GGAGAGG    TCTA
                                ||| |||||||    ||||
                                CTT CCTCTCT    AGAT
                                  A      AAT_
GAM541  CYP8B1  3'  GAGGAGGAGGGAGAGTGTCTCT 20504     A    A    ___
                                GAG AGGAG GGGAG   CTCT
                                ||| ||||| |||||   ||||
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                                CTC TCCTC CTCTC   GAGA
                                  C    C    ACA
GAM541  DAAM2   3'  GAGAAGGGGTGGGAGGGCC   45174       AGA    CT
                                GAGAAGG   GGGAG  CT
                                |||||||   |||||  ||
                                CTCTTCC   CCCTC  GG
                                    CCA    CC
GAM541  EPHA8   3'  GAGGGAGAGGGGGCTC     33895     AA      A
                                GAG  GGAGAGGG GCTC
                                |||  |||||||| ||||
                                CTC  CCTCTCCC CGAG
                                  __       C
GAM541  GNAZ    3'  GAGAGGGAGGGAGATCT     13181      A  A      C
                                GAGA GG GAGGGAG TCT
                                |||| || ||||||| |||
                                CTCT CC CTCCCTC AGA
                                  _ _      T
GAM541  HMGA2   5'  GAGGAGGAGAGGAGGAGGCGCT 18518     A      __   _ T
                                GAG AGGAGAGG  GAG C CT
                                |||  ||||||||  |||  |  ||
                                CTC TCCTCTCC  CTC G GA
                                  C       TC   C C
GAM541  HOXC13  3'  GAGAGGAGAGAGGAGCCCTAT  40664      A     _
                                GAGA GGAGAG GGAGCTCTAT
                                |||| |||||| ||||||||||
                                CTCT CCTCTC CCTCGGGATA
                                  _     T
GAM541  KCNE1L  3'  GAGAGGGAGGGAAAAGATGTCT 29372      A  A      CTCTA_
                                GAGA GG GAGGGAG     TCT
                                |||| || |||||||     |||
                                CTCT CC CTCCCTT     AGA
                                  _ _      TTCTAC
GAM541  LZTS1   3'  GAGGGGGAGAGGATATCT    34265     AA      AGCTC
                                GAG  GGAGAGGG    TATCT
                                |||  ||||||||    |||||
                                CTC  CCTCTCCT    ATAGA
                                  CC       _____
GAM541  MCC     3'  GAGGGGGAGAGTGAGTGCT   14382     AA     G   CT
                                GAG  GGAGAG GAG  CT
                                |||  |||||| |||  ||
                                CTC  CCTCTC CTC  GA
                                  CC     A   AC
GAM541  MSX2    3'  GAGAGGGAGAGGAAACCCT   42294      A
                                GAGA GGAGAGGGAGCTCT
                                |||| ||||||||||||||
                                CTCT CCTCTCCTTTGGGA
                                  C
GAM541  NEUD4   3'  GAGGGAGGGAGGGAGAGGCCCT 21621     A_   A     ___
                                GAG  AGG GAGGGA   GCTCT
                                |||  ||| ||||||   |||||
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                                CTC  TCC CTCCCT   CGGGA
                                  CC   _     CTC
GAM541  NR1I2    5'  GAGAGGGAGAGGGAGACCAC   35104      A         CT
                                GAGA GGAGAGGGAG  CTAT
                                |||| ||||||||||  ||||
                                CTCT CCTCTCCCTC  GGTG
                                  C         T_
GAM541  PDE4A    3'  GAGAAGGGGGGAGGGGACAGGC 26255        A__     A____
           TCT                    GAGAAGG   GAGGG    GCTCT
                                |||||||   |||||    |||||
                                CTCTTCC   CTCCC    CGAGA
                                    CCC    CTGTC
GAM541  PFC      5'  GAGAGGAGGTCCCGCTTTATCT 15226      A    AGGGA   C
                                GAGA GGAG    GCT TATCT
                                |||| ||||    ||| |||||
                                CTCT CCTC    CGA ATAGA
                                  _   CAGGG   A
GAM541  PPP2R5D  3'  AGAAGAGGGACCATTCT     26452          G  CTA
                                AGGAGAGGGA CT   TCT
                                |||||||||| ||   |||
                                TCTTCTCCCT GG   AGA
                                      _ TA_
GAM541  PRKACA   3'  GGAGAGGGGCAGCTGCTTTGTC 15580         __   _ A__
           T                    GGAGAGGG  AGCT CT   TCT
                                ||||||||  |||| ||   |||
                                CCTCTCCC  TCGA GA   AGA
                                     CG    C  AAC
GAM541  PSAP     3'  GGAGGTGGGGGAGCCCTA    42967      A___
                                GGAG    GGGAGCTCTA
                                ||||    ||||||||||
                                CCTC    CCCTCGGGAT
                                  CACC
GAM541  PSCD4    3'  GAGAGGGGAAGGGAGTAGACTA 30125      A  AG     CT__
                                GAGA GG  AGGGAG    CTA
                                |||| ||  ||||||    |||
                                CTCT CC  TCCCTC    GAT
                                  C  CT     ATCT
GAM541  PTMS     3'  GAGGGGAGGGGGGGCAGCT    15884     AA   A_  _
                                GAG  GGAG  GGG AGCT
                                |||  ||||  ||| ||||
                                CTC  CCTC  CCC TCGA
                                  C_   CC   G
GAM541  PYGM     5'  GAGGGAGAGGTGAGCTCCAC   24696     AA      _
                                GAG  GGAGAGG GAGCTCTAT
                                |||  ||||||| |||||||||
                                CTC  CCTCTCC CTCGAGGTG
                                  __      A
GAM541  RAD52    3'  GAGAGGAGGGTGCTGTCT    39559      A   A  GA   CTA
                                GAGA GGAG GG  GCT   TCT
                                |||| |||| ||  |||   |||
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                                CTCT CCTC CC  CGA   AGA
                                  _   _ A_  C__
GAM541  SCD     3'  GAGGGAGAGAGAGGCTTTCT  22830    AA       CT  A
                                GAG  GGAGAGGGAG  CT TCT
                                |||  ||||||||||  || |||
                                CTC  CCTCTCTCTC  GA AGA
                                  __        C_  A
GAM541  SDC4    3'  GGGAAGGGAGGCCCTATCTA  16525    AG     _
                                GG  AGGGAG CTCTATCTA
                                ||  |||||| |||||||||
                                CC  TCCCTC GGGATAGAT
                                 CT     C
GAM541  SEZ6L   5'  GAGGAGGAGAGGAGATCTA  34422    A      G  C
                                GAG AGGAGAGG AG TCTA
                                ||| |||||||| || ||||
                                CTC TCCTCTCC TC AGAT
                                  C       _  T
GAM541  SLC18A1 5'  AAGAGGGGAGGGAGTCT    16819     A  A     C
                                GAGA GG GAGGGAG TCT
                                |||| || ||||||| |||
                                TTCT CC CTCCCTC AGA
                                  C  _      _
GAM541  SLC4A1  3'  GAAGAGGGAGGGCTCAGATCTA 7354          __   T_
                                GGAGAGGGA  GCTC  ATCTA
                                |||||||||  ||||  |||||
                                CTTCTCCCT  CGAG  TAGAT
                                      CC    TC
GAM541  SORD    3'  GAGAAGAGGAAAGATTTTCT  16965      GA     GC_
                                GAGAAG  GAGGGA   TCT
                                ||||||  ||||||   |||
                                CTCTTC  CTTTCT   AGA
                                   TC     AAA
GAM541  SYNGR3  3'  AGAGGGAGGTGTCTGTCT    20092       C__   A
                                AGAGGGAG   TCT TCT
                                ||||||||   ||| |||
                                TCTCCCTC   AGA AGA
                                     CAC   C
GAM541  TBXA2R  3'  GAGAAGGGGTGGGAGCTCT   9854        AGA
                                GAGAAGG   GGGAGCTCT
                                |||||||   |||||||||
                                CTCTTCC   CCCTCGAGA
                                    CCA
GAM541  TCF12   3'  AGGAGAGGTCACCTTCTATCTA 17339       GA  __
                                AGGAGAGG  GC  TCTATCTA
                                ||||||||  ||  ||||||||
                                TCCTCTCC  TG  AGATAGAT
                                     AG  GA
GAM541  TEAD2   5'  GAGAAAGTTGCCGGGAGCT   18764       AGA__
                                GAGAAGG    GGGAGCT
                                |||||||    |||||||
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                                CTCTTTC    CCCTCGA
                                    AACGG
GAM541  TLX1    5'  GAGGGAGAGAGGGGGCGCC   24337    AA      A  T
                                GAG  GGAGAGGG GC CT
                                |||  |||||||| || ||
                                CTC  TCTCTCCC CG GG
                                  CC       C  C
GAM541  TRAP100  3'  GGAGCCACGAGGAGCTTTAT  31348     A____     C
                                GGAG    GGGAGCT TAT
                                ||||    ||||||| |||
                                CCTC    TCCTCGA ATA
                                  GGTGC      A
GAM541  WFS1    3'  AGGAGAGGGAATCTCATCT   25638          _  T
                                AGGAGAGGGAG CTC ATCT
                                |||||||||| ||| ||||
                                TCCTCTCCCTT GAG TAGA
                                       A  _
GAM541  WNT2    3'  GAGGAAGAGGGGGCTTCC    18107    AA      A  _
                                GAG  GGAGAGGG GCT CT
                                |||  |||||||| ||| ||
                                CTC  CTTCTCCC CGA GG
                                  __       C   A
GAM541  WNT8B   3'  AAGAGGAAAGTGGCTTTAT   40584     A    GGA   C
                                GAGA GGAGAG   GCT TAT
                                |||| ||||||   ||| |||
                                TTCT CCTTTC   CGA ATA
                                  _     AC_   A
GAM541  ZFP36L1  3'  GAGGGGGAGAGGGAGGGCACAT 22284     AA       __  TCTA
           TCT                    GAG  GGAGAGGGA  GC    TCT
                                |||  |||||||||  ||    |||
                                CTC  CCTCTCCCT  CG    AGA
                                  CC        CC  TGTA
GAM542  ABH     3'  TGGAAACTCACTTCTACCTTCC 40743          _ _  AC
                                TGGAAACTTACT C GCC  CC
                                |||||||||||| | |||  ||
                                ACCTTTGAGTGA G TGG  GG
                                       A A   AA
GAM542  BAK1    3'  AGAAGGCACTGTCACCCCCCA  45104     ACT   CGC
                                GGAA   TACT   CACCCCCCA
                                ||||   ||||   |||||||||
                                TCTT   GTGA   GTGGGGGGT
                                  CC_    CA_
GAM542  CDKN2D   3'  GGACGCTCCCCCCCACCCCCCA  38613     AA  A   G
                                GGA  CTT CTC CCACCCCCCA
                                |||  ||| ||| ||||||||||
                                CCT  GAG GGG GGTGGGGGGT
                                  GC   _   _
GAM542  COL5A1   5'  TGGGGACCTCGGCACCCCCC   6421     AA  TTA   C
                                TGG  AC   CTCG CACCCCCC
                                |||  ||   |||| ||||||||
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                                ACC  TG   GAGC GTGGGGGG
                                  CC  ___    C
GAM542  FBXL2    3'  TGGAAACCTATTAACATGCCTT 29122         ____  TC   AC
            CC                    TGGAAACTT    AC  GCC  CC
                                  |||||||||    ||  |||  ||
                                  ACCTTTGGA    TG  CGG  GG
                                       TAAT  TA   AA
GAM542  GGA1     3'  TGGGGGTGTAGGCGTCACCCCC 30051     AAACTTACT  C
            CA                    TGG        CG CACCCCCCA
                                  |||        || |||||||||
                                  ACC        GC GTGGGGGGT
                                    CCCACATCC  A
GAM542  HTR2A    3'  TGAAAACTTGCTCAGTGTGCCT 8389          A  ______  AC
            TCC                    TGGAAACTT CTC     GCC  CC
                                  |||||||||  |||     |||  ||
                                  ACTTTTGAA GAG     CGG  GG
                                       C   TCACA   AA
GAM542  IRS1     5'  GAAATCCACGCCGCCCCCC   24419      C  ACT    A
                                  GAAA TT   CGCC CCCCCC
                                  ||||  ||   ||||  ||||||
                                  CTTT AG   GCGG GGGGGG
                                    _  GT_    C
GAM542  S100A5   3'  TGGAAACTTTATTTCCTCCC   16446         ACTCG  A
                                  TGGAAACTT     CC CCC
                                  |||||||||     ||  |||
                                  ACCTTTGAA     GG GGG
                                       ATAAA  A
GAM542  SPTA1    3'  TAGAAACTTTGACACCCCTCA  17098         ACTCGC     C
                                  TGGAAACTT      CACCCC CA
                                  |||||||||      ||||||  ||
                                  ATCTTTGAA      GTGGGG GT
                                       ACT___      A
GAM542  TDGF1    3'  TGGAAACTTGCCCTTCCA    17366         A  G_
                                  TGGAAACTT CTC  CCA
                                  |||||||||  |||  |||
                                  ACCTTTGAA GGG  GGT
                                       C   AA
GAM542  B3GNT3   3'  GTGGACACAGGAGTTTCTGGC  30680         AT   _  A
                                  GTGGGCACA  AGTT CT GC
                                  |||||||||  ||||  ||  ||
                                  CACCTGTGT  TCAA GA CG
                                       CC    A  C
GAM542  BACE2    3'  GTGGGCACAGGAGAAAGC    39995         AT  TTCT
                                  GTGGGCACA  AG    AGC
                                  |||||||||  ||    |||
                                  CACCCGTGT  TC    TCG
                                       CC  TT__
GAM542  CLDN14   5'  GTGGGCACACGTGCCACT    29082         ATA  _
                                  GTGGGCACA   GTT CT
                                  |||||||||   |||  ||
```

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                                CACCCGTGT  CGG GA
                                     GCA  T
GAM542  FCER2   5'  GCGGGCACAATCACAGC    12813        AGTTC
                                GTGGGCACAAT   TAGC
                                ||||||||||    ||||
                                CGCCCGTGTTA   GTCG
                                      GT___
GAM542  GH2     3'  GTGGGCACTGGAGTAGC    35434       AAT  TCT
                                GTGGGCAC  AGT  AGC
                                ||||||||  |||  |||
                                CACCCGTG  TCA  TCG
                                    ACC  ___
GAM542  IDUA    3'  ATGGGCACAGTGCAG      6812        ATA  TC
                                GTGGGCACA  GT  TAG
                                |||||||||  ||  |||
                                TACCCGTGT  CA  GTC
                                    ___  C_
GAM542  KCNJ10  3'  GGCGACCATGGTTCTAGC   13871    _  A  A
                                GGC AC AT GTTCTAGC
                                ||| || || ||||||||
                                CCG TG TA CAAGATCG
                                  C  G  C
GAM542  LGI1    3'  GTAGTGCTTGGTTCTAGC   22997    _  ACAATA
                                GTGG GC    GTTCTAGC
                                |||| ||    ||||||||
                                CATC CG    CAAGATCG
                                  A  AAC___
GAM542  LLGL1   3'  CGGGATAGTTCTGGC      42502     CACA      A
                                TGGG   ATAGTTCT GC
                                ||||   |||||||| ||
                                GCCC   TATCAAGA CG
                                  ____      C
GAM542  MAP2    3'  GTGGACACAAATCTAGC    36504        TAGT
                                GTGGGCACAA   TCTAGC
                                ||||||||||   ||||||
                                CACCTGTGTT   AGATCG
                                      T___
GAM542  NDST1   3'  GTGGGATGTCCTAG       11372     CACA  A
                                GTGGG   AT GTTCTAG
                                |||||   || |||||||
                                CACCC   TA CAGGATC
                                  ____  _
GAM542  OLFM1   3'  GTGGGCTGCAGTTCCAGC   26778      ACAA
                                GTGGGC   TAGTTCTAGC
                                ||||||   ||||||||||
                                CACCCG   GTCAAGGTCG
                                   AC__
GAM542  PDGFRB  5'  GTGGGCACAGTTCCAG     42341        ATA
                                GTGGGCACA  GTTCTAG
                                |||||||||  |||||||
```

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                                CACCCGTGT  CAAGGTC
                                     ___
GAM542  PLXNB3   3'  TGGGCACAGTGCCTGGC    23952       ATA  _  A
                                TGGGCACA  GT TCT GC
                                ||||||||  || ||| ||
                                ACCCGTGT  CA GGA CG
                                    ___ C  C
GAM542  PPP1CC   5'  GTGGTGCTTCAAGTTCTAG   43918    _ ACAAT
                                GTGG GC    AGTTCTAG
                                |||| ||    ||||||||
                                CACC CG    TCAAGATC
                                  A  AAGT_
GAM542  SARDH    3'  GGGCACAAGTTCTGGC     28250      AT    A
                                GGGCACA  AGTTCT GC
                                |||||||  |||||| ||
                                CCCGTGT  TCAAGA CG
                                   __    C
GAM542  SERPINH2 3'  GTGGAGTGAATTCTAGC    10298     CACAAT
                                GTGGG    AGTTCTAGC
                                |||||    |||||||||
                                CACCT    TTAAGATCG
                                  CAC___
GAM542  SIAH2    3'  GTGGATCTATAGTTCTAG    22866     CACA
                                GTGGG   ATAGTTCTAG
                                |||||   ||||||||||
                                CACCT   TATCAAGATC
                                  AGA_
GAM542  SLC25A1  3'  GTGGGCACAGGGTCATAG   25604       ATA  C
                                GTGGGCACA  GTT TAG
                                |||||||||  ||| |||
                                CACCCGTGT  CAG ATC
                                     CC_  T
GAM543  B4GALT1  3'  TGGGTTTGTGACAGACAGACC  11293    AACTC      GT_
                                TGG   GTGACAGAT  CT
                                |||   |||||||||  ||
                                ACC   CACTGTCTG  GG
                                  CAAA_       TCT
GAM543  BACE     3'  TGGGGTGAGGAGATGTCT   39974    AACTC   C_
                                TGG   GTGA  AGATGTCT
                                |||   ||||  ||||||||
                                ACC   CACT  TCTACAGA
                                  C____   CC
GAM543  EHD3     3'  TGGTGCTGTTGGATGTCTA   31119    AA  C  GACA
                                TGG  CT GT   GATGTCTA
                                |||  || ||   ||||||||
                                ACC  GA CA   CTACAGAT
                                  AC  _  AC__
GAM543  PFKFB4   3'  TGGGGCTCTGACAGATG    21299    AA  G
                                TGG  CTC TGACAGATG
                                |||  ||| |||||||||
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                                ACC  GAG ACTGTCTAC
                                  CC  _
GAM543  SDPR    3'  TGGAGTCCGTGACAGGTC    21651     AC       AT
                                TGGA  TCGTGACAG  GTC
                                ||||  |||||||||  |||
                                ACCT  GGCACTGTC  CAG
                                  CA       __
GAM544  CDH1    3'  TACAGTGAGCTATGATCACAT  20368      TT  A  C
                                TACAGT  GC TA GATCACAT
                                ||||||  || || ||||||||
                                ATGTCA  CG AT CTAGTGTA
                                   CT  _  A
GAM544  GBE1    3'  GCTGTATTTGCATAAACCA   6688     ACA       C
                                GCT   GTTTGCATA GATCA
                                |||   ||||||||| |||||
                                CGA   TAAACGTAT TTGGT
                                  CA_       _
GAM544  GHR     3'  GCTATGGTTTGCATTCAAT   6713      CA      A
                                GCTA  GTTTGCAT CGAT
                                ||||  |||||||| ||||
                                CGAT  CAAACGTA GTTA
                                  AC       A
GAM544  MAP3K5  3'  CAGTGGTGCACGATCACAT   25436     T_  AT
                                CAGT  TGC  ACGATCACAT
                                ||||  |||  ||||||||||
                                GTCA  ACG  TGCTAGTGTA
                                  CC  __
GAM544  POLH    3'  GCTAAGTTTGCAACCAC     27101     C      TACG
                                GCTA AGTTTGCA   ATCAC
                                |||| ||||||||   |||||
                                CGAT TCAAACGT   TGGTG
                                  _      ____
GAM545  CYP39A1  3'  AGATACGTTTACAATAAAGAA  32462    G       TAC_
                                AGA TACGTTTAC   GAGAA
                                ||| |||||||||   |||||
                                TCT ATGCAAATG   TTCTT
                                  _       TTAT
GAM545  CYP3A43  3'  GAGATAGTCTTATGAGAACTA  38399    TAC   AC  C
                                GAG   GTTT  TA GAGAACTA
                                |||   ||||  || ||||||||
                                CTC   CAGA  AT CTCTTGAT
                                  TAT   __  A
GAM545  IRS2    3'  AGGTAACATCTGCGAGAACT   40694    A  _    ACTA
                                AG GTA CGTTT   CGAGAACT
                                || ||| |||||   ||||||||
                                TC CAT GTAGA   GCTCTTGA
                                  _  T    C___
GAM545  NDUFS2  5'  AGGGTCGTTTACCGTCGAACT  21238    A  A      ACGA
                                AG GT CGTTTACT   GAACT
                                || || ||||||||   |||||
```

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                                TC CA GCAAATGG    CTTGA
                                 C _       CAG_
GAM546  CD164    3'  AGGTACAATAGTGCTAGCA   25679     _  TCAA      C
                                AGG ACA    ATAGTGC AGCA
                                ||| |||    ||||||| ||||
                                TCC TGT    TATCACG TCGT
                                  A _____      A
GAM546  CNTNAP2  3'  TAGGACATCAAAGGAAATAGTA 30493          _____
                                TAGGACATCAA     ATAGTG
                                ||||||||||     ||||||
                                ATCCTGTAGTT     TATCAT
                                       TCCTT
GAM546  GRB10    3'  GGCAATATCATGGCCAGCAC   23661    A  TCAAATA  _
                                GG CA      GTG CCAGCAC
                                || ||      ||| |||||||
                                CC GT      TAC GGTCGTG
                                 _  TATAG__   C
GAM546  HADHB    3'  TAGGACACAGATAAGAACAAG  6768         CAAAT  T  C
                                TAGGACAT     AG GC AG
                                ||||||||     || || ||
                                ATCCTGTG     TC TG TC
                                     TCTAT  T  T
GAM546  HHLA1    5'  TAGGACATCTAATTAGAGAGTG 25053         A  _____
          C                      TAGGACATC AAT     AGTGC
                                ||||||||| |||     |||||
                                ATCCTGTAG TTA     TCACG
                                     A   ATCTC
GAM546  HIP1     3'  GGGGGTCAAATAGTCAGC    23756    ACA       GC
                                GG   TCAAATAGT  CAGC
                                ||   |||||||||  ||||
                                CC   AGTTTATCA  GTCG
                                 CCC       __
GAM546  SERPIND1 3'  GGACATCAAGAATGGTGC    6774          __  A
                                GGACATCAA  AT GTGC
                                |||||||||  || ||||
                                CCTGTAGTT  TA CACG
                                     CT  C
GAM546  SLC14A2  5'  GAGCCAAGATAGTGCCAG    28398    CA   _
                                GA  TCAA ATAGTGCCAG
                                ||  |||| ||||||||||
                                CT  GGTT TATCACGGTC
                                 C_    C
GAM546  SMAP     3'  TAGGACATTAACATAGCCCA   27453        CAA_    G
                                TAGGACAT    ATAGT CCA
                                ||||||||    ||||| |||
                                ATCCTGTA    TATCG GGT
                                     ATTG    _
GAM546  UBE4A    3'  GATATCAAATAGCAACTGGCAC 21972    C         _ CA
                                GA ATCAAATAGTG C  GCAC
                                || ||||||||||| |  ||||
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                                CT TAGTTTATCGT G  CGTG
                                 A         T AC
GAM547  ATF2     3'  ACTGTTGTACTGCAG       12435         TAAACT
                                ACTGTTGT     ACTGCAG
                                ||||||||     |||||||
                                TGACAACA     TGACGTC
                                     _______
GAM547  CDH18    5'  TGCTGTCACTCTGCTGCAGAC  22343         AA  A
                                TGTTGTTA  CT CTGCAGAC
                                ||||||||  || ||||||||
                                ACGACAGT  GA GACGTCTG
                                     GA  C
GAM547  HMGA2    5'  CTGTTGCTTAGGCTGCCGC   18512         AAA_  A
                                CTGTTGTT    CT CTGC
                                ||||||||    || ||||
                                GACAACGA    GA GGCG
                                     ATCC  C
GAM547  LGS      3'  CTGTTGTTAATTACAAA     32442          ACTAC
                                CTGTTGTTAA     TGCAGA
                                ||||||||||     ||||||
                                GACAACAATT     ATGTTT
                                      A____
GAM547  MYD88    3'  TGATGTCCAGCTGCTGCAGAC  14722    T    AAA  A
                                TG TGTT   CT CTGCAGAC
                                || ||||   || ||||||||
                                AC ACAG   GA GACGTCTG
                                 T    GTC  C
GAM547  TADA2L   3'  TCCTCAAAAGACTACTGCAGA  39427    G    ___
                                TT TTAA   ACTACTGCAGA
                                || ||||   ||||||||||
                                AG AGTT   TGATGACGTCT
                                 G    TTC
GAM547  TFCP2    5'  TTGCTCAACTACTGCAGA     24925       A
                                TTGTT AACTACTGCAGA
                                ||||| ||||||||||
                                AACGA TTGATGACGTCT
                                   G
GAM547  TRDN     3'  TAATTGCCTGAACTACTGTGGA 25878    T     A_       CA
           C                     C GTTGTT  AACTACTG  GAC
                                | ||||||  ||||||||  |||
                                A TAACGG  TTGATGAC  CTG
                                 T     AC       AC
GAM548  MAG      5'  GAGTGATCGCTGAATC      38746      ATAGT
                                GAGT    TCGTTGAATC
                                ||||    ||||||||||
                                CTCA    AGCGACTTAG
                                  CT____
GAM548  MFRP     3'  AGTACATTTTTGTTGAATC   36423        GTTC_
                                AGTATA    GTTGAATC
                                ||||||    ||||||||
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                                TCATGT    CAACTTAG
                                   AAAAA
GAM548  P23     3'  CGGGTATAAGCTGAATC    27339    A    TTC
                                CG GTATAG   GTTGAATC
                                || ||||||   ||||||||
                                GC CATATT   CGACTTAG
                                 C    ____
GAM548  RBM8A   3'  GAGATAATTTTGTTGAATC   23013    T    C_
                                GAG ATAGTT  GTTGAATC
                                ||| ||||||  ||||||||
                                CTC TATTAA  CAACTTAG
                                  _     AA
GAM548  SNTB1   3'  GAGTATAGTCCCAGAAT    34280         GTT
                                GAGTATAGTTC   GAAT
                                ||||||||||   ||||
                                CTCATATCAGG   CTTA
                                      GT_
GAM549  TNP1    3'  TGCTGTTCTTGTTGCTGCT   40476       G   C  GAA
                                TGCTGTTC TGT GC   GCT
                                |||||||| ||| ||   |||
                                ACGACAAG ACA CG   CGA
                                     A   A  A__
GAM550  APOL1   3'  CCGCCTTGGCCTCCCAAAGTGC 18934      C      _____
                                CCGCTT GGCCTCCC    TGC
                                |||||| ||||||||    |||
                                GGCGGA CCGGAGGG    ACG
                                   A       TTTC
GAM550  ARHGAP6 3'  GCTTGGCCTCCCTGGTCC    30219     C       CACG
                                GCTT GGCCTCCCTG    CC
                                |||| ||||||||||    ||
                                CGAA CCGGAGGGAC    GG
                                  _        CA__
GAM550  CHN2    5'  CCGCTCCGCGCCTTTGCACGCC 19810       _   CCC
            C                    CCGCTTCG GCCT   TGCACGCCC
                                |||||||| ||||   |||||||||
                                GGCGAGGC CGGA   ACGTGCGGG
                                     G    A__
GAM550  CHRNA4  5'  CCGCTTCGGCCGCCGGGCC   8848          T  CTGCAC
                                CCGCTTCGGCC CC     GCC
                                |||||||||| ||     |||
                                GGCGAAGCCGG GG     CGG
                                      C  CC_____
GAM550  DPYSL3  5'  GCTCCGGCTCGCCCGCGCC   10771       C  _    AC
                                GCTTCGGC TC CCTGC  GCC
                                |||||||| || |||||  |||
                                CGAGGCCG AG GGGCG  CGG
                                     _ C    ___
GAM550  EFNB1   5'  CGCTTCGGGGCTGCGCGCCC  20716       CCTCC   A
                                CGCTTCGG    CTGC CGCCC
                                ||||||||    |||| |||||
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                                GCGAAGCC    GACG GCGGG
                                    CC___   C
GAM550  EPB49   5'  CCGCTTCGCCTTCTCCTG    12725       G  _ _
                                CCGCTTCG CCT C CCTG
                                |||||||| ||| | ||||
                                GGCGAAGC GGA G GGAC
                                    _   A A
GAM550  FLI1    5'  CCTGGGCCCTCCCTGCGTGCCC 44118    C   _     AC
                                CTT GGCC TCCCTGC  GCCC
                                ||| |||| |||||||  ||||
                                GGA CCGG AGGGACG  CGGG
                                  C   G     CA
GAM550  HMGA2   5'  CCGCTTCGCCTCGACCGCC   18505       G   CCT  A
                                CCGCTTCG CCTC   GC CGCC
                                |||||||| ||||   || ||||
                                GGCGAAGC GGAG   TG GCGG
                                    _   C__  _
GAM550  HUNK    5'  CTTCGGCTTCCCCGGC     31067       C    CAC
                                CTTCGGC TCCCTG   GC
                                ||||||| ||||||   ||
                                GAAGCCG AGGGGC   CG
                                    A    ___
GAM550  JUND    5'  CCGCTCGGCCCTGCGC     23801      T    TCC   AC
                                CCGCT CGGCC   CTGC  GC
                                ||||| |||||   ||||  ||
                                GGCGA GCCGG   GACG  CG
                                  _    ____   __
GAM550  KCNQ3   5'  CCGCTTCGCCTTCTCCGCTGCT 21126       G ___  _   AC
          GC                    CCGCTTCG CC   TCC CTGC  GC
                                |||||||| ||   ||| ||||  ||
                                GGCGAAGC GG   AGG GACG  CG
                                    _ AAG   C   A_
GAM550  KIF1B   3'  CCGCCTCGGCCTCCCCAAGTGC 31461            CAC
                                CCGCTTCGGCCTCCCTG   GC
                                ||||||||||||||||   ||
                                GGCGGAGCCGGAGGGGT   CG
                                        TCA
GAM550  LETM1   5'  CCGCTCCGGCCTCCTGCGCTGC 29500          C   AC_
          C                     CCGCTTCGGCCTCC TGC   GCC
                                |||||||||||||| |||   |||
                                GGCGAGGCCGGAGG ACG   CGG
                                        _   CGA
GAM550  MAPT    3'  GCCTCGGCCTCCCCCGTGGCC  32580          GCAC
                                GCTTCGGCCTCCCT    GCC
                                ||||||||||||||   |||
                                CGGAGCCGGAGGGG    CGG
                                        GCAC
GAM550  NAT8    5'  GCTAGGCCTCCCTGCACGCC   19551    TC
                                GCT  GGCCTCCCTGCACGCC
                                |||  ||||||||||||||||
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                                CGA  CCGGAGGGACGTGCGG
                                  T_
GAM550  PPOX    5'  CCTTTTCGGTCTCTCCTAC   7179    GC    C  _
                                CC  TTCGG CTC CCTGC
                                ||  ||||| ||| |||||
                                GG  AAGCC GAG GGATG
                                 AA    A  A
GAM550  PRKY    3'  GCTTCAGCTTCCCCAAATCC  15701       C    GCACG
                                GCTTCGGC TCCCT    CC
                                |||||||| |||||    ||
                                CGAAGTCG AGGGG    GG
                                     A    TTTA_
GAM550  RBL1    3'  CCGCCTTGGCCTCCCAAAGTCC 16175      C      TGCACG
                                CCGCTT GGCCTCCC     CC
                                |||||| ||||||||     ||
                                GGCGGA CCGGAGGG     GG
                                   A       TTTCA_
GAM550  RCN1    3'  CCGTTTGGCTTCCCAAGGATCC 16201    C  C   C    TGCACG
                                CCG TT GGC TCCC     CC
                                ||| || ||| ||||     ||
                                GGC AA CCG AGGG     GG
                                 _  A   A    TTCCTA
GAM550  TCF1    3'  GCTTCGGCCTCCCTGGGC    8090            CAC
                                GCTTCGGCCTCCCTG   GC
                                ||||||||||||||   ||
                                CGAAGCCGGAGGGAC   CG
                                          C__
GAM551  PRDM1   5'  GCGCGGTCGCTGCTC      10183     ACGATC  C
                                GCGC     GG TGCTGTTT
                                ||||     || ||||||||
                                CGCG     CC GCGACGAG
                                  _______  A
GAM552  ACCN1   3'  GCTTCTTTCCAGCACTGGGGCC 9913    CCCC_   CGA
                                GC    TCC   GCTGGGGCC
                                ||    |||   |||||||||
                                CG    AGG   TGACCCCGG
                                 AAGAA   TCG
GAM552  ADD1    3'  CGGCCCCCTCCTCGACAGCT   30517          _   __
                                CGGCCCCCTCC CGA  GCT
                                |||||||||| |||  |||
                                GCCGGGGGAGG GCT  CGA
                                       A   GT
GAM552  ALDH8A1 3'  CAGCCTCCCAAGTAGCTGGGGC 35451      _   TCCCG
                                CGGCC CCC    AGCTGGGGC
                                ||||| |||    |||||||||
                                GTCGG GGG    TCGACCCCG
                                   A   TTCA_
GAM552  ARHGDIA 3'  GCTCCCTCCTGAAGCCAGGCC  20208    C     C_    TG  G
                                GC CCCTCC  GAGC  GG CC
                                || ||||||  ||||  || ||
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                                CG GGGAGG  TTCG  CC GG
                                 A     AC    GT _
GAM552  ASC      5'  GGTCCCCTCCCACCCAGGCC  29944    C       GA   G
                                GG CCCCTCCC  GCT GGGCC
                                || ||||||||  ||| |||||
                                CC GGGGAGGG  TGG TCCGG
                                 A       __  G
GAM552  ASIC4    5'  GGTGCCCTCCCGAGTGG     33066    CC        C
                                GG  CCCTCCCGAG TGG
                                ||  ||||||||||| |||
                                CC  GGGAGGGCTC ACC
                                 AC         _
GAM552  ATP5J    5'  CGGCCTCGTTCCGGGGC     11769      CCCTCC  AG
                                CGGCC     CG  CTGGGGC
                                |||||     ||  |||||||
                                GCCGG     GC  GGCCCCG
                                   A_____  AA
GAM552  AXIN1    5'  CGGCCCCCATCTCGGCGGC   41376        _  C  A  TGG
                                CGGCCCCC TC CG GC   GGC
                                |||||||| || || ||   |||
                                GCCGGGGG AG GC CG   CCG
                                     T  A  _  ___
GAM552  BACH2    5'  CAGCCCCCTCCCGGCAGC    34781           A  TGG
                                CGGCCCCCTCCCG GC   GGC
                                |||||||||||| ||   |||
                                GTCGGGGGAGGGC CG   TCG
                                           _  ___
GAM552  BARHL1   3'  GGCCCCTTCCTGCCCCGCC   33468      C   CGA   GGG
                                GGCCCC TCC   GCT   GCC
                                |||||| |||   |||   |||
                                CCGGGG AGG   CGG   CGG
                                   A  A__   GG_
GAM552  BCAR1    3'  GCCTCCCTCCTGGGG      41942    _     CGAGC
                                GCC CCCTCC    TGGGG
                                ||| ||||||    |||||
                                CGG GGGAGG    ACCCC
                                  A    _____
GAM552  BLTR2    5'  GGCCTCTCCTGGGGC      33369     CC   CGAGC
                                GGCC  CTCC    TGGGGC
                                ||||  ||||    ||||||
                                CCGG  GAGG    ACCCCG
                                  A_   _____
GAM552  CACNB1   3'  CGGGTCCTCTCCCCTGGGGCC  8780     CC  _    GAG
                                CGG  CC CTCCC   CTGGGGCC
                                |||  || |||||   ||||||||
                                GCC  GG GAGGG   GACCCCGG
                                  CA  A    ___
GAM552  CARKL    3'  GGCCCCCTCCTGGAAGC     29999         CGAGC   _
                                GGCCCCCTCC    TGGG GC
                                ||||||||||    |||| ||
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                                CCGGGGGAGG    ACCT CG
                                      _____   T
GAM552  CCNF    3'  GCCTCCCTCCCACGGGC    12075    _      AGCTG
                                GCC CCCTCCCG    GGGC
                                ||| ||||||||    ||||
                                CGG GGGAGGGT    CCCG
                                  A       G____
GAM552  CDA     3'  CAGTCCCTGTAGGCTGGGGCC  12144    CC    CCCGA
                                CGG  CCCT    GCTGGGGCC
                                |||  ||||    |||||||||
                                GTC  GGGA    CGACCCCGG
                                  A_   CATC_
GAM552  CELSR3   5'  GGCCCCCTCCCGGG       10839          GAGCTG
                                GGCCCCCTCCC     GGG
                                ||||||||||     |||
                                CCGGGGGAGGG     CCC

                                       _______
GAM552  CELSR3   3'  CAGCCCTTCAAGAGCTGGGG   10827       CC  CC
                                CGGCCC  TC  GAGCTGGGG
                                ||||||  ||  |||||||||
                                GTCGGG  AG  CTCGACCCC
                                   A_  TT
GAM552  CLTC    5'  GGTCTCCTCCTGTCACTGGGGC 22153    CCC    CGA_
                                GG   CCTCC   GCTGGGGC
                                ||   |||||   ||||||||
                                CC   GGAGG   TGACCCCG
                                 AGA    ACAG
GAM552  COG4    3'  CAGCTCCTTGGCTGGGGC    31720     CCCC   CGA
                                CGGC   TCC   GCTGGGGC
                                ||||   |||   ||||||||
                                GTCG   AGG   CGACCCCG
                                  _____  AAC
GAM552  COL17A1  3'  GGCTTTCCTAGGCTGGGGC   39082    CCCC   CGA
                                GGC   TCC   GCTGGGGC
                                |||   |||   ||||||||
                                CCG   AGG   CGACCCCG
                                  AA__  ATC
GAM552  CSNK1G2  3'  CCCCCTCCCAGGAGGGCC    10609        G  CT
                                CCCCCTCCC AG  GGGGCC
                                ||||||||| ||  ||||||
                                GGGGGAGGG TC  TCCCGG
                                      _ C_
GAM552  DGCR2    3'  GGCCCCCTCCTGAGGGCGGCC  23098         C   CT  _
                                GGCCCCCTCC GAG  GG GGCC
                                |||||||||| |||  || ||||
                                CCGGGGGAGG CTC  CC CCGG
                                      A   __  G
GAM552  DUX4    5'  CGGCTCCCTCCCGCCCGC    43758     C      AG  GGG
                                CGGC CCCTCCCG  CT   GC
                                |||| ||||||||  ||   ||
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                                GCCG GGGAGGGC  GG   CG
                                  A       G_ ___
GAM552  ECH1     3'  CGGCCCCCTGGCTGGGGCC   40865         CCCGA
                                CGGCCCCCT    GCTGGGGCC
                                |||||||||    |||||||||
                                GCCGGGGGA    CGACCCCGG
                                     C____
GAM552  EDN3     3'  AGCCTTGAGCTGGGGC      6481       CCCTCCC
                                GGCC      GAGCTGGGGC
                                ||||      ||||||||||
                                TCGG      CTCGACCCCG
                                  AA_____
GAM552  EGFL4    3'  CAGCCCCCTCCCATGGG     41560           AGC
                                CGGCCCCCTCCCG   TGGG
                                ||||||||||||   ||||
                                GTCGGGGGAGGGT   ACCC
                                       ___
GAM552  EN2      3'  GGCCTCATTTCTGGGACC    10960     CCC  CCGAG
                                GGCC   TC    CTGGGGCC
                                ||||   ||    ||||||||
                                CCGG   AG    GACCCTGG
                                  ___  TAAA_
GAM552  FAT2     3'  GCCCCTCTCCTGGGAC      11076      _   CGAGC
                                GCCCC CTCC    TGGGGC
                                ||||| ||||    ||||||
                                CGGGG GAGG    ACCCTG
                                  A   _____
GAM552  FGFR3    3'  CGGCCCCTCCCTGGAAACC   6614        C    GAGCT GG
                                CGGCCCC TCCC    G  GCC
                                ||||||| ||||    |  |||
                                GCCGGGG AGGG    C  TGG
                                    _   AC___ TT
GAM552  FMNL     3'  CGGTCCTCGGGGCTGGGGC   25298     CCC    CCGA
                                CGG   CCTC    GCTGGGGC
                                |||   ||||    ||||||||
                                GCC   GGAG    CGACCCCG
                                  A__    CCC_
GAM552  FPGS     3'  CGGCCCCCCTTCCTCGAGGGCC 22428         __   _   GCTG
                                CGGCCCCC  TCC CGA    GGGCC
                                ||||||||  ||| |||    |||||
                                GCCGGGGG  AGG GCT    CCCGG
                                    GA   A   _____
GAM552  GCGR     3'  CAGCCCTAGCTGGGG       6691        CCTCCCG
                                CGGCCC      AGCTGGGG
                                ||||||      ||||||||
                                GTCGGG      TCGACCCC
                                  A_______
GAM552  GCN5L2   3'  GGCCCCCTTCAGTTTGGGC   40812         CC G  CTG
                                GGCCCCCT  C AG   GGGC
                                ||||||||  | ||   ||||
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                              CCGGGGGA  G TC   CCCG
                                  A_ _  AAA
GAM552  GGA1    3'  CAGCCCCTCGCTGGGGC    30045       C  CCGA
                              CGGCCCC TC   GCTGGGGC
                              ||||||| ||   ||||||||
                              GTCGGGG AG   CGACCCCG
                                  _ _____
GAM552  GPC1    3'  GGCCTCTGTCCCTGGGGCC   13253     CCC_   GAGC
                              GGCC   TCCC   TGGGGCC
                              ||||   ||||   |||||||
                              CCGG   AGGG   ACCCCGG
                                AGAC   _____
GAM552  GPR30   5'  GGCCTCTTCCCCACCAGGGCC 11314     CCC   GA  TG
                              GGCC   TCCC  GC  GGGCC
                              ||||   ||||  ||  |||||
                              CCGG   AGGG  TG  CCCGG
                                AGA    G_  GT
GAM552  GRB10   3'  GGCCAGCGAGCTGGGGC    23662     CCCTCC
                              GGCC     CGAGCTGGGGC
                              ||||     ||||||||||
                              CCGG     GCTCGACCCCG
                                TC_____
GAM552  HDAC5   3'  CAGCCCCCTCCTGGTCTTAGC 40161         CGAG  GG
                              CGGCCCCCTCC   CT  GGC
                              ||||||||||    ||  |||
                              GTCGGGGGAGG   GA  TCG
                                    ACCA  A_
GAM552  HIP12   3'  GGTCCCCTCCCTGAGGGCC   42404    C      GAGCT
                              GG CCCCTCCC    GGGGCC
                              || ||||||||    ||||||
                              CC GGGGAGGG    TCCCGG
                               A       AC___
GAM552  HOXB3   5'  GCCCCCCTCCTCCGGGG     13439      TC  GAG
                              GCCCCC  CC   CTGGGG
                              ||||||  ||   ||||||
                              CGGGGG  GG   GGCCCC
                                 GA  A__
GAM552  HR      5'  CGGCCCCCTCCCGGG      32916          GAGCTG
                              CGGCCCCCTCCC     GGG
                              ||||||||||||     |||
                              GCCGGGGGAGGG     CCC
                                      _______
GAM552  ICMT    3'  GGTCCCCTTGGCCTGGGGCC  29658    C    CCCGAG
                              GG CCCCT     CTGGGGCC
                              || |||||     ||||||||
                              CC GGGGA     GACCCCGG
                               A    ACCG__
GAM552  IFNGR2  5'  GCCTCTTCCCGAGCGGC    24385     CCC       TGG
                              GCC   TCCCGAGC   GGC
                              |||   ||||||||   |||
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                                CGG  AGGGCTCG  CCG
                                  AGA      ___
GAM552  IL15    5'  CAGTTCCCTCCCGGGGGGC  8224     CC      AGCT
                                CGG  CCCTCCCG  GGGGC
                                |||  ||||||||  |||||
                                GTC  GGGAGGGC  CCCCG
                                  AA      C___
GAM552  IL2RA   3'  GGTCTCCTAGGGAGCTGGGG  7672    CCCC   C___
                                GG   CTCC   GAGCTGGGG
                                ||   ||||   |||||||||
                                CC   GAGG   CTCGACCCC
                                 A___   ATCC
GAM552  IL2RB   5'  GGCCATCTCTCCAGGGC    9387      CC  _  GAGCT
                                GGCC  CTC CC    GGGGC
                                ||||  ||| ||    |||||
                                CCGG  GAG GG    TCCCG
                                  TA  A  _____
GAM552  ITGA5   3'  GGCTTCAGGGAGGCTGGGGCC  41499    CCCC  CC_  _
                                GGC   TC   GAG CTGGGGCC
                                |||   ||   ||| ||||||||
                                CCG   AG   CTC GACCCCGG
                                  A___  TCC   C
GAM552  KCNA7   3'  CGGCCTCCCAAAGTGCTGGGG  36652     CCC    ___
                                CGGCC   TCCCGA   GCTGGGG
                                |||||   ||||||   |||||||
                                GCCGG   AGGGTT   CGACCCC
                                   ___     TCA
GAM552  KCNC4   5'  CGGCCCCCTCTGCGG      22527         CCGAGC  G
                                CGGCCCCCTC     TG GG
                                ||||||||||     || ||
                                GCCGGGGGAG     AC CC
                                     _______  G
GAM552  KCNH2   3'  GCCCCTCTCACTGGGGC    6948       _  CCGA
                                GCCCC CTC    GCTGGGGC
                                ||||| |||    ||||||||
                                CGGGG GAG    TGACCCCG
                                  A  _____
GAM552  LIM2    3'  CAGCTCCCTCCCATGGGC    36183     C     GAGCTG
                                CGGC CCCTCCC     GGGC
                                |||| |||||||     ||||
                                GTCG GGGAGGG     CCCG
                                  A      TA_____
GAM552  LIMK1   5'  GGCCCGGCGGGGCTGGGGC   32532     CCTCC  A_
                                GGCCC    CG  GCTGGGGC
                                |||||    ||  ||||||||
                                CCGGG    GC  CGACCCCG
                                   CC___  CC
GAM552  LOXL1   5'  GGCCTTGTCCCGAGCGGGAC   41185     CCC      T
                                GGCC   TCCCGAGC GGGGC
                                ||||   |||||||| |||||
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                                CCGG  AGGGCTCG CCCTG
                                  AAC      _
GAM552  MB      3'  GCTCTCTCTTGAACCCGGGGCC 23858   CCC  CC   _
                                GC  CTC  GAGCT GGGGCC
                                ||  |||  ||||| ||||||
                                CG  GAG  CTTGG CCCCGG
                                 AGA  AA   G
GAM552  MBP     3'  GGCCCCCTCTCTGTGC     14377        CCGAG  GG
                                GGCCCCCTC    CTG  GC
                                |||||||||    |||  ||
                                CCGGGGGAG    GAC  CG
                                     A____   A_
GAM552  MFI2    5'  GGCTGGGGCCGGGCTGGGGC  25467    CCCCTC  A
                                GGC     CCG GCTGGGGC
                                |||     ||| ||||||||
                                CCG     GGC CGACCCCG
                                  ACCCC_  C
GAM552  MMP14   3'  GGCCCCCTGCTTGGCTTGGCC  22639       CCCGA  GG
                                GGCCCCCT    GCT  GGCC
                                ||||||||    |||  ||||
                                CCGGGGGA    CGA  CCGG
                                    CGAAC   A_
GAM552  MMP15   3'  CAGCCCCCTCTCCCTGGGGC  14558         _  GAG
                                CGGCCCCCTC CC   CTGGGGC
                                |||||||||| ||   |||||||
                                GTCGGGGGAG GG   GACCCCG
                                     A  ____
GAM552  MUC5B   3'  GGCGCCCTCCCGAAAGGGG   42499    C       CT
                                GGC CCCTCCCGAG  GGGG
                                ||| ||||||||||  ||||
                                CCG GGGAGGGCTT  CCCC
                                  C        T_
GAM552  MYO1C   3'  CCTCCCAAAGTGCTGGGG    41469        ____
                                CCTCCCGA   GCTGGGG
                                ||||||||   |||||||
                                GGAGGGTT   CGACCCC
                                    TCA
GAM552  MYO1D   3'  GGCCTTCTCAGCAGCTGGGGC  43500     CC   CCG
                                GGCC  CTC   AGCTGGGGC
                                ||||  |||   |||||||||
                                CCGG  GAG   TCGACCCCG
                                  AA   TCG
GAM552  NBS1    5'  CGGCTCCTCAGGGCTGGGGCC  42986     CC   CCGA
                                CGGC  CCTC    GCTGGGGCC
                                ||||  ||||    |||||||||
                                GCCG  GGAG    CGACCCCGG
                                  A_    TCC_
GAM552  NGFR    3'  GGCCCCCTTCTGGCCAAGCT   14782        _ ____
                                GGCCCCCT C   CCGAGCT
                                |||||||| |   |||||||
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                                CCGGGGGA G   GGTTCGA
                                     A ACC
GAM552  NR2E3    3'  GGTCCCCACTCCCGGGGCC   32286    _   _    GAGCT
                                GG CCCC CTCCC    GGGGCC
                                || |||| |||||    ||||||
                                CC GGGG GAGGG    CCCCGG
                                 A   T   _____
GAM552  OTP      3'  GGCCTCGCGGGCTGGGGC    36997     CCC  C  A
                                GGCC   TC CG GCTGGGGC
                                ||||   || || ||||||||
                                CCGG   AG GC CGACCCCG
                                   ___  C  C
GAM552  PAX5     3'  GGCCTTCCCCAAGCTGGGCC  32516     CC T        G
                                GGCC  C CCCGAGCTGGG CC
                                ||||  | ||||||||||| ||
                                CCGG  G GGGTTCGACCC GG
                                  AA _        _
GAM552  PCDH7    5'  CGCCCCCCTCCTCCGGGGCC  37113    G      CGAG
                                CG CCCCCTCC   CTGGGGCC
                                || ||||||||   ||||||||
                                GC GGGGGAGG   GGCCCCGG
                                 G      A___
GAM552  PFKFB3   5'  CGGCCCGCCTCCCGGGGC    44435      _    GAGCT
                                CGGCCC CCTCCC    GGGGC
                                |||||| ||||||    |||||
                                GCCGGG GGAGGG    CCCCG
                                   C    _____
GAM552  PIK3R2   3'  CGGCCCCCTTGTGGGG     22745        CCCGAGC
                                CGGCCCCCT     TGGGG
                                |||||||||     |||||
                                GCCGGGGGA     ACCCC
                                     AC_____
GAM552  PITX1    3'  CGGCGCGGTGAGCTGGGGC   15323     CCCCTCCC
                                CGGC      GAGCTGGGGC
                                ||||      ||||||||||
                                GCCG      CTCGACCCCG
                                  CGCCA___
GAM552  PLCB2    3'  CAGCCTCAGAAGGCTGGGGC  21319     CCC  CC  _
                                CGGCC  TC  GAG CTGGGGC
                                |||||  ||  ||| |||||||
                                GTCGG  AG  TTC GACCCCG
                                   ___  TC  C
GAM552  PLXNB2   3'  CGGCCGGAGGGAGCTGGGGC  29645     CCCTCCC
                                CGGCC     GAGCTGGGGC
                                |||||     ||||||||||
                                GCCGG     CTCGACCCCG
                                  CCTCC__
GAM552  PPP2CB   5'  GGCGGCCGGGCTGGGGC    20001    CCCCTC  A
                                GGC    CCG GCTGGGGC
                                |||    ||| ||||||||
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                                CCG     GGC CGACCCCG
                                  CC____  C
GAM552  PPP5C   3'  GACCCTCTCTCTGGGG     26490      C   CCGAG
                                GGCCC CTC    CTGGGG
                                ||||| |||    ||||||
                                CTGGG GAG    GACCCC
                                   A  A____
GAM552  PRDM2   3'  CGGCCCCCTTCCTGCCGC    31969        C  GA   GGG
                                CGGCCCCCT CC  GCT   GC
                                ||||||||| ||  |||   ||
                                GCCGGGGGA GG  CGG   CG
                                     A  A_  ___
GAM552  PRX     3'  GGATTCCCACGGCTGGGGCC  34129    CCCCC    A_
                                GG    TCCCG  GCTGGGGCC
                                ||    |||||  |||||||||
                                CC    AGGGT  CGACCCCGG
                                 TA___    GC
GAM552  RAF1    3'  GGCTTCCTTCTCCCAGGGCC  44334     __ C_    GAGCT
                                GGC  CC  CTCCC    GGGGCC
                                |||  ||  |||||    ||||||
                                CCG  GG  GAGGG    TCCCGG
                                 AA  AA   _____
GAM552  RNH     5'  GGCCCCCTTCTGGGG      40605        CCCGAG
                                GGCCCCCT     CTGGGG
                                ||||||||     ||||||
                                CCGGGGGA     GACCCC
                                   A_____
GAM552  RUNX1   3'  GCGTCCCCTGGGTGCTGGGGCC 12023    __    CCCGA
                                GC  CCCCT    GCTGGGGCC
                                ||  |||||    |||||||||
                                CG  GGGGA    CGACCCCGG
                                 CA    CCCA_
GAM552  RXRA    3'  CAGCTCCAGGGCTGGGGC    16415     CCCC   CGA
                                CGGC    TCC   GCTGGGGC
                                ||||    |||   ||||||||
                                GTCG    AGG   CGACCCCG
                                  ____  TCC
GAM552  SCN1B   5'  CGCCCCCCTCCCGGG      9779     G       GAGCTG
                                CG CCCCCTCCC     GGG
                                || |||||||||     |||
                                GC GGGGGAGGG     CCC
                                 G       _______
GAM552  SDC4    3'  GGCCCCAGCTGGGGC      16524       CTCCCG
                                GGCCCC     AGCTGGGGC
                                ||||||     |||||||||
                                CCGGGG     TCGACCCCG
                                   _______
GAM552  SEPN1   3'  GGCCCCTCCTGGCTGGGGC   42429       C   CGA
                                GGCCCC TCC   GCTGGGGC
                                |||||| |||   ||||||||
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                                CCGGGG AGG   CGACCCCG
                                   _   AC_
GAM552  SLC21A9  3'  GCAGACCTGGGCTGGGGCC   28565    CC_  CCCGA
                                GC   CCT    GCTGGGGCC
                                ||   |||    |||||||||
                                CG   GGA    CGACCCCGG
                                 TCT   CC___
GAM552  SLC29A1  3'  GGCTCCCTCCCCAGGGC     22417     C      GAGC
                                GGC CCCTCCC    TGGGGC
                                ||| |||||||    ||||||
                                CCG GGGAGGG    GTCCCG
                                  A      _____
GAM552  SLC2A6   3'  GGCTGCCTGGGCTGGGGC    32772     CC   CCCGA
                                GGC  CCT    GCTGGGGC
                                |||  |||    ||||||||
                                CCG  GGA    CGACCCCG
                                  AC   CC___
GAM552  SMG1     5'  CGGCCCACGACGCTGGGGCC   31507       CCTCC  _
                                CGGCCC    CGA GCTGGGGCC
                                ||||||    ||| |||||||||
                                GCCGGG    GCT CGACCCCGG
                                   T_____   G
GAM552  SOLH     3'  CGGCCCCCGTCGGGTGTTGGGG 24826         _  CCGAGC
           C                     CGGCCCCC TC     TGGGGC
                                ||||||||  ||     ||||||
                                GCCGGGGG AG     ACCCCG
                                     C  CCCACA
GAM552  STIM1    3'  GGGTCTGGGGAGCTGGGGC   41134    CCCC  CCC
                                GG    CT   GAGCTGGGGC
                                ||    ||   ||||||||||
                                CC    GA   CTCGACCCCG
                                 CA__  CCC
GAM552  TCFL4    3'  GGCCCCTCCCTGAGATGGCC   41830       C   _   CTGG
                                GGCCCC TCCC GAG    GGCC
                                ||||||  |||| |||    ||||
                                CCGGGG AGGG CTC    CCGG
                                   _    A   TA__
GAM552  TK1      3'  CGACTTCCTCCTGGAGTGG    17552      CC    C_   C
                                CGGC  CCTCC  GAG TGG
                                ||||  |||||  ||| |||
                                GCTG  GGAGG  CTC ACC
                                  AA    AC   _
GAM552  TMEPAI   5'  CGGCGCCCGGAGCTGGGGCC   33603      C   TCCC
                                CGGC CCC    GAGCTGGGGCC
                                |||| |||    ||||||||||
                                GCCG GGG    CTCGACCCCGG
                                  C   C___
GAM552  TMEPAI   5'  CGGCCTCCCCTCGGCAGC    33602       C    C  A  TGG
                                CGGCC CCTC CG GC   GGC
                                ||||| |||| || ||   |||
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                                GCCGG GGGG GC CG   TCG
                                  A    A  _ ___
GAM552  TNFSF7   5'  CAGCCCCCTCCCGGGGC     10356          GAGCT
                                CGGCCCCCTCCC    GGGGC
                                ||||||||||||    |||||
                                GTCGGGGGAGGG    CCCCG
                                        _____
GAM552  TRPV4    3'  GGTCCCTCGCCTCTGGGGCC  41349    CC    _ GAG
                                GG  CCCTC CC   CTGGGGCC
                                ||  ||||| ||   ||||||||
                                CC  GGGAG GG   GACCCCGG
                                 A_    C  A__
GAM552  USP11    5'  GGTCCCCTCCCTGCAGTATGCC 21634    C       GA  TGGG_
                                GG CCCCTCCC  GC    GCC
                                || ||||||||  ||    |||
                                CC GGGGAGGG  CG    CGG
                                 A       A_  TCATA
GAM552  VIPR2    3'  CGCGCCCCAGCTGGGG      18010    _    CTCCCG
                                CG GCCCC     AGCTGGGG
                                || |||||     ||||||||
                                GC CGGGG     TCGACCCC
                                 G    _______
GAM552  WBP2     3'  CGGCACCTCTCCCGAGGC    43812     _ C      GCTGG
                                CGGC CC CTCCCGA    GGC
                                |||| || |||||||    |||
                                GCCG GG GAGGGCT    CCG
                                  T  A      ______
GAM552  WHSC1    3'  GCTCCCTCCCGAGGAGGCC   39369    C        CT
                                GC CCCTCCCGAG  GGGGCC
                                || ||||||||||  ||||||
                                CG GGGAGGGCTC  CTCCGG
                                 A         __
GAM552  WNT2     3'  GGCCCCCCCATCCTGGGGCC   18108        CCCGAG
                                GGCCCCCT     CTGGGGCC
                                ||||||||     ||||||||
                                CCGGGGGG     GACCCCGG
                                     TAG___
GAM552  XYLB     3'  GGATCCCTCCTGTCTGGGGCC  23023    CC     CGAG
                                GG  CCCTCC    CTGGGGCC
                                ||  ||||||    ||||||||
                                CC  GGGAGG    GACCCCGG
                                 TA     ACA_
GAM552  ZNF76    3'  GGCCCCCTTCTTGAGCAGGGCC 18310         _ CC    T
                                GGCCCCCT C  GAGC GGGGCC
                                |||||||| |  |||| ||||||
                                CCGGGGGA G  CTCG TCCCGG
                                     A AA    _
GAM552  ALDH3A2  3'  GAGTGTGGGGACAGAGTCC   42915     C_    CC    _
                                GAG  TGGGG  CGGA TCC
                                |||  |||||  |||| |||
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                                CTC  ACCCC  GTCT AGG
                                  AC    T_   C
GAM552  CHRNB4   3'  CCTCTGAGCTGGGAAGAATC  8869     CC      CCC
                                CCTC  GAGCTGGGG  GGATC
                                ||||  |||||||||  |||||
                                GGAG  CTCGACCCT  CTTAG
                                  A_      T__
GAM552  GATA4    3'  CGGGCTGGAGCAGGGGTCC   13110    A      CC  A
                                CG GCTGGGGC  GG TCC
                                || ||||||||  || |||
                                GC CGACCTCG  CC AGG
                                 C       TC  C
GAM552  HCK      5'  CTCGCGGGCAGCCCGGATCC  40940    C  A  TGG
                                CTC CG GC   GGCCCGGATCC
                                ||| || ||   ||||||||||
                                GAG GC CG   TCGGGCCTAGG
                                  C  C  ___
GAM552  HSPA4    5'  CGGGCTCGGGCCCGGGTCC   44850    A   G      A
                                CG GCT GGGCCCGG TCC
                                || ||| |||||||| |||
                                GC CGA CCCGGGCC AGG
                                 C   G       C
GAM552  KCNN4    3'  CCTCCCAGAATCCTGGATC   13922       GAGCT   _  C
                                CCTCCC    GGGG CC GGATC
                                ||||||    |||| || |||||
                                GGAGGG    TCTT GG CCTAG
                                   _____   A  A
GAM552  KIF3B    3'  CCCACCTGGGGCCTGGATC   22031     AG      C
                                CCCG  CTGGGGCC GGATC
                                ||||  |||||||| |||||
                                GGGT  GACCCCGG CCTAG
                                  G_      A
GAM552  MCCC2     5'  TCCCTGGCTGGGGCGGA    35252     GA      CC
                                TCCC  GCTGGGGC  GGA
                                ||||  ||||||||  |||
                                AGGG  CGACCCCG  CCT
                                  AC      __
GAM552  NQO1     3'  CCTCTTGAGCCCAGTCGGAT  9477      CC    G  GCC
                                CCTC  GAGCT GG   CGGAT
                                ||||  ||||| ||   |||||
                                GGAG  CTCGG TC   GCCTA
                                  AA    G  A__
GAM552  NSD1     3'  CTCCTTGGTTGGGGCCCACTGG 35361     CGAGC      ___
           AT                    CTCC    TGGGGCCC   GGAT
                                ||||    ||||||||  ||||
                                GAGG    ACCCCGGG   CCTA
                                  AACCA       TGA
GAM552  ORC4L    3'  GAACTAGAAAACCTGGGTC   41607        __   C  A
                                GAGCTGGG  GCC GG TC
                                ||||||||  ||| || ||
```

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                                CTTGATCT  TGG CC AG
                                    TT   A  C
GAM552  PACE     3'  CCTCCCAGCTGGGGTCC     15033       G       C
                                CCTCCC AGCTGGGG CC
                                |||||| |||||||| ||
                                GGAGGG TCGACCCC GG
                                   _       A
GAM552  PHLDA3   3'  CCCCTGAGCTGGGCATGTC   29611      C       GCC  GA
                                CTCC GAGCTGGG   CG  TC
                                |||| ||||||||   ||  ||
                                GGGG CTCGACCC   GT  AG
                                  A       ___  AC
GAM552  RARB     5'  CCTTCCGAATGCGTTCCGGATC 32059     C    C  GGGC
              C                  CCT CCGAG TG    CCGGATCC
                                ||| ||||| ||    ||||||||
                                GGA GGCTT AC    GGCCTAGG
                                  A    _  GCAA
GAM552  RNF4     3'  TCCTCGAGCTGGGTGAACCGGG 16358     _       GC__    A
              TC                  TCC CGAGCTGGG    CCGG TC
                                ||| |||||||||    |||| ||
                                AGG GCTCGACCC    GGCC AG
                                  A        ACTT    C
GAM552  SMARCD2  5'  CCTGCCCGGGAGATTCCGGATC 16914     _   AGCT    C__
              C                  CCT CCCG    GGGG   CCGGATCC
                                ||| ||||    ||||   ||||||||
                                GGA GGGC    CCTC   GGCCTAGG
                                  C    _____    TAA
GAM552  TCF1     3'  CCTCCACGGGTTGGGGCGCC   8089       _ AGC     _
                                CCTCC CG   TGGGGC CC
                                ||||| ||   |||||| ||
                                GGAGG GC   ACCCCG GG
                                   T  CCA     C
GAM552  TMEPAI   3'  CTTCCAGCTGGGGGCCCTCC   33607    C  G      _   GGA
                                CT CC AGCTGGGG CCC   TCC
                                || || |||||||| |||   |||
                                GA GG TCGACCCC GGG   AGG
                                 A  _       C   ____
GAM552  TOP3B    5'  CTCCCGAGCTCGCGGGTCC    19464          _ _  C
                                CTCCCGAGCT G GGG CC
                                |||||||||| | ||| ||
                                GAGGGCTCGA C CCC GG
                                      G G   A
GAM552  TRPM4    3'  CCTCCCAGGCTGGGACTGGTTC 32779        A       CC  A
                                CCTCCCG GCTGGGGC  GG TC
                                ||||||| ||||||||  || ||
                                GGAGGGT CGACCCTG  CC AG
                                    C       A_  A
GAM552  WFS1     3'  CCTGTCGGGCTGGGGCCACA   25639     CC  A       _
                                CCT  CG GCTGGGGCC CG
                                |||  || |||||||| ||
```

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                                GGA  GC CGACCCCGG GT
                                  CA  C        T
GAM553  ADAMTS13  5'  CCCTTAGAGGAGGCCTAAG   40040     GAAAA  CCC
                                CCCT    AG   GGCCTGAG
                                ||||    ||   ||||||||
                                GGGA    TC   CCGGATTC
                                  ATC__  CT_
GAM553  APAF1    5'  CCCCGGAGGGAGCCCGGC    29816     T  AAA
                                CCCC GA   AGCCCGGC
                                |||| ||   ||||||||
                                GGGG CT   TCGGGCCG
                                  C  CCC
GAM553  CALCR    3'  CCTGGAAAAGCCTGAG      11944     A   AGCCC
                                CCTG AAA    GGCCTGAG
                                |||| |||    ||||||||
                                GGAC TTT    TCGGACTC
                                  C  _____
GAM553  CEACAM1  3'  CCCTGAAAGAGGTACCTGAG  11830       A  CCCG
                                CCCTGAAA AG    GCCTGAG
                                |||||||| ||    |||||||
                                GGGACTTT TC    TGGACTC
                                    C  CA__
GAM553  CMA1     5'  CCCAGAGAGGCTGCCTGAGC   12299     T  AAAA  CCG
                                CCC GA    GC   GCCTGAGC
                                ||| ||    ||   ||||||||
                                GGG CT    CG   CGGACTCG
                                  T  CTC_  A__
GAM553  COG2     3'  CTTTAGAAAGCCCAGGAG    28879    GAA_       CCT
                                CT    AAAGCCCGG   GAG
                                ||    |||||||||   |||
                                GA    TTTCGGGTC   CTC
                                  AATC        ___
GAM553  CXorf6   3'  CTGAAGAAGCCCAGTTCTG   24238      A      C_
                                CTGAA AAGCCCGG  CTG
                                ||||| ||||||||  |||
                                GACTT TTCGGGTC  GAC
                                   C       AA
GAM553  CYP46    3'  CCCCTGAAGAGGGCTTTAGGGA 27422        AA  CCC   CT____
            G                    CCCCTGAA  AG   GGC     GAG
                                ||||||||  ||   |||     |||
                                GGGGACTT  TC   CCG     CTC
                                    C_  ___   AAATCC
GAM553  EBF      3'  CCTCTTAAAAAGGCCTGAG   42368    _  G    GCCC
                                CC CT AAAAA    GGCCTGAG
                                || || |||||    ||||||||
                                GG GA TTTTT    CCGGACTC
                                  A  A    _____
GAM553  ESRRG    3'  CCCTGAAAAAGTTACATAG   42445          CCCG  CTG
                                CCCTGAAAAAG    GC   AG
                                ||||||||||    ||   ||
```

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                                GGGACTTTTTC   TG  TC
                                      AA__  TA_
GAM553  FCN2    3'  CCCTGAGGCCGGCCTGG    31888      AAAA  C    A
                                CCCTGA   GCC GGCCTG G
                                ||||||   ||| |||||| |
                                GGGACT   CGG CCGGAC C
                                   C___  _    C
GAM553  FE65L2  5'  CCCGGGGGAGGGCCTGAG   39326     AAAA CCC
                                CCTG   AG  GGCCTGAG
                                ||||   ||  ||||||||
                                GGGC   TC  CCGGACTC
                                  CCCC ___
GAM553  GAS11   3'  CCCCTGGAGAATCCCACTGGGC 11212      AAAAAG   GC  A
                                CCCCTG    CCCG  CTG GC
                                ||||||    ||||  ||| ||
                                GGGGAC    GGGT  GAC CG
                                   CTCTTA   __  C
GAM553  GNAO1   3'  CTGGAAAGCCCGGCCTGAGC  44940    AA
                                CTG  AAAGCCCGGCCTGAGC
                                |||  ||||||||||||||||
                                GAC  TTTCGGGCCGGACTCG
                                  C_
GAM553  GPRK5   3'  CCTCGGAAAACAGACCTGAG  23633    GAA   CC
                                CCT   AAAGC  GGCCTGAG
                                |||   |||||  ||||||||
                                GGA   TTTTG  CTGGACTC
                                  GCC    T_
GAM553  GRM7    5'  CCTCCGGGAAAGCCCAGGGGC  9184    _  AA    ___
                                CC CTG  AAAGCCC   GGC
                                || |||  |||||||   |||
                                GG GGC  TTTCGGG   CCG
                                 A  CC      TCC
GAM553  H4FG    3'  CCCTGAAAAGGGCCT       18639         AGCCC
                                CCCTGAAAA    GGCCT
                                |||||||||    |||||
                                GGGACTTTT    CCGGA
                                     C_____
GAM553  HCFC1   3'  CCCCAGCCTCGGAGCCTGGCCT 43387     TGAAAA__   C
           GAG                    CCCC       AGCC GGCCTGAG
                                ||||       |||| ||||||||
                                GGGG       TCGG CCGGACTC
                                  TCGGAGCC   A
GAM553  MAGEL2  5'  CCCTGAAAGGGCTGCTCCAGC  33299        AA___  _
                                CCCTGAAA    GC CCGGC
                                ||||||||    || |||||
                                GGGACTTT    CG GGTCG
                                     CCCGA  A
GAM553  MCF2    3'  CCCCGAAAAGAATTTCTGGGC  23862         AGCCCGGC   A
                                CCCTGAAAA       CTG GC
                                |||||||||       ||| ||
```

```
                                GGGGCTTTT      GAC CG
                                     CTTAAA__  C
GAM553  MECP2   3'  CCACTGAAAGGGCCTATGGC  22581   _    AA  C__
                                CC CTGAAA  GCC  GGC
                                || ||||||  |||  |||
                                GG GACTTT  CGG  CCG
                                 T    CC  ATA
GAM553  MHC2TA  3'  TGAGGAAGCCCAACTAGC   6990    AA      CTG
                                TGA  AAGCCCGGC  AGC
                                |||  |||||||||  |||
                                ACT  TTCGGGTTG  TCG
                                  CC       A__
GAM553  MIR16   3'  CCTAAAAAGCCTGGAAAAG  32495       A  C  CCT
                                CCTGAAAA GCC GG  GAG
                                |||||||| ||| ||  |||
                                GGATTTTT CGG CC  TTC
                                     _  A  TT_
GAM553  MSL3L1  3'  CCCCTGAAGGAGTCAGC    38582       AA  CC
                                CCCCTGAA  AG  CGGC
                                ||||||||  ||  ||||
                                GGGGACTT  TC  GTCG
                                     CC  A_
GAM553  MUC1    3'  CCCTGAAGAACCTGA      43771       AAAGCCC
                                CCCTGAA     GGCCTGA
                                |||||||     |||||||
                                GGGACTT     TTGGACT
                                    C_______
GAM553  NPR1    3'  CCCAGCCCGGCCTGA      44577    TGAAAA
                                CCC     AGCCCGGCCTGA
                                |||     ||||||||||||
                                GGG     TCGGGCCGGACT
                                  _______
GAM553  RNF4    3'  CCCCTGAGAGAACCTGAG   16351       AAA  CCC
                                CCCCTGA  AG  GGCCTGAG
                                |||||||  ||  ||||||||
                                GGGGACT  TC  TTGGACTC
                                    C__  ____
GAM553  ROM1    5'  CCCGGCCCGGCTTGA      7260      AAAAA     C
                                CCTG    GCCCGGC TGA
                                ||||    ||||||| |||
                                GGGC    CGGGCCG ACT
                                  ______     A
GAM553  SELPLG  3'  CCGAGGAAGCCCAGAG     40673     AA     GCCT
                                CTGA  AAGCCCG   GAG
                                ||||  |||||||   |||
                                GGCT  TTCGGGT   CTC
                                  CC     _____
GAM553  SHMT1   3'  CCCCTCAAAGGGCCCGAG   20022      G  AAGCCC
                                CCCCT AAA     GGCCTGAG
                                ||||| |||     ||||||||
```

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                                GGGGA TTT     CCGGGCTC
                                  G   C_____
GAM553  SOX10    3'  CTGGGAAGCCCAGGGAG     28002     AAA      CCT
                                CTG   AAGCCCGG   GAG
                                |||   ||||||||   |||
                                GAC   TTCGGGTC   CTC
                                  CC_       C__
GAM553  SPOCK    3'  CCTTAGAAAAAGCCCTTGAG   41732     __       GGCC
                                CCT  GAAAAAGCCC    TGAG
                                |||  ||||||||||    ||||
                                GGA  CTTTTTCGGG    ACTC
                                  AT         A___
GAM553  TAP2     3'  CCTGGAAGACCTGAACCCTGAG 8082      AAA  _  C  __
                                CCTG   AAG CC GG  CCTGAG
                                ||||   ||| || ||  ||||||
                                GGAC   TTC GG CT  GGACTC
                                  C__   T  A  TG
GAM553  TEC      3'  CCTGAAAAACGTCCGGGAG    17384        GC_   CCT
                                CCTGAAAAA   CCGG   GAG
                                |||||||||   ||||   |||
                                GGACTTTTT   GGCC   CTC
                                     GCA    ___
GAM553  TMEPAI   3'  CCCTCGGGAAAGCCCGCC     33597     _ AA      G
                                CCCT G  AAAGCCCG CC
                                |||| |  |||||||| ||
                                GGGA C  TTTCGGGC GG
                                  G CC       _
GAM553  WHSC1    3'  CCTCCGGGAAAGCCCAAGGC   39359    _   AA      __
                                CC CTG  AAAGCCC  GGC
                                || |||  |||||||  |||
                                GG GGC  TTTCGGG  CCG
                                 A   CC      TT
GAM553  WHSC1    5'  CCTCCGGGAAAGCCCAAGGC   39359    _   AA      __
                                CC CTG  AAAGCCC  GGC
                                || |||  |||||||  |||
                                GG GGC  TTTCGGG  CCG
                                 A   CC      TT
GAM553  ZNF24    3'  CTGAAGAAAAAGACCTGAG    28087      A   CCC
                                CTGAA AAG   GGCCTGAG
                                |||||  |||   ||||||||
                                GACTT TTT   CTGGACTC
                                  C   TT_
GAM553  AKR1B1   3'  ACCTGGTAGATTTTG       11568        GCT   C
                                ACCTGGT   GGA TTTG
                                |||||||   ||| ||||
                                TGGACCA   TCT AAAC
                                    ___   A
GAM553  CDKN2C   3'  TCTTCAACTTGGGTGTTGA    38568         CT_   C
                                TCTTCAAC   GGTG TGG
                                ||||||||   |||| |||
```

```
                                AGAAGTTG  CCAC ACT
                                    AAC   A
GAM553  SELE    3'  CCTTGCCTGCTGGACTTT   7803     GG__
                                CCT   TGCTGGACTTT
                                |||   ||||||||||
                                GGA   ACGACCTGAAA
                                  ACGG
GAM554  ABR     3'  CCCCAGCCCTGAGGGCCCGG  35007    G   ___
                                CCC AGCT  GGGGCCCGG
                                ||| ||||  |||||||||
                                GGG TCGG  TCCCGGGCC
                                  G   GAC
GAM554  APBA2   3'  CCCGGGCGGCCCTGCCCGG   24279     A  T  G___
                                CCCG GC GG   GCCCGG
                                |||| || ||   ||||||
                                GGGC CG CC   CGGGCC
                                  C  _  GGGA
GAM554  BCL10   5'  CCCAAGACGGTGGCTTGG    19403      C  _  CC
                                CCCGAG TGG GGC  GG
                                |||||| ||| |||  ||
                                GGGTTC GCC CCG  CC
                                   T   A   AA
GAM554  CACNA1A  3'  CCCGGCCCGCGGGGCCTGG   35726     A  ___    C
                                CCCG GCT  GGGGCC GG
                                |||| |||  |||||| ||
                                GGGC CGG  CCCCGG CC
                                  _  GCG    A
GAM554  CACNG3  5'  CCTGGAGCTGCCAGCTCGG   27232   C_    G_  C
                                CC  GAGCTG  GGC CGG
                                ||  ||||||  ||| |||
                                GG  CTCGAC  TCG GCC
                                 AC     GG   A
GAM554  CD1D    5'  CCCAAGCCCAGACCCCGG    44296       G    _
                                CCCGAGCT GGGCCC GG
                                |||||||| |||||| ||
                                GGGTTCGG TCTGGG CC
                                    G     G
GAM554  CDH11   5'  CCGAGCCGCCAGTCCCTGG   38029       G_ _  _
                                CCGAGCTG  GG CCC GG
                                ||||||||  || ||| ||
                                GGCTCGGC  TC GGG CC
                                    GG  A   A
GAM554  CDH16   3'  CCCAGCTAGAGCTGCCTGG   19785    G      __ _
                                CCC AGCTGGGGC  CC GG
                                ||| |||||||||  || ||
                                GGG TCGATCTCG  GG CC
                                  _       AC  A
GAM554  CDS2    5'  CCGGAGCAGGCAGCTCGG    19212    C   T  _  C
                                CC GAGC GG GGC CGG
                                || |||| || ||| |||
```

```
                                GG CTCG CC TCG GCC
                                 C   T G   A
GAM554  CETP    5'  CCCGAGCCGTTCAGCCTGG   6340        G__   C
                                CCCGAGCTG  GGCC GG
                                |||||||||  |||| ||
                                GGGCTCGGC  TCGG CC
                                     AAG   A
GAM554  CLDN3   5'  CCGGGGCCGCTGGGCCTGG   10564    A_  __   C
                                CCG  GCTG  GGGCC GG
                                |||  ||||  ||||| ||
                                GGC  CGGC  CCCGG CC
                                  CC   GA   A
GAM554  CNP     3'  CCTGGAAGTAGGGCTCGG    37555    C_  C    C
                                CC  GAG TGGGGC CGG
                                ||  ||| |||||| |||
                                GG  CTT ATCCCG GCC
                                 AC  C    A
GAM554  CPNE6   3'  CCCAGGGGGCACACCTGG    25732    G  CT   ___ _
                                CCC AG  GGGGC  CC GG
                                ||| ||  |||||  || ||
                                GGG TC  CCCCG  GG CC
                                  _ __    TGT  A
GAM554  CRHR1   3'  CCAGAGGCCCTGGGCCCGG   20436    C  _ G_
                                CC GAG CT  GGGCCCGG
                                || ||| ||  ||||||||
                                GG CTC GG  CCCGGGCC
                                 T  C  GA
GAM554  DDX3    5'  CCCTAGTCTCAGCCTCGG    35814    G  _  G  G  _
                                CCC AG CT GG CC CGG
                                ||| || || || || |||
                                GGG TC GA TC GG GCC
                                  A  A  G  _  A
GAM554  DVL1    5'  CCGCGCGCTCAGGGCCCGG   40407    _  A  _
                                CC CG GCT GGGGCCCGG
                                || || ||| |||||||||
                                GG GC CGA TCCCGGGCC
                                 C  G  G
GAM554  E2F1    3'  CCTGAACTGGCCCCCTGG    44486    C     GG  _
                                CC GAGCTGG  CCC GG
                                || |||||||  ||| ||
                                GG CTTGACC  GGG CC
                                 A      GG  A
GAM554  E2F2    5'  CCTCGGCACCTGGGGTCCGG  19871    _  A_  _   C
                                CC CG  GC TGGGG CCGG
                                || ||  || ||||| ||||
                                GG GC  TG ACCCC GGCC
                                 A  CG  G    A
GAM554  EGFL4   3'  CCGGGGCCTAGCGCCCGG    41564    A_  _  G
                                CCG  GC TGG GCCCGG
                                |||  || ||| ||||||
```

```
                                GGC  CG ATC CGGGCC
                                  CC  G   G
GAM554  EXTL3   3'  CCCCAGCTGGTGAGCCCTGG   11029     G     _ _   _
                                CCC AGCTGG G GCCC GG
                                ||| |||||| | |||| ||
                                GGG TCGACC C CGGG CC
                                  G     A T    A
GAM554  FGF2    5'  CCCAAGCTGCAGCGCCCGG   12832          _ _
                                CCCGAGCTG GG GCCCGG
                                ||||||||| || ||||||
                                GGGTTCGAC TC CGGGCC
                                     G  G
GAM554  FGFR1   5'  CCGGAGCTGGTGCCCCGG    31933    C      G   _
                                CC GAGCTGG GCCC GG
                                || ||||||| |||| ||
                                GG CTCGACC CGGG CC
                                 C      A    G
GAM554  FMR2    5'  CCCAGCTAAAAGTGTCCGG   12956    G      C___
                                CCC AGCTGGGG   CCGG
                                ||| ||||||||   ||||
                                GGG TCGATTTT   GGCC
                                  _      CACA
GAM554  GALR1   5'  CCCGGAGCTGGACCTTCTCGG  11197     _     G ____
                                CCCG AGCTGGG CC   CGG
                                |||| ||||||| ||   |||
                                GGGC TCGACCT GG   GCC
                                  C      _ AAGA
GAM554  GPC6    5'  CCGAGCCGCAGAATCCTGG   25040       G ___ C
                                CCGAGCTG GG  CC GG
                                |||||||| ||  || ||
                                GGCTCGGC TC  GG CC
                                     G  TTA  A
GAM554  HIS1    5'  CCCAGTTCCCTAGGCCCGG   26989     AG_ G_
                                CCCG  CT  GGGCCCGG
                                ||||  ||  ||||||||
                                GGGT  GG  TCCGGGCC
                                  CAA  GA
GAM554  HPCAL1  3'  CCCAGGCCCGGGGCCCGG   39543     A  _
                                CCCG GCT GGGGCCCGG
                                |||| ||| |||||||||
                                GGGT CGG CCCCGGGCC
                                  C  G
GAM554  HSD17B1 5'  CCCAAAGGACAGGGTTCGG   7657       C__   CC
                                CCCGAG  TGGGG  CGG
                                ||||||  |||||  |||
                                GGGTTT  GTCCC  GCC
                                   CCT    AA
GAM554  HYAL1   3'  CCGGAGCTAGACAGCCTGG   37640    C     __   C
                                CC GAGCTGG  GGCC GG
                                || |||||||  |||| ||
```

```
                                GG CTCGATC  TCGG CC
                                 C      TG   A
GAM554  JUN     5'  CCCGAACCACCAGCCCGG   13738       GG_
                                CCCGAGCT  GGCCCGG
                                ||||||||  |||||||
                                GGGCTTGG  TCGGGCC
                                    TGG
GAM554  LASS2   5'  CCGAGGCCCCGAGGCCTGG   42669     ___     C
                                CCGAG  CTGGGGCC GG
                                |||||  |||||||| ||
                                GGCTC  GGCTCCGG CC
                                  CGG      A
GAM554  LDLR    5'  CCTAGCTGGAAACCCTGG    8022    G     _  _
                                CC AGCTGGGG CCC GG
                                || |||||||| ||| ||
                                GG TCGACCTT GGG CC
                                 A       T  A
GAM554  LEPR    5'  CCCGAACTGGGGCCGCGG    14132          _
                                CCCGAGCTGGGGCC CGG
                                |||||||||||||| |||
                                GGGCTTGACCCCGG GCC
                                        C
GAM554  LTBR    5'  CCCGAGCCCAGAGCCTGG    14253       G  _  C
                                CCCGAGCT GG GCC GG
                                |||||||| || ||| ||
                                GGGCTCGG TC CGG CC
                                    G  T  A
GAM554  LY6E    3'  CCTGAGCTGGGGGATCGG    14275   C       CC_
                                CC GAGCTGGGG  CGG
                                || |||||||||  |||
                                GG CTCGACCCC  GCC
                                 A       CTA
GAM554  MFI2    5'  CCGGGCTGGGGCTGGGTCCGGC 25465    A      _____   III
                                CCG GCTGGGGC    CCGG  C
                                ||| ||||||||    ||||  |
                                GGC CGACCCCG    GGCC  G
                                  C       ACCCA   III
GAM554  MLLT1   3'  CCCGGCGGTGGGGGCCCGG   25479    A  T___
                                CCCG GC   GGGGCCCGG
                                ||||  ||  |||||||||
                                GGGC CG   CCCCGGGCC
                                  _  CCAC
GAM554  MMP25   3'  CCCAAGCTGGGTGGCCTGG   35380         __  C
                                CCCGAGCTGGG  GCC GG
                                ||||||||||  ||| ||
                                GGGTTCGACCC  CGG CC
                                       AC  A
GAM554  MNT     3'  CCCAGAGCCACGGGTCTGG   33706    _    _  CCC
                                CCC GAGCTG GGG  GG
                                ||| |||||| |||  ||
```

```
                                GGG CTCGGT CCC   CC
                                  T     G   AGA
GAM554  MYBBP1A  3'  CCAGAGCAGGATGCCCGG    30956    C    T   _
                                CC GAGC GGG GCCCGG
                                || |||| ||| ||||||
                                GG CTCG CCT CGGGCC
                                 T    T   A
GAM554  MYLK2    3'  CCCGAGCCTCCCAGCCTGG    37518        GG__    C
                                CCCGAGCT    GGCC GG
                                ||||||||    |||| ||
                                GGGCTCGG    TCGG CC
                                     AGGG    A
GAM554  MYO1C    5'  CCCAGGGCCGACGCCCGG    41465      A_     G
                                CCCG  GCTGG GCCCGG
                                ||||  ||||| ||||||
                                GGGT  CGGCT CGGGCC
                                  CC     G
GAM554  NAGLU    5'  CCCGAAGGCTAAGCCCGG    7050        __      G
                                CCCGA  GCTGGG CCCGG
                                |||||  |||||| |||||
                                GGGCT  CGATTC GGGCC
                                   TC     _
GAM554  NRXN2    5'  CCAGGGCCCAAGCCTCGG    31472     A_   G    _
                                CCG  GCT GGGCC CGG
                                |||  ||| ||||| |||
                                GGT  CGG TTCGG GCC
                                  CC   G    A
GAM554  NT5C     5'  CCGGAGCTGCGAGCTCTCGG   31099    C     _    C__
                                CC GAGCTG GGGC   CGG
                                || |||||| ||||   |||
                                GG CTCGAC CTCG   GCC
                                 C     G    AGA
GAM554  ONECUT2  3'  CCCCAGCTAGGAATCCGG    22138     G       C_
                                CCC AGCTGGGG  CCGG
                                ||| ||||||||  ||||
                                GGG TCGATCCT  GGCC
                                  G       TA
GAM554  PABPC4   5'  CCGGGGCGCGGGGCTCGG    19221     A_ _     C
                                CCG  GC TGGGGC CGG
                                |||  || |||||| |||
                                GGC  CG GCCCCG GCC
                                  CC  C     A
GAM554  PGF      5'  CCCGACGGGGAGCGGCCCGG   15247      G T  _____
                                CCCGA C GGG    GCCCGG
                                ||||| | |||    ||||||
                                GGGCT G CCC    CGGGCC
                                   _ C   TCGC
GAM554  PKIB     5'  CCCGGAGCTGCGACTCGG    37163      _    G   C
                                CCCG AGCTG GGC CGG
                                |||| ||||| ||| |||
```

```
                                GGGC TCGAC CTG GCC
                                  C    G   A
GAM554  PKIB    5'  CCCAAGCTCTGCGGCCCGG   37162       __ G
                                CCCGAGCT  G GGCCCGG
                                ||||||||  | |||||||
                                GGGTTCGA  C CCGGGCC
                                    GA G
GAM554  POU5F1  5'  CCCAAGCCGGGGGCCTGG    15468         _ C
                                CCCGAGCTGGGG CC GG
                                |||||||||||| || ||
                                GGGTTCGGCCCC GG CC
                                      C  A
GAM554  POV1    5'  CCCGAGCTCCGCAGGGCTCGG  18843       ____   C
                                CCCGAGCT   GGGGC CGG
                                ||||||||   ||||| |||
                                GGGCTCGA   TCCCG GCC
                                    GGCG    A
GAM554  PPARA   5'  CCCTGAGCTTCAGCCTGG    22768    _   GG   C
                                CCC GAGCT  GGCC GG
                                ||| |||||  |||| ||
                                GGG CTCGA  TCGG CC
                                  A    AG   A
GAM554  PPP2R5D 3'  CCCTGGAACCTGGGTCCGG   26455    __   G  C
                                CCC  GAGCT GGG CCGG
                                |||  ||||| ||| ||||
                                GGG  CTTGG CCC GGCC
                                  AC    A  A
GAM554  REQ     3'  CCCGAGCTGCTGGCCTGG    26541       G_  C
                                CCCGAGCTG  GGCC GG
                                |||||||||  |||| ||
                                GGGCTCGAC  CCGG CC
                                    GA   A
GAM554  RGS3    3'  CCCGAGAGCCCAGGCCTGG   39124    __   G   C
                                CCC  GAGCT GGGCC GG
                                |||  ||||| ||||| ||
                                GGG  CTCGG TCCGG CC
                                  CT    G    A
GAM554  SHOX    3'  CCCGGGCTGGACGCACGG    27815    A    _ C
                                CCCG GCTGGG GC CGG
                                |||| |||||| || |||
                                GGGC CGACCT CG GCC
                                  C    G  T
GAM554  SLC1A5  5'  CCCAGGCTCTTAGGTCCGG   24744    A  G__  C
                                CCCG GCT   GGG CCGG
                                |||| |||   ||| ||||
                                GGGT CGA   TCC GGCC
                                  C  GAA  A
GAM554  SLC20A1 5'  CCACGGGCACACGGCCCGG   40449   _ A _ G
                                CC CG GC TG GGCCCGG
                                || || || || |||||||
```

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                                GG GC CG GT CCGGGCC
                                 T  C  T  G
GAM554  SLC3A2   5' CCCGCGCTGAGACCCTGG    14399     A       _
                                CCCG GCTGGGGCCC GG
                                |||| |||||||||| ||
                                GGGC CGACTCTGGG CC
                                  G        A
GAM554  SLC7A4   3' CCCGAAGCCCAGCCCCTGG   42186     _  G  G  _
                                CCCGA GCT GG CCC GG
                                ||||| ||| || ||| ||
                                GGGCT CGG TC GGG CC
                                  T   G  G   A
GAM554  SMARCA5  5' CCAGAGGCCCGAGTCCGG    18779    C  _  G   C
                                CC GAG CT GGG CCGG
                                || ||| || ||| ||||
                                GG CTC GG CTC GGCC
                                 T   C  G   A
GAM554  SMARCD3  5' CCCGGGACCCCGGCCCGG    16925     A_  GG
                                CCCG  GCT  GGCCCGG
                                ||||  |||  |||||||
                                GGGC  TGG  CCGGGCC
                                  CC   GG
GAM554  SOX11    3' CCCGGGGCGCGCGTGCCCGG  17011     A_  _  GG_
                                CCCG  GC TG   GCCCGG
                                ||||  || ||   ||||||
                                GGGC  CG GC   CGGGCC
                                  CC  C  GCA
GAM554  THBD     5' CGAGTTTATAAGTGCCCGG   7424      C___   _
                                CGAG    TGGG GCCCGG
                                ||||    |||| ||||||
                                GCTC    ATTC CGGGCC
                                  AAAT    A
GAM554  TOP3A    5' CCCGGAGCCGCTCCCCGG    21463     _    GGG
                                CCCG AGCTG   CCCGG
                                |||| |||||   |||||
                                GGGC TCGGC   GGGCC
                                  C    GAG
GAM554  UBA52    3' CCAGGGCCACGGGGCCTGG   17780     A_  __    C
                                CCG  GCT  GGGGCC GG
                                |||  |||  |||||| ||
                                GGT  CGG  CCCCGG CC
                                  CC   TG    A
GAM554  UBQLN1   5' CCAGAGCCGGCAGGCCTGG   30277    C     __   C
                                CC GAGCTGG  GGCC GG
                                || |||||||  |||| ||
                                GG CTCGGCC  CCGG CC
                                 T     GT   A
GAM554  UNC119   3' CCCAGCTAAGTTGTCCGG    38343    G     GC__
                                CCC AGCTGGG   CCGG
                                ||| |||||||   ||||
```

```
                                GGG TCGATTC   GGCC
                                  _     AACA
GAM554  USP7     5'  CCGGGGCTGCGAGCCCGG    18450    A_   _
                                CCG  GCTG GGGCCCGG
                                |||  |||| ||||||||
                                GGC  CGAC CTCGGGCC
                                  CC   G
GAM554  VIPR1    3'  CCGGGGCTGGCCGCGCCCGG  21506    A_   G___
                                CCG  GCTGG   GCCCGG
                                |||  |||||   ||||||
                                GGC  CGACC   CGGGCC
                                  CC    GGCG
GAM554  ADRA1A   5'  GCCACCTCCCGGGCTGGCGC  37808    C     A    G
                                GCC CCTCCCG GCTGG GC
                                ||| ||||||| ||||| ||
                                CGG GGAGGGC CGACC CG
                                  T     C    G
GAM554  ALDH3B1  3'  CCTCCTCGGGCCCGG      45062      CGAGC G
                                CCTCC    T GGGCCCGG
                                |||||    | ||||||||
                                GGAGG    A CCCGGGCC
                                  _____ G
GAM554  ANXA6    3'  GCCCCTTCCTTAGTCTCTGG  19714      C   CG  ___
                                GCCCC TCC  AG   CTGG
                                ||||| |||  ||   ||||
                                CGGGG AGG  TC   GACC
                                   A   AA  AGA
GAM554  ARSA     5'  GCCCTTCCCTGAGACCCG    7933      CC    GAGC     _
                                GCCC  TCCC   TGGGGCCC G
                                ||||  ||||   |||||||| |
                                CGGG  AGGG   ACTCTGGG C
                                  A_   ____      G
GAM554  BACH2    5'  GCCCCCTCCCGGCAGCCGG   34790         __
                                GCCCCCTCCCG  AGCTGG
                                ||||||||||  ||||||
                                CGGGGGAGGGC  TCGGCC
                                       CG
GAM554  C21orf2  3'  GCTTCCTGTGCCAGGCCCGG  22303   CC   CCCGA  TG  G
                                GC  CCT    GC  GG CCCGG
                                ||  |||    ||  || |||||
                                CG  GGA    CG  CC GGGCC
                                 AA   CA___  GT  _
GAM554  CACNA1A  3'  GCCCTTCCTGGAGCCCG    35733     CC   CGAGC
                                GCCC  TCC    TGGGGCCCG
                                ||||  |||    |||||||||
                                CGGG  AGG    ACCTCGGGC
                                  A_   _____
GAM554  CLU      3'  CCTGGAGGCTGGGGCCTGG   12294     CCC   _      C
                                CCT   GAG CTGGGGCC GG
                                |||   ||| |||||||| ||
```

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                                GGA  CTC GACCCCGG CC
                                  C__  C      A
GAM554  COL18A1  3' GCTTCCTCCGAGCCGCCG   36132   CC   C    GGGC
                                GC  CCTCC GAGCTG   CCG
                                ||  ||||| ||||||   |||
                                CG  GGAGG CTCGGC   GGC
                                 AA   _    ____
GAM554  CSNK1G2  3' CCCCCTCCCAGGAGGGCCTGG 10610       G  CT    C
                                CCCCCTCCC AG  GGGGCC GG
                                |||||||||  ||  |||||| ||
                                GGGGGAGGG TC  TCCCGG CC
                                      _ C_    A
GAM554  CTSD    3' GCCTCATCCTCAACGGGCCCGG 12528    CCC  CG  TG
                                GCC  TCC  AGC  GGGCCCGG
                                |||  |||  |||  ||||||||
                                CGG  AGG  TTG  CCCGGGCC
                                  AGT  AG  __
GAM554  CYLN2   5' GCCTCCTCCTCTCGGGCCCGG  18052    C   CGAG  G
                                GCC CCTCC   CT GGGCCCGG
                                ||| |||||   || ||||||||
                                CGG GGAGG   GA CCCGGGCC
                                  A   A___  G
GAM554  DDX11   3' GCCTTCCCTGGGGGTGCCTGG  36177    CCC   GAGCT  _  C
                                GCC  TCCC    GGG GCC GG
                                |||  ||||    ||| ||| ||
                                CGG  AGGG    CCC CGG CC
                                  A__   ACC__  A  A
GAM554  DLEC1   3' CTCCAGCTGGGGCCTGG    28824     CG       C
                                CTCC  AGCTGGGGCC GG
                                ||||  |||||||||| ||
                                GAGG  TCGACCCCGG CC
                                   __       A
GAM554  DMPK    5' GCCCCTCCCCGGGCCGGGGGCT 20613      CT   A    _ C
          CGG                    GCCCC  CCCG GCTGGGG C CGG
                                |||||  |||| ||||||| | |||
                                CGGGG  GGGC CGGCCCC G GCC
                                   AG   C     C A
GAM554  ECH1    3' GCCCCCTGGCTGGGGCCTGG  40866       CCCGA      C
                                GCCCCCT    GCTGGGGCC GG
                                |||||||    ||||||||| ||
                                CGGGGGA    CGACCCCGG CC
                                    C____       A
GAM554  EN2     3' CCTCATTTCTGGGACCCTGG  10939     CCGAG      _
                                CCTC    CTGGGGCCC GG
                                ||||    ||||||||| ||
                                GGAG    GACCCTGGG CC
                                  TAAA_       A
GAM554  F2RL3   3' GCCCCTGCCCGGGGCCCG    19519     CT  GAGCT
                                GCCCC  CCC    GGGGCCCG
                                |||||  |||    ||||||||
```

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                                CGGGG  GGG    CCCCGGGC
                                  AC  _____
GAM554  GATA3   5'  GCCCTCTCGCCGGGCCCGG   13096     C  CCGA    G
                                GCCC CTC   GCTGGG CCCGG
                                |||| |||   |||||| |||||
                                CGGG GAG   CGGCCC GGGCC
                                  A  ____    _
GAM554  GNL1    5'  GCCCCCGCCGCAGGGGCCCGG  45564      T  CGA  T
                                GCCCCC CC   GC GGGGCCCGG
                                |||||| ||   || |||||||||
                                CGGGGG GG   CG CCCCGGGCC
                                   C  ___  T
GAM554  GYG2    5'  CCTCTGTCCGGAAGCCCG    19389     CCGAG    _
                                CCTC    CTGGG GCCCG
                                ||||    ||||| |||||
                                GGAG    GGCCT CGGGC
                                  ACA__    T
GAM554  HADH2   3'  GCTTCCTCCCAAGCTGGAG   21054    CC
                                GC  CCTCCCGAGCTGGGG
                                ||  ||||||||||||||
                                CG  GGAGGGTTCGACCTC
                                 AA
GAM554  HCN4    5'  ACCTCCTCCCGGGCCC     24217     C     GAGCTG
                                GCC CCTCCC     GGGCCC
                                ||| ||||||     ||||||
                                TGG GGAGGG     CCCGGG
                                  A    _______
GAM554  HIP12   3'  CCCCTCCCTGAGGGCCCTGG   42396       GAGCT     _
                                CCCCTCCC    GGGGCCC GG
                                ||||||||    ||||||| ||
                                GGGGAGGG    TCCCGGG CC
                                    AC___      A
GAM554  HR      5'  GCCCCCTCCCGGGCCCCG    32920         GAGCT   G
                                GCCCCCTCCC    GGG CCCG
                                ||||||||||    ||| ||||
                                CGGGGGAGGG    CCC GGGC
                                      _____  G
GAM554  IFNGR2  5'  GCCTCTTCCCGAGCGGCAGCGG 24386    CCC      TGG   C_
                                GCC   TCCCGAGC   GGC  CGG
                                |||   ||||||||   |||  |||
                                CGG   AGGGCTCG   CCG  GCC
                                  AGA       ___   TC
GAM554  KCNC4   5'  GCCCCCTCTGCGGCTTGG    22529       C_  A   G
                                GCCCCCTC  CG GCT GG
                                ||||||||  || ||| ||
                                CGGGGGAG  GC CGA CC
                                    AC  _   A
GAM554  LY6E    3'  CCTTCCTGAGCTGGGGGATCGG 14276    C   C       CC_
                                CC TCC GAGCTGGGG   CGG
                                || ||| |||||||||   |||
```

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                                GG AGG CTCGACCCC   GCC
                                 A  A       CTA
GAM554  MAD2L2   5'  CCCGCCCGAGATCGGGCCCGG  26801    T    CTG
                                CCC CCCGAG   GGGCCCGG
                                ||| ||||||   ||||||||
                                GGG GGGCTC   CCCGGGCC
                                  C     TAG
GAM554  MADH1    5'  GCTTTCTCCTGGAGCCG    25340    CCC   CGAGC     C
                                GC   CTCC    TGGGGCC G
                                ||   ||||    ||||||| |
                                CG   GAGG    ACCTCGG C
                                 AAA   _____      A
GAM554  MMP25    3'  GCCCCTCCCCGGGCTCGG    35385     CT   A   G
                                GCCCC  CCCG GCT GG
                                |||||  |||| ||| ||
                                CGGGG  GGGC CGA CC
                                   AG   C   G
GAM554  MNT      3'  GCTCTCTCCCAGAGCCACGGGT 33717    CCC    _    _  CCC
            CTGG                  GC   CTCCC GAGCTG GGG   GG
                                ||   ||||| |||||| |||   ||
                                CG   GAGGG CTCGGT CCC   CC
                                 AGA    T     G   AGA
GAM554  NR2E3    3'  CCCCACTCCCGGGGCCTGG   32285     _    GAGCT     C
                                CCCC CTCCC    GGGGCC GG
                                |||| |||||    |||||| ||
                                GGGG GAGGG    CCCCGG CC
                                  T    _____     A
GAM554  OTP      3'  CCTCGCGGGCTGGGGCTTGG   36992     C  A      CC
                                CCTC CG GCTGGGGC  GG
                                |||| || ||||||||  ||
                                GGAG GC CGACCCCG  CC
                                  C  C       AA
GAM554  P3       5'  GCCCTTCCCTGCCAGGCCCGG  33381     CC   GA  TG  G
                                GCCC  TCCC  GC  GG CCCGG
                                ||||  ||||  ||  || |||||
                                CGGG  AGGG  CG  CC GGGCC
                                  A_   A_  GT  _
GAM554  PCSK5    5'  GCCCCCTCTGCTGGCCCG    26234       CCGA   GG
                                GCCCCCTC   GCT  GGCCCG
                                ||||||||   |||  ||||||
                                CGGGGGAG   CGA  CCGGGC
                                    A___   __
GAM554  PIN1L    3'  GCCCCCTCCCAGCCATTTTGG  26323         G   GG___
                                GCCCCCTCCC AGCT    GG
                                |||||||||| ||||    ||
                                CGGGGGAGGG TCGG    CC
                                      _   TAAAA
GAM554  PRX      3'  GCCCCCACCCGAGCCTTGG   34122       T      GG
                                GCCCCC CCCGAGCT  GG
                                |||||| ||||||||  ||
```

```
                                CGGGGG GGGCTCGG  CC
                                   T       AA
GAM554  RAP1    5'  ACCCCCTCCCGAGCGCCG    33265           TGGG  C
                                GCCCCCTCCCGAGC   GCC G
                                |||||||||||||    ||| |
                                TGGGGGAGGGCTCG   CGG C
                                      _____  A
GAM554  SCN1B   5'  CCCCCTCCCGGGCCGCCG    9778          A   GGGC
                                CCCCCTCCCG GCTG   CCG
                                |||||||||| ||||   |||
                                GGGGGAGGGC CGGC   GGC
                                      C  ____
GAM554  SHH     3'  GCCCCCTCCCGCGCCCCTCCCC 6795          A  GGGG_
           CGG                    GCCCCCTCCCG GCT    CCCGG
                                |||||||||| |||    |||||
                                CGGGGGAGGGC CGG    GGGCC
                                      G  GGAGG
GAM554  SLC29A1 3'  GCTCCCTCCCCAGGGCCTGG  22415   C     GAGC     C
                                GC CCCTCCC   TGGGGCC GG
                                || |||||||   ||||||| ||
                                CG GGGAGGG   GTCCCGG CC
                                 A     _____     A
GAM554  SLC6A8  5'  GCTCCTGCCCGCGGCTCGG   24773   CC  _   A_  G
                                GC  CCT CCCG  GCT GG
                                ||  ||| ||||  ||| ||
                                CG  GGA GGGC  CGA CC
                                 A_  C   GC  G
GAM554  SORCS2  3'  GCTCCTTCCAGAGCCCAGACCC 34058   C  C  C    G
           GG                    GC CC TCC GAGCT GGGCCCGG
                                || || ||| ||||| ||||||||
                                CG GG AGG CTCGG TCTGGGCC
                                 A  A  T    G
GAM554  STAT1   5'  GCCTCTCCCGAGCGCGCTGG  40215    CC      _  G_
                                GCC  CTCCCGAGC TG  GG
                                |||  ||||||||| ||  ||
                                CGG  GAGGGCTCG GC  CC
                                  A_       C  GA
GAM554  TAZ     3'  GCTCCCTCCTGAAGCCAGCCC  31768   C    C_   GG
                                GC CCCTCC  GAGCT  GGCCC
                                || ||||||  |||||  |||||
                                CG GGGAGG  TTCGG  TCGGG
                                 A     AC    __
GAM554  TIMM44  3'  CCCCTCCCGGGCCAGCTGG   43427        ____
                                CCCCTCCCG   AGCTGG
                                |||||||||   ||||||
                                GGGGAGGGC   TCGACC
                                      CCGG
GAM554  TNFAIP2 3'  GCCCCCTCTCAGGCTGAGA   26638        C  A
                                GCCCCCTC CG GCTGGGG
                                |||||||| || |||||||
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```
                                CGGGGGAG GT CGACTCT
                                    A  C
GAM554  TNFSF7   5'  GCCCCCTCCCGGGGCTCCTGG  10358         GAGCT   _ _
                                GCCCCCTCCC    GGGGC CC GG
                                ||||||||||    ||||| || ||
                                CGGGGGAGGG    CCCCG GG CC
                                     _____    A  A
GAM554  TNXB     5'  CCCTCCCGCCTGGCCTGG    37152       GA  GG   C
                                CCCTCCC  GCT  GGCC GG
                                |||||||  |||  |||| ||
                                GGGAGGG  CGG  CCGG CC
                                   __  A_   A
GAM554  TOP3B    5'  GCTCTCCCGAGCTCGCGG    19466    CCC       _ G
                                GC   CTCCCGAGCT G GG
                                ||   |||||||||| | ||
                                CG   GAGGGCTCGA C CC
                                 A__        G G
GAM554  ZNF278   5'  GCCCCCTCCCACTAGCCCG   36792         AGCTGG
                                GCCCCCTCCCG    GGCCCG
                                ||||||||||     ||||||
                                CGGGGGAGGGT    TCGGGC
                                      GA____
GAM554  ZNF74    5'  GCCCCCTCCCCGCGCCCG    18300         GA  TGGG
                                GCCCCCTCCC  GC   GCCCG
                                |||||||||  ||   |||||
                                CGGGGGAGGG  CG   CGGGC
                                     G_  ____
GAM555  ATBF1    5'  GGCGTCCGGGTCCCCGGCC   27851    __   ATCC
                                GGC  CCGG   CCCCGGTT
                                |||  ||||   ||||||||
                                CCG  GGCC   GGGGCCGG
                                  CA   CA__
GAM555  BACE2    3'  GGGGCCTGTGGCTCTGGTTCC  29050      C__  A  CCCCC
                                GGGGCC   GG TC    GGTTCC
                                ||||||   || ||    ||||||
                                CCCCGG   CC AG    CCAAGG
                                   ACA  G  A____
GAM555  BARX1    3'  TGGGACCTGGGTCTGGCT    34629       C  A  CCCCC
                                TGGGGCC GG TC    GGTT
                                |||||||  || ||    ||||
                                ACCCTGG CC AG    CCGA
                                   A  C  A____
GAM555  LAMC2    3'  TGGGGTCCAGATCCTTGATCAT 33124      C       CCCCG_
          TC                      TGGGG CCGGATCC     GTTC
                                |||||  ||||||||     ||||
                                ACCCC GGTCTAGG     TAAG
                                  A       AACTAG
GAM555  NPTX1    3'  TGGGGCCCGGCTTCCCTGGT   14845         ATCC   C
                                TGGGGCCCGG    CCC GGT
                                ||||||||||    ||| |||
```

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                                ACCCCGGGCC   GGG CCA
                                     GAA_  A
GAM555  OA1     3'  TGGGGTCTGGACCCCCAGC   7083      CCC  TC
                                TGGGG  GGA  CCCCCGGT
                                |||||  |||  ||||||||
                                ACCCC  CCT  GGGGGTCG
                                   AGA  __
GAM555  PCDHB2  5'  TAGGGCCCGGATTTCCCGG   33195         CCC
                                TGGGGCCCGGAT  CCCGG
                                ||||||||||||  |||||
                                ATCCCGGGCCTA  GGGCC
                                      AA_
GAM555  PPP2R5E  5'  GGTACGGGGTCCCTCCGGTTCC 26474   CC  A_  C
                                GG  CGG  TCCC CCGGTTCC
                                ||  |||  |||| ||||||||
                                CC  GCC  AGGG GGCCAAGG
                                 AT  CC   A
GAM555  SEZ6L   5'  TGGGGTCCGGGTCCCCCGGT  34428     C   ATC
                                TGGGG CCGG  CCCCCGGT
                                ||||| ||||  ||||||||
                                ACCCC GGCC  GGGGGCCA
                                   A   CA_
GAM555  UCP2    5'  GGCCCGATCCCCTTGGTT   17845      G    CC
                                GGCCCG ATCCCC  GGTT
                                |||||| ||||||  ||||
                                CCGGGC TAGGGG  CCAA
                                   _     AA
GAM555  ACHE    3'  CCTGAGTGGGGCCCTTCCCC  8561    C  C     GGA
                                CC GAG TGGGGCCC  TCCCC
                                || ||| ||||||||  |||||
                                GG CTC ACCCCGGG  AGGGG
                                 A  _      A__
GAM555  ALK     5'  GAGCTGGGGTCTGTCCCC   43835       CCCGGA
                                GAGCTGGGG    TCCCC
                                |||||||||    |||||
                                CTCGACCCC    AGGGG
                                     AGAC__
GAM555  AQP7    5'  CCCCAGCTGGGGCTCAGCTATC 10118    G      C  __
           CC                    CCC AGCTGGGGC CGG  ATCCC
                                |||  ||||||||| |||  |||||
                                GGG TCGACCCCG GTC  TAGGG
                                  G       A  GA
GAM555  ASH1    5'  CTGGGTCCACGGCGGATCCC  32976     G  ____
                                CTGGG CC   CGGATCCC
                                ||||| ||   ||||||||
                                GACCC GG   GCCTAGGG
                                   A  TGCC
GAM555  CD8A    3'  CCTGAGCTGGGAGACAAGGTCC 12090   C      CC __  A
           C                     CC GAGCTGGGG  C  GG TCCC
                                || |||||||||  |  || ||||
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                                GG CTCGACCCT  G  CC AGGG
                                 A        CT TT  _
GAM555  CENTD2   5'  GCTGGGGCCCCCCGGCCCC    31597          __  AT
                                GCTGGGGCCC  GG  CCCC
                                ||||||||||  ||  ||||
                                CGACCCCGGG  CC  GGGG
                                      GG  __
GAM555  CHRM1    3'  CCAAAGCCCGGATCCTCC    45423    TG         _
                                C  GGGCCCGGATCC CC
                                |  ||||||||||||  ||
                                G  TTCGGGCCTAGG GG
                                 GT          A
GAM555  CISH     3'  CCAGCTGGGGCTGATGTCCCC  30026    G       CCGGA
                                CC AGCTGGGGC    TCCCC
                                || |||||||||    |||||
                                GG TCGACCCCG    AGGGG
                                 _       ACTAC
GAM555  CIT      3'  CCGAGCTGAGGCCCCGATGACC 43045           G  __  _
              TCC                   CCGAGCTGGGGCCC GAT  CC CC
                                ||||||||||||||  |||  || ||
                                GGCTCGACTCCGGG CTA  GG GG
                                       G   CT  A
GAM555  COL17A1  3'  CCTAGGCTGGGGCTTGAAC   39079    GA_      CC
                                CC   GCTGGGGC  GGAT
                                ||   ||||||||  ||||
                                GG   CGACCCCG  CTTG
                                 ATC       AA
GAM555  COX15    3'  CCGAGCTGGGGCACCTGCTC   20424          _  GGA
                                CCGAGCTGGGGC CC   TC
                                ||||||||||||  ||   ||
                                GGCTCGACCCCG GG   AG
                                       T  ACG
GAM555  CRAT     3'  GCTGGGGCCTGCAGGCCCCC   19664          __  AT
                                GCTGGGGCC  CGG  CCCC
                                |||||||||  |||  ||||
                                CGACCCCGG  GTC  GGGG
                                      AC   CG
GAM555  CST      5'  CGGGCTGTGGCTGGCTGCCCC  22171    A   G   CC  AT_
                                CG GCTG GGC  GG   CCCC
                                || |||| |||  ||   ||||
                                GC CGAC CCG  CC   GGGG
                                 C    A   A_  GAC
GAM555  DDAH2    5'  CGGCTGGGGCCCCACCCCC   30355    A       GGAT
                                CG GCTGGGGCCC    CCCCC
                                || ||||||||||    |||||
                                GC CGACCCCGGG    GGGGG
                                 _        GT__
GAM555  ECEL1    5'  CCCGAGCGGGGGCCTGAGCC   22091        T     CG  T
                                CCCGAGC GGGGCC  GA CC
                                |||||||  ||||||  || ||
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                                GGGCTCG CCCCGG  CT GG
                                    C     A_  C
GAM555  ECH1    3'  CCCTGGCTGGGGCCTGGGAC  40864    GA       C_
                                CCC  GCTGGGGCC  GGAT
                                |||  |||||||||  ||||
                                GGG  CGACCCCGG  CCTG
                                  AC        AC
GAM555  EPAC    5'  CCAGAGCTGGGCTATCCTCC  25915    C      GCCCGG   _
                                CC GAGCTGGG     ATCC CC
                                || ||||||||     |||| ||
                                GG CTCGACCC     TAGG GG
                                 T       GA____    A
GAM555  EPB49   3'  GAGCTGGGGCCTGTTCCC    12729          CGGA
                                GAGCTGGGGCC    TCCC
                                ||||||||||    ||||
                                CTCGACCCCGG    AGGG
                                      ACA_
GAM555  ESPN    3'  CCCGAGCTCGGGGCCTGCCTCC 36443        _     CGGA
                                CCCGAGCT GGGGCC    TCC
                                |||||||| ||||||    |||
                                GGGCTCGA CCCCGG    AGG
                                    G     ACGG
GAM555  FZD5    5'  CCGGGCCGGGGCTTCTCC    41044     A       CCGGA
                                CCG GCTGGGGC     TCC
                                ||| ||||||||     |||
                                GGC CGGCCCCG     AGG
                                  C       AAG__
GAM555  GARP    3'  CCTGGGCTGAGGCCTGGGCCC  24308    GA_       C  AT
                                CC   GCTGGGGCC GG  CC
                                ||   ||||||||| ||  ||
                                GG   CGACTCCGG CC  GG
                                 ACC        A  CG
GAM555  GPR48   3'  AGCTGGGACAGTCCC       32980          CC  A
                                AGCTGGGGC  GG TCCC
                                |||||||||  || ||||
                                TCGACCCTG  TC AGGG
                                      __  _
GAM555  GPR48   5'  CGGGCTGGAGCGGGGGTC    32985    A       CC  A
                                CG GCTGGGGC  GG TC
                                || ||||||||  || ||
                                GC CGACCTCG  CC AG
                                 C       CC  C
GAM555  HLX1    3'  GCAAGGCCCGGATCCCC     34986    T
                                GC GGGGCCCGGATCCCC
                                || ||||||||||||||||
                                CG TTCCGGGCCTAGGGG
                                 _
GAM555  HSPA4   5'  CGGGCTCGGGCCCGGGTCC    44850    A  G       A
                                CG GCT GGGCCCGG TCC
                                || ||| |||||||| |||
```

```
                                GC CGA CCCGGGCC AGG
                                 C  G      C
GAM555  IL10RA   3'  CCTGGCTGGGGCCAGCCCC   40621   GA      C  AT
                                CC  GCTGGGGCC GG  CCCC
                                ||  ||||||||| ||  ||||
                                GG  CGACCCCGG TC  GGGG
                                 AC       _ __
GAM555  KIF3B    3'  GAGTTTGGGCCGAATCC    22037    CTG    C
                                GAG   GGGCC GGATCC
                                |||   ||||| ||||||
                                CTC   CCCGG CTTAGG
                                 AAA    _
GAM555  LRP3     5'  CGGGCTAGGGCTCGGGCTCC  42164   A      C  A_
                                CG GCTGGGGC CGG  TCC
                                || |||||||| |||  |||
                                GC CGATCCCG GCC  AGG
                                 C       A  CG
GAM555  MTMR3    3'  CCCTGAGTCTGGATTTCCC   34393    _  _    G__
                                CCC GAG CTGGG   CCC
                                ||| ||| |||||   |||
                                GGG CTC GACCT   GGG
                                 A  A    AAA
GAM555  NPTX1    5'  CGGCTGGGGCTCGGCTC    14836    A      C  A
                                CG GCTGGGGC CGG TC
                                || |||||||| ||| ||
                                GC CGACCCCG GCC AG
                                 _      A  G
GAM555  NR1H2    3'  CCTGGACTGGGGCTTATCCC  43118   GA_     CCGG
                                CC  GCTGGGGC   ATCCC
                                ||  ||||||||   |||||
                                GG  TGACCCCG   TAGGG
                                 ACC      AA__
GAM555  NRL      3'  CCTGGGCTGTGCATCCCC   26134   GA_   GG  CCGG
                                CC  GCTG  GC   ATCCCC
                                ||  ||||  ||   ||||||
                                GG  CGAC  CG   TAGGGG
                                 ACC   A_ ____
GAM555  NSD1     3'  CCTTGGTTGGGGCCCACTGGAT 35360   GAGC_     ___
                                CC    TGGGGCCC  GGAT
                                ||    ||||||||  ||||
                                GG    ACCCCGGG  CCTA
                                 AACCA      TGA
GAM555  PACE     3'  CCCAGCTGGGGTCCAAACCC  15031    G      C
                                CCC AGCTGGGG CCGGATCC
                                ||| |||||||| ||||||||
                                GGG TCGACCCC GGTTTGGG
                                  _      A
GAM555  PACSIN1  3'  CCAGCTGGGGCTGCAGCCCC  45146   G      C_  AT
                                CC AGCTGGGGC  CGG  CCCC
                                || |||||||||  |||  ||||
```

```
                                GG TCGACCCCG  GTC  GGGG
                                 _       AC   __
GAM555  PCDHB2   5'  CTAGGGCCCGGATTTCCC    33193           CC
                                CTGGGGCCCGGAT  CCC
                                ||||||||||||  |||
                                GATCCCGGGCCTA  GGG
                                      AA
GAM555  PDCL     5'  CCCTAGCTCGCTCCGGATCC   23932     G   GGG _
                                CCC AGCT   GC CCGGATCC
                                ||| ||||   || ||||||||
                                GGG TCGA   CG GGCCTAGG
                                  A   G__  A
GAM555  PDE5A    5'  CCCCAGCTGGGGTCCGTCCC   37904     G      C   GA
                                CCC AGCTGGGG CCG  TCCC
                                ||| |||||||| |||  ||||
                                GGG TCGACCCC GGC  AGGG
                                  G       A  __
GAM555  PODXL    3'  CCCAGAGCCTCTCCGGGTTCTC 23959     _    GGGG  C  A  C
            C                    CCC GAGCT    CC GG TC CC
                                ||| |||||    || || || ||
                                GGG CTCGG    GG CC AG GG
                                  T    AGA_  C  A  A
GAM555  PPP1R7   3'  CCCGTGGCTGGGCAGTTC    15509     A_     GCC   A
                                CCCG  GCTGGG   CGG TC
                                ||||  ||||||   ||| ||
                                GGGC  CGACCC   GTC AG
                                  AC     ____  A
GAM555  RXRA     3'  CCAGGGCTGGGGCCCGAAGACC 16417     A_          TC
            C                    CCG  GCTGGGGCCCGGA  CCC
                                |||  ||||||||||||  |||
                                GGT  CGACCCCGGGCTT  GGG
                                  CC           CT
GAM555  SDC4     3'  CCCCAGCTGGGGCCTCATCAGC 16521     G        _  GATC
            CC                    CCC AGCTGGGGCC CG    CCC
                                ||| ||||||||| ||    |||
                                GGG TCGACCCCGG GT    GGG
                                  G        A  AGTC
GAM555  SHMT2    3'  CCTGAGCTGGGTCCCAGCTC   24004    C      G    A
                                CC GAGCTGGG CCCGG TC
                                || |||||||| ||||| ||
                                GG CTCGACCC GGGTC AG
                                 A       A    G
GAM555  SIRT2    3'  CCCGGTTGGGGCTCAGCTGTCC 36144     AGC     C   A__
            C                    CCCG   TGGGGC CGG   TCCC
                                ||||   |||||| |||   ||||
                                GGGC   ACCCCG GTC   AGGG
                                  CA_     A  GAC
GAM555  SLC9A3R2 3'  CCGGGGCTGGGGCTGAT     41524     A_      CCG
                                CCG  GCTGGGGC   GAT
                                |||  ||||||||   |||
```

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                                GGC  CGACCCCG   CTA
                                  CC       A__
GAM555  SPI1    5'  CCGAGTCGGTCAGATCCCC   17074      C   GGCC
                                CCGAG TGG    CGGATCCCC
                                ||||| |||    |||||||||
                                GGCTC GCC    GTCTAGGGG
                                   A   A___
GAM555  TBL1X   3'  CGAGCTGGTGACTTCC      24876        _   CCGGA
                                CGAGCTGG GGC     TCC
                                |||||||| |||     |||
                                GCTCGACC CTG     AGG
                                    A   A____
GAM555  TNP2    5'  CCCAGGCTGGGGCAGCTC    24055      A       CC  A
                                CCCG GCTGGGGC  GG TC
                                |||| ||||||||  || ||
                                GGGT CGACCCCG  TC AG
                                  C       __ G
GAM555  TOP3B   5'  CCCGAGCTCGCGGGTCCTCC   19462         _ _   C  GGA
                                CCCGAGCT G GGG CC   TCC
                                |||||||| | ||| ||   |||
                                GGGCTCGA C CCC GG   AGG
                                    G G   A  ___
GAM556  ABL2    5'  CCCTGGCCCTGAGCGGCTGGG  28725     C    CCTCC  A
                                CCC GGCCC     CG GCTGGG
                                ||| |||||     || ||||||
                                GGG CCGGG     GC CGACCC
                                  A     ACTC_ _
GAM556  ADCY2   3'  TCCTCGGCCTCCCAAAATATTG 42147     C    CCC      C___
           GG                     TCC CGGCC   TCCCGAG    TGGG
                                ||| |||||   |||||||    ||||
                                AGG GCCGG   AGGGTTT    ACCC
                                  A     ___       TATA
GAM556  AF1Q    5'  TCCCCGCCCCCTCCTGCC    27728       G       CGA
                                TCCCCG CCCCCTCC   GCT
                                |||||| ||||||||   |||
                                AGGGGC GGGGGAGG   CGG
                                   _       A__
GAM556  AK3     5'  CGGCCCCCTACCTCTGG     30181         C  GAG
                                CGGCCCCCT CC   CTGG
                                |||||||| ||   ||||
                                GCCGGGGGA GG   GACC
                                    T  A__
GAM556  AKAP13  5'  TCCCCCGCGGGCCGAGCTGGG  28486      G  CCCCTC
                                TCCCC GC     CCGAGCTGGG
                                ||||| ||     ||||||||||
                                AGGGG CG     GGCTCGACCC
                                  G  CCC___
GAM556  ALDH3A2 5'  TCCCCGGCTCTGGCAGCGGGCT 42920         CCCCTCC_  A
           GGG                    TCCCCGGC       CG GCTGGG
                                ||||||||       || ||||||
```

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                                AGGGGCCG       GC CGACCC
                                    AGACCGTC  C
GAM556  ANKH     3'  TCCTTGGCCTCCCAAAGTGTTG 38327     CC    CCC      C___
            GG                   TCC  GGCC   TCCCGAG    TGGG
                                 |||  ||||   |||||||    ||||
                                 AGG  CCGG   AGGGTTT    ACCC
                                   AA    ___       CACA
GAM556  AP2M1    5'  TCCTCGGCCCCCTGCTCTGCCG 19823     C        CCCGA
            G                    TCC CGGCCCCCT     GCTGG
                                 |||  |||||||||     |||||
                                 AGG GCCGGGGGA     CGGCC
                                   A        CGAGA
GAM556  ASC      5'  CCCTTGGTCCCCTCCCACCCAG 29940     C_  C        AG TG
            G                    CCC  GG CCCCTCCCG  C  GG
                                 |||  ||  |||||||||  |  ||
                                 GGG  CC GGGGAGGGT  G  CC
                                   AA  A        G_ GT
GAM556  BARHL1   3'  CCCTTGGCCCCTTCCTGCC    33461     C_     C   CGA
                                 CCC  GGCCCC TCC   GCT
                                 |||  |||||| |||   |||
                                 GGG  CCGGGG AGG   CGG
                                   AA     A   A__
GAM556  CD34     5'  CCCGCCCCCTCCGCCCGGG    12113      G       C AG
                                 CCCG CCCCCTCC G  CTGGG
                                 ||||  |||||||  |  |||||
                                 GGGC GGGGGAGG C  GGCCC
                                   _       _ G_
GAM556  CYLN2    5'  CCCCGGCCTCCTCCTCTCGGG  18047         C     CGAGC
                                 CCCCGGCC CCTCC     TGGG
                                 ||||||||  |||||     ||||
                                 GGGGCCGG GGAGG     GCCC
                                     A     AGA__
GAM556  CYP1A2   3'  CCCCGGCCTCCCAAAATGCTGG 42900         CCC      ___
            G                    CCCCGGCC   TCCCGA   GCTGGG
                                 ||||||||   ||||||   ||||||
                                 GGGGCCGG   AGGGTT   CGACCC
                                     ___       TTA
GAM556  DUX4     5'  TCCCCGGCTCCCTCCCGCCCG  43761         C       AG
                                 TCCCCGGC CCCTCCCG  CTG
                                 |||||||| ||||||||  |||
                                 AGGGGCCG GGGAGGGC  GGC
                                     A       G_
GAM556  EPB49    3'  TCCCTCGCGGAGGCTGAGCTGG 12736      CG  CCCCTCCC
            G                    TCCC  GC       GAGCTGGG
                                 ||||  ||       ||||||||
                                 AGGG  CG       CTCGACCC
                                   AG  CCTCCGA_
GAM556  FBXW1B   3'  TCCCCTGCCCCCTCCCTTCCCC 37996       G        GAG___
            CTGGG                    TCCCC GCCCCCTCCC     CTGGG
                                 |||||  ||||||||||      |||||
```

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                                AGGGG CGGGGGAGGG     GACCC
                                  A         AAGGGG
GAM556  FOXD2    5'  CCCCGGGAATCCGAGCTGGG  20957       CCCCCTC
                                CCCCGG      CCGAGCTGGG
                                ||||||      ||||||||||
                                GGGGCC      GGCTCGACCC
                                   CTTA___
GAM556  GAS7     3'  CCTCGGCCTCCCAAAGAGCTGG 18883    C    _  TCCC
             G                   CC CGGCC CCC    GAGCTGGG
                                 || ||||| |||    ||||||||
                                 GG GCCGG GGG    CTCGACCC
                                  A    A  TTT_
GAM556  HUNK     5'  TCCCCGGCTTCTCCCGCCG   31081        CCC    GA
                                TCCCCGGC   CTCCC  GCTG
                                ||||||||   |||||  ||||
                                AGGGGCCG   GAGGG  CGGC
                                     AA_    __
GAM556  IFNW1    5'  TCCTGGCTTTACTGAGCTGGG  13486     CC   CCCCTCCC
                                TCC  GGC       GAGCTGGG
                                |||  |||       ||||||||
                                AGG  CCG       CTCGACCC
                                  A_   AAATGA__
GAM556  IL1RL1LG 3'  CCAGGCCCCCTTCCTGG     27795    C       C  GAGC
                                CC GGCCCCCT CC    TGG
                                || |||||||| ||    |||
                                GG CCGGGGGA GG    ACC
                                 T       A _____
GAM556  ITGAL    3'  TCCTTGGCCTCCCAAAGTGCTG 13624     CC    CCC     ___
             GG                   TCC  GGCC   TCCCGA   GCTGGG
                                  |||  ||||   ||||||   ||||||
                                  AGG  CCGG   AGGGTT   CGACCC
                                    AA    ___      TCA
GAM556  KCNJ5    3'  CCTCGGCCTCCCAAAATGCTGG 9433     C    CCC     ___
             G                    CC CGGCC   TCCCGA   GCTGGG
                                  || |||||   ||||||   ||||||
                                  GG GCCGG   AGGGTT   CGACCC
                                   A    ___      TTA
GAM556  LIM2     3'  CAGCTCCCTCCCATGGG     36182      C       AGC
                                  CGGC CCCTCCCG   TGGG
                                  |||| ||||||||   ||||
                                  GTCG GGGAGGGT   ACCC
                                    A      ___
GAM556  LY6E     3'  GGCTTTCCTTCCTGAGCTGGG  14281     C__  C   C
                                  GGC   CC TCC GAGCTGGG
                                  |||   || ||| ||||||||
                                  CCG   GG AGG CTCGACCC
                                    AAA  A   A
GAM556  MAFF     3'  TCCTTGGACTCCCAAAGTGCTG 29516     CC  CCCC      ___
             GG                   TCC  GG   CTCCCGA   GCTGGG
                                  |||  ||    |||||||   ||||||
```

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                                AGG  CC    GAGGGTT   CGACCC
                                  AA  T___      TCA
GAM556  MBD3     3'  TCTCCAGTCTCAAGGAGCTGGG 19424    C   CCCC  CC_
                                TC CCGG    CTC   GAGCTGGG
                                || ||||    |||   ||||||||
                                AG GGTC    GAG   CTCGACCC
                                 A    A___   TTC
GAM556  MS4A1    3'  CCTCGGCCTCCCAAAGGGCTGG 6597     C    CCC     ___
              G                  CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||  ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A    ___      TCC
GAM556  MYO1C    3'  CCGCCTCCCAAAGTGCTGGG   41467    _      ___
                                CC CCTCCCGA   GCTGGG
                                || ||||||||   ||||||
                                GG GGAGGGTT   CGACCC
                                 C       TCA
GAM556  PCDHA9   3'  CCTTGGCCTCCCAAAATGTTGG 36542    CC   CCC      C___
              G                  CC  GGCC   TCCCGAG    TGGG
                                ||  ||||   |||||||    ||||
                                GG  CCGG   AGGGTTT    ACCC
                                 AA    ___      TACA
GAM556  PCOLN3   3'  GCCTTGGCTTCCAAGCTGGG   15752     CC__  C
                                GCC    CT CCGAGCTGGG
                                |||    || ||||||||||
                                CGG    GA GGTTCGACCC
                                  AACC  A
GAM556  PIP5K1A  5'  TCCCCGCCCCCTCCG       18657       G      CGAGCT
                                TCCCCG CCCCCTCC     G
                                |||||| ||||||||     |
                                AGGGGC GGGGGAGG     C
                                    _      _______
GAM556  PNOC     5'  TCCCCGGCTCCCTCCGATGG   26351        C     C  GC
                                TCCCCGGC CCCTCC GA  TGG
                                |||||||| |||||| ||  |||
                                AGGGGCCG GGGAGG CT  ACC
                                     A     _  __
GAM556  POLR2E   3'  CCCCGGCTCAGCTGAGCTGGG  40916       CCCCTCCC
                                CCCCGGC       GAGCTGGG
                                |||||||       ||||||||
                                GGGGCCG       CTCGACCC
                                    AGTCGA__
GAM556  PRX      3'  TCCTCGGCCCCCTCCTTGG   34134     C        CGAGC
                                TCC CGGCCCCCTCC     TGG
                                ||| ||||||||||     |||
                                AGG GCCGGGGGAGG     ACC
                                  A         A____
GAM556  PTPRF    3'  CCCTGCCCCTCAGCAAGCTGGG 39030     G    C  C_
                                CCC GCCCC TC  CGAGCTGGG
                                ||| ||||| ||  |||||||||
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                                GGG CGGGG AG  GTTCGACCC
                                  A    _ TC
GAM556  RNH      5'  TCCATGGCCCCCTTCTGG    40611     CC      CCCGAG
                                TCC  GGCCCCCT     CTGG
                                |||  ||||||||     ||||
                                AGG  CCGGGGGA     GACC
                                  TA       A_____
GAM556  SFRS2IP   5'  CCTCGGCCTCCCAAACTGCTGG 21791    C    CCC     ___
              G                   CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||  ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A    ____     TGA
GAM556  SLC1A5   5'  TCCTTGGCCCTAGGAGCTGGG  24749    CC    CCTCCC
                                TCC  GGCCC     GAGCTGGG
                                |||  |||||     ||||||||
                                AGG  CCGGG     CTCGACCC
                                  AA    ATC___
GAM556  UBE2G2   3'  CCTTGGCCTCCCAAAGAGCTGG 42121    CC   _   TCCC
              G                   CC  GGCC CCC    GAGCTGGG
                                ||  |||| |||    ||||||||
                                GG  CCGG GGG    CTCGACCC
                                 AA    A   TTT_
GAM556  WEE1     5'  CCGGGTCTCTGCGAGCTGGG   18086     CCCC   C_
                                CCGG    CTC  CGAGCTGGG
                                ||||    |||  |||||||||
                                GGCC    GAG  GCTCGACCC
                                  CA__   AC
GAM556  WHSC1    3'  CCTGGCGGCTCGAGCTGGG    39362    C   CCC   CC
                                CC GGC   CTC  GAGCTGGG
                                || |||   |||  ||||||||
                                GG CCG   GAG  CTCGACCC
                                 A  CC_   __
GAM556  WW45     3'  CCTCGGCCTCCCAAAATGCTGG 34818    C    CCC     ___
              G                   CC CGGCC   TCCCGA   GCTGGG
                                || |||||   ||||||  ||||||
                                GG GCCGG   AGGGTT   CGACCC
                                 A    ____     TTA
GAM556  ACADS    3'  CCGGGGTTGGGGTGGAGGCCCC 6153     AGC_    CCC  TT_
                                CCG    TGGGG   GG   CCCC
                                |||    |||||   ||   ||||
                                GGC    ACCCC   CC   GGGG
                                  CCCA    A__  TCC
GAM556  ACHE     3'  CCTGAGTGGGGCCCTTCCCC   8561     C   C       GG
                                CC GAG TGGGGCCC  TTCCCC
                                || ||| ||||||||  ||||||
                                GG CTC ACCCCGGG  AAGGGG
                                 A   _       __
GAM556  ALK      5'  GAGCTGGGGTCTGTCCCC    43835          CCCG
                                GAGCTGGGG    GTTCCC
                                |||||||||    ||||||
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                                CTCGACCCC   CAGGGG
                                     AGA_
GAM556  ALOX5   3'  GCTGGGGCAGCTGGCC     44910        CC   CC
                                GCTGGGGC  GGTT  CC
                                ||||||||  ||||  ||
                                CGACCCCG  TCGA  GG
                                    __   CC
GAM556  AQP6    3'  CCCGGCTGGGATTCC      38238     A     GCCCG
                                CCCG GCTGGG    GTTCC
                                |||| ||||||    |||||
                                GGGC CGACCC    TAAGG
                                  _    _____
GAM556  AQP7    5'  CCCCAGCTGGGGCTCAGCTATC 10118     G       C   __
           CC                     CCC AGCTGGGGC CGGT  TCCC
                                ||| |||||||| ||||  ||||
                                GGG TCGACCCCG GTCG  AGGG
                                  G       A   AT
GAM556  ATP8B2  3'  CCCGAGTGGGGCTGGCTCCC  42202       C     CC
                                CCCGAG TGGGGC  GGTTCCC
                                ||||||  ||||||  |||||||
                                GGGCTC ACCCCG  CCGAGGG
                                   _     A_
GAM556  BLK     3'  CCTAGGCTGGGGTTGCCCC   11843    GA_     CCCG
                                CC  GCTGGGG   GTTCC
                                ||  |||||||   |||||
                                GG  CGACCCC   CGGGG
                                 ATC      AA__
GAM556  CENTD2  5'  GCTGGGGCCCCCGGCCCC    31597          __
                                GCTGGGGCCC  GGTTCC
                                ||||||||||  ||||||
                                CGACCCCGGG  CCGGGG
                                     GG
GAM556  CISH    3'  CCAGCTGGGGCTGATGTCCCC  30026    G       CC  _
                                CC AGCTGGGGC  GGT TCCCC
                                || |||||||||  ||| |||||
                                GG TCGACCCCG  CTA AGGGG
                                 _       A_  C
GAM556  CIT     3'  CCGAGCTGAGGCCCCGATGACC 43045            _  TC  _
           TCC                    CCGAGCTGGGGCCC GGT  CC CC
                                |||||||||||||| |||  || ||
                                GGCTCGACTCCGGG CTA  GG GG
                                       G   CT  A
GAM556  COL9A1  5'  CCCGGCTCTGCAGCCTGGTTCC 12335     AG_  G   C
           CC                     CCCG   CTG GGCC GGTTCCCC
                                ||||   ||| |||| ||||||||
                                GGGC   GAC TCGG CCAAGGGG
                                  CGA   G   A
GAM556  COX15   3'  CCGAGCTGGGGCACCTGCTC  38514           _  G
                                CCGAGCTGGGGC CC GTTC
                                ||||||||||| || ||||
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                                GGCTCGACCCCG GG CGAG
                                      T  A
GAM556  CRAT    3'  GCTGGGGCCTGCAGGCCCCC  19664        __  TT
                                GCTGGGGCC  CGG  CCCC
                                |||||||||  |||  ||||
                                CGACCCCGG  GTC  GGGG
                                     AC   CG
GAM556  CST     5'  CGGGCTGTGGCTGGCTGCCCC  22171    A   G   CC   _
                                CG GCTG GGC  GGTT CCCC
                                || |||| |||  |||| ||||
                                GC CGAC CCG  CCGA GGGG
                                 C   A  A_   C
GAM556  DDAH2   5'  CGGCTGGGGCCCCACCCCC   30355    A       G TT
                                CG GCTGGGGCCC G  CCC
                                || ||||||||| |  |||
                                GC CGACCCCGGG T  GGG
                                 _        G GG
GAM556  DUSP1   5'  CGGCTTCTTCGCGGTTCCCCC  20653    A  GGGGCC
                                CG GCT     CGGTTCCCCC
                                || |||     ||||||||||
                                GC CGA     GCCAAGGGGG
                                 _  AGAAGC
GAM556  ECEL1   5'  CCCGAGCGGGGGCCTGAGCC   22091       T    C  TT
                                CCCGAGC GGGGCC GG  CC
                                ||||||| |||||| ||  ||
                                GGGCTCG CCCCGG CT  GG
                                    C     A  C_
GAM556  ELMO2   3'  CCTCAGCTGGGTTTTCCC    35221    CG     GCCCGG
                                CC  AGCTGGG     TTCCC
                                ||  |||||||     |||||
                                GG  TCGACCC     AAGGG
                                 AG      AA____
GAM556  EPB49   5'  CCCGGGCTGGCGCGTCC     12724     A    G  CCG
                                CCCG GCTGG GC   GTTC
                                |||| ||||| ||   ||||
                                GGGC CGACC CG   CAGG
                                  C    G  ___
GAM556  EPB49   3'  GAGCTGGGGCCTGTTCCC    12729          CG
                                GAGCTGGGGCC  GTTCCC
                                ||||||||||  ||||||
                                CTCGACCCCGG  CAAGGG
                                      A_
GAM556  ESPN    3'  CCCGAGCTCGGGGCCTGCCTCC 36443        _     CG  TC
                                CCCGAGCT GGGGCC  GT  CC
                                |||||||| ||||||  ||  ||
                                GGGCTCGA CCCCGG  CG  GG
                                    G     A_  GA
GAM556  FZD5    5'  CCGGGCCGGGGCTTCTCCC   41045     A      CCGG
                                CCG GCTGGGGC   TTCCC
                                ||| ||||||||   |||||
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                                GGC CGGCCCCG   GAGGG
                                  C      AA__
GAM556  GARP     3'  CCTGGGCTGAGGCCTGGGCCC  24308    GA_      C  TT
                                CC   GCTGGGGCC GG  CC
                                ||   ||||||||| ||  ||
                                GG   CGACTCCGG CC  GG
                                  ACC       A  CG
GAM556  GUCY1A3  5'  CCCGGCTGGGGTCTCTAAGCTC 41835     A     CCC___
              C                  CCCG GCTGGGG     GGTTCC
                                ||||| |||||||     ||||||
                                GGGC CGACCCC     TCGAGG
                                  _      AGAGAT
GAM556  HCFC1    3'  CCAAGGACGCCTGGTTCCCC   43385      CT  G   C
                                CCGAG  GG GCC GGTTCCCC
                                |||||  || ||| ||||||||
                                GGTTC  CT CGG CCAAGGGG
                                  __ G   A
GAM556  HSPA4    5'  CGGGCTCGGGCCCGGGTCC   44850    A   G      T
                                CG GCT GGGCCCGG TCC
                                || ||| |||||||| |||
                                GC CGA CCCGGGCC AGG
                                 C   G       C
GAM556  IL10RA   3'  CCTGGCTGGGGCCAGCCCC   40621    GA       C
                                CC  GCTGGGGCC GGTTCC
                                ||  ||||||||| ||||||
                                GG  CGACCCCGG TCGGGG
                                 AC       _
GAM556  KCNJ5    3'  CCCCAGCTGCTGGGGTTCCCCC 9432      G    G_  CCC
                                CCC AGCTG  GG   GGTTCCCCC
                                |||  |||||  ||   |||||||||
                                GGG TCGAC  CC   CCAAGGGGG
                                  G    GA  ___
GAM556  KCNK10   5'  CCCGGGCTGGCGGCCACTGCGT 34511      A    _   CG_  _
              CC                  CCCG GCTGG GGCC   GT TCC
                                |||| ||||| ||||   || |||
                                GGGC CGACC CCGG   CG AGG
                                  C    G    TGA  C
GAM556  LRP1     5'  CCCCAGTTGGGGGGTCCCCC   14208     G  C    CCC
                                CCC AG TGGGG   GGTTCCCC
                                ||| || |||||   ||||||||
                                GGG TC ACCCC   CCAGGGGG
                                  G  A    ___
GAM556  LRP3     5'  CGGGCTAGGGCTCGGGCTCC   42164    A      C  _
                                CG GCTGGGGC CGG TTCC
                                || |||||||| ||| ||||
                                GC CGATCCCG GCC GAGG
                                 C       A  C
GAM556  LYL1     5'  CCCGGCGGCCCGGTTTCC    24576      A  TGG       C
                                CCCG GC   GGCCCGGTT CC
                                ||||  ||   |||||||| ||
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                                GGGC CG   CCGGGCCAA GG
                                  _ ___       A
GAM556  MAF     5'  CCGGGCTGGGGCGCTTC    23824    A      CC G
                                CCG GCTGGGGC  G TTC
                                ||| ||||||||  | |||
                                GGC CGACCCCG  C AAG
                                  C       __ G
GAM556  MYH11   3'  CCTGGGCTGGAGCGTTCTTCC 35626   GA_     CCG   CC
                                CC   GCTGGGGC   GTTC  CC
                                ||   ||||||||   ||||  ||
                                GG   CGACCTCG   CAAG  GG
                                 ACC        ___    AA
GAM556  NPTX1   5'  CGGCTGGGGCTCGGCTC    14836    A      C
                                CG GCTGGGGC CGGTTC
                                || |||||||| ||||||
                                GC CGACCCCG GCCGAG
                                 _       A
GAM556  NR1H2   3'  CCTGGACTGGGGCTTATCCC  43118    GA_      CCGGT
                                CC   GCTGGGGC    TCCC
                                ||   ||||||||    ||||
                                GG   TGACCCCG    AGGG
                                 ACC       AAT__
GAM556  PACE    3'  CCCAGCTGGGGTCCAAACCC  15031    G      C    TT
                                CCC AGCTGGGG CCGG  CCC
                                ||| |||||||| ||||  |||
                                GGG TCGACCCC GGTT  GGG
                                  _       A   T_
GAM556  PACSIN1 3'  CCAGCTGGGGCTGCAGCCCC  45146    G       C_
                                CC AGCTGGGGC  CGGTTCC
                                || |||||||||  |||||||
                                GG TCGACCCCG  GTCGGGG
                                 _        AC
GAM556  PAX3    3'  CCGAGCTGGGCTTGGCT     7748          G CC
                                CCGAGCTGGG C  GGTT
                                ||||||||||  |  ||||
                                GGCTCGACCC G  CCGA
                                       _ AA
GAM556  PDE5A   5'  CCCCAGCTGGGGTCCGTCCC  37904    G      C   GT
                                CCC AGCTGGGG CCG  TCCC
                                ||| |||||||| |||  ||||
                                GGG TCGACCCC GGC  AGGG
                                  G       A  __
GAM556  PITX1   3'  CCTGGGCTGGGGGCACCGTCCC 15321    GA_     _ _  GT
                                CC   GCTGGGG C CCG  TCCC
                                ||   ||||||| | |||  ||||
                                GG   CGACCCC G GGC  AGGG
                                 ACC      C T  __
GAM556  PNUTL2  5'  CCCGGGCGGGGCCGGCTCC   38647     A  T     C
                                CCCG GC GGGGCC GGTTCC
                                |||| || |||||| ||||||
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                                GGGC CG CCCCGG CCGAGG
                                  C _    _
GAM556  POU2AF1  5'  GAGCTGAGGCTGTTTCC    26369        CCGG
                                GAGCTGGGGC   TTCC
                                ||||||||||   ||||
                                CTCGACTCCG   AAGG
                                     ACA_
GAM556  PPP1R7   3'  CCCGTGGCTGGGCAGTTCTTCC 15510    A_    GCC    CC
                                CCCG  GCTGGG  CGGTTC  CC
                                ||||  ||||||  ||||||  ||
                                GGGC  CGACCC  GTCAAG  GG
                                  AC     ___     AA
GAM556  PPP3CA   5'  GAGCACGCCTCCCGGTTC    9612      _ GGG
                                GAGC TG   CCCGGTTC
                                |||| ||   ||||||||
                                CTCG GC   GGGCCAAG
                                  T  GGA
GAM556  RANBP9   5'  CCAGAGCTGGGGTCGGGGCCCC 24250    C       CC   TT
                                CC GAGCTGGGG  CGG  CCCC
                                || |||||||||  |||  ||||
                                GG CTCGACCCC  GCC  GGGG
                                 T       A_   CC
GAM556  RXRA     3'  CCAGGGCTGGGGCCCGAAGACC 16417     A_         TT_
           C                     CCG  GCTGGGGCCCGG   CCC
                                |||  ||||||||||||   |||
                                GGT  CGACCCCGGGCT   GGG
                                  CC          TCT
GAM556  SDC4     3'  CCCCAGCTGGGGCCTCATCAGC 16521     G        _ GTTC
           CC                    CCC AGCTGGGGCC CG    CCC
                                ||| ||||||||||  ||    |||
                                GGG TCGACCCCGG GT    GGG
                                  G         A  AGTC
GAM556  SECTM1   3'  CCTGGCTGGGGGCTCCCC    16539    GA      CCCG
                                CC  GCTGGGG    GTTCCCC
                                ||  |||||||    |||||||
                                GG  CGACCCC    CGAGGGG
                                 AC      _____
GAM556  SHMT2    3'  CCTGAGCTGGGTCCCAGCTC   24004    C       G
                                CC GAGCTGGG CCCGGTTC
                                || |||||||| ||||||||
                                GG CTCGACCC GGGTCGAG
                                 A       A
GAM556  SIRT2    3'  CCCGGTTGGGGCTCAGCTGTCC 36144      AGC     C   __
           C                     CCCG   TGGGGC CGGT  TCCC
                                ||||   |||||| ||||  ||||
                                GGGC   ACCCCG GTCG  AGGG
                                  CA_     A   AC
GAM556  SLC21A9  3'  CCTGGGCTGGGGCCCAGC    28561    GA_
                                CC   GCTGGGGCCCGGT
                                ||   ||||||||||||
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                                GG  CGACCCCGGGTCG
                                 ACC
GAM556  SLC2A6   3'  CCTGGGCTGGGGCTGTGGCT  32767   GA_     CC_
                                CC  GCTGGGGC  GGTT
                                ||  ||||||||  ||||
                                GG  CGACCCCG  CCGA
                                 ACC      ACA
GAM556  SLC9A3R2 3'  CCGGGGCTGGGGCTGATT   41525    A_     CC
                                CCG GCTGGGGC GGTT
                                ||| ||||||||  ||||
                                GGC CGACCCCG CTAA
                                 CC      A_
GAM556  SMURF1   3'  CCATGAGACCCTGGTTTCC   45186    AGC     _   C
                                CCG  TGGGGCCC GGTT CC
                                |||  |||||||| |||| ||
                                GGT  ACTCTGGG CCAA GG
                                 ___      A   A
GAM556  SRC      3'  CCCCAGCCCTTCTCCTGGTTCC 24032    G   GGGG_ C
                                CCC AGCT    CC GGTTCC
                                ||| ||||    || ||||||
                                GGG TCGG    GG CCAAGG
                                 G   GAAGA  A
GAM556  TBL1X    3'  CGAGCTGGTGACTTCCTCC   24877       _  CCGG   _
                                CGAGCTGG GGC   TTCC CC
                                |||||||| |||   |||| ||
                                GCTCGACC CTG   AAGG GG
                                    A  ____   A
GAM556  TNP2     5'  CCCAGGCTGGGGCAGCTC   24055    A      CC
                                CCCG GCTGGGGC  GGTTC
                                |||| ||||||||  |||||
                                GGGT CGACCCCG  TCGAG
                                  C      __
GAM556  WHSC1    3'  CGAGCTGGGTCCTCC      39363       GC  GGT
                                CGAGCTGGG  CC   TCC
                                |||||||||  ||   |||
                                GCTCGACCC  GG   AGG
                                    A_  ___
GAM556  WIF1     3'  CCTGAGCTGGGCGCCTGCT   41165   C      _  CG
                                CC GAGCTGGG GCC  GTT
                                || ||||||| |||  |||
                                GG CTCGACCC CGG  CGA
                                 A      G   A_
GAM557  SOX11    3'  AGGTCAAACACTGCGGCGGCGT 17001        CG_ TA
           TC                    AGGTCAAGC   G  GCGGCGTTC
                                ||||||||||  |  |||||||||
                                TCCAGTTTG   C  CGCCGCAAG
                                    TGA GC
GAM557  BCLG     3'  TTCCTCAGGTTCTCAATG    39827       CCGGAAGAC
                                TTTCTCAGG       CAATG
                                |||||||||       |||||
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                                AAGGAGTCC        GTTAC
                                     AAGA_____
GAM557  FLT1     3'  CTCAGGCCAGCCAGTG      12911          AAGA   A
                                CTCAGGCCGG    CCA TG
                                ||||||||||    ||| ||
                                GAGTCCGGTC    GGT AC
                                     _____   C
GAM557  SDHC     3'  TTTCCCAGGCTGGAGATAAGAA 42983          C   A  CC__
           TGA                    TTTCTCAGGC GGA GA    AATGA
                                ||||||||||| ||| ||    |||||
                                AAAGGGTCCG CCT CT    TTACT
                                     A   _  ATTC
GAM557  SFRP1    3'  TCTCTCGGAGACCAAT      16576      AGGC    A
                                TCTC    CGGA GACCAAT
                                ||||    |||| |||||||
                                AGAG    GCCT CTGGTTA
                                  A___    _
GAM557  STAT1    3'  TTTCACAGGTAAACCAATG    40220      T    CCGGA
                                TTTC CAGG     AGACCAATG
                                |||| ||||     |||||||||
                                AAAG GTCC     TTTGGTTAC
                                  T    A____
GAM557  TGM3     3'  TTTCCCAGGCCGGACAGCATG  17507            AGACCA
                                TTTCTCAGGCCGGA     ATG
                                ||||||||||||||     |||
                                AAAGGGTCCGGCCT     TAC
                                      GTCG__
GAM557  VHL      3'  TTTCCCAGGCTGGAGTGCAATG 8125           C   AGAC
                                TTTCTCAGGC GGA    CAATG
                                |||||||||| |||    |||||
                                AAAGGGTCCG CCT    GTTAC
                                     A   CAC_
GAM558  ANK1     3'  GCAGCTCCTCCGACGCAGCC   33861    G       A  A  TG
                                G AGCTCCTCC AC CA  GCC
                                | |||||||| || ||  |||
                                C TCGAGGAGG TG GT  CGG
                                 G        C  C  __
GAM558  APPBP2   3'  GGAGCTCCCTGATGCACCCAAC 26882          _________
                                GGAGCTCCT       CCAAC
                                |||||||||       |||||
                                CCTCGAGGG       GGTTG
                                     ACTACGTG
GAM558  DLEC1    3'  GGAGCTCCTTTGGGTGGCC    28829         CCAACACA
                                GGAGCTCCT       TGGCC
                                |||||||||       |||||
                                CCTCGAGGA       ACCGG
                                     AACCC___
GAM558  INPPL1   3'  GGAGCTCCTCCGCTGTGG     11464          AACACA
                                GGAGCTCCTCC     TGG
                                ||||||||||     |||
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                                CCTCGAGGAGG     ACC
                                      CGAC__
GAM558  MYL1    5'  GGAGTTCCTCCAAAAGAACC  38606     C      CACAT
                                GGAG TCCTCCAA    GGCC
                                |||| ||||||||    ||||
                                CCTC AGGAGGTT    TTGG
                                  A       TTC__
GAM558  MYO1E   3'  GGAGCTCCTCTGCCC      22656         CAACACA  G
                                GGAGCTCCTC      TG CC
                                ||||||||||      || ||
                                CCTCGAGGAG      AC GG
                                      _______  G
GAM558  RAD51L3 3'  GGAGCTCCTGCAGCACAT   39473        C  A
                                GGAGCTCCT CA CACAT
                                ||||||||| || |||||
                                CCTCGAGGA GT GTGTA
                                      C  C
GAM558  AK1     3'  TGGCCAGGCTGCTCTCGAA   7881        A     TC
                                TGGCCAGG TGCTCT  CGAG
                                |||||||| ||||||  ||||
                                ACCGGTCC ACGAGA  GCTT
                                     G     __
GAM558  APM1    3'  GGCCAGGAGTTCGAGAC    22015        TGCTCTTC
                                GGCCAGGA       CGAGAC
                                ||||||||       ||||||
                                CCGGTCCT       GCTCTG
                                     CAA_____
GAM558  BRIP1   3'  GGCCAGGAGTTCGAGAC    36781        TGCTCTTC
                                GGCCAGGA       CGAGAC
                                ||||||||       ||||||
                                CCGGTCCT       GCTCTG
                                     CAA_____
GAM558  CNN2    3'  GGCCAGGAGTTCGAGAC    20404        TGCTCTTC
                                GGCCAGGA       CGAGAC
                                ||||||||       ||||||
                                CCGGTCCT       GCTCTG
                                     CAA_____
GAM558  COLQ    5'  TGGCCAGGGTCTGGCGAG   38697        ATGC   TC
                                TGGCCAGG    TCT  CGAG
                                ||||||||    |||  ||||
                                ACCGGTCC    AGA  GCTC
                                     C___    CC
GAM558  CYP1A2  3'  TGGCCAGGCTGCTTTCCAA  8917         A   C
                                TGGCCAGG TGCT TTCCGA
                                |||||||| |||| ||||||
                                ACCGGTCC ACGA AAGGTT
                                     G    _
GAM558  DBT     3'  TGGCCAGGGTGGTCTCGAA   12556        A  C   TC
                                TGGCCAGG TG TCT  CGAG
                                |||||||| || |||  ||||
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                                ACCGGTCC AC AGA  GCTT
                                     C  C   __
GAM558  EPHA2    3'  GGCCAGGGTGTCATCCGAGACC 20740       A  C  T
                                GGCCAGG TG TC TCCGAGACC
                                ||||||| || || |||||||||
                                CCGGTCC AC AG AGGCTCTGG
                                    C  _  T
GAM558  FUT6     3'  TGGCCAGGATGGTCTCGA    6655          C   TC
                                TGGCCAGGATG TCT  CGA
                                |||||||||||| |||  |||
                                ACCGGTCCTAC AGA  GCT
                                      C   __
GAM558  GABRE    5'  TGTTCAGGATGCGAGA     35080    GC      TCTTCC
                                TG  CAGGATGC     GAGA
                                ||  ||||||||     ||||
                                AC  GTCCTACG     CTCT
                                 AA       _______
GAM558  IL1RL1LG 3'  GGCCAGGAAATCCGAG     27796        TGCTCT
                                GGCCAGGA     TCCGAG
                                ||||||||     ||||||
                                CCGGTCCT     AGGCTC
                                     TT_____
GAM558  ITK      3'  TGGTCAGGATGCTGCTTCC   24450     C       _
                                TGG CAGGATGCT CTTCC
                                ||| ||||||||| |||||
                                ACC GTCCTACGA GAAGG
                                  A        C
GAM558  LYL1     5'  GGCCAGGATAGCCGAG      24579         CTCTT
                                GGCCAGGATG    CCGAG
                                ||||||||||    |||||
                                CCGGTCCTAT    GGCTC
                                      C_____
GAM558  MHC2TA   3'  GCCAGGATGCTGAG       6985          CTTCC
                                GCCAGGATGCT    GAG
                                ||||||||||    |||
                                CGGTCCTACGA    CTC
                                       ______
GAM558  MTRF1    5'  GGTCGGAACCTTCCGAGACC   20188    CCA   T  T
                                GG   GGA GC CTTCCGAGACC
                                ||   ||| || ||||||||||
                                CC   CCT TG GAAGGCTCTGG
                                 AG_  _ _
GAM558  NHLH1    5'  TGGCCAGGTACTGGGGCC    24661        A   CTT_
                                TGGCCAGG TGCT    CC
                                |||||||| ||||    ||
                                ACCGGTCC ATGA    GG
                                     _   CCCC
GAM558  NRXN2    3'  GGTTGGGGTGTTTTCCAAGAC  31489    CCA  A  CTC
                                GG   GG TG   TTCCGAGAC
                                ||   || ||   |||||||||
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                                CC   CC AC   AAGGTTCTG
                                 AAC  C  AA_
GAM558  OAS3     3'  TGGCCAGGATGCATCTGCTGGG 26185          _   TCCGA_
              GAC                   TGGCCAGGATGC TCT      GAC
                                ||||||||||| |||     |||
                                ACCGGTCCTACG AGA     CTG
                                      T   CGACCC
GAM558  PIGR     3'  GGCCAGGAGTTCGAGAC     43708        TGCTCTTC
                                GGCCAGGA       CGAGAC
                                ||||||||       ||||||
                                CCGGTCCT       GCTCTG
                                    CAA_____
GAM558  PSD      5'  TGGCCAGGATGGTCTCGA    15792          C   TC
                                TGGCCAGGATG TCT  CGA
                                |||||||||| |||  |||
                                ACCGGTCCTAC AGA  GCT
                                      C   __
GAM558  PTAFR    3'  TGGCCAGGATGGTCTCGA    9631           C   TC
                                TGGCCAGGATG TCT  CGA
                                |||||||||| |||  |||
                                ACCGGTCCTAC AGA  GCT
                                      C   __
GAM558  PTGES    3'  GGCCAGGAGTTCGAGAC     22183        TGCTCTTC
                                GGCCAGGA       CGAGAC
                                ||||||||       ||||||
                                CCGGTCCT       GCTCTG
                                    CAA_____
GAM558  RBBP9    3'  GGCCAGGAGTTCGAGAC     43139        TGCTCTTC
                                GGCCAGGA       CGAGAC
                                ||||||||       ||||||
                                CCGGTCCT       GCTCTG
                                    CAA_____
GAM558  SULT2A1  3'  TGGCCAGGATGGTCTCGA    43474          C   TC
                                TGGCCAGGATG TCT  CGA
                                |||||||||| |||  |||
                                ACCGGTCCTAC AGA  GCT
                                      C   __
GAM558  TSN      5'  GCTAGGGTCCTCCGAG      21495    C   ATGC
                                GC AGG    TCTTCCGAG
                                || |||    |||||||||
                                CG TCC    AGGAGGCTC
                                 A   C___
GAM558  XRCC3    3'  GGCCAGGATACACCGGGACC   24105          TCTT   A
                                GGCCAGGATGC    CCG GACC
                                ||||||||||    ||| ||||
                                CCGGTCCTATG    GGC CTGG
                                      T___   C
GAM559  MADH7    3'  ATTTACAAGTAATAATATA    25362      T
                                ATTT TAGGTAATAATATA
                                |||| ||||||||||||||
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                                TAAA GTTCATTATTATAT
                                  T
GAM559  RAP1A   3'  TCTAAATTCTTCACATAATATA 16153          AGGTA
                                TCTAAATTTTT    ATAATATA
                                ||||||||||    ||||||||
                                AGATTTAAGAA    TATTATAT
                                     GTG__
GAM560  GAS7    3'  ACGAGCTGGATGAGGT     25260     A  CTC
                                ACGA CT   GGATGAGGT
                                |||| ||   |||||||||
                                TGCT GA   CCTACTCCA
                                  C ___
GAM560  RUNX1   3'  TCAACGAATTTTAAGAGGT   12028       CTCTCG  T
                                TCAACGAA     GA GAGGT
                                ||||||||     || |||||
                                AGTTGCTT     TT CTCCA
                                    AAAA__ _
GAM560  BSN     3'  TCCCCAGGTGTACAGACGAG  18415        A     A
                                TCTCCAGGT TACAGA GAG
                                ||||||||| |||||| |||
                                AGGGGTCCA ATGTCT CTC
                                     C     G
GAM560  EPHA1   3'  TCTGGGGTGCAGAGCAGG   23436    CCA   ATACAGA
                                TCT   GGT     AGAGCGGG
                                |||   |||     ||||||||
                                AGA   CCA     TCTCGTCC
                                  CC_   CG_____
GAM560  GNPI    3'  TCCTAGGTAAGCAGGAGAGCGG 24187    _    TA   A
            G                    TCC AGGTA  CAG AGAGCGGG
                                ||| |||||  ||| ||||||||
                                AGG TCCAT  GTC TCTCGCCC
                                  A    TC   C
GAM560  GPD1    3'  TCTCCAGGTGCGTAGCTGG   40658        ATACAGAAG  _
                                TCTCCAGGT       AGC GG
                                |||||||||       ||| ||
                                AGAGGTCCA       TCG CC
                                     CGCA_____   A
GAM560  GPR30   5'  TCTCCAGGCGGAGGG      11318        ATACAGAA   C
                                TCTCCAGGT      GAG GG
                                |||||||||       ||| ||
                                AGAGGTCCG      CTC CC
                                     C________  _
GAM560  GPR81   3'  TCCCCAGGTAACTGAGGGGCGG 37191         T  A  AGA
            G                    TCTCCAGGTA AC GA   GCGGG
                                |||||||||| || ||   |||||
                                AGGGGTCCAT TG CT   CGCCC
                                     _ A  CCC
GAM560  MKKS    5'  AGGTATTTGGAAAACAGG    33110       ACA    G
                                AGGTAT   GAAGA CGGG
                                ||||||   ||||| ||||
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                                TCCATA   CTTTT GTCC
                                   AAC    _
GAM560  PRNP     3'  TCCAGGTAAATGGACAAAGG  7186         TACA  A   C
                                TCCAGGTA    GA GAG GG
                                ||||||||    || ||| ||
                                AGGTCCAT    CT TTT CC
                                     TTAC  G   _
GAM560  PSCD4    3'  TCTCCAGGTGCTGCAGGCGATG 30134         ATA_   AA  GC
          GG                      TCTCCAGGT    CAG  GA  GGG
                                ||||||||||    |||  ||  |||
                                AGAGGTCCA    GTC  CT  CCC
                                     CGAC   CG  A_
GAM560  SLC7A4   3'  CCCAAGCAGGTGTGGGAGGGCG 42185         TACAGA__  A
          GG                      TCCAGGTA       AG GCGGG
                                ||||||||       || |||||
                                GGGTTCGT       TC CGCCC
                                     CCACACCC  C
GAM560  TEAD2    3'  TCTCCAAGACATGCAGAGGAGT 18770         _   A    A   C
          GGG                       TCTCCAGG TAT CAGA GAG GGG
                                ||||||||| ||| |||| ||| |||
                                AGAGGTTC GTA GTCT CTC CCC
                                     T   C    C   A
GAM560  WNT8B    3'  TCCCTAGGTCTGGGAGAGCGGG 40588      C    ATACA  A
                                TCTC AGGT     GA GAGCGGG
                                |||| ||||     || |||||||
                                AGGG TCCA     CT CTCGCCC
                                  A   GACC_  _
GAM561  ALEX2    5'  AAGGAAGACAGACCCTCCA   31323       A  CCA
                                AAGGAA AC   AGACCCTCCA
                                ||||||  ||   ||||||||||
                                TTCCTT TG   TCTGGGAGGT
                                   C  ___
GAM561  APBB2    3'  TAAGAAAAAGACCTTCC     43678         ACCCA    C
                                TAAGGAAA     AGACC TCC
                                ||||||||     ||||| |||
                                ATTCTTTT     TCTGG AGG
                                     _____     A
GAM561  ARNT2    3'  TAAGAAAAGCCTCAACTCTCCT 31362         A  _   GAC_
          CCA                       TAAGGAAA CC CAA    CCTCCA
                                ||||||||  || |||    ||||||
                                ATTCTTTT GG GTT    GGAGGT
                                     C  A   GAGA
GAM561  C7       3'  AGGAAAACCACCCTC       8228          CAAG
                                AGGAAAACC    ACCCTC
                                |||||||||    ||||||
                                TCCTTTTGG    TGGGAG
                                     _____
GAM561  CRKL     3'  AAGGAAGACCCTTTCC      23304       AAACCCA     __
                                AAGGA      AGACCC  TCC
                                |||||      ||||||  |||
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                                TTCCT      TCTGGG  AGG
                                  _______     AA
GAM561  ENTPD1   5'  CAAGGAAAACTTCCCCT     12125          CCAAGA
                                TAAGGAAAAC     CCCT
                                ||||||||||     ||||
                                GTTCCTTTTG     GGGA
                                     AAG___
GAM561  HOXD3    3'  GGCCAGGCCCAAGACTCTCCA  27900    AAAA_       C
                                GG    CCCAAGAC CTCCA
                                ||    |||||||| |||||
                                CC    GGGTTCTG GAGGT
                                 GGTCC       A
GAM561  IL2RB    3'  GGGAACCCAAGGTCCTC     9389     AA       AC
                                GG  AACCCAAG  CCTC
                                ||  ||||||||  ||||
                                CC  TTGGGTTC  GGAG
                                 C_       CA
GAM561  KRTHA5   3'  AAGGAAAACCTGACCC      14018          CAA
                                AAGGAAAACC   GACCC
                                ||||||||||   |||||
                                TTCCTTTTGG   CTGGG
                                     A__
GAM561  LAMC2    3'  TAAGGAAAGCTGAGACTCCCC  33119         ACCCA    C
                                TAAGGAAA     AGAC CTCC
                                ||||||||     |||| ||||
                                ATTCCTTT     TCTG GGGG
                                     CGAC_    A
GAM561  NORE1    3'  AAGGAAAATGACTCTCC     36425         CCCAA   C
                                AAGGAAAA     GAC CTCC
                                ||||||||     ||| ||||
                                TTCCTTTT     CTG GAGG
                                     A_____   A
GAM561  PROK1    3'  TAAGGAAACACCCTAATTGCCT 37104         _   _  GAC
                                TAAGGAAA ACCC AA   CCT
                                |||||||| |||| ||   |||
                                ATTCCTTT TGGG TT   GGA
                                     G    A  AAC
GAM561  PRPS2    3'  AAGGAAAATTCAAAATCCA    15729         CC    CCC
                                AAGGAAAA  CAAGA   TCCA
                                ||||||||  |||||   ||||
                                TTCCTTTT  GTTTT   AGGT
                                     AA    ____
GAM561  RAB26    3'  AAGGGCCTGGAGACCCTC     30742      AAAA  CA_
                                AAGG    CC   AGACCCTC
                                ||||    ||   ||||||||
                                TTCC    GG   TCTGGGAG
                                  C____  ACC
GAM561  RAD9     3'  CAAGGAAAACTTGTCAGCTCCA 21369          CCAAGACC
                                TAAGGAAAAC       CTCCA
                                ||||||||||       |||||
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                                GTTCCTTTTG       GAGGT
                                     AACAGTC_
GAM561  RANBP7   3'  TAAAGAAAATACTCCCTC    26892         CCCAAGA
                                TAAGGAAAA      CCCTC
                                |||||||||      |||||
                                ATTTCTTTT      GGGAG
                                     ATGA___
GAM561  SALL2    3'  TAAGGAAAATACAAGGGGCC   41901         CC    AC_
                                TAAGGAAAA  CAAG   CC
                                |||||||||  ||||   ||
                                ATTCCTTTT  GTTC   GG
                                     AT    CCC
GAM561  SERPINA3 3'  AGGAGGCCCAGGACCCTCCA   41455      AAA    A
                                AGGA   CCCA GACCCTCCA
                                ||||   |||| |||||||||
                                TCCT   GGGT CTGGGAGGT
                                  CC_    C
GAM561  SRRM2    3'  GGAAAGGGAGCCCTCCA     32277       ACCCA  A
                                GGAAA     AG CCCTCCA
                                |||||     || |||||||
                                CCTTT     TC GGGAGGT
                                   CCC__  _
GAM561  TCL1A    3'  GGGAAACCCAACCTC       35028     A       GAC
                                GG AAACCCAA   CCTC
                                || ||||||||   ||||
                                CC TTTGGGTT   GGAG
                                 C       ___
GAM561  TGFBR2   5'  AAGACCAAGACCCTCC      17467      AAAC
                                AGGA    CCAAGACCCTCC
                                ||||    ||||||||||||
                                TTCT    GGTTCTGGGAGG
                                  _____
GAM561  TM4SF6   3'  TAAGGAAAATACAACAATTCC  17586         CC   GACCC
                                TAAGGAAAA  CAA     TCC
                                |||||||||  |||     |||
                                ATTCCTTTT  GTT     AGG
                                     AT   GTTA_
GAM561  WNT10B   3'  AGCTTCCCCTCAAGACCCTCCA 18142     AAAA_  _
                                GG     CC CAAGACCCTCCA
                                ||     || ||||||||||||
                                TC     GG GTTCTGGGAGGT
                                 GAAGG  A
GAM561  AKAP13   3'  TGAGTACTTGGAAAGATGCCTT 28488            CCCT_
                                TGAGTACTTGGGA     CCTT
                                ||||||||||||     ||||
                                ACTCATGAACCTT     GGAA
                                       TCTAC
GAM561  CD8A     3'  TGAGTGGTTCTTATTTCCTTAT 12094       A___    GGACCC
           C                    TGAGT    CTTG     TCCTTATC
                                |||||    ||||     ||||||||
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                                ACTCA   GAAT     AGGAATAG
                                  CCAA   AA____
GAM561  CSK     3'  TGGGTACTTTCTTTCTCCTTAT 20472    A     GGGACC
            C                    TG GTACTT     CTCCTTATC
                                 || ||||||     |||||||||
                                 AC CATGAA     GAGGAATAG
                                  C     AGAAA_
GAM561  MGST2   5'  TGAATGCTGACCTTCCTTATC  14497      A  TGG   C
                                 TGAGT CT   GACC TCCTTATC
                                 ||||| ||   |||| ||||||||
                                 ACTTA GA   CTGG AGGAATAG
                                   C ___    A
GAM561  SUSP1   3'  TGAGCACTTCAGTTCTTTAT   31797        G  ACCC  C
                                 TGAGTACTT GG    TC TTAT
                                 ||||||||| ||    || ||||
                                 ACTCGTGAA TC    AG AATA
                                       G  A___  A
GAM562  ABCB9   3'  TCCTCTGCCCCACCGGG     33358    G  _  AG
                                 TC TC GC  TCCACCGGG
                                 || || ||  |||||||||
                                 AG AG CG  GGGTGGCCC
                                  G  A  __
GAM562  ALP     5'  TCCTCCCGCCCACCGGG     30930    G  GCA
                                 TC TC   GTCCACCGGG
                                 || ||   ||||||||||
                                 AG AG   CGGGTGGCCC
                                  G  GG_
GAM562  CDKN2C  5'  TCGCCGCAGTTCCGGG      38567         CCA
                                 TCGTCGCAGT   CCGGG
                                 ||||||||||   |||||
                                 AGCGGCGTCA   GGCCC
                                       A__
GAM562  CLASP1  3'  TCGCCGCAGGTCCGGG      42249         TCCA
                                 TCGTCGCAG    CCGGG
                                 |||||||||    |||||
                                 AGCGGCGTC    GGCCC
                                       CA__
GAM562  DAG1    5'  TCGCGCGAGCACGTACCGGG   20528     T   _   CC__
                                 TCG CGC AGT    ACCGGG
                                 ||| ||| |||    ||||||
                                 AGC GCG TCG    TGGCCC
                                   _   C   TGCA
GAM562  ESR2    5'  CCGTCGCAGCTCGGG       11013          CCAC
                                 TCGTCGCAGT    CGGG
                                 ||||||||||    ||||
                                 GGCAGCGTCG    GCCC
                                       A___
GAM562  HCN2    3'  TCCTCTCAGCCACTGGG     10175    G  G   T    C
                                 TC TC CAG CCAC GGG
                                 || || ||| |||| |||
```

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                                AG AG GTC GGTG CCC
                                 G A  _   A
GAM562  HRC     3'  CGTCGCAGTCGAGCGACTGGG  13461         C____  C
                                CGTCGCAGTC    AC GGG
                                ||||||||||    || |||
                                GCAGCGTCAG    TG CCC
                                     CTCGC  A
GAM562  ITPKB   3'  TCGTGCTCCACCGGG      13656     C  AG
                                TCGT GC  TCCACCGGG
                                |||| ||  |||||||||
                                AGCA CG  AGGTGGCCC
                                  _ __
GAM562  KIFC3   5'  TCGCCGCAGCGCCCGGG     24465         CCA
                                TCGTCGCAGT   CCGGG
                                ||||||||||   |||||
                                AGCGGCGTCG   GGCCC
                                     CG_
GAM562  MADD    5'  ATCGAAGTCTCCACCGGG    39063     C  __
                                GTCG AG  TCCACCGGG
                                |||| ||  |||||||||
                                TAGC TC  AGGTGGCCC
                                  T  AG
GAM562  MLLT2   5'  TCGGCGCAGCCCCGGG     25510     T    T  A
                                TCG CGCAG CC CCGGG
                                ||| ||||| || |||||
                                AGC GCGTC GG GGCCC
                                 C    _ _
GAM562  NLGN2   5'  CCGTGTTCACCACCGGG     44750     CG_  GT
                                TCGT   CA  CCACCGGG
                                ||||   ||  ||||||||
                                GGCA   GT  GGTGGCCC
                                  CAA  __
GAM562  ORC2L   5'  TCGCGCCCGACCACCGGG    26196     T   AGT_
                                TCG CGC    CCACCGGG
                                ||| |||    ||||||||
                                AGC GCG    GGTGGCCC
                                  _   GGCT
GAM562  RGS19IP1 3' TCATCGCAGGGTCCGGG     41699         TCCA
                                TCGTCGCAG    CCGGG
                                |||||||||    |||||
                                AGTAGCGTC    GGCCC
                                     CCA_
GAM562  RTN2    3'  CCTGACACCCACCGGG      24723    GTC   G
                                TC   GCA TCCACCGGG
                                ||   ||| |||||||||
                                GG   TGT GGGTGGCCC
                                 AC_  _
GAM562  SORCS2  5'  TCCTCGCCGCCACCGGG     34065    G    A T
                                TC TCGC G CCACCGGG
                                || |||| | ||||||||
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                                AG AGCG C GGTGGCCC
                                 G   G _
GAM562  TDGF1    3'  TCATTGCAGTCCAGCCTGGG  17365     C      _ _
                                TCGT GCAGTCCA CC GGG
                                |||| |||||||| || |||
                                AGTA CGTCAGGT GG CCC
                                  A       C  A
GAM562  TP73     5'  CCGTCGCAGCCCCGGG     24067        T  A
                                TCGTCGCAG CC CCGGG
                                ||||||||| || |||||
                                GGCAGCGTC GG GGCCC
                                    _ _
GAM562  UCN      3'  TCGCAGCCCCAAACCGGG   17842        ___
                                TCGCAGTCC   ACCGGG
                                |||||||||   ||||||
                                AGCGTCGGG   TGGCCC
                                      GTT
GAM562  CCNK     3'  TTCAGAACTGCTTTTATTTG  44201         CCC
                                TTCAGGACTGC   TATTTG
                                ||||||||||   ||||||
                                AAGTCTTGACG   ATAAAC
                                      AAA
GAM562  CLECSF12 3'  TTCGGGACTACCCTGACCGACA 44128    A       CTAT
          T                      TTC GGACTGCCC    TTGACAT
                                ||| |||||||||    |||||||
                                AAG CCTGATGGG    GGCTGTA
                                  C        ACT_
GAM562  EDG8     3'  GGGGTGCCCCACCCTTGGCAT  44207    AC     TA_   A
                                GG  TGCCCC   TTTG CAT
                                ||  ||||||   |||| |||
                                CC  ACGGGG   GAAC GTA
                                 CC     TGG    C
GAM562  FACL3    3'  TTCAAGTATTTTCCTATTTGA  20885       ACTGCC
                                TTCAGG     CCTATTTGA
                                ||||||     |||||||||
                                AAGTTC     GGATAAACT
                                    ATAAAA
GAM562  TAF7L    5'  AGACAATACCTTATTTGACAT  36056     __   CC
                                GGAC  TGCC  TATTTGACAT
                                ||||  ||||  ||||||||||
                                TCTG  ATGG  ATAAACTGTA
                                  TT    A_
GAM563  ACN      3'  CATTTGGTATGTATGTA     31407         CGTAA
                                TATTTGGTA    GTATGTA
                                |||||||||    |||||||
                                GTAAACCAT    CATACAT
                                      A____
GAM563  COL4A5   3'  ATTTGGTATGTAACATG     37896        C   G
                                ATTTGGTA GTAA TATG
                                |||||||| |||| ||||
```

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                                TAAACCAT CATT GTAC
                                   A   _
GAM563  ESRRBL1  3'  TAATATGTGAGTATGTATA   32841      C  A
                                TGGTA GT AGTATGTATA
                                ||||| || ||||||||||
                                ATTAT CA TCATACATAT
                                   A  C
GAM563  FGF13    3'  TATTCGGTGCGTATTTGGGTAT 37983        A   AGTAT
           A                     TATTTGGT CGTA    GTATA
                                ||||||||| ||||    |||||
                                ATAAGCCA GCAT    CATAT
                                   C    AAACC
GAM563  PLSCR1   3'  TATTTGGTAGTAAAATG    34411        C    T
                                TATTTGGTA GTAAG ATG
                                ||||||||| ||||| |||
                                ATAAACCAT CATTT TAC
                                   _    _
GAM563  SFRS7    3'  TCTGAATGTAGGTATGTAT   40472      TAC  A
                                TTTGG   GTA GTATGTAT
                                |||||   ||| ||||||||
                                AGACT   CAT CATACATA
                                   TA_  C
GAM563  UQCRB    3'  TTAGCACAGGAGTATGTATA  26658       TA
                                TTGGTACG  AGTATGTATA
                                ||||||||  ||||||||||
                                AATCGTGT  TCATACATAT
                                   CC
GAM563  MAB21L1  3'  TACGGAGTGTTACGGTGTAC  24589       A_   AAC
                                TACGGAGT  TATG   TGTAT
                                ||||||||  ||||   |||||
                                ATGCCTCA  ATGC   ACATG
                                   CA   C__
GAM563  NCALD    3'  GGAATATATAAAATATAC    36765         CT
                                GGAGTATATGAA  GTATAC
                                ||||||||||||  ||||||
                                CCTTATATATTT  TATATG
                                   __
GAM563  NYX      3'  GGAGTAAATGAACTGGAT    35445       T      T
                                GGAGTA ATGAACTG AT
                                |||||| |||||||| ||
                                CCTCAT TACTTGAC TA
                                   T      C
GAM564  ACADSB   3'  TCTCTCCCTCATTCCTTAT   11500     A      GG
                                TCTC CCCTCATT  CTTAT
                                |||| ||||||||  |||||
                                AGAG GGGAGTAA  GAATA
                                  A      G_
GAM564  PKHD1    3'  CCTCACTTCCCCAGCTTATTAT 39804       __    TTG
                                TCTCAC  CCTCA   GCTTATTAT
                                ||||||  |||||   |||||||||
```

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                                GGAGTG  GGGGT   CGAATAATA
                                   AA    ___
GAM564  SYNGR1   3'  TCACACCCTCATCTGTGCCT   21770    T       _ _
                                TC CACCCTCAT TG GCTT
                                || ||||||||| || ||||
                                AG GTGGGAGTA AC CGGA
                                 T       G  A
GAM564  TNFSF6   3'  TCAGCCTCTTTAGCTTATTAT  8475     C    A
                                TCA CCTC TTGGCTTATTAT
                                ||| |||| ||||||||||||
                                AGT GGAG AATCGAATAATA
                                  C    A
GAM565  ACCN2    3'  CAGCAGAGCTTTCAACTCCTC  33434       _ CTAAGA
                                CAGCAG GC     AGCTCCTC
                                |||||| ||     ||||||||
                                GTCGTC CG     TTGAGGAG
                                   T  AAAG__
GAM565  AP1B1    3'  GCAGGCCCTGGGCTCCTC    10036        AAGAA
                                GCAGGCCT    GCTCCTC
                                ||||||||    |||||||
                                CGTCCGGG    CGAGGAG
                                     ACC__
GAM565  AP1G1    3'  CAGCAGTTCTCTTCAGCTCCTC 10048       GC  AAGA
                                CAGCAG  CT    AGCTCCTC
                                ||||||  ||    ||||||||
                                GTCGTC  GA    TCGAGGAG
                                   AA  GAAG
GAM565  APBB2    5'  CAGAAGGCAAGCTCCT      43677     C    CTAAG
                                CAG AGGC     AAGCTCCT
                                ||| ||||     ||||||||
                                GTC TCCG     TTCGAGGA
                                  T   ______
GAM565  APEX     5'  GCAGCCTAGCTCCT       38772      G   AAGA
                                GCAG CCT    AGCTCCT
                                |||| |||    |||||||
                                CGTC GGA    TCGAGGA
                                  _  _____
GAM565  AQP3     3'  CAGTGGCCTAAGGTGCT     40582     CA       AA
                                CAG  GGCCTAAG  GCT
                                |||  ||||||||  |||
                                GTC  CCGGATTC  CGA
                                  A_       CA
GAM565  ARHC     5'  CAGCAAGCCTGGTCCT      23166          AAGAAGC
                                CAGCAGGCCT      TCCT
                                ||||||||||      ||||
                                GTCGTTCGGA      AGGA
                                     CC_____
GAM565  ATP11A   3'  ACAGGCCTGGGGGAATGGCCTC 44168         AA__   GCT
                                GCAGGCCT    GAA   CCTC
                                ||||||||    |||   ||||
```

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                                TGTCCGGA   CTT   GGAG
                                     CCCC   ACC
GAM565  BACH2    3'  AGTAGGCCAAGAAATTC     34774    C    T     C
                                AG AGGCC AAGAAG TC
                                || ||||| |||||| ||
                                TC TCCGG TTCTTT AG
                                 A    _     A
GAM565  BCAT1    3'  ACAGATGAAGCTCCT       42372       CCTAA
                                GCAGG    GAAGCTCCT
                                |||||    |||||||||
                                TGTCT    CTTCGAGGA
                                  A____
GAM565  CERD4    3'  GCAGGCCTGAGCTTCCTC    28950         AA  A  _
                                GCAGGCCT  GA GCT CCTC
                                ||||||||  || ||| ||||
                                CGTCCGGA  CT CGA GGAG
                                    __ _  A
GAM565  CHP      5'  GCCGTGCCGGGAGCTCCTC   28522    AG_  TAA  A
                                GC   GCC   GA GCTCCTC
                                ||   |||   || |||||||
                                CG   CGG   CT CGAGGAG
                                 GCA   CC_ _
GAM565  CMAR     5'  AGTAGTCCTAGCTCCT      23291    C  G   AAGA
                                AG AG CCT    AGCTCCT
                                || || |||    |||||||
                                TC TC GGA    TCGAGGA
                                 A  A  _____
GAM565  CYP1A1   3'  CAGAGGCCTAAGGACCT     7971      C       AAGCT
                                CAG AGGCCTAAG     CCT
                                ||| |||||||||     |||
                                GTC TCCGGATTC     GGA
                                  _       CT___
GAM565  DGCR2    3'  CAGCAGGCCAAGCTC       23087         TAAG
                                CAGCAGGCC    AAGCTC
                                |||||||||    ||||||
                                GTCGTCCGG    TTCGAG
                                      ____
GAM565  DGKE     5'  CAGCAGGCCTTGGCCGCCTC  18888          AAGAA  _
                                CAGCAGGCCT     GCT CCTC
                                ||||||||||     ||| ||||
                                GTCGTCCGGA     CGG GGAG
                                     AC___   C
GAM565  DTX1     5'  GCAGGCCCAGCTCCT       20651         AAGA
                                GCAGGCCT    AGCTCCT
                                ||||||||    |||||||
                                CGTCCGGG    TCGAGGA
                                      ____
GAM565  EBP      3'  GCAGGCAGAGAGCTCCTC    27309       CTA  _
                                GCAGGC   AGA AGCTCCTC
                                ||||||   ||| ||||||||
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                                CGTCCG   TCT TCGAGGAG
                                   ___   C
GAM565  EHD3    3'  CAGCAGGCTAGCCCACTC    31107        CTAAGA    _
                                CAGCAGGC     AGCTC CTC
                                ||||||||     ||||| |||
                                GTCGTCCG     TCGGG GAG
                                    A_____    T
GAM565  EHF     3'  GGTTCTGAAAAGAAGCTCCTC  29116    C_  ___
                                GG  CT   AAGAAGCTCCTC
                                ||  ||   ||||||||||||
                                CC  GA   TTCTTCGAGGAG
                                 AA  CTT
GAM565  EIF2B5  3'  GCCGGGCCTGCTTAGCTCCTC  41535    A_    AAGA
                                GC  GGCCT    AGCTCCTC
                                ||  |||||    ||||||||
                                CG  CCGGA    TCGAGGAG
                                 GC    CGAA
GAM565  ENAM    3'  CAGAGGCCTAATCTC       36673     C       GAAG
                                CAG AGGCCTAA    CTC
                                ||| ||||||||    |||
                                GTC TCCGGATT    GAG
                                 _       A___
GAM565  FASN    3'  CAGGGGCCCAGCTCCT      19930     CA     AAGA
                                CAG  GGCCT    AGCTCCT
                                |||  |||||    |||||||
                                GTC  CCGGG    TCGAGGA
                                 C_    _____
GAM565  GNAT1   3'  GCCAGACGGAAGCTCCT     6740     _    CTAA
                                GC AGGC    GAAGCTCCT
                                || ||||    |||||||||
                                CG TCTG    CTTCGAGGA
                                 G   C___
GAM565  GPX4    3'  CAGCAGGCCATGGGACCTTCCT 13281          TAA_  AGC
          C                      CAGCAGGCC    GA   TCCTC
                                |||||||||    ||   |||||
                                GTCGTCCGG    CT   AGGAG
                                     TACC  GGA
GAM565  GSTM1   3'  CAGCAGGCTGAGTATGGGCTCC 40445         CTAAGAA__
          TC                     CAGCAGGC        GCTCCTC
                                |||||||         |||||||
                                GTCGTCCG        CGAGGAG
                                    ACTCATACC
GAM565  GSTM2   3'  CAGCAGGCTGAGTATGGGCTCC 9194          CTAAGAA__
          TC                     CAGCAGGC        GCTCCTC
                                |||||||         |||||||
                                GTCGTCCG        CGAGGAG
                                    ACTCATACC
GAM565  GSTM4   3'  CAGCAGGCTGAGTATGGGCTCC 9199          CTAAGAA__
          TC                     CAGCAGGC        GCTCCTC
                                |||||||         |||||||
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                                GTCGTCCG       CGAGGAG
                                    ACTCATACC
GAM565  GTF2I   3'  AACAGGTCCGAAAAGCTCTTC  37432      C TA      C
                                AGCAGG C  AGAAGCTC TC
                                |||||| |  |||||||| ||
                                TTGTCC G  TTTTCGAG AG
                                   A GC       A
GAM565  HCFC1   3'  GCAAGCCTTGCTCCT      43393        AAGAA
                                GCAGGCCT    GCTCCT
                                ||||||||    ||||||
                                CGTTCGGA    CGAGGA
                                    A____
GAM565  HIP1    5'  CAGAAGGTCTGTGCCCCT    23751    C   C  AAGAA
                                CAG AGG CT    GCTCCT
                                ||| ||| ||    ||||||
                                GTC TCC GA    CGGGGA
                                  T   A  CA___
GAM565  HIRA    3'  GCAGGCCTGGGACTGCCT    17741        AAGAA  _
                                GCAGGCCT    GCT CCT
                                ||||||||    ||| |||
                                CGTCCGGA    TGA GGA
                                    CCC__   C
GAM565  HOXC6   3'  CAGCAGGCCCAGGAGCCGGCTC 21072          A  A   C_
                                CAGCAGGCCTA GA GCT  CTC
                                |||||||||| || |||  |||
                                GTCGTCCGGGT CT CGG  GAG
                                      C  _   CC
GAM565  HSF4    5'  CAGCGCGCCGCCAGCTCCTC  40762     AG   TAAGA
                                CAGC  GCC    AGCTCCTC
                                ||||  |||    ||||||||
                                GTCG  CGG    TCGAGGAG
                                  CG   CGG__
GAM565  IRF1    3'  AGCAGGGTAGAGCTCCTC    42037      CCTA   A
                                AGCAGG    AGA GCTCCTC
                                ||||||    ||| |||||||
                                TCGTCC    TCT CGAGGAG
                                   CA__   _
GAM565  KIF3C   3'  GCAGGCAGGAGCTCCTC     13954      CTA  A
                                GCAGGC   AG AGCTCCTC
                                ||||||   || ||||||||
                                CGTCCG   TC TCGAGGAG
                                   ___  C
GAM565  KLHL3   3'  GCAGGCCTTTCCCTGAGGCTTC 44642        AA____  A   C
          TC                      GCAGGCCT     GA GCT CTC
                                ||||||||     || ||| |||
                                CGTCCGGA     CT CGA GAG
                                    AAGGGA  C   A
GAM565  KRT16   5'  CAGGTAGGCCAGCTCCT    45449    C_    TAAGA
                                CAG  AGGCC    AGCTCCT
                                |||  |||||    |||||||
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```
                                GTC  TCCGG    TCGAGGA
                                  CA    _____
GAM565  LDHB    5'  GCAGGCCCAGGAGGACTC    14120        A  A_
                                GCAGGCCTA GA  GCTC
                                |||||||||  ||  ||||
                                CGTCCGGGT CT  TGAG
                                     C  CC
GAM565  MAT1A   3'  AGCAGGCCAAGGACTGCTC   44899        TAA  A_
                                AGCAGGCC   GA  GCTC
                                ||||||||   ||  ||||
                                TCGTCCGG   CT  CGAG
                                    TTC  GA
GAM565  MEOX1   3'  CAGCTGGTTCCAAAGCTCCTC  30395     A  CCTAA
                                CAGC GG    GAAGCTCCTC
                                ||||  ||    ||||||||||
                                GTCG CC    TTTCGAGGAG
                                  A  AAGG_
GAM565  MPO     3'  CAACAGGCCCAGTTCCT     6999          AAGA  C
                                CAGCAGGCCT    AG TCCT
                                ||||||||||    ||  ||||
                                GTTGTCCGGG    TC AGGA
                                     _____  A
GAM565  MPZ     3'  CAGCAGGCCGGAGCTC      8035          TAA  A
                                CAGCAGGCC   GA GCTC
                                |||||||||   ||  ||||
                                GTCGTCCGG   CT CGAG
                                     C__  _
GAM565  MYO15A  3'  CAGGGGCCTAAGGTAACTC   32182     CA      A_
                                CAG  GGCCTAAG  AGCTC
                                |||  ||||||||  |||||
                                GTC  CCGGATTC  TTGAG
                                  C_       CA
GAM565  MYO1E   3'  CAGCAGGCCAGCTTACCC    22653         TAAGA   __
                                CAGCAGGCC    AGCT  CCT
                                |||||||||    ||||  |||
                                GTCGTCCGG    TCGA  GGG
                                     _____    AT
GAM565  NPTX1   3'  GCAAAGCAGGAAGCTCCTC   14838     _  CTAA
                                GCAG GC    GAAGCTCCTC
                                ||||  ||    ||||||||||
                                CGTT CG    CTTCGAGGAG
                                  T  TC__
GAM565  NR1I2   3'  GCAGGCCTCCTGGCTTCTC   35105        AAGAA  C
                                GCAGGCCT    GCT CTC
                                ||||||||    ||| |||
                                CGTCCGGA    CGA GAG
                                    GGAC_   A
GAM565  NRXN2   3'  CAGGCCTGAGCCCCT       31471        AA  A
                                CAGGCCT  GA GCTCCT
                                |||||||  ||  ||||||
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```
                                GTCCGGA  CT CGGGGA
                                   __ _
GAM565  NT5M    3'  CAGTGGCCTCAACTCCT    33646    CA    AAGAA
                                CAG  GGCCT    GCTCCT
                                |||  |||||    ||||||
                                GTC  CCGGA    TGAGGA
                                  A_    GT___
GAM565  OSR1    3'  CAGCAGGCTCCCTCCT     23034        _  AAGAAG
                                CAGCAGGC CT     CTCCT
                                |||||||| ||     |||||
                                GTCGTCCG GG     GAGGA
                                    A  ______
GAM565  P4HB    3'  GCAGCCACCAGCTCCTC    9547      G  TAAGA
                                GCAG CC    AGCTCCTC
                                |||| ||    ||||||||
                                CGTC GG    TCGAGGAG
                                  _  TGG__
GAM565  PIGN    3'  AGAAAAAAAAAGAAGCTCCT  29545    C   CCT
                                AG AGG   AAGAAGCTCCT
                                || |||   ||||||||||
                                TC TTT   TTCTTCGAGGA
                                 T   TTT
GAM565  PKD1    3'  CAGCAGGCCTGGGCGCTGCTC  7134          AAGAA   C
                                CAGCAGGCCT    GCT CTC
                                ||||||||||    ||| |||
                                GTCGTCCGGA    CGA GAG
                                     CCCG_   C
GAM565  PLAG1   3'  CAGGAGCCAAAGCTCCT    15345    CA    TAA
                                CAG  GGCC   GAAGCTCCT
                                |||  ||||   |||||||||
                                GTC  TCGG   TTTCGAGGA
                                  C_   ___
GAM565  RAB3A   3'  GCAGGCCTGGCCACCTC    16063        AAGAA  _
                                GCAGGCCT    GCT CCTC
                                ||||||||    ||| ||||
                                CGTCCGGA    CGG GGAG
                                    C____   T
GAM565  RAI3    5'  CAGCAGGCGAGCTCCT     19566        CTAA  A
                                CAGCAGGC    GA GCTCCT
                                ||||||||    || ||||||
                                GTCGTCCG    CT CGAGGA
                                   ____  _
GAM565  RASSF1  3'  GCAGGCCTGGAGCAGCTTCTC  28427        A_  A    C
                                GCAGGCCT  AG AGCT CTC
                                ||||||||  || |||| |||
                                CGTCCGGA  TC TCGA GAG
                                    CC  G    A
GAM565  RORC    3'  CAGCAGGCCATAGGGAGAGGC  22811         TA____   A
                                CAGCAGGCC     AGA GC
                                |||||||||     ||| ||
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                                GTCGTCCGG     TCT CG
                                     TATCCC   C
GAM565  SCN4A    3'  GCAGGCCAGCTCCT       7321        TAAGA
                                GCAGGCC    AGCTCCT
                                |||||||    |||||||
                                CGTCCGG    TCGAGGA
                                     _____
GAM565  SH3BP2   3'  CAGTGGGCCCAAGTGCTGACCT 16626     CA      AA  __
           C                     CAG  GGCCTAAG  GCT  CCTC
                                |||  ||||||||  |||  ||||
                                GTC  CCGGGTTC  CGA  GGAG
                                  AC       A_   CT
GAM565  SPR      3'  CAGCAGGCATGAATGCT     17093        CTAA  _
                                CAGCAGGC    GAA GCT
                                ||||||||    ||| |||
                                GTCGTCCG    CTT CGA
                                     TA__   A
GAM565  STK10    3'  GCAGGCCTGGCTCCT       25620        AAGAA
                                GCAGGCCT    GCTCCT
                                ||||||||    ||||||
                                CGTCCGGA    CGAGGA
                                     C____
GAM565  TACC1    3'  CAGCAGCCTAAGGGAACCT    26591       G     AAGCT
                                CAGCAG CCTAAG    CCT
                                ||||||| ||||||    |||
                                GTCGTC GGATTC    GGA
                                   _     CCTT_
GAM565  TAL1     3'  CAGCAGCCTAAGAACGCCCTC  17279       G      _  T
                                CAGCAG CCTAAGAA GC CCTC
                                ||||||| |||||||| || ||||
                                GTCGTC GGATTCTT CG GGAG
                                   _       G  _
GAM565  TCF2     3'  CAGCAGGCCAGAGCTC      27020        TA   A
                                CAGCAGGCC  AGA GCTC
                                |||||||||  ||| ||||
                                GTCGTCCGG  TCT CGAG
                                     __   _
GAM565  TCF20    3'  ACAGGCCTGGACCTCCTC    42528        AA  AG
                                GCAGGCCT  GA  CTCCTC
                                ||||||||  ||  ||||||
                                TGTCCGGA  CT  GAGGAG
                                     C_  G_
GAM565  TCF8     3'  CAGCAGGCCAGGGATGCAGCCT 36233        TAA  A  T_
           C                     CAGCAGGCC   GA GC  CCTC
                                |||||||||   || ||  ||||
                                GTCGTCCGG   CT CG  GGAG
                                     TCC  A  TC
GAM565  TNFAIP1  3'  CAGCAGGCTGCCAGGTTTCTC 34474        __  AGAAG
                                CAGCAGGC  CTA    CTC
                                ||||||||  |||    |||
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                                GTCGTCCG GGT    GAG
                                    AC   CCAAA
GAM565  TNP2     5' CAGCAGGCCTAGCT       24054         AAGA
                                CAGCAGGCCT   AGCT
                                ||||||||||   ||||
                                GTCGTCCGGA   TCGA
                                     _____
GAM565  TNS      3' CAGCAGGCCCAGGAGCTC    35467          A  A
                                CAGCAGGCCTA GA GCTC
                                |||||||||||  || ||||
                                GTCGTCCGGGT CT CGAG
                                      C  _
GAM565  UBE2H    3' CAGCAGGCCTCTTCCT      17804         AAGAAGC
                                CAGCAGGCCT      TCCT
                                ||||||||||      ||||
                                GTCGTCCGGA      AGGA
                                      GA_____
GAM565  UNC13    5' ACGGGTCTGGCAGCTCCTC   26858    A  C  AAGA
                                GC GG CT    AGCTCCTC
                                || || ||    ||||||||
                                TG CC GA    TCGAGGAG
                                 C  A  CCG_
GAM565  WBP2     3' CAGTCAGGAAGCTCCT      43809     _   CCTAAG
                                CAG CAGG     AAGCTCCT
                                ||| ||||     ||||||||
                                GTC GTCC     TTCGAGGA
                                  A  _______
GAM565  ZNF41    3' CAACAGGCCTTCCTCCT     41912         AAGAAG
                                CAGCAGGCCT     CTCCT
                                ||||||||||     |||||
                                GTTGTCCGGA     GAGGA
                                      AG_____
GAM565  CADPS    3' ACTTGCCTTTTGTTTTTCAA  42189    _  GG   CCA
                                GCT GCC  TTG   TTTTTCAA
                                ||| |||  |||   ||||||||
                                TGA CGG  AAC   AAAAAGTT
                                  A   AA  ___
GAM565  CHRNA4   3' GCTGCCGGGTGCGCCATCTTT 8852        T__
                                GCTGCCGG   TGCCATTTTT
                                ||||||||   ||||||||||
                                CGACGGCC   GCGGTAGAAA
                                     CAC
GAM565  MS4A12   3' GAGTTGCAGAATCATTTTTCA 32814    C   C  TTGC
                                GAG TGC GG    CATTTTTCA
                                ||| ||| ||    |||||||||
                                CTC ACG CT    GTAAAAAGT
                                  A   T  TA__
GAM565  ZNF36    3' GAGTTGTTGTTGCCATTTC   45293    C  CCG
                                GAG TG   GTTGCCATTTT
                                ||| ||   ||||||||||
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                                CTC AC   CAACGGTAAAG
                                  A  AA_
GAM566  DDX26    3'  TAGCCAACAATGCATGT     29097          CGACATC
                                TAGCCAACAA      CGTGT
                                ||||||||||      |||||
                                ATCGGTTGTT      GTACA
                                      AC_____
GAM566  DISC1    3'  TAGCCAACATGGTGAAGCCCTG 33049         ACGACAT_  G
              T                  TAGCCAACA       CC TGT
                                 |||||||||       || |||
                                 ATCGGTTGT       GG ACA
                                      ACCACTTC  G
GAM566  GPR56    3'  GCCAGCAATCTACCCGTGT   24999      A   CGAC
                                GCCA CAA    ATCCGTGT
                                |||| |||    ||||||||
                                CGGT GTT    TGGGCACA
                                  C   AGA_
GAM566  ITGB1BP2 3'  GCCAACAATATCCTGGTA    29362        CGAC    GT
                                GCCAACAA    ATCC  GTA
                                ||||||||    ||||  |||
                                CGGTTGTT    TAGG  CAT
                                     A___    AC
GAM566  MHC2TA   3'  GCCAACAATGTCAGTGC     6984         CGACA  C
                                GCCAACAA     TC GTGT
                                ||||||||     || ||||
                                CGGTTGTT     AG CACG
                                     AC___  T
GAM566  RHD      3'  TAGCCAACATGGTGAAACCCTG 32167          AC__  C    G
              T                  TAGCCAACA    GA ATCC TGT
                                 |||||||||    || |||| |||
                                 ATCGGTTGT    CT TGGG ACA
                                      ACCA  T   _
GAM566  SET      3'  GCCAGCAACTGTCCCGTGTA   16561      A    GACA
                                GCCA CAAC    TCCGTGTA
                                |||| ||||    ||||||||
                                CGGT GTTG    GGGCACAT
                                  C    ACA_
GAM566  ARCN1    3'  TTGGGTAGCAACAGCAGCAGAC 11661      A  ATC  C
              A                  TTGG TA   AT GTAGCAGACA
                                 |||| ||   || ||||||||||
                                 AACC AT   TG CGTCGTCTGT
                                   C  CGT  T
GAM566  DOCK1    3'  TGGATAATCATTGGTGGAC    10720          CGTAGCA
                                TGGATAATCAT      GAC
                                ||||||||||      |||
                                ACCTATTAGTA      CTG
                                      ACCAC__
GAM566  GNAS     3'  TTGGAGCGTTCGTAGCAGGCA  38669       TAATCA       A
                                TTGGA     TCGTAGCAG CA
                                |||||     ||||||||| ||
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                                AACCT     AGCATCGTC GT
                                   CGCA__         C
GAM566  HSPA4    3'  TTGGATAACGCAAC        44857         TCAT
                                TTGGATAA    CGTAGC
                                ||||||||    ||||||
                                AACCTATT    GCGTTG
                                     ____
GAM566  ITGAL    3'  TTGGATAAATACATGCAGGCA  13627         TCAT   A    A
                                TTGGATAA    CGT GCAG CA
                                ||||||||    ||| |||| ||
                                AACCTATT    GTA CGTC GT
                                     TAT_  _    C
GAM566  PK428    5'  TTGGATAATGCATCAGCGGCA  18810          _    _ TA
                                TTGGATAAT CATC G  GCA
                                ||||||||| |||| |  |||
                                AACCTATTA GTAG C  CGT
                                     C    T GC
GAM566  UBD      3'  TTGGGAAATCATCAGAAGA    26917      AT      GT  C
                                TTGG  AATCATC  AG AGA
                                ||||  |||||||  || |||
                                AACC  TTAGTAG  TC TCT
                                  CT       __  T
GAM566  USP6     3'  TTGGATAATAGTTAACAGA    45035          CATCG
                                TTGGATAAT    TAGCAGA
                                |||||||||    |||||||
                                AACCTATTA    ATTGTCT
                                     TCA__
GAM567  MME      3'  GAAGAATCTCAGCATCAGTCAA 28599        CC_   A
            A                    GAAGAA   CAG ATCAGTCAAA
                                ||||||   ||| ||||||||||
                                CTTCTT   GTC TAGTCAGTTT
                                   AGA   G
GAM567  NLGN1    3'  TCAAAGAACTCAGAACTATAAT 31389          C     C__
            CA                     TCGAAGAAC CAGAAT   AGTCA
                                |||||||||| ||||||   |||||
                                AGTTTCTTG GTCTTG   TTAGT
                                     A     ATA
GAM567  COX15    3'  CGGCTTCAACTTCTCAAG    38515    A     ACTC     G
                                CG CTTCAA    CTTTTC AAG
                                || ||||||    |||||| |||
                                GC GAAGTT    GAAGAG TTC
                                 C     ____     _
GAM567  COX6B    5'  CGGCTTCAGCTCCCTCCCAGGA 12405    A     AA     TT  A_
            GG                     CG CTTCA  CTCCTT  CG  AGG
                                || |||||  ||||||  ||  |||
                                GC GAAGT  GAGGGA  GT  TCC
                                 C    C_     GG  CC
GAM567  EPB72    3'  CGACTTCATGCTTGGAAG    19898         AACTC   TTC
                                CGACTTCA    CTT   GAAG
                                ||||||||    |||   ||||
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                                GCTGAAGT    GAA   CTTC
                                    AC___   C__
GAM567  ERBB3    3'  CTCAAACTCCTTGCCTCAGG   12754          T  GA
                                TTCAAACTCCTT TC  AGG
                                |||||||||||| ||  |||
                                GAGTTTGAGGAA GG  TCC
                                      C  AG
GAM567  GATA4    3'  CGACTTCAAGTTTCTTCCCA   13109        ACTC   TT
                                CGACTTCAA   CTT  CG
                                |||||||||   |||  ||
                                GCTGAAGTT   GAA  GT
                                     CAAA   GG
GAM567  MKI67    3'  CTTCAAAGGAGATTTCGGAGG  14521       CTCCT    A
                                CTTCAAA    TTTCG AGG
                                |||||||    ||||| |||
                                GAAGTTT    AAAGC TCC
                                    CCTCT    C
GAM567  SERPINE1 3'  CTTCAAACTTCTCTCCCAGG   8288         C     GA
                                CTTCAAACT CTTTTC  AGG
                                ||||||||| ||||||  |||
                                GAAGTTTGA GAGAGG  TCC
                                     A     G_
GAM568  COL6A1   3'  TAGCACCGTTAATCTCGAGGGT 12332        CT_   CACTAT
           CT                  TAGCACCG   ATC     GTCT
                               ||||||||   |||     ||||
                               ATCGTGGC   TAG     CAGA
                                    AAT   AGCTCC
GAM568  HIP12    3'  CAGCGCCCGGGCCGCTATGTCT 42393     A_   CTAT  A
           C                   TAGC  CCG    CC CTATGTCTC
                               ||||  |||    || |||||||||
                               GTCG  GGC    GG GATACAGAG
                                 CG   CC__  C
GAM568  SFRS1    3'  GCATTGCTACCCACCTAAGTC  27959     CC        AT_
                               GCA  GCTATCCACT   GTC
                               |||  ||||||||||   |||
                               CGT  CGATGGGTGG   CAG
                                 AA         ATT
GAM568  UBQLN3   3'  CAGCACCTCCACTATGT     32718       GCTA
                               TAGCACC    TCCACTATGT
                               |||||||    ||||||||||
                               GTCGTGG    AGGTGATACA
                                    ____
GAM568  FKBP10   3'  TAGAGGTCTGTGCTGTG     34960      A  GAC
                               TGGA GT   GTGCTGTG
                               |||| ||   ||||||||
                               ATCT CA   CACGACAC
                                 C  GA_
GAM568  PPP2CB   3'  TAGTGGAAGTTAGCTTGTGAAT 20003          GACGT   _
                               TAGTGGAAGT    GCT GTGAAT
                               ||||||||||    ||| ||||||
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                                ATCACCTTCA    CGA CACTTA
                                      AT___   A
GAM569  CBFA2T3  3'  GAGAAAGTGTGTGATAGTCATA 23262      TGCCA  CT
            G                  GAGAA    TG  ATAGTCATAG
                               |||||    ||  ||||||||||
                               CTCTT    AC  TATCAGTATC
                                  TCAC_  AC
GAM569  DISC1    3'  GAGAATGCAGTGCTGTACAATA 33036        CA   __    CA
            CTAG                GAGAATGC  TGCT  ATAGT  TAG
                               ||||||||  ||||  |||||  |||
                               CTCTTACG  ACGA  TGTTA  ATC
                                    TC   CA    TG
GAM569  EMS1     3'  GAGAGGCCATGCTGTGACAT   39740     AT      ATAGT
                               GAGA  GCCATGCT    CAT
                               ||||  ||||||||    |||
                               CTCT  CGGTACGA    GTA
                                 C_      CACT_
GAM569  PAX5     3'  GAGGATGCTCTGCCATAG    32509     A   CA
                               GAG ATGC  TGCTATAG
                               ||| ||||  ||||||||
                               CTC TACG  ACGGTATC
                                 C   AG
GAM569  STAC     3'  GATGCCATGTCAACATAG    17135    A     CTA   T
                               GA TGCCATG   TAG CATAG
                               || |||||||   ||| |||||
                               CT ACGGTAC   GTT GTATC
                                _      A__   _
GAM569  ART3     3'  TGTGGATCCCTATAGTTATT   10139     TAAA
                               TGTG   ATCTTTATAGTTATT
                               ||||   ||||||||||||||
                               ACAC   TAGGGATATCAATAA
                                 C___
GAM569  TFDP2    5'  TGGTAAAATCTTTGTAG     26621    T        A
                               TG GTAAAATCTTT TAG
                               || ||||||||||| |||
                               AC CATTTTAGAAA ATC
                                _         C
GAM570  CDK2     3'  CCAGTGGTTTTGTTTTACTTG  12201            C_
                               TCAGTGGTTTTGTTT  CTTG
                               ||||||||||||||  ||||
                               GGTCACCAAAACAAA  GAAC
                                        AT
GAM570  MEOX2    3'  ATGGTTTATTCTTGATA     25449       T   TC
                               GTGGTTT GTT  CTTGATA
                               ||||||| |||  |||||||
                               TACCAAA TAA  GAACTAT
                                  _  __
GAM570  SOX11    3'  AGTGGTTTGTTTCTCTGTAG   17003        T    C   A
                               AGTGGTTT GTTTC TTG TAG
                               |||||||| ||||| ||| |||
```

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                                TCACCAAA CAAAG GAC ATC
                                   _    A  _
GAM570  ZNF83    3'  TCAGTGTTTTTGTTTCTCTCAA 32893       G       _  TG
                                TCAGTG TTTTGTTTC CT  A
                                |||||| |||||||| ||  |
                                AGTCAC AAAACAAAG GA  T
                                   A       A  GT
GAM570  CASP7    3'  AACATGACTCTACCACTGTT  10270        CAC   AAGT
                                AACATGAC  CTG   CTGTT
                                ||||||||  |||   |||||
                                TTGTACTG  GAT   GACAA
                                    A__   GGT_
GAM570  CASP7    3'  AACATGACTCTACCACTGTTA 10271        CAC   AAGT
                                AACATGAC  CTG   CTGTTA
                                ||||||||  |||   ||||||
                                TTGTACTG  GAT   GACAAT
                                    A__   GGT_
GAM570  CNN2     3'  TGAGGGTCTGAAGTCTGTT   20407     CCAC
                                TGA   CTGAAGTCTGTT
                                |||   ||||||||||||
                                ACT   GACTTCAGACAA
                                  CCCA
GAM570  CTSH     3'  CATGTGGTTTGAGTCTGTT   20499     ACCACC  A
                                CATG     TGA GTCTGTT
                                ||||     ||| |||||||
                                GTAC     ACT CAGACAA
                                  ACCAA_  _
GAM570  FCGR2A   3'  ATGACCACATGGCATAACGTTA 44276        C  AA  C_
                                ATGACCAC TG  GT  TGTTA
                                |||||||| ||  ||  |||||
                                TACTGGTG AC  TA  GCAAT
                                    T  CG  TT
GAM570  GCH1     3'  AACATGACCAAAGTGAAGTCTG 6699          CC_
          TT                    AACATGACCA   TGAAGTCTGTT
                                ||||||||||   ||||||||||
                                TTGTACTGGT   ACTTCAGACAA
                                     TTC
GAM570  MLLT4    3'  AACATGACCCTTGAAAT     25521         ACC
                                AACATGACC   TGAAGT
                                |||||||||   ||||||
                                TTGTACTGG   ACTTTA
                                    GA_
GAM570  PRKAA2   3'  ACATGACCACAGTCTTCTGTT 26499         CTGAAG
                                ACATGACCAC     TCTGTT
                                ||||||||||     ||||||
                                TGTACTGGTG     AGACAA
                                     TCAGA_
GAM570  SCA1     3'  AACAGACCAGTCTGT       7268       T    CCTGAA
                                AACA GACCA     GTCTGT
                                |||| |||||     ||||||
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                                TTGT CTGGT     CAGACA
                                  _   ______
GAM570  TIRAP    5'  CATGACCAGCTGAGGAACTG  38090        C   AGT_
                                CATGACCA CTGA   CTG
                                |||||||| ||||   |||
                                GTACTGGT GACT   GAC
                                    C   CCTT
GAM570  XK       3'  AACATGGTTACCTGTGAACTG  34353      ACC    AAGT
                                AACATG  ACCTG   CTG
                                ||||||  |||||   |||
                                TTGTAC  TGGAC   GAC
                                   CAA    ACTT
GAM570  XPNPEP1  3'  AACATGACCATCATGGAGC   33781         CC_  A
                                AACATGACCA  TG AGT
                                ||||||||||  || |||
                                TTGTACTGGT  AC TCG
                                      AGT  C
GAM571  CNTN3    3'  GATTTTGTTTAATATTTGG   42482         __
                                GATTTTGTT  GTATTTGG
                                |||||||||  ||||||||
                                CTAAAACAA  TATAAACC
                                     AT
GAM571  IL1F5    3'  GATTTTGATTGTATCTTGGGTT 29353        _      __
                                GATTTTG TTGTATTT  GGTT
                                ||||||| ||||||||  ||||
                                CTAAAAC AACATAGA  CCAA
                                    T       AC
GAM571  EFEMP1   5'  TTTATCTGCATGTGGTAGGAGT 33126          GTCCGCAA
           C                     TTTATCTGTATG       AGTC
                                ||||||||||||       ||||
                                AAATAGACGTAC       TCAG
                                      ACCATCC_
GAM571  MIR16    3'  TTTATTAGTATGGCCACAAGT  32499      CT     T     A
                                TTTAT  GTATGG CCGCAA GT
                                |||||  |||||| |||||| ||
                                AAATA  CATACC GGTGTT CA
                                   AT     _     _
GAM572  DHFR     3'  CCTATCCTGTACTTCTTTCTGC 8992         A  GG  ___  A
           C                     CCTATCCT TA  TC   CT CC
                                |||||||| ||  ||   || ||
                                GGATAGGA AT  AG   GA GG
                                    C  GA  AAA  C
GAM572  DNAI2    5'  CCCTATCTCCACAGGTCCTGCC 35746        _         A
                                CCCTATC CTATAGGTCCT CC
                                ||||||| |||||||||| ||
                                GGGATAG GGTGTCCAGGA GG
                                    A         C
GAM572  DSS1     3'  CCCATCCTGGGTTCTCTGCC   26703        ATA  _ _  A
                                CCTATCCT   GGT C CT CC
                                ||||||||   ||| | || ||
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                                GGGTAGGA  CCA G GA GG
                                   C__  A A  C
GAM572  DUSP6   3'  CCTACCCTATCATTTGGTTCTA 42327        A____  C
            CC                  CCTATCCTAT    GGT CTACC
                                ||||||||||    ||| |||||
                                GGATGGGATA    CCA GATGG
                                   GTAAA  A
GAM572  GAS11   3'  CCCCTGGTCCTACATCACCTAC 11213      A_     GGT
            C                   CCCCT  TCCTATA  CCTACC
                                |||||  |||||||  ||||||
                                GGGGA  AGGATGT  GGATGG
                                  CC     AGT
GAM572  HEPH    5'  CCCCTATCCGGTTCT      39856        TATA  C
                                CCCCTATCC   GGT CT
                                |||||||||   ||| ||
                                GGGGATAGG   CCA GA
                                   ____  A
GAM572  HRH2    3'  CCCCCATCCTGTGCACC    35289        ATAG  _
                                CCCCTATCCT   GT CC
                                ||||||||||   || ||
                                GGGGGTAGGA   CG GG
                                   CA__  T
GAM572  MEFV    3'  TACTTCTATCCCAATCCAGTC  6971     CC      TA__
                                TAC  CTATCCTA   GGTC
                                |||  ||||||||   ||||
                                ATG  GATAGGGT   TCAG
                                  AA      TAGG
GAM572  MTA1L1  3'  CCAAGACATCTGTGGGTCCTAC 21883   CC__   CTATA
            C                   CC   TATC    GGTCCTACC
                                ||   ||||    |||||||||
                                GG   GTAG    CCAGGATGG
                                 TTCT   ACAC_
GAM572  OLIG2   3'  CCAATCCACAAGTGGTTCTAC  25143   T   T    C___
                                CC ATCC ATAGGT   CTAC
                                || |||| ||||||   ||||
                                GG TAGG TGTTCA   GATG
                                 T   _     CCAA
GAM572  PDE4B   3'  CACCCCTGTCCTCTCTGCC   15146      A   ATAG
                                TACCCCT TCCT   GTC
                                ||||||| ||||   |||
                                GTGGGGA AGGA   CGG
                                   C   GAGA
GAM572  PDE4B   5'  CACCCCTGTCCTCTCTGCC   15146      A   ATAG
                                TACCCCT TCCT   GTC
                                ||||||| ||||   |||
                                GTGGGGA AGGA   CGG
                                   C   GAGA
GAM572  PPP2R5B 3'  CCCTTGTCAAGTCCTGCC   26445     ATCCTA      A
                                CCCT     TAGGTCCT CC
                                ||||     |||||||| ||
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                                GGGA     GTTCAGGA GG
                                  ACA___       C
GAM572  TNC      3'  TACCCCTGTACATCCTAC    13470        ATCCTA  G
                                TACCCCT     TA GTCCTAC
                                |||||||     || |||||||
                                ATGGGGA     AT TAGGATG
                                    C_____  G
GAM572  TULP1    3'  CATCTCCGTCCTACC       17725      _ ATAG
                                TATC CT    GTCCTACC
                                |||| ||    ||||||||
                                GTAG GG    CAGGATGG
                                  A ____
GAM572  FBXL7    5'  CAGTGGGAGGGGGTGC      29394        ACTA T   A
                                TAGTGGGA    G GGG GTGC
                                ||||||||    | ||| ||||
                                GTCACCCT    C CCC CACG
                                    ____ _   _
GAM572  GNAI1    3'  GTGGGGTGGGGAGTGCT     13167      AACTA    _
                                GTGGG    GTGGG AGTGCT
                                |||||    ||||| ||||||
                                CACCC    CACCC TCACGA
                                   _____    C
GAM572  GPR4     5'  GTGGGTGGGAGTGC        40891      AACTAG
                                GTGGG     TGGGAGTGC
                                |||||     |||||||||
                                CACCC     ACCCTCACG
                                   _______
GAM572  RRAD     3'  TAGTGGGAGCGGGTGGGA    20020        ACTA
                                TAGTGGGA    GTGGGA
                                ||||||||    ||||||
                                ATCACCCT    CACCCT
                                     CGCC
GAM573  CABC1    3'  CCTTTGGCTGGAACTGGTG   33680       _     CTA
                                CCTTTGG TGGAAC   GTG
                                ||||||| ||||||   |||
                                GGAAACC ACCTTG   CAC
                                    G     AC_
GAM573  CD69     5'  CTTTGCTGGAGCTCTTGTT   12137      G   AC  AG
                                CTTTG TGGA  CT  TGTT
                                ||||| ||||  ||  ||||
                                GAAAC ACCT  GA  ACAA
                                   G   C_  GA
GAM573  HDLBP    3'  ACCTTGGTTTAGTGTT      42742      T   GGAACC
                                ACCTT GGT     TAGTGTT
                                ||||| |||     |||||||
                                TGGAA CCA     ATCACAA
                                   _  A_____
GAM573  SIAT4C   3'  CCTTGGTGGGGCCATCGCT   26578        AA  TAG
                                CTTTGGTGG  CC   TGTT
                                |||||||||  ||   ||||
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                                GGAACCACC  GG   GCGA
                                     CC  TA_
GAM573  TXNIP    3'  ACCTTTGGTGGGGCAGT     26998          AACC
                                ACCTTTGGTGG    TAGT
                                ||||||||||    ||||
                                TGGAAACCACC    GTCA
                                     CC__
GAM573  ADCY6    5'  CACCACTAGTAGCTCA      34164         CACCA   G
                                CACCACTAGT    GGT TCA
                                ||||||||||    ||| |||
                                GTGGTGATCA    TCG AGT
                                      _____  _
GAM573  ADCY7    3'  CCACTAGTCTACCCAGCACC   9984          _  A  TG
                                CCACTAGTC ACC GG  TC
                                ||||||||| ||| ||  ||
                                GGTGATCAG TGG TC  GG
                                     A   G  GT
GAM573  CD4      3'  CACCACTAGCCACTGGTGAGAG 8324           CA    TCA_
           CC                    CACCACTAGTCAC  GGTG    CC
                                ||||||||||||  ||||    ||
                                GTGGTGATCGGTG  CCAC    GG
                                      A_    TCTC
GAM573  CDKN2B   3'  CCACTAGTTATGTTAC      38541        CACCAG    C
                                CCACTAGT     GTGT AC
                                ||||||||     |||| ||
                                GGTGATCA     TACA TG
                                     A_____    A
GAM573  CISH     3'  CACTAGTCACTGTC       40356          CAGG
                                CACTAGTCAC    TGTC
                                ||||||||||    ||||
                                GTGATCAGTG    ACAG
                                      _____
GAM573  CLASP2   3'  CCATTAGATGCCAGGTGC    42078     C   TCA
                                CCA TAG   CCAGGTGT
                                ||| |||   ||||||||
                                GGT ATC   GGTCCACG
                                  A   TAC
GAM573  CNTN3    3'  ACTAGTCATTCAGATTGT    42478        C_    _
                                ACTAGTCA  CAGGT GT
                                ||||||||  ||||| ||
                                TGATCAGT  GTCTA CA
                                     AA    A
GAM573  COL4A5   3'  ACTAGTCAGCATGTTATC    37894        C  GG_
                                ACTAGTCA CA   TGTC
                                ||||||||  ||   ||||
                                TGATCAGT GT   ATAG
                                     C  ACA
GAM573  DLST     3'  CACCACTAGGTACTAACAC   12571         TC  CAGGTGT
                                CACCACTAG  AC      CAC
                                |||||||||  ||      |||
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                                GTGGTGATC  TG      GTG
                                     CA  ATT____
GAM573  GJB3     5'  CACTAGTTGCCAGGGCC     35835        CA    T
                                CACTAGT  CCAGG GTC
                                |||||||  ||||| |||
                                GTGATCA  GGTCC CGG
                                    AC    _
GAM573  GRIN2B   3'  CTGGTCACCAGGGTTGCC    9121     A       __
                                CT GTCACCAGG  TGTC
                                || |||||||||  ||||
                                GA CAGTGGTCC  ACGG
                                 C        CA
GAM573  HNRPF    3'  CTAGTCACCATTTCCACC    22455          GGTG
                                CTAGTCACCA    TCACC
                                ||||||||||    |||||
                                GATCAGTGGT    GGTGG
                                     AAA_
GAM573  IL10     3'  ACCATAGTGTGTCA        8193       C    CACCAG
                                ACCA TAGT     GTGTCA
                                |||| ||||     ||||||
                                TGGT ATCA     CACAGT
                                  _   _______
GAM573  IL13RA1  3'  CACCACTATCATCACTTTTTGC 11441         __    CAGG
                                CACCACTA  GTCAC    TGT
                                ||||||||  |||||    |||
                                GTGGTGAT  TAGTG    ACG
                                     AG    AAAA
GAM573  KCNA6    5'  CCGCTGGTACCGAAGCGCC    13810    A  A  C  _
                                CC CT GT ACC AGGTGTC
                                || || || ||| |||||||
                                GG GA CA TGG TTCGCGG
                                 C  C  _   C
GAM573  MLLT7    3'  CACCACTAGCACCCTGCC     25527         T    AGG
                                CACCACTAG CACC   TGTC
                                |||||||||  ||||   ||||
                                GTGGTGATC GTGG   ACGG
                                     _    G__
GAM573  PCDH9    5'  CACTAGCCAGCACTGTCAC    44396         C  GG
                                CACTAGTCA CA  TGTCAC
                                |||||||||  ||  ||||||
                                GTGATCGGT GT  ACAGTG
                                     C  G_
GAM573  PTBP1    3'  CCACAGTCACCAAGAGCC     36717      T        T
                                CCAC AGTCACCAGG GTC
                                ||||  |||||||||| |||
                                GGTG TCAGTGGTTC CGG
                                  _         T
GAM573  RNF12    5'  CACCATTAGACACATCATC    32033       C   T   CAGG
                                CACCA TAG CAC    TGTC
                                |||||  ||| |||    ||||
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                                GTGGT ATC GTG   GTAG
                                  A  T  TA__
GAM573  RPL15   3'  ACCACTAATCACTGAATGCC  16390          CA
                                ACCACTAGTCAC  GGTGTC
                                ||||||||||||  ||||||
                                TGGTGATTAGTG  TTACGG
                                      AC
GAM573  RPS6KA1  3'  ACCACGCAGGGGTGTTC    40378     _  TCACCA   CA
                                ACCAC TAG     GGTGT  C
                                ||||| |||     |||||  |
                                TGGTG GTC     CCACA  G
                                  C  C_____    AC
GAM573  STX8    3'  CTGTCATTGCCAGGTGTCAC  22140   A   ___
                                CT GTCA   CCAGGTGTCAC
                                || ||||   ||||||||||
                                GA CAGT   GGTCCACAGTG
                                 _   AAC
GAM573  SYNGR1   3'  ACTATGTCACCAGAAGTCACC  21749     _       T
                                ACTA GTCACCAGG GTCACC
                                |||| ||||||||| ||||||
                                TGAT CAGTGGTCT CAGTGG
                                  A       T
GAM573  TAF4B    5'  CACTTTGGTCACCAGGGTC   44549     A__       T
                                CACT   GTCACCAGG GTC
                                ||||   ||||||||| |||
                                GTGA   CAGTGGTCC CAG
                                  AAC       _
GAM573  TNFRSF8  3'  CACCACTAGATGCTGGAGCC  10311         TCACCA  T
                                CACCACTAG     GG GTC
                                |||||||||     || |||
                                GTGGTGATC     CC CGG
                                     TACGA_  T
GAM573  TRAF5    3'  ACTGTCACCAAAATACA    21467     A       TGT
                                ACT GTCACCAGG   CA
                                ||| |||||||||   ||
                                TGA CAGTGGTTT   GT
                                  _       TAT
GAM573  WWOX     3'  CACTGTCATCCTCAC       39109     A   _  AGGTG
                                CACT GTCA CC    TCAC
                                |||| |||| ||    ||||
                                GTGA CAGT GG    AGTG
                                  _   A  _____
GAM573  WWOX     3'  CTACTCCCTCTGGGTGTCAC  39113     G  A  A___
                                CTA TC CC   GGTGTCAC
                                ||| || ||   ||||||||
                                GAT AG GG   CCACAGTG
                                 G  _  AGAC
GAM574  C8A      3'  ATGATCCAAAGTGCTGTAA   8157      CTG TG T
                                ATG   C  G GTGCTGTAA
                                |||   |  | |||||||||
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                                TAC   G  T CACGACATT
                                  TA_ GT T
GAM574  DTNB     3'  ATGGTGCTAATATTGTAGATAA 37598     C       GC    A
                                ATG TGCTGGTGT  TGTA ATAA
                                ||| |||||||||  |||| ||||
                                TAC ACGATTATA  ACAT TATT
                                  C        __    C
GAM574  GGT2     5'  ATGCCGCTGGTGTGCCAGCTCA 43922              _  AA
              TA                   ATGCTGCTGGTGTGCT GT  ATA
                                ||||||||||||||| ||  |||
                                TACGGCGACCACACGG CG  TAT
                                         T  AG
GAM574  GLP1R    3'  TGCTGCTGTGTGTCACCAT    13144         _   _
                                TGCTGCTG GTGT GCTGT
                                |||||||| |||| |||||
                                ACGACGAC CACA TGGTA
                                     A   G
GAM574  GPR23    5'  ATGTGCTGATGCCTGTAGATAA 41315     C       G    A
                                ATG TGCTGGTGT CTGTA ATAA
                                ||| ||||||||| ||||| ||||
                                TAC ACGACTACG GACAT TATT
                                  _        _    C
GAM574  H3F3B    3'  ATGATGCTGGTGTGAATAA    23703     C        CT
                                ATG TGCTGGTGTG  GTAA
                                ||| ||||||||||  ||||
                                TAC ACGACCACAC  TATT
                                  T        T_
GAM574  NEDD4    3'  ATGCTGTGGTGTTTGGAAA    43097       C     GC  T
                                ATGCTG TGGTGT  TG AAA
                                |||||| ||||||  || |||
                                TACGAC ACCACA  AC TTT
                                   _     A_  C
GAM574  CD2AP    3'  ACATTATGAACACCAGG     29067      CAC  AG
                                ACAT   GT  GCACCAGG
                                ||||   ||  ||||||||
                                TGTA   TA  TGTGGTCC
                                  A__  CT
GAM574  CPLX2    5'  CTAGCACACGTGCACCG     27396        ATC    AG    A
                                CTAGCAC   ACGT  GCACC G
                                |||||||   ||||  ||||| |
                                GATCGTG   TGCA  CGTGG C
                                   ____   __    C
GAM574  DIO3     3'  CAGCACATCAGTGTCACTGGG  10688          C  AGG   CA
                                TAGCACATCA GT   CAC  GG
                                |||||||||| ||   |||  ||
                                GTCGTGTAGT CA   GTG  CC
                                      _  CA_   AC
GAM574  GPC3     3'  CAGCACATGTGCTGGGCACCAG 21020         CAC  A_
              G                   TAGCACAT   GT  GGCACCAGG
                                ||||||||   ||  |||||||||
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                                GTCGTGTA  CG  CCGTGGTCC
                                    CA_  AC
GAM574  NT5C3   3'  TAGCAACATTGTAAACACCA  32410     _  CAC
                                TAGCA CAT  GTAGGCACCA
                                ||||| |||  ||||||||||
                                ATCGT GTA  CATTTGTGGT
                                   T  A__
GAM574  PDGFB   3'  GCACAGAGGCACCAG      15177      TCACGT
                                GCACA    AGGCACCAG
                                |||||    |||||||||
                                CGTGT    TCCGTGGTC
                                   C_____
GAM574  SORCS2  3'  CCAGCACATCACCAGCCAG  34050         G  GCA
                                CTAGCACATCAC TAG  CCAG
                                |||||||||||| |||  ||||
                                GGTCGTGTAGTG GTC  GGTC
                                          _  ___
GAM574  TCTA    3'  CCAGCCCTGTAGGCACTG   35278     ACATCAC      CA
                                CTAGC     GTAGGCAC  G
                                |||||     ||||||||  |
                                GGTCG     CATCCGTG  C
                                   GGA____      AC
GAM574  TEM7    3'  CTAGCACACGTTTTCCCA   33807      ATC   AGGCA
                                CTAGCAC  ACGT   CCA
                                |||||||  ||||   |||
                                GATCGTG  TGCA   GGT
                                   ___   AAAG_
GAM575  ABCC3   3'  CTGATGCCCTCCACCTGC   33420     _  TATC    C
                                CTGGT CCC   TCCACC GC
                                ||||| |||   |||||| ||
                                GACTA GGG   AGGTGG CG
                                   C  ____     A
GAM575  ABR     3'  CTGGTTCCACCACCCGCC   35009     C  TATCT
                                CTGGT CC    CCACCCGCC
                                ||||| ||    |||||||||
                                GACCA GG    GGTGGGCGG
                                   A  T____
GAM575  ABR     3'  CTGGCTCCTGACTCCTGCC   35008     TC  AT   ACCC
                                CTGG  CCT  CTCC   GCC
                                ||||  |||  ||||   |||
                                GACC  GGA  GAGG   CGG
                                  GA  CT   A___
GAM575  AGR2    5'  CTGGATTTCCTCACCCACCTGC 26921     TC__  ATC    C
          C                      CTGG   CCT   TCCACC GCC
                                ||||   |||  |||||| |||
                                GACC   GGA   GGGTGG CGG
                                  TAAA  GT_    A
GAM575  AP1B1   5'  TGGTCCCTTATCTGTAGCC   10044       _   CCACCC
                                TGGTCCCT ATCT    GCC
                                |||||||| ||||    |||
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                                ACCAGGGA TAGA     CGG
                                    A   CAT___
GAM575  APAF1   5'  CTGGTTCTATCCCTTTTGCC  29819      CC      CACCC
                                CTGGT  CTATCTC    GCC
                                |||||  |||||||    |||
                                GACCA  GATAGGG    CGG
                                   A_      AAAA_
GAM575  ARNT2   3'  CTGATCCCCTAATGTCTGCC  31357         A____  _
                                CTGGTCCCT    TCT CC
                                |||||||||    ||| ||
                                GACTAGGGG    AGA GG
                                     ATTAC   C
GAM575  C18orf1 3'  TGGCCCCTATTTCCTGCC    41235         C   ACCC
                                TGGTCCCTAT TCC    GCC
                                |||||||||| |||    |||
                                ACCGGGGATA AGG    CGG
                                     A   A___
GAM575  CD34    3'  CTGGTCCCATGGTCCTGCC   12116        TATC   ACCC
                                CTGGTCCC   TCC    GCC
                                ||||||||   |||    |||
                                GACCAGGG   AGG    CGG
                                     TACC   A___
GAM575  CERD4   3'  CTGGATGCCTCCACCTGC    28947     TCCCTA      C
                                CTGG     TCTCCACC GC
                                ||||     |||||||| ||
                                GACC     GGAGGTGG CG
                                  TAC___       A
GAM575  CHRNE   3'  TGGTTCCCACCCGC       6347      CCCTA  T
                                TGGT    TC CCACCCGC
                                ||||    || ||||||||
                                ACCA    AG GGTGGGCG
                                  _____  _
GAM575  COL4A4  5'  CTGGATCCGCGCCCACCTGCC  6401      _  CTATC     C
                                CTGG TCC    TCCACC GCC
                                |||| |||    |||||| |||
                                GACC AGG    GGGTGG CGG
                                  T   CGC__     A
GAM575  CPN1    5'  CTAGCCTCTTCACCCGC     10570       CCTA   C
                                CTGGTC    TCT CACCCGC
                                ||||||    ||| |||||||
                                GATCGG    AGA GTGGGCG
                                   ____   A
GAM575  DES     3'  CTAGTCCCCCTGGCTACCTGCC 43563         ATCTCC   C
                                CTGGTCCCT     ACC GCC
                                |||||||||     ||| |||
                                GATCAGGGG     TGG CGG
                                     GACCGA   A
GAM575  DTX1    5'  TGGTCCCTGTTCCCCGCC    20652        ATCTCCA
                                TGGTCCCT      CCCGCC
                                ||||||||      ||||||
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                                ACCAGGGA      GGGCGG
                                    CAAG___
GAM575  F2RL3    3'  CCGGTCCCTGACCCG       19516         ATCTCC
                                CTGGTCCCT     ACCCG
                                |||||||||     |||||
                                GGCCAGGGA     TGGGC
                                    C_____
GAM575  FBXL7    5'  GGTCCCCATCCGCCCGCC    29411         TC   A
                                GGTCCCTA  TCC CCCGCC
                                ||||||||  ||| ||||||
                                CCAGGGGT  AGG GGGCGG
                                    __  C
GAM575  G6PD     5'  CCGGTTTCCCCGCCTGC     7599        CCCTA    A  C
                                CTGGT    TCTCC CC GC
                                |||||    ||||| || ||
                                GGCCA    AGGGG GG CG
                                   A____    C  A
GAM575  GAS11    3'  CTGGTCCCCATCTCTGCAGCC  11214            CACCC
                                CTGGTCCCTATCTC    GCC
                                ||||||||||||||    |||
                                GACCAGGGGTAGAG    CGG
                                      ACGT_
GAM575  GFI1     3'  CTGGTCCCCATTTGACTTTGCC 23553           CTCCACCC
                                CTGGTCCCTAT       GCC
                                ||||||||||        |||
                                GACCAGGGGTA       CGG
                                     AACTGAAA
GAM575  GPC5     5'  CTGGTCCCCTTTACCCGCC   20919         ATCTCC
                                CTGGTCCCT     ACCCGCC
                                |||||||||     |||||||
                                GACCAGGGG     TGGGCGG
                                    AAA___
GAM575  GPT      5'  GGCCCCGCCCCACCCG      23636        TAT
                                GGTCCC   CTCCACCCG
                                ||||||   |||||||||
                                CCGGGG   GGGGTGGGC
                                   C__
GAM575  GPX3     5'  CTGATCCCTGGCCACCGTCC   13277         ATCT    CG
                                CTGGTCCCT   CCACC  CC
                                |||||||||   |||||  ||
                                GACTAGGGA   GGTGG  GG
                                    CC__    CA
GAM575  HIVEP1   5'  CCGGTCCCCCGCTCCGTCCGCC 13377         AT   AC
                                CTGGTCCCT  CTCC  CCGCC
                                |||||||||  ||||  |||||
                                GGCCAGGGG  GAGG  GGCGG
                                    GC   CA
GAM575  HMGA2    3'  CGGTTTTTCTCACCCGCC    18511      CCCTA   C
                                TGGT    TCTC ACCCGCC
                                ||||    |||| |||||||
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                                GCCA    AGAG TGGGCGG
                                  AAA__   _
GAM575  HS3ST3A1  5'  CTGGTCCCCTTGCCCGCC    25805        ATCTCCA
                                CTGGTCCCT      CCCGCC
                                |||||||||      ||||||
                                GACCAGGGG      GGGCGG
                                    AAC____
GAM575  KCNJ6    5'  GGTCTCCACCCCTCCGCCCGCC 13859     _  TA_    A
                                GGTC CC   TCTCC CCCGCC
                                |||| ||   ||||| ||||||
                                CCAG GG   GGAGG GGGCGG
                                  A  TGG    C
GAM575  KLF8     5'  CTGTTCCCCTCACACCCGCC   28533     G   TAT   _
                                CTG TCCC   CTC CACCCGCC
                                ||| ||||   ||| ||||||||
                                GAC AGGG   GAG GTGGGCGG
                                  A   ___   T
GAM575  MATK     5'  CTGGTGTCTTCCTGCCACCCGC 40309      CC  A  _
              C                  CTGGT  CT TCT CCACCCGCC
                                |||||  || ||| |||||||||
                                GACCA  GA GGA GGTGGGCGG
                                   CA  A   C
GAM575  MGAT5    5'  CTAGTCCCACCACCTGC     14471        TATCT    C
                                CTGGTCCC    CCACC GC
                                ||||||||    ||||| ||
                                GATCAGGG    GGTGG CG
                                    T_____    A
GAM575  NAGA     5'  CGGTCCCCAAGTTGCCCGCC   7036         TCTCCA
                                TGGTCCCTA     CCCGCC
                                |||||||||     ||||||
                                GCCAGGGGT     GGGCGG
                                    TCAAC_
GAM575  POLD1    3'  CTGGTCCCGCCCCCGC      15439        TATCT  A
                                CTGGTCCC    CC CCCGC
                                ||||||||    || |||||
                                GACCAGGG    GG GGGCG
                                    C_____  _
GAM575  POLH     3'  TGGTCCCTTTTCTGTGCC    27103        A_   CCACCC
                                TGGTCCCT  TCT     GCC
                                ||||||||  |||     |||
                                ACCAGGGA  AGA     CGG
                                    AA   CA_____
GAM575  PPP2R2B  5'  CTGGTCCCGCCCGCCCGCC   21332        TATC   A
                                CTGGTCCC    TCC CCCGCC
                                ||||||||    ||| ||||||
                                GACCAGGG    GGG GGGCGG
                                    C___   C
GAM575  PTPRF    5'  CTGGTCCCGCTCCCGC      39034        TAT  CCA
                                CTGGTCCC   CT   CCCGC
                                ||||||||   ||   |||||
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                                GACCAGGG  GA  GGGCG
                                   C__  ___
GAM575  RAI14   5' CTGCTCCACCCCGCCCGCC  31801    G  CTAT   A
                                CTG TCC   CTCC CCCGCC
                                ||| |||   |||| ||||||
                                GAC AGG   GGGG GGGCGG
                                  G  T___   C
GAM575  SLC9A5  3' CTGATCCCTAGAAAGTCACCTG 21387        TCTC__   C
           CC                    CTGGTCCCTA    CACC GCC
                                ||||||||||    |||| |||
                                GACTAGGGAT    GTGG CGG
                                     CTTTCA   A
GAM575  STK11   3' CTGGTCTCCACACCCGCC   7833      CCTA  TC
                                CTGGTC   TC  CACCCGCC
                                ||||||   ||  ||||||||
                                GACCAG   AG  GTGGGCGG
                                   ____  GT
GAM575  TSC     3' CTGATCAGGCTCCATCTGCC  32832     CCTAT   CCC
                                CTGGTC   CTCCA  GCC
                                ||||||   |||||  |||
                                GACTAG   GAGGT  CGG
                                   TCC__   AGA
GAM575  WWOX    5' CTGGCCCCCCTATCGCCCGC  39114       ATC  CA
                                CTGGTCCCT  TC  CCCGC
                                |||||||||  ||  |||||
                                GACCGGGGG  AG  GGGCG
                                     GAT  C_
GAM575  ADRB3   3' AGGTGAGTGGGAAGGTAGA   6175      G     CAC  T
                                AGGTG AGTGGGA  AG TAGA
                                ||||| |||||||  || ||||
                                TCCAC TCACCCT  TC ATCT
                                  _     ___  C
GAM575  CACNA1G 3' AGGTGAGTGGGAAAGT     33128     G     CAC
                                AGGTG AGTGGGA  AGT
                                ||||| |||||||  |||
                                TCCAC TCACCCT  TCA
                                  _     T__
GAM575  CACNA2D2 3' AGGTGGGGTGGGGCAG     25702      A    ACA
                                AGGTGG GTGGG  CAG
                                |||||| |||||  |||
                                TCCACC CACCC  GTC
                                   C    C__
GAM575  COL10A1  3' GGTGGGGTAGAGTTAGA    7964      A   GACAC
                                GGTGG GTGG    AGTTAGA
                                ||||| ||||    |||||||
                                CCACC CATC    TCAATCT
                                  C   _____
GAM575  ENIGMA   3' AGGTGGGTGGGGCAG      41632      A    ACA
                                AGGTGG GTGGG  CAG
                                |||||| |||||  |||
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                                TCCACC CACCC   GTC
                                  _    C__
GAM575  FCRH3    3'  AGATGGATGATGTGTGGTTGGA 38111       G   GACACA   A
                G                  AGGTGGA TGG     GTT GAG
                                   ||||||| |||     ||| |||
                                   TCTACCT ACT     CAA CTC
                                     _  ACACAC   C
GAM575  FLOT1    3'  GGTGGAGTGGGATCATCAG   25134          _ _
                                   GGTGGAGTGGGA CA CAG
                                   |||||||||||| || |||
                                   CCACCTCACCCT GT GTC
                                          A  A
GAM575  FXR2     3'  GGAGGGGTGCAGGTTGGA    22162      T   ACA  _  A
                                   GGAG GGG   CAG TT GA
                                   |||| |||   ||| || ||
                                   CCTC CCC   GTC AA CT
                                     _  AC_   C  C
GAM575  HSF4     5'  GGTGGGGTGAGATGAGT     40770      A     CAC
                                   GGTGG GTGGGA   AGT
                                   ||||| ||||||   |||
                                   CCACC CACTCT   TCA
                                      C     AC_
GAM575  HSF4     5'  GGTGGGGTGGGGTGAGA     40771      A    ACACA  T
                                   GGTGG GTGGG    GT AGA
                                   ||||| |||||    || |||
                                   CCACC CACCC    CA TCT
                                      C    _____  C
GAM575  KCNK3    3'  AGGGGAGTGGGGCTGAG     13897     T      ACACA   A
                                   AGG GGAGTGGG    GTT GAG
                                   ||| ||||||||    ||| |||
                                   TCC CCTCACCC    CGA CTC
                                    _      _____  _
GAM575  PRKACA   3'  GGAGGGGTGGGAGTAGA     15581    T  A     CACA  T
                                   GG GG GTGGGA    GT AGA
                                   || || ||||||    || |||
                                   CC CC CACCCT    CA TCT
                                    T  C     ____  _
GAM575  RING1    5'  AGGTGGTGTGGGTTAG      16332       A    ACACAG
                                   AGGTGG GTGGG     TTAG
                                   |||||| |||||     ||||
                                   TCCACC CACCC     AATC
                                      A    ______
GAM575  SLC17A7  3'  GGTGGAGAGGGAACCTTTAG  33696       T   C  AG
                                   GGTGGAG GGGA AC  TTAG
                                   ||||||| |||| ||  ||||
                                   CCACCTC CCCT TG  AATC
                                       T   _  GA
GAM575  SLC7A5   3'  AGGCTGGAGTGGGGCACACAG  18536    _       __
                                   AGG TGGAGTGGG  ACACAG
                                   ||| |||||||||  ||||||
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```
                                TCC ACCTCACCC  TGTGTC
                                  G       CG
GAM576  ANGPT1   3'  TGTATATATTTCCCTTACAT  40249         C     TG
                                TGTATATATT CTCTTG  T
                                |||||||||| ||||||  |
                                ACATATATAA GGGAAT  A
                                      A     GT
GAM576  MBNL     3'  TGTATTGAGAGAGTTTGTGTTG 34328      ATATTCCTC
          T                      TGTAT       TTGTGTTGT
                                |||||       |||||||||
                                ACATA       AACACAACA
                                   ACTCTCTCA
GAM576  SC5DL    3'  TACTATGTATCTTGACTGTA  44913    G      C  _
                                TA TATGTATC TG TTGTA
                                || |||||||| || |||||
                                AT ATACATAG AC GACAT
                                  G       A  T
GAM576  SNX3     3'  AGTATGTATCTTATGTGT    19135         C  _
                                AGTATGTATC TGT TGT
                                |||||||||| ||| |||
                                TCATACATAG ATA ACA
                                      A   C
GAM577  BAPX1    3'  AGCGGCACTGCGGTGGGCGC  10156        CA_  AA_
                                AGCGGTAC   GGT   CGC
                                ||||||||   |||   |||
                                TCGCCGTG   CCA   GCG
                                     ACG   CCC
GAM577  C14orf2  3'  AGCAGTACCAGGTAGCAG    22205          AC
                                AGCGGTACCAGGTA  GCGG
                                ||||||||||||||  ||||
                                TCGTCATGGTCCAT  CGTC
                                                __
GAM577  COX7A1   5'  AGCGGTACCAGGGAATAC    12406          T  CG
                                AGCGGTACCAGG AA  C
                                |||||||||||| ||  |
                                TCGCCATGGTCC TT  G
                                      C  AT
GAM577  DR1      5'  GCGGTACCGGGCGG        40441        A  TAAC
                                GCGGTACC GG    GCGG
                                |||||||| ||    ||||
                                CGCCATGG CC    CGCC
                                   _  _____
GAM577  OLFM1    5'  GCGGCTGCGTGGACGCGGAC  26773      ACCA_  TA
                                GCGGT    GG  ACGCGGAC
                                |||||    ||  ||||||||
                                CGCCG    CC  TGCGCCTG
                                   ACGCA  __
GAM578  PPP1CB   3'  TAAGTTAACAGGTTTCTCA   15506          A
                                TAAGTTAACAG GTTTTTTA
                                |||||||||| ||||||||
```

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                                ATTCAATTGTC CAAAGAGT
                                          _
GAM578  APAF1    3'  TAAGCCTGTAAACTAGCT    29826         T
                                TAAGCTTGT AACTAGCT
                                ||||||||| ||||||||
                                ATTCGGACA TTGATCGA
                                      T
GAM578  BUB3     3'  TAAGATTGAAAACTAGCT    21805      C   TT
                                TAAG TTG  AACTAGCT
                                |||| |||  ||||||||
                                ATTC AAC  TTGATCGA
                                  T   TT
GAM578  CLCN6    3'  TAAGCTTGGGACAGCT      34721         TTA  T
                                TAAGCTTG   AC AGCT
                                ||||||||   || ||||
                                ATTCGAAC   TG TCGA
                                     CC_  _
GAM578  CPT2     3'  CAAGCCTGTAGCTGGCT     6431          TAA  A
                                TAAGCTTGT   CT GCT
                                |||||||||   || |||
                                GTTCGGACA   GA CGA
                                     TC_  C
GAM578  ETV5     3'  TAAGCTTGTGTCCAGGCT    20854         TAA   _
                                TAAGCTTGT   CTAG CT
                                |||||||||   |||| ||
                                ATTCGAACA   GGTC GA
                                     CA_   C
GAM578  JAG1     3'  CAAGTATTCAACTAGCT     6850       CTTG
                                TAAG   TTAACTAGCT
                                ||||   ||||||||||
                                GTTC   AGTTGATCGA
                                  ATA_
GAM578  SMARCD1  3'  CAAGATCAACTAGCT       40080      CTT
                                TAAG   GTTAACTAGCT
                                ||||   ||||||||||
                                GTTC   TAGTTGATCGA
                                       ___
GAM578  TFRC     3'  AGCCTGTTAGCACGTACTGGCT 17424          _______  A   III
           A                    AGCTTGTTA     ACT GCT   A
                                |||||||||     ||| |||   |
                                TCGGACAAT     TGA CGA   T
                                     CGTGCA   C   III
GAM579  EIF2C1   3'  TGGGGTCAGGGCCAGAT     29189         AAGA
                                TGGGGTCG    CTAGAT
                                ||||||||    ||||||
                                ACCCCAGT    GGTCTA
                                     CCC_
GAM579  NCALD    3'  TAGAATCACAGGACTGGAT    36771         AA_   A
                                TGGGGTCG   GACT GAT
                                ||||||||   |||| |||
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                                ATCTTAGT  CTGA CTA
                                    GTC   C
GAM579  ROBO1   3'  TGGGGTCAGACCTGAT    39490      GA   A
                                TGGGGTC  AGACT GAT
                                |||||||  ||||| |||
                                ACCCCAG  TCTGG CTA
                                   __    A
GAM579  SCNN1G  3'  TGGTGGTCCTGACTAGAT   9796    _   GAA
                                TGG GGTC  GACTAGAT
                                ||| ||||  ||||||||
                                ACC CCAG  CTGATCTA
                                  A   GA_
GAM579  SP3     5'  TGGAATCTGGACTAGAT    44385      GAA
                                TGGGGTC  GACTAGAT
                                |||||||  ||||||||
                                ACCTTAG  CTGATCTA
                                    AC_
GAM579  SRI     3'  TGGTGTAACAGACTAGAT   17111    G  CGA
                                TGG GT   AGACTAGAT
                                ||| ||   |||||||||
                                ACC CA   TCTGATCTA
                                  A  TTG
GAM579  STIM1   3'  TGGGGTGGAACAGAT     41137      C   GAC
                                TGGGGT GAA   TAGAT
                                |||||| |||   |||||
                                ACCCCA CTT   GTCTA
                                   C  ___
GAM579  TEM5    3'  TAGGGCATGACTAGAT     37243      CGAA
                                TGGGGT   GACTAGAT
                                ||||||   ||||||||
                                ATCCCG   CTGATCTA
                                   TA__
GAM579  BAZ2A   3'  GTTTCACACATTCACTAG   30312        TC_
                                GTTTCACAC  CACTAG
                                |||||||||  ||||||
                                CAAAGTGTG  GTGATC
                                     TAA
GAM579  CD53    3'  TTAGTTTCACCACT       8156        CACT
                                TTAGTTTCA   CCACT
                                |||||||||   |||||
                                AATCAAAGT   GGTGA
                                    ____
GAM579  KCNA3   3'  TTAGTTTCATTTCCTCCCAG  13798        CAC  A_
                                TTAGTTTCA  TCC  CTAG
                                |||||||||  |||  ||||
                                AATCAAAGT  AGG  GGTC
                                     AA_   AG
GAM579  MOX2    3'  TCAACATCATTCCACTAGC   42523     TT  CAC
                                TTAG  TCA  TCCACTAGC
                                ||||  |||  |||||||||
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                                AGTT  AGT   AGGTGATCG
                                  GT   A__
GAM579  RRAS2    3'  TTAGCTTCACAGAAAGGACTAG 29313          CTCC__
             CCA                   TTAGTTTCACA     ACTAGCCA
                                |||||||||||     ||||||||
                                AATCGAAGTGT     TGATCGGT
                                     CTTTCC
GAM579  USP9Y    3'  CTAGTTTTCAATACTAGCCA   41957       _  CACTCC
                                TTAGTTT CA     ACTAGCCA
                                |||||||  ||     ||||||||
                                GATCAAA GT     TGATCGGT
                                   A  TA____
GAM579  USP9Y    5'  TTAGTTTCAAGCTCGCTAA    41963        CA   CA
                                TTAGTTTCA  CTC  CTAG
                                |||||||||  |||  ||||
                                AATCAAAGT  GAG  GATT
                                     TC   C_
GAM579  ZNF174   5'  GCTAGCCTTTACTAGCCAA    18361     TCACA  CC
                                GTT    CT  ACTAGCCAA
                                |||    ||  |||||||||
                                CGA    GA  TGATCGGTT
                                  TCG__  AA
GAM580  ABCD1    5'  TCAGGGCCTTGAGAGG      6206          C   CTGC
                                TCAGGGCCT GAG    GG
                                |||||||||  |||    ||
                                AGTCCCGGA CTC    CC
                                     A   T___
GAM580  AES      3'  TACCAGGGTGAGAGGGCTGTGG 10058         CCTCGA_   C
             C                    TATCAGGG      GCTG GGC
                                |||||||||      |||| |||
                                ATGGTCCC      CGAC CCG
                                     ACTCTCC    A
GAM580  CA3      5'  CAGGGTTTCTAACCGGC     23208       CC  G   TG
                                CAGGG  TC AGC  CGGC
                                |||||  ||  |||  ||||
                                GTCCC  AG TTG  GCCG
                                   AA  A   __
GAM580  CDK4     5'  TATCGGGGCCCCGGAGCCG    38142       A       _
                                TATC GGGCCTCG AGCTG
                                ||||  ||||||||  |||||
                                ATAG CCCGGGGC TCGGC
                                   C       C
GAM580  CRHR1    3'  TCAGTGGGGGCTGCGGC      20449      _  CCTCGA
                                TCAG GG     GCTGCGGC
                                ||||  ||     ||||||||
                                AGTC CC     CGACGCCG
                                  A  CC_____
GAM580  CSF2     3'  TATCAGGGTCAGTGTGG      8899          CC  G  C  C
                                TATCAGGG  TC AG TG GG
                                ||||||||  ||  ||  ||  ||
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                                ATAGTCCC  AG TC AC CC
                                   __  _  _  A
GAM580  DMPK    3'  TCAGGGCCTCAGCCTGGC    20622         G   GC
                                TCAGGGCCTC AGCT  GGC
                                |||||||||| ||||  |||
                                AGTCCCGGAG TCGG  CCG
                                     _   A_
GAM580  FAT     5'  CCGGGGCCTCGCCGGGC    23489    A     GA   C
                                TC GGGCCTC  GCTG GGC
                                || |||||||  |||| |||
                                GG CCCGGAG  CGGC CCG
                                 C      __   _
GAM580  NUCB1   3'  TATCAGGGTTCACCGG     26160        CC   AGCTG
                                TATCAGGG  TCG    CGG
                                ||||||||  |||    |||
                                ATAGTCCC  AGT    GCC
                                     A_   G____
GAM580  RFX1    3'  TCAGAGTTTGCAGCTGCGGC  16299      CCTCG
                                TCAGGG    AGCTGCGGC
                                ||||||    |||||||||
                                AGTCTC    TCGACGCCG
                                    AAACG
GAM580  SHANK2  3'  CAGGGCCTTGCTGGGG     39328        CGA   C
                                CAGGGCCT   GCTG GG
                                ||||||||   |||| ||
                                GTCCCGGA   CGAC CC
                                     A__    C
GAM580  WTAP    5'  ATCGGGGCCTCGAGGC     22225    A        CT
                                ATC GGGCCTCGAG  GC
                                ||| ||||||||||  ||
                                TAG CCCGGAGCTC  CG
                                  C        __
GAM580  ADCY2   3'  GGGCACCTGCCAGGCTCGC   42145         G   C  GC
                                GGGCACCTG CCGG GT  CGC
                                ||||||||| |||| ||  |||
                                CCCGTGGAC GGTC CG  GCG
                                     _   _  A_
GAM580  ADCY8   5'  CAGGGGGCCTGGCCGGCG    9996       CA
                                CAGGG  CCTGGCCGGCG
                                |||||  ||||||||||
                                GTCCC  GGACCGGCCGC
                                   CC
GAM580  ARF3    3'  CAGGGCCCTGGCCACACTTGC  11668       A      _  G
                                CAGGGC CCTGGCCG GC TGC
                                |||||| |||||||| || |||
                                GTCCCG GGACCGGT TG ACG
                                     _       G  A
GAM580  BAI2    5'  GGGGACCTGGCCGGGCGC    11797     C        C
                                GGG ACCTGGCCGG GTGC
                                ||| ||||||||| ||||
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                                CCC TGGACCGGCC CGCG
                                  C        _
GAM580  CD5     5'  AGGGTGTCTGGCCGGGT     30542      CAC       C
                                AGGG   CTGGCCGG GT
                                ||||   |||||||| ||
                                TCCC   GACCGGCC CA
                                  ACA       _
GAM580  COX15    3'  GGGCACCTGCTCGCCAGTGT   38516          ___     C
                                GGGCACCTG   GCCGG GT
                                |||||||||   ||||| ||
                                CCCGTGGAC   CGGTC CA
                                     GAG    A
GAM580  DDX11    3'  GGGTGCCTGGCCGGGGGC    36179     CA        CGT
                                GGG  CCTGGCCGG   GC
                                |||  |||||||||   ||
                                CCC  GGACCGGCC   CG
                                  AC        CC_
GAM580  DDX38    5'  GGGCGCCGGCGCTGC       30414      ACCTG      _
                                GGGC    GCCGGCG TGC
                                ||||    ||||||| |||
                                CCCG    CGGCCGC ACG
                                  _____       G
GAM580  EYA1     5'  AGGCGCCTGGCCGCTGCCGC   7987       A       G G
                                GGGC CCTGGCCG C TGCCGC
                                |||| |||||||| | ||||||
                                TCCG GGACCGGC G ACGGCG
                                  C       _ _
GAM580  GPR62    3'  CAGGGCACCTGCTGTGACCTG  44871           GCC_   G
                                CAGGGCACCTG    GGC TG
                                ||||||||||    ||| ||
                                GTCCCGTGGAC    CTG AC
                                     GACA   G
GAM580  KCNJ12   3'  CAGGGCACTGGGCCCGTTCTGC 34246         CT    GG   GCC
                                CAGGGCAC  GGCC  CGT   GC
                                ||||||||  ||||  |||   ||
                                GTCCCGTG  CCGG  GCA   CG
                                     AC    __   AGA
GAM580  MAT1A    3'  CAGGGCACTGGCTGCCTG    44903         C    CG  G
                                CAGGGCAC TGGC  GC TG
                                |||||||| ||||  || ||
                                GTCCCGTG ACCG  CG AC
                                     _    A_  G
GAM580  MSI1     3'  GGGCACCTGGCCCCTTGC    14646           GGCG
                                GGGCACCTGGCC    TGC
                                ||||||||||||    |||
                                CCCGTGGACCGG    ACG
                                     GGA_
GAM580  PIGR     5'  CAGGGCACTGGACGCTGCTGC  43700         C   C  G G   C
                                CAGGGCAC TGG CG C TGC GC
                                |||||||| ||| || | ||| ||
```

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                                GTCCCGTG ACC GC G ACG CG
                                     _  T  _ _  A
GAM580  PTPN1    3'  GGGGGGCTGTTGGCGTGCCGC  15902     CAC   GCC
                                GGG  CTG  GGCGTGCCGC
                                |||  |||  ||||||||||
                                CCC  GAC  CCGCACGGCG
                                  CCC  AA_
GAM580  SLC7A5   3'  GGGTGCCTGGCCGCGGTG    18554     CA      G  _
                                GGG  CCTGGCCG CG TG
                                |||  |||||||| || ||
                                CCC  GGACCGGC GC AC
                                  AC       _ C
GAM580  SORCS2   5'  GGGCGCCTGGCTCCGTGCCGC  34060      A     CGG
                                GGGC CCTGGC  CGTGCCGC
                                |||| ||||||  ||||||||
                                CCCG GGACCG  GCACGGCG
                                   C     AG_
GAM580  THPO     5'  GGGGTGTCTGGCTGGCGTG   7853      CAC_    C
                                GGG   CTGGC GGCGTG
                                |||   ||||| ||||||
                                CCC   GACCG CCGCAC
                                  CACA    A
GAM580  VIPR2    3'  GGGCACCTGGCCTGGGCCG   18022           _ CGT
                                GGGCACCTGGCC GG  GCCG
                                |||||||||||| ||  ||||
                                CCCGTGGACCGG CC  CGGC
                                      A ___
GAM581  ADAMTS13 3'  CTGCAGCTGCTTTGGTCCA   40033          GC  AAAA
                                CTGCAGCTGCT  TGG   CCG
                                ||||||||||  |||   |||
                                GACGTCGACGA  ACC   GGT
                                      A_  A___
GAM581  ALEX1    5'  CTGCAGCTACTGCGGGCCG   32485           T  AAAA
                                CTGCAGCTGCTGC GG   CCG
                                |||||||||||| ||   |||
                                GACGTCGATGACG CC   GGC
                                      C _____
GAM581  AOC3     3'  TGAGCTGCTGCTGTCACG    19022    C       GAAAAC
                                TG AGCTGCTGCTG     CG
                                || ||||||||||      ||
                                AC TCGACGACGAC     GC
                                 _         AGT___
GAM581  APLP2    3'  GCGGCTGCTGCTTGGCAGTCGA 44922    A       _ AAAAC
                                GC GCTGCTGCT GG    CGA
                                || |||||||| ||    |||
                                CG CGACGACGA CC    GCT
                                 C       A  GTCA_
GAM581  ATRX     5'  CTGTAGCTGCTGCTGGAA    39607    C
                                CTG AGCTGCTGCTGGAA
                                ||| ||||||||||||||
```

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                                GAC TCGACGACGACCTT
                                  A
GAM581  BAZ1B    5'  CTGGCGGCTGCTGGGGCCG   37086    CA  T      AAAA
                                CTG  GC GCTGCTGG   CCG
                                |||  || ||||||||   |||
                                GAC  CG CGACGACC   GGC
                                  __  C      CC__
GAM581  CACNA1A  5'  CTGAGGCTGCCGGGGCTGG   35732    CA     ___
                                CTG  GCTGCT   GCTGG
                                |||  ||||||   |||||
                                GAC  CGACGG   CGACC
                                  TC     CCC
GAM581  CEP2     5'  GCGGCTACTGGACACGA     28440    T      AAAC
                                GC GCTGCTGGA   CGA
                                || |||||||||   |||
                                CG CGATGACCT   GCT
                                 C       GT__
GAM581  CYP1A2   3'  CAGCTACTTGGGAGGCCGA   8912       GCT   AAA
                                CAGCTGCT   GGA   CCGA
                                ||||||||   |||   ||||
                                GTCGATGA   CCT   GGCT
                                    AC_   CC_
GAM581  DAAM2    3'  CTGCAGCTGTTCTGCCTGG   45173        __   _
                                CTGCAGCTG  CTGC TGG
                                |||||||||  |||| |||
                                GACGTCGAC  GACG ACC
                                     AA   G
GAM581  DAZ      3'  CTGCAGCTGATGAAGACTGG   19850       CT____
                                CTGCAGCTG     GCTGG
                                |||||||||     |||||
                                GACGTCGAC     TGACC
                                     TACTTC
GAM581  DGCR2    3'  CTGCGCTGCTGAGGAGGGGCCG 23092      A      CT   AAA_
                                CTGC GCTGCTG  GGA    CCG
                                |||| |||||||  |||    |||
                                GACG CGACGAC  CCT    GGC
                                  _      T_   CCCC
GAM581  EGFL5    5'  CTGCTGTTGCTGCTGCTGG   44524     A___
                                CTGC   GCTGCTGCTGG
                                ||||   ||||||||||
                                GACG   CGACGACGACC
                                  ACAA
GAM581  FABP2    3'  TGAGCCCTGGAAAA       6588     C    GCTG
                                TG AGCT    CTGGAAAA
                                || ||||    ||||||||
                                AC TCGG    GACCTTTT
                                 _   _____
GAM581  GABRB2   5'  GCGGCTGCCGGGGACCG     34870    T      AAA
                                GC GCTGCTGG   ACCG
                                || ||||||||   ||||
```

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                                CG CGACGGCC   TGGC
                                 C       CC_
GAM581  GLS      5'  CTGCTGCTGCTGCTGCGCGCCG 31376      A        GAAAA
                A                CTGC GCTGCTGCTG     CCGA
                                 |||| ||||||||||     ||||
                                 GACG CGACGACGAC     GGCT
                                   A         GCGC_
GAM581  GNAS     3'  TGTAGCTGCTGCTGGCCACCA  38667    C          AAA
                                 TG AGCTGCTGCTGG   ACCG
                                 || ||||||||||||   ||||
                                 AC TCGACGACGACC   TGGT
                                  A          GG_
GAM581  HK1      5'  CAGCTGCTGTAGCCG       37915          C   AAAA
                                 CAGCTGCTG TGG    CCG
                                 |||||||| |||    |||
                                 GTCGACGAC ATC    GGC
                                        _  _____
GAM581  HPCAL1   5'  CCGCAGCTGCTGCGCCGG    39544            __
                                 CTGCAGCTGCTGC  TGG
                                 ||||||||||||  |||
                                 GGCGTCGACGACG  GCC
                                       CG
GAM581  HRH1     3'  CTGCAGCTTCTGAAACCG    9251          G   CTGGA
                                 CTGCAGCT CTG     AAACCG
                                 |||||||| |||     ||||||
                                 GACGTCGA GAC     TTTGGC
                                    A   ______
GAM581  HS3ST3B1 5'  CTGCAACTGGAACGGAAAGTCG 25794          CT  T     AC
                                 CTGCAGCTG  GC GGAAA  CG
                                 |||||||||  || |||||  ||
                                 GACGTTGAC  TG CCTTT  GC
                                       CT  _     CA
GAM581  MAB21L1  5'  TGCGGCTGCTAGAGCTGG    24592     A     ___
                                 TGC GCTGCT   GCTGG
                                 ||| ||||||   |||||
                                 ACG CGACGA   CGACC
                                   C      TCT
GAM581  MAN1A1   5'  CCGCGGCTGCGGGGCTGG    45095     A    T__
                                 CTGC GCTGC   GCTGG
                                 |||| |||||   |||||
                                 GGCG CGACG   CGACC
                                    C     CCC
GAM581  MTMR1    5'  CTGGGCTGCCGGGAGCCG    43154     CA      CT   AAA
                                 CTG  GCTGCTG  GGA   CCG
                                 |||  |||||||  |||   |||
                                 GAC  CGACGGC  CCT   GGC
                                   C_       __   C__
GAM581  MYOZ1    5'  CTGAGCTGCTGTGACC      34554     C       C  GAAA
                                 CTG AGCTGCTG TG    ACC
                                 ||| |||||||| ||    |||
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                                GAC TCGACGAC AC    TGG
                                  _      _ _____
GAM581  NEK6     5'  GCTGCCGCTGGGGGACCG    30824          AAA
                                GCTGCTGCTGG   ACCG
                                ||||||||||   ||||
                                CGACGGCGACC   TGGC
                                      CCC
GAM581  NPPB     5'  CTGCTGCTGCTGCTGCGA    14826     A       _
                                CTGC GCTGCTGCTG GA
                                |||| |||||||||| ||
                                GACG CGACGACGAC CT
                                  A        G
GAM581  NRAP     3'  CTGTGCTGCTGTGAAAC     40193     CAGC      GA
                                CTG   TGCTGCTG  AAAC
                                |||   ||||||||  ||||
                                GAC   ACGACGAC  TTTG
                                 _____       AC
GAM581  P23      3'  GCGGCTGCTGCTAGGGAGTCGA 27344    A        AAAAC
                                GC GCTGCTGCTGG    CGA
                                || ||||||||||     |||
                                CG CGACGACGATC    GCT
                                 C         CCTCA
GAM581  P53AIP1  5'  CTGTGCTGCTGTGACTGG    35231     CA     ___
                                CTG  GCTGCTG   CTGG
                                |||  |||||||   ||||
                                GAC  CGACGAC   GACC
                                  A_      ACT
GAM581  PDGFB    3'  TGAGCTGCTGGGCAAGACCG   15197    C      CT _ A
                                TG AGCTGCTG  GG AA ACCG
                                || ||||||||  || || ||||
                                AC TCGACGAC  CC TT TGGC
                                 _       __ G  C
GAM581  PDYN     3'  CTGCTGCTGCTGCTGCCG    35921     A       GAAAA
                                CTGC GCTGCTGCTG    CCG
                                |||| ||||||||||    |||
                                GACG CGACGACGAC    GGC
                                  A        _____
GAM581  PIM1     5'  CTGCTGCTGCTGCTGCTGCCG  44965     A       GAAAA
                                CTGC GCTGCTGCTG    CCG
                                |||| ||||||||||    |||
                                GACG CGACGACGAC    GGC
                                  A        GAC__
GAM581  PODXL    5'  CTGCCGCTGCAGCAGAGCCG  23972     A    T  T   AAA
                                CTGC GCTGC GC GGA   CCG
                                |||| ||||| || |||   |||
                                GACG CGACG CG TCT   GGC
                                  G    T _   C__
GAM581  POR      3'  CTGTGCTGCCAGGGGCCGG   45300     CA     _____
                                CTG  GCTGCT    GCTGG
                                |||  ||||||    |||||
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```
                                GAC  CGACGG   CGGCC
                                  A_     TCCC
GAM581  PRX      3'  GCAGCTGCACCTCGGGGAGTCG 34121        T  ____  AAAC
              A                   GCAGCTGC GCT   GGA   CGA
                                  |||||||| |||   |||   |||
                                  CGTCGACG TGG   CCT   GCT
                                      _  AGCC  CA__
GAM581  PXMP3    5'  CTGCAGCTCCCTCAAGACTGG  7229        G  _____
                                  CTGCAGCT CT    GCTGG
                                  |||||||| ||    |||||
                                  GACGTCGA GG    TGACC
                                       G  AGTTC
GAM581  RAD52    3'  CTGCAGCTGCTTCTGCCGG   39558         ___
                                  CTGCAGCTGCT   GCTGG
                                  ||||||||||   |||||
                                  GACGTCGACGA   CGGCC
                                         AGA
GAM581  RALBP1   3'  CTGCACTGCCGGGGGCCGG   27699      G   ____
                                  CTGCA CTGCT   GCTGG
                                  ||||| |||||   |||||
                                  GACGT GACGG   CGGCC
                                     _    CCCC
GAM581  RXRA     3'  CTGCAGCTCCAGGGCTGG    16423       G  ___
                                  CTGCAGCT CT   GCTGG
                                  |||||||| ||   |||||
                                  GACGTCGA GG   CGACC
                                      _ TCC
GAM581  SCA1     5'  TGCAGCTGCTGTTGCTCTGG  7297          _____
                                  TGCAGCTGCTG    CTGG
                                  ||||||||||    ||||
                                  ACGTCGACGAC    GACC
                                         AACGA
GAM581  STAU     5'  CTGCTGGCTGCTGCTCCG    32693     A_      GGAAAA
                                  CTGC  GCTGCTGCT     CCG
                                  ||||  |||||||||     |||
                                  GACG  CGACGACGA     GGC
                                    AC       _______
GAM581  STIM1    3'  CTGCAACTGCTAGGGGAA    41125          CT
                                  CTGCAGCTGCTG  GGAA
                                  ||||||||||||  ||||
                                  GACGTTGACGAT  CCTT
                                         CC
GAM581  TARBP2   3'  CTGCAGCAGTAAAAACCG    39530       TGCTGCTG
                                  CTGCAGC       GAAAACCG
                                  |||||||       ||||||||
                                  GACGTCG       TTTTTGGC
                                      TCA_____
GAM581  TTC3     3'  ACTTGCTGCTGCAAACTGA   17711     _     GA   C
                                  GCT GCTGCTG  AAAC GA
                                  ||| |||||||  |||| ||
```

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                                TGA CGACGAC  TTTG CT
                                  A      G_   A
GAM581  WASF3    3'  CTACAGCTGCAGGGCTGA    27382          T__
                                CTGCAGCTGC   GCTGG
                                ||||||||||  |||||
                                GATGTCGACG   CGACT
                                      TCC
GAM581  AGRN     3'  TCTGTCTGCAGCACGGC     44257    CAG        CC
                                TC   CTGCAGCGCG  GC
                                ||   ||||||||||  ||
                                AG   GACGTCGTGC  CG
                                 ACA         __
GAM581  ANGPT4   5'  TCCTGCTGCAGCCAACAGTGGC 31988     A       G  C  C_
                                TCC GCTGCAGC CG CG  GGC
                                ||| |||||||| || ||  |||
                                AGG CGACGTCG GT GT  CCG
                                  A       _ T  CA
GAM581  ANKRD3   5'  TCTAGCCAGCGCCGCGGC    33970    C    CAGC
                                TC AGCTG    GCGCCGCGGC
                                || |||||    ||||||||||
                                AG TCGGT    CGCGGCGCCG
                                 A    _____
GAM581  ANXA6    5'  TCCAGCCGCAGCGGAGGC    19716           CGCC
                                TCCAGCTGCAGCG    GC
                                ||||||||||||    ||
                                AGGTCGGCGTCGC    CG
                                      CTC_
GAM581  BCL7A    5'  GCGGCTCCGCGCCGCGGC    34214    T  AG
                                GC GC  CGCGCCGCGGC
                                || ||  ||||||||||
                                CG CG  GCGCGGCGCCG
                                 C  AG
GAM581  CA6      3'  GCTGCAGCGGACAGGC      10233         C  CGC
                                GCTGCAGCG GC   GGC
                                |||||||| ||   |||
                                CGACGTCGC TG   CCG
                                      C  T__
GAM581  DGUOK    3'  TCCAGCTGTACTTTCAGGCGGC 38963         CA  GCGCC_
                                TCCAGCTG  GC     GCGGC
                                ||||||||  ||     |||||
                                AGGTCGAC  TG     CGCCG
                                     A_  AAAGTC
GAM581  DNAH9    5'  TCCAGCTGCATCGGTGC     21670          G  C____
                                TCCAGCTGCA CG    GC
                                |||||||||| ||    ||
                                AGGTCGACGT GC    CG
                                      A  CAIII
GAM581  DUOX1    5'  TCCAGCTGCGGCCACGGC    32656          AGC C
                                TCCAGCTGC   G GCCGCGGC
                                |||||||||   | ||||||||
```

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                                AGGTCGACG  C CGGTGCCG
                                    ___ _
GAM581  DUSP6   5'  CCCAGCTGCAGCCGCTGGC   42326         G  CGC
                                TCCAGCTGCAGC CGC  GGC
                                |||||||||||| |||  |||
                                GGGTCGACGTCG GCG  CCG
                                      _  A__
GAM581  EGFR    5'  TCCGGCGCAGCGCGGC     23398    A  T     CC
                                TCC GC GCAGCGCG  GC
                                ||| || ||||||||  ||
                                AGG CG CGTCGCGC  CG
                                  C _      __
GAM581  EGLN1   5'  TCCGGCGCAGCGCCGG     35179    A  T     GCCG
                                TCC GC GCAGCGC   CGG
                                ||| || |||||||   |||
                                AGG CG CGTCGCG   GCC
                                  C _     ____
GAM581  FOXG1B  5'  TCCGGCAGCAGCGCAGTGCCGC 23513    A  T    C_____ CGCG
          G                      TCC GC GCAGCG     GC   G
                                ||| || ||||||      ||   |
                                AGG CG CGTCGC     CG   C
                                  C  T    GTCAIII  GCGC
GAM581  GATA6   5'  CAGCTTGGCGCCGCGGC    23538     GCAGC
                                CAGCT    GCGCCGCGGC
                                |||||    ||||||||||
                                GTCGA    CGCGGCGCCG
                                   AC___
GAM581  GEMIN5  5'  TCCAGCTGCACTCCAAGG   44844       AGC  G   C
                                TCCAGCTGC   GC CCG GG
                                |||||||||   || ||| ||
                                AGGTCGACG   TG GGT CC
                                     ___  A   T
GAM581  GNAQ    5'  TCCGCTGCAGCCCGCCGGC   13177    A     G   GC
                                TCC GCTGCAGC CGCC  GGC
                                ||| ||||||| ||||  |||
                                AGG CGACGTCG GCGG  CCG
                                  _      G   __
GAM581  GNB1    5'  TCCAGTCCCGCCGCGG     13210     _ GCAGCG
                                TCCAG CT     CGCCGCGG
                                |||||  ||     ||||||||
                                AGGTC GG     GCGGCGCC
                                   A _______
GAM581  GRB10   5'  CCCGGGCGCGCGCGCCGCGGC  23650    A_  T  A
                                TCC  GC GC GCGCGCCGCGGC
                                |||  || || ||||||||||||
                                GGG  CG CG CGCGCGGCGCCG
                                  CC  _ _
GAM581  GSTM1   3'  TCCAGCTGCGCTGCACAGC   40447        A  _   C
                                TCCAGCTGC GC GCGC GC
                                |||||||| || |||| ||
```

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                                AGGTCGACG CG CGTG CG
                                     _ A   T
GAM581  GSTM2   3'  TCCAGCTGCGCTGCACAGC   9196        A _   C
                                TCCAGCTGC GC GCGC GC
                                ||||||||| || |||| ||
                                AGGTCGACG CG CGTG CG
                                     _ A   T
GAM581  GSTM4   3'  TCCAGCTGCGCTGCACAGC   9203        A _   C
                                TCCAGCTGC GC GCGC GC
                                ||||||||| || |||| ||
                                AGGTCGACG CG CGTG CG
                                     _ A   T
GAM581  HDGF    5'  TCCGGCGCGGCCACGG     21066    A TGCA   C
                                TCC GC   GCG GCCGCGG
                                ||| ||   ||| |||||||
                                AGG CG   CGC CGGTGCC
                                  C _____  _
GAM581  IDH2    3'  TCCACTGCAGCCATGGGTGGC  13478    G     G  CCGC_
                                TCCA CTGCAGC CG    GGC
                                |||| ||||||| ||    |||
                                AGGT GACGTCG GT    CCG
                                  _     _ ACCCA
GAM581  IHPK3   5'  TCCAGCTGCACGCCTGC    38374       AGC    _
                                TCCAGCTGC  GCGCC GC
                                |||||||||  ||||| ||
                                AGGTCGACG  TGCGG CG
                                     ___    A
GAM581  ITGA11  3'  CCCAGCTGCAGCCAGGCCG  29196         GC_
                                TCCAGCTGCAGC  GCCG
                                ||||||||||||  ||||
                                GGGTCGACGTCG  CGGC
                                      GTC
GAM581  ITK     3'  TCCAGCTGTGGCTTGACTGC  24444       CA  GC_  C
                                TCCAGCTG  GC  GC GC
                                ||||||||  ||  || ||
                                AGGTCGAC  CG  TG CG
                                    AC  AAC  A
GAM581  JAG2    5'  TCGAGCGCAGCGCCGCGGC   13733   C  T   GC
                                TC AGC GCAGC  GCCGCGGC
                                || ||| |||||  ||||||||
                                AG TCG CGTCG  CGGCGCCG
                                 C  _    __
GAM581  LARGE   5'  CCCGGCTCCAAATGCCGCGGC 21860    A  G  CGC
                                TCC GCT CAG   GCCGCGGC
                                ||| ||| |||   ||||||||
                                GGG CGA GTT   CGGCGCCG
                                  C  G  TA_
GAM581  LIMK1   3'  TCCAGCTGTGGGCCCAGTGGC  32539       CAGC  G  C_
                                TCCAGCTG   GC CCG  GGC
                                ||||||||   || |||  |||
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                                AGGTCGAC   CG GGT  CCG
                                    ACC_ _  CA
GAM581  MAML1   5'  TCCGCGCTACCGCCGCGGC   31296    A  T  A  G
                                TCC GC GC GC CGCCGCGGC
                                ||| || || || |||||||||
                                AGG CG CG TG GCGGCGCCG
                                  _ _ A  _
GAM581  MAPK14  5'  TCCAGCTGCTGCGCCCGC    40018        A   G
                                TCCAGCTGC GCGC CCGC
                                ||||||||| |||| ||||
                                AGGTCGACG CGCG GGCG
                                    A   _
GAM581  MBD3    3'  CCCAGCTGTCAGCAAGCCGTGG 19416        _   C   C
          C                      TCCAGCTG CAGCG GCCG GGC
                                ||||||||| ||||| |||| |||
                                GGGTCGAC GTCGT CGGC CCG
                                    A   T   A
GAM581  MPO     3'  CCCAGCTGCAGCTGGCGC    7002          __ C___
                                TCCAGCTGCAGC  G   GC
                                |||||||||||  |   ||
                                GGGTCGACGTCG  C   CG
                                    AC GIII
GAM581  MYBPH   3'  CAGGCTGCAGCACCTGGC    22649    _     GC  GC
                                CAG CTGCAGC  GCC  GGC
                                ||| |||||||  |||  |||
                                GTC GACGTCG  TGG  CCG
                                  C     __  A_
GAM581  MYL2    3'  TCCAACTGTAGGATGTGCGGC  41335       C  CGCGCC
                                TCCAGCTG AG     GCGGC
                                ||||||||  ||     |||||
                                AGGTTGAC TC     CGCCG
                                    A  CTACA_
GAM581  NME1    5'  TCCGGCTGCAGCCGCCAGC   7073     A      G   _
                                TCC GCTGCAGC CGCC GC
                                ||| ||||||| |||| ||
                                AGG CGACGTCG GCGG CG
                                  C       _   T
GAM581  NT5C    3'  TCCAGCTGCTGCCCGCGGC   31102        AGC  G
                                TCCAGCTGC   GC CCGCGGC
                                |||||||||   || |||||||
                                AGGTCGACG   CG GGCGCCG
                                    A__  _
GAM581  OXTR    3'  CAGGCTGCAGCCCTGG      9522     _     GCG  GC
                                CAG CTGCAGC   CC  GG
                                ||| |||||||   ||  ||
                                GTC GACGTCG   GG  CC
                                  C      ____  A_
GAM581  PGLS    3'  TCCAGCAGCAGCACGACGTGGC 28985       T      C  C
                                TCCAGC GCAGCGCG CG GGC
                                ||||||  |||||||| || |||
```

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                                AGGTCG CGTCGTGC GC CCG
                                   T      T  A
GAM581  PPT2    3'  TCTGGCTGCAGCTCTTCAGGCG 39927    CA      GCGCC__
            GC                   TC  GCTGCAGC      GCGGC
                                ||  ||||||||      |||||
                                AG  CGACGTCG      CGCCG
                                 AC       AGAAGTC
GAM581  PREB    5'  ACTGCCCGCACCGCGGC     30137      AG
                                GCTGC  CGCGCCGCGGC
                                |||||  ||||||||||
                                TGACG  GCGTGGCGCCG
                                  G_
GAM581  PTK2B   3'  TCCAGCTGCAGCCTGAGC    19924          GCGCC
                                TCCAGCTGCAGC    GC
                                ||||||||||||    ||
                                AGGTCGACGTCG    CG
                                       GACT_
GAM581  RAX     3'  TCCAGCTGCAGGGCTGAGG   30247          C  GCCGC
                                TCCAGCTGCAG GC    GG
                                ||||||||||| ||    ||
                                AGGTCGACGTC CG    CC
                                      C  ACT__
GAM581  SIAH2   5'  TCCAGCTGGCAGCGCAGGGGGC 22867        _      CCGC
                                TCCAGCTG CAGCGCG   GGC
                                |||||||| |||||||   |||
                                AGGTCGAC GTCGCGT   CCG
                                     C      CCC_
GAM581  SKI     3'  TCCAGCTGTAGTTGGGGGACGC 16735        C  CGCGC___
            GGC                  TCCAGCTG AG       CGCGGC
                                ||||||||  ||       ||||||
                                AGGTCGAC TC       GCGCCG
                                     A  AACCCCCT
GAM581  SLC6A12 3'  TCCAGCTGGGGGTGCCTGTGGC 16802        CAGCGC   GC_
                                TCCAGCTG     GCC   GGC
                                ||||||||     |||   |||
                                AGGTCGAC     CGG   CCG
                                     CCCCA_   ACA
GAM581  SOX18   5'  TCCAGCTGGGCGCGGC     32945        CA    CC
                                TCCAGCTG  GCGCG  GC
                                ||||||||  |||||  ||
                                AGGTCGAC  CGCGC  CG
                                     C_    __
GAM581  STIP1   3'  TCCGTGCTGCTCGCCGCGG   27734     A_    AGCG
                                TCC  GCTGC   CGCCGCGG
                                |||  |||||   ||||||||
                                AGG  CGACG   GCGGCGCC
                                  CA    A___
GAM581  STK24   3'  TCTGGCTGCAGCACAGTGCCGC 18707    CA       C_______ CGCG
            G                    TC  GCTGCAGCG     GC   G
                                ||  |||||||||      ||   |
```

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                                AG  CGACGTCGT      CG    C
                                 AC        GTCAIII  GCGC
GAM581  TNFRSF6B  3'  CAGCTGCAAGGCCGCGCGGC  37280         __  G   C
                                CAGCTGCA  GC CGC GCGGC
                                ||||||||  || ||| |||||
                                GTCGACGT  CG GCG CGCCG
                                     TC  _   _
GAM581  WRN       5'  CCCCGCCCAGCGCGCCGCGG  8133      A   G
                                TCC GCT CAGCGCGCCGCGG
                                ||| ||| ||||||||||||
                                GGG CGG GTCGCGCGGCGCC
                                  G  _
GAM582  A1BG      3'  CAACTAAGCACTTGGGGAA   39087   C   TTT    _
                                A ACT   GCATT GGGGAA
                                | |||   ||||| ||||||
                                G TGA   CGTGA CCCCTT
                                 T   TT_    A
GAM582  ABCB4     5'  CACATTATGCTCCTTGGGGA  7768      C  T   A__
                                CACA TT TGC   TTGGGGA
                                |||| || |||   |||||||
                                GTGT AA ACG   AACCCCT
                                  _ T   AGG
GAM582  ACAD8     3'  CACACCTTTGCTCTAGAA    30789          A
                                CACACTTTTGC TTGGGG
                                |||||||||||| ||||||
                                GTGTGGAAACG GATCTT
                                       A
GAM582  AHR       3'  TAACTTTGTATTTGGGGAA   11549   C    TGCA
                                A ACTTT    TTGGGGAA
                                | |||||    ||||||||
                                A TGAAA    AACCCCTT
                                 T    CATA
GAM582  AP2B1     3'  CACACTTTTCCTTCTGGAA   10481        GCA  GG
                                CACACTTTT   TT  GGAA
                                |||||||||   ||  ||||
                                GTGTGAAAA   AA  CCTT
                                      GG_  GA
GAM582  AQP6      5'  CTATTAGAGATTGGGGAA    11639    T   C__
                                CT TTG   ATTGGGGAA
                                || |||   |||||||||
                                GA AAT   TAACCCCTT
                                  T   CTC
GAM582  ARCN1     3'  ACACTCTTTGCAGGGA      11646        _   TTG
                                ACACTTTT GCA   GGGA
                                |||||||| |||   ||||
                                TGTGAGAA CGT   CCCT
                                     A   ___
GAM582  ATP5J     5'  CACACTTCTAGTCGCGGGA   11768          CA  _
                                CACACTTTTG  TTG GGGA
                                ||||||||||  ||| ||||
```

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                                GTGTGAAGAT  AGC CCCT
                                     C_  G
GAM582  ATSV    3'  CACCCTTTCCTGGGGAA    20220       GCA
                                CACTTTT  TTGGGGAA
                                |||||||  ||||||||
                                GTGGGAA  GACCCCTT
                                   AG_
GAM582  AXL     3'  CACACCCCCACAGTTGGGGA  34881       TG _
                                CACACTTT  CA TTGGGGA
                                ||||||||  || |||||||
                                GTGTGGGG  GT AACCCCT
                                     GT  C
GAM582  B4GALT1  3'  CACATTCATGCTGGGGAA   11279     C  T   AT
                                CACA TT TGC  TGGGGAA
                                |||| || |||  |||||||
                                GTGT AG ACG  ACCCCTT
                                  A  T  __
GAM582  BAIAP3   3'  CACACTGGGCCTGGGGAA   19454       TTT  A
                                CACACT  GC TTGGGGAA
                                ||||||  || ||||||||
                                GTGTGA  CG GACCCCTT
                                   CC_ _
GAM582  BAK1    3'  ACACTTTCTGGGGA       45103        GCAT
                                ACACTTTT   TGGGGA
                                ||||||||   ||||||
                                TGTGAAAG   ACCCCT
                                     _____
GAM582  BAZ2B    5'  ACACCTTTTTCGGGAA     30320        GCA
                                ACACTTTT  TTGGGGA
                                ||||||||  |||||||
                                TGTGGAAA  AGCCCTT
                                     A__
GAM582  BCAT1    3'  ACATTTTTGGCACCAGGGA   42374     C    _  TG
                                ACA TTTTG CAT  GGGA
                                ||| ||||| |||  ||||
                                TGT AAAAC GTG  CCCT
                                  A    C  GT
GAM582  BCL11B   3'  CACATTTTGCTTAGAG      39744     C     A
                                CACA TTTTGC TTGGGG
                                |||| |||||| ||||||
                                GTGT AAAACG AATCTC
                                     _    _
GAM582  C18orf1  3'  CACACTTTGCTGGAA       41212        T  AT
                                CACACTTT GC  TGGGG
                                |||||||| ||  |||||
                                GTGTGAAA CG  ACCTT
                                     _ ___
GAM582  CACNG3   5'  CACTGGAGCCCATTGGGGAA  27230     TTT __
                                CACT  GC  ATTGGGGAA
                                ||||  ||  |||||||||
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                                GTGA  CG  TAACCCCTT
                                  CCT  GG
GAM582  CANX    3'  CACACATTTGCTTCAAGGA   44661      T    A TG
                                CACAC TTTGC T  GGGA
                                ||||| ||||| |  ||||
                                GTGTG AAACG A  TCCT
                                   T    A GT
GAM582  CAT     3'  CATTTTCCCCTGGGGAA    11986    C   GCA
                                CA TTTT   TTGGGGAA
                                || ||||   ||||||||
                                GT AAAG   GACCCCTT
                                 A   GG_
GAM582  CD1D    3'  CACACCTTTGCACTTCTGA   44294           GGG
                                CACACTTTTGCATT   GA
                                ||||||||||||||   ||
                                GTGTGGAAACGTGA   CT
                                         AGA
GAM582  CDH6    3'  ACACTTTTGTTTAAGGGAA   22320        CATT
                                ACACTTTTG   GGGGAA
                                |||||||||   ||||||
                                TGTGAAAAC   TCCCTT
                                     AAAT
GAM582  CLN5    5'  CACACTTTGCAGTCCAGGAA  27078       T  _  G
                                CACACTTT GCA TT GGGAA
                                |||||||| ||| || |||||
                                GTGTGAAA CGT AG TCCTT
                                    _  C  G
GAM582  COL1A2  3'  CATACTTTTAATTGGGAA    6386    C     C
                                CA ACTTTTG ATTGGGGA
                                || ||||||| ||||||||
                                GT TGAAAAT TAACCCTT
                                 A     _
GAM582  DAF     3'  ACACTTTTAGGAAAGGAA    8205        CATT
                                ACACTTTTG   GGGGAA
                                |||||||||   ||||||
                                TGTGAAAAT   TTCCTT
                                     CCT_
GAM582  DAPP1   3'  CACAGTTTTGTCATTAGAA   30812     C    _
                                CACA TTTTG CATTGGGG
                                |||| ||||| ||||||||
                                GTGT AAAAC GTAATCTT
                                  C    A
GAM582  DDX11   3'  CACACTTTTATTTAAGGA    36167        CA
                                CACACTTTTG  TTGGGGA
                                ||||||||||  |||||||
                                GTGTGAAAAT  AATTCCT
                                     A_
GAM582  DDX11   3'  CAGACCTGATGTTGGGGAA   36168   CT   CA_
                                CA  TTTG   TTGGGGAA
                                ||  ||||   ||||||||
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                                GT  GGAC   AACCCCTT
                                 CT    TAC
GAM582  DYT1    3'  CACCTTTTGCAAAACGGAG   6472      A       T__
                                CAC CTTTTGCA   TGGGG
                                ||| ||||||||   |||||
                                GTG GAAAACGT   GCCTC
                                  _       TTT
GAM582  EGFL5   5'  CACATTTATTGCAGTTCGGG   44518     CTT_    _ G
                                CACA    TTGCA TT GGG
                                ||||    ||||| || |||
                                GTGT    AACGT AA CCC
                                  AAAT     C  G
GAM582  EPHA8   3'  CATTTTTGCATTGTCAGGA    33892    C         __
                                CA TTTTGCATTG  GGGA
                                || ||||||||||  ||||
                                GT AAAACGTAAC  TCCT
                                 A         AG
GAM582  EPHB2   3'  CACACTTTCTCTCCAGGGAA   32663          GCA TG
                                CACACTTTT   T  GGGAA
                                |||||||||   |  |||||
                                GTGTGAAAG   G  CCCTT
                                     AGA GT
GAM582  FGFR2   3'  ACAGTTGCCCTGTTGGGGAA   35706    TT    A___
                                AC  TTGC    TTGGGGAA
                                ||  ||||    ||||||||
                                TG  AACG    AACCCCTT
                                 TC    GGAC
GAM582  FLRT2   3'  ACACTTTTAAAGGGA       29834         CATT
                                ACACTTTTG    GGGGA
                                |||||||||    |||||
                                TGTGAAAAT    TCCCT
                                     T___
GAM582  GAP43   3'  CACACTGTTTGACTTGGGA    13045       _    CA
                                CACACT TTTG  TTGGGG
                                |||||| ||||  ||||||
                                GTGTGA AAAC  AACCCT
                                   C    TG
GAM582  GRLF1   3'  CACACTCCTGGGGA        44223        TTGCA
                                CACACTT    TTGGGGA
                                |||||||    |||||||
                                GTGTGAG    GACCCCT
                                     _____
GAM582  IL12B   3'  CACATTTTGCATAATAGGGA   13518     C       __
                                CACA TTTTGCAT  TGGGGA
                                |||| ||||||||  ||||||
                                GTGT AAAACGTA  ATCCCT
                                  _       TT
GAM582  ITGBL1  5'  CACTTCTGCAAGGTGGGG    21985          T__
                                CACTTTTGCA   TGGGG
                                ||||||||||   |||||
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                                GTGAAGACGT   ACCCC
                                     TCC
GAM582  ITPKB    3'  CACACTACATTGGGGAA     13642       TTT
                                CACACT   GCATTGGGGAA
                                ||||||   ||||||||||||
                                GTGTGA   TGTAACCCCTT
                                  ___
GAM582  KIAA0442 3'  ACCCTTTTGCATATATGAA   31786    A       TGGG
                                AC CTTTTGCAT    GAA
                                || |||||||||    |||
                                TG GAAAACGTA    CTT
                                 G        TATA
GAM582  KIF3B    3'  CACTTTTAGTACAGACGGGG   22030       ___    T_
                                CACTTT   TGCA  TGGGG
                                ||||||   ||||  |||||
                                GTGAAA   ATGT  GCCCC
                                    ATC    CT
GAM582  M17S2    3'  CACACTTCTGTAAACAGAG    36586         CAT_
                                CACACTTTTG    TGGGG
                                ||||||||||    |||||
                                GTGTGAAGAC    GTCTC
                                     ATTT
GAM582  MAP3K7IP1 3'  CACGCCTGGCTCTGGGGAA   25922     A   TT  A
                                CAC CTT  GC TTGGGGAA
                                ||| |||  || ||||||||
                                GTG GGA  CG GACCCCTT
                                  C   C_  A
GAM582  MBL2     3'  CTTATTACATGTTGGGGAA    6961      _     __
                                CTT TTGCAT  TGGGGAA
                                ||| ||||||  |||||||
                                GAA AATGTA  ACCCCTT
                                  T     CA
GAM582  MBNL     3'  CACATTTTGCATTTTTGA     34309      C       GGG
                                CACA TTTTGCATT   GA
                                |||| |||||||||   ||
                                GTGT AAAACGTAA   CT
                                  _        AAA
GAM582  MVK      3'  CACACTTCTCCGGGAA      41338         GCA
                                CACACTTTT   TTGGGGA
                                |||||||||   |||||||
                                GTGTGAAGA   GGCCCTT
                                     ___
GAM582  NDUFS5   3'  CACACTTTGACAAGGAG     21242        T   TT
                                CACACTTT GCA  GGGG
                                |||||||| |||  ||||
                                GTGTGAAA TGT  CCTC
                                     C   T_
GAM582  OCA2     3'  ACATTTTGTCCTTGGGGA    41188     C    CA_
                                ACA TTTTG   TTGGGGA
                                ||| |||||   |||||||
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                                TGT AAAAC   AACCCCT
                                  _    AGG
GAM582  PACE4    5'  CATTTCACCTGGGGAA     39687    C   TG A
                                CA TTT  C TTGGGGAA
                                || |||  | ||||||||
                                GT AAA  G GACCCCTT
                                  _  GT _
GAM582  PDE4D    3'  CACACTTTGGCAAGAG      43892        T   TT
                                CACACTTT GCA  GGGG
                                |||||||| |||  ||||
                                GTGTGAAA CGT  TCTC
                                     C  __
GAM582  PIK3R3   3'  CAATTGACAGTTTGGGGAA   41436   TT  _ __
                                C  TTG CA  TTGGGGAA
                                |  ||| ||  ||||||||
                                G  AAC GT  AACCCCTT
                                 TT   T  CA
GAM582  PPP1R12B 3'  CACACTTTCGTGGGA       36968         CAT
                                CACACTTTTG   TGGGG
                                ||||||||||   |||||
                                GTGTGAAAGC   ACCCT
                                       ___
GAM582  PPP4C    3'  CACCCTCTTGGGGGA       15530     A     CATT
                                CAC CTTTTG    GGGGA
                                ||| ||||||    |||||
                                GTG GAGAAC    CCCCT
                                  G     _____
GAM582  PRKAB1   3'  CATTCCCTCTTGGGGAA     26501    C    GCA
                                CA TTTT   TTGGGGAA
                                || ||||   ||||||||
                                GT AGGG   AACCCCTT
                                 A   AG_
GAM582  PRKCN    3'  CACATCTTAAACTTTGGGGAA  25157     _   TT  A
                                CACA CTT  GC TTGGGGAA
                                |||| |||  || ||||||||
                                GTGT GAA  TG AACCCCTT
                                  A   TT  A
GAM582  PSEN2    3'  CACACTCTTTGCGCATCTCAG  29810         ___    GG
                                CACACTTTT   GCATT  GG
                                |||||||||   |||||  ||
                                GTGTGAGAA   CGTAG  TC
                                     ACG    AG
GAM582  PSMC1    3'  CACGCTTTATTGGGAA      15831     A   TGC
                                CAC CTTT   ATTGGGGA
                                ||| ||||   ||||||||
                                GTG GAAA   TAACCCTT
                                  C   ___
GAM582  RAD52    3'  CACACCTGAAATGGGGAA    39555        TTGCAT
                                CACACTT     TGGGGAA
                                |||||||     |||||||
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                                GTGTGGA     ACCCCTT
                                    CTTT__
GAM582  SERPINB13 3'  CACAATATCTGTTGGGGAA   29621     CT_   CA
                                CACA   TTTG  TTGGGGAA
                                ||||   ||||  ||||||||
                                GTGT   AGAC  AACCCCTT
                                  TAT   __
GAM582  SERPINE1  3'  CACCCTGTAATTGGGGAA    8285       TGC
                                CACTTT   ATTGGGGAA
                                ||||||   |||||||||
                                GTGGGA   TAACCCCTT
                                    CAT
GAM582  SLC1A2    3'  CACATTTCTGCATCTTGGGA   41596     C       G_
                                CACA TTTTGCATT  GGGA
                                |||| |||||||||  ||||
                                GTGT AAGACGTAG  CCCT
                                  A        AA
GAM582  SNX9      3'  ACACTTTTCCATCTAATGGGGA 32145        G  ____
                                ACACTTTT CAT    TGGGGA
                                |||||||| |||    ||||||
                                TGTGAAAA GTA    ACCCCT
                                    G   GATT
GAM582  SPARC     3'  ACATTTTAAACATTGGGG    17062     C   T_
                                ACA TTT  GCATTGGGG
                                ||| |||  |||||||||
                                TGT AAA  TGTAACCCC
                                  A   TT
GAM582  STAU      3'  CACACTTCTGTGTACAG     32691         CAT  G
                                CACACTTTTG   TG GG
                                ||||||||||   || ||
                                GTGTGAAGAC   AT TC
                                      AC_  G
GAM582  TEM8      3'  ACACTGTGAGCCTGGGGAA   38171      TTT_  A
                                ACACT    GC TTGGGGAA
                                |||||    || ||||||||
                                TGTGA    CG GACCCCTT
                                   CACT  _
GAM582  TMEM2     3'  ACACTTTATGCGTCGGGG    30149        _   A
                                ACACTTT TGC TTGGGG
                                ||||||| ||| ||||||
                                TGTGAAA ACG AGCCCC
                                    T   C
GAM582  TMEM2     3'  CAGACTTTTGCTGCAGGAA   30151    C       AT
                                CA ACTTTTGC  TGGGGA
                                || ||||||||  ||||||
                                GT TGAAAACG  GTCCTT
                                 C       AC
GAM582  TNS       3'  CACATGCCTTGGGGA       35465      CTTT   A
                                CACA    TGC TTGGGGA
                                ||||    ||| |||||||
```

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                                GTGT   ACG AACCCCT
                                  ____  G
GAM582  TRAF1    3'  CTCCTGCGTGTTGGGGAA   24943       A__
                                CTTTTGC  TTGGGGAA
                                |||||||  ||||||||
                                GAGGACG  AACCCCTT
                                   CAC
GAM582  TRIM14   3'  CACATTTCTGACTGGAG    37695     C   C
                                CACA TTTTG ATTGGGG
                                |||| ||||| |||||||
                                GTGT AAGAC TGACCTC
                                  A   _
GAM582  VEGF     3'  CACATTCTTGGGCAGGGGA   17943     C   CATT
                                CACA TTTTG   GGGGA
                                |||| |||||   |||||
                                GTGT AGAAC   CCCCT
                                  A    CCGT
GAM582  ZFP36L1  3'  CACATATGAACTGGGGAA    22280    TTT  C
                                CAC  TG ATTGGGGAA
                                |||  || |||||||||
                                GTG  AC TGACCCCTT
                                 TAT  T
GAM582  ZNF141   3'  TTTTGCATTTCCAGGGGA    18350       ____
                                TTTTGCATT   GGGGA
                                |||||||||   |||||
                                AAAACGTAA   CCCCT
                                    AGGT
GAM582  ZNF26    3'  CACACTTTCAATGGGAA     43795       GCAT
                                CACACTTTT   TGGGGA
                                |||||||||   ||||||
                                GTGTGAAAG   ACCCTT
                                    TT__
GAM582  FMR2     3'  AGTGTGTGTGTGTGTGTA    12950      CAG   A
                                AGTGTG  GTGTG GTA
                                ||||||  ||||| |||
                                TCACAC  CACAC CAT
                                   ACA   A
GAM582  FOXF2    3'  TAAGTGGCAGGTGTGTGGC   11129      T      A_
                                TAAGTG GCAGGTGTG  GT
                                ||||||| |||||||||  ||
                                ATTCAC CGTCCACAC  CG
                                  _       AC
GAM582  HRH1     3'  GTGTGCAAGCTGCATAA     9254        GTGA
                                GTGTGCAGGT   GTAA
                                ||||||||||   ||||
                                CACACGTTCG   TATT
                                    ACG_
GAM583  DLG5     3'  ACAGAAATTGACCTTTATTTG  44442     TGTGGA
                                ACAG    GACCTTTATTTG
                                ||||    ||||||||||||
```

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                                TGTC     CTGGAAATAAAC
                                  TTTAA_
GAM583  EPAC     3'  GTGTGGAGACCTCTCTATTGC  25917           AT_
                                GTGTGGAGACCTTT   TTGC
                                ||||||||||||||  ||||
                                CACACCTCTGGAGA   AACG
                                      GAT
GAM583  FE65L2   3'  CACTGAGGGATTTTTATTTGC  39316    G  T  A  CC
                                CA TG GG GA  TTTATTTGC
                                || || || ||  |||||||||
                                GT AC CC CT  AAATAAACG
                                 G  T  _  AA
GAM583  MGAT4B   3'  CACAGTGTGGGGGCCGCCTGC  38264         AGA  TTTA
                                TACAGTGTGG   CC    TTTGC
                                ||||||||||  ||    |||||
                                GTGTCACACC   GG    GGACG
                                     CCC  C___
GAM583  PRKY     3'  TACAGTGTGGAATTCTGGTTGC  15706          AC  TTAT
                                TACAGTGTGGAG  CT    TTGC
                                ||||||||||||  ||    ||||
                                ATGTCACACCTT  GA    AACG
                                      AA  CC__
GAM583  TKTL1    3'  TACAGTGTGGAGGCTCT     29315           AC
                                TACAGTGTGGAG  CTTT
                                ||||||||||||  ||||
                                ATGTCACACCTC  GAGA
                                      C_
GAM583  TRPC6    3'  TAAGTGTGGGGATTCATCTG   21485   C      A  CC
                                A AGTGTGG GA  TTTATTTG
                                | |||||||  ||  ||||||||
                                A TCACACC CT  AAGTAGAC
                                 T      C  __
GAM583  ATP8B2   3'  TGTAAACTGTGTGGCCAAAAGG  42222           A__  TGC
           GA                     TGTAAACTGTGT   CAG   GGA
                                ||||||||||||  |||   |||
                                ACATTTGACACA   GTT   CCT
                                      CCG   TTC
GAM583  CBFA2T2  3'  TGCAAACTGAGCTTCAGTGTGG  22979         T  A_    C
           AA                     TGTAAACTG GT  CAGTG GGAA
                                |||||||||  ||  ||||| ||||
                                ACGTTTGAC CG  GTCAC CCTT
                                     T  AA    A
GAM583  CD59     3'  TGTAACTGTGTGTGGCAAA   8306       A     ACA  _
                                TGTAA CTGTGT   GTG CGGA
                                ||||| ||||||   ||| ||||
                                ACATT GACACA   CAC GTTT
                                  _     ____  C
GAM583  CLK2     3'  TGGAAACTGTGTGGATGGAA   41280    T       ACA  C
                                TG AAACTGTGT   GTG GGA
                                || |||||||||   ||| |||
```

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                                AC TTTGACACA   TAC CTT
                                 C       CC_  _
GAM583  CRTL1    5'  TGTGAGTGTGTGTGCAGAA   12454    AAAC    ACA
                                TGT   TGTGT  GTGCGGAA
                                |||   |||||  ||||||||
                                ACA   ACACA  CACGTCTT
                                  CTC_    ___
GAM583  DDEF1    3'  TGTAAACTGTGTACACAGA   40569           AGT
                                TGTAAACTGTGTAC  GCGGA
                                ||||||||||||||  |||||
                                ACATTTGACACATG  TGTCT
                                          ___
GAM583  IL7R     3'  TGCAGACTGTGTAGTGGG    13516     A     AC   C
                                TGTA ACTGTGT  AGTG GG
                                |||| |||||||  |||| ||
                                ACGT TGACACA  TCAC CC
                                  C      __   _
GAM583  ITGA4    5'  TGTAAACCCCAGTGTGG     9427        GTGTA    C
                                TGTAAACT    CAGTG GG
                                ||||||||    ||||| ||
                                ACATTTGG    GTCAC CC
                                     G____    A
GAM583  MX2      3'  TGTAACTGTGTGCTACGG    14698      A     ACAG
                                TGTAA CTGTGT   TGCGG
                                |||||  ||||||   |||||
                                ACATT GACACA   ATGCC
                                   _     CG__
GAM583  PIK3CA   3'  TATTAACAGTGCAGTGTGGAA  26319    A   T   TA    C
                                TGT AAC GTG  CAGTG GGAA
                                ||| ||| |||  ||||| ||||
                                ATA TTG CAC  GTCAC CCTT
                                  A   T   __    A
GAM583  PPP1R11  3'  TGTAACTGTGTATGGCAAAA  45511      A      CAGT
                                TGTAA CTGTGTA   GCGGAA
                                |||||  |||||||   ||||||
                                ACATT GACACAT   CGTTTT
                                   _      AC__
GAM583  PPP1R3C  3'  TGTGAGTTGTGTACACTGAC  23994    AAAC      G  _
                                TGT   TGTGTACA TG C
                                |||   ||||||||  || |
                                ACA   ACACATGT AC G
                                  CTCA       G  T
GAM583  PPP4R1   3'  TGTAAATGTGTACAGCA     23079       C
                                TGTAAA TGTGTACAGTG
                                ||||||  ||||||||||
                                ACATTT ACACATGTCGT
                                       _
GAM583  PROML1   3'  TGTAAACTGGTGTGTGTTCAGC 25688         _____    A
                                TGTAAACT    GTGT CAGT
                                ||||||||    |||| ||||
```

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                                ACATTTGA    CACA GTCG
                                    CCACA   A
GAM583  RHBG    3'  TGTAACTGTGTGACGTGGG   33824      A    ACA  C
                                TGTAA CTGTGT  GTG GG
                                ||||| ||||||  ||| ||
                                ACATT GACACA  CAC CC
                                  _    CTG  _
GAM583  SLC6A12  3'  TGCAAGAACAGTGCGGAA   16803      ACTGTGT
                                TGTAA     ACAGTGCGGAA
                                |||||     ||||||||||
                                ACGTT     TGTCACGCCTT
                                  CT_____
GAM583  TM4SF4   5'  TGTGAACTGTGTCCTTGGA   21459    A      ACAGTGC
                                TGT AACTGTGT     GGA
                                ||| ||||||||     |||
                                ACA TTGACACA     CCT
                                  C      GGAA___
GAM583  UBE2B    3'  TGCGAATTATATAGTGCGGAA  17798    TA  C    AC
                                TG  AA TGTGT  AGTGCGGAA
                                ||  || |||||  |||||||||
                                AC  TT ATATA  TCACGCCTT
                                 GC  A    __
GAM584  NPY2R    5'  CAGAGCGGCTGGGCGGTTGGCG 9488         A  T  A_  A
          CT                    CAGAGCGGC GG CG  TG CGCT
                                |||||||||| || ||  || ||||
                                GTCTCGCCG CC GC  AC GCGA
                                     A  C  CA  C
GAM584  NR2E1    3'  CAGGGCGGCAGGTCATAGCT   17574    A       G   AC
                                CAG GCGGCAGGTC ATG  GCT
                                ||| |||||||||| |||  |||
                                GTC CGCCGTCCAG TAT  CGA
                                  C        _  __
GAM584  SFRP5    3'  GATGACGCGTACAGGGGCG   16594        TC   CTTGA
                                GATGACGC  GCA    GGCG
                                ||||||||  |||    ||||
                                CTACTGCG  TGT    CCGC
                                     CA   CC___
GAM585  ATP6IP1  3'  ACCCGTGTACTGCTTATTG   10143     AT    CTATATG
                                ACCC  TGTAC      TATTG
                                ||||  |||||      |||||
                                TGGG  ACATG      ATAAC
                                  C_    ACGA___
GAM585  PKDREJ   3'  ACCCATATGTACCTTTTTGT   25875       _     ATA
                                ACCCAT TGTACCT   TGT
                                ||||||  |||||||  |||
                                TGGGTA ACATGGA   ACA
                                   T      AAA
GAM585  POP4     3'  TGTCCACATATGTATTGT    27367     A  _
                                TGT CC TATATGTATTGT
                                ||| ||  ||||||||||||
```

```
                                ACA GG GTATACATAACA
                                  _ T
GAM585  STC1    3'  TGTAGATATATGTATTGT    17186     CC
                                TGTA  TATATGTATTGT
                                ||||  ||||||||||||
                                ACAT  ATATACATAACA
                                  CT
GAM585  TLL1    3'  ACCCAATTGTATTCAATGT   29731      _    CCTAT
                                ACCCA TTGTA    ATGT
                                ||||| |||||    ||||
                                TGGGT AACAT    TACA
                                   T    AAGT_
GAM585  UCP3    3'  TAGGCATGCCTAATGGGTTT  17855    ACA    __
                                TAG   CATGT  AGTGGGTTT
                                |||   |||||  |||||||||
                                ATC   GTACG  TTACCCAAA
                                  C__    GA
GAM586  EPB41L2  3'  TATACATAGGGTCAAAGGCAAA 11007         CTAG    A
           G                     TATACGTAGG    GAAG CAAAG
                                ||||||||||    |||| |||||
                                ATATGTATCC    TTTC GTTTC
                                      CAG_    C
GAM586  SRI     3'  TATACATATTACCGAAGGCAAA 17110        G_  AG    A
           G                     TATACGTA  GCT  GAAG CAAAG
                                ||||||||  |||  |||| |||||
                                ATATGTAT  TGG  CTTC GTTTC
                                     AA   __    C
GAM586  CDH20   3'  CCACCCTTGTCAGAACACC   36681     G  GC_  _
                                CCA CC   TTA AACACC
                                ||| ||   ||| ||||||
                                GGT GG   AGT TTGTGG
                                  G  AAC   C
GAM586  EMS1    5'  CCAGCCGCTCCCAGGCACC   39738          AAA__
                                CCAGCCGCTT    CACC
                                ||||||||||    ||||
                                GGTCGGCGAG    GTGG
                                      GGTCC
GAM586  GALC    3'  CCAGCCACCTGGAAAAAC    6672          _____
                                CCAGCCGCTT    AAAC
                                ||||||||||    ||||
                                GGTCGGTGGA    TTTG
                                      CCTT
GAM586  GALNS   3'  CCAGCCACCTCGGGCACC    8008          AAA_
                                CCAGCCGCTT    CACC
                                ||||||||||    ||||
                                GGTCGGTGGA    GTGG
                                      GCCC
GAM586  GDF5    5'  CCAGCCGCTGAATGACACC    8144          T __
                                CCAGCCGCT AA  ACACC
                                ||||||||| ||  |||||
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                                GGTCGGCGA TT  TGTGG
                                     C  AC
GAM586  IL6R     3'  CCAGCCGCTTCTCCACACC   8170          AA__
                                CCAGCCGCTT    ACACC
                                ||||||||||    |||||
                                GGTCGGCGAA    TGTGG
                                     GAGG
GAM586  MLH3     5'  CCAACCGCCTCGGACGCC    30779          AA_  A
                                CCAGCCGCTT   AC CC
                                ||||||||||   || ||
                                GGTTGGCGGA   TG GG
                                     GCC  C
GAM586  STCH     3'  CCAACCACTGTAAATACC    28079          _    C
                                CCAGCCGCT TAAA ACC
                                ||||||||| |||| |||
                                GGTTGGTGA ATTT TGG
                                     C    A
GAM586  STK11    3'  CCAGCAGCTCCCAAACACC   7831        C   __
                                CCAGC GCTT  AAACACC
                                ||||| ||||  |||||||
                                GGTCG CGAG  TTTGTGG
                                   T    GG
GAM587  ARD1     5'  GCGCTCCGAAGCGACGCC    18572          AAA
                                GCGCTCCGAA   CGACGCC
                                ||||||||||   |||||||
                                CGCGAGGCTT   GCTGCGG
                                     C__
GAM587  BZRP     5'  ACGCTCCGGGAAGGGCACTGCC 28698         AAAAACGA   C
                                GCGCTCCG       CGC GCC
                                ||||||||       ||| |||
                                TGCGAGGC       GTG CGG
                                     CCTTCCC_   A
GAM587  CACNA1C  3'  GCGCCCCGGGACCCTCGCCGCC 8755          AAAAACGA
                                GCGCTCCG       CGCCGCC
                                ||||||||       |||||||
                                CGCGGGGC       GCGGCGG
                                     CCTGGGA_
GAM587  CALCB    3'  GCTCCGAAAGAACCA       44711          AAC  C
                                GCTCCGAAA   GA GCCG
                                |||||||||   || ||||
                                CGAGGCTTT   CT TGGT
                                     ___  _
GAM587  CDC34    5'  GCGCTCCAGCAGCTCTGGCGCC 20355         AAAAACGA__
           GCC                    GCGCTCCG         CGCCGCC
                                ||||||||         |||||||
                                CGCGAGGT         GCGGCGG
                                     CGTCGAGACC
GAM587  CNTNAP2  5'  GCGCTCCAAGAGCTCGC     30487          AAAAC  C  _
                                GCGCTCCGA    GA GC CGC
                                |||||||||    || || |||
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                                CGCGAGGTT    CT CG GCG
                                      _____ _  A
GAM587  EP300    5'  GCGCTCCGCGCCGCCGC     10987        AAAAA  A
                                GCGCTCCG    CG CGCCGC
                                ||||||||    || ||||||
                                CGCGAGGC    GC GCGGCG
                                     _____  G
GAM587  FGF2     5'  CTCCGCGGACGCCGCC      12837      AAAAAC
                                CTCCG     GACGCCGCC
                                |||||     |||||||||
                                GAGGC     CTGCGGCGG
                                  GC____
GAM587  FLT1     5'  CGCTCCGAGCCGCCGC      12910        AAAACGA
                                CGCTCCGA      CGCCGC
                                ||||||||      ||||||
                                GCGAGGCT      GCGGCG
                                     CG_____
GAM587  IGJ      5'  GCGCTCCGGCGCCATGGCCGC  40342        AAAAA  AC
                                GCGCTCCG    CG  GCCGC
                                ||||||||    ||  |||||
                                CGCGAGGC    GT  CGGCG
                                     CGCG_  AC
GAM587  IRS2     5'  GCGCTCCGGGAAGCCGGGGTGC 40706        A_  AA  A____
           GCC                    GCGCTCCG  AA  CG    CGCC
                                ||||||||  ||  ||    ||||
                                CGCGAGGC  TT  GC    GCGG
                                     CC  CG  CCCAC
GAM587  KCNS3    5'  CGCTCTGCGACGCCGC      13934      CGAAAAA
                                CGCTC      CGACGCCGC
                                |||||      |||||||||
                                GCGAG      GCTGCGGCG
                                  AC_____
GAM587  M11S1    5'  GCGCTCCGTGGGCGCAGGCCGC 25329        AAAAA  AC_
                                GCGCTCCG    CG   GCCGC
                                ||||||||    ||   |||||
                                CGCGAGGC    GC   CGGCG
                                     ACCC_  GTC
GAM587  PITPN    3'  GCGTCCGAAAATGGCC      26340     C       ACGAC
                                GCG TCCGAAAA     GCC
                                ||| ||||||||     |||
                                CGC AGGCTTTT     CGG
                                  _       AC___
GAM587  RTN2     5'  GCGCCCACGACGCCG       24725       CGAAAA
                                GCGCTC     ACGACGCCG
                                ||||||     |||||||||
                                CGCGGG     TGCTGCGGC
                                     _______
GAM587  SPK      5'  ACGCTCCGACGGGTGACGC    22070         AAAAC
                                GCGCTCCGA    GACGC
                                |||||||||    |||||
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                                TGCGAGGCT    CTGCG
                                     GCCCA
GAM587  TCN2    5'  CGCTCCGAGAGACGCAGC    7404        AAAAC    C
                                CGCTCCGA    GACGC GC
                                ||||||||    ||||| ||
                                GCGAGGCT    CTGCG CG
                                     CT___    T
GAM587  ZNF198  5'  GCGCTCCGCGGAACGAACC    18369       AAA    C
                                GCGCTCCG   AACGA GCC
                                ||||||||   ||||| |||
                                CGCGAGGC   TTGCT TGG
                                     GCC    _
GAM587  CYLN2   5'  TCTCGGGCCCGGGCGCGC    18062       AAAC  _
                                TCTCGGGCC    GC CGT
                                |||||||||    || |||
                                AGAGCCCGG    CG GCG
                                     GCC_  C
GAM587  IGFBP4  3'  TCTTGGGCTAAGTGCCAGTC   11408    C    C  AC   _
                                TCT GGGC AA  GCC GTC
                                ||| |||| ||  ||| |||
                                AGA CCCG TT  CGG CAG
                                  A    A  CA   T
GAM587  NPY2R   5'  TCTCAGGCCAAGCGCGCC    9502          A   C
                                TCTCGGGCCAA CGC GTC
                                |||||||||||| ||| |||
                                AGAGTCCGGTT GCG CGG
                                     C   _
GAM587  OSCAR   3'  TCTCGGGCTGCAGTGC      39312       CAAAC  C  C
                                TCTCGGGC    GC GT GT
                                ||||||||    || || ||
                                AGAGCCCG    CG CA CG
                                     A____  T  _
GAM587  PTGFRN  5'  CCTCGGGCCGGACGTCATCG   42589       AA   C
                                TCTCGGGCC  ACG CGTCG
                                |||||||||  ||| |||||
                                GGAGCCCGG  TGC GTAGC
                                     CC   A
GAM587  RPP30   3'  TCTCGGGCCGGGCGCAGT    26940       AAA   C
                                TCTCGGGCC   CGC GT
                                |||||||||   ||| ||
                                AGAGCCCGG   GCG CA
                                     CCC   T
GAM587  SORCS2  3'  CCTCGGGCTGAGCGACAGCACG 34052       CAAA  _ C  _
          T                     TCTCGGGC    CG C GT CGT
                                ||||||||    || | || |||
                                GGAGCCCG    GC G CG GCA
                                     ACTC  T T  T
GAM587  TCL1B   3'  TCGGGCCAAAGTGTCAGCAGA  22257         CGCC   _
                                TCGGGCCAAA    GTC GTAGA
                                ||||||||||    ||| |||||
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```
                                AGCCCGGTTT   CAG CGTCT
                                      CA__   T
GAM588  ELMO1    3'  GCTCTTGTCCCACCAGTGGAC  39049       G      A_
                                GCTCTTG CCCACCAG  GAC
                                ||||||| ||||||||  |||
                                CGAGAAC GGGTGGTC  CTG
                                    A       AC
GAM588  FMOD     3'  TTGGCCCATTGCAGATGCTG   12935       C__   GACA
                                TTGGCCCA   CAGA   CTG
                                ||||||||   ||||   |||
                                AACCGGGT   GTCT   GAC
                                     AAC   AC__
GAM588  HSPG2    3'  TCTGGGCCCACCCAGCCACTG  24370     T      AG  A
                                TCT GGCCCACC  AG CACTG
                                ||| ||||||||  || |||||
                                AGA CCGGGTGG  TC GTGAC
                                  C       G_  G
GAM588  ITGA1    5'  GCTCTTGGTCTCTGAAATCTCA 41846       CCCACCA   ___
            CTG                    GCTCTTGG      GAGA   CACTG
                                ||||||||      ||||  |||||
                                CGAGAACC      CTTT   GTGAC
                                     AGAGA__   AGA
GAM588  LAMP2    3'  GCTCTTGGCTCACCGCAACCTC 30386        C   AGA   A_
            TG                   GCTCTTGGC CACC   GAC  CTG
                                ||||||||| ||||   |||  |||
                                CGAGAACCG GTGG   TTG  GAC
                                     A   CG_   GA
GAM588  ODC1     3'  GCTTTTGGCCCATTCTGCCA   14921     C      _____
                                GCT TTGGCCCA     CCA
                                ||| ||||||||     |||
                                CGA AACCGGGT     GGT
                                  A       AAGAC
GAM588  SLC7A7   5'  GCTCTTGGCTCAGCACT     19577        CCAC   AGA
                                GCTCTTGGC    CAG   CACT
                                |||||||||    |||   ||||
                                CGAGAACCG    GTC   GTGA
                                     A___   ___
GAM589  CACNA2D2 3'  GAGTGTGTAAGGGCCAGA    25716    T      AACA
                                GA GTGTGTAA    CCGGA
                                || ||||||||    |||||
                                CT CACACATT    GGTCT
                                 _       CCC_
GAM589  CD1B     3'  AATGTGTGTAAAATCAGG     12083          _  CC
                                GATGTGTGTAAAA CA  GG
                                |||||||||||| ||  ||
                                TTACACACATTTT GT  CC
                                       A  __
GAM589  FMR1     3'  GATGTGTGCAAGGTACCAA    12940          AAC
                                GATGTGTGTAA   ACCGG
                                ||||||||||   |||||
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                                CTACACACGTT   TGGTT
                                      CCA
GAM589  HD      3'  TGTGTGTAAAATTATAGA    13369          CACC
                                TGTGTGTAAAA    GGA
                                ||||||||||    |||
                                ACACACATTTT    TCT
                                      AATA
GAM589  KPNA1    3'  GATGTGTGTAAGAGA      44317          AAACACC
                                GATGTGTGTA      GGAGA
                                ||||||||||      |||||
                                CTACACACAT      TCTCT
                                      _______
GAM589  LARS2    3'  CGCTGTGGCTTGGACACCGGAG 31679    A    T  AAA_
                                CG TGTG GT    ACACCGGAG
                                || |||| ||    |||||||||
                                GC ACAC CG    TGTGGCCTC
                                 G   _  AACC
GAM589  NPY2R    5'  TGTGTGTAGGAGCAGAGA    9504         AAACAC
                                TGTGTGTA     CGGAGA
                                ||||||||     ||||||
                                ACACACAT     GTCTCT
                                     CCTC__
GAM589  NPY2R    3'  TGTGTGTAGGAGCAGAGA    9504         AAACAC
                                TGTGTGTA     CGGAGA
                                ||||||||     ||||||
                                ACACACAT     GTCTCT
                                     CCTC__
GAM589  OGT      3'  TGTGTTTAAAACACCCTAGGA  18791      G       ___
                                TGTGT TAAAACACC   GGA
                                ||||| |||||||||   |||
                                ACACA ATTTTGTGG   CCT
                                   A        GAT
GAM589  PTEN     3'  TGTGTGTAAATAGCTGGAGA   7222          ACACC
                                TGTGTGTAAA    GGAGA
                                ||||||||||    |||||
                                ACACACATTT    CCTCT
                                      ATCGA
GAM589  RET      3'  GATGTGGTGGGCCCGGGGGAC  33934       T  AAAACA   A_
                                GATGTG GT     CCGG  GAC
                                |||||| ||     ||||  |||
                                CTACAC CA     GGCC  CTG
                                   _  CCCG__    CC
GAM589  RFP      3'  GAAAGTATGAAACACTGGAG   27131    T_    TA     C
                                GA  GTGTG  AAACAC GGAG
                                ||  |||||  |||||| ||||
                                CT  CATAC  TTTGTG CCTC
                                 TT    __     A
GAM589  SIAT1    3'  ATGTGTGTGGCAGGAG      16719        AAAA  CC
                                ATGTGTGT    CA  GGAG
                                ||||||||    ||  ||||
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                                TACACACA   GT  CCTC
                                    CC__  __
GAM589  SPON1    3'  GATGTGTGTAGGAA       41668          AAACACC
                                GATGTGTGTA      GGAG
                                ||||||||||      ||||
                                CTACACACAT      CCTT
                                    ________
GAM589  THBD     3'  TGTGCAAAGTGGATACTGGAGA 7435         AC_____  C
          C                      TGTGTAAA     AC GGAGAC
                                ||||||||      || ||||||
                                ACACGTTT     TG CCTCTG
                                    CACCTA  A
GAM589  APAF1    3'  GCCTGGCATGTGCGCACA    29822     CTT   ATACA
                                GCC   TGG    TGCGCACA
                                |||   |||    ||||||||
                                CGG   ACC    ACGCGTGT
                                  ___   GTAC_
GAM589  C14orf1  3'  GCCTTTTGGATACACACA    28415     C
                                GCC TTTGGATACATGCG
                                ||| ||||||||||||||
                                CGG AAACCTATGTGTGT
                                  A
GAM589  CACNB2   3'  GCTTGTTGGATACATCAACTAC 8793     CCT        GC  _
          A                     GC   TTGGATACAT  GC ACA
                                ||   ||||||||||  || |||
                                CG   AACCTATGTA  TG TGT
                                 AAC         GT  A
GAM589  DDX10    3'  GCCCTTTGGGAATGGGGCA   20574         ATAC   C_
                                GCCCTTTGG    ATG  GCA
                                |||||||||    |||  |||
                                CGGGAAACC    TAC  CGT
                                    CT__   CC
GAM589  F7       3'  GCATATCTGTGTGTGCGCACA  6558     CC_   GATACA
                                GC   TTTG     TGCGCACA
                                ||   ||||     ||||||||
                                CG   AGAC     ACGCGTGT
                                 TAT    ACAC__
GAM589  GSPT1    3'  CCTTTGTAACATGTGCACACA  13307       GAT    C
                                CCTTTG   ACATG GCACACA
                                ||||||   ||||| |||||||
                                GGAAAC   TGTAC CGTGTGT
                                   AT_    A
GAM589  LAMB1    5'  CCTCTGCTCATGCGCATAC    14064       GATA      C
                                CCTTTG    CATGCGCA AC
                                ||||||    |||||||| ||
                                GGAGAC    GTACGCGT TG
                                   GA__       A
GAM589  MSR1     3'  GCCCTTTGGTTGTACATG     39818         A__
                                GCCCTTTGG   TACATG
                                |||||||||   ||||||
```

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                                CGGGAAACC   ATGTAC
                                     AAC
GAM589  PPP1R3C   3'  GCCCTTTGTGTATACTTTTCAC 23989        GA  C  GCG_
           ACA                    GCCCTTTG  TA AT    CACACA
                                |||||||  || ||    ||||||
                                CGGGAAAC  AT TG    GTGTGT
                                     AC  A  AAAA
GAM589  RET     3'  CCCTCTGGGTGTGTGCGCACAC 33931        ATACA
           A                     CCCTTTGG    TGCGCACACA
                                ||||||||    ||||||||||
                                GGGAGACC    ACGCGTGTGT
                                     CACAC
GAM589  RGL     3'  GCATACCAAATACATGTGCA   31542    CCT TG      C
                                GC   T  GATACATG GCA
                                ||   |  |||||||| |||
                                CG   G  TTATGTAC CGT
                                 TAT GT       A
GAM589  TMEM1    3'  GCTTTTTAGATACACATTGCA  17597    CC        GC_
                                GC  TTTGGATACAT   GCA
                                ||  ||||||||||   |||
                                CG  AAATCTATGTG   CGT
                                 AA         TAA
GAM590  NHLH1    5'  GACAAGGGGCAGCGT      24651        T  CATTCT
                                GACAAGGG GC     GCGT
                                |||||||| ||     ||||
                                CTGTTCCC CG     CGCA
                                     _  T_____
GAM590  PRKY     3'  AGACAAGGGTTTCATCATG    15683         GC    C
                                AGACAAGGGT  CATT TG
                                ||||||||||  |||| ||
                                TCTGTTCCCA  GTAG AC
                                     AA    T
GAM590  RAI3     3'  GGGTGCCAGCAAGTTG      19569        TTCT  __
                                GGGTGCCA    GC  GTTG
                                ||||||||    ||  ||||
                                CCCACGGT    CG  CAAC
                                     ____  TT
GAM590  TRIM9    3'  AGCAAGGGCCTTCTGCGTT    38137    A    GT   A
                                AG CAAGG  GCC TTCTGCGTT
                                || |||||  ||| |||||||||
                                TC GTTCC  CGG AAGACGCAA
                                  _    __   _
GAM590  APRT     3'  GGGCAGCCGGTGCCCC      7929        T   ACGACACG   A
                                GGGCAG CCG       GCC CC
                                |||||| |||       ||| ||
                                CCCGTC GGC       CGG GG
                                   _   CA_______   _
GAM590  BDKRB2   5'  GGGCAGCCTGATGTCCCCACC  8405         C  CGACACGG
                                GGGCAGTC GA       CCACC
                                ||||||||  ||       |||||
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                                CCCGTCGG CT       GGTGG
                                     A  ACAGG___
GAM590  BTC      5'  GGGCGTCTGCTCGGCCAC    45540      A   CGACGACA
                                GGGC GTC       CGGCCAC
                                |||| |||       |||||||
                                CCCG CAG       GCCGGTG
                                  _   ACGA____
GAM590  ECH1     5'  GGGCAGTCGATTTCCGGTTGCC 40868        C  CGACA ___
                                GGGCAGTC GA     CG   GCC
                                |||||||| ||     ||   |||
                                CCCGTCAG CT     GC   CGG
                                     _  AAAG_  CAA
GAM590  FTH1     5'  GGGCAGTCCGAGGGTGCGG    42792          CGACA
                                GGGCAGTCCGA     CGG
                                ||||||||||     |||
                                CCCGTCAGGCT     GCC
                                      CCCAC
GAM590  HMX1     3'  GGGCAGTCTGTGGGGACAGTCA 33214        CGACGAC    C
              CC                  GGGCAGTC       ACGG CACC
                                |||||||       |||| ||||
                                CCCGTCAG       TGTC GTGG
                                     ACACCCC    A
GAM590  JUN      3'  GGGCAGCCCGCAGGCGGCC    13746          A  ACA
                                GGGCAGTCCG CG   CGGCC
                                |||||||||| ||   |||||
                                CCCGTCGGGC GT   GCCGG
                                      _  CC_
GAM590  LRP1     3'  GGGCAGTCCGACGGGGCAGGGC 14221           A__  C
              C                   GGGCAGTCCGACG   CA GGCC
                                ||||||||||||   || ||||
                                CCCGTCAGGCTGC   GT CCGG
                                      CCC  C
GAM590  MEN1     3'  GGGTAATTCAAACACGGCTACC 39194     C   C   CG      C
                                GGG AGT CGA  ACACGGC ACC
                                ||| ||| |||  ||||||| |||
                                CCC TTA GTT  TGTGCCG TGG
                                  A   A   __      A
GAM590  PAX2     3'  GGGCAGTCCGGCTGGCAC     19635          ACGACAC   C
                                GGGCAGTCCG      GGC AC
                                ||||||||||      ||| ||
                                CCCGTCAGGC      CCG TG
                                      CGA_____   _
GAM590  PPGB     3'  GGGCAGTCCTGGCGGCAGAACC 7176          GA_  A  CG
                                GGGCAGTCC   CG CA  GCC
                                |||||||||   || ||  |||
                                CCCGTCAGG   GC GT  TGG
                                      ACC  C  CT
GAM590  RPS6KA2  5'  GGGCAGGCCGCGCCGGCCACC  34468       T   A  ACA
                                GGGCAG CCG CG   CGGCCACC
                                ||||||| ||| ||   ||||||||
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                                CCCGTC GGC GC   GCCGGTGG
                                   C   _  G__
GAM590  SEPN1    3'  GGGCAGTCCGGGGTATGGCC   42432          ACGACAC
                                GGGCAGTCCG      GGCC
                                ||||||||||      ||||
                                CCCGTCAGGC      CCGG
                                     CCCATA_
GAM590  TRPV1    5'  AGGCAGTCCTGCGGCCAC    38791          GACGACA
                                GGGCAGTCC      CGGCCAC
                                |||||||||      |||||||
                                TCCGTCAGG      GCCGGTG
                                     AC_____
GAM590  UNRIP    5'  GGGCAATCCGGTGGCA      28423          ACGACAC   C
                                GGGCAGTCCG      GGC A
                                ||||||||||      ||| |
                                CCCGTTAGGC      CCG T
                                     CA_____  _
GAM591  CAV3     3'  AAGGGCCATTGTGCTTCTGTGG 37844     A  _  ATACGA
           C                     AAG GCC TTG     TCTGTGGC
                                 ||| ||| |||     ||||||||
                                 TTC CGG AAC     AGACACCG
                                   C  T  ACGA__
GAM591  ELK3     5'  AGGCGTCTGCAGACGGTCTGTG 23418    A  C_  AT_  A
           GC                    AG GC  TTG   ACG TCTGTGGC
                                 || ||  |||   ||| ||||||||
                                 TC CG  GAC   TGC AGACACCG
                                  _ CA   GTC   C
GAM591  FCGR2B   3'  AAGAGCCTTGATGTCAAGAAGA 19657          ACGATCTGT
           GC                    AAGAGCCTTGAT       GGC
                                 ||||||||||||       |||
                                 TTCTCGGAACTA       TCG
                                      CAGTTCTTC
GAM591  LIG4     5'  AAGAGTCTGTGACATCTTTGTG 14162      C  _    CGATC
           G                     AAGAG CT TGATA    TGTGG
                                 ||||| || |||||    |||||
                                 TTCTC GA ACTGT    ACACC
                                   A  C    AGAA_
GAM591  PPP2R5E  5'  AAGAATCCGAAGATGATCTGTG 26463      _  TT_  AC
           GC                    AAGAG CC   GAT  GATCTGTGGC
                                 ||||| ||   |||  ||||||||||
                                 TTCTT GG   CTA  CTAGACACCG
                                   A  CTT  __
GAM591  RGS2     3'  AACAGTACTGATGATCTGTGG  16312    G  CC    AC
                                 AA AG  TTGAT  GATCTGTGG
                                 || ||  |||||  |||||||||
                                 TT TC  GACTA  CTAGACACC
                                  G  AT    __
GAM591  SLC7A7   5'  AAGTGCCTTCCAGGATCTGTGG 19575     A    GA  C
                                 AAG GCCTT  TA GATCTGTGG
                                 ||| |||||  || |||||||||
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                                TTC CGGAA  GT CTAGACACC
                                  A    G_  C
GAM591  CLASPIN  3'  TCCATGAGTTGTTGA      35224       TTAA
                                TCCATG   GGTTGTTGA
                                ||||||   |||||||||
                                AGGTAC   TCAACAACT
                                   ____
GAM591  DLEC1    3'  TCCATGCTGGGGCCAGCGCTG  28851        AA  TT   GA
                                TCCATGTT  GG  GTT  CGCTG
                                ||||||||  ||  |||  |||||
                                AGGTACGA  CC  CGG  GCGAC
                                    __  C_  TC
GAM591  SACS     3'  CAGTTAAGGTTTTCCGTTG   30762    T       ____
                                CA GTTAAGGTT    GTTG
                                || |||||||||    ||||
                                GT CAATTCCAA    CAAC
                                 _       AAGG
GAM592  DSG2     3'  CTGTGTGTCTGTAAGGCTCA  12607     T  A  GC_
                                CTGT GT TC   AAGGCTCA
                                |||| || ||   ||||||||
                                GACA CA AG   TTCCGAGT
                                  _ C  ACA
GAM592  KRTHA7   5'  TACCTGTTGTGGTGCCATCA  19085         ATC  AAGGC
                                TACCTGTTGT   GC    TCA
                                ||||||||||   ||    |||
                                ATGGACAACA   CG    AGT
                                     CCA  GT___
GAM592  KRTHA8   5'  TACCTGTTGTGGTGCCATCA  27669         ATC  AAGGC
                                TACCTGTTGT   GC    TCA
                                ||||||||||   ||    |||
                                ATGGACAACA   CG    AGT
                                     CCA  GT___
GAM592  VNN1     3'  CCTGTTGTGCCCTACTC     21685        ATC  AAG
                                CCTGTTGT   GC   GCTC
                                ||||||||   ||   ||||
                                GGACAACA   CG   TGAG
                                    ___  GGA
GAM592  GDF2     5'  TGCAGGCGGCCGTGCT      32130      ACACGT  AA
                                TGCA     GG  GCCGTGCT
                                ||||     ||  ||||||||
                                ACGT     CC  CGGCACGA
                                  _______  GC
GAM592  P4HB     3'  ACAGGCCACAGGCCGTGCTG  9541      ACA  TG AA
                                GCA   CG  G  GCCGTGCTG
                                |||   ||  |  |||||||||
                                TGT   GT  C  CGGCACGAC
                                  CCG  GT __
GAM592  PFKFB4   3'  TGCACATGAATGGAAGGCTGTG 21298      ACAC_      _ C
            CTGC                   TGCA     GTGGAAG C GTGCTGC
                                ||||     ||||||| | |||||||
```

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                                ACGT    TACCTTC G CACGACG
                                  GTACT     C A
GAM593  ADCY8   5'  CGGACAAAGCCTGCGGC    10004       AACC   CC  A
                                CGGACAA   AGTT  CGG C
                                |||||||   ||||  ||| |
                                GCCTGTT   TCGG  GCC G
                                    ____   AC  _
GAM593  CTBP2   5'  GATGAAACCCTCGTCCCGGACG 35600    CA    AGT_
                                GA  AAACC   TCCCGGACG
                                ||  |||||   |||||||||
                                CT  TTTGG   AGGGCCTGC
                                 AC    GAGC
GAM593  DDC     3'  CAGACAAAATCACAACCCTCTG 8984         C  GTT  ___
           GA                    CGGACAAAA CA   CCC   GGA
                                |||||||||  ||   |||   |||
                                GTCTGTTTT GT   GGG   CCT
                                     A  GTT   AGA
GAM593  GRAF    3'  GGGGAAACCAGTCAGA     31451    ACA      TCC
                                GG   AAACCAGT   CGGA
                                ||   ||||||||   ||||
                                CC   TTTGGTCA   GTCT
                                 CC_      ___
GAM593  KCNK4   5'  CGGGCAAAACCAGGGA     37829     A       TTCCC
                                CGG CAAAACCAG    GGA
                                ||| |||||||||    |||
                                GCC GTTTTGGTC    CCT
                                 C       _____
GAM593  PRIM2A  5'  GGCAGCCAGCTGTTCCCGG   9621     A  AAA    ___
                                GG CA   CCAGT   TCCCGG
                                || ||   |||||   ||||||
                                CC GT   GGTCG   AGGGCC
                                 _ C__     ACA
GAM593  APOL1   3'  TCCAACTGTTCTAACTCT    18940        C   CCG   G
                                TCCAACTG TTC   AAC TCT
                                |||||||| |||   ||| |||
                                AGGTTGAC AAG   TTG AGA
                                     _   A__   _
GAM593  BCL11B  3'  AACTACTTCCTTTTGCGAGACG 39741          _________  ACGTC
           T                     AACTGCTTCC       CGA    T
                                ||||||||||       |||    |
                                TTGATGAAGG       GCT    A
                                     AAAACIII   CTGCA
GAM593  ELF3    3'  CAGCTGCTTCCTTTGCTCG   20750    A      CGAAC T
                                CA CTGCTTCC    G CTCG
                                || ||||||||    | ||||
                                GT GACGAAGG    C GAGC
                                 C       AAA__ _
GAM593  GAD1    5'  TCCAGCTGCTTCCTCGTTCTCG 30295      A      _  AACG
                                TCCA CTGCTTCC CG    TCTCG
                                |||| |||||||| ||    |||||
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                                AGGT GACGAAGG GC    AGAGC
                                  C       A  A___
GAM593  NUP62    5'  TCCAACTGCCTTTCCCGCCCTT 29605          __     AACG_
              TC                    TCCAACTGCT  TCCCG     TC
                                |||||||||| |||||    ||
                                AGGTTGACGG  AGGGC    AG
                                     AA     GGGAA
GAM594  HMGA2    5'  TGAGTGTGTGTGAGTGTGAGT  18530         GTAGCGCT
                                TGAGTGTG       GTGTGAGT
                                ||||||||       ||||||||
                                ACTCACAC       CACACTCA
                                     ACACT___
GAM594  HMGA2    5'  TGAGTGTGTGTGAGTGTGTGTG 18531         _ _  CGC
              AGT                    TGAGTGTG GT AG   TGTGTGAGT
                                |||||||| || ||   |||||||||
                                ACTCACAC CA TC   ACACACTCA
                                     A  C  AC_
GAM594  KCNK7    5'  GAGGAGGTGCTGTGTGG     37858     TGT   AGC       A
                                GAG   GGT   GCTGTGTG G
                                |||   |||   |||||||| |
                                CTC   CCA   CGACACAC C
                                  CT_   ___       C
GAM594  MICB     3'  TGGGTGTGGTGGTGCCTGT    25477     A      A__  G
                                TG GTGTGGT   GC CTGT
                                || |||||||   || ||||
                                AC CACACCA   CG GACA
                                 C       CCA  _
GAM594  MS4A1    3'  TGACTGTGACTGTGTGG      6603      G    GTAGC       A
                                TGA TGTG     GCTGTGTG G
                                ||| ||||     |||||||| |
                                ACT ACAC     TGACACAC C
                                  G    ______       C
GAM594  NPR1     3'  GCGTGTGCCTGTGTGAG      44582       GTA  G
                                GTGTG   GC CTGTGTGAG
                                |||||   || |||||||||
                                CGCAC   CG GACACACTC
                                   A__  _
GAM594  RHD      3'  TGGGTGTGGTAGTGCGCACTTG 32169     A        C  T TG GA
              T                     TG GTGTGGTAG GC G  T  GT
                                || |||||||| || |  |  ||
                                AC CACACCATC CG C  G  CA
                                 C        A  _ GT AA
GAM594  CCR2     3'  CCTGGTTCTAGAAGCCCAGTGT 8498      G   CCAA__
                                CC TGG      AAGCCCAGTGT
                                || |||      ||||||||||
                                GG ACC      TTCGGGTCACA
                                 _   AAGATC
GAM594  FAT2     3'  CCTTTGGCCAAAAGTGCC     11074     CG        C_
                                CC  TGGCCAAAAG  CC
                                ||  ||||||||||  ||
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                                GG  ACCGGTTTTC  GG
                                 AA         AC
GAM594  JRKL     5'  CCTCTTGGCCAAAAGACTTGT  19090    CCG        CCCAG
                                CC   TGGCCAAAAG    TGT
                                ||   ||||||||||    |||
                                GG   ACCGGTTTTC    ACA
                                 AGA        TGA__
GAM594  KCNK4    5'  CCTTGGACCGGAGCCCAGTGT  37826    G  _  AAA
                                CC TGG CC   AGCCCAGTGT
                                || ||| ||   ||||||||||
                                GG ACC GG   TCGGGTCACA
                                 A  T  CC_
GAM594  PPP1R3D  5'  CCTCCGTGCTCAGAAGCC    26426    _    GC  A
                                CC CCGTG  CA AAGCC
                                || |||||  || |||||
                                GG GGCAC  GT TTCGG
                                 A    GA  C
GAM594  PTGIS    3'  CCCTTGGGAATGTGAGCCCAGT 9671      G   CCAAA__
                GT                CCC TGG      AGCCCAGTGT
                                ||| |||      ||||||||||
                                GGG ACC      TCGGGTCACA
                                  A   CTTACAC
GAM594  TEM8     3'  CCCTGGGTGATGAAGCCCAGTG 38177     G   CCAA__
                T                 CCC TGG     AAGCCCAGTGT
                                ||| |||     ||||||||||
                                GGG ACC     TTCGGGTCACA
                                  _  CACTAC
GAM594  USP6     5'  CCTCTGGCAGCCCAGC      45028    CG    CAAA
                                CC  TGGC    AGCCCAGT
                                ||  ||||    ||||||||
                                GG  ACCG    TCGGGTCG
                                 AG   _____
GAM595  PIK3C2B  3'  GATTTTGCAGTGAGTCGAGA   15292      CTTT__
                                GATT     TGAGTCGAGA
                                ||||     ||||||||||
                                CTAA     ACTCAGCTCT
                                  AACGTC
GAM595  BCL11A   3'  AGAAAGGCTCAAAGTT      39704      T   ACC
                                AGAA GGC   TCAAAGTT
                                |||| |||   ||||||||
                                TCTT CCG   AGTTTCAA
                                  T  ___
GAM595  COL1A2   3'  AGAAGAAATGGCAAAGAGAAAG 6383       AG      CCTC_
                TTT                AGAA  AATGGCA    AAAGTTT
                                ||||  |||||||    |||||||
                                TCTT  TTACCGT    TTTCAAA
                                  CT      TTCTC
GAM595  DAZ      3'  AAAAAGAATGGTACCTCA    19846          C
                                AGAAAGAATGG ACCTCA
                                |||||||||| ||||||
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```
                                TTTTTCTTACC TGGAGT
                                      A
GAM595  MYCL2    3'  AGAGAGAGCTGGGTTTCAAAGT 23894     A  A_   CACC
             TT                  AGA AGA  TGG    TCAAAGTTT
                                 ||| |||  |||    |||||||||
                                 TCT TCT  ACC    AGTTTCAAA
                                   C   CG   CAA_
GAM595  RBBP9    3'  AGAAAGAGGTCAACAAAGTTT  43135        AT  _  CCT
                                 AGAAAGA  GG CA   CAAAGTTT
                                 |||||||  || ||   ||||||||
                                 TCTTTCT  CC GT   GTTTCAAA
                                     __  A  T__
GAM595  RCN1     3'  AGAAAGAATTGCAATTTACCAA 16198         G   CC___    A
             GGTTT                   AGAAAGAAT GCA     TCAA GTTT
                                 |||||||||| |||     |||| ||||
                                 TCTTTCTTA CGT     GGTT CAAA
                                      A   TAAAT    C
GAM595  ULBP2    5'  AAGATGAATCACCTCAAGGTTT 36095      A  ___       A
                                 AAGA TGG  CACCTCAA GTTT
                                 |||| |||  |||||||| ||||
                                 TTCT ACT  GTGGAGTT CAAA
                                   _  TA       C
GAM596  CHRNA4   3'  TACTGTAGCAGGAAGTCCT   8855      C         CGGCG
                                 TAC GTAGCAGGAG    CCT
                                 ||| ||||||||||    |||
                                 ATG CATCGTCCTT    GGA
                                   A         CA___
GAM596  IDH2     3'  GCAGCCATGGGTGGCGCCTCC  13477      A__  AGC
                                 GTAGC   GG   GGCGCCTCC
                                 |||||   ||   |||||||||
                                 CGTCG   CC   CCGCGGAGG
                                    GTA  CA_
GAM596  WRN      5'  CCGAGTACAAGCCGGCGCCTCC 8134      TA_    AG
                                 CCG   GCAGG  CGGCGCCTCC
                                 |||   |||||  ||||||||||
                                 GGC   TGTTC  GCCGCGGAGG
                                   TCA    G_
GAM596  SLC7A5   3'  GCCGTGTCCGGCTTCGT     18548          AAGCC
                                 GCCGTGTCCGG    TCGT
                                 ||||||||||    ||||
                                 CGGCACAGGCC    AGCA
                                       GA___
GAM596  SNRP70   5'  GCGTCTGTCCGGAGGCTCG   44214    CG_      A  C
                                 GC   TGTCCGGA GC TCG
                                 ||   |||||||| || |||
                                 CG   ACAGGCCT CG AGC
                                  CAG       C  _
GAM597  ATP6V1A1 3'  AGGAGCTTGCTGAGGAAAA   11775      CCCC
                                 AGGA    GCTGAGGAAGA
                                 ||||    ||||||||||
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                                TCCT   CGACTCCTTTT
                                  CGAA
GAM597  BAPX1   3'  GGACTTCAGAGAAGGAAGA   10161     CC  CT  _
                                GGAC  CG  GA GGAAGA
                                ||||  ||  || ||||||
                                CCTG  GT  CT CCTTCT
                                  AA  CT  T
GAM597  DYRK3   5'  GGACCCCGCTCGGGGAGAGGCG 18718         GA  A   C
                                GGACCCCGCT  GG AGA GCG
                                ||||||||||  || ||| |||
                                CCTGGGGCGA  CC TCT CGC
                                      GC  C   C
GAM597  EXTL3   3'  CCTCTCGCTGAGGAGGGCG   11033    C__       AGAC
                                CC   CGCTGAGGA   GCG
                                ||   |||||||||   |||
                                GG   GCGACTCCT   CGC
                                 AGA       CC__
GAM597  FBXL4   5'  GACCCGGAAGGAAGACGCG   29133      CGCT
                                GACCC   GAGGAAGACGCG
                                |||||   ||||||||||||
                                CTGGG   TTCCTTCTGCGC
                                  CC__
GAM597  IL24    3'  GGACCCATGGCCAAGGGCG   27787      C__  TG   AAGAC
                                GGACCC   GC  AGG    GCG
                                ||||||   ||  |||    |||
                                CCTGGG   CG  TCC    CGC
                                   TAC  GT  _____
GAM597  JUNB    3'  GGACCCCAGTGGGAGGCG    13757        C  A   AGAC
                                GGACCCCG TG GGA    GCG
                                |||||||| || |||    |||
                                CCTGGGGT AC CCT    CGC
                                     C  _   C___
GAM597  MYB     5'  GGCTCCGCCGAGAGCCGCG   40532    ACC       AAGA
                                GG   CCGCTGAGG   CGCG
                                ||   |||||||||   ||||
                                CC   GGCGGCTCT   GCGC
                                 GA_       CG__
GAM597  RAB3A   5'  CAGGACCCCGGTGCGTTGA   16060          C  AG__
                                CAGGACCCCG TG   GA
                                |||||||||| ||   ||
                                GTCCTGGGGC AC   CT
                                      C  GCAA
GAM597  RDBP    3'  CAGAGGCTGAGGGAGA     16230     ACCCC      A
                                CAGG    GCTGAGG AGA
                                ||||    ||||||| |||
                                GTCT    CGACTCC TCT
                                  C_____      C
GAM597  TFG     5'  CAGGTCTCCGCTGAATGGGCGG 25868     ACC      ___  AA
            ACGCG                   CAGG   CCGCTGA   GG  GACGCG
                                ||||   |||||||   ||  ||||||
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                                GTCC  GGCGACT  CC CTGCGC
                                  AGA     TAC GC
GAM597  HDAC7A  3' TCTCAGGGTCCTCTCCAGT  32476       _  C  C
                                TCTCAGGG CCTC TCCG GT
                                |||||||| |||| |||| ||
                                AGAGTCCC GGAG AGGT CA
                                    A  _  _
GAM597  HIS1    3' TCTCAGGGCCTCCCTACGT  26996          CC
                                TCTCAGGGCCTCCT GCGT
                                |||||||||||||| ||||
                                AGAGTCCCGGAGGG TGCA
                                       A_
GAM597  MASP1   3' TCTCAGGGGCTTCTCTGGC  40107       C C  C_
                                TCTCAGGG CT CTC GC
                                |||||||| || |||  ||
                                AGAGTCCC GA GAG CG
                                    C A  AC
GAM597  SRRM1   3' TCTCAGGGCCTTTTCACGCA  25191         CC _
                                TCTCAGGGCCT TC CGCG
                                |||||||||||  || ||||
                                AGAGTCCCGGA AG GCGT
                                      AA T
GAM598  CIS4    3' CCCGAGTTTAATTACAGAA  20129      C    ATA
                                CCCGAG TTTAAT  TATAGAA
                                |||||| ||||||  |||||||
                                GGGCTC AAATTA  ATGTCTT
                                  _   ____
GAM598  RERE    3' AGCTTCAAGATATATAGAAA  29021       T
                                AGCTTTAA ATATATAGAAA
                                |||||||| ||||||||||
                                TCGAAGTT TATATATCTTT
                                    C
GAM598  TDG     3' CCCAGCTTTAATATCTACCAGA 17352    G        ATA_
                                CCC AGCTTTAATAT   TAGA
                                ||| ||||||||||   ||||
                                GGG TCGAAATTATA   GTCT
                                  _        GATG
GAM598  APXL    3' GGTGCGTGACTGTGTTTTT  11624   CA  CTC  G
                                GG  CGT  AC GTGTTTTT
                                ||  |||  || ||||||||
                                CC  GCA  TG CACAAAAA
                                 AC  C__  A
GAM598  CNTN3   3' AGTCACGTCTTCAACAATTTTT 42479   G    _ _  G
          T                      AG CACGTCT CA CGGT TTTT
                                || ||||||| || |||| ||||
                                TC GTGCAGA GT GTTA AAAA
                                 A     A T  A
GAM598  FOSB    3' GGCACGTGGAATGTTTTTCA  27542       CTCAC
                                GGCACGT   GGTGTTTTTCA
                                |||||||   ||||||||||
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                                CCGTGCA    TTACAAAAAGT
                                   CC___
GAM598  INPP5A   3' AGGCCATGTGTGTTTTT    24403     A  CTCACG
                                AGGC CGT    GTGTTTTT
                                |||| |||    ||||||||
                                TCCG GTA    CACAAAAA
                                  _  CA____
GAM598  KLK10    3' AGGCACGTCATTGTTCCC    15768        TCACGG
                                AGGCACGTC    TGTTTTT
                                |||||||||    |||||||
                                TCCGTGCAG    ACAAGGG
                                     TA____
GAM598  NQO1     3' AGGCTGTCTCCCATTTTTC   9476      AC    ACGGT
                                AGGC  GTCTC    GTTTTTC
                                ||||  |||||    |||||||
                                TCCG  CAGAG    TAAAAAG
                                  A_    GG___
GAM598  RANBP3   5' AGGCACATTTTGCACCTGTTTT 28748       CT__  GG
           TCA                    AGGCACGT   CAC  TGTTTTTCA
                                |||||||||   |||  |||||||||
                                TCCGTGTA   GTG  ACAAAAAGT
                                    AAAC   G_
GAM598  SLT      5' GGTGCGTCGTGCTCTT     37177    CA   TCACG
                                GG  CGTC    GTGTTTTT
                                ||  ||||    ||||||||
                                CC  GCAG    CACGAGAA
                                 AC   ______
GAM598  STAT1    3' GGTGTATCTGGATGTTTTTCA 28729    CAC   CAC
                                GG   GTCT   GGTGTTTTTCA
                                ||   ||||  ||||||||||
                                CC   TAGA   CTACAAAAAGT
                                 ACA   C__
GAM598  UBL3     3' AGGCACATTTTGTTTTTTC   28262       CTCACG  G
                                AGGCACGT     GT TTTTTC
                                ||||||||     || ||||||
                                TCCGTGTA     CA AAAAAG
                                    AAA___  _
GAM598  VBP1     3' AGCATGTCTCACAGTTTTC   17924     C       GTT
                                GGCA GTCTCACGGT   TTTC
                                |||| ||||||||||   ||||
                                TCGT CAGAGTGTCA   AAAG
                                  A       ___
GAM599  ADAM12   3' CCAGTCCAGAAGACAGA     18467     C_      TAT
                                CCA  CCAGAAGAT   AGA
                                |||  |||||||||  |||
                                GGT  GGTCTTCTG   TCT
                                  CA       ___
GAM599  AIPL1    3' CCAGAAGAATTAAAAACA    40817       TTATA
                                CCAGAAGA    GAAAACA
                                ||||||||    |||||||
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                                GGTCTTCT    TTTTTGT
                                    TAA__
GAM599  ATP7A    3'  CACCCAGAGAAAAAAAC     6258        A  TTAT
                                CACCCAGA GA    AGAAAAC
                                |||||||| ||    |||||||
                                GTGGGTCT CT    TTTTTTG
                                    _ _____
GAM599  BIG1     3'  CCACCCAAAAGAAAAGAAAA  26957          TTAT
                                CCACCCAGAAGA    AGAAAA
                                ||||||||||||    ||||||
                                GGTGGGTTTTCT    TCTTTT
                                      TT__
GAM599  CERD4    3'  CCACCCAGAGGAATCCCAG   28945        A  TTA_
                                CCACCCAGA GA    TAG
                                ||||||||| ||    |||
                                GGTGGGTCT CT    GTC
                                     C  TAGG
GAM599  CKTSF1B1 3'  CCCAGGAGGGCACAAAAA    30083      A  AT
                                CCCAG AG  TATAGAAA
                                ||||| ||  ||||||||
                                GGGTC TC  GTGTTTTT
                                   C  CC
GAM599  CRADD    3'  CCATCTGAAGATCATCAAAAA  19176     CCCA       A
                                CCA    GAAGATTAT GAAAA
                                |||    ||||||||| |||||
                                GGT    CTTCTAGTA TTTTT
                                  AGA_       G
GAM599  CSF3     3'  CCACCCAGAAAAACAGGAGACA 8901           TT    AAA
                                CCACCCAGAAGA  ATAG   ACA
                                ||||||||||||  ||||   |||
                                GGTGGGTCTTTT  TGTC   TGT
                                      __    CTC
GAM599  DNASE1   5'  CACCTGAGAGTGCAGAAAACA  23351     CA  A  TTA
                                CACC  GA GA   TAGAAAACA
                                ||||  || ||   |||||||||
                                GTGG  CT CT   GTCTTTTGT
                                  A_  _  CAC
GAM599  EGR2     3'  CCCAACCTATTGTAGAAAAC   7581       AAG   A
                                CCCAG   ATT TAGAAAAC
                                |||||   ||| ||||||||
                                GGGTT   TAA ATCTTTTG
                                   GGA   C
GAM599  ELK1     3'  CCACTGGGGGACTGACAGAAAA 23407     CCAGAA   _
           CA                    CCAC     GATT ATAGAAAACA
                                ||||     |||| ||||||||||
                                GGTG     CTGA TGTCTTTTGT
                                  ACCCC_   C
GAM599  ERBB2IP  3'  CCAGATTTTTATAGAAAA    33096      AGA
                                CCAGA   TTATAGAAAA
                                |||||   ||||||||||
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                                GGTCT   AATATCTTTT
                                   AAA
GAM599  FRAT2    3'  CCACCAGAAAATAAGAAAA   28969      C      TAT
                                CCACC AGAAGAT   AGAAAA
                                ||||| |||||||   ||||||
                                GGTGG TCTTTTA   TCTTTT
                                   _      T__
GAM599  GFI1     3'  CCAGAAGATCTAAAAACA    23551          ATA
                                CCAGAAGATT   GAAAACA
                                ||||||||||   |||||||
                                GGTCTTCTAG   TTTTTGT
                                      A__
GAM599  GLO1     3'  CACCCAAAAAGGAAA       27468          GATTAT  A
                                CACCCAGAA     AG AAA
                                |||||||||     || |||
                                GTGGGTTTT     TC TTT
                                      _______ C
GAM599  GLRX     3'  CATCCAGAAGAAAACCAAGA   13148    C       TT  __
                                CA CCAGAAGA  AT  AGA
                                || ||||||||  ||  |||
                                GT GGTCTTCT  TG  TCT
                                 A       TT  GT
GAM599  HEM1     3'  CACCAGAAGATAGAAAA     23738      C     TTA
                                CACC AGAAGA   TAGAAAA
                                |||| ||||||   |||||||
                                GTGG TCTTCT   ATCTTTT
                                   _     ____
GAM599  HTR1D    3'  CAGAAGTTAAGAAAACA     9260        A   T
                                CAGAAG TTA AGAAAACA
                                |||||| ||| ||||||||
                                GTCTTC AAT TCTTTTGT
                                   _  _
GAM599  KCNC3    3'  CCTCCAGAAGATTCTAAG    22499    AC        AT_
                                CC  CCAGAAGATT   AG
                                ||  ||||||||||   ||
                                GG  GGTCTTCTAA   TC
                                 A_         GAT
GAM599  KL       3'  CACCCAAAAAGAGAA       22003          GATTAT   A
                                CACCCAGAA     AGA AA
                                |||||||||     ||| ||
                                GTGGGTTTT     TCT TT
                                      _______  C
GAM599  LETM1    3'  CCACCCAGAGGGCACAG     29497          A AT
                                CCACCCAGA G  TATAG
                                ||||||||| |  |||||
                                GGTGGGTCT C  GTGTC
                                      _ CC
GAM599  MEN1     5'  CCACCCAGGAGACAGA      39166          A    TAT
                                CCACCCAG AGAT   AGA
                                |||||||| ||||   |||
```

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                                GGTGGGTC TCTG   TCT
                                    C   ___
GAM599  MSX2     3'  GAAGATTACACCAAGAAAACA  42293        ____
                                GAAGATTAT   AGAAAACA
                                |||||||||   ||||||||
                                CTTCTAATG   TCTTTTGT
                                   TGGT
GAM599  MUC12    3'  CCACCCAGGAGGAGACAG    45329        A  ATT
                                CCACCCAG AG   ATAG
                                |||||||| ||   ||||
                                GGTGGGTC TC   TGTC
                                    C  CTC
GAM599  MUC4     5'  CCACCAGGAAAGAAAA      39666      CA   GATTAT
                                CCACC  GAA     AGAAAA
                                |||||  |||     ||||||
                                GGTGG  CTT     TCTTTT
                                  TC  _______
GAM599  MYO1C    3'  CCCCCAGAAGGGCATAGA    41466    A      AT
                                CC CCCAGAAG  TATAGA
                                || ||||||||  ||||||
                                GG GGGTCTTC  GTATCT
                                 _       CC
GAM599  NKTR     3'  CCACCCAAAGCCATGAAAA   23926        A A   A
                                CCACCCAGA G TTAT GAAAA
                                ||||||||| | |||| |||||
                                GGTGGGTTT C GGTA CTTTT
                                       _ _   _
GAM599  PPT2     3'  CCAGCCAGAAGACTCAG     39915     C        A
                                CCA CCAGAAGATT TAG
                                ||| |||||||||| |||
                                GGT GGTCTTCTGA GTC
                                  C        _
GAM599  PXF      3'  CCAGGAGAACTATAGAAA    16007     A  _
                                CCAG AGA TTATAGAAA
                                |||| ||| |||||||||
                                GGTC TCT GATATCTTT
                                  C   T
GAM599  RAB7L1   3'  CCTCCCAGAACTGGGATGGAAA 19432    A      GATTATA_
           A                     CC CCCAGAA       GAAAA
                                || |||||||       |||||
                                GG GGGTCTT       CTTTT
                                 A      GACCCTAC
GAM599  SCP2     3'  CACCCAGAGCATAGGAAAAACA 16485        AGAT    __
                                CACCCAGA   TATAG  AAAACA
                                ||||||||   |||||  ||||||
                                GTGGGTCT   GTATC  TTTTGT
                                    C___     CT
GAM599  SLC35A1  3'  CCCATTAACATTATAGAAAACA 26947      G_  G
                                CCCA  AA ATTATAGAAAACA
                                ||||  || ||||||||||||
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                                GGGT  TT TAATATCTTTTGT
                                  AA  G
GAM599  SRY      3'  CCAGAGAAAAGAAAACA     17118      A  TTAT
                                CCAGA GA    AGAAAACA
                                ||||| ||    ||||||||
                                GGTCT CT    TCTTTTGT
                                  _  TT__
GAM599  TGFBR2   3'  TAACCCAGAAGTGAGAA     17475   C       ATTAT
                                C ACCCAGAAG     AGAA
                                | |||||||||     ||||
                                A TGGGTCTTC     TCTT
                                 T        AC___
GAM599  TLE1     3'  CACCCAGAAAGAAAGAA     22917          ATTAT
                                CACCCAGAAG     AGAA
                                ||||||||||     ||||
                                GTGGGTCTTT     TCTT
                                      CTT__
GAM599  TRPS1    5'  CAGAAGACACAGAAGACA    30457        T     A
                                CAGAAGAT ATAGAA ACA
                                |||||||| |||||| |||
                                GTCTTCTG TGTCTT TGT
                                   _     C
GAM599  UC28     3'  CCCTTCAGAAGATTTGTAG   34686    ACC       A_
                                CC   CAGAAGATT  TAG
                                ||   |||||||||  |||
                                GG   GTCTTCTAA  ATC
                                 GAA        AC
GAM599  UNC13    3'  CCACCCAAGAAGAAAATA    26862        _    TT
                                CCACCCA GAAGA  ATA
                                ||||||| |||||  |||
                                GGTGGGT CTTCT  TAT
                                    T     TT
GAM599  ZIC3     3'  CAGAATTTGTTAGAAAACA   18245      GATTA
                                CAGAA     TAGAAAACA
                                |||||     |||||||||
                                GTCTT     ATCTTTTGT
                                   AAACA
GAM599  GBAS     3'  CACAGAAATGTATGTAG     11234     A   TGG
                                CACA GGA   GTATGTAG
                                |||| |||   ||||||||
                                GTGT CTT   CATACATC
                                  _   TA_
GAM599  PPP1R3C  3'  TCTCCACAAGGATACGTA    23992     A         G
                                TCT CCACAAGGATG GTA
                                ||| |||||||||| |||
                                AGA GGTGTTCCTAT CAT
                                  _         G
GAM599  RBM8A    3'  TACCTACTGGGTATGT      23014      _  AAGGA
                                TACC AC     TGGGTATGT
                                |||| ||     |||||||||
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                                ATGG TG    ACCCATACA
                                  A _____
GAM600  ABCC1   3'  CTTCCAGGAGGACAGG     33402        ACCAATCA
                                TTTCCAGGA      ACAGG
                                |||||||||      |||||
                                GAAGGTCCT      TGTCC
                                    CC_______
GAM600  ADCY6   5'  TCCCCAATCAACAGG      34178    AGGAA
                                TCC    CCAATCAACAGG
                                |||    ||||||||||||
                                AGG    GGTTAGTTGTCC
                                 ______
GAM600  DSCR3   3'  TTTCTGGGAACCAAGTTTCAAG 25833     CA      TCAA
                                TTTC  GGAACCAA   CAGG
                                ||||  ||||||||   ||||
                                AAAG  CCTTGGTT   GTTC
                                  AC       CAAA
GAM600  NPY2R   3'  TTTCCAGGAATTAAACAG    9505         CCAATC
                                TTTCCAGGAA     AACAG
                                ||||||||||     |||||
                                AAAGGTCCTT     TTGTC
                                    AAT___
GAM600  ZNF175  5'  TTCCCAGGAGCCAGAAGC    28369        A   ATCAAC
                                TTTCCAGGA CCA     AGGC
                                ||||||||| |||     ||||
                                AAGGGTCCT GGT     TTCG
                                    C   C_____
GAM600  BAZ2A   3'  CAGCAGTAGTTGTCCCTGAGGA 30303       TA   GTG_   A
                                CAGCAGTA  TTG    TGA GGA
                                ||||||||  |||    ||| |||
                                GTCGTCAT  AAC    ACT CCT
                                    C_   AGGG   _
GAM600  CLASP1  3'  ACAGTGTACTTGAAGGA    42230      A    GGTG
                                GCAGT TATT    TGAAGGA
                                ||||| ||||    |||||||
                                TGTCA ATGA    ACTTCCT
                                  C    _____
GAM600  CNP     3'  AGTTATGGTGTGAAGG     37554     ATAT
                                AGT    TGGTGTGAAGG
                                |||    ||||||||||||
                                TCA    ACCACACTTCC
                                  AT__
GAM600  CNTNAP2 3'  CAGCAGTGTGATTGGATGGAA  30483       AT_    _  T
                                CAGCAGT   ATTGG TG GAA
                                |||||||   ||||| || |||
                                GTCGTCA   TAACC AC CTT
                                    CAC    T  _
GAM600  EXTL2   3'  AGCATTATATAAGAAGGA    11016      G    TGGTGT
                                AGCA TATAT     GAAGGA
                                |||| |||||     ||||||
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                                TCGT ATATA     CTTCCT
                                  A    TT____
GAM600  F11     3'  CAGCGTGTTACTGTGGAGGAA  6552      A  ATA   G    A
                                CAGC GT   TTG TGTG AGGAA
                                |||| ||   ||| |||| |||||
                                GTCG CA   AAT ACAC TCCTT
                                  _ C__   G    C
GAM600  GALNT7   3'  CAGCATGACTGTGAAGGA    38352      GTATAT  _
                                CAGCA     TGG TGTGAAGGA
                                |||||     ||| |||||||||
                                GTCGT     ACT ACACTTCCT
                                  _______  G
GAM600  GLUL    3'  GTAGATGAAATGAAGGA     13156     TAT   T
                                GTA   TGG GTGAAGGA
                                |||   ||| ||||||||
                                CAT   ACT TACTTCCT
                                  CT_   T
GAM600  IL1R1   3'  GCCAGTGTGGAGTGAGGG    9360     _  ATAT   T    A
                                GC AGT    TGG GTGA GG
                                || |||    ||| |||| ||
                                CG TCA    ACC CACT CC
                                 G   C___   T    C
GAM600  ITGAM    3'  CAGCGCTGGTGTGGAGGA    43510      A  ATAT      A
                                CAGC GT    TGGTGTG AGGA
                                |||| ||    ||||||| ||||
                                GTCG CG    ACCACAC TCCT
                                  _ _____       C
GAM600  NPR1    3'  CAGGGTAGGGAGGTGTGGAGG  44576     CA   TATT     A
                                CAG  GTA    GGTGTG AGG
                                |||  |||    |||||| |||
                                GTC  CAT    CCACAC TCC
                                  C_   CCCT     C
GAM600  PRV1    3'  CAGCGGTGAAGAATCGTGGGGG 43873      A  ATATTGG    AA
           AA                     CAGC GT      TGTG  GGAA
                                |||| ||      ||||  ||||
                                GTCG CA      GCAC  CCTT
                                  C  CTTCTTA    CC
GAM600  PYGM     5'  GCAGGGGTGGTGTGAGGGA   24697      TATAT      A
                                GCAG     TGGTGTGA GGA
                                ||||     |||||||| |||
                                CGTC     ACCACACT CCT
                                  CCC__       C
GAM600  STAT1    3'  CAGCAGTATGTAAAAG      28728        ATATTG
                                CAGCAGT     GTGTGAAGG
                                |||||||     |||||||||
                                GTCGTCA     TACATTTTC
                                           _______
GAM601  ATP11A   3'  TTCATGATATGTGCATATG   44197        GCCTCTCA
                                TTCATGA       TGCATATG
                                |||||||       ||||||||
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                                AAGTACT       ACGTATAC
                                    ATAC____
GAM601  CLCN3    3'  ATGAGCCTTTGTTGTGGTGCAT 12270        CTCA_____    A
            GTG                   ATGAGCCT        TGCAT TG
                                |||||||||        ||||| ||
                                TACTCGGA        ACGTA AC
                                    AACAACACC     C
GAM601  MTNR1B   3'  TTCATGAGTTTGTCATGC    25559        CCTC
                                TTCATGAG    TCATGC
                                ||||||||    ||||||
                                AAGTACTC    AGTACG
                                    AAAC
GAM601  PTGFR    3'  TCATGACCATGCATGTG     9661        GCCTC       A
                                TCATGA     TCATGCAT TG
                                ||||||     |||||||| ||
                                AGTACT     GGTACGTA AC
                                   ______       C
GAM601  SMURF1   3'  TCGTGAGTTTATTGCATATG   45201    A    CCTCTCA
                                TC TGAG       TGCATATG
                                || ||||       |||||||||
                                AG ACTC       ACGTATAC
                                 C    AAATA__
GAM601  COL11A1  3'  TGGATGAGAATGAGCACCATAT 12347    A       CT_  T
            T                    TG ATGAGAGT   CA CCATATT
                                || |||||||||   || |||||||
                                AC TACTCTTA   GT GGTATAA
                                 C       CTC  _
GAM601  CREBL1   3'  GAATGAGAGGAGCCCTATATTC 20432         TCTCA  _
                                GAATGAGAG     TCC ATATTC
                                |||||||||     ||| ||||||
                                CTTACTCTC     GGG TATAAG
                                     CTC__   A
GAM601  EPS8     3'  TGAATGACAGACACCATATTC  20814        G  TCT  T
                                TGAATGA AG   CA CCATATTC
                                ||||||| ||   || ||||||||
                                ACTTACT TC   GT GGTATAAG
                                    G  T__  _
GAM601  FDX1     3'  TGAAGTCCACTCATCCATGTTC 41270     G   ___       A
                                TGA AGTC   TCATCCAT TTC
                                ||| ||||   |||||||| |||
                                ACT TCAG   AGTAGGTA AAG
                                  _   GTG       C
GAM601  RNMT     3'  AAATGAGGAAATCCATATT    19141        AGTCTC
                                GAATGAG     ATCCATATT
                                |||||||     |||||||||
                                TTTACTC     TAGGTATAA
                                    CTT___
GAM601  ROS1     3'  TGAATGAGAGTGTTTATCTC   16365          _______
                                TGAATGAGAG     TCTC
                                ||||||||||     ||||
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                                ACTTACTCTC     AGAG
                                     ACAAAT
GAM602  ARHI     3'  TACGTATTGACAACATGGATGT 21701     A  G       _  CC
                                TAC TA TGACAACG GG  GT
                                ||| || |||||||| ||  ||
                                ATG AT ACTGTTGT CC  CA
                                  C  A       A  TA
GAM602  ATP8A2   3'  CACGTAGTGACAGCTG      45253     A       ACGG  CG
                                TAC TAGTGACA    GC  TG
                                ||| ||||||||    ||  ||
                                GTG ATCACTGT    CG  AC
                                  C       _____  __
GAM602  LHX2     3'  ACAGTGACACAAATGTTGTG   21981         A    CC__
                                ATAGTGACA CGGG    GTG
                                ||||||||| ||||    |||
                                TGTCACTGT GTTT    CAC
                                     _    ACAA
GAM602  POU2AF1  3'  TAATAGTGACGATGGTGC    26376   C       AAC  GCC
                                A ATAGTGAC   GG   GTGC
                                | ||||||||   ||   ||||
                                A TATCACTG   CT   CACG
                                 T       ____ AC_
GAM603  HLX1     5'  GGGTGGGTGGGCGCGC      34991    TTAA   T    T
                                GG    TGG TGGG CGCGC
                                ||    ||| |||| |||||
                                CC    ACC ACCC GCGCG
                                 C____   C    _
GAM603  HUNK     3'  TAAGCGAGGTTGGGTTGTGCAG 31078       TAAT       CGC
                                TAGGT    GGTTGGGT   GCAG
                                |||||    ||||||||   ||||
                                ATTCG    CCAACCCA   CGTC
                                   CT__       ACA
GAM603  DCD      3'  TAAAGCCTGCTGCTCCTGGGT  38233          AAC  A    A
                                TAAAGCCTGC   GT TTCTG GT
                                ||||||||||   || ||||| ||
                                ATTTCGGACG   CG AGGAC CA
                                     A__  _    C
GAM603  ICAM1    5'  TGAGGTTGCAACTCTGAG    43436   A  CC     GTAT
                                A AG  TGCAAC    TCTGAG
                                | ||  ||||||    ||||||
                                A TC  ACGTTG    AGACTC
                                 C  CA     _____
GAM603  MASP1    3'  GCCCAAATGTGTTCTGAGT    40101       C  C  A
                                GCCTG AA GT TTCTGAGT
                                ||||| || || ||||||||
                                CGGGT TT CA AAGACTCA
                                   _  A  C
GAM603  RAB30    5'  CTGCGATGTCCTGAGT      30934      AAC  A
                                CTGC   GT TTCTGAGT
                                ||||   || ||||||||
```

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                                GACG   TA AGGACTCA
                                  C__  C
GAM604  MPP6     3'  TCAACGCATTTCTTTA      32396          GAATCT
                                TCAATGCATT     TCTTTA
                                ||||||||||     ||||||
                                AGTTGCGTAA     AGAAAT
                                       _______
GAM604  ITGB3    3'  TTCTTGGGCATTTGGGGGT   6842      GTCA       AACAC
                                TTC    GGCATTTG    GGT
                                |||    ||||||||    |||
                                AAG    CCGTAAAC    CCA
                                  AAC_       CC___
GAM605  AICDA    3'  CGCAGCTTTATCATTCTGTTT  34040     G         GCAA
                                CGC AGCTTTATCA    GTTT
                                ||| ||||||||||    ||||
                                GCG TCGAAATAGT    CAAA
                                  _         AAGA
GAM606  SCN3A    3'  GTAATTGCACAACTTTG     27952      C  A
                                GTAA TG CATAACTTTG
                                |||| || ||||||||||
                                CATT AC GTGTTGAAAC
                                  A  _
GAM606  TLR4     3'  TACTTAGTAGGCAATAACTTTG 17564          ACTGAC
                                TATTTAGTA     ATAACTTTG
                                |||||||||     |||||||||
                                ATGAATCAT     TATTGAAAC
                                     CCGT__
GAM606  CPSF6    3'  ACATGCTAGTCAGGTGCTTTTA 28130         CCGAC   C_
                                ACGTGCTA    CAG  GCTTTTA
                                ||||||||    |||  |||||||
                                TGTACGAT    GTC  CGAAAAT
                                    CA___   CA
GAM607  AQP6     5'  GCCATGTGTATTGCACCC    11640      C  AC
                                GCCA GT  ATTGTACCT
                                |||| ||  |||||||||
                                CGGT CA  TAACGTGGG
                                  A  CA
GAM607  BCAS1    3'  GCCGTTGTCACTGAGCCTCAAA 18922     AC_ A    TA
          AG                      GCC   GT CATTG  CCTCAAAAG
                                |||   || |||||  |||||||||
                                CGG   CA GTGAC  GGAGTTTTC
                                  CAA  _    TC
GAM607  CLCA2    5'  GCTGCATACATTGTGTCA    27223    CA        ACC
                                GC  CGTACATTGT   TCA
                                ||  ||||||||||   |||
                                CG  GTATGTAACA   AGT
                                 AC         C__
GAM607  RNTRE    3'  ACATACTTTTGTACCTTGAAAG 31244        A_       CA
                                ACGTAC  TTGTACCT  AAAG
                                ||||||  ||||||||  ||||
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                                TGTATG  AACATGGA  TTTC
                                   AA       AC
GAM607  TM4SF4   3'  GCCATGATGACAGCCTCAAAAG 21456     CGTACAT  _ _
                                GCCA      TG TA CCTCAAAAG
                                ||||      || || |||||||||
                                CGGT      AC GT GGAGTTTTC
                                  ACT_____  T  C
GAM607  ADAM11   3'  GGCCGAGACGGTGGGTGC    34656         CT_
                                GGCCGAGATG   GGTGC
                                ||||||||||   |||||
                                CCGGCTCTGC   CCACG
                                      CAC
GAM607  AGTR1    5'  GGCCGGCTGCGCTGGTGC    28916      AGA_
                                GGCCG    TGCTGGTGC
                                |||||    |||||||||
                                CCGGC    GCGACCACG
                                   CGAC
GAM607  ARHGEF1  3'  TGGCCGAGGCTCATGC      21737        AT   G
                                TGGCCGAG  GCT GTGC
                                ||||||||  ||| ||||
                                ACCGGCTC  CGA TACG
                                     __   G
GAM607  CDKN2C   5'  TGGCTGGATGCTGACGTGC   38571     CGA     __
                                TGGC   GATGCTG  GTGC
                                ||||   |||||||  ||||
                                ACCG   CTACGAC  CACG
                                  AC_      TG
GAM607  DBN1     3'  TGGCCAGAGGCTGATGC     38944      G   T
                                TGGCC AGA GCTGGTGC
                                ||||| ||| ||||||||
                                ACCGG TCT CGACTACG
                                   _  C
GAM607  DIA1     3'  TGGCCGTGTGACCGGTGC    28795       AGAT
                                TGGCCG    GCTGGTGC
                                ||||||    ||||||||
                                ACCGGC    TGGCCACG
                                   ACAC
GAM607  DYRK1A   3'  TGGTGGAGATACCACGTGC   39007     CC       _
                                TGG  GAGATGCTG GTGC
                                |||  ||||||||| ||||
                                ACC  CTCTATGGT CACG
                                  AC        G
GAM607  EGR4     3'  TGTCCGGCGAGCTGGTGC    12680    G   A_  T
                                TG CCG  GA GCTGGTGC
                                || |||  || ||||||||
                                AC GGC  CT CGACCACG
                                 A   CG  _
GAM607  ENDOGL1  3'  TAGCTGAGGGTGATGGTG    23017      C   A_  C
                                TGGC GAG  TG TGGTG
                                |||| |||  || |||||
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                                ATCG CTC  AC ACCAC
                                  A  CC  T
GAM607  EXT2    3'  TGACTCAGCGGCTGGTGC    7591      CG  AT
                                TGGC  AG  GCTGGTGC
                                ||||  ||  ||||||||
                                ACTG  TC  CGACCACG
                                  AG  GC
GAM607  FAAH    5'  TGGCCGAGTGCCTGTGC     45467       A   G
                                TGGCCGAG TGCT GTGC
                                |||||||| |||| ||||
                                ACCGGCTC ACGG CACG
                                    _   A
GAM607  FANCG   5'  TGGCCGAGGCTGGGC      21560       AT    T
                                TGGCCGAG  GCTGG GC
                                ||||||||  ||||| ||
                                ACCGGCTC  CGACC CG
                                   __    _
GAM607  GNA11   3'  TGGCACGAGAACCACTGC    44052     _   T   G
                                TGGC CGAGA GCTG TGC
                                |||| ||||| |||| |||
                                ACCG GCTCT TGGT ACG
                                  T    _   G
GAM607  HTR4    3'  TGACCGAGATAGGACGC     9303         CT  _
                                TGGCCGAGATG  GG TGC
                                ||||||||||  || |||
                                ACTGGCTCTAT  CC GCG
                                    __ T
GAM607  IL10RA  3'  TGGCATGAGCTGGTGC     40629     CGA  T
                                TGGC   GA GCTGGTGC
                                ||||   || ||||||||
                                ACCG   CT CGACCACG
                                  TA_  _
GAM607  IL12RB2 5'  TGACCGAGGTGAGGTGC    11435       A  CT
                                TGGCCGAG TG  GGTGC
                                ||||||||  ||  |||||
                                ACTGGCTC AC  CCACG
                                    C  T_
GAM607  IL6R    3'  GGTCCAGGCTGCTGGTGC    8184    _  AGA
                                GG CCG   TGCTGGTGC
                                || |||   |||||||||
                                CC GGT   ACGACCACG
                                 A  CCG
GAM607  KCNK4   3'  TGACCGACCTGGGTGC     37840       GA  CT
                                TGGCCGA  TG  GGTGC
                                |||||||  ||  |||||
                                ACTGGCT  AC  CCACG
                                   GG  __
GAM607  KIAA0857 5' TGGCCGAGCCGGTGC      42477       GAT
                                TGGCCGA   GCTGGTGC
                                |||||||   ||||||||
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                                ACCGGCT  CGGCCACG
                                   ___
GAM607  KRT3    3'  TGGCTGCGATGCTGATGC   38384    CGA
                                TGGC  GATGCTGGTGC
                                ||||  ||||||||||
                                ACCG  CTACGACTACG
                                  ACG
GAM607  M11S1   5'  TGGCCGAGGGCATCGTGC   25333      AT  TG_
                                TGGCCGAG  GC  GTGC
                                ||||||||  ||  ||||
                                ACCGGCTC  CG  CACG
                                    C_  TAG
GAM607  MCCC2   5'  TGGCCTGGAGCCGGTGC    35253     GA  T
                                TGGCC  GA GCTGGTGC
                                |||||  || ||||||||
                                ACCGG  CT CGGCCACG
                                  AC  _
GAM607  NRXN1   5'  TAGCCGAGGCGAATGC     39849      AT  TG
                                TGGCCGAG  GC  GTGC
                                ||||||||  ||  ||||
                                ATCGGCTC  CG  TACG
                                    __  CT
GAM607  PIK3CG  5'  TAGCCGAGAAGGAAGTGC   15306       TGCT
                                TGGCCGAGA   GGTGC
                                |||||||||   |||||
                                ATCGGCTCT   TCACG
                                     TCCT
GAM607  PLAUR   3'  TGGCCTGAGGTCACACAGC  15373    _  ___   T
                                TGGCC GAG  ATGC GGT
                                ||||| |||  |||| |||
                                ACCGG CTC  TGTG TCG
                                  A  CAG   _
GAM607  PPP2R4  3'  TGGCCGAGTGACCAGGC    41334      A  _ TG T
                                TGGCCGAG TG C  G GC
                                |||||||| || |  | ||
                                ACCGGCTC AC G  C CG
                                    _  T GT _
GAM607  PRELP   3'  TGGCCGGCACAGGTGC     15552     AGA  T
                                TGGCCG  TGC GGTGC
                                ||||||  ||| |||||
                                ACCGGC  GTG CCACG
                                   C__  T
GAM607  RAF1    3'  TGGCCGAGTGCCTTGC     44337      A   GG
                                TGGCCGAG TGCT  TGC
                                |||||||| ||||  |||
                                ACCGGCTC ACGG  ACG
                                    _  A_
GAM607  RFP     5'  TGGCCGGGCCGATGC      27135      AGAT
                                TGGCCG   GCTGGTGC
                                ||||||   ||||||||
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                                ACCGGC   CGGCTACG
                                   C___
GAM607  SLC18A3  5'  TGGCCGAGGGACATGC     16839       AT  TG
                                TGGCCGAG  GC  GTGC
                                ||||||||  ||  ||||
                                ACCGGCTC  TG  TACG
                                     CC  __
GAM607  SNX9     3'  TGGAAGTGCTGGTGC      32163     CC   A
                                TGG  GAG TGCTGGTGC
                                |||  ||| |||||||||
                                ACC  TTC ACGACCACG
                                  __  _
GAM607  SURF4    3'  TGGTGCAGAACTGGTGC     37661     CCG   T
                                TGG   AGA GCTGGTGC
                                |||   ||| ||||||||
                                ACC   TCT TGACCACG
                                  ACG  _
GAM607  TMPRSS4  3'  TGGCCGAGCTAGGGC      33395       GAT    T
                                TGGCCGA   GCTGG GC
                                |||||||   ||||| ||
                                ACCGGCT   CGATC CG
                                    ___    C
GAM607  WASF3    3'  TGGCCGGCTGGTGC       27393       AGAT
                                TGGCCG   GCTGGTGC
                                ||||||   ||||||||
                                ACCGGC   CGACCACG
                                   ____
GAM607  XRCC5    3'  TGGCAGAGATTGGGC      34496     C    GC   T
                                TGGC GAGAT  TGG GC
                                |||| |||||  ||| ||
                                ACCG CTCTA  ACC CG
                                  T    __  _
GAM607  ZNF289   3'  GGCTGAGACTGCCGGTGC    42256     C   _
                                GGC GAGA TGCTGGTGC
                                ||| |||| |||||||||
                                CCG CTCT ACGGCCACG
                                  A   G
GAM607  ZNF7     5'  TGGCCGAGAGACCTCGC     18263        T   GG
                                TGGCCGAGA GCT  TGC
                                ||||||||| |||  |||
                                ACCGGCTCT TGG  GCG
                                     C   A_
GAM607  ZYX      3'  GGCCGAGGGCGCGGGTGC    18437       A_   T
                                GGCCGAG  TGC GGTGC
                                |||||||  ||| |||||
                                CCGGCTC  GCG CCACG
                                    CC   C
GAM608  ATP7A    3'  TTAAAGTTTTGGAAACATCTTG 6269         C  AC   C
                                TTGAAGTT TG  GAA TATCTTG
                                |||||||| ||  ||| |||||||
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                                AATTTCAA AC  CTT GTAGAAC
                                     A __  T
GAM608  NHLH1   3'  TGAGATGTGGCCCACTCGTTG  24659       CCGATCAAGA
                                TGAGAT        ACTCGTTG
                                ||||||        ||||||||
                                ACTCTA        TGAGCAAC
                                   CACCGGG___
GAM609  IL1R1   3'  GGCTTCTGCTGCAAAAT     9364      A  GAG
                                GGC TC   TGTTGCAAAAT
                                ||| ||   ||||||||||
                                CCG AG   ACGACGTTTTA
                                  A ___
GAM609  NET1    3'  TCCAGCATTTGCAAAA      25230         CGAGTG
                                TCCGGCAT     TTGCAAAA
                                ||||||||     ||||||||
                                AGGTCGTA     AACGTTTT
                                   _______
GAM610  ADAR    3'  GAGGAAATGGACCGCAGG    31904        CAA    CTT
                                GAGGAAA   ACTGT   GG
                                |||||||   |||||   ||
                                CTCCTTT   TGGCG   CC
                                    ACC    T__
GAM610  ADRBK2  3'  GAGAAAACAAACTTCACAGG   23129           G  TT_
                                GAGGAAACAAACT TC   GG
                                |||||||||||| ||   ||
                                CTCTTTTGTTTGA AG   CC
                                      _  TGT
GAM610  ATP10C  3'  GAGGAAACCAGGACTCTGTTTG 35980         AAA____   C
           GAA                    GAGGAAAC      CTGT TTGGAA
                                ||||||||      |||| ||||||
                                CTCCTTTG      GACA AACCTT
                                    GTCCTGA   _
GAM610  CCNG1   5'  GAGGGGGACTGTCCTGG     19768      AAACAA
                                GAGG     ACTGTCTTGG
                                ||||     ||||||||||
                                CTCC     TGACAGGACC
                                  CCC___
GAM610  CLASP1  3'  GAGGAAACAAGTTGG       42240          ACTGTC
                                GAGGAAACAA     TTGG
                                ||||||||||     ||||
                                CTCCTTTGTT     AACC
                                     C_____
GAM610  CREB1   3'  GAGGCAGGTGTTGGAACA    39596      AAACAAACT  C
                                GAGG        GT TTGGAACA
                                ||||        || ||||||||
                                CTCC        CA AACCTTGT
                                  GTC_______  C
GAM610  DEFA6   3'  GAGGAAACAAAGTTGATGG   12565          CTGTCT
                                GAGGAAACAAA     TGG
                                ||||||||||      |||
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                                CTCCTTTGTTT     ACC
                                      CAACT_
GAM610  EIF4EBP1  3'  GAGGGGGCAGGTGCCCTGA   19887      AAA  AAC
                                GAGG   CA   TGTCTTGG
                                ||||   ||   ||||||||
                                CTCC   GT   ACGGGACT
                                  CCC  CC_
GAM610  FCRH3     3'  GGAAACAAAATATTTGGA    38113         C   C
                                GGAAACAAA TGT TTGGA
                                ||||||||| ||| |||||
                                CCTTTGTTT ATA AACCT
                                      T   _
GAM610  FOXD2     3'  GAGGAAACGAACTTCCTTG   20964         A    GT
                                GAGGAAAC AACT  CTTG
                                |||||||| ||||  ||||
                                CTCCTTTG TTGA  GAAC
                                     C    AG
GAM610  GALC      3'  GAGGAAACAAATTGTGG     6673          C   CTT
                                GAGGAAACAAA TGT   GG
                                |||||||||| |||   ||
                                CTCCTTTGTTT ACA   CC
                                      A   ___
GAM610  GAS7      3'  GAGGAAACACATTCATACCGG  25270         AACT_  C
                                GAGGAAACA    GT TTGG
                                |||||||||    || ||||
                                CTCCTTTGT    TA GGCC
                                     GTAAG  T
GAM610  KLF8      3'  GAGGAAAAAATTGTCCCA    28534        C   C
                                GAGGAAA AAA TGTCTTG
                                ||||||| ||| |||||||
                                CTCCTTT TTT ACAGGGT
                                    _   A
GAM610  MKI67     3'  GGAAACAAACGTGGAGACA    14524         TGTCT   _
                                GGAAACAAAC    TGGA ACA
                                ||||||||||    |||| |||
                                CCTTTGTTTG    ACCT TGT
                                      C____    C
GAM610  NCL       3'  AGGACTGTATACTGTCTTGGAA 41049      AACAA_
                                AGGA     ACTGTCTTGGAA
                                ||||     ||||||||||||
                                TCCT     TGACAGAACCTT
                                  GACATA
GAM610  PPARBP    5'  GAGGAAACAAGTTGGCTCG   21929         AC  T
                                GAGGAAACAA  TG CTTG
                                ||||||||||  || ||||
                                CTCCTTTGTT  AC GAGC
                                      CA  C
GAM610  PPT2      5'  GAGGAAACAGGCGGA       23123         AACT  CTT
                                GAGGAAACA   GT   GGA
                                |||||||||   ||   |||
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                                CTCCTTTGT   CG  CCT
                                    C___ ___
GAM610  RAI3    3'  GAGGCAAACTGTTCCCG    19568     AAA      _
                                GAGG  CAAACTGT CTTG
                                ||||  |||||||| ||||
                                CTCC  GTTTGACA GGGC
                                  ___      A
GAM610  TAP2    3'  GAGACAGATGGGCTGGAACA  8083     GAA  AAC  TC
                                GAG  ACA  TG TTGGAACA
                                |||  |||  ||  ||||||||
                                CTC  TGT  AC  GACCTTGT
                                  ___  CT_  CC
GAM610  TGFBR3  3'  GAGGGCAGCACCCATCTTGGGA 17490     AAACAAA       A
           CA                     GAGG      CTGTCTTGG ACA
                                ||||      ||||||||| |||
                                CTCC      GGTAGAACC TGT
                                  CGTCGTG       C
GAM611  ABCD2   3'  ACACTTCGTCTAACT      23147     CTCC
                                ACAC   TCGTCTAACT
                                ||||   ||||||||||
                                TGTG   AGCAGATTGA
                                  A___
GAM611  FIGF    3'  TACAGTTTTCCTCATCTGCTCT 20922     ACACC       AA
                                TACA   TCCTCGTCT  CTCT
                                ||||   |||||||||  ||||
                                ATGT   AGGAGTAGA  GAGA
                                  CAAA_       C_
GAM611  HPSE    3'  TACAGAATCTCCTCGCCT   27419     ACAC
                                TACA   CTCCTCGTCT
                                ||||   ||||||||||
                                ATGT   GAGGAGCGGA
                                  CTTA
GAM611  NDRG2   3'  CAGCACCTCCCAGGTTAGCTCT 32191    A      C_  C  A
                                CA CACCTCCT  GT TA CTCT
                                || ||||||||  || || ||||
                                GT GTGGAGGG  CA AT GAGA
                                 C       TC  _  C
GAM611  PABPC4  5'  TACGGCCCTCCCCGCGACT   19230    AACA       CTA
                                TAC   CCTCCTCGT   ACT
                                |||   |||||||||   |||
                                ATG   GGAGGGGCG   TGA
                                  CCG_       C__
GAM611  PCDHA9  3'  TACAGCACCCCCTTTGCTC   36551     A      CGTCTAA
                                TACA CACCTCCT      CTC
                                |||| ||||||||      |||
                                ATGT GTGGGGGA      GAG
                                  C       AAC_____
GAM611  TJP1    5'  ACCTCCTCCTCCTCT      17532         G  TAA
                                ACCTCCTC TC   CTCT
                                |||||||| ||   ||||
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                                TGGAGGAG AG   GAGA
                                    G  ___
GAM612  ABH      3'  CCATGTCAAACACTTCTCT   40739     A  T__
                                CCA GTT   TACTTCTCT
                                ||| |||   |||||||||
                                GGT CAG   GTGAAGAGA
                                  A   TTT
GAM612  ADCY7    3'  CCAAGTTGTCTCTAAACA    9983        TTACT
                                CCAAGTT    TCTCTAAACA
                                |||||||    ||||||||||
                                GGTTCAA    AGAGATTTGT
                                    C____
GAM612  ATRX     3'  CCAAGTTTTATTTCAAAC    39606         C   TCT
                                CCAAGTTTTA TTC   AAAC
                                |||||||||| |||   ||||
                                GGTTCAAAAT AAG   TTTG
                                     A  ___
GAM612  COL17A1  3'  CCCCAAGTGCCATTTTCT    39078        T  C_
                                CCCCAAGT TTA  TTCT
                                |||||||| |||  ||||
                                GGGGTTCA GGT  AAGA
                                    C   AA
GAM612  DISC1    3'  CCCAAGTTTTGCTTCACT    33032         A   T
                                CCCAAGTTTT CTTC CT
                                |||||||||| ||||| ||
                                GGGTTCAAAA GAAG GA
                                     C   T
GAM612  EFNA3    3'  CCCCAAGTTTGGTACCAAACA  22396          TACTTCT
                                CCCCAAGTTT      CTAAACA
                                ||||||||||      |||||||
                                GGGGTTCAAA      GGTTTGT
                                     CCAT___
GAM612  GALNT7   5'  CCCCAAGTCCTCTCT      38355        TTTA
                                CCCCAAGT   CTTCTCT
                                ||||||||   |||||||
                                GGGGTTCA   GGAGAGA
                                    _____
GAM612  KCNF1    5'  CCCGAGCCTTTTCTAAACA   13828    A  TTTA  C
                                CCC AGT   CTT TCTAAACA
                                ||| |||   ||| ||||||||
                                GGG TCG   GAA AGATTTGT
                                  C  _____  A
GAM612  LPHH1    3'  GTTTCACAATTTCTCTAAACA  29389      ___
                                GTTTTAC   TTCTCTAAACA
                                |||||||   ||||||||||
                                CAAAGTG   AAGAGATTTGT
                                    TTA
GAM612  NPY2R    5'  CCCCAAGTTTGATACTCT    9490         TACTT
                                CCCCAAGTTT    CTCT
                                ||||||||||    ||||
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                                GGGGTTCAAA    GAGA
                                      CTAT_
GAM612  PIAS1    3'  GCTTGTATACTTTTCTAAACA  32078     ___    C
                                GTTT   TACTT TCTAAACA
                                ||||   ||||| ||||||||
                                CGAA   ATGAA AGATTTGT
                                  CAT    A
GAM612  PIWIL1   3'  CCCAAGTTTCATCCA      43751         CTTC
                                CCCAAGTTTTA   TCTA
                                ||||||||||   ||||
                                GGGTTCAAAGT   AGGT
                                     ____
GAM612  POU5F1   3'  CCAGGTTTTCTTTCCCTA   15467    A    AC
                                CCA GTTTT  TTCTCTA
                                ||| |||||  |||||||
                                GGT CAAAA  AAGGGAT
                                  C    GA
GAM612  RNF28    3'  CCCTAGTCCCTGCTCTCT   37197    A    AC
                                CCC AGTTTT  TTCTCT
                                ||| ||||||  ||||||
                                GGG TCAGGG  GAGAGA
                                  A     AC
GAM612  SPTAN1   3'  CCTAAGTCTTATTCCAAGCTAA 17100   C      C   ___
                                CC AAGTTTTA TTCT   CTAA
                                || |||||||| ||||   ||||
                                GG TTCAGAAT AAGG   GATT
                                 A      _   TTC
GAM612  TAF7     5'  CCAAGTCTTTTCTCTAAA   24861        AC
                                CCAAGTTTT  TTCTCTAAA
                                |||||||||  |||||||||
                                GGTTCAGAA  AAGAGATTT
                                     __
GAM612  TNFSF4   3'  CCCTTAAGCATTCTCTAAA   17748    __   TTTAC
                                CCC  AAGT    TTCTCTAAA
                                |||  ||||    |||||||||
                                GGG  TTCG    AAGAGATTT
                                  AA   T____
GAM612  UNC13    3'  CCCCAAATTTTTCCTTAAA   26863         ACT  TC
                                CCCCAAGTTTT   TC  TAAA
                                ||||||||||   ||  ||||
                                GGGGTTTAAAA   AG  ATTT
                                     ___  GA
GAM613  FCGR2A   3'  GGGGGGTAGGTATCTTCTT    44279    CAA_   C
                                GG    AGGT ATCTTCTT
                                ||    |||| ||||||||
                                CC    TCCA TAGAAGAA
                                 CCCA   _
GAM613  PACE4    3'  GTGAGACAAAGGTCATCTT    15056     A
                                GTGA GGCAAAGGTCATCTT
                                |||| ||||||||||||||
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                                CACT CTGTTTCCAGTAGAA
                                   _
GAM613  PROL4    3'  TGAAGGAAGTTATCTTCTT   28523       CAA   C
                                TGAAGG  AGGT ATCTTCTT
                                ||||||  |||| ||||||||
                                ACTTCC  TTCA TAGAAGAA
                                   ___   A
GAM613  GRM7     3'  GGTTGTTTTTTTCCACTAAATT 9189        ___   CAGG__
              GG                  GGTTGTTT  TCCAC    GG
                                ||||||||  |||||    ||
                                CCAACAAA  AGGTG    CC
                                    AAA   ATTTAA
GAM613  IKBKB    3'  GGCTGCCCCATGTCAGGGGGTC 41807      TT   C__
              GA                  GGTTGT  TCCA  CAGGGGGTCGA
                                ||||||  ||||  ||||||||||
                                CCGACG  GGGT  GTCCCCCAGCT
                                   __   ACA
GAM613  OXTR     3'  GGTTGTTTCCACTTTTTGG   9528        T   CAGG_
                                GGTTGTTT CCAC    GG
                                |||||||| ||||    ||
                                CCAACAAA GGTG    CC
                                   _   AAAAA
GAM613  SAS      3'  GGTTGTTTTCTCCTTGG    25589        CA  AG
                                GGTTGTTTTC  CC  GG
                                |||||||||  ||  ||
                                CCAACAAAAG  GG  CC
                                    A_  AA
GAM614  AF1Q     3'  TGGAGTAGACAGATA      27730    A   AACATT
                                TG GAGTA    GACGGATA
                                || |||||    ||||||||
                                AC CTCAT    CTGTCTAT
                                  _   _______
GAM614  AOC2     3'  TGAGAGGAACATTGAGGG    41819      TA      C
                                TGAGAG  AACATTGA GG
                                ||||||  |||||||| ||
                                ACTCTC  TTGTAACT CC
                                   C_      C
GAM614  KRT13    5'  TGAGAGCAGGTGCAGATA    14010       AACAT  A
                                TGAGAGTA    TG CGGATA
                                ||||||||    || ||||||
                                ACTCTCGT    AC GTCTAT
                                    CC___  _
GAM614  MTMR8    3'  TGAGAATAAATGTAAATGGATA 31758         CATT  C
              AA                  TGAGAGTAAA   GA GGATAAA
                                ||||||||||   || |||||||
                                ACTCTTATTT   TT CCTATTT
                                    ACAT  A
GAM614  STXBP1   3'  TGAGAGCAGGCACTGAGGG   17211        AA    C
                                TGAGAGTA  CATTGA GG
                                ||||||||  |||||| ||
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                                ACTCTCGT  GTGACT CC
                                    CC     C
GAM614  SVIL     3'  TGAGAGTAAAATTGTAGA    34739          C    AC
                                TGAGAGTAAA ATTG  GGA
                                |||||||||| ||||  |||
                                ACTCTCATTT TAAC  TCT
                                      _   A_
GAM614  GRIN2A   3'  ATAACATCACCATTGGCA    9104        TC     _
                                ATAAC  TATCAT GGCA
                                |||||  |||||| ||||
                                TATTG  GTGGTA CCGT
                                   TA     A
GAM614  LMO1     5'  ATAACCCTGTCTCTGGCA    14177         A  A_
                                ATAACTCT TC  TGGCA
                                |||||||| ||  |||||
                                TATTGGGA AG  ACCGT
                                     C  AG
GAM614  PCDH9    5'  ACAATGACCACCATGGCA    44395      CT_
                                ATAA   CTATCATGGCA
                                ||||   ||||||||||||
                                TGTT   GGTGGTACCGT
                                  ACT
GAM615  BSN      3'  TGGGGATTCCTTTTTACCTGCT 18422      AA   CA
                                TGG  GAT  TTTTTTTACCTGCT
                                |||  |||  ||||||||||||||
                                ACC  CTA  GGAAAAATGGACGA
                                  C_  A_
GAM615  GARP     3'  TGGGTGAGGCTTTTTACCTG   24321      AA  TCAT
                                TGG  GA   TTTTTTACCTG
                                |||  ||   ||||||||||
                                ACC  CT   GAAAAATGGAC
                                  CA  CC__
GAM615  SIM2     3'  TGGAAGCTCATTTTTTAAACAC 22885        A       T_ _
            TGCT                    TGGAAG TCATTTTTT  AC CTGCT
                                |||||| |||||||||  || |||||
                                ACCTTC AGTAAAAAA  TG GACGA
                                   G        TT  T
GAM615  SYT4     3'  TGGAGGACATTTTTTTA     41661      A  T
                                TGGA GA CATTTTTTTA
                                |||| || ||||||||||
                                ACCT CT GTAAAAAAAT
                                  C  _
GAM615  ADAM29   3'  CTGGGAGGGTGTCACCCGA   44619     A_       G
                                CTG  AGGGTGTCG TTGG
                                |||  ||||||||| ||||
                                GAC  TCCCACAGT GGCT
                                  CC        G
GAM615  ARF1     3'  CCTGAAGGTGGGTAGG      43305         G  TC   T
                                CCTGAAGG TG  GGT GG
                                |||||||| ||  ||| ||
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                                GGACTTCC AC  CCA CC
                                   _ __   T
GAM615  CRABP1   3'  CCTGGGGGGTGGGGGTGGG   40751     AA    TC   T
                                CCTG  GGGTG  GGT GG
                                ||||  |||||  ||| ||
                                GGAC  CCCAC  CCA CC
                                  CC    CC   C
GAM615  EXTL2    3'  CCTGGAAGAGCTGGTTGGCAGG 11017     _     GTC      A
           G                     CCTG AAGGGT   GGTTGGCA GG
                                ||||  ||||||   |||||||| ||
                                GGAC TTCTCG   CCAACCGT CC
                                  C     A__       C
GAM615  FOSB     3'  CCAGGAGGGTCGGCTGGCAGGG 27533    TGAA   T        A
                                CC    GGG GTCGGTTGGCA GG
                                ||    ||| ||||||||||| ||
                                GG    TCC CAGCCGACCGT CC
                                 TCC_  _         C
GAM615  GALGT    5'  CCCGGGGGCGGTTGGCGG    11179     AA   T T      AA
                                CCTG  GGG G CGGTTGGC  G
                                ||||  ||| | ||||||||  |
                                GGGC  CCC C GCCAACCG  C
                                  __   _ _       CC
GAM615  HOXD4    3'  CCTGGAGGGGTGGAGTGG    31172     A    T  C  T_
                                CCTG AGGG GT GG  TGG
                                |||| |||| || ||  |||
                                GGAC TCCC CA CC  ACC
                                  C    _ _  TC
GAM615  NR2E1    3'  CCTGAAGGGTTTGTTAGTTGA  17575          __  CG
                                CCTGAAGGGT  GT  GTTGG
                                ||||||||||  ||  |||||
                                GGACTTCCCA  CA  CAACT
                                      AA  AT
GAM615  RET      3'  CCTGAAGGTGGGTAAGG     33932        G  TC   T_
                                CCTGAAGG TG  GGT  GG
                                |||||||| ||  |||  ||
                                GGACTTCC AC  CCA  CC
                                   _ __   TT
GAM615  SCRT1    3'  TGAAGGGGCCGGCAAG      36372        TGTCG
                                TGAAGGG    GTTGGCAAG
                                |||||||    |||||||||
                                ACTTCCC    CGGCCGTTC
                                   _____
GAM615  SHANK2   3'  CTGGTGGGTGGGCTGGCAGGG  29456     AA    TC      A
                                CTG  GGGTG  GGTTGGCA GG
                                |||  |||||  |||||||| ||
                                GAC  CCCAC  CCGACCGT CC
                                  CA     __       C
GAM615  SLC1A4   3'  TGGGAGGGTAAAAGTTGGCAAG 16759    A_     TC
           G                     TG  AGGGTG  GGTTGGCAAGG
                                ||  ||||||  ||||||||||
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                                AC  TCCCAT  TCAACCGTTCC
                                 CC     TT
GAM615  SLC6A8   3'  CCTGGAGGGGTGCGGTGGG   24758     AA_    T   T
                                CCTG   GGGTG CGGT GG
                                ||||   ||||| |||| ||
                                GGAC   CCCAC GCCA CC
                                  CTC    _   C
GAM615  SUV39H1  3'  CTGAAGGTGGGTGGG      17222       G  TC   T
                                CTGAAGG TG  GGT GG
                                ||||||| ||  ||| ||
                                GACTTCC AC  CCA CC
                                    _ __  C
GAM616  GPRK6    3'  TGCTGGTGGGGGCCTCGGGCT  13275    CA  T   A_   CG
                                TGC  GT GGGG  TTGG  GCT
                                |||  || ||||  ||||  |||
                                ACG  CA CCCC  AGCC  CGA
                                  AC  C   GG   __
GAM616  INHBB    3'  TGTCAGTTGAGGGTTCTCGCT  13568    C       A  GG  G
                                TG CAGTTGGGG TT  CG CT
                                || |||||||| ||  || ||
                                AC GTCAACTCC AA  GC GA
                                 A       C  GA  _
GAM616  PLTP     3'  TGCCAGCTTGGGGATTGA    26348        _
                                TGCCAGTT GGGGATTGG
                                |||||||| |||||||||
                                ACGGTCGA CCCCTAACT
                                    A
GAM616  ALPL     3'  GCTGGAGGCCAGAAGTGGGTTT 7890        G  A  _   C
          G                      GCTGGAGG CA AA TGGG TTG
                                |||||||| || || |||| |||
                                CGACCTCC GT TT ACCC AAC
                                    G  C  C   A
GAM616  ETF1     3'  GCTGGAGGGTGAGGC       21830         CAAAA  _
                                GCTGGAGGG    TG GGC
                                |||||||||    || |||
                                CGACCTCCC    AC CCG
                                     _____  T
GAM616  FBXL11   3'  GCTGGGAGGCAGGTTGGGGCTT 29432      AG   AAAT_
          G                      GCTGG  GGCA    GGGCTTG
                                |||||  ||||    |||||||
                                CGACC  CCGT    CCCGAAC
                                  CT    CCAAC
GAM616  HR       3'  GCAGGAGGGCAGAAGGTTG   32919    T      AAAT   C
                                GC GGAGGGCA    GGG TTG
                                || ||||||||    ||| |||
                                CG CCTCCCGT    TCC AAC
                                 T       CT__   _
GAM616  KCNK3    3'  GCTGGAGGCCAGTTAGCTTG   13906        G  AAATG
                                GCTGGAGG CA    GGCTTG
                                |||||||| ||    ||||||
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                                CGACCTCC GT    TCGAAC
                                    G  CAA__
GAM616  LNK      3'  GCTGGAGGGAGGGAACTTA   24204        CAAAAT
                                GCTGGAGGG     GGGCTTG
                                |||||||||     |||||||
                                CGACCTCCC     CTTGAAT
                                    TCC___
GAM616  MAP3K7IP1 3'  GGAGGGGTGGGCTTG      25930       CAAAA
                                GGAGGG    TGGGCTTG
                                ||||||    ||||||||
                                CCTCCC    ACCCGAAC
                                  C____
GAM616  NOS1     3'  AGCTGGAAATGGGT       8369        GGGCAA     C
                                AGCTGGA     AATGGG T
                                |||||||     |||||| |
                                TCGACCT     TTACCC A
                                   _______     A
GAM616  NUP98    3'  TAGATGGAGGGTGGGAAATGCT 32234     C      CAAAATGG
              T                  TAG TGGAGGG       GCTT
                                 ||| |||||||       ||||
                                 ATC ACCTCCC       CGAA
                                   T      ACCCTTTA
GAM616  OBP2A    3'  GCTGGAGGGTAGGTCC      31041        CAAAA   _
                                GCTGGAGGG    TGGG CT
                                |||||||||    |||| ||
                                CGACCTCCC    ATCC GG
                                    _____   A
GAM616  OBP2B    3'  GCTGGAGGGTAGGTCC      31036        CAAAA   _
                                GCTGGAGGG    TGGG CT
                                |||||||||    |||| ||
                                CGACCTCCC    ATCC GG
                                    _____   A
GAM616  PCSK2    5'  GCTGGAGGGGAAGCC       15128        CAAAAT
                                GCTGGAGGG     GGGCT
                                |||||||||     |||||
                                CGACCTCCC     TTCGG
                                    C_____
GAM616  PPL      3'  GCTGCAAGGAGTGGGCTT    15494     G   CAAAA
                                GCTG AGGG    TGGGCTT
                                ||||  ||||    |||||||
                                CGAC TTCC    ACCCGAA
                                  G   TC___
GAM616  PPP1R12B 3'  TGGAAGGCAAGGACT       36959        AAT
                                TGGAGGGCAA   GGGCT
                                ||||||||||   |||||
                                ACCTTCCGTT   CCTGA
                                    ___
GAM616  RHO      3'  GCTGAAGATGGGCT        8062        GGCAAA
                                GCTGGAG     ATGGGCT
                                |||||||     |||||||
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                              CGACTTC     TACCCGA
                                          ______
GAM616  RNF6     5' TGGGAGGCGGGATAGGCTTG  25582     AG   AAA
                              TGG  GGC   ATGGGCTTG
                              |||  |||   |||||||||
                              ACC  CCG   TATCCGAAC
                                CT   CCC
GAM616  WIG1     3' AGCTGGGGCATGAAAATGGGCT 45384       AG   ___
           TG                   AGCTGG  GGCA   AAATGGGCTTG
                              ||||||  ||||   ||||||||||
                              TCGACC  CCGT   TTTACCCGAAC
                                 __   ACT
GAM617  CDC25B   3' ACAAAGGAGCGTTTCAGG    34844       AG    _ GACGCG
                              ACAAAG  GCGTT C     AGG
                              ||||||  ||||| |     |||
                              TGTTTC  CGCAA G     TCC
                                 CT    A _______
GAM617  CRH      5' CAGAGAGACGTCTCCGGGG    8894     A       T GA  CGA
                              CA AGAGGCGT C  CG   GG
                              || ||||||||| |  ||   ||
                              GT TCTCTGCA G  GC   CC
                               C       _ AG  C__
GAM617  DPP6     3' GAGGCGCTGCTGCGGGGA    39130        CGAC   A
                              GAGGCGTT    GCG GGA
                              ||||||||    ||| |||
                              CTCCGCGA    CGC CCT
                                   CGA_   C
GAM617  FGF18    5' GAGGCGCCTGGCCGGTGCGGGG 38006        _____   AC   A
           A                   GAGGCGT    TCG  GCG GGA
                              |||||||    |||  ||| |||
                              CTCCGCG    GGC  CGC CCT
                                  GACC   CA   C
GAM617  FZD1     3' AGAGGCGCGCGAGGA      18608        TTCGA
                              AGAGGCG     CGCGAGGA
                              |||||||     ||||||||
                              TCTCCGC     GCGCTCCT
                                          ______
GAM617  JUND     3' GGAAAGAGGCAGCGCGAGG   23806   C       TTCGA
                              A AAAGAGGCG     CGCGAGG
                              | |||||||||     |||||||
                              C TTTCTCCGT     GCGCTCC
                               C        C_____
GAM617  MLLT4    3' AAGAGGCGTTTTCTAAGGA   25522          CGACGC
                              AAGAGGCGTT     GAGGA
                              ||||||||||     |||||
                              TTCTCCGCAA     TTCCT
                                    AAGA__
GAM617  PLEK     3' ACAGGGAGGCGTTGGCTCAGG  15387     AA       CGAC  G_
                              ACA  GAGGCGTT    GC  AGG
                              |||  ||||||||    ||  |||
```

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                                TGT  CTCCGCAA   CG  TCC
                                  CC       C___  AG
GAM617  SCN4A    3'  AAAGAGACGGGGCGTGG     7312          TTCGAC   A
                                AAAGAGGCG     GCG GG
                                |||||||||     ||| ||
                                TTTCTCTGC     CGC CC
                                     CC____   A
GAM617  SLC16A2  3'  ACAAAGAGGCAGAGTGAGG   27147          TTC  CGC
                                ACAAAGAGGCG   GA   GAGG
                                ||||||||||   ||   ||||
                                TGTTTCTCCGT   CT   CTCC
                                      ___  CA_
GAM617  TEX15    3'  AAAGAGGCTTATCCTGGGGA  36323         __   GACGCGA
                                AAAGAGGC  GTTC      GGA
                                ||||||||  ||||      |||
                                TTTCTCCG  TAGG      CCT
                                     AA   ACC_____
GAM617  WHSC1    3'  GAGGCGCTCCCTCCCGAGGA  39364         GACG_
                                GAGGCGTTC    CGAGGA
                                |||||||||    ||||||
                                CTCCGCGAG    GCTCCT
                                     GGAGG
GAM617  ZFHX1B   5'  AAGAAGCCGCGAAG       31335        GTTCGA
                                AAGAGGC     CGCGAGG
                                |||||||     |||||||
                                TTCTTCG     GCGCTTC
                                      _______
GAM617  ZNF192   5'  AGAGGCGCCCCGTCGTGG    26672          GA  _  A
                                AGAGGCGTTC  CG CG GG
                                ||||||||||  || || ||
                                TCTCCGCGGG  GC GC CC
                                     __  A  A
GAM617  ZNF35    3'  CAAAGAGGTGTCTCATTAGG  18282         C   CGA  CG
                                CAAAGAGG GTT   CG  AGG
                                |||||||| |||   ||  |||
                                GTTTCTCC CAG   GT  TCC
                                     A   A__  AA
GAM618  ACHE     5'  GGAGCTGGAGGCGGCCGATG  8564       ACG  TAAG
                                GGAG   GG   GGCCGATG
                                ||||   ||   ||||||||
                                CCTC   CC   CCGGCTAC
                                  GA_  TCCG
GAM618  ADH1A    5'  CAGGAGACTGGTGAGTCC     8571          G   A  GG
                                CAGGAGAC GGT AG  CC
                                |||||||| ||| ||  ||
                                GTCCTCTG CCA TC  GG
                                     A   C  A_
GAM618  IFITM2   3'  GAGGATAAAGGGCTGATGC   26971    C     _    C
                                GA GGGTAA GGGC GATGC
                                || |||||| |||| |||||
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                                CT CCTATT CCCG CTACG
                                 _     T    A
GAM618  IGFBP1   5'  CAGCAGACAGGGGCCGATG   8243      G      TAAG
                                CAG AGACGGG    GGCCGATG
                                ||| |||||||    ||||||||
                                GTC TCTGTCC    CCGGCTAC
                                  G      ____
GAM618  LTBR     5'  GGGACGGGACTCAGGGCCGATG 14258    A     TA__
                                GG GACGGG    AGGGCCGATG
                                || ||||||    ||||||||||
                                CC CTGCCC    TCCCGGCTAC
                                 _     TGAG
GAM618  PTGFRN   3'  CAGGGGGTGGGGTAGGGTCG   42586     AGAC_    A   C
                                CAGG     GGGTA GGG CG
                                ||||     ||||| ||| ||
                                GTCC     CCCAT CCC GC
                                  CCCAC     _   A
GAM618  SOX12    3'  GGTGACAGGAAGGGCCGGTGC  28054    A     T      A
                                GG GACGGG AAGGGCCG TGC
                                || |||||| |||||||| |||
                                CC CTGTCC TTCCCGGC ACG
                                 A     _       C
GAM618  TRPM2    5'  CAGGAAGATGAGGCTGATG    17689      GAC    AA    C
                                CAGGA   GGGT  GGGC GATG
                                |||||   ||||  |||| ||||
                                GTCCT   TCTA  TCCG CTAC
                                  ____    C_    A
GAM618  USH2A    3'  CAGGAGGAGGGTAAGGCCA    28301       AC       G
                                CAGGAG  GGGTAAGG CCG
                                ||||||  |||||||| |||
                                GTCCTC  CCCATTCC GGT
                                   CT       _
GAM618  XRCC3    3'  AGAGGTGGGTGAGGAGGAGC   24098      AC    A    CC  T
                                GGAG  GGGT AGGG  GA GC
                                ||||  |||| ||||  || ||
                                TCTC  CCCA TCCT  CT CG
                                  CA    C    C_ _
GAM619  C5R1     3'  GAATAACATTCTTGAAATGA   11918         AAG      C
                                GAATAGCAT   TTTGAAA GA
                                |||||||||   ||||||| ||
                                CTTATTGTA   GAACTTT CT
                                     A__       A
GAM620  SQLE     3'  TGGTACTATGCTATATATATCC 17109    A   G  A
          TC                      TG TAC AT CTATATGTATTCTT
                                || ||| || ||||||||||||||
                                AC ATG TA GATATATATAGGAG
                                 C   A  C
GAM620  ROS1     3'  AGTTATAGACCACCATGACATT 16364          AA     T_
                                AGTTATAGAC  ATTAT  CATT
                                ||||||||||  |||||  ||||
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                                TCAATATCTG  TGGTA  GTAA
                                     G_    CT
GAM620  SOCS5    3'  GAGGTTACAGATACTCAT    30421    A      CAAAT
                                GA GTTATAGA    TATTCAT
                                || ||||||||    |||||||
                                CT CAATGTCT    ATGAGTA
                                 C      _____
GAM620  TTC3     3'  GAAGTTATGTACAAAACACACT 17714        AG    T__
             CATT                GAAGTTAT  ACAAA   TATTCATT
                                |||||||| |||||  ||||||||
                                CTTCAATA  TGTTT   GTGAGTAA
                                     CA    TGT
GAM621  DNA2L    3'  TCTAGAATACTGAAATAC    45038         AA
                                TCTAGAATAC  AAATAT
                                ||||||||||  ||||||
                                AGATCTTATG  TTTATG
                                      AC
GAM621  DYRK2    3'  TAGAACACAAAAAGTTTCT    27041           TATGG
                                TAGAATACAAAAA    TCT
                                ||||||||||||    |||
                                ATCTTGTGTTTTT    AGA
                                       CAA__
GAM621  PGK1     3'  TCTAGAATGCACAATGGT    7114         A  AAAAT
                                TCTAGAAT CA    ATGGT
                                |||||||| ||    |||||
                                AGATCTTA GT    TACCA
                                     C  GT___
GAM621  SEPP1    3'  TCCATCATAAAAAATATGGT   23999     GA   C
                                TCTA  ATA AAAAATATGGT
                                ||||  ||| ||||||||||
                                AGGT  TAT TTTTTATACCA
                                  AG  _
GAM621  SMARCA3  3'  TCTGGAATGCAAATATGGT    40057     A    ACAA
                                TCT GAAT    AAATATGGT
                                ||| ||||    |||||||||
                                AGA CTTA    TTTATACCA
                                  C    CG__
GAM621  STC1     3'  TCTAACTTAGAATATGGTCTA  17185      AATACAAA
                                TCTAG       AATATGGTCTA
                                |||||       ||||||||||
                                AGATT       TTATACCAGAT
                                   GAATC___
GAM621  UTY      3'  TAGAAACAAAAATCACAAATCT 28317       T       AT__
                                TAGAA ACAAAAAT    GGTCT
                                ||||| ||||||||    |||||
                                ATCTT TGTTTTTA    TTAGA
                                   _       GTGT
GAM622  CYP1A1   5'  GGGTGGACTCTTGGAGCCT    7975     A       TCACA
                                GG TGGACTCTT    AGCCT
                                || |||||||||    |||||
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                                CC ACCTGAGAA    TCGGA
                                 C       CC___
GAM622  LAIR1   3'  GATGGACTCGGCCATGGGC   14054       TT  CAA
                                GATGGACTC  TCA  GC
                                |||||||||  |||  ||
                                CTACCTGAG  GGT  CG
                                     CC   ACC
GAM622  RBBP5   3'  TGGGTGGAGCACAGGCC    22807    A  CTCTTT   A
                                TGG TGGA     CACA GCC
                                ||| ||||     |||| |||
                                ACC ACCT     GTGT CGG
                                  C   C_____   C
GAM622  TAL1    3'  TGGATGGATCAACATAGGCCT  17293       C  TTT  CAA
                                TGGATGGA TC   CA   GCCT
                                |||||||| ||   ||   ||||
                                ACCTACCT AG   GT   CGGA
                                     _ TT_  ATC
GAM623  CDH19   3'  TAGATGACATTGAAAAAT    34502       CTA
                                TAGATGACA   AAGAAT
                                |||||||||   ||||||
                                ATCTACTGT   TTTTTA
                                     AAC
GAM624  FZD4    5'  GGCCAGCATCGGGGGGTAGC   29159       C   AAGCA
                                GGCCGGCA CGG    AGC
                                |||||||| |||    |||
                                CCGGTCGT GCC    TCG
                                     A   CCCA_
GAM624  ABCC3   5'  GCGGCGGGCAGAGCGGGCGCC  33423    _ C    CA
                                GCG C GGCGG  CGGGCGCC
                                ||| | |||||  ||||||||
                                CGC G CCGTC  GCCCGCGG
                                  C C    TC
GAM624  ABL1    5'  GCCCGGCCCCCGGGCGCC    28713   G    GGCA
                                GC CCGGC    CGGGCGCC
                                || |||||    ||||||||
                                CG GGCCG    GCCCGCGG
                                 _    GGG_
GAM624  ADAM12  5'  GCCCGGCGGCGAGCGC     18472   G      AC
                                GC CCGGCGGC  GGGCGC
                                || ||||||||  ||||||
                                CG GGCCGCCG  CTCGCG
                                 _      ___
GAM624  ADAM23  5'  GCTCGGCGCGCATGGTGCC   19205   _   _  C  GC
                                GC CGGCG GCA GG  GCC
                                || ||||| ||| ||  |||
                                CG GCCGC CGT CC  CGG
                                 A    G   A A_
GAM624  ADAMTS8 5'  GCCCGGCGGCGGGAGCGC    28163   G      AC
                                GC CCGGCGGC  GGGCGC
                                || ||||||||  ||||||
```

```
                                CG GGCCGCCG  CTCGCG
                                 _      CC
GAM624  ADCY6   5' GCGTGGTGGCGGGCGCC    34172    CC  C   AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A   __
GAM624  AF5Q31  5' GCGGCGGCGGCAGCGATGCGCC 30855    C      _  _
                                GCG CGGCGGCA CGG GCGCC
                                ||| |||||||| ||| |||||
                                CGC GCCGCCGT GCT CGCGG
                                  C       C   A
GAM624  AP1M1   5' GCGACGGTGGGGACTGC    37170    C   C  CAC   _
                                GCG CGG GG   GGGC GC
                                ||| ||| ||   |||| ||
                                CGC GCC CC   CCTG CG
                                  T   A ____   A
GAM624  AQP5    5' GCCGGCGGGGGGGCGCC     11629        CAC
                                GCCGGCGG   GGGCGCC
                                ||||||||   |||||||
                                CGGCCGCC   CCCGCGG
                                     C__
GAM624  AQP6    3' GCGTGGTGGCAGGCGCC    38248    CC  C    CG
                                GCG  GG GGCA  GGCGCC
                                |||  || ||||  ||||||
                                CGC  CC CCGT  CCGCGG
                                  A_  A   __
GAM624  AXUD1   5' GCGGCGGCGGCGGGAGACTGCC 37490    C      AC_   _
                                GCG CGGCGGC   GGGC GCC
                                ||| |||||||   |||| |||
                                CGC GCCGCCG   TCTG CGG
                                  C      CCC    A
GAM624  BAALC   5' GCGGCGGCGACATCGCG    36039    C      CGG
                                GCG CGGCGGCA   GCG
                                ||| ||||||||   |||
                                CGC GCCGCTGT   CGC
                                  C       AG_
GAM624  BAPX1   3' GCACTGCGGTGGGCGCC    10160    CG   CAC
                                GCGC  GCGG   GGGCGCC
                                ||||  ||||   |||||||
                                CGTG  CGCC   CCCGCGG
                                   A_   A__
GAM624  BCL7C   5' GCGCCAGGCCCGGGCGCC   21923      GC   A
                                GCGCCG  GGC CGGGCGCC
                                ||||||  ||| ||||||||
                                CGCGGT  CCG GCCCGCGG
                                    __   G
GAM624  BCR     5' GCCCGGCCCCGGGCGCC    20248    G    GGCA
                                GC CCGGC    CGGGCGCC
                                || |||||    ||||||||
```

```
                                CG GGCCG   GCCCGCGG
                                 _    GG__
GAM624  BMP3    5'  GCCGGCGGCGGAGCC      10189        AC  C
                                GCCGGCGGC  GGG GCC
                                |||||||||  ||| |||
                                CGGCCGCCG  CCT CGG
                                     __  _
GAM624  BTAF1   5'  GCGCCGGCGGTTCGGAGC   43666         CA  _
                                GCGCCGGCGG  CGG GC
                                ||||||||||  ||| ||
                                CGCGGCCGCC  GCC CG
                                      AA  T
GAM624  C21orf2 5'  GCCCGACCGGCGGGCGCC   22302   G   _  AC
                                GC CCGGC GGC  GGGCGCC
                                || ||||| |||  |||||||
                                CG GGCTG CCG  CCCGCGG
                                 _    G  __
GAM624  CAPZA1  5'  GCGCCCGCGCCCGCGCC    43716     G  G ACGG
                                GCGCC GCG C   GCGCC
                                ||||| ||| |   |||||
                                CGCGG CGC G   CGCGG
                                   G  _ GG__
GAM624  CARPX   5'  GCGGCGGCGGCAGCAGCC   33574    C      CGG  _
                                GCG CGGCGGCA  GC GCC
                                ||| ||||||||  || |||
                                CGC GCCGCCGT  CG CGG
                                  C       ____  T
GAM624  CDC45L  5'  GCCCGGCGGCACGAGGCC   18606   G         C
                                GC CCGGCGGCACGGG GCC
                                || ||||||||||||| |||
                                CG GGCCGCCGTGCTC CGG
                                 _          _
GAM624  CDKN2B  3'  GCTCCGCCACGCGGGCGC   38547   G  G G  A
                                GC CCG C GC CGGGCGC
                                || ||| | || |||||||
                                CG GGC G TG GCCCGCG
                                 A  _ G  C
GAM624  CENPB   5'  GCCGGCGGCGCGGATCTGC   43015       A   C__
                                GCCGGCGGC CGGG  GC
                                |||||||| ||||  ||
                                CGGCCGCCG GCCT  CG
                                     C   AGA
GAM624  CHST1   5'  GCGGCGGCGGCAGCAGCC   18908    C      CGG  _
                                GCG CGGCGGCA  GC GCC
                                ||| ||||||||  || |||
                                CGC GCCGCCGT  CG CGG
                                  C       ____  T
GAM624  CIS4    5'  GCGCCGGCGCGACTGCC     20130       G ACG  _
                                GCGCCGGCG C  GGC GCC
                                ||||||||| |  ||| |||
```

```
                                CGCGGCCGC G   CTG CGG
                                    _ ____   A
GAM624  CNTFR   5'  GCGCCGGCTGGAGCCGCC    12302        _  CAC  G
                                GCGCCGGC GG   GG CGCC
                                |||||||| ||   || ||||
                                CGCGGCCG CC   TC GCGG
                                    A ____  G
GAM624  CTSD    3'  GCTGGCGCGCGGACGCC     12530    C    G A
                                GC GGCG C CGGGCGCC
                                || |||| | ||||||||
                                CG CCGC G GCCTGCGG
                                 A   _ C
GAM624  DDX26   5'  CGCTGGGGCGGGCGCC      29091     C  C   AC
                                CGC GG GGC  GGGCGCC
                                ||| || |||  |||||||
                                GCG CC CCG  CCCGCGG
                                  A _   __
GAM624  DNM2    5'  GCGCCGGCGGCCCCCGGC    22384          ACG_
                                GCGCCGGCGGC   GGC
                                ||||||||||   |||
                                CGCGGCCGCCG   CCG
                                      GGGG
GAM624  DNMT1   5'  GCGGCGGCAGCGCAGGCGCC  10715     C      A
                                GCG CGGCGGC CGGGCGCC
                                ||| ||||||| ||||||||
                                CGC GCCGTCG GTCCGCGG
                                  C      C
GAM624  DPP6    3'  GCGCCGGGAGGAGGCGC     39131       C_  CAC
                                GCGCCGG  GG   GGGCGC
                                |||||||  ||   ||||||
                                CGCGGCC  CC   TCCGCG
                                    CT  ____
GAM624  DRG2    5'  GCGGTGGCGGCGGCACC     10787     CC     ACG
                                GCG  GGCGGC   GGCGCC
                                |||  ||||||   ||||||
                                CGC  CCGCCG   CCGTGG
                                  CA     ____
GAM624  DSC3    5'  GCGCCGGGAGGGTGCC      35944       C  CAC   C
                                GCGCCGG GG   GGG GCC
                                ||||||| ||   ||| |||
                                CGCGGCC CT   CCC CGG
                                    _ ____   A
GAM624  EGLN1   5'  GCGCAGGGCATACGGGCGCC  35166     C_   GC
                                GCGC  GGCG  ACGGGCGCC
                                ||||  ||||  |||||||||
                                CGCG  CCGT  TGCCCGCGG
                                  TC   A_
GAM624  EGLN1   5'  GCGCCGGCAGCCGC        35167          ACGGG
                                GCGCCGGCGGC    CGC
                                ||||||||||    |||
```

```
                                CGCGGCCGTCG    GCG
                                       _____
GAM624  EGR4    5'  GCGCCGGCTGTGGGGCGCC   12676        GGCAC
                                GCGCCGGC    GGGCGCC
                                ||||||||    |||||||
                                CGCGGCCG    CCCGCGG
                                     ACAC_
GAM624  EIF1A   5'  GCTCGGCGGCAGCAAATGGCGC 44808   _      _ ___
              C                  GC CGGCGGCA CG   GGCGCC
                                || |||||||| ||   ||||||
                                CG GCCGCCGT GT   CCGCGG
                                 A       C  TTA
GAM624  EMX2    5'  GCGCCGAGGAGCGGGCGCC   44690       C  CA
                                GCGCCGG GG  CGGGCGCC
                                ||||||| ||  ||||||||
                                CGCGGCT CC  GCCCGCGG
                                     _  TC
GAM624  EN2     5'  GCGCCCGCGGTCAGCGCGCC   10956      G   CA  _
                                GCGCC GCGG  CGG GCGCC
                                ||||| ||||  ||| |||||
                                CGCGG CGCC  GTC CGCGG
                                   G   A_   G
GAM624  FAAH    5'  GCGCCGGCCGCCAGGCGCC   11055        G  A
                                GCGCCGGC GC CGGGCGCC
                                |||||||| || ||||||||
                                CGCGGCCG CG GTCCGCGG
                                     G  _
GAM624  FANCE   5'  GCCGGGGCACGGGTGCC    34898      C       C
                                GCCGG GGCACGGG GCC
                                ||||| |||||||| |||
                                CGGCC CCGTGCCC CGG
                                   _       A
GAM624  FBXL7   5'  GCCGGCGGGCGCAGCGCC    29403        CA  _
                                GCCGGCGG  CG GGCGCC
                                ||||||||  || ||||||
                                CGGCCGCC  GC TCGCGG
                                     C_  G
GAM624  FBXW1B  5'  GCCCCGGCGGCCCCGCC    37991    G       ACGGG
                                GC CCGGCGGC    CGCC
                                || ||||||||    ||||
                                CG GGCCGCCG    GCGG
                                 G       GG___
GAM624  FGF18   5'  GCGGCCGGGACCGGGCGCC   38007    _   C   A
                                GCG CCGG GGC CGGGCGCC
                                ||| |||| ||| ||||||||
                                CGC GGCC CTG GCCCGCGG
                                  C   _  _
GAM624  FGFR1   5'  GCGCTCGGTGCTCGGCGCC   31943     _  CG  A   G
                                GCGC CGG  GC CGG CGCC
                                |||| |||  || ||| ||||
```

```
                                CGCG GCC  CG GCC GCGG
                                  A  A_  A  _
GAM624  FHL2    5'  GCGCGGGGGGCGGGCGCC   11111     C  C   AC
                                GCGC GG GGC  GGGCGCC
                                |||| || |||  |||||||
                                CGCG CC CCG  CCCGCGG
                                  C  C  __
GAM624  FMR2    5'  GCGGCGGCGGGCGGGCGCC   12969     C     CA
                                GCG CGGCGG  CGGGCGCC
                                ||| ||||||  ||||||||
                                CGC GCCGCC  GCCCGCGG
                                  C     C_
GAM624  FOXD2   5'  CGCCGGCGGCCCCCGCC     20961          ACGGG
                                CGCCGGCGGC    CGCC
                                ||||||||||    ||||
                                GCGGCCGCCG    GCGG
                                      GGG__
GAM624  FUT1    3'  GCGTGGTGGCGGGCGCC     6634      CC  C   AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A  __
GAM624  FVT1    5'  GCGCGGCGGGCGGGCGCC    13031     C    CA
                                GCGC GGCGG  CGGGCGCC
                                |||| |||||  ||||||||
                                CGCG CCGCC  GCCCGCGG
                                  _    C_
GAM624  G6PD    5'  GCCCCGGCGGCCTCGCGCGC  7604     G      A_  G
                                GC CCGGCGGC  CG GCGC
                                || ||||||||  || ||||
                                CG GGCCGCCG  GC CGCG
                                 G       GA  G
GAM624  GCGR    5'  GCGCTCGGGTCGGGCGCC    6693      _  CGGCA
                                GCGC CGG    CGGGCGCC
                                |||| |||    ||||||||
                                CGCG GCC    GCCCGCGG
                                  A  CA___
GAM624  GFI1    5'  GCGTCCCGCGGGCGCC      23554     _  G  GGCAC
                                GCG CC GC    GGGCGCC
                                ||| || ||    |||||||
                                CGC GG CG    CCCGCGG
                                  A  G  _____
GAM624  GNB5    5'  GCCGCGGCGGGCGCC       32109     G   AC
                                GCCG CGGC  GGGCGCC
                                |||| ||||  |||||||
                                CGGC GCCG  CCCGCGG
                                  _   __
GAM624  GPI     5'  GCGCCGGCAGCGCGC       6749          ACGG
                                GCGCCGGCGGC   GCGC
                                ||||||||||   ||||
```

```
                                CGCGGCCGTCG   CGCG
                                      ____
GAM624  GSTM3   5'  GCCCACGCGCGGGCGCC    42762    G  G A
                                GCC GCG C CGGGCGCC
                                ||| ||| | ||||||||
                                CGG TGC G GCCCGCGG
                                  G  _ C
GAM624  HAGH    5'  GCGTCGGCGCGTCGCAGCC   23712    C   GCA  G_ _
                                GCG CGGCG  CG  GC GCC
                                ||| |||||  ||  || |||
                                CGC GCCGC  GC  CG CGG
                                  A    ___  AG  T
GAM624  HCN4    5'  GCCCGGCTCCAGGCGCC    24224   G   GGCA
                                GC CCGGC   CGGGCGCC
                                || |||||   ||||||||
                                CG GGCCG   GTCCGCGG
                                 _    AG__
GAM624  HK1     3'  GCGCCGGCAGGCCCTGGCGCC  37917       _  ACG
                                GCGCCGGC GGC  GGCGCC
                                |||||||| |||  ||||||
                                CGCGGCCG CCG  CCGCGG
                                     T  GGA
GAM624  HNRPDL  5'  GCAGCGCAGCGCGGGCGCC   24175   _ CG   A
                                GC GC  GCGGC CGGGCGCC
                                || ||  ||||| ||||||||
                                CG CG  CGTCG GCCCGCGG
                                 T __    C
GAM624  HR      5'  GGCCGGCACCGGGCGCC    32926   C    G A
                                G GCCGGCG C CGGGCGCC
                                | ||||||| | ||||||||
                                C CGGCCGT G GCCCGCGG
                                 _     _ _
GAM624  HTRA3   5'  GCCGGGCGCCGGGCGCC    44832     CG  A
                                GCCGG  GC CGGGCGCC
                                |||||  || ||||||||
                                CGGCC  CG GCCCGCGG
                                   CG  _
GAM624  IL12RB2 5'  GCAGCCGGGCGGGCGCC    11429   _   CGGCA
                                GC GCCGG   CGGGCGCC
                                || |||||   ||||||||
                                CG CGGCC   GCCCGCGG
                                 T   C____
GAM624  ILF1    5'  GCCGCTCCGCGCGGGCGCC   21109    GCG_ A
                                GCCG   GC CGGGCGCC
                                ||||   || ||||||||
                                CGGC   CG GCCCGCGG
                                  GAGG  C
GAM624  ILF1    5'  GCGCCGGTGGCGCGCC     21110      C  ACGG
                                GCGCCGG GGC   GCGCC
                                ||||||| |||   |||||
```

```
                                CGCGGCC CCG   CGCGG
                                   A  ____
GAM624  INSM1   5' GCCCCGGCGGCCCTCAGTGCC 13577   G     A__  GC
                                GC CCGGCGGC  CGG  GCC
                                || ||||||||  |||  |||
                                CG GGCCGCCG  GTC  CGG
                                 G      GGA  A_
GAM624  KCNF1   5' GGCTGGCATCCGGGCGCC   13835   _   __
                                GGC GGCA  CGGGCGCC
                                ||| ||||  ||||||||
                                CCG CCGT  GCCCGCGG
                                  A   AG
GAM624  KCNH1   5' GCTCGGGGTCCGGCGGGCG  13843   _  ____   AC
                                GC CGG   CGGC  GGGCG
                                || |||   ||||  |||||
                                CG GCC   GCCG  CCCGC
                                 A  CCAG   __
GAM624  KCNMB4  5' GCGGCGGCGGCGGCAGCGCC  30946   C     ACG
                                GCG CGGCGGC  GGCGCC
                                ||| |||||||  ||||||
                                CGC GCCGCCG  TCGCGG
                                  C     CCG
GAM624  KCNS2   5' GCGCCGGCCGCCCGCGCC   42831       G  ACGG
                                GCGCCGGC GC   GCGCC
                                |||||||| ||   |||||
                                CGCGGCCG CG   CGCGG
                                     G  GG__
GAM624  KCNS2   5' GCGCCGCGCGGGGGCGC    42830      _   CAC
                                GCGCCG GCGG  GGGCGC
                                |||||| ||||  ||||||
                                CGCGGC CGCC  CCCGCG
                                   G   ___
GAM624  KCNS2   5' GCCCGCGGCCGAGGCC     42828    G   A   C
                                GCC GCGGC CGGG GCC
                                ||| ||||| |||| |||
                                CGG CGCCG GCTC CGG
                                  G   _  _
GAM624  LENG4   3' ACGCCGGCGGCATGAAGC   35877         C_
                                GCGCCGGCGGCA  GGGC
                                ||||||||||||  ||||
                                TGCGGCCGCCGT  TTCG
                                      AC
GAM624  LENG4   3' GCAGCTGCGCGGGCGCC    35886   C  G  A
                                GC GGC GC CGGGCGCC
                                || ||| || ||||||||
                                CG TCG CG GCCCGCGG
                                 _  A  C
GAM624  LLGL1   5' GCGCCCGGCTGCAGGCGCC  42504     GG   A_
                                GCGCC  CGGC  CGGGCGCC
                                |||||  ||||  ||||||||
```

```
                                CGCGG  GCCG  GTCCGCGG
                                  __    AC
GAM624  LMO4    5'  GCCCGGCGGCCCCCGCC    27653    G      ACGGG
                                GC CCGGCGGC    CGCC
                                || ||||||||    ||||
                                CG GGCCGCCG    GCGG
                                 _       GGG__
GAM624  LYZ     3'  GCGTGGTGGCGGGCGCC    6954     CC  C   AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A  __
GAM624  MADD    5'  GCTCCGAGCGGGCGCC     39074    G   GC   AC
                                GC CCG  GGC  GGGCGCC
                                || |||  |||  |||||||
                                CG GGC  TCG  CCCGCGG
                                 A  __  __
GAM624  MAP2K2  5'  GCCGGCGGCGGCGGCGCC    36208        ACG
                                GCCGGCGGC   GGCGCC
                                |||||||||   ||||||
                                CGGCCGCCG   CCGCGG
                                     CCG
GAM624  MAP3K1  5'  GCTCGGCGGCGGGCGCC     42706    _     AC
                                GC CGGCGGC  GGGCGCC
                                || |||||||  |||||||
                                CG GCCGCCG  CCCGCGG
                                 A      __
GAM624  MAZ     5'  GCCTCGGCCGCGGGCGCC    43851     GG   A_
                                GCC  CGGC  CGGGCGCC
                                |||  ||||  ||||||||
                                CGG  GCCG  GCCCGCGG
                                  A_   GC
GAM624  MBNL    5'  GCCCGCGCGGGCGCC      34314     G   GCA
                                GCC GCG   CGGGCGCC
                                ||| |||   ||||||||
                                CGG CGC   GCCCGCGG
                                  G  ____
GAM624  MCM5    3'  GCGCTAGAGGCGGGCGCC    41007     CG C   AC
                                GCGC  G GGC  GGGCGCC
                                ||||  | |||  |||||||
                                CGCG  C CCG  CCCGCGG
                                   AT T  __
GAM624  MDFI    5'  GCGCCTGCTCCGGGCGCC    24618      G  GGCA
                                GCGCC GC    CGGGCGCC
                                ||||| ||    ||||||||
                                CGCGG CG    GCCCGCGG
                                   A  AG__
GAM624  MGAT3   5'  GCGGCTGCGGCGGGCGCC    14462     CCG    AC
                                GCG   GCGGC  GGGCGCC
                                |||   |||||  |||||||
```

```
                                CGC  CGCCG  CCCGCGG
                                  CGA   __
GAM624  MTCP1   5'  GCGCCTGCCCAGGCGCC    30581     G  GGCA
                                GCGCC GC   CGGGCGCC
                                ||||| ||   ||||||||
                                CGCGG CG   GTCCGCGG
                                  A  G___
GAM624  MTMR1   5'  GCCGGCGGTGGCGCC      43156       CACG
                                GCCGGCGG   GGCGCC
                                ||||||||   ||||||
                                CGGCCGCC   CCGCGG
                                    A___
GAM624  MUCDHL  3'  GCTGGGGACGGGCGCC     34939   C  C  C
                                GC GG GG ACGGGCGCC
                                || || || |||||||||
                                CG CC CC TGCCCGCGG
                                 A  _  _
GAM624  MYCL2   3'  GCGTGGTGGCAGGCGCC    23902    CC  C   CG
                                GCG  GG GGCA  GGCGCC
                                |||  || ||||  ||||||
                                CGC  CC CCGT  CCGCGG
                                 A_  A   __
GAM624  MYO3A   5'  GCGCTGGCTACGGGCGC    41116    C   GGC
                                GCGC GGC   ACGGGCGC
                                |||| |||   ||||||||
                                CGCG CCG   TGCCCGCG
                                  A  A__
GAM624  NEDD4L  5'  GCTGCGGCGCGGACGGCC   31619   CG   A    _
                                GC  GCGGC CGGGCG CC
                                ||  ||||| |||||| ||
                                CG  CGCCG GCCTGC GG
                                 A_    C     C
GAM624  NEO1    5'  GCTCGGCTCCCGGGCGCC    14754   _   GGCA
                                GC CGGC   CGGGCGCC
                                || ||||   ||||||||
                                CG GCCG   GCCCGCGG
                                 A   AGG_
GAM624  NFIA    5'  GCGCCGGCCCGGCCGGGTGCC 43216       __  A   C
                                GCGCCGGC  GGC CGGG GCC
                                ||||||||  ||| |||| |||
                                CGCGGCCG  CCG GCCC CGG
                                    GG  _   A
GAM624  NLGN2   5'  GCTGGAAGCGGCGGGCGCC   44757   GCC_    AC
                                GC   GGCGGC  GGGCGCC
                                ||   ||||||  |||||||
                                CG   TCGCCG  CCCGCGG
                                 ACCT    __
GAM624  NLGN2   5'  GCCACGAGGCGGGCGCC    44754    G   CA
                                GCCG CGG  CGGGCGCC
                                |||| |||  ||||||||
```

```
                                CGGT GCT  GCCCGCGG
                                  _  CC
GAM624  NMB     5'  GCCCCGGCGGCGGAGCC    43950   G     AC  C
                                GC CCGGCGGC  GGG GCC
                                || ||||||||  ||| |||
                                CG GGCCGCCG  CCT CGG
                                 G      __  _
GAM624  NPTX2   5'  GCGCCGTCGGGGCGC      45207      G  CACG
                                GCGCCG CGG   GGCGC
                                |||||| |||   |||||
                                CGCGGC GCC   CCGCG
                                   A  ____
GAM624  NRXN1   5'  GCCGGCGGGTGGGGGGCC   22048       CAC  C
                                GCCGGCGG  GGG GCC
                                ||||||||  ||| |||
                                CGGCCGCC  CCC CGG
                                     CAC  C
GAM624  OCRL    5'  GCGCCGGGCGCCGGGCGCC   11481       CG  A
                                GCGCCGG  GC CGGGCGCC
                                |||||||  || ||||||||
                                CGCGGCC  CG GCCCGCGG
                                   CG  _
GAM624  OCRL    5'  GCTCCGCGCCGGGCGCC    11482   G  G  G A
                                GC CCG CG C CGGGCGCC
                                || ||| || | ||||||||
                                CG GGC GC G GCCCGCGG
                                 A  _  _ _
GAM624  OLFM1   5'  GCTCCGGCGGCGGCGCC    26774   G     ACG
                                GC CCGGCGGC  GGCGCC
                                || ||||||||  ||||||
                                CG GGCCGCCG  CCGCGG
                                 A     ___
GAM624  PDAP1   5'  GCGGCGGCGGCGGCGGCGCC  45202    C     ACG
                                GCG CGGCGGC  GGCGCC
                                ||| |||||||  ||||||
                                CGC GCCGCCG  CCGCGG
                                  C     CCG
GAM624  PDPK1   5'  CGCGTCGGCGCGGGCGCC   15210    CGG   A
                                CGC  CGGC CGGGCGCC
                                |||  |||| ||||||||
                                GCG  GCCG GCCCGCGG
                                  CA_   C
GAM624  PFKFB3  5'  GCGCCGGCGCGCGGCCGGGCG 44437        _  A__
                                GCGCCGGCG GC  CGGGCG
                                ||||||||| ||  ||||||
                                CGCGGCCGC CG  GCCCGC
                                     G  CCG
GAM624  PML     3'  GCCTGCTTGACGGGCGCC   37729    G  GGC
                                GCC GC  ACGGGCGCC
                                ||| ||  |||||||||
```

```
                                CGG CG   TGCCCGCGG
                                  A  AAC
GAM624  POLR2E   3'  ACGTCCCACCAGCGGGCGCC  40911    __  G   AC
                                GCG  CCG CGGC  GGGCGCC
                                |||  ||| ||||  |||||||
                                TGC  GGT GTCG  CCCGCGG
                                  AG   G   __
GAM624  PPIC     5'  GCGCTACCGGCACGGGCGC   9607     CGG
                                GCGC   CGGCACGGGCGC
                                ||||   ||||||||||||
                                CGCG   GCCGTGCCCGCG
                                  ATG
GAM624  PPP2R5A  5'  GCACGGGGGTGCGGGTGCC   26436     C  C  CA   C
                                GCGC GG GG  CGGG GCC
                                |||| || ||  |||| |||
                                CGTG CC CC  GCCC CGG
                                  C  _  AC   A
GAM624  PTEN     5'  GCGCCGGGAGCCCGGGCGCC  7215       C   A
                                GCGCCGG GGC CGGGCGCC
                                ||||||| ||| ||||||||
                                CGCGGCC TCG GCCCGCGG
                                    C   G
GAM624  PTK7     5'  GCACCGGAGCGCGGGCGCC   15861      C   A
                                GCGCCGG GGC CGGGCGCC
                                ||||||| ||| ||||||||
                                CGTGGCC TCG GCCCGCGG
                                    _   C
GAM624  PTP4A2   5'  GCGGCGGCGGCGGCGGCGC   38636    C     ACG
                                GCG CGGCGGC   GGCGC
                                ||| |||||||   |||||
                                CGC GCCGCCG   CCGCG
                                  C      CCG
GAM624  PXN      5'  GCCGGACCACGGGCGCC    16026     CGG
                                GCCGG   CACGGGCGCC
                                |||||   ||||||||||
                                CGGCC   GTGCCCGCGG
                                   TG_
GAM624  RAB3A    5'  GCGGCGGCGGCAGCAGCG   16064    C      CG
                                GCG CGGCGGCA  GGCG
                                ||| |||||||  ||||
                                CGC GCCGCCGT  TCGC
                                  C       CG
GAM624  RB1CC1   5'  CGCCGGCGTCCCGGGCGCC   31312       GCA
                                CGCCGGCG   CGGGCGCC
                                ||||||||   ||||||||
                                GCGGCCGC   GCCCGCGG
                                    AGG
GAM624  RNPEPL1  5'  GCTCGGAGCCGGGCGCC    32884    _  C   A
                                GC CGG GGC CGGGCGCC
                                || ||| ||| ||||||||
```

```
                                CG GCC TCG GCCCGCGG
                                 A  _  _
GAM624  ROR2     5'  GCGCGGGGTCGGGCGCC     21261      C  C  CA
                                GCGC GG GG  CGGGCGCC
                                |||| || ||  ||||||||
                                CGCG CC CC  GCCCGCGG
                                  _  _  A_
GAM624  RRAD     3'  GCCCGGCGGCTGCGC       20019    G      ACGG
                                GC CCGGCGGC   GCGC
                                || ||||||||   ||||
                                CG GGCCGCCG   CGCG
                                 _      A___
GAM624  RREB1    5'  GCGGCGGCGGCGGCGGCGC   16398    C      ACG
                                GCG CGGCGGC   GGCGC
                                ||| |||||||   |||||
                                CGC GCCGCCG   CCGCG
                                  C      CCG
GAM624  RRM2B    5'  CGCCGAAGCTACGGGCGC    42718      C  _
                                CGCCGG GGC ACGGGCGC
                                |||||| ||| ||||||||
                                GCGGCT TCG TGCCCGCG
                                   _  A
GAM624  SECTM1   3'  GCCTCGGTCACCGGGCGCC   16543     GG  _  _
                                GCC  CGG CAC GGGCGCC
                                |||  ||| ||| |||||||
                                CGG  GCC GTG CCCGCGG
                                  A_  A  G
GAM624  SERPINB9 3'  GCGTGGTGGCGGGCGCC     19997     CC  C  AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A  __
GAM624  SGT      5'  GCGCTTGCGCACCGCGGTGCC  16616     CG  G  _ _ C
                                GCGC  GCG CAC G GG GCC
                                ||||  ||| ||| | || |||
                                CGCG  CGC GTG C CC CGG
                                   AA  _  G G  A
GAM624  SH3BP2   3'  GCGTGGTGGCGGGCGCC     16634     CC  C  AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A  __
GAM624  SIAT8E   5'  GCGCCGGTGCCGGGTAGCC   40835       CG  A  C_
                                GCGCCGG  GC CGGG  GCC
                                |||||||  || ||||  |||
                                CGCGGCC  CG GCCC  CGG
                                   A_  _   AT
GAM624  SLC1A2   5'  ACGCCGGCGATGCGC       41595         CACGG
                                GCGCCGGCGG    GCGC
                                ||||||||||    ||||
```

```
                                TGCGGCCGCT    CGCG
                                     A____
GAM624  SLC25A15  5'  GCGCCGGCGTGGCCGC     30669        GCAC  G
                                GCGCCGGCG   GG CGC
                                |||||||||   || |||
                                CGCGGCCGC   CC GCG
                                     A___  G
GAM624  SLC6A8   5'  GCGGCGGCGGCTGCAGCC    24771    C     ACGG  _
                                GCG CGGCGGC   GC GCC
                                ||| |||||||   || |||
                                CGC GCCGCCG   CG CGG
                                  C     A___  T
GAM624  SLC6A9   5'  GCAGCCCAGCACGGGTGC    27987    _  GG       C
                                GC GCC  CGGCACGGG GC
                                || |||  ||||||||| ||
                                CG CGG  GTCGTGCCC CG
                                 T  __       A
GAM624  SMAC     5'  GCGTGGTGGCGGGCGCC     39898    CC  C   AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A  __
GAM624  SOX4     5'  GCCTCGGCTCGGCGGGCGCC   16986    GG   A___
                                GCC  CGGC   CGGGCGCC
                                |||  ||||   ||||||||
                                CGG  GCCG   GCCCGCGG
                                  A_   AGCC
GAM624  STAT5B   5'  GCTCGGCCCCTCGGGCGCC   29721    _   GGCA
                                GC CGGC   CGGGCGCC
                                || ||||   ||||||||
                                CG GCCG   GCCCGCGG
                                 A   GGGA
GAM624  TACC1    5'  CGCCGGCAGCCGGCGCC     26594        A  G
                                CGCCGGCGGC CGG CGCC
                                |||||||||| ||| ||||
                                GCGGCCGTCG GCC GCGG
                                     _  _
GAM624  TERF2    3'  GCGTGATGGCGGGCGCC     24910    CC GC   AC
                                GCG  G  GGC  GGGCGCC
                                |||  |  |||  |||||||
                                CGC  C  CCG  CCCGCGG
                                  A_ TA  __
GAM624  TESK1    5'  GCCCGATCCCGGGCGCC     26612    G   CGGCA
                                GC CCGG    CGGGCGCC
                                || ||||    ||||||||
                                CG GGCT    GCCCGCGG
                                 _   AGG__
GAM624  THBD     5'  GCGCCGCGTGCAGGCGCC    7426       G  GCA
                                GCGCCG CG   CGGGCGCC
                                |||||| ||   ||||||||
```

```
                                CGCGGC GC   GTCCGCGG
                                   _ AC_
GAM624  TIMP3    5'  CGCCGGCGGGGCTGC       7447          CACG  _
                                CGCCGGCGG    GGC GC
                                |||||||||    ||| ||
                                GCGGCCGCC    CCG CG
                                     ____   A
GAM624  TNFRSF12 5'  GCCCTCCGACGGGCGCC     19125    G  GG  GC
                                GC CC  CG  ACGGGCGCC
                                || ||  ||  |||||||||
                                CG GG  GC  TGCCCGCGG
                                 _ AG  __
GAM624  UBE3A    5'  CGGCGGATGGCGGGCGCC    39278       CA__
                                CGGCGG   CGGGCGCC
                                ||||||   ||||||||
                                GCCGCC   GCCCGCGG
                                   TACC
GAM624  UMPS     5'  GCCCCGGCGTCCGGCGCC    7503     G     GCA   G
                                GC CCGGCG   CGG CGCC
                                || |||||||  ||| ||||
                                CG GGCCGC   GCC GCGG
                                 G     AG_  _
GAM624  VARS2    5'  GCCCCGGCAGCCGGCGCC    26661    G       A   G
                                GC CCGGCGGC CGG CGCC
                                || |||||||| ||| ||||
                                CG GGCCGTCG GCC GCGG
                                 G       _  _
GAM624  WASF3    5'  GCGCCGGGGCTGCGC       27386        C   ACGG
                                GCGCCGG GGC   GCGC
                                |||||||  |||   ||||
                                CGCGGCC CCG   CGCG
                                   _  A___
GAM624  WDR8     5'  CGCCTGCCGCGGGCGCC     32822      G  G  AC
                                CGCC GC GC  GGGCGCC
                                ||||  ||  ||  |||||||
                                GCGG CG CG  CCCGCGG
                                  A  G  __
GAM624  WIG1     5'  GCGCCGGCAGTCTCCGCGCC  45386          CACGG
                                GCGCCGGCGG    GCGCC
                                ||||||||||    |||||
                                CGCGGCCGTC    CGCGG
                                     AGAGG
GAM624  WNT4     5'  GCCGCCGCGGGCGCC       36255      G  GCA
                                GCCG CG   CGGGCGCC
                                ||||  ||   ||||||||
                                CGGC GC   GCCCGCGG
                                  G  ___
GAM624  WW45     5'  GCGCCGGCCGTCTCCGCC    34822         GGCA  GG__
                                GCGCCGGC   CG   CGCC
                                ||||||||   ||   ||||
```

```
                                CGCGGCCG   GC   GCGG
                                     ____ AGAG
GAM624  WW45    5' GCTCCGCGCCGGGCGCC    34823   G  G  G A
                                GC CCG CG C CGGGCGCC
                                || ||| || | ||||||||
                                CG GGC GC G GCCCGCGG
                                 A  _ _ _
GAM624  ZNF264  3' GCGTGGTGGCGGGCGCC    18273    CC  C  AC
                                GCG  GG GGC  GGGCGCC
                                |||  || |||  |||||||
                                CGC  CC CCG  CCCGCGG
                                  A_  A  __
GAM624  ZNF278  5' GCGCCGGCGCGCAGC      36795         _  CGGGC
                                GCGCCGGCG GCA    GC
                                ||||||||| |||    ||
                                CGCGGCCGC CGT    CG
                                     G  _____
GAM624  ZNF278  5' GCGGCGGCGGCAGAGTAGGCC 36817    C      C  C__
                                GCG CGGCGGCA GGG  GCC
                                ||| |||||||| |||  |||
                                CGC GCCGCCGT CTC  CGG
                                  C       _  ATC
GAM624  ZNF32   5' GCGCCAGCGCCGGCGCC    45042        G A  G
                                GCGCCGGCG C CGG CGCC
                                ||||||||| | ||| ||||
                                CGCGGTCGC G GCC GCGG
                                     _ _  _
GAM625  ALX3    3' TGTCCAGGCGGGGGTG     27073        _ TCCCCGA
                                TGTCCAGG GG     GGGTG
                                |||||||| ||     |||||
                                ACAGGTCC CC     CCCAC
                                     G  ________
GAM625  CCR9    3' TGTCCAGGGGTTCACTGGCAAG 36301          CCC  AG  TG
                                TGTCCAGGGGT  CG  GG  AG
                                ||||||||||  ||  ||  ||
                                ACAGGTCCCCA  GT  CC  TC
                                      A__  GA  GT
GAM625  CORO2A  3' GGTGTCCCTGAGGGTGAG   38064   G   C
                                GG GTCCC GAGGGTGAG
                                || ||||| |||||||||
                                CC CAGGG CTCCCACTC
                                 A    A
GAM625  EGFL4   5' TGTCGGGGGAGAAGGTGAGGGT 41587    CA   TCCCC__
           GAG                  TGTC  GGGG     GAGGGTGAG
                                ||||  ||||     |||||||||
                                ACAG  CCCC     CTCCCACTC
                                  C_   TCTTCCA
GAM625  FBXL3A  5' TGTTCAGGGATCCCCGGCG  29131    C        GAG
                                TGT CAGGGGTCCCC  GGTG
                                ||| ||||||||||  ||||
```

```
                                ACA GTCCCTAGGGG  CCGC
                                  A       ___
GAM625  GPR61    3'  TGTCCAGGGGACTGGAGGTG  44268        TCCCC   G
                                TGTCCAGGGG    GAGG TG
                                ||||||||||    |||| ||
                                ACAGGTCCCC    CTCC AC
                                     TGAC_   _
GAM625  JRK      3'  TGTCCAGGGGCGGTG      44506         CCCCGAG
                                TGTCCAGGGGT     GGTG
                                ||||||||||      ||||
                                ACAGGTCCCCG     CCAC
                                          _______
GAM625  MAP3K14  3'  TGGCCAGGGGCAGGGCAGGGTG 19547    T      CCCCG
           AG                     TG CCAGGGGT    AGGGTGAG
                                || ||||||||    ||||||||
                                AC GGTCCCCG    TCCCACTC
                                  C       TCCCG
GAM625  MEF2D    3'  TGTCAGGTGTGGGGGTG    25427     C   G  CCCCGA
                                TGTC AGG GT     GGGTG
                                |||| ||| ||     |||||
                                ACAG TCC CA     CCCAC
                                  _   A  CC____
GAM625  MTMR1    5'  TGTCCAGGGTCTCCACGCTGGG 43161        G_   C  A_
                                TGTCCAGGG  TCC CG  GGG
                                |||||||||  ||| ||  |||
                                ACAGGTCCC  AGG GC  CCC
                                     AG   T  GA
GAM625  PLXNB2   3'  TCCAGGGGAGGGTG       29649        TCCCCG
                                TCCAGGGG     AGGGTG
                                ||||||||     ||||||
                                AGGTCCCC     TCCCAC
                                          _______
GAM625  PRELP    3'  TCCCTGCCTCGAGGGTG     15551     AGGG T  C
                                TCC    G CC CGAGGGTG
                                |||    | || ||||||||
                                AGG    C GG GCTCCCAC
                                  GA__ _  A
GAM625  SLC6A8   3'  TGTCCAGGGTCCCTTCCTGGG  24792        GT  __  GA
                                TGTCCAGGG  CC  CC  GGG
                                |||||||||  ||  ||  |||
                                ACAGGTCCC  GG  GG  CCC
                                     AG  AA  A_
GAM625  TNFAIP2  3'  TGTCCGGGGATCCCTGAG    26644      A       C
                                TGTCC GGGGTCCC GAG
                                |||||  |||||||| |||
                                ACAGG CCCTAGGG CTC
                                   C       A
GAM625  TRPM2    3'  TGTCCAGGGAAGGGTG      17699         GTCCCC
                                TGTCCAGGG     GAGGGTG
                                |||||||||     |||||||
```

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                                ACAGGTCCC     TTCCCAC
                                       _______
GAM626  ELOVL4   3'  TATGTTATAGCTTACAAAA   35543          TTA TG
                                TATGTTATAGCTT   A  GAA
                                |||||||||||||   |  |||
                                ATACAATATCGAA   T  TTT
                                      ___ GT
GAM626  ERBB4    3'  GTTATAACTTTAATGGA     23457          T
                                GTTATAGCTTT AATGGA
                                |||||||||||| ||||||
                                CAATATTGAAA TTACCT
                                          _
GAM626  F8       3'  TATGTTATAGTTTCCAAAGA  6569          C     T
                                TATGTTATAG TTTTAA GGA
                                |||||||||| |||||| |||
                                ATACAATATC AAGGTT TCT
                                      A     _
GAM627  ADARB1   3'  GGAGGTACCTACGGAGAAA   31881   A        AAA
                                A AGGTACTTATG   AGGAA
                                | ||||||||||||   |||||
                                C TCCATGGATGC   TCTTT
                                 C          C__
GAM627  ALMS1    3'  AAAGGGACTTATTCTTGAGAAA 31527      T     GAAAA
                                AAAGG ACTTAT     GGAAA
                                ||||| ||||||     |||||
                                TTTCC TGAATA     TCTTT
                                   C      AGAAC
GAM627  ALOX5    3'  AAAGGTACTGGCCTCGGAGGAA 44909         TATGAAA_
                                AAAGGTACT       AGGAA
                                |||||||||       |||||
                                TTTCCATGA       TCCTT
                                      CCGGAGCC
GAM627  AMPH     3'  AGCTACAATGGAAAGGAAA   11597    G   TT   A
                                AG TAC  ATG AAAGGAAA
                                || |||  ||| ||||||||
                                TC ATG  TAC TTTCCTTT
                                 G   T_   C
GAM627  AP1G1    3'  AAAGGTACTTTTGATACAGA   10046         A   AAA
                                AAAGGTACTT TGA   GGA
                                |||||||||| |||   |||
                                TTTCCATGAA ACT   TCT
                                      A   ATG
GAM627  APLP2    3'  AAAGGGGAGGAAAAAGGAAAAA 44914      TACTTAT
                                AAAGG      GAAAAGGAAAAA
                                |||||      ||||||||||||
                                TTTCC      TTTTTCCTTTTT
                                   CCTCC__
GAM627  CACNG7   3'  AGGGACCAATGAAAAGGA    36685     T   T
                                AGG ACT ATGAAAAGGA
                                ||| ||| ||||||||||
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```
                                TCC TGG TACTTTTCCT
                                  C   T
GAM627  CLCN4    3'  GGCACTTAGTGAAAAGGAA   12288        _
                                GGTACTTA TGAAAAGGAA
                                |||||||| ||||||||||
                                CCGTGAAT ACTTTTCCTT
                                     C
GAM627  CLCN5    5'  AAAGGATTTATGAAACAAAA  6355       TAC       AG
                                AAAGG   TTATGAAA  GAA
                                |||||   ||||||||  |||
                                TTTCC   AATACTTT  TTT
                                   TA_       GT
GAM627  CNN3     3'  AGGCAGAAAAAGGAAAA     40368      CTTAT
                                AGGTA    GAAAAGGAAAA
                                |||||    ||||||||||||
                                TCCGT    TTTTTCCTTTT
                                   C_____
GAM627  COL19A1  3'  AAAGATGCTTAAAATTAGGAAA 12364       A    T  AA
              AA                  AAAGGT CTTA GA  AGGAAAAA
                                |||||| |||| ||  ||||||||
                                TTTCTA GAAT TT  TCCTTTTT
                                   C    T  AA
GAM627  CTBP2    3'  AAGGGACTGATAAAGGAAAAA  35597     T   T    AA
                                AAGG ACT ATGA  AGGAAAAA
                                |||| ||| ||||  ||||||||
                                TTCC TGA TATT  TCCTTTTT
                                  C   C   __
GAM627  CUGBP1   3'  AAAGGAAAAAAAAAGGAAA   27274      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTTT___
GAM627  CYP24    5'  GGTACCTCTTGAAAAGGGAAA  8949        A_      A
                                GGTACTT  TGAAAAGG AAA
                                |||||||  |||||||| |||
                                CCATGGA  ACTTTTCC TTT
                                     GA       C
GAM627  DPYSL2   3'  AAAGGTGACAGAAAAGGA    10741       ACTTAT
                                AAAGGT     GAAAAGGA
                                ||||||     ||||||||
                                TTTCCA     CTTTTCCT
                                   CTGT__
GAM627  EHD4     3'  AAAGGTTTTATATGAAAGG   40205       ACT_     A
                                AAAGGT    TATGAAA GG
                                ||||||    ||||||| ||
                                TTTCCA    ATACTTT CC
                                   AAAT      _
GAM627  ELK4     3'  AAAGGAGAAAAGAAAAGGAA  34747       TACTTAT
                                AAAGG      GAAAAGGAA
                                |||||      |||||||||
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```
                                TTTCC      CTTTTCCTT
                                   TCTTTT_
GAM627  EMX2     5' AAAGGAAAGGAAAAAGGAAA  44675      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTTCC__
GAM627  ESRRG    3' AAAGGAAAGGGAAAAGGAAA  42441      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      CTTTTCCTTT
                                   TTTCC__
GAM627  ESRRG    3' AAAGGAAAGGGAAAAAGGAAA 42440      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   TTTCCC_
GAM627  FBXW1B   3' AGTACTTATGAGAAAAAGA   37987          __
                                GGTACTTATGA  AAAGGA
                                ||||||||||  ||||||
                                TCATGAATACT  TTTTCT
                                      CT
GAM627  FCMD     3' AAAGGTCACTTCAGGAAGGGGA 27506       _   AT_   AA
                                AAAGGT ACTT   GAA  GGA
                                |||||| ||||   |||  |||
                                TTTCCA TGAA   CTT  CCT
                                   G   GTC   CC
GAM627  FPGS     3' AAGGCACTGGGAGGAGGAA   22421        TAT  AA
                                AAGGTACT   GA  AGGAA
                                ||||||||   ||  |||||
                                TTCCGTGA   CT  TCCTT
                                     CC_  CC
GAM627  GALNT7   3' AAGGTGTGAAAAGGA      38349      ACTTA
                                AAGGT    TGAAAAGGA
                                |||||    |||||||||
                                TTCCA    ACTTTTCCT
                                   C____
GAM627  GNB3     3' AAAGGTAGAAAAAGGA      13215       CTTAT
                                AAAGGTA    GAAAAGGA
                                |||||||    ||||||||
                                TTTCCAT    TTTTTCCT
                                    C____
GAM627  GRAF     3' AAAGTGTACCAAAAAGG     31433     _    TAT
                                AAAG GTACT   GAAAAGG
                                |||| |||||   |||||||
                                TTTC CATGG   TTTTTCC
                                  A    ___
GAM627  GRIN2B   3' AGAACTGTGAAAAGGA      9119      T   TA
                                AGG ACT  TGAAAAGGA
                                ||| |||  |||||||||
```

```
                                TCT TGA  ACTTTTCCT
                                  _  C_
GAM627  GRINL1A  3'  AGGTAAGAAAAAGGAAAAA   42995      CTTAT
                                AGGTA    GAAAAGGAAAAA
                                |||||    ||||||||||||
                                TCCAT    TTTTTCCTTTTT
                                   TC___
GAM627  IFIT4    5'  GCTTTTATGAAAGGGGAAA   43369    AC      A_
                                GT  TTATGAAA  GGAAA
                                ||  ||||||||  |||||
                                CG  AATACTTT  CCTTT
                                 AA       CC
GAM627  LAG3     5'  AAAGGAGGTCAGAAAAGGAAA  14040      TAC   T
                                AAAGG   TTA GAAAAGGAAA
                                |||||   ||| ||||||||||
                                TTTCC   AGT CTTTTCCTTT
                                   TCC   _
GAM627  MID1     3'  AAAGGAACTATTAAAAGGAA   37783      T   TATG
                                AAAGG ACT    AAAAGGAA
                                ||||| |||    ||||||||
                                TTTCC TGA    TTTTCCTT
                                   T   TAA_
GAM627  MID1     3'  AAAGGAACTATTAAAAGGAA   37783      T   TATG
                                AAAGG ACT    AAAAGGAA
                                ||||| |||    ||||||||
                                TTTCC TGA    TTTTCCTT
                                   T   TAA_
GAM627  MN1      3'  GGTAAGAAAAGGAAAAA     14588      CTTAT
                                GGTA    GAAAAGGAAAAA
                                ||||    ||||||||||||
                                CCAT    CTTTTCCTTTTT
                                  T____
GAM627  MS4A4A   3'  AAGGTACTTTCTATGGGGAAA  35849         ATGAAAA
                                AAGGTACTT      GGAAA
                                |||||||||      |||||
                                TTCCATGAA      CCTTT
                                     AGATACC
GAM627  NHLH1    3'  AAGGAGCAAGAAAAGGAAA   24646      TACTTAT
                                AAGG      GAAAAGGAAA
                                ||||      ||||||||||
                                TTCC      CTTTTCCTTT
                                  TCGTT__
GAM627  OAS2     3'  AAAGGCAGGCTCAGAAGGAAAA 32546        __   T  AA
                                AAAGGTA  CTTA GA  AGGAAAA
                                |||||||  |||| ||  |||||||
                                TTTCCGT  GAGT CT  TCCTTTT
                                    CC   _ __
GAM627  PATE     3'  AAGGATAACACAGAAAGGAAAA 39638      TACT   GA
           A                     AAGG    TAT  AAAGGAAAAA
                                ||||    |||  ||||||||||
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                                TTCC   GTG  TTTCCTTTTT
                                  TATT   TC
GAM627  PAX5    3'  AAAGATACTAAAGAAGGA    32505        TAT  AA
                                AAAGGTACT   GA  AGGA
                                |||||||||   ||  ||||
                                TTTCTATGA   CT  TCCT
                                    TTT  __
GAM627  PCDH11X  5'  AGGTAAACGAAAGGGA     37293      CTT     A
                                AGGTA   ATGAAA GGA
                                |||||   |||||| |||
                                TCCAT   TGCTTT CCT
                                   T__     C
GAM627  PCDH11Y  5'  AGGTAAACGAAAGGGA     37333      CTT     A
                                AGGTA   ATGAAA GGA
                                |||||   |||||| |||
                                TCCAT   TGCTTT CCT
                                   T__     C
GAM627  PIK3CG   3'  GGAGGCAGGGAAAAAGGAA   15305   A    CTTAT
                                A AGGTA    GAAAAGGAA
                                | |||||    |||||||||
                                C TCCGT    TTTTTCCTT
                                 C    CCC__
GAM627  PIK3R3   5'  GGAGGGAGAATGAAGAGGAAAA 41444   A   TACTT    A
          A                      A AGG    ATGAA AGGAAAAA
                                | |||    ||||| |||||||||
                                C TCC    TACTT TCCTTTTT
                                 C   CTCT_    C
GAM627  POU3F4   3'  AAAGGGAAAGAAAAAGGAAA   7168       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   CTTTC__
GAM627  POU3F4   3'  AAAGGGAAAAAAAGGAAA    7167       TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                   CTT_____
GAM627  PSCD4    3'  AGATATCCCTGAAAAGGAA   30120      _  A
                                AGGTA CTT TGAAAAGGAA
                                ||||| ||| ||||||||||
                                TCTAT GGG ACTTTTCCTT
                                   A  _
GAM627  PUM2     3'  AAAGGTTTCACGCAAAGGAAAA 31657       AC    A
          A                      AAAGGT  TTATG AAAGGAAAAA
                                ||||||  ||||| ||||||||||
                                TTTCCA  AGTGC TTTCCTTTTT
                                   A_    G
GAM627  RAB5C    5'  AGGCACTTAGTGGGGAGG    40805        _  AAA
                                AGGTACTTA TG   AGG
                                |||||||| ||   |||
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                                TCCGTGAAT AC   TCC
                                     C  CCC
GAM627  RORC     3'  AGGGTTCATGGGAAAGGAAAA  22810     TAC    A_
                                AGG   TTATG  AAAGGAAAA
                                |||   |||||  |||||||||
                                TCC   AGTAC  TTTCCTTTT
                                  CA_    CC
GAM627  SH3GL2   3'  GGTAAAAGTGGAAAGGAAA   16683      CTTA  A
                                GGTA    TG AAAGGAAA
                                ||||    || ||||||||
                                CCAT    AC TTTCCTTT
                                   TTTC  C
GAM627  SIAH1    3'  GGTACAAAAAAAGGAAAAA   16712      TTAT
                                GGTAC    GAAAAGGAAAAA
                                |||||    ||||||||||||
                                CCATG    TTTTTCCTTTTT
                                   TT__
GAM627  SIAT1    3'  AGGTATTGAAAAGGAA      16717      CTTA
                                AGGTA    TGAAAAGGAA
                                |||||    ||||||||||
                                TCCAT    ACTTTTCCTT
                                   A___
GAM627  SLC17A2  5'  AAGGCTAACTTGGAAAAGGA   25181       __   AT
                                AAGGT  ACTT  GAAAAGGA
                                |||||  ||||  ||||||||
                                TTCCG  TGAA  CTTTTCCT
                                   AT    C_
GAM627  SRC      3'  AGACGTATGAAAGGAAAA    24029    T  T      A
                                GG AC TATGAAA GGAAAA
                                || || ||||||| ||||||
                                TC TG ATACTTT CCTTTT
                                 _  C      _
GAM627  STK24    3'  GGAGGAGGATGAAGAAGGAAAA 18704    A   TACTT    _
           A                     A AGG     ATGAA AAGGAAAAA
                                | |||     ||||| |||||||||
                                C TCC     TACTT TTCCTTTTT
                                 C   TCC__     C
GAM627  TFDP1    3'  AAGATGCTTATGAAACAAA    28273       A       AG
                                AAGGT CTTATGAAA  GA
                                ||||| |||||||||  ||
                                TTCTA GAATACTTT  TT
                                   C        GT
GAM627  UBE2G2   3'  TGAGCCCCTTGTGAGAAGGAAA 42129    A   A_   A   A
           A                     A GGT  CTT TGA AAGGAAAA
                                | |||  ||| ||| ||||||||
                                A TCG  GAA ACT TTCCTTTT
                                 C   GG   C   C
GAM627  UBE2V1   3'  AAAGGAACTTGAGGAGGA    35339       T   TA   AA
                                AAAGG ACT  TGA  AGGA
                                ||||| |||  |||  ||||
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                                TTTCC TGA  ACT  TCCT
                                  T  __  CC
GAM627  VSX1    3'  AAAGGAAACGCAGGAAAGGAAA 31094      T_ T T   A
                                AAAGG  AC TA GAAA GGAAA
                                |||||  || || |||| |||||
                                TTTCC  TG GT CTTT CCTTT
                                  TT  C  C   _
GAM627  WHSC1   3'  AAAGGAAAAAGGAAA      39345      TACTTAT
                                AAAGG      GAAAAGGAAA
                                |||||      ||||||||||
                                TTTCC      TTTTTCCTTT
                                  _______
GAM628  CCNH    3'  TCTAGCTCTTTTGAAGATGG  10301    GC      CCC  CC
                                TC  AGCTCTTT   GG  TGG
                                ||  ||||||||   ||  |||
                                AG  TCGAGAAA   TC  ACC
                                 A_       ACT  T_
GAM628  HOXB9   3'  TCGGACTCTCCTGGCCTGGCT  35847    CAGCT    C
                                TCG    CTTTCC GGCCTGGCT
                                |||    |||||| |||||||||
                                AGC    GAGAGG CCGGACCGA
                                 CT___     A
GAM628  IL17B   3'  TCGGGCTGCTGGCCTGGC    30896    CA  _  TTCCC
                                TCG  GCT CT    GGCCTGGC
                                |||  ||| ||    ||||||||
                                AGC  CGA GA    CCGGACCG
                                 C_  C  _____
GAM628  PI3     5'  GCAGTCCAGCTTGGCCTGGCT  15279     C  TTCCC
                                GCAG TCT    GGCCTGGCT
                                |||| |||    |||||||||
                                CGTC AGG    CCGGACCGA
                                  _  TCGAA
GAM628  REQ     3'  TCCCAGCTCCCTGGCCTGGCT  26550    G    TTT  C
                                TC CAGCTC   CC GGCCTGGCT
                                || ||||||   || |||||||||
                                AG GTCGAG   GG CCGGACCGA
                                 G     ___  A
GAM628  SIGLEC11 5'  TCTGGCTTCTGGGCCGGCCTGG 38087    GCA  _  TTC
            CT                   TC   GCT CT   CCGGCCTGGCT
                                ||   ||| ||   ||||||||||
                                AG   CGA GA   GGCCGGACCGA
                                 AC_   A  CCC
GAM628  SNX9    3'  GCAACTCTTTCTTTTTGG    32155          CCGGCC
                                GCAGCTCTTTC     TGG
                                ||||||||||     |||
                                CGTTGAGAAAG     ACC
                                      AAAA__
GAM628  WSX1    3'  TCCCAGCTCTGCCTGG      22120    G     TTCCCG
                                TC CAGCTCT     GCCTGG
                                || |||||||     ||||||
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                                AG GTCGAGA     CGGACC
                                 G     _______
GAM628  AKAP1    3'  GCTGGTCGAGGCTGCGCAGCG  40225    GAC_   A  G
                                GT   CGAG GC TGCGCAGCG
                                ||   |||| || |||||||||
                                CG   GCTC CG ACGCGTCGC
                                 ACCA   _ _
GAM628  CAPN10   3'  CGTGACCGGGTAGCCAACG   35769        AG_   GTGCG
                                CGTGACCG   AGC    CAGCG
                                ||||||||   |||    |||||
                                GCACTGGC   TCG    GTTGC
                                     CCA   _____
GAM628  DDX3     5'  CGTGACCGTAGGTGTCGCGTGC 35815        _ A____
              G                  CGTGACCG AG    GCGTGCG
                                ||||||||| ||    |||||||
                                GCACTGGC TC    CGCACGC
                                     A  CACAG
GAM628  EN2      5'  CCGAGGGCGTGCGCGGCG    10934      A      A
                                CCGAG GCGTGCGC GCG
                                ||||| |||||||| |||
                                GGCTC CGCACGCG CGC
                                   C       C
GAM628  GMDS     3'  GCGGCCGGGACAGCGCAGCG   11299     A   A  G  T
                                GTG CCG GA CG GCGCAGCG
                                ||| ||| || || ||||||||
                                CGC GGC CT GT CGCGTCGC
                                  C   C  _  _
GAM628  HPCAL1   5'  CGCGACCGGGGAAGGTGGC   39545        A_   C   C
                                CGTGACCG  GAG GTG GC
                                ||||||||  ||| ||| ||
                                GCGCTGGC  CTT CAC CG
                                     CC   C   _
GAM628  LASS1    3'  CGTGGTTGAGCGCCGGC     34603      ACCGA     G  CA
                                CGTG    GAGCGT CG  GC
                                ||||    |||||| ||  ||
                                GCAC    CTCGCG GC  CG
                                  CAA__     _  __
GAM628  RANBP2L1 5'  GTGACGAGCGTGCGGC      37024      CGA       CA
                                GTGAC   GAGCGTGCG  GC
                                |||||   |||||||||  ||
                                CACTG   CTCGCACGC  CG
                                   ____       __
GAM628  RENT1    5'  CGGACCGAGAGGTAACAG    16250    T       C   C
                                CG GACCGAGAG GTG GCAG
                                || ||||||||| ||| ||||
                                GC CTGGCTCTC CAT TGTC
                                  _       _  _
GAM628  SDC2     3'  GTAATTGAGGGACACAGCG   42571      CC   AGCGT
                                GTGA  GAG    GCGCAGCG
                                ||||  |||    ||||||||
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                                CATT  CTC    TGTGTCGC
                                  AA  CC___
GAM628  SLC38A3  5'  CGCGGTTGGGAACGTGCGGCG  27760     ACCGA       CA
                                CGTG    GAGCGTGCG  GCG
                                ||||    |||||||||  |||
                                GCGC    CTTGCACGC  CGC
                                  CAACC       __
GAM629  CISH     5'  GGTGGGGACAGTGGCTGG    40361    AT     ___
                                GG  TGGGGA   TGGCTGG
                                ||  ||||||   |||||||
                                CC  ACCCCT   ACCGACC
                                 __     GTC
GAM629  KPNB1    5'  TGGGGGTTGGGGGGTCGGGTG   13980    A  A     A_   C
                                TG GG TTGGGG  TGG TG
                                || || ||||||  ||| ||
                                AC CC AACCCC  GCC AC
                                 C  C     CA   C
GAM629  NPEPPS   3'  TGGGGGTTGGGGGGTGGAAC    26723    A  A     A   CT
                                TG GG TTGGGG TGG  GGC
                                || || |||||| |||  |||
                                AC CC AACCCC ACC  TTG
                                 C  C     C   __
GAM629  PLIN     3'  AGGGTTGGGGATGAACTG     15395     A        _
                                AGG TTGGGGATGG CTG
                                ||| |||||||||| |||
                                TCC AACCCCTACT GAC
                                  C         T
GAM629  SGCB     3'  TGAGAATTGGGGATATAAACAT 6929              GCT
                                TGAGGATTGGGGATG   GGCAT
                                ||||||||||||||   |||||
                                ACTCTTAACCCCTAT   TTGTA
                                          AT_
GAM629  XRCC3    5'  TGGGGCTTGGGGATGACCCGC  24112    A  A         G
                                TG GG TTGGGGATGGCT GC
                                || || ||||||||||| ||
                                AC CC AACCCCTACTGG CG
                                 C  G           G
GAM630  GAN      3'  TGCTCATTGAGAAGGCAGAATG 35154    _    C  TATTA
                                TG TCAT TG    GCAGAATG
                                || |||| ||    ||||||||
                                AC AGTA AC    CGTCTTAC
                                 G   _  TCTTC
GAM630  LMO2     3'  TCTGTCATTTTTATTAAGC    24550         CTG    _
                                TCTGTCAT   TATTA GC
                                ||||||||   ||||| ||
                                AGACAGTA   ATAAT CG
                                     AAA    T
GAM630  MBNL     3'  TCTGTCATTGTATTAGC      34324         C
                                TCTGTCAT TGTATTAGC
                                |||||||| |||||||||
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                                AGACAGTA ACATAATCG
                                      _
GAM630  SLC1A1   3'  TCTTCATAAATTAGCAGAATG  20037     G    CTGT
                                TCT TCAT    ATTAGCAGAATG
                                ||| ||||    ||||||||||||
                                AGA AGTA    TAATCGTCTTAC
                                  _    TT__
GAM631  CLCA1    5'  TACCATTATATATATACAGA   10507      C       C
                                TACCA TATATATA ACAGA
                                ||||| |||||||| |||||
                                ATGGT ATATATAT TGTCT
                                   A       A
GAM631  EHHADH   3'  CATTACTCTATCACAGAATTG  12683    C   A_   A
                                CA TAT  TAT CACAGAATTG
                                || |||  ||| ||||||||||
                                GT ATG  ATA GTGTCTTAAC
                                 A   AG  _
GAM631  EIF2C1   3'  CTTTATAAAACACAGAATTG   29178    A    T_
                                CT TATA  ACACAGAATTG
                                || ||||  ||||||||||
                                GA ATAT  TGTGTCTTAAC
                                 A    TT
GAM632  PPP2CA   3'  AGTTATATGGTTTTACAA    15513       T       T
                                AGTTAT TGGTTTTA CAA
                                |||||| |||||||| |||
                                TCAATA ACCAAAAT GTT
                                   T      _
GAM632  RNF6     3'  GTTATTTGGTTCTAGCAA    25579            T
                                GTTATTTGGTTTTA CAA
                                |||||||||||||| |||
                                CAATAAACCAAGAT GTT
                                         C
GAM633  CXCL16   3'  CGCAAGGGCTGAGGCCAG    35196         CA    AG
                                CGCAAGGGC  AGGC  AG
                                |||||||||  ||||  ||
                                GCGTTCCCG  TCCG  TC
                                      AC    G_
GAM633  DDX11    3'  GCAGGGGCTGCAAGAGCTTC   36176     A    CAAG   _
                                GCA GGGC    GCA GAGCTTC
                                ||| ||||    ||| |||||||
                                CGT CCCG    CGT CTCGAAG
                                  C    A___   T
GAM633  MFNG     3'  TCGCAAGGGGTGGGGAGCAAGG 14420         CCAA__   __
           AGCTT                  TCGCAAGGG     GGCA  GAGCTT
                                |||||||||     ||||  ||||||
                                AGCGTTCCC     TCGT  CTCGAA
                                      CACCCC    TC
GAM633  MTA1L1   5'  TCGCGGGGGCAGGGCT     21895      AA   CCAA    A
                                TCGC  GGG    GGCAG GCT
                                ||||  |||    ||||| |||
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                                AGCG  CCC   CCGTC CGA
                                  __  ____    C
GAM633  SRD5A1   3' AAGGGCCACGAGGAGCTTC   9824        AGGCA
                                AAGGGCCA    GAGCTTC
                                ||||||||    |||||||
                                TTCCCGGT    CTCGAAG
                                    GCTC_
GAM634  BLAME    3' GGAGTGCTGTGTATTTT    33489    CAC    GAG
                                GGA   TGCTG   GTATTTT
                                |||   |||||   |||||||
                                CCT   ACGAC   CATAAAA
                                  C__    A__
GAM634  FCER2    3' AGGGTGCTGTTGGGGGCACT   12810    ACA   C   A
                                AGG   CTG TGG GGTATT
                                |||   ||| ||| ||||||
                                TCC   GAC ACC CCGTGA
                                  CAC   A   C
GAM634  KAI1     3' GGACGCTGTGGGGAGCATTTTT 13787     A   CT  AG
                                GGAC CTG  GG  GTATTTTT
                                |||| |||  ||  ||||||||
                                CCTG GAC  CC  CGTAAAAA
                                  C   AC  CT
GAM634  LPIN2    3' GGACACTGCTCGGGGGGCA   31214         _ A_
                                GGACACTGCT GG  GGTA
                                |||||||||| ||  ||||
                                CCTGTGACGA CC  CCGT
                                      G  CC
GAM634  PIK3CG   3' AGACACTGTTAACATAGTTTTT 15301        CTG  G  _
                                GGACACTG   GA GTA TTTTT
                                ||||||||   || ||| |||||
                                TCTGTGAC   TT TAT AAAAA
                                    AA_  G   C
GAM634  RANBP3   5' AGGCATTGCTGGACTCATTTTT 28749     A  C      GG
                                AGG CA TGCTGGA  TATTTTT
                                ||| || |||||||  |||||||
                                TCC GT ACGACCT  GTAAAAA
                                  _ A      GA
GAM634  SFRP5    3' GGGTGTGGCTGGAGGCACT   16597    ACACT
                                GG    GCTGGAGGTATT
                                ||    ||||||||||||
                                CC    CGACCTCCGTGA
                                  CACAC
GAM635  BSN      3' GCCAGATTGTAGATGTGT    18401     AG  _
                                GCCA  TT TAGATGTGT
                                ||||  || |||||||||
                                CGGT  AA ATCTACACA
                                  CT  C
GAM635  C18orf2  3' TGCTGAGTTTAGAACCAGTGT 36410     CA       T___
                                TGC  AGTTTAGA    GTGT
                                |||  ||||||||    ||||
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                                ACG  TCAAATCT    CACA
                                  AC       TGGT
GAM635  CYP8B1   3'  TGCCAAGTTCTGCAT      20512         AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ACGGTTCAAG   ACGTA
                                             ___
GAM635  E2F3     3'  TACCAAGTCCAGTGTGT     12630          A
                                TGCCAAGTTTAG TGTGT
                                |||||||||||| |||||
                                ATGGTTCAGGTC ACACA
                                             _
GAM635  EPB41L2  3'  TGCCAGCTTTAAATGGT     11009      AG       T
                                TGCCA  TTTAGATG GT
                                |||||  |||||||| ||
                                ACGGT  AAATTTAC CA
                                   CG       _
GAM635  FAP      5'  TGCCAAGTTTCAAAAGAT    20892          _____
                                TGCCAAGTTT    AGAT
                                ||||||||||    ||||
                                ACGGTTCAAA    TCTA
                                      GTTT
GAM635  GDI2     3'  TGCCAAATTTTAAATGTGT    11259          _
                                TGCCAAGTTT AGATGTGT
                                |||||||||| ||||||||
                                ACGGTTTAAA TTTACACA
                                      A
GAM635  GNAZ     3'  TGCCATCTCCAGATGTGT     13186      AG
                                TGCCA  TTTAGATGTGT
                                |||||  ||||||||||
                                ACGGT  AGGTCTACACA
                                   AG
GAM635  JAM3     3'  TGCCAAATTACGGTGTGT     37268         TAGA
                                TGCCAAGTT    TGTGT
                                |||||||||    |||||
                                ACGGTTTAA    ACACA
                                      TGCC
GAM635  KCNE1L   3'  TGCCAAGTGTTGGACGTGT   29377         _ A
                                TGCCAAGT TT GATGTGT
                                |||||||| || |||||||
                                ACGGTTCA AA CTGCACA
                                     C  C
GAM635  LIMD1    3'  TACCAAGTCCTTGTGT      30634         AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||   |||||
                                ATGGTTCAGG   ACACA
                                      A__
GAM635  LOXL2    3'  CCAAGTTTCAAGTATGTGT   14195         AG___
                                CCAAGTTT    ATGTGT
                                ||||||||    ||||||
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                                GGTTCAAA    TACACA
                                    GTTCA
GAM635  MMP19    5' TGCATTTCCAGATGTGT    35595    CAAG
                                TGC   TTTAGATGTGT
                                |||   ||||||||||
                                ACG   AGGTCTACACA
                                  TAA_
GAM635  MTMR7    3' GCCACAAACCAGATGTGT    42905    AGT_
                                GCCA   TTAGATGTGT
                                ||||   ||||||||||
                                CGGT   GGTCTACACA
                                  GTTT
GAM635  OPCML    3' TGCAGAGACAGATGTGT    14955    CA  TT
                                TGC  AG  TAGATGTGT
                                |||  ||  |||||||||
                                ACG  TC  GTCTACACA
                                  TC  T_
GAM635  PATE     3' TGGCAAGCTCAAGTGTGT    39647    C       A
                                TG CAAGTTTAG TGTGT
                                || |||||||| |||||
                                AC GTTCGAGTT ACACA
                                 C       C
GAM635  PCSK1    3' TGCCAAGTCCCAAGTGT    7757         AGAT
                                TGCCAAGTTT   GTGT
                                ||||||||||   ||||
                                ACGGTTCAGG   CACA
                                     GTT_
GAM635  PLS1     3' TACCAAACTAGGATGTGT    15412      GT TA
                                TGCCAA  T  GATGTGT
                                ||||||  |  |||||||
                                ATGGTT  A  CTACACA
                                   TG TC
GAM635  RAB23    3' TACCATACAAAGATGTGT    32220      AG TT
                                TGCCA  T  AGATGTGT
                                |||||  |  ||||||||
                                ATGGT  G  TCTACACA
                                  AT TT
GAM635  SLC21A9  3' TGCCAAGTCTGGGTGT     28571        AGAT
                                TGCCAAGTTT   GTGT
                                ||||||||||   ||||
                                ACGGTTCAGA   CACA
                                     CC__
GAM635  TAGLN2   3' TGCCCCAGATGTGT      18686     AAGT
                                TGCC   TTAGATGTGT
                                ||||   ||||||||||
                                ACGG   GGTCTACACA
                                  ____
GAM635  TNFRSF1A 3' TGCCAAGTTTCTATTAGTGT  9870         AGAT__
                                TGCCAAGTTT    GTGT
                                ||||||||||    ||||
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                                ACGGTTCAAA     CACA
                                     GATAAT
GAM635  TRIM     3'  TGCCAAGTCCTTCTGTGT    32303          AGA
                                TGCCAAGTTT   TGTGT
                                ||||||||||  |||||
                                ACGGTTCAGG   ACACA
                                     AAG
GAM635  XRCC3    3'  TGCAGCCAGATGTGT      24109     CA    T
                                TGC  AGTT AGATGTGT
                                |||  |||| ||||||||
                                ACG  TCGG TCTACACA
                                  __   _
GAM636  ACAD8    3'  TCATGATTTACATTCAGAGGTG 30791     A      AAT     A
                                TCA TGATTTG   TTCAGA GTG
                                ||| |||||||   |||||| |||
                                AGT ACTAAAT   AAGTCT CAC
                                  _      GT_     C
GAM636  EMX2     3'  TCAAGGATTTGAAACAG     44697      T       TTT
                                TCAA GATTTGAA   CAG
                                |||| ||||||||   |||
                                AGTT CTAAACTT   GTC
                                  C       T__
GAM636  MPHOSPH9 3'  TCAAAGATTTGCAGAGGT    35568      T     AATTT    A
                                TCAA GATTTG    CAGA GT
                                |||| ||||||    |||| ||
                                AGTT CTAAAC    GTCT CA
                                  T     _____   C
GAM636  NEK6     3'  TCAAATGATTTCCTTCAGAGGT 30827      _     GAA      A
           G                     TCAA TGATTT   TTTCAGA GTG
                                |||| ||||||   ||||||| |||
                                AGTT ACTAAA   GAAGTCT CAC
                                  T     G__      C
GAM636  PPEF1    3'  TGACTATGAATTTCAGGGGTG  26412       _        AA
                                TGATT TGAATTTCAG  GTG
                                ||||| ||||||||||  |||
                                ACTGA ACTTAAAGTC  CAC
                                   T         CC
GAM637  CDH16    3'  CATGCCTGGTGATGG       19784         A   CAT
                                CATGCCTG TGA   TGG
                                |||||||| |||   |||
                                GTACGGAC ACT   ACC
                                     C  ___
GAM637  DNMT1    3'  ATCAGTGCATGTTGGGGA    10714      _  C  ATGACA
                                ATCA TGC TG     TTGGGGA
                                |||| ||| ||     |||||||
                                TAGT ACG AC     AACCCCT
                                  C  T _______
GAM637  DVL3     3'  TGCCTGATGGGGTGGGG     20692          ACAT
                                TGCCTGATG    TGGGG
                                |||||||||    |||||
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                                ACGGACTAC   ACCCC
                                    CCC_
GAM637  SLC38A2  3' ATGCCTGATGAGCGAAG    33273        CAT
                                ATGCCTGATGA  TGGGG
                                ||||||||||  |||||
                                TACGGACTACT  GCTTC
                                    C__
GAM638  ABCC5    3' TGCCACCTCAAAAAGCAG    25028    CT
                                TGCC TTTCAAAAAGCAG
                                ||||  ||||||||||||
                                ACGG GGAGTTTTTCGTC
                                  T_
GAM638  ADAMTS13 3' GCCCCCCAAAGGCAG      40036     TT   AA
                                GCCCT TCAAA GCAG
                                ||||| ||||| ||||
                                CGGGG GGTTT CGTC
                                  __   C_
GAM638  ADARB1   3' TGCCCTTTCCACTTACACAG  31886       AAAA_
                                TGCCCTTTTCA   GCAG
                                ||||||||||   ||||
                                ACGGGAAAGGT   TGTC
                                    GAATG
GAM638  AK1      3' TGCCCTTTTCAGACCCTCAG  7880        AAAAG_
                                TGCCCTTTTCA    CAG
                                ||||||||||    |||
                                ACGGGAAAAGT    GTC
                                    CTGGGA
GAM638  ANK1     5' TGCCCTTCTGCCCAGCAG   33877       CAAAA
                                TGCCCTTTT   AGCAG
                                |||||||||   |||||
                                ACGGGAAGA   TCGTC
                                    CGGG_
GAM638  ASB1     5' GCCCCTCGGGCAGGAAGCAG  32030      T__ AA
                                GCCCTTT  CA AAGCAG
                                |||||||  || ||||||
                                CGGGGAG  GT TTCGTC
                                   CCC  CC
GAM638  ATP2A3   3' CCCCCAGGAAAGAAGCAG   23190     TTC  _
                                CCCTT  AAA AAGCAG
                                |||||  ||| ||||||
                                GGGGG  TTT TTCGTC
                                  TCC  C
GAM638  AXIN1    3' TGCCCTTTTTGGTCAGCAG  41394       CAAAA
                                TGCCCTTTT   AGCAG
                                |||||||||   |||||
                                ACGGGAAAA   TCGTC
                                    ACCAG
GAM638  CAPON    3' TACCCTCCAAAGCA       41936       TCAA
                                TGCCCTTT   AAAGCA
                                ||||||||   ||||||
```

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                                ATGGGAGG   TTTCGT
                                    ____
GAM638  CBFA2T2  3'  TACCCTTTGCAAGCAG     22976       TCAAA
                                TGCCCTTT    AAGCAG
                                ||||||||    ||||||
                                ATGGGAAA    TTCGTC
                                    CG___
GAM638  CCNF     3'  CCCTTTCCATGCAGGAGCAG  12072       AAA___
                                CCCTTTTCA    AGCAG
                                |||||||||    |||||
                                GGGAAAGGT    TCGTC
                                     ACGTCC
GAM638  CPNE7    3'  TGCCCCTTCTCATCGGGGCAG 30873     _    AAAA_
                                TGCCC TTTTCA    GCAG
                                ||||| ||||||    ||||
                                ACGGG AAGAGT    CGTC
                                   G     AGCCC
GAM638  CTPS     3'  TGCCCTTTCAACTGCAG     44803       T   AAA
                                TGCCCTTT CAA   GCAG
                                |||||||| |||   ||||
                                ACGGGAAA GTT   CGTC
                                    _  GA_
GAM638  DAG1     3'  TGCCCTCTTGAGAGCAG     20529       CAAAA
                                TGCCCTTTT    AGCAG
                                |||||||||    |||||
                                ACGGGAGAA    TCGTC
                                     CTC__
GAM638  DMD      5'  GCCTCACAAAAGCAG       19705    CTTT  _
                                GCC   TCA AAAAGCAG
                                |||   ||| ||||||||
                                CGG   AGT TTTTCGTC
                                  _____  G
GAM638  DOCK1    3'  CCTTTGAAGAAAAAGCAG    10717      TC__
                                CCTTT   AAAAAGCAG
                                |||||   |||||||||
                                GGAAA   TTTTTCGTC
                                   CTTC
GAM638  DSC3     3'  TGCTACCAAAAAGCAG      35948    CCTTT
                                TGC    TCAAAAAGCAG
                                |||    ||||||||||
                                ACG    GGTTTTTCGTC
                                  AT___
GAM638  ECHS1    3'  TGTCCTCTCCAAGCAG      19874    C      AAA
                                TG CCTTTTCA   AGCAG
                                || ||||||||   |||||
                                AC GGAGAGGT   TCGTC
                                 A      ___
GAM638  EDAR     5'  GCCCTCTCAGAAGCAG      35307       CAAA
                                GCCCTTTT   AAGCAG
                                ||||||||   ||||||
```

```
                                CGGGAGAG   TTCGTC
                                    TC__
GAM638  ENTPD6   5' TGCCCTTTTCCGGGGAGCAG  10344        AAAA_
                                TGCCCTTTTC    AGCAG
                                ||||||||||    |||||
                                ACGGGAAAAG    TCGTC
                                     GCCCC
GAM638  EPHB2    3' TGTCCCTTTCATCAACAG    32684    C      AAA
                                TG CCTTTTCA   AGCAG
                                || ||||||||   |||||
                                AC GGGAAAGT   TTGTC
                                 A       AG_
GAM638  EXTL3    3' TGCCCCTTCCAGCA       11040         AAAA
                                TGCCCTTTTCA   GCA
                                ||||||||||    |||
                                ACGGGGAAGGT   CGT
                                      ____
GAM638  F2R      3' GCTCCCATAAAAAGCAG    12797    _   TTTC
                                GC CCT    AAAAAGCAG
                                || |||    |||||||||
                                CG GGG    TTTTTCGTC
                                 A   TA__
GAM638  FGF7     3' TACCCTTTCCACTTGAGCAG  12862         AAA_
                                TGCCCTTTTCA   AGCAG
                                ||||||||||    |||||
                                ATGGGAAAGGT   TCGTC
                                     GAAC
GAM638  HAS3     3' TGCACTTTTAAAAGCAG     39777    C    CA
                                TGC CTTTT  AAAAGCAG
                                ||| |||||  ||||||||
                                ACG GAAAA  TTTTCGTC
                                  T    __
GAM638  HLCS     3' CCCTTTTCCATCTGAAGCAG  7638         AAA___
                                CCCTTTTC     AAGCAG
                                ||||||||     ||||||
                                GGGAAAAG     TTCGTC
                                     GTAGAC
GAM638  HMGA1    5' CCCTTCTCTAAGGAGCAG    44162         _  AA
                                CCCTTTTC AA  AGCAG
                                |||||||| ||  |||||
                                GGGAAGAG TT  TCGTC
                                     A  CC
GAM638  HSPA4    3' TGCCCCAAAAAGCAG       44856      TTTT
                                TGCCC    CAAAAAGCAG
                                |||||    ||||||||||
                                ACGGG    GTTTTTCGTC
                                      ____
GAM638  JAG1     3' CTTTTCAAGTCTAAAGCAG   6854         ____
                                CTTTTCAA    AAAGCAG
                                ||||||||    |||||||
```

```
                                GAAAAGTT   TTTCGTC
                                    CAGA
GAM638  JUP     3'  GCCCAGGACAGAAAAGCAG   13775     TTTT  _
                                GCCC   CA AAAAGCAG
                                ||||   || ||||||||
                                CGGG   GT TTTTCGTC
                                  TCCT  C
GAM638  KCNS3   5'  TGCCCTTCTCAGCA       13936         AAAA
                                TGCCCTTTTCA   GCA
                                ||||||||||   |||
                                ACGGGAAGAGT   CGT
                                     ____
GAM638  LDB2    3'  TGCAAGTCAAAAAGCAG     10523     CCTTT
                                TGC    TCAAAAAGCAG
                                |||    ||||||||||
                                ACG    AGTTTTTCGTC
                                  TTC__
GAM638  MAGEA2  3'  TGCTCTCTTCAAAGAGGCAG  41309     C       AA_
                                TGC CTTTTCAAA  GCAG
                                ||| |||||||||  ||||
                                ACG GAGAAGTTT  CGTC
                                  A       CTC
GAM638  MAGEA8  3'  TGCTCTCTTCAAACACAG    23847     C       AA
                                TGC CTTTTCAAA  GCAG
                                ||| |||||||||  ||||
                                ACG GAGAAGTTT  TGTC
                                  A       G_
GAM638  MAGEA9  3'  TGCTCTCTTCAAACACAG    23851     C       AA
                                TGC CTTTTCAAA  GCAG
                                ||| |||||||||  ||||
                                ACG GAGAAGTTT  TGTC
                                  A       G_
GAM638  MAPK8IP1 3' TGCCCCTCCTCAAGCAG     24163         CAAA
                                TGCCCTTTT   AAGCAG
                                |||||||||   ||||||
                                ACGGGGAGG   TTCGTC
                                     AG__
GAM638  MCM7    3'  TGCCCCTTCCCAAGGGGCAG  25409         AAAAA_
                                TGCCCTTTTC    GCAG
                                ||||||||||    ||||
                                ACGGGGAAGG    CGTC
                                     GTTCCC
GAM638  MFNG    3'  TGCCCTTTTTCAATTCAG    14421         _  AAAG
                                TGCCCTTTT CAA   CAG
                                ||||||||| |||   |||
                                ACGGGAAAA GTT   GTC
                                     A  AA__
GAM638  MMP19   5'  GCCCCTCCCAAAGGGCAG    35586       TT   AA
                                GCCCTT  CAAA  GCAG
                                ||||||  ||||  ||||
```

```
                                CGGGGA  GTTT  CGTC
                                   GG    CC
GAM638  MYC      5'  TGCCCTTCTCGAGGCAG     14714          AAAAA
                                TGCCCTTTTC    GCAG
                                ||||||||||    ||||
                                ACGGGAAGAG    CGTC
                                     CTC__
GAM638  NFKBIL2  5'  GCTCTTCTCAAAGGCAG     30241    C       AA
                                GC CTTTTCAAA  GCAG
                                || |||||||||  ||||
                                CG GAAGAGTTT  CGTC
                                 A        C_
GAM638  NOS1     3'  TGCCTTTTCACTTTAACAG   8380      C     AAA_
                                TGCC TTTTCA    AGCAG
                                |||| ||||||    |||||
                                ACGG AAAAGT    TTGTC
                                  _     GAAA
GAM638  NPTX1    3'  GCCCTCTCTGGGAAGCAG    14839        CAAA
                                GCCCTTTT    AAGCAG
                                ||||||||    ||||||
                                CGGGAGAG    TTCGTC
                                     ACCC
GAM638  PLAU     3'  TGCCCTTTTTAACTCCTGCAG  42882          C  AAA__
                                TGCCCTTTT AA    GCAG
                                |||||||||  ||    ||||
                                ACGGGAAAA TT    CGTC
                                     A  GAGGA
GAM638  POLS     3'  CCTGCTTCAAAAGGGCAG    28118     _      A_
                                CCT TTTCAAAA  GCAG
                                |||  ||||||||  ||||
                                GGA GAAGTTTT  CGTC
                                  C       CC
GAM638  PRKCN    3'  GCCCTGGCTAAAAAGCAG    25159       TTTC
                                GCCCT    AAAAAGCAG
                                |||||    |||||||||
                                CGGGA    TTTTTCGTC
                                   CCGA
GAM638  PTTG1IP  5'  GCCTCAAAAAGCAG        20288     CTTT
                                GCC    TCAAAAAGCAG
                                |||    ||||||||||
                                CGG    AGTTTTTCGTC
                                    _____
GAM638  RENT1    3'  TACCCCCCAGAAGCAG      16257         TCAAA
                                TGCCCTTT    AAGCAG
                                ||||||||    ||||||
                                ATGGGGGG    TTCGTC
                                     TC___
GAM638  SLC16A2  3'  TGCCCTCTAAGCAA        27159         TCAAA
                                TGCCCTTT    AAGCAG
                                ||||||||    ||||||
```

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                                ACGGGAGA    TTCGTT
                                        _____
GAM638  SMCX    3'  GCCCACCCCCCAAGAAGCAG  20071     __  TT   A
                                GCCC  TT  CAA AAGCAG
                                ||||  ||  ||| ||||||
                                CGGG  GG  GTT TTCGTC
                                  TG  GG   C
GAM638  SOX12   3'  TGCTCCTCCCATTAAGGCAG  28062    C   TT  AA  _
                                TGC CTT  CA  AAG CAG
                                ||| |||  ||  ||| |||
                                ACG GGA  GT  TTC GTC
                                  A   GG  AA   C
GAM638  TCF2    3'  GCCCTTTTCTTGGAGCAG    27028        AAAA
                                GCCCTTTTC   AGCAG
                                |||||||||   |||||
                                CGGGAAAAG   TCGTC
                                      AACC
GAM638  TGFBR3  3'  TGCCCTTTCCAATCTCAG    17494          AAAG
                                TGCCCTTTTCAA   CAG
                                ||||||||||||   |||
                                ACGGGAAAGGTT   GTC
                                       AGA_
GAM638  TLX1    5'  TGCCCTTCTTTAAAACA     24348        CAA
                                TGCCCTTTT   AAAGCA
                                |||||||||   ||||||
                                ACGGGAAGA   TTTTGT
                                      AA_
GAM638  TMEPAI  3'  TGCCTTTTCACCTACGCAG   33627     C     AAAA_
                                TGCC TTTTCA    GCAG
                                |||| ||||||    ||||
                                ACGG AAAAGT    CGTC
                                  _     GGATG
GAM638  ZIC1    5'  TGCCCTTTTAAAGGCA      18239        CA   A
                                TGCCCTTTT  AAA GCA
                                |||||||||  ||| |||
                                ACGGGAAAA  TTT CGT
                                      __   C
GAM638  ZNF236  3'  TGCCCTTTCAAAATAACAG   28868        T    _
                                TGCCCTTT CAAAA AGCAG
                                |||||||| ||||| |||||
                                ACGGGAAA GTTTT TTGTC
                                      _    A
GAM639  AF1Q    3'  TAGCACAAATCACCATCAATAT 27727          __  GAT
                                TAGCACAAAT  CCA   ATAT
                                ||||||||||  |||   ||||
                                ATCGTGTTTA  GGT   TATA
                                      GT   AGT
GAM639  GCNT1   3'  GCACAGGTCACATCTT      11248      AA  CAGAT
                                GCACA  TC    ATATCTT
                                |||||  ||    |||||||
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                                CGTGT  AG    TGTAGAA
                                  CC _____
GAM639  KLHL3    3'  GCACAAATCTATCT       44641         CAGATA
                                GCACAAATC     TATCT
                                |||||||||     |||||
                                CGTGTTTAG     ATAGA
                                      ______
GAM639  LRRC2    3'  AGCCCCTCTTCAGATATATTTT 35994     ACAAATC       C
              C                  AGC      CAGATATAT TTC
                                |||      ||||||||| |||
                                TCG      GTCTATATA AAG
                                  GGGAGAA       A
GAM639  TBXA2R   5'  GCACTGGTTCAGGCACACCTTC 9856      AAATC   A
                                GCAC    CAG TATATCTTC
                                ||||    ||| |||||||||
                                CGTG    GTC GTGTGGAAG
                                  ACCAA   C
GAM639  TLR3     5'  TAGTCCAAATCCAGACATTTC  17561     CA          A
                                TAG  CAAATCCAGATAT TC
                                |||  |||||||||||||| ||
                                ATC  GTTTAGGTCTGTA AG
                                  AG          A
GAM639  MGA      5'  AATTGGATGTTGAAGGCA    41720        ACC
                                AATTGGGT   GAAGGCG
                                ||||||||   |||||||
                                TTAACCTA   CTTCCGT
                                     CAA
GAM640  EN2      3'  TGGATTTTATACCACCTGT    10964          TG T
                                TGGATTTTATGC  C CTGT
                                ||||||||||||  | ||||
                                ACCTAAAATATG  G GACA
                                       GT _
GAM640  MAPK4    3'  TCTGGGGGTCTCCTGCTCTGT  15667     T  A    ATG
                                TCTG GG TTTT   CTGCTCTGT
                                |||| || ||||   |||||||||
                                AGAC CC AGAG   GACGAGACA
                                  C  C   ___
GAM640  TRPV3    3'  TCTTGGATTTTGTTGAAATCTG 45445     G       ATGCTGC
              T                  TCT TGGATTTT       TCTGT
                                ||| ||||||||       |||||
                                AGA ACCTAAAA       AGACA
                                  _       CAACTTT
GAM640  XRCC2    3'  TGTGAATTTTTGCTTCTGT   24096         A   GC
                                TGTGGATTTT TGCT  TCTGT
                                |||||||||| ||||  |||||
                                ACACTTAAAA ACGA  AGACA
                                      _   __
GAM641  FZD3     3'  TTTGATGCAATATAAAAA    32638     A
                                TTT ATGCAATGTAAAAG
                                |||  ||||||||||||||
```

```
                                AAA TACGTTATATTTTT
                                  C
GAM641  ADORA2B  3'  AACTTTTATTTTTCCATTGCC  8610      GCATTATC
                                AGCT       TTCCATTGCC
                                ||||       ||||||||||
                                TTGA       AAGGTAACGG
                                  AAATAAA_
GAM641  C18orf1  3'  AAGATGCAACTTTCCATTGC  41203     C    TT TC
                                AAG TGCA  A  TTCCATTGC
                                ||| ||||  |  |||||||||
                                TTC ACGT  T  AAGGTAACG
                                  T   __ GA
GAM641  CACNB2   5'  AAGCTGCACTGTGCC      8788          ATCTTCCAT
                                AAGCTGCATT       TGCC
                                ||||||||||       ||||
                                TTCGACGTGA       ACGG
                                      C_________
GAM641  DDT      3'  AAGCTGGTTATCTCCAGGCC  10668       CA     T   TT
                                AAGCTG  TTATCT CCA  GCC
                                ||||||  |||||| |||  |||
                                TTCGAC  AATAGA GGT  CGG
                                   C_     _  C_
GAM641  GOT2     3'  AAACTGCATTATTTCCCTTGC  45232          C    A
                                AAGCTGCATTAT TTCC TTGC
                                |||||||||||| |||| ||||
                                TTTGACGTAATA AGGG AACG
                                      A   _
GAM641  INPP5D   3'  GCTGCACTATTTCAAGAGCC  44422          C   CATT
                                GCTGCATTAT TTC    GCC
                                |||||||||| |||    |||
                                CGACGTGATA AAG    CGG
                                      _   TTCT
GAM641  MASP1    3'  AGCTGGGTCCCATTGC      40093       CATTATC
                                AGCTG      TTCCATTGC
                                |||||      |||||||||
                                TCGAC      AGGGTAACG
                                  CC_____
GAM641  MLLT2    3'  AAGTTGCAGTTCCATTGC    25490     C    TTATC
                                AAG TGCA    TTCCATTGC
                                ||| ||||    |||||||||
                                TTC ACGT    AAGGTAACG
                                  A   C____
GAM641  PCLO     3'  TGCATTATCTTCTGCC      45309          CAT
                                TGCATTATCTTC   TGCC
                                ||||||||||||   ||||
                                ACGTAATAGAAG   ACGG
                                       ___
GAM641  PCP4     3'  AAGCTACTCACAATTCCATTG  26229        A    C_
                                AAGCTGC TTAT  TTCCATTG
                                ||||||| ||||  ||||||||
```

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                                TTCGATG AGTG  AAGGTAAC
                                   _    TT
GAM641  PDE4C    3'  GCTTTACCATCCATTGCC    9558     A    T
                                GC TTATC TCCATTGCC
                                || ||||| |||||||||
                                CG AATGG AGGTAACGG
                                 A    T
GAM641  PGM1     3'  AACTTGCACCATCATTTCATTG 15256     _      _ C
          CC                      AGCT GCATTATC TT CATTGCC
                                |||| |||||||| || |||||||
                                TTGA CGTGGTAG AA GTAACGG
                                  A       T A
GAM641  SDHC     3'  AGCTGGCATTGTTTCCACTG  42974      _   ATC
                                AGCTG CATT   TTCCATTG
                                ||||| ||||   ||||||||
                                TCGAC GTAA   AAGGTGAC
                                   C    CA_
GAM641  TRIP15   3'  AGCTGCACTGTTTATTTGCC  20158        ATCTTCCA
                                AGCTGCATT       TTGCC
                                |||||||||       |||||
                                TCGACGTGA       AACGG
                                     CAAATA__
GAM641  UBE3A    3'  AAGCTGCATTTTTCCTGC    39275        ATC    AT
                                AAGCTGCATT   TTCC  TGC
                                ||||||||||   ||||  |||
                                TTCGACGTAA   AAGG  ACG
                                     A__    __
GAM642  PSEN1    3'  GGGCATACATCTCATTTGCTG  28740        CCG  ACCA
                                GGGTATACA   CG    CTG
                                |||||||||   ||    |||
                                CCCGTATGT   GT    GAC
                                     AGA  AAAC
GAM642  RAD21    3'  GGGTATACACTGAAGTCTG    26528        CGC  CCA
                                GGGTATACAC   GA   CTG
                                ||||||||||   ||   |||
                                CCCATATGTG   CT   GAC
                                     A__  TCA
GAM643  MARK3    5'  CGTTGAACCCCATTCGTGA    14357         A   C  C
                                CGTTGAACCC CAT CG GA
                                |||||||||| ||| || ||
                                GCAACTTGGG GTA GC CT
                                     _   A  A
GAM644  TRIM9    3'  AGGGTGACTGGCACATGT    31552      AAATAAA
                                AGGGT      GGCACATGT
                                |||||      |||||||||
                                TCCCA      CCGTGTACA
                                   CTGA___
GAM644  AMY1A    5'  CAGTGTCCTTTCCAGAAACTAT 44303       A      ____
          TT                      CAGTGT CCTTTCT    ACTATTT
                                ||||||| |||||||    |||||||
```

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                                GTCACA GGAAAGG    TGATAAA
                                   _      TCTT
GAM644   AMY2A    5'  CAGTGTCCTTTCCAGAAACTAT 8689        A     _____
                TT                  CAGTGT CCTTTCT    ACTATTT
                                    |||||| |||||||    |||||||
                                    GTCACA GGAAAGG    TGATAAA
                                       _      TCTT
GAM644   AMY2B    5'  CAGTGTCCTTTCCAGAAACTAT 34158       A     _____
                TT                  CAGTGT CCTTTCT    ACTATTT
                                    |||||| |||||||    |||||||
                                    GTCACA GGAAAGG    TGATAAA
                                       _      TCTT
GAM644   PON1     3'  GTTTACCTTTCTATTATTT   7778     G        C
                                    GT TACCTTTCTA TATTT
                                    || |||||||||| |||||
                                    CA ATGGAAAGAT ATAAA
                                     A         A
GAM645   ACLY     3'  CACAGTTTCTAAGCATGTC    42153
                                    TACAGTTTCTAAGCGTGTT
                                    |||||||||||||||||||
                                    GTGTCAAAGATTCGTACAG

GAM645   BACH2    3'  TTTCTAACTGTTTTGT      34813        G G
                                    TTTCTAA C TGTTTTGT
                                    ||||||| | ||||||||
                                    AAAGATT G ACAAAACA
                                       _ _
GAM645   CYP4F3   3'  ACAGTTTGGCAGTGTTTTGT   9450        CTAA  _
                                    ACAGTTT    GC GTGTTTTGT
                                    |||||||    || |||||||||
                                    TGTCAAA    CG CACAAAACA
                                        C___  T
GAM645   DLG5     3'  TACAGTTTTTCATAGTTTGTC  44462        CTAAG    T
                                    TACAGTTT     CGTG TTTGTC
                                    ||||||||     |||| ||||||
                                    ATGTCAAA     GTAT AAACAG
                                         AA___    C
GAM645   LPL      3'  TACGTTTCTTTCTTGTTTTGT  6942      A     AAGCG
                                    TAC GTTTCT     TGTTTTGT
                                    ||| ||||||     ||||||||
                                    ATG CAAAGA     ACAAAACA
                                      _      AAGA_
GAM645   MTR      3'  TGAGTTTCTAGGCCCTTATTTT 7020     C       A  G__
                GT                    A AGTTTCTA GC   TGTTTTGT
                                      | |||||||| ||   ||||||||
                                      A TCAAAGAT CG   ATAAAACA
                                       C       C  GGA
GAM645   NR3C1    3'  TACAGCTTCTATTTTG      6755           AAGCGT
                                    TACAGTTTCT     GTTTTG
                                    ||||||||||     ||||||
```

```
                                ATGTCGAAGA     TAAAAC
                                       ______
GAM645  SNAI2    3'  TACATTCTCCTGTGTTTTGT   16883      G    AAGC
                                TACA TTTCT    GTGTTTTGT
                                |||| |||||    |||||||||
                                ATGT AGAGG    CACAAAACA
                                  A    A___
GAM645  TRIP15   3'  TACAATTTCTGAGCTGCACTGT 20159          A  G  T
                                TACAGTTTCT AGC TGT TTGT
                                |||||||||| ||| ||| ||||
                                ATGTTAAAGA TCG ACG GACA
                                      C   _  T
GAM645  DSC3     3'  GTTTATTTTTTAAACTATCACT 35945             ACCA
                                GTTTATTTTTTAAACTG   ACT
                                ||||||||||||||||    |||
                                CAAATAAAAAATTTGAT   TGA
                                          AG__
GAM645  OPCML    3'  TTTATTTTTTAGACTGAGGGCC 14957          A   ___
                                TTTATTTTTTA ACTGA  CC
                                |||||||||| |||||  ||
                                AAATAAAAAAT TGACT  GG
                                      C    CCC
GAM645  SLC2A8   3'  GTTTATTTTTTAAACTCAAC  31032            GAC
                                GTTTATTTTTTAAACT  CAAC
                                ||||||||||||||   ||||
                                CAAATAAAAAATTTGA  GTTG
                                       ___
GAM645  TNFAIP1  3'  TTATTTTTTAAAAACCAA    34484          CT
                                TTATTTTTTAAA  GACCAA
                                ||||||||||||  ||||||
                                AATAAAAAATTT  TTGGTT
                                       __
GAM646  PACSIN1  3'  GGGCTCAGGAGACTC       45159        AGAAAC
                                GGGCTCG     GGAGATTT
                                |||||||     ||||||||
                                CCCGAGT     CCTCTGAG
                                      _______
GAM646  HIVEP2   3'  AATTACATTTATTACAAAGCAG 27549         CTTCTTCTCT
            AT                    AATTACAT        GCAGAT
                                  ||||||||        ||||||
                                  TTAATGTA        CGTCTA
                                      AATAATGTTT
GAM646  PCDH11Y  3'  TTACATCTCACTGCAGAT    37363         CTTCT
                                TTACATCTT    CTGCAGAT
                                |||||||||    ||||||||
                                AATGTAGAG    GACGTCTA
                                      T____
GAM647  ATRN     3'  TCCCAGGTGTCTCCAG      40281         T A
                                TCCCAGGT G TTTCCAG
                                |||||||| | |||||||
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```
                                AGGGTCCA C AGAGGTC
                                     _ _
GAM647  BARX1    3'  TCCCAGGTTAGAGCCCAG    34627          ATT
                                TCCCAGGTTG   TCCAG
                                ||||||||||   |||||
                                AGGGTCCAAT   GGGTC
                                      CTC
GAM647  BRCA1    3'  TGGCCCAGACTCTTCCAG    28654    T    GT GA
                                TG CCCAG  T  TTTCCAG
                                || |||||  |  |||||||
                                AC GGGTC  A  GAAGGTC
                                 C    TG __
GAM647  BTG1     3'  GTCTTGTAAAATTTCCAG    11911     CCAG  T_
                                GTC   GT  GATTTCCAG
                                |||   ||  |||||||||
                                CAG   CA  TTAAAGGTC
                                  AA__  TT
GAM647  CACNA1C  3'  TGTTCCGGTTAACTCCAG    8761      C  A      T
                                TGT CC GGTTGATT CCAG
                                ||| || |||||||| ||||
                                ACA GG CCAATTGA GGTC
                                  A  _      _
GAM647  CDC42    3'  TGTCCCAGATTACTCTCCAG   12163           A
                                TGTCCCAGGTTG TTTCCAG
                                |||||||||||| |||||||
                                ACAGGGTCTAAT AGAGGTC
                                      G
GAM647  CLTCL1   3'  TGTCCAGGTGTGGTCCAG    41888      C   _  ATT
                                TGTCC AGGT TG   TCCAG
                                ||||| |||| ||   |||||
                                ACAGG TCCA AC   AGGTC
                                   _   C  C__
GAM647  CMAR     3'  TGTCCAGGTTGTCC        23299       C      ATT
                                TGTCC AGGTTG   TCC
                                ||||| ||||||   |||
                                ACAGG TCCAAC   AGG
                                   _     ___
GAM647  DDB2     3'  TGCCCCAGGTCCCA        6464           GATTT
                                TGTCCCAGGTT    CCA
                                ||||||||||     |||
                                ACGGGGTCCAG    GGT
                                      _____
GAM647  DLEC1    3'  TCACCTCGATTTCCAG      28850    _  AGG
                                TC CC   TTGATTTCCAG
                                || ||   ||||||||||
                                AG GG   AGCTAAAGGTC
                                 T  ___
GAM647  DYT1     3'  TGCTTGGGCTCATTTCCAG   6479      CCCA   G
                                TGT    GGTT ATTTCCAG
                                |||    |||| ||||||||
```

```
                                ACG   CCGA TAAAGGTC
                                  AAC_   G
GAM647  EDG8    3'  ATCCCAGGAGTTCCAG     44203       TTGAT
                                GTCCCAGG   TTCCAG
                                ||||||||   ||||||
                                TAGGGTCC   AAGGTC
                                    TC___
GAM647  FAT2    3'  TGTTCCTGGTTTTCCAG    11079    C  A   GAT
                                TGT CC GGTT   TTCCAG
                                ||| || ||||   ||||||
                                ACA GG CCAA   AAGGTC
                                  A  A   ___
GAM647  GGA3    3'  TGTCCCAGGATCACATCCAG  39788       TTGATT
                                TGTCCCAGG    TCCAG
                                |||||||||    |||||
                                ACAGGGTCC    AGGTC
                                     TAGTGT
GAM647  GLUD1   3'  TGTCCCAGACTCATCCAG   23592       GT G TT
                                TGTCCCAG  T A  TCCAG
                                ||||||||  | |  |||||
                                ACAGGGTC  A T  AGGTC
                                     TG G __
GAM647  HCS     3'  TCCTGTATCATTTCCAG    33235    CAG   G
                                TCC   GTT ATTTCCAG
                                |||   ||| ||||||||
                                AGG   TAG TAAAGGTC
                                  ACA  _
GAM647  HUNK    3'  TCCCGCTTGTTTCCAG     31082     AG   GA
                                TCCC  GTT  TTTCCAG
                                ||||  |||  |||||||
                                AGGG  CGA  AAAGGTC
                                   __  AC
GAM647  ICMT    3'  TGTCCCAGGCTGCACAG    29662         ATTTC
                                TGTCCCAGGTTG    CAG
                                ||||||||||||    |||
                                ACAGGGTCCGAC    GTC
                                      GT___
GAM647  KCNH3   3'  TGCCCCAGGGATCCA      42090       TT  TT
                                TGTCCCAGG  GA  TCCA
                                |||||||||  ||  ||||
                                ACGGGGTCC  CT  AGGT
                                     __  __
GAM647  KCNJ10  3'  TGCTTCGGGGGATCTCCAG  13874    CCCA  TT
                                TGT   GG  GATTTCCAG
                                |||   ||  |||||||||
                                ACG   CC  CTAGAGGTC
                                  AAG_  CC
GAM647  KNS2    3'  TGCCCCAGGTCTCC       24475         GATT
                                TGTCCCAGGTT   TCC
                                ||||||||||   |||
```

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                                ACGGGGTCCAG   AGG
                                      ____
GAM647  LAMB2   5'  TCCCAGGTCTGTCCAG     14075        GATT
                                TCCCAGGTT   TCCAG
                                |||||||||   |||||
                                AGGGTCCAG   AGGTC
                                     AC__
GAM647  LU      3'  TGTCCCAGGCTGGGCC     24565         ATTT
                                TGTCCCAGGTTG   CC
                                ||||||||||||   ||
                                ACAGGGTCCGAC   GG
                                       CC__
GAM647  MAPK12   5'  TGTCCCAGGTGCCGACCCC   16474         __   TT
                                TGTCCCAGGT  TGAT  C
                                |||||||||  ||||  |
                                ACAGGGTCCA  GCTG  G
                                      CG   GG
GAM647  MARS    3'  TGCCCAGGTTGTTAAGCAG   45428   T      ATTTC
                                TG CCCAGGTTG    CAG
                                || |||||||||    |||
                                AC GGGTCCAAC    GTC
                                 _       AATTC
GAM647  MMP25    3'  GTCCCAGGTCCCCACCAG    35391         GA TT
                                GTCCCAGGTT  T  CCAG
                                |||||||||  |  ||||
                                CAGGGTCCAG  G  GGTC
                                      G_ GT
GAM647  NCSTN    5'  TCCCGGGTCAGCCCCAG    43943     A   GAT
                                TCCC GGTT   TTCCAG
                                |||| ||||   ||||||
                                AGGG CCAG   GGGGTC
                                  C   TC_
GAM647  NR4A2    3'  TGCTCAGTTATTTCCAG    26167    CC   GTTG
                                TGT  CAG   ATTTCCAG
                                |||  |||   ||||||||
                                ACG  GTC   TAAAGGTC
                                 A_   AA__
GAM647  NRAP    3'  TGGCCCAGGCCATCTTCAG   40200   T     G   C
                                TG CCCAGGTT ATTT CAG
                                || |||||||| |||| |||
                                AC GGGTCCGG TAGA GTC
                                 C      _   A
GAM647  NRXN1    5'  TCCCAGATTTCCAG       39850        GATT
                                TCCCAGGTT   TCCAG
                                |||||||||   |||||
                                AGGGTCTAA   AGGTC
                                      ____
GAM647  OAS2    3'  TGTTACAGGGCTATTTCCAG  32557    CC   TTG
                                TGT  CAGG   ATTTCCAG
                                |||  ||||   ||||||||
```

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                                ACA  GTCC   TAAAGGTC
                                  AT    CGA
GAM647  PBX2     3'  TGTCCCAGTCCTGCCC      15111        G_   ATT
                                TGTCCCAG  TTG   TCC
                                ||||||||  |||   |||
                                ACAGGGTC  GAC   GGG
                                    AG   ___
GAM647  PHKB     3'  TATCTTTTGATTTCCAG     7124       CCAGG
                                TGTC    TTGATTTCCAG
                                ||||    ||||||||||
                                ATAG    AACTAAAGGTC
                                  AA___
GAM647  PIK3CG   3'  TCCAAAGAATTTCCAG      15307     C   TT
                                TCC AGG  GATTTCCAG
                                ||| |||  |||||||||
                                AGG TTC  TTAAAGGTC
                                  T   __
GAM647  PTK2B    3'  TGCCCCAGGTCCTCCCTCAG   19927          GA TT _
                                TGTCCCAGGTT  T  C CAG
                                ||||||||||  |  | |||
                                ACGGGGTCCAG  A  G GTC
                                     G_ GG A
GAM647  RAMP1    3'  TGTCCCAAGGCTCCA       25198        _   TGATT
                                TGTCCCA GGT    TCCA
                                |||||| |||    ||||
                                ACAGGGT CCG    AGGT
                                    T  _____
GAM647  RFP      3'  TGTCCCAGAATCCTTCCAG   27136         TTGA
                                TGTCCCAGG   TTTCCAG
                                |||||||||   |||||||
                                ACAGGGTCT   GAAGGTC
                                     TAG_
GAM647  ROR1     5'  TGTCCGGGTCGCACCAG     22704       CA    ATTT
                                TGTCC  GGTTG   CCAG
                                |||||  |||||   ||||
                                ACAGG  CCAGC   GGTC
                                   C_    GT__
GAM647  RPE      3'  TCCCAGATCCTTTCCAG     41641         GA
                                TCCCAGGTT  TTTCCAG
                                |||||||||  |||||||
                                AGGGTCTAG  AAAGGTC
                                     G_
GAM647  SOX10    5'  TGTCCCAAGGTGTGCGGTCCAG 28017        _  _  ATT
                                TGTCCCA GGT TG   TCCAG
                                ||||||| ||| ||   |||||
                                ACAGGGT CCA AC   AGGTC
                                    T   C  GCC
GAM647  STAT6    5'  TGCCCCAGCCCGCTGTTTCC   17158         ___    A
                                TGTCCCAG   GTTG TTTCC
                                ||||||||   |||| |||||
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                                ACGGGGTC   CGAC AAAGG
                                    GGG   _
GAM647  STC1     3'  GTTCCTGGAATTTCCAG     17180    C  A  TT
                                GT CC GG  GATTTCCAG
                                || || ||  |||||||||
                                CA GG CC  TTAAAGGTC
                                 A  A  __
GAM647  TOP3A    3'  TGTCCTCTAAGTTTCCAG    21466      CAGG   _
                                TGTCC    TTGA TTTCCAG
                                |||||    |||| |||||||
                                ACAGG    GATT AAAGGTC
                                   A___    C
GAM647  USF2     3'  TGTCTCAGTACCTCCAG     17905     C   GTTG
                                TGTC CAG    ATTTCCAG
                                |||| |||    ||||||||
                                ACAG GTC    TGGAGGTC
                                  A   A___
GAM647  ZK1      5'  TGCCTCAGAACTTCCAG     25173     C   GTT
                                TGTC CAG   GATTTCCAG
                                |||| |||   |||||||||
                                ACGG GTC   TTGAAGGTC
                                  A   ___
GAM647  ZNF136   5'  TGTCCCAGCTTCCTCCC     40879        G  GA
                                TGTCCCAG TT  TTTCC
                                |||||||| ||  |||||
                                ACAGGGTC AA  GAGGG
                                     G  G_
GAM648  ADAMTS3  5'  CGAGTTCACTTTCCA       30642        CCAA
                                CGAGTTCAT    TTCCA
                                |||||||||    |||||
                                GCTCAAGTG    AAGGT
                                     A___
GAM648  C8orf1   3'  CGAGTTCAATGAAGACATTCCA 20272        TCCA____
                                CGAGTTCA       ATTCCA
                                ||||||||       ||||||
                                GCTCAAGT       TAAGGT
                                     TACTTCTG
GAM648  CFTR     3'  CGAGCTCCAATTCCA       7949       TCA
                                CGAGT   TCCAATTCCA
                                |||||   ||||||||||
                                GCTCG   AGGTTAAGGT
                                   ___
GAM648  GARP     5'  CCAGTTCATCTGTCTCCA    24306   G      CAA
                                C AGTTCATC   TTCCA
                                | ||||||||   |||||
                                G TCAAGTAG   GAGGT
                                 G       ACA
GAM648  KHK      3'  GAGTTGGCCCCAATTCCA    27054      CA_
                                GAGTT   TCCAATTCCA
                                |||||   ||||||||||
```

```
                                CTCAA  GGGTTAAGGT
                                   CCG
GAM648  MARK3   5' CGAGTCCACGGCAGTTCC   14355       C_ A
                                CGAGTTCAT  CA TTCC
                                |||||||||  || ||||
                                GCTCAGGTG  GT AAGG
                                     CC  C
GAM648  NDRG1   3' CGAGTAACCCCAATTCCA   40577     TCA
                                CGAGT  TCCAATTCCA
                                |||||  ||||||||||
                                GCTCA  GGGTTAAGGT
                                   TTG
GAM648  NEU1    3' GAGTTCACATTGATTCAATTC 7728       C_______
                                GAGTTCAT     CAATTC
                                ||||||||     ||||||
                                CTCAAGTG     GTTAAG
                                     TAACTAA
GAM648  NQO2    5' CGAGTCCAGCAATCTTCC   9480       TC   __
                                CGAGTTCA  CAAT  TCC
                                ||||||||  ||||  |||
                                GCTCAGGT  GTTA  AGG
                                     C_   GA
GAM648  PKP2    3' GAATTCACATTTTGATTCCA  21317       CCA___
                                GAGTTCAT     ATTCCA
                                ||||||||     ||||||
                                CTTAAGTG     TAAGGT
                                     TAAAAC
GAM648  PRSS11  3' CGTGCTCCCAATTCCA     15765    A   AT
                                CG GTTC  CCAATTCCA
                                || ||||  |||||||||
                                GC CGAG  GGTTAAGGT
                                  A   __
GAM648  SIAH2   3' CCAGCCATCCAATTTCA    22861   G  T      C
                                C AGT CATCCAATT CA
                                | ||| |||||||| ||
                                G TCG GTAGGTTAA GT
                                 G  _       A
GAM648  SLC4A5  5' GAGCTCACAGCTGAATTCCA  39429       CC___
                                GAGTTCAT    AATTCCA
                                ||||||||    |||||||
                                CTCGAGTG    TTAAGGT
                                     TCGAC
GAM648  THBD    3' CAAGCTCCCAATTCCA     7422       AT
                                CGAGTTC  CCAATTCCA
                                |||||||  |||||||||
                                GTTCGAG  GGTTAAGGT
                                      __
GAM648  TMEM1   3' CAAGTTCAATTCCA       17589       TCCA
                                CGAGTTCA   ATTCCA
                                ||||||||   ||||||
```

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                              GTTCAAGT   TAAGGT
                                  ____
GAM648  TSLP    5'  CGTGGACACCCAATTCCA   37500   AGTT
                              CG   CATCCAATTCCA
                              ||   ||||||||||||
                              GC   GTGGGTTAAGGT
                                ACCT
GAM648  UTX     5'  CGAATTCACAACTCCA     41603       TC
                              CGAGTTCA  CAATTCCA
                              ||||||||  ||||||||
                              GCTTAAGT  GTTGAGGT
                                  __
GAM648  AKAP1   3'  CCCAATTTCAACAGTGCAA   40224     AC   TCCTGG
                              CCCAA  TCA    AGTGCAA
                              |||||  |||    |||||||
                              GGGTT  AGT    TCACGTT
                                 AA   TG____
GAM648  ATP11B  3'  CCCAAACTGATCTTTACA    44306       C   CTGGAG
                              CCCAAACT ATC    TGCA
                              |||||||| |||    ||||
                              GGGTTTGA TAG    ATGT
                                  C   AA____
GAM648  BMP6    3'  CCAAACTCAGCTTGCTACA   11860       TC  GGAG
                              CCAAACTCA  CT   TGCA
                              |||||||||  ||   ||||
                              GGTTTGAGT  GA   ATGT
                                   C_  ACG_
GAM648  CADPS   5'  CCCCGGCTTGGAGTGCAA   42191    AAA  CATCC
                              CCC   CT   TGGAGTGCAA
                              |||   ||   ||||||||||
                              GGG   GA   ACCTCACGTT
                                GCC  _____
GAM648  CALCR   3'  CCCAAATTCATTTTCTCTGTAG 11943      C  ___ _  G
                              CCCAAA TCA   TC CTG AG
                              ||||||  |||   || ||| ||
                              GGGTTT AGT   AG GAC TC
                                 A   AAA  A   A
GAM648  CRHR1   3'  CCACACCTGGAGTG      20435    AACT  T
                              CCA   CA CCTGGAGTG
                              |||   || |||||||||
                              GGT   GT GGACCTCAC
                                  ____ _
GAM648  CYP26A1 5'  CCCAAAGTTCATCTTTAATTGC 38405      C_   CTG  G
                              CCCAAA  TCATC   GA TGC
                              ||||||  |||||   || |||
                              GGGTTT  AGTAG   TT ACG
                                 CA    AAA  A
GAM648  CYP4A11 3'  CCCGAGCTCTGGAAGTGCA   8935     AAA   ATCC   _
                              CCC   CTC   TGGA GTGCA
                              |||   |||   |||| |||||
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                                GGG   GAG    ACCT CACGT
                                  CTC   ____    T
GAM648   DAZL     3'  AAACTCATGTCCATGGCAG   42772        __  _  _
                                AAACTCA  TCC TGG AG
                                |||||||  ||| ||| ||
                                TTTGAGT  AGG ACC TC
                                    AC   T   G
GAM648   FVT1     3'  CCAACTCATCTTGAATA     13027      A     CTG
                                CCAA CTCATC   GAGTG
                                |||| ||||||   |||||
                                GGTT GAGTAG   CTTAT
                                  _     AA_
GAM648   GLUD1    3'  CCCAGACTCATCCAGAA     23587      A       T
                                CCCA ACTCATCC GGAG
                                |||| |||||||| ||||
                                GGGT TGAGTAGG TCTT
                                  C       _
GAM648   HNRPF    3'  CAAACTCATGGTGCAA      22454          CCTGGA
                                CAAACTCAT     GTGCAA
                                |||||||||     ||||||
                                GTTTGAGTA     CACGTT
                                     C_____
GAM648   HYAL1    3'  CCACAAACTCAGTAGGAGTGCA 37639    _       TCCT
           A                     CC CAAACTCA    GGAGTGCAA
                                || ||||||||    |||||||||
                                GG GTTTGAGT    CCTCACGTT
                                 T       CAT_
GAM648   IL1RL2   3'  CCTAGCCTCATCCTGCAGCA   40478    CAAA       G
                                CC    CTCATCCTG AGTG
                                ||    ||||||||| ||||
                                GG    GAGTAGGAC TCGT
                                 ATCG        G
GAM648   LNPEP    3'  AACTCCAAAGAGTGCAAA    24556      ATCCT
                                AACTC    GGAGTGCAAA
                                |||||    ||||||||||
                                TTGAG    TCTCACGTTT
                                   GTT__
GAM648   MAML1    3'  CCCAGGACTAAGGCGGAGTGCA 31279      A_   CATCC
                                CCCA  ACT    TGGAGTGCA
                                ||||  |||    |||||||||
                                GGGT  TGA    GCCTCACGT
                                  CC   TTCC_
GAM648   MELK     3'  CCCACACTCATCCGGCAG    31333      A       T _
                                CCCA ACTCATCC GG AG
                                |||| |||||||| || ||
                                GGGT TGAGTAGG CC TC
                                  G       _ G
GAM648   MEN1     5'  CCCAAAGTTTGTCTCCTGTAAG 39167        CTCA___    _
                                CCCAAA      TCCTG GAG
                                ||||||      ||||| |||
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                                GGGTTT      AGGAC TTC
                                   CAAACAG     A
GAM648  NET1     3'  CAAACTCATTATTTGCA     25228         CC  GAG
                                CAAACTCAT  TG   TGCA
                                |||||||||  ||   ||||
                                GTTTGAGTA  AT   ACGT
                                     __  AA_
GAM648  PCDH7    5'  CCCAGAGTCATCCCCTCAGCG  37110      AAC      GG_
                                CCCA   TCATCCT   AGTG
                                ||||   |||||||   ||||
                                GGGT   AGTAGGG   TCGC
                                  CTC      GAG
GAM648  PCDHA2   3'  CCCAAACTATATTTTTACAAA  36467        CATCCTGGAG
                                CCCAAACT         TGCAAA
                                ||||||||         ||||||
                                GGGTTTGA         ATGTTT
                                     TATAAAA___
GAM648  PTK7     3'  CCCAGGCCATCCTGAGCG    15858      AA T      G
                                CCCA  C CATCCTG AGTG
                                ||||  | |||||||  ||||
                                GGGT  G GTAGGAC TCGC
                                  CC _      _
GAM648  PTPRA    5'  CAAACTCATTCTTGGCCTTG   38906         _ C   AG_
                                CAAACTCAT C TGG   TG
                                |||||||||  | |||   ||
                                GTTTGAGTA G ACC   AC
                                     A A   GGA
GAM648  RNF26    3'  CCCAAAGTCAGGTGCA      36753       C   TCCTG A
                                CCCAAA TCA     G GTGCA
                                ||||||  |||     |  |||||
                                GGGTTT AGT     C CACGT
                                   C   _____ _
GAM648  RRM2B    3'  CCCAAACTCATCTGACCACA   42713           CTG  G
                                CCCAAACTCATC   GA TGCA
                                ||||||||||||   ||  ||||
                                GGGTTTGAGTAG   CT GTGT
                                       A__   G
GAM648  SFRP4    3'  CCCAGCCTCATCCTGTAAG    16583      AA        _
                                CCCA  CTCATCCTG GAG
                                ||||  |||||||||  |||
                                GGGT  GAGTAGGAC TTC
                                  CG         A
GAM648  SH3BP2   3'  CCTGAACTCATCTTGAAG    16629     CA       C
                                CC  AACTCATC TGGAG
                                ||  ||||||||  |||||
                                GG  TTGAGTAG ACTTC
                                 AC        A
GAM648  STARD4   3'  CCCAAAGTCATTTAGAATG   40123       C    CC
                                CCCAAA TCAT  TGGAGTG
                                ||||||  ||||  |||||||
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                                GGGTTT AGTA  ATCTTAC
                                   C   A_
GAM648  TCF19    5'  CCCAAATTCAGAGTGCAA    45555      C   TCCTG
                                CCCAAA TCA    GAGTGCAA
                                |||||| |||    ||||||||
                                GGGTTT AGT    CTCACGTT
                                   A  _____
GAM648  TIMM23   3'  CCCAAACTGTCCTTAATA    41118       CA   GG
                                CCCAAACT  TCCT  AGTG
                                ||||||||  ||||  ||||
                                GGGTTTGA  AGGA  TTAT
                                    C_   A_
GAM648  TLL1     3'  CAAACTCATCTAAATGTA    29733        C   _
                                CAAACTCATC TGGA GTG
                                |||||||||| |||| |||
                                GTTTGAGTAG ATTT CAT
                                      _   A
GAM648  TNS      3'  CCCAGGGTCACTAGAGTGCA   35469     AAC   TC
                                CCCA   TCA  CTGGAGTGCA
                                ||||   |||  ||||||||||
                                GGGT   AGT  GATCTCACGT
                                  CCC   __
GAM648  TNXB     5'  CCTGACTCATCCACGGCAG    37153    AA      _  _
                                CC  ACTCATCC TGG AG
                                ||  |||||||| ||| ||
                                GG  TGAGTAGG GCC TC
                                 AC       T   G
GAM649  ALEX1    5'  TTAACCCGAGCACAAAACA    32486     T   A
                                TTG TTC AGCACAAAACA
                                ||| ||| ||||||||||
                                AAT GGG TCGTGTTTTGT
                                  T   C
GAM649  APPL     3'  TTTTGGTAAGCACAAAA     29018      TTTC
                                TTTTG    AAGCACAAAA
                                |||||    ||||||||||
                                AAAAC    TTCGTGTTTT
                                   CA__
GAM649  BCL11B   3'  GTTTTTTAAACACAAAACA    35649      GTTTC
                                GTTTT    AAGCACAAAACA
                                |||||    ||||||||||||
                                CAAAA    TTTGTGTTTTGT
                                   AA___
GAM649  FACL5    3'  GTTATGTTTATCACAAAACAAA 42016     T    CAAG
                                GTT TGTTT    CACAAAACAAA
                                ||| |||||    ||||||||||
                                CAA ACAAA    GTGTTTTGTTT
                                  T    TA__
GAM649  FGF5     3'  ATTTTGTTTCAGTCACACTGAA 37581          AG   ___
            ACAAA                  GTTTTGTTTCA  CACA   AAACAAA
                                ||||||||||  ||||   |||||||
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                                TAAAACAAAGT  GTGT   TTTGTTT
                                     CA    GAC
GAM649  FGF5    3'  ATTTTGTTTCAGTCACATTGAA 37582          AG   ___
            ACAAA                   GTTTTGTTTCA  CACA   AAACAAA
                                |||||||||||  ||||  |||||||
                                TAAAACAAAGT  GTGT   TTTGTTT
                                     CA    AAC
GAM649  FGF5    3'  CCTCAAGCATAAAGCAAA    20916        C   A
                                TTTCAAGCA AAA CAAA
                                ||||||||| ||| ||||
                                GGAGTTCGT TTT GTTT
                                     A   C
GAM649  FOXD2   3'  TTTTCTTTTAAGCACAAAGCA  20978     G   C       A
                                TTTT TTT AAGCACAAA CA
                                |||| ||| ||||||||| ||
                                AAAA AAA TTCGTGTTT GT
                                  G   A       C
GAM649  GAS7    3'  TTTGTTTCAGAGCGGCAA    25292         _   A_
                                TTTGTTTCA AGC  CAA
                                ||||||||| |||  |||
                                AAACAAAGT TCG  GTT
                                     C   CC
GAM649  IRS2    3'  ATTTTGTTAAAACAAAACAAA  40695         TCAAGC
                                GTTTTGTT     ACAAAACAAA
                                ||||||||     ||||||||||
                                TAAAACAA     TGTTTTGTTT
                                     TTT___
GAM649  ITSN1   3'  GCACATTCAAGCACAGAACA   16657    TTTGT        A
                                GT    TTCAAGCACA AACA
                                ||    |||||||||| ||||
                                CG    AAGTTCGTGT TTGT
                                 TGT__        C
GAM649  ITSN1   3'  GCTTTGTTTCATGAAACA    16659          ___
                                GTTTTGTTTCA   AGCA
                                ||||||||||   ||||
                                CGAAACAAAGT   TTGT
                                      ACT
GAM649  RPE65   3'  TGCTTTCAAGCATAAAACA   7266       _     C
                                TGTTT CAAGCA AAAACA
                                ||||| |||||| ||||||
                                ACGAA GTTCGT TTTTGT
                                   A     A
GAM649  ZFP37   3'  TGCTTAAGTACAAAACAA    18212      C   C
                                TGTTT AAG ACAAAACAA
                                ||||| ||| |||||||||
                                ACGAA TTC TGTTTTGTT
                                   _  A
GAM649  ACVR1   3'  AAAGCTATGCAAAGC       9957         CCCTT
                                AGAGCTAT    CAAAGC
                                ||||||||    ||||||
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                                TTTCGATA    GTTTCG
                                    C____
GAM649  ADAMTS3  3'  GAACCTGCCTTCAAAGCC    30643      ATC
                                GAGCT   CCTTCAAAGCC
                                |||||   ||||||||||
                                CTTGG   GGAAGTTTCGG
                                   AC_
GAM649  ADORA1   3'  AGAGCTTCCAAAGC       8586       ATCCC
                                AGAGCT    TTCAAAGC
                                ||||||    ||||||||
                                TCTCGA    AGGTTTCG
                                    _____
GAM649  ARHGDIA  3'  GAGCCATCTCCACAGCC     20206        _  TTCAA
                                GAGCTATC CC    AGCC
                                |||||||| ||    ||||
                                CTCGGTAG GG    TCGG
                                    A  TG___
GAM649  AVPR2    3'  GAGCTTCTCAAAGC       6285       A  CCT
                                GAGCT TC   TCAAAGC
                                ||||| ||   |||||||
                                CTCGA AG   AGTTTCG
                                  _ ___
GAM649  BAP1     3'  GGATCACCTTTTTCAAAGCC   21645    T  _  ___
                                C ATC CCT   TCAAAGCC
                                | ||| |||   ||||||||
                                C TAG GGA   AGTTTCGG
                                 C   T   AAA
GAM649  BPI      5'  AGAGCTGCCAAAACCTCAAGGC 11898       AT C___     A
           C                     AGAGCT  C    CTTCAA GCC
                                ||||||  |    |||||| |||
                                TCTCGA  G    GGAGTT CGG
                                   CG TTTT     C
GAM649  CASP8    3'  AGTTATCCCCCTGACAAGCC   37866    C       CA__
                                AG TATCCCTT    AAGCC
                                || ||||||||    |||||
                                TC ATAGGGGG    TTCGG
                                 A       ACTG
GAM649  CDH1     3'  AACTAACCCCCTTTAGGGCC   20356      _     CAAA_
                                AGCTA TCCCTT     GCC
                                ||||| ||||||     |||
                                TTGAT GGGGGA     CGG
                                   T      AATCC
GAM649  CDK7     5'  AAAGCTACCTTAAAGCC     12208        TC    C
                                AGAGCTA  CCTT AAAGCC
                                |||||||  |||| ||||||
                                TTTCGAT  GGAA TTTCGG
                                   __   _
GAM649  CLECSF2  5'  AGAAACTCTCTTCAAAG     23060      CTA  C
                                AGAG   TC CTTCAAAG
                                ||||   || ||||||||
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                                TCTT   AG GAAGTTTC
                                  TG_  A
GAM649  COL4A3   3'  AAAGCATCTTCAAAGC     36373      TATCC
                                AGAGC    CTTCAAAGC
                                |||||    |||||||||
                                TTTCG    GAAGTTTCG
                                  TA___
GAM649  EMP1     3'  AGAGCTACCACTGAGCC     10890         C  TCAA
                                AGAGCTATC CT    AGCC
                                ||||||||| ||    ||||
                                TCTCGATGG GA    TCGG
                                     T  C___
GAM649  ERBB4    3'  GACCTATCCCTAAGC      23455    G       TCA
                                GA CTATCCCT   AAGC
                                || ||||||||   ||||
                                CT GATAGGGA   TTCG
                                 G       ___
GAM649  EZH1     3'  AGGCTTTCTCAAAGC      12777    A   A  CCT
                                AG GCT TC   TCAAAGC
                                || ||| ||   |||||||
                                TC CGA AG   AGTTTCG
                                 _   A  ___
GAM649  FAAH     3'  AGAGCCACCAAAGC       45465        CCCTT
                                AGAGCTAT    CAAAGC
                                ||||||||    ||||||
                                TCTCGGTG    GTTTCG
                                      _____
GAM649  GAN      3'  AGAGTTACCATACCAAAGCC  35138     C    CCT
                                AGAG TATC   TCAAAGCC
                                |||| ||||   ||||||||
                                TCTC ATGG   GGTTTCGG
                                  A    TAT
GAM649  GHR      3'  AAAGCTAACTTCAAAG      6710        TCC
                                AGAGCTA   CTTCAAAG
                                |||||||   ||||||||
                                TTTCGAT   GAAGTTTC
                                    T__
GAM649  HLA-DMA  5'  GAGCTACCAACCCAGC      25937        __  TCAA
                                GAGCTATC  CCT    AGC
                                ||||||||  |||    |||
                                CTCGATGG  GGG    TCG
                                     TT  _____
GAM649  HS3ST3A1 5'  AGAGCATCCCCCCGGCGGGCC 25800      T      AAA__
                                AGAGC ATCCCTTC    GCC
                                ||||| ||||||||    |||
                                TCTCG TAGGGGGG    CGG
                                   _      CCGCC
GAM649  IL10RA   3'  AGGCCTGTCCCCTCACAGC   40620    A  A_      A
                                AG GCT  TCCCTTCA AGC
                                || |||  |||||||| |||
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                                TC CGG  AGGGGAGT TCG
                                 _  AC       G
GAM649  LPHH1    3'  AGAGTCATCTCTTCAAGC    29385     C   C     A
                                AGAG TATC CTTCAA GC
                                |||| |||| |||||| ||
                                TCTC GTAG GAAGTT CG
                                  A   A    _
GAM649  MMP1     3'  AGAGTTATCCCTTGC      14542     C      CAAA
                                AGAG TATCCCTT   GC
                                |||| ||||||||   ||
                                TCTC ATAGGGAA   CG
                                  A      ____
GAM649  MMP16    3'  GAGACTATCCAAAGC      35438     _     CTTC
                                GAG CTATCC   AAAGC
                                ||| ||||||   |||||
                                CTC GATAGG   TTTCG
                                  T    ____
GAM649  MN1      5'  GAGGGAGACCCTTCAAAGCC  14582     CTAT_
                                GAG    CCCTTCAAAGCC
                                |||    ||||||||||||
                                CTC    GGGAAGTTTCGG
                                 CCTCT
GAM649  MUTYH    5'  AGAGGTAGCCTTCAAAGCC   29222     C  TC
                                AGAG TA  CCTTCAAAGCC
                                |||| ||  ||||||||||
                                TCTC AT  GGAAGTTTCGG
                                  C  C_
GAM649  NLGN3    3'  AGAGCTATCCTGCTCTTTAAAG 33281          ____  C
           C                     AGAGCTATCC   CTT AAAGC
                                ||||||||||   ||| |||||
                                TCTCGATAGG   GAA TTTCG
                                      ACGA  A
GAM649  OVOL1    5'  AGGCTCATGTTCAAAGCC   21271    A  ATCCC
                                AG GCT    TTCAAAGCC
                                || |||    |||||||||
                                TC CGA    AAGTTTCGG
                                 _  GTAC_
GAM649  PCOLN3   3'  AGGCTGTGCCCAAAGCC    15746    A  AT_  TTC
                                AG GCT   CCC   AAAGCC
                                || |||   |||   ||||||
                                TC CGA   GGG   TTTCGG
                                 _  CAC   ___
GAM649  PDE4B    3'  AGGCTACCTCTTCAAAG     15145    A    C
                                AG GCTATC CTTCAAAG
                                || |||||| ||||||||
                                TC CGATGG GAAGTTTC
                                 _     A
GAM649  PODXL    3'  AGAGCTACTACAGCCGGAGCC 23953        CCCT_  AA
                                AGAGCTAT    TC  AGCC
                                ||||||||    ||  ||||
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                              TCTCGATG    GG  TCGG
                                  ATGTC  CC
GAM649  PRex1    3'  GAGCCATCCCGAGGGAGCC   34072        TTCAA
                              GAGCTATCCC    AGCC
                              ||||||||||    ||||
                              CTCGGTAGGG    TCGG
                                   CTCCC
GAM649  RRM2B    3'  AGAACTATCTCTTATAACAGC  42710        C  CAA__
                              AGAGCTATC CTT    AGC
                              ||||||||| |||    |||
                              TCTTGATAG GAA    TCG
                                   A  TATTG
GAM649  SCN4A    3'  ACAGTCCCAGATTCAAAGCC  7315    TA   ___
                              GC  TCCC   TTCAAAGCC
                              ||  ||||   |||||||||
                              TG  AGGG   AAGTTTCGG
                                TC    TCT
GAM649  SLC10A2  3'  AGAGCTATCATTTTAGAAAGC  7812        CCTTC__
                              AGAGCTATC      AAAGC
                              |||||||||      |||||
                              TCTCGATAG      TTTCG
                                   TAAAATC
GAM649  SLC12A7  3'  AAAGCTATCTCTTCAGTGCC  27327        C    AA
                              AGAGCTATC CTTCA  GCC
                              ||||||||| |||||  |||
                              TTTCGATAG GAAGT  CGG
                                   A    CA
GAM649  SORCS1   3'  AGAGCTACCAAAGC       38096        CCCTT
                              AGAGCTAT    CAAAGC
                              ||||||||    ||||||
                              TCTCGATG    GTTTCG
                                   _____
GAM649  SOX10    3'  AGGCTCCTCAAAGC       27993    A   ATCC
                              AG GCT    CTTCAAAGC
                              || |||    |||||||||
                              TC CGA    GGAGTTTCG
                               _  ____
GAM649  SURF4    3'  GCTGTTCACTCCAAAGCC    37658     A_  C
                              GCT  TC CTTCAAAGCC
                              |||  || ||||||||||
                              CGA  AG GAGGTTTCGG
                                CA  T
GAM649  TADA2L   5'  AGAGCTACGCGCTCCAGGGC  39425        CC_    AA
                              AGAGCTAT   CTTCA  GC
                              ||||||||   |||||  ||
                              TCTCGATG   GAGGT  CG
                                   CGC    CC
GAM649  TIMP3    3'  AGAGGTGTCCCTCCAGCC    7440      CTA      AA
                              AGAG   TCCCTTCA  GCC
                              ||||   ||||||||  |||
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                                TCTC  AGGGAGGT  CGG
                                  CAC      __
GAM649  ZNF22    3'  AGGGCTATCCAAAGC      45044    A     CTTC
                                AG GCTATCC   AAAGC
                                || |||||||   |||||
                                TC CGATAGG   TTTCG
                                 C     _____
GAM650  CA3      3'  GAAATTAAAAATAAATGGCC  23211       T_   TT
                                GAAATTAA  ATGA  TGGCC
                                ||||||||  ||||  |||||
                                CTTTAATT  TATT  ACCGG
                                     TT   T_
GAM650  IFRD1    3'  GAAATTAAACTTTGGC     41107       TATGA
                                GAAATTAA    TTTGGC
                                ||||||||    ||||||
                                CTTTAATT    AAACCG
                                     TG___
GAM650  SERPINB4 3'  GAAAGTATGATTTGG      42226     TTAA
                                GAAA   TATGATTTGG
                                ||||   ||||||||||
                                CTTT   ATACTAAACC
                                  C___
GAM650  ZNF255   5'  TAATAAAATTAATATGAT    25101     CG
                                TAA  AAATTAATATGAT
                                |||  ||||||||||||
                                ATT  TTTAATTATACTA
                                  AT
GAM651  ACCN2    5'  CTGTCCGCCCGCCCGCGCGC  33443          T  A
                                CTGTCCGCCTGT CC CGCGC
                                |||||||||||| || |||||
                                GACAGGCGGGCG GG GCGCG
                                       _ C
GAM651  BMX      5'  ACGCGTCCGCCCACGC      11887     T      TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
                                TGCG CAGGCGG    GTGCG
                                  _     ______
GAM651  DPYSL2   3'  CTGTCTGCGGTTCCACG     10749      C  CT
                                CTGTC GC  GTTCCACG
                                ||||| ||  ||||||||
                                GACAG CG  CAAGGTGC
                                   A  C_
GAM651  HCN4     5'  GCTGTCCGTCTGTCTCGC    24226        C    CCA
                                GCTGTCCG CTGTT   CGC
                                |||||||| |||||   |||
                                CGACAGGC GACAG   GCG
                                     A    A__
GAM651  PXR1     5'  ACGCGTCCGCCCACGC      7231      T      TGTTC
                                ACGC GTCCGCC    CACGC
                                |||| |||||||    |||||
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                                TGCG CAGGCGG    GTGCG
                                  _    _____
GAM651  SCG3    5' CGCTGTCCGCCCTGTGGGTGC 29883          GTTCCAC
                                CGCTGTCCGCCT     GC
                                ||||||||||||     ||
                                GCGACAGGCGGG     CG
                                      ACACCCA
GAM651  SLC5A5  5' CGCTGTCTGTCTCTGCG    7825       CGCC   CCAC
                                CGCTGTC   TGTT   GCG
                                |||||||   ||||   |||
                                GCGACAG   ACAG   CGC
                                   ____   AGA_
GAM651  SLC5A5  5' GCTGTCTGTCTGTCCTGC   7826       CGC    CAC
                                GCTGTC  CTGTTC  GC
                                ||||||  ||||||  ||
                                CGACAG  GACAGG  CG
                                   ACA    A__
GAM652  CADPS   3' TGATAGGATCGCCCCCTTG  42197    C
                                TGA AGGATCGTCCCCTTG
                                ||| ||||||||||||||
                                ACT TCCTAGCGGGGGAAC
                                  A
GAM652  SIM2    3' TGACAGGATTTTTCCATGTTG 22883        CG_  CC_
                                TGACAGGAT  TCC  TTG
                                |||||||||  |||  |||
                                ACTGTCCTA  AGG  AAC
                                     AAA  TAC
GAM652  ZNF79   5' ACAGCCACTCTTTGGCTCG  44352     GA  _ CCC
                                ACAG  TCG TC  TTGGCTCG
                                ||||  ||| ||  ||||||||
                                TGTC  GGT AG  AACCGAGC
                                  __  G  A__
GAM653  ANPEP   3' GAGGTGCTCAGGCAGCCTGG  10097    AA  GCCCGAC
                                GAG  GC     GCGGCCTGG
                                |||  ||     |||||||||
                                CTC  CG     CGTCGGACC
                                  CA  AGTC___
GAM653  ASIP    3' CGAGAAGCGCCCCGCGTCCCCG 11714         GA   G_
                                CGAGAAGCGCCC  CGCG  CCTG
                                ||||||||||||  ||||  ||||
                                GCTCTTCGCGGG  GCGC  GGGC
                                      __   AG
GAM653  BACH1   5' CGAGAGCGCCCGGCGG     10146      A     AC
                                CGAGA GCGCCCG  GCGG
                                |||||  |||||||  ||||
                                GCTCT CGCGGGC  CGCC
                                  _     __
GAM653  CACNG6  5' CGGGAGCGAGGAGCGGCCTGG 36695    A  A   CCC  C
                                CG GA GCG   GA GCGGCCTGG
                                || || |||   || |||||||||
```

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                                GC CT CGC   CT CGCCGGACC
                                 C  _   TC_  _
GAM653  CARKL    3'  CGGGGAGCATCTACGGCCTGG  29992    AGA    CCCGAC
                                CG   AGCG     GCGGCCTGG
                                ||   ||||     |||||||||
                                GC   TCGT     TGCCGGACC
                                 CCC    AGA___
GAM653  CD7      3'  GAGAAGCACCGTGGGGCCTGG  26003          CGACGC
                                GAGAAGCGCC     GGCCTGG
                                ||||||||||     |||||||
                                CTCTTCGTGG     CCGGACC
                                     CACC__
GAM653  CSNK1G2  3'  CGAGAAGCACCCGCCT      10612           GACGCG
                                CGAGAAGCGCCC     GCCT
                                ||||||||||||     ||||
                                GCTCTTCGTGGG     CGGA
                                          _______
GAM653  DLX2     3'  CGGGAAGCCTCGCGCGCCTGG  20587    A    GCC  A    G
                                CG GAAGC   CG CGCG CCTGG
                                || |||||   || |||| |||||
                                GC CTTCG   GC GCGC GGACC
                                 C    GA_  _   _
GAM653  EGFL6    5'  AGGGGCGCTCGCGGCCTG    31775    AA    CCGA
                                AG  GCGC    CGCGGCCTG
                                ||  ||||    |||||||||
                                TC  CGCG    GCGCCGGAC
                                 CC    A___
GAM653  GALNT2   3'  GAGGGGCGCTCCGGCCTG    21004     AA    _  GACGC
                                GAG  GCGC CC     GGCCTG
                                |||  |||| ||     ||||||
                                CTC  CGCG GG     CCGGAC
                                  CC    A  _____
GAM653  GAS11    3'  AGAAGCGCCTGACTTACTGG   11209         C   GCG  C
                                AGAAGCGCC GAC   GC TGG
                                ||||||||| |||   || |||
                                TCTTCGCGG CTG   TG ACC
                                     A   AA_  _
GAM653  MATK     5'  CGAGGCGCCGCGGCCTG     40306      AA     CGAC
                                CGAG  GCGCC    GCGGCCTG
                                ||||  |||||    ||||||||
                                GCTC  CGCGG    CGCCGGAC
                                   __    _____
GAM653  MGAM     3'  GAGAGGCGTCCCTGCAGCCTGG 43657      A   _   GAC
                                GAGA GCG CCC   GCGGCCTGG
                                |||| ||| |||   |||||||||
                                CTCT CGC GGG   CGTCGGACC
                                  C   A   A__
GAM653  MTMR3    3'  GAAGTGCTACACAGCCTGG    34394      C  CCG
                                GAAG GC   ACGCGGCCTGG
                                |||| ||   ||||||||||
```

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                                CTTC CG   TGTGTCGGACC
                                  A A__
GAM653  SLIT3    5'  CGGGGAGCGCGGGCGGCCTGG  16866    AGA    CCGAC
                                CG   AGCGC    GCGGCCTGG
                                ||   |||||    |||||||||
                                GC   TCGCG    CGCCGGACC
                                 CCC    CC___
GAM653  SUV39H2  5'  GAGGCGGGTCAGCGGCCTGG   36015     AA   CCCGAC
                                GAG  GCG     GCGGCCTGG
                                |||  |||     |||||||||
                                CTC  CGC     CGCCGGACC
                                  __  CCAGT_
GAM653  TOP3A    3'  GAGAAGCCCTGGGCAGCCTGG  21464      GC    GAC
                                GAGAA  GCCC   GCGGCCTGG
                                |||||  ||||   |||||||||
                                CTCTT  CGGG   CGTCGGACC
                                   __   ACC
GAM653  TRPC6    5'  CGGGAACGCCCGACTGGCCTGG 21482    A   G      GC
                                CG GAA CGCCCGAC  GGCCTGG
                                || ||| |||||||||  |||||||
                                GC CTT GCGGGCTG  CCGGACC
                                 C   _       A_
GAM653  TRPV1    5'  CGGGGAGCATCTACGGCCTGG  38794    AGA    CCCGAC
                                CG   AGCG     GCGGCCTGG
                                ||   ||||     |||||||||
                                GC   TCGT     TGCCGGACC
                                 CCC    AGA___
GAM653  BCL2L2   5'  TGCCGGGATCCGGGCC      19750         CC   ACAA
                                TGCCGGGA  CCG    GGCC
                                ||||||||  |||    ||||
                                ACGGCCCT  GGC    CCGG
                                    A_   _____
GAM653  CRIM1    3'  GCTGGGTCGCAAGGCCTT    32373    C   ACCC  A
                                GC GGG    CG CAAGGCCTT
                                || |||    || |||||||||
                                CG CCC    GC GTTCCGGAA
                                 A   A___  _
GAM653  EGFR     3'  TGCTGGGGCCATGAAGGCCTTC 23400     C   A  CC  CA
                                TGC GGG CC  GA  AGGCCTTC
                                ||| ||| ||  ||  ||||||||
                                ACG CCC GG  CT  TCCGGAAG
                                  A   C  TA  __
GAM653  GCK      5'  GCTGGGACCCCTCAGCCTTC   37928    C      GACAA
                                GC GGGACCCC    GGCCTTC
                                || |||||||    |||||||
                                CG CCCTGGGG    TCGGAAG
                                 A       AG___
GAM653  GPR44    3'  TGCTGTGGGCCAGGCCTT    21963     C__   A  CCGACA
                                TGC   GGG CC     AGGCCTT
                                |||   ||| ||     |||||||
```

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                                ACG   CCC GG     TCCGGAA
                                  ACA  _ _______
GAM653  IL1RAP   3'  TACCGGGATAAGGGCTT    13505        CCCCGAC    C
                                TGCCGGGA      AAGG CTT
                                ||||||||      |||| |||
                                ATGGCCCT      TTCC GAA
                                    A_______    C
GAM653  LENG4    3'  TGCTGGGGTCCCGAGGTGGC   35893     C   AC     CAA
                                TGC GGG  CCCGA   GGC
                                ||| |||  |||||   |||
                                ACG CCC  GGGCT   CCG
                                  A   CA    CCA
GAM653  RFC1     3'  GGGAAAAAACAAGGCTTTC    16275      CCCC       C
                                GGGA    GACAAGGC TTC
                                ||||    |||||||| |||
                                CCCT    TTGTTCCG AAG
                                  TTT_       A
GAM654  AVPR1A   5'  TGGGATCGTGGCGCTTTCC    8735         CGCTC  A   C
                                TGGGATCG     GG GCT TCC
                                ||||||||     || ||| |||
                                ACCCTAGC     CC CGA AGG
                                    A____  G   A
GAM654  CIAS1    3'  GGATCGCAGCTCTC        22207        GCTCGG
                                GGATCGC     AGCTCTC
                                |||||||     |||||||
                                CCTAGCG     TCGAGAG
                                  _______
GAM654  GAS1     3'  TGGGACGCGGGCTCTC      13076       T   GCTC  A
                                TGGGA CGC    GG GCTCTC
                                ||||| |||    || ||||||
                                ACCCT GCG    CC CGAGAG
                                  _  _____ _
GAM654  IL8      3'  TGGGGTCCAGACAGAGCTCTC  45394      A  G  CT
                                TGGG TC CG  CGGAGCTCTC
                                |||| || ||  ||||||||||
                                ACCC AG GT  GTCTCGAGAG
                                  C  _  CT
GAM654  ADAM8    3'  GAAGAGCACGGAGGGGAACCTG 9965          A   CT  T_
                                GGAGAGCAC GAG  GG  CCTG
                                |||||||| |||  ||  ||||
                                CTTCTCGTG CTC  CC  GGAC
                                    C   C_  TT
GAM654  ASB2     5'  GGAGAGCCAGGGAGAGACTGAC 32052        A   AGCT  TC
                                GGAGAGC CAG    GG  CTGAC
                                ||||||| |||    ||  |||||
                                CCTCTCG GTC    CT  GACTG
                                    _  CCT_  CT
GAM654  BMP1     3'  GGGGCTGCAGAGCTGGC     25988     AGA  A_
                                GG   GC  CAGAGCTGGT
                                ||   ||  ||||||||||
```

```
                                CC   CG  GTCTCGACCG
                                 C__  AC
GAM654  CD3E     3'  GAGGAGCACAGGGCTGGC    8813    GA      A
                                G  GAGCACAG GCTGGT
                                |  |||||||| ||||||
                                C  CTCGTGTC CGACCG
                                 TC       C
GAM654  CELL     3'  GGAGGGCATGGAACTGGCCTCC 12227     A   CA      __
              TG                   GGAG GCA  GAGCTGGT  CCTG
                                |||| |||  ||||||||  ||||
                                CCTC CGT  CTTGACCG  GGAC
                                  C   AC       GA
GAM654  COL4A2   3'  GGAGAACATGGAGCTGGC    12319        CA
                                GGAGAGCA  GAGCTGGT
                                ||||||||  ||||||||
                                CCTCTTGT  CTCGACCG
                                     AC
GAM654  CUL3     3'  GGAAGCACAGGATATCTGA    18738     G      AGCTG   C
                                GGA AGCACAG     GTC TGA
                                ||| |||||||     ||| |||
                                CCT TCGTGTC     TAG ACT
                                  _      CTA__   _
GAM654  EXTL1    5'  GGAGGGCTCGGGGTCCTGA    20868      A  ACAGAGCT
                                GGAG GC       GGTCCTGA
                                |||| ||       ||||||||
                                CCTC CG       CCAGGACT
                                  C  AGCC_____
GAM654  FBXL7    3'  GGAGAGCACTGTGATTCTGA   29407         AGAGC    C
                                GGAGAGCAC     TGGT CTGA
                                |||||||||     |||| ||||
                                CCTCTCGTG     ACTA GACT
                                     AC___    A
GAM654  GBF1     3'  GGGAAGCACTGGTCCTGA    20079    AG   ACAGA
                                GG  AGC     GCTGGTCCTGA
                                ||  |||     ||||||||||
                                CC  TCG     TGACCAGGACT
                                 CT  ______
GAM654  HOXB6    3'  GGAGAGCAGGTCTCCTG     40823        CAGAGCT  __
                                GGAGAGCA      GG  TCCTG
                                ||||||||      ||  |||||
                                CCTCTCGT      CC  AGGAC
                                     ________  AG
GAM654  HOXB7    3'  GGGAGCATGGGGCTGGGGGAC  21069    A    CAGA    TCCT
                                GG GAGCA   GCTGG   GAC
                                || |||||   |||||   |||
                                CC CTCGT   CGACC   CTG
                                  _    ACCC    CC__
GAM654  ITGA3    3'  GGCAGAGCCAGGCTGGC     24263    _    A   A
                                GG AGAGC CAG GCTGGT
                                || ||||| ||| ||||||
```

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                                CC TCTCG GTC CGACCG
                                 G    _  _
GAM654  LAMC2    3'  GGAGAGCAGTGGTGCAATCTTG 33117        CAGA_ T   C
                                GGAGAGCA    GC GGTC TG
                                ||||||||    || |||| ||
                                CCTCTCGT    CG TTAG AC
                                     CACCA  _   A
GAM654  LANGERIN 5'  GGGAGCACAGGTGCTTCTGGC  31846    A      AG____
                                GG GAGCACAG     CTGGT
                                || ||||||||     |||||
                                CC CTCGTGTC     GACCG
                                 _      CACGAA
GAM654  LDOC1    3'  GGAGAGCAGTGGCTCCTG    29490        CAGA C  _
                                GGAGAGCA   G TGG TCCTG
                                ||||||||   | ||| |||||
                                CCTCTCGT   C ACC AGGAC
                                    _____ _  G
GAM654  MECP2    3'  GGGGACACAGAGTTCTGGC   22604    A G     __
                                GG GA CACAGAG  CTGGT
                                || || |||||||  |||||
                                CC CT GTGTCTC  GACCG
                                 C  _      AA
GAM654  MT1L     3'  GAGAGCACAGCTGTCCTG    44947         AGCTG
                                GAGAGCACAG    GTCCTG
                                ||||||||||    ||||||
                                CTCTCGTGTC    CAGGAC
                                     GA___
GAM654  MYBL2    3'  GGTGAGCACAGGAGCACCCCTG 14704    A      _  T G
                                GG GAGCACAG AGC G TCCTG
                                || |||||||| ||| | |||||
                                CC CTCGTGTC TCG T GGGAC
                                 A      C  _ G
GAM654  NXF5     3'  GGAGGGCTCAGAGCTGGAGGAG 37619     A  A       TCCT
          A                      GGAG GC CAGAGCTGG   GA
                                ||||  || |||||||||   ||
                                CCTC CG GTCTCGACC   CT
                                  C  A       TCCT
GAM654  PAK4     3'  GGAGAGGGTGGGGGGCCCTGAC 25250      CACAGAGCT
                                GGAGAG       GGTCCTGAC
                                ||||||       |||||||||
                                CCTCTC       CCGGGACTG
                                   CCACCCC__
GAM654  PTAFR    5'  GGAATGATCAGCTGGTCCTG  9630      AGCACAG
                                GGAG      AGCTGGTCCTG
                                ||||      ||||||||||
                                CCTT      TCGACCAGGAC
                                  ACTAG__
GAM654  RASSF1   3'  GAGGGGTGCAGAGCCATACCTG 28426    AGCA_      GT
                                GAG    CAGAGCTG  CCTG
                                |||    ||||||||  ||||
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                                CTC    GTCTCGGT  GGAC
                                  CCCAC       AT
GAM654  SLC21A2  3'  GGGAGACAGAGCTGTCTG    24802    A  C       GTC
                                GG GAG ACAGAGCTG   CTG
                                || ||| |||||||||   |||
                                CC CTC TGTCTCGAC   GAC
                                 _  _       A__
GAM654  TNFRSF6B 5'  GAAGGGCACAGAGCGTGGC    32353     A       _
                                GGAG GCACAGAGC TGGT
                                |||| ||||||||| ||||
                                CTTC CGTGTCTCG ACCG
                                  C       C
GAM654  TRPS1    3'  GAGAACGCATGAGCTGGTCCTG 30462       A  _
                                GAGAGC CA GAGCTGGTCCTG
                                |||||| || ||||||||||||
                                CTCTTG GT CTCGACCAGGAC
                                    C  A
GAM654  UBE2L6   3'  GGAGAGCTGGAGAACTGGC    20122       AC_
                                GGAGAGC   AGAGCTGGT
                                |||||||   |||||||||
                                CCTCTCG   TCTTGACCG
                                    ACC
GAM654  ZNF26    5'  GGAGAGCAGGAGGCTGAT     43802        CA  _
                                GGAGAGCA  GAG CTGGT
                                ||||||||  ||| |||||
                                CCTCTCGT  CTC GACTA
                                     C_  C
GAM655  CSF3     3'  GACATGATTCCTCCTGTC     8902           G  C
                                GACATGATTCCT CC GTC
                                |||||||||||| || |||
                                CTGTACTAAGGA GG CAG
                                       _  A
GAM655  PIGR     3'  CGACATGATTCTGAAGGTGAT  43702          C  CCC  C
                                CGACATGATTC TG   GT GAT
                                |||||||||||  ||   ||  |||
                                GCTGTACTAAG AC   CA CTA
                                       _  TTC  _
GAM655  AGRN     3'  ACCCAGGCAGGCGGCAGAGG   44244    G   AC   C
                                AC CAG  GTA GGCGGCAGAGG
                                || |||  ||| ||||||||||||
                                TG GTC  CGT CCGCCGTCTCC
                                 G  __  _
GAM655  AMT      5'  GCAGACGGCGCACAGAGGC    7908        GTAC   _
                                GCAGAC    GGCG GCAGAGGC
                                ||||||    |||| ||||||||
                                CGTCTG    CCGC TGTCTCCG
                                    _____   G
GAM655  AP1M1    3'  CGCAGACGTGGGTGACA      37167         AC  C
                                CGCAGACGT  GG GGCA
                                |||||||||  || ||||
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                                GCGTCTGCA  CC CTGT
                                     C_  A
GAM655  APPBP2   5'  ACGCGGGCGCACGGCAGAAGGC 26869      AGA        CA
                                ACGC   CGTACGGCGG  GAGGC
                                ||||   ||||||||||  |||||
                                TGCG   GCGTGCCGTC  TTCCG
                                  CCC        __
GAM655  ATP6V0B  5'  GCGGCGACGGCGGCGGGGG   19726    AGA  T      AGA
                                GC   CG ACGGCGGC   GG
                                ||   || ||||||||   ||
                                CG   GC TGCCGCCG   CC
                                 CC_  _       CCC
GAM655  BTEB1    5'  GCGGGCGACGGCAGCCCAGGC  10217    AGA  T      AG
                                GC   CG ACGGCGGC  AGGC
                                ||   || ||||||||  ||||
                                CG   GC TGCCGTCG  TCCG
                                 CCC  _       GG
GAM655  CACNG3   3'  GCTGGGCGTGGGGCAGAGG   27238    AGA_   AC  C
                                GC    CGT  GG GGCAGAGG
                                ||    |||  || ||||||||
                                CG    GCA  CC CCGTCTCC
                                 ACCC   __  _
GAM655  CAPN5    5'  CGCGGGCGCTGGAGCGGAGGC  44928     AGA   AC  C   A
                                CGC   CGT  GG GGC GAGGC
                                |||   |||  || ||| |||||
                                GCG   GCG  CC TCG CTCCG
                                  CCC   A_  _   C
GAM655  DRD2     3'  CGTCAGAGTGTGGCAGAGGC   9013     _    C  ACGGC
                                CG CAGA GT    GGCAGAGGC
                                || |||| ||    |||||||||
                                GC GTCT CA    CCGTCTCCG
                                 A    _  CA___
GAM655  EEF1A2   3'  GCAGACATGCGCCTGGCGGGGG 41518         A ____    CAGA
                                GCAGACGT C    GGCGG    GG
                                |||||||| |    |||||    ||
                                CGTCTGTA G    CCGCC    CC
                                     C CGGA    C___
GAM655  EPAS1    3'  GACGGCGTCGGCAGAGG     11002      TA  G
                                GACG  CG CGGCAGAGG
                                ||||  || |||||||||
                                CTGC  GC GCCGTCTCC
                                  C_  A
GAM655  EPHB6    5'  GACGCTGGCGGCAGGGGC    20798       AC       A
                                GACGT  GGCGGCAG GGC
                                |||||  |||||||| |||
                                CTGCG  CCGCCGTC CCG
                                   A_       C
GAM655  FLNA     3'  CGCAGCACGGCACAGGGCAGGG 11133       _  _    C    A
            GC                    CGCAG ACG TACGG GGCAG GGC
                                |||||| ||| ||||| ||||| |||
```

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                                GCGTC TGC GTGTC CCGTC CCG
                                  G  C   _   C
GAM655  GM2A    5'  GCAAGGTCTGTGGCGGCAGAGG 42689     AC  AC__
                                GCAG  GT   GGCGGCAGAGG
                                ||||  ||   ||||||||||
                                CGTT  CA   CCGCCGTCTCC
                                  C_  GACA
GAM655  HTRA3   5'  GCGGGCGTCAGGGCGGCAGGGG 44834    AGA  AC_     A
          C                      GC  CGT  GGCGGCAG GGC
                                ||  |||  |||||||| |||
                                CG  GCA  CCGCCGTC CCG
                                 CCC  GTC      C
GAM655  ITM2B   5'  GCTCCGCGGCGGCAGAGGC   35094    AGA  TA
                                GC  CG  CGGCGGCAGAGGC
                                ||  ||  ||||||||||||
                                CG  GC  GCCGCCGTCTCCG
                                 AG_  __
GAM655  KRTHB6  3'  CGACAGGCGCTGGCGGAGGC   14033   _  A  AC   CAG
                                CG CAG CGT  GGCGG  AGGC
                                || ||| |||  |||||  ||||
                                GC GTC GCG  CCGCC  TCCG
                                 T  C  A_   ___
GAM655  LASS1   3'  CGCGCGCAGGCGGCAGGGGC  34599    AGA   C     A
                                CGC  CGTA GGCGGCAG GGC
                                |||  |||| |||||||| |||
                                GCG  GCGT CCGCCGTC CCG
                                  C__  _      C
GAM655  LETM1   5'  CGCGGACGGCTGACAGAGGC  29501    A  GTAC  _
                                CGC GAC   GGC GGCAGAGGC
                                ||| |||   ||| |||||||||
                                GCG CTG   CCG CTGTCTCCG
                                  C  _____  A
GAM655  MAPRE3  5'  CGGGGGCGCTGCGGCAGAGGC  29531   CAGA  ACG
                                CG   CGT   GCGGCAGAGGC
                                ||   |||   ||||||||||
                                GC   GCG   CGCCGTCTCCG
                                 CCCC  A__
GAM655  NHP2L1  3'  GCAGGGAGCACGTGGCAGAGGC 22680     AC_   GC
                                GCAG  GTACG  GGCAGAGGC
                                ||||  |||||  |||||||||
                                CGTC  CGTGC  CCGTCTCCG
                                  CCT   A_
GAM655  P53AIP1 5'  GCAGGTCTGAGCAGAGG    35232     AC  ACGGC
                                GCAG  GT   GGCAGAGG
                                ||||  ||   ||||||||
                                CGTC  CA   TCGTCTCC
                                  __ GAC__
GAM655  PIK3R2  3'  CGCAGACGGGCCCAGGGG   22744       TAC  GG  A
                                CGCAGACG  GGC  CAG GG
                                ||||||||  |||  ||| ||
```

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                                GCGTCTGC   CCG  GTC CC
                                    ___   G_   C
GAM655  PNUTL1   5'  CGCGACAACAAGCGGCGGAGGC 15428     A   T  _    A
                                CGC GACG ACG GCGGC GAGGC
                                ||| |||| ||| ||||| |||||
                                GCG CTGT TGT CGCCG CTCCG
                                  _   _  T   C
GAM655  PTGER3   5'  ACGCGGCGCGGGCGGCGGCGGA 9640      AGA_  TA     A
          GG                      ACGC   CG  CGGCGGC GAGG
                                ||||   ||  ||||||| ||||
                                TGCG   GC  GCCGCCG CTCC
                                  CCGC  CC      C
GAM655  REQ      3'  ACACGGGGCAGGTGGCAGAGGC 26539     AGAC   C  C
                                ACGC   GTA GG GGCAGAGGC
                                ||||   ||| || |||||||||
                                TGTG   CGT CC CCGTCTCCG
                                  CCC_  _ A
GAM655  RGL      3'  GCAGATGCAGGCAGAGG     31541      C   CGGC
                                GCAGA GTA   GGCAGAGG
                                ||||| |||   ||||||||
                                CGTCT CGT   CCGTCTCC
                                  A  _____
GAM655  USF2     3'  GCGGGACGTTGGCAGAGG    17897    A_    ACGGC
                                GC  GACGT   GGCAGAGG
                                ||  |||||   ||||||||
                                CG  CTGCA   CCGTCTCC
                                 CC    A_____
GAM655  WEE1     5'  CGCGGACTTTCCGGCAGAGGC  18090     A   GTACGG
                                CGC GAC     CGGCAGAGGC
                                ||| |||     ||||||||||
                                GCG CTG     GCCGTCTCCG
                                  C  AAAG__
GAM656  ARHGDIA  3'  CCTGTCCGTCGTCCGTCCGTCA 20203    _    CCC   G_     C
                                CC GTCCG   TCG  TGTCCG CA
                                || |||||   |||  |||||| ||
                                GG CAGGC   AGC  GCAGGC GT
                                 A    ___   AG     A
GAM656  HNRPDL   5'  TCTGCCCTCGGTTCGCCA    24181    C       GTC
                                TC GCCCTCGGT   CGCCA
                                || |||||||||   |||||
                                AG CGGGAGCCA   GCGGT
                                 A       A__
GAM656  HPCAL1   5'  TCAGTCCGCCCGTCCGC     39549    C       TCGGT
                                TC GTCCGCCC    GTCCGC
                                || ||||||||    ||||||
                                AG CAGGCGGG    CAGGCG
                                 T      _____
GAM656  PDGFB    5'  TCCGTCTGCCCGCCTGCTCGCC 15194       C   TCGG  TC
                                TCCGTC GCCC    TG  CGCC
                                |||||| ||||    ||  ||||
```

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                                AGGCAG CGGG   AC  GCGG
                                   A   CGG_  GA
GAM656  RAD51L3  5'  TCCGCCCGCCCGGGATCCGCC  39474         TC  TG
                                TCCGTCCGCCC  GG  TCCGCC
                                ||||||||||  ||  ||||||
                                AGGCGGGCGGG  CC  AGGCGG
                                      __  CT
GAM656  UBE2B    5'  TCCCTCCGCCCTCCGC     17797     G     TCGGTG
                                TCC TCCGCCC     TCCGC
                                ||| |||||||     |||||
                                AGG AGGCGGG     AGGCG
                                  G     _______
GAM656  XYLB     5'  TCCGTCAGTCCGTCCGTCCGCC 23027       CG_  C  GG
           A                     TCCGTC   CC TC  TGTCCGCCA
                                ||||||   || ||  |||||||||
                                AGGCAG   GG AG  GCAGGCGGT
                                   TCA  C  __
GAM656  SIAT4C   3'  GCCACAGCGACGAGCC      26579     CGT  A
                                GCC   CG CGACGAGCC
                                |||   || |||||||||
                                CGG   GT GCTGCTCGG
                                  T__  C
GAM657  CDYL     3'  TCATACTTAAGCTATTCAG   22088         T   _
                                TCATACTTAA CTAT CAG
                                |||||||||| |||| |||
                                AGTATGAATT GATA GTC
                                      C   A
GAM657  PIP5K1B  3'  ATACTTAATTTACCAATGTG  18664         C    GACG
                                ATACTTAAT TATCA   GTG
                                ||||||||| |||||   |||
                                TATGAATTA ATGGT   CAC
                                     A    TA__
GAM658  BLMH     3'  TCTGAAGAGGTTCCTGG     7551        A      AA
                                TCTGAA GAGGTTT  GG
                                |||||| |||||||  ||
                                AGACTT CTCCAAG  CC
                                   _      GA
GAM658  LZTS1    3'  CCTCTGTCGTTTGAGGAT    34263       AAAGAG   A
                                TCTCTG     GTTT AGGAT
                                ||||||     |||| |||||
                                GGAGAC     CAAA TCCTA
                                   AG_____   C
GAM658  XPR1     3'  CCTGAAAGAGGTATGTGG    21848          TTAA
                                TCTGAAAGAGGT   GG
                                ||||||||||||   ||
                                GGACTTTCTCCA   CC
                                       TACA
GAM658  ZNFN2A1  5'  TCTGAGAGAGGTCTGATGG   41365      A      AA_
                                TCTGA AGAGGTTT   GG
                                ||||| ||||||||   ||
```

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                                AGACT TCTCCAGA   CC
                                  C       CTA
GAM659  TRHDE    3'  TGAGAATATCATTTCTGTTTT  30113     A       AAA
                                TGA AATATCATT   TTGTTTT
                                ||| |||||||||   |||||||
                                ACT TTATAGTAA   GACAAAA
                                  C       A__
GAM659  TRIM37   3'  TTCATTTAAAATTACATTTGTA 31627      A       A  T
           G                     TTCA TTTAAAAT AT TTTGTAG
                                |||| |||||||| || |||||||
                                AAGT AAATTTTA TG AAACATC
                                  _       A  T
GAM660  RRM2     3'  GAATTGGCTCCCATTA      9758       GC    TCC
                                GAATT  GGTT   CCCATTA
                                |||||  ||||   |||||||
                                CTTAA  CCGA   GGGTAAT
                                  __   ____
GAM660  SLC1A3   3'  GGAATACTTCCCCCATT     20043      T  GGT
                                GGAAT GC   TTCCCCCATT
                                ||||| ||   ||||||||||
                                CCTTA TG   AAGGGGGTAA
                                  _ ____
GAM660  TEGT     3'  AGGAGCTGGAGATCCCCATTAG 42094      ATT  _  TTTC
                                AGGA   GC GG    CCCCATTAG
                                ||||   || ||    |||||||||
                                TCCT   CG CC    GGGGTAATC
                                  ____ A  TCTA
GAM660  ARF4L    3'  GCCTGGGGAGACTCCCCA    43071        T   AAAGA
                                GCCTGGG AGG     CCCA
                                ||||||| |||     ||||
                                CGGACCC TCT     GGGT
                                    C   GAG__
GAM660  BACH2    3'  GCCTGGGCAGGAAAGCC     34791             A
                                GCCTGGGTAGGAAAG CC
                                |||||||||||||| ||
                                CGGACCCGTCCTTTC GG
                                                _
GAM660  BAT3     5'  GCCTAGGTGGGAGGGAGCC   21583         A   AA  C
                                GCCTGGGT GGA  GA CC
                                |||||||| |||  || ||
                                CGGATCCA CCT  CT GG
                                    C   CC  C
GAM660  FXYD6    3'  GCCTGCCAGAGACCCAA     35118       GGTA   AA
                                GCCTG   GGA  GACCCAA
                                |||||   |||  |||||||
                                CGGAC    TCT  CTGGGTT
                                  GG__   __
GAM660  HOXB1    3'  GCCTGGGTTGGGAGAGCC    13429         A  AA   C
                                GCCTGGGT GG  AGA CC
                                |||||||| ||  ||| ||
```

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                                CGGACCCA CC  TCT GG
                                    A  C_   C
GAM660  JAK2     5'  GCCCGGGCCGAGGGGCCCGACC 22476        __   AAAGA   A
            G                    GCCTGGGT  AGG    CCC ACCG
                                 ||||||||  |||    ||| ||||
                                 CGGGCCCG  TCC    GGG TGGC
                                     GC   CC___   C
GAM660  MSH6     5'  GCCGGCAAGGCCCAAC     6761     TG     AAAGA
                                 GCC  GGTAGG    CCCAAC
                                 |||  ||||||    ||||||
                                 CGG  CCGTTC    GGGTTG
                                   __     C____
GAM660  PRKY     3'  GCCGAGGGGACCCAAC     15698     T_   TAGGAAA
                                 GCC  GGG      GACCCAAC
                                 |||  |||      ||||||||
                                 CGG  CCC      CTGGGTTG
                                   CT  ________
GAM660  PUM2     3'  GCCTAGGTAGTTTTGCCCAA  31660         GAAAGA
                                 GCCTGGGTAG     CCCAA
                                 ||||||||||     |||||
                                 CGGATCCATC     GGGTT
                                      AAAAC_
GAM660  TNFRSF6B 5'  GCCCGGGTAGGGCCGGCC    37283          AAAGAC  AA
                                 GCCTGGGTAGG     CC  CC
                                 ||||||||||     ||  ||
                                 CGGGCCCATCC     GG  GG
                                       C_____  CC
GAM660  TOP3B    3'  GCCTGGGTGAGGGAGGAC    19465        _   AAA
                                 GCCTGGGT AGG   GAC
                                 ||||||||  |||   |||
                                 CGGACCCA TCC   CTG
                                     C   CTC
GAM660  TPS1     3'  GCCTGGGCAGGGGAGGGCC   41304          AA  AC
                                 GCCTGGGTAGG  AG  CC
                                 ||||||||||  ||  ||
                                 CGGACCCGTCC  TC  GG
                                       CC  CC
GAM660  WHSC1    3'  GCCTGGCTGGGGAGGCCCA   39367       GTA  AA  A
                                 GCCTGG   GG  AG CCCA
                                 ||||||   ||  || ||||
                                 CGGACC   CC  TC GGGT
                                    GA_  CC  C
GAM661  APBA2    3'  GAAGTCTTCCTACGGGTAGC  24280         GA  ATAA
                                 GGAGTCTTC  TA   TAGC
                                 |||||||||  ||   ||||
                                 CTTCAGAAG  AT   ATCG
                                      G_  GCCC
GAM661  BN51T    3'  GCAGTTTTCATCTATAATAGCC 44674   G   C   ATA
                                 G AGT TTCG   ATAATAGCC
                                 | ||| ||||   |||||||||
```

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                                C TCA AAGT   TATTATCGG
                                 G   A    AGA
GAM661  CACNA1A  3'  GGAGCCCCGGTAGTAGC     35738        T  ATAA  A
                                GGAGTCT CG    TA TAGC
                                ||||||| ||    || ||||
                                CCTCGGG GC    AT ATCG
                                    _  C___  C
GAM661  NPTX2    3'  GGAGCCTTCTTCTAATGGC    45208         GATAA    A
                                GGAGTCTTC     TAAT GC
                                |||||||||     |||| ||
                                CCTCGGAAG     ATTA CG
                                      AAG__    C
GAM661  PCDH9    3'  GGACTCTTCGATAGTAAC     44402      G        A
                                GGA TCTTCGATA TAAT
                                ||| |||||||||| ||||
                                CCT AGAAGCTAT ATTG
                                  G         C
GAM661  UBL3     3'  GGGATCTTCAAAAGTAGCC    28267     AG      TAATAA
                                GG  TCTTCGA      TAGCC
                                ||  |||||||      |||||
                                CC  AGAAGTT      ATCGG
                                 CT      TTC___
GAM662  BPGM     3'  TCAATAATGATTTCTTGAA    11894     TAC        C
                                TC   AATGATTTC TGAA
                                ||   |||||||||| ||||
                                AG   TTACTAAAG ACTT
                                 TTA         A
GAM662  DRD1     5'  TCTCAAAGCCCCTGGAGCTTG  9008      A   TGAT     A
                                TCT CAA    TTCCTG AGCTTG
                                ||| |||    |||||| ||||||
                                AGA GTT    GGGGAC TCGAAC
                                  _  TC__     C
GAM662  MALT1    3'  TCTCAAAGTCCTGAAGTTT    27693     A   TGATT      C
                                TCT CAA     TCCTGAAG TT
                                ||| |||     |||||||| ||
                                AGA GTT     AGGACTTC AA
                                  _  TC___       A
GAM663  ACADS    3'  AGGCGGAGCTGCCAATGGTCG  6151         A     GC_
                                AGGCGGAG TGCCGA   TCG
                                |||||||| ||||||   |||
                                TCCGCCTC ACGGTT   AGC
                                     G     ACC
GAM663  ACN      3'  AGGAGGAGATGCTGATTCA    31406     C       C  GC
                                AGG GGAGATGC GA  TCG
                                ||| |||||||| ||  |||
                                TCC CCTCTACG CT  AGT
                                  T       A  A_
GAM663  ADARB1   3'  AGGCGGCGATGCTGGGCC     31867       A    CGAGCTC
                                AGGCGG GATGC      GGCC
                                |||||| |||||      ||||
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                                TCCGCC CTACG      CCGG
                                   G    AC_____
GAM663  AP2B1   5'  GGCGGGGGTGGCGGCGGGAGCC 10487      AGA  C  A  TC_
                                GGCGG   TG CG GC   GGCC
                                |||||   || || ||   ||||
                                CCGCC   AC GC CG   TCGG
                                   CCC  C  _  CCC
GAM663  ARIH1   5'  GGCGGGGACGCCGAGGCC    25093      A      GCTC
                                GGCGG GATGCCGA    GGCC
                                ||||| ||||||||    ||||
                                CCGCC CTGCGGCT    CCGG
                                   C       ____
GAM663  COL1A1  3'  AGGGGAGATGTTGCAAGAGCCA 6362     C     C__   CTC
                                AGG GGAGATG   CGAG   GGCCA
                                ||| |||||||   ||||   |||||
                                TCC CCTCTAC   GTTC   TCGGT
                                  _      AAC   ___
GAM663  CX3CR1  3'  AGGTGGAGATGCATGAGGTCA  43290    C      C_  C
                                AGG GGAGATGC  GAG TCG
                                ||| ||||||||  ||| |||
                                TCC CCTCTACG  CTC AGT
                                  A       TA   C
GAM663  FOXD2   5'  AGCGGCTCGGGCTCGGCC    20951      AGATGC  A
                                GGCGG     CG GCTCGGCC
                                |||||     || ||||||||
                                TCGCC     GC CGAGCCGG
                                   GA____  C
GAM663  GLUD1   5'  AGGGGAGGTGCGTGATGGTCG  23586    C   A  C_  GC_
                                AGG GGAG TGC  GA   TCG
                                ||| |||| |||  ||   |||
                                TCC CCTC ACG  CT   AGC
                                  _   C   CA  ACC
GAM663  KCNS3   5'  AGGTGGAGATGCCACACGCTC  13931    C       GA__
                                AGG GGAGATGCC    GCTC
                                ||| |||||||||    ||||
                                TCC CCTCTACGG    CGAG
                                  A       TGTG
GAM663  LASS1   3'  AGGCGGAGGCTGCGCGGCC   34591       AT  CGA  T
                                AGGCGGAG  GC   GC CGGCC
                                ||||||||  ||   || |||||
                                TCCGCCTC  CG   CG GCCGG
                                     __  A__  C
GAM663  MXI1    5'  GGCGGGCGGGCCAGCTCGGCC  39022      AGAT   G
                                GGCGG   GCC AGCTCGGCC
                                |||||   ||| |||||||||
                                CCGCC   CGG TCGAGCCGG
                                   CGCC  _
GAM663  NT5C    5'  GGGGGCGCGGGCTCGGCC    31101    C  AGAT  _  A
                                GG GG   GC CG GCTCGGCC
                                || ||   || || ||||||||
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                                CC CC    CG GC CGAGCCGG
                                 _ ____  C  C
GAM663  PCTK1    5' AGCCGGCCATGAGCTTGGCC  37461    G   AG  GCC    C
                                AG CGG  AT   GAGCT GGCC
                                || |||  ||   ||||| ||||
                                TC GCC  TA   CTCGA CCGG
                                 G   GG ___    A
GAM663  SCNN1A   3' GGCAGAGGTGCCGGGGC    9782        A    AGCTC
                                GGCGGAG TGCCG    GGC
                                ||||||| |||||    |||
                                CCGTCTC ACGGC    CCG
                                    C    C____
GAM663  SIAH2    5' AGGCGGAGGGCTGGAC     22860        ATGCCGA   C
                                AGGCGGAG     GCT GGC
                                ||||||||     ||| |||
                                TCCGCCTC     CGA CTG
                                     C_______  C
GAM663  SLC9A3R1 3' GGTGGAATGCTGGCTCG    43250    C   A   CGA
                                GG GGAG TGC   GCTCG
                                || |||| |||   |||||
                                CC CCTT ACG   CGAGC
                                 A   _  AC_
GAM663  TPS1     3' GGTGTAGATGCCAGGCC    41305    CGG      AGCTC
                                GG   AGATGCCG    GGCC
                                ||   ||||||||    ||||
                                CC   TCTACGGT    CCGG
                                 ACA      ______
GAM663  ZNF216   5' AGGCGGAGGTGGCGCCGCC   25649        A  CCGA   CG
                                AGGCGGAG TG    GCT  GCC
                                |||||||| ||    |||  |||
                                TCCGCCTC AC    CGG  CGG
                                    C  CG__   __
GAM664  BDKRB2   3' TGGGGGGTCTCAGCACTGTGAT 8409      AT       AGAC
                                TGGG  GTCTCAGCA   GTGAT
                                ||||  |||||||||   |||||
                                ACCC  CAGAGTCGT   CACTA
                                  CC       GA__
GAM664  CA9      5' TGGGGTGTCCCAGCACACG   10234     A        AG
                                TGGG TGTCTCAGCA  ACG
                                |||| ||||||||||  |||
                                ACCC ACAGGGTCGT  TGC
                                  C        G_
GAM664  DSC3     3' TGGGTGTTTCAGTAGCCGT   35950     A   C   CA  A
                                TGGG TGT TCAG  AG CGT
                                |||| ||| ||||  || |||
                                ACCC ACA AGTC  TC GCA
                                  _  A   A_  G
GAM664  GJA1     3' TGGAATGTTTTAGCAGGGAC  6733         CTC    A_
                                TGGGATGT   AGCA  GAC
                                ||||||||   ||||  |||
```

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                                ACCTTACA  TCGT  CTG
                                    AAA   CC
GAM665  CCRL1    3'  ACCACGGCGTCTGAGAT    32427        CACAC
                                ACCACGGTG    GAGAT
                                |||||||||    |||||
                                TGGTGCCGC    CTCTA
                                    AGA__
GAM665  CDC25B   3'  TACCACGGTTCCTACAGAGAT  34858        GC__  C
                                TACCACGGT   ACA GAGAT
                                |||||||||   ||| |||||
                                ATGGTGCCA   TGT CTCTA
                                    AGGA  _
GAM665  MAP3K13  3'  CAGTATAGTCACGAGATC    21795      CA__
                                CGGTG   CACGAGATC
                                |||||   |||||||||
                                GTCAT   GTGCTCTAG
                                   ATCA
GAM665  NOTCH3   3'  TACTCGGTACACGGGATC    7740     CA      ACGA
                                TAC  CGGTGCAC   GATC
                                |||  ||||||||   ||||
                                ATG  GCCATGTG   CTAG
                                  A_      CC__
GAM666  CRSP9    3'  GAGGTTATCATCAAAGTTTT   20176     ACCAA   G
                                GAGG    GTC AAAGTTTT
                                ||||    ||| ||||||||
                                CTCC    TAG TTTCAAAA
                                  AATAG  _
GAM667  ABCC3    3'  TCCGAAAAGTGGGAGTA     33428     AA      TC
                                TCC  AAGAGTGGG  GTA
                                |||  |||||||||  |||
                                AGG  TTTTCACCC  CAT
                                  C_       T_
GAM667  CMAR     5'  TCCAAGTGGAGTCATAC     23295     AAAG    _
                                TCCA   AGTGG GTCGTAC
                                ||||   ||||| |||||||
                                AGGT   TCACC CAGTATG
                                  _____    T
GAM667  DGCR2    3'  CCTGGAAGAGTGGGCCCCCA  23091    AA_       GTA
                                CC   AAGAGTGGGTC   CA
                                ||   ||||||||||   ||
                                GG   TTCTCACCCGG   GT
                                 ACC         GG_
GAM667  IL7R     3'  CAGGAAGAGTGGTCAAAGCAA  13515    A_      G   TA_
                                CA  AAGAGTGG TCG   CAA
                                ||  |||||||| |||   |||
                                GT  TTCTCACC AGT   GTT
                                 CC       _  TTC
GAM667  MEN1     3'  GAGATTGGTTGTACAACA    39181     TG_   C
                                GAG   GGT GTACAACA
                                |||   ||| ||||||||
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                                CTC   CCA CATGTTGT
                                  TAA   A
GAM667  NCYM     5'  TCCAAAAGGGCGGGAGGAGCA  26746        A     TC__
                                TCCAAAAG GTGGG    GTA
                                |||||||| |||||    |||
                                AGGTTTTC CGCCC    CGT
                                     C     TCCT
GAM667  PIP5K1B  3'  TCCAAAAAGGTGATTGGCA    18668        A    GTC
                                TCCAAAAG GTGG   GTA
                                |||||||| ||||   |||
                                AGGTTTTT CACT   CGT
                                     C    AAC
GAM667  RELN     3'  AAAAGAATGGAGAGCAACA    45351          TCGTA
                                AAAAGAGTGGG    CAACA
                                ||||||||||     |||||
                                TTTTCTTACCT    GTTGT
                                      CTC__
GAM667  SEPP1    3'  AAGAGTATGATACAACA     41086        GGTC
                                AAGAGTG    GTACAACA
                                |||||||    ||||||||
                                TTCTCAT    TATGTTGT
                                    AC__
GAM667  TCF8     3'  TCCAAAAGAGGTTCCACA     36239         TGGG  G
                                TCCAAAAGAG    TC TACA
                                ||||||||||    || ||||
                                AGGTTTTCTC    AG GTGT
                                      CA__  _
GAM667  TEC      3'  TCCTGAGAGGCTGTACAAC    17390     AAAA   T    C
                                TCC    GAG GGGT GTACAAC
                                |||    ||| |||| |||||||
                                AGG    CTC TCCG CATGTTG
                                  A___   _    A
GAM667  WHSC1    3'  TCACAGGAGAGTGGGTGTCA   39380    _ AA       C  A
                                TC CA  AGAGTGGGT GT CA
                                || ||  |||||||| || ||
                                AG GT  TCTCACCCA CA GT
                                 T  CC        _ _
GAM668  PTBP1    3'  TCGAAGTCCAGGTACAGACT   15853       CG    A
                                TCGAAG  CCAG TACAGATT
                                ||||||  |||| ||||||||
                                AGCTTC  GGTC ATGTCTGA
                                   A_    C
GAM669  BACH2    3'  TATCCTACTGCATGAACTGACA 34802      AC     ACGT
           A                     TATC  ACTGCG    GCTGACAA
                                ||||  ||||||    ||||||||
                                ATAG  TGACGT    TGACTGTT
                                  GA     ACT_
GAM669  OPHN1    3'  TATCACACTCTGGGGACTGTGG 14971         GC___   _   C
           TG                    TATCACACT    GAC GTG TG
                                |||||||||     ||| ||| ||
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                                ATAGTGTGA    CTG CAC AC
                                     GACCC   A   C
GAM669  RGL     5'  TCACACAGCACTGACA     31545       T  GACGT
                                TCACAC GC    GCTGACA
                                |||||| ||    |||||||
                                AGTGTG CG    TGACTGT
                                   T  ______
GAM669  TCF12   3'  TATCACACTACCTGCC     17344          GACG
                                TATCACACTGC    TGCT
                                ||||||||||    ||||
                                ATAGTGTGATG    ACGG
                                      G___
GAM669  TCF8    3'  CACACCTGTGCTGACA     36231       GCGAC
                                CACACT    GTGCTGACA
                                ||||||    |||||||||
                                GTGTGG    CACGACTGT
                                   A____
GAM670  CCR2    3'  CCTGGTTCTAGAAGCCCAGTGT 8498     G   CCAA__
                                CC TGG     AAGCCCAGTGT
                                || |||     ||||||||||
                                GG ACC     TTCGGGTCACA
                                 _  AAGATC
GAM670  FAT2    3'  CCTTTGGCCAAAAGTGCC    11074    CG        C_
                                CC  TGGCCAAAAG  CC
                                ||  ||||||||||  ||
                                GG  ACCGGTTTTC  GG
                                 AA         AC
GAM670  JRKL    5'  CCTCTTGGCCAAAAGACTTGT  19090    CCG        CCCAG
                                CC   TGGCCAAAAG    TGT
                                ||   ||||||||||    |||
                                GG   ACCGGTTTTC    ACA
                                 AGA        TGA__
GAM670  KCNK4   5'  CCTTGGACCGGAGCCCAGTGT  37826    G  _  AAA
                                CC TGG CC   AGCCCAGTGT
                                || ||| ||   ||||||||||
                                GG ACC GG   TCGGGTCACA
                                 A   T  CC_
GAM670  PPP1R3D 5'  CCTCCGTGCTCAGAAGCC    26426    _    GC  A
                                CC CCGTG  CA AAGCC
                                || |||||  || |||||
                                GG GGCAC  GT TTCGG
                                 A    GA  C
GAM670  PTGIS   3'  CCCTTGGGAATGTGAGCCCAGT 9671      G   CCAAA__
            GT                   CCC TGG      AGCCCAGTGT
                                ||| |||      ||||||||||
                                GGG ACC      TCGGGTCACA
                                 A   CTTACAC
GAM670  TEM8    3'  CCCTGGGTGATGAAGCCCAGTG 38177     G   CCAA__
            T                    CCC TGG     AAGCCCAGTGT
                                ||| |||     ||||||||||
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                                GGG ACC     TTCGGGTCACA
                                  _  CACTAC
GAM670  USP6    5' CCTCTGGCAGCCCAGC     45028    CG   CAAA
                                CC  TGGC   AGCCCAGT
                                ||  ||||   ||||||||
                                GG  ACCG   TCGGGTCG
                                 AG   ____
GAM671  PCOLCE2  3' AGACAAGATTGTAACACCT   30042       A      C
                                AGACAA ATTGTAAC ACTT
                                |||||| |||||||| ||||
                                TCTGTT TAACATTG TGGA
                                   C      _
GAM672  GABRE    3' TTTACATATTTCCCCATTTCA  35082         A   TC
                                TTTACATATT CCCT  TTCA
                                |||||||||| ||||  ||||
                                AAATGTATAA GGGG  AAGT
                                      A   TA
GAM673  CUL3     3' TCTAGATCTGATTTTTACA   18745     A     GT
                                TCTA ATCTGAT  TTTTGCA
                                |||| |||||||  |||||||
                                AGAT TAGACTA  AAAATGT
                                  C     __
GAM673  PSG7     3' TGTAAAAGTTTGAGGT      15808          GTGAT  T
                                TGTAAAAGTT    TG AGGT
                                ||||||||||    || ||||
                                ACATTTTCAA    AC TCCA
                                      ______ _
GAM674  AXIN1    3' CCTGGCCGTGACACCCGTG   41375    C      G  GAG
                                CC GGCCGTGA CG   CCGTG
                                || |||||||| ||   |||||
                                GG CCGGCACT GT   GGCAC
                                 A       _ G__
GAM674  BAIAP3   3' TCCCCGGCCTGGGAGCCCCG  19458        G  AGC     G
                                TCCCCGGCC TG   GGAGCC TG
                                ||||||||| ||   |||||| ||
                                AGGGGCCGG AC   CCTCGG GC
                                     _ ___      G
GAM674  INMT     3' GGGCGTGAGCAAGCTGAGCTGT 27678    C      ____   C
           G                     GG CGTGAGCG    GAGC GTG
                                || ||||||||    |||| |||
                                CC GCACTCGT    CTCG CAC
                                 C       TCGA    A
GAM674  NMB      5' GCCCTGAGCAGCGGAGCCGTG  43952     G    ___
                                GCC TGAGC   GGAGCCGTG
                                ||| |||||   |||||||||
                                CGG ACTCG   CCTCGGCAC
                                  G    TCG
GAM674  TERF2    5' TCCTCGGCTGTGACGCCGC   24916     C   C   GCGGA
                                TCC CGGC GTGA    GCCGT
                                ||| |||| ||||    |||||
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                                AGG GCCG CACT    CGGCG
                                  A   A   G____
GAM675  ACCN2   5'  GACCGGTGGCGGGCTCAGCG  33444    A       G
                                GAC CGGTGGCGGGC CGGTG
                                ||| |||||||||| |||||
                                CTG GCCACCGCCCG GTCGC
                                  _       A
GAM675  COG7    3'  GCATGGTGGCCACGGTGG   42657   A C    GGG
                                G CA GGTGGC  CGCGGTGG
                                | || ||||||  ||||||||
                                C GT CCACCG  GTGCCACC
                                 _ A    ___
GAM675  CTBP2   5'  GGCGGCGGTGGCGGTGGC   10624       GC
                                GGTGGCGG  GCGGTGGC
                                ||||||||  ||||||||
                                CCGCCGCC  CGCCACCG
                                     AC
GAM675  CTGF    5'  GGAGCGGAGGGCGCGGTGGCG  12503   C   C
                                A GGTGG GGGCGCGGTGGCG
                                | ||||| ||||||||||||
                                C TCGCC CCCGCGCCACCGC
                                 C    T
GAM675  CYP26A1 5'  CAGAGGCGGCGCGGTGGCG   38404    T   G
                                CGG GGCGG CGCGGTGGCG
                                ||| ||||| ||||||||||
                                GTC CCGCC GCGCCACCGC
                                  T   _
GAM675  DRPLA   3'  CACGGTGGGGGGAGGGTG   12584       C  CGC
                                CACGGTGG GGG  GGTG
                                |||||||| |||  ||||
                                GTGCCACC CCC  CCAC
                                     _  CTC
GAM675  ELK1    5'  GGTGGTGGTGGCGGTGGCG   23414     C  GC
                                GGTGG GG  GCGGTGGCG
                                ||||| ||  |||||||||
                                CCACC CC  CGCCACCGC
                                   A  AC
GAM675  ENO2    5'  GGTGGCGGTGGCGGTGGC   12714       GC
                                GGTGGCGG  GCGGTGGC
                                ||||||||  ||||||||
                                CCACCGCC  CGCCACCG
                                     AC
GAM675  GAL     5'  CGGTGGCGGGTCTGGGCG   45048       CGC_
                                CGGTGGCGGG   GGTG
                                ||||||||||   ||||
                                GCCACCGCCC   CCGC
                                      AGAC
GAM675  GAL     5'  GGTCCGGGTGCGGTGGC    45053    GG  C
                                GGT  CGGG GCGGTGGC
                                |||  |||| ||||||||
```

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                                CCA  GCCC CGCCACCG
                                  G_   A
GAM675  IRS1    3'  GACACGGTGGTGGGCACATCAG 24420          C      GT
                                GACACGGTGG GGGCGCG  GG
                                |||||||||| |||||||  ||
                                CTGTGCCACC CCCGTGT  TC
                                      A      AG
GAM675  LGMN    5'  GACCGTGGTGGCAGTGGTGGCG 24684     AC_      GCGC
                                GAC   GGTGGCGG   GGTGGCG
                                |||   ||||||||   |||||||
                                CTG   CCACCGTC   CCACCGC
                                  GCA      A___
GAM675  MAF     5'  CGGTGGCGGCGGTGG      23828         GGC
                                CGGTGGCG   GCGGTGG
                                ||||||||   |||||||
                                GCCACCGC   CGCCACC

                                   ___
GAM675  MAPRE3  5'  GACAGGTGGCGGGGGCG    29532     C       C
                                GACA GGTGGCGGG GCG
                                |||| ||||||||| |||
                                CTGT CCACCGCCC CGC
                                  _       C
GAM675  PKIG    3'  CACGGTGCGAAGGTGG     28190       G   CGC
                                CACGGTG CGGG   GGTGG
                                ||||||| ||||   |||||
                                GTGCCAC GCTT   CCACC

                                  _   ___
GAM675  PTMS    5'  CGGAACCTGGCGCGGTGGCG  15882    T   G_
                                CGG GGC  GGCGCGGTGGCG
                                ||| |||  ||||||||||||
                                GCC TTG  CCGCGCCACCGC
                                  _  GA
GAM675  PYGB    3'  CACAGTGGTGGTCAGGGTGG  16043        C  G  C
                                CACGGTGG GG CG GGTGG
                                |||||||| || || |||||
                                GTGTCACC CC GT CCACC
                                     A  A  C
GAM675  RRP22   5'  GACAGGTGGCGGGCGCG    27007     C
                                GACA GGTGGCGGGCGCG
                                |||| ||||||||||||
                                CTGT CCACCGCCCGCGC

                                  _
GAM675  SLC20A2 3'  GGTGTGGTGGCGGTGGCA   27576     GC  GC
                                GGTG  GG  GCGGTGGCG
                                ||||  ||  |||||||||
                                CCAC  CC  CGCCACCGT
                                  A_  AC
GAM675  SLC6A8  5'  GGTGGCGGCGGCGGCGGTGGCG 24783         __  _
                                GGTGGCGG  GCG CGGTGGCG
                                ||||||||  ||| ||||||||
```

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                                CCACCGCC  CGC GCCACCGC
                                    GC   C
GAM675  SLC7A8   3'  GCACGGTGGGGCGGTGG    29288   A    GGC   C
                                G CACGGT   GGG GCGGTGG
                                | ||||||   ||| |||||||
                                C GTGCCA   CCC CGCCACC
                                _     ___   _
GAM675  STK10    5'  GGCCGGGGGCGCGGTGGC    25621    _ C
                                GGT GG GGGCGCGGTGGC
                                ||| || ||||||||||||
                                CCG CC CCCGCGCCACCG
                                  G _
GAM675  USF2     3'  GGCGGCGGCTGCGTGGTGG   17902       __  C
                                GGTGGCGG  GCG GGTGG
                                ||||||||  ||| |||||
                                CCGCCGCC  CGC CCACC
                                    GA   A
GAM675  WNT1     5'  GACGCGGCGGTGGCGGCAGTGG 24082    A    CG   _
            CG                    GAC CGGTGG  GGCG CGGTGGCG
                                ||| ||||||  |||| ||||||||
                                CTG GCCGCC  CCGC GTCACCGC
                                  C     A_   C
GAM676  ACVRL1   5'  GGGTCCGGCGCGGCCCCGG   6166     C      AGAA
                                GGG CCGGCGCGG   GG
                                ||| |||||||||   ||
                                CCC GGCCGCGCC   CC
                                  A       GGGG
GAM676  AF5Q31   5'  TCGAGCCCGCCCAGGGGGCGG  30859       G G   AGAA
                                TCGGGCCCG C CGG   GGCGG
                                ||||||||| | |||   |||||
                                AGCTCGGGC G GTC   CCGCC
                                    _ G   CC__
GAM676  ARHGAP6  3'  GGGCCCGGGTATGGAGGCGG  30222       CGC_   GAA
                                GGGCCCGG   GGA  GGCGG
                                ||||||||   |||  |||||
                                CCCGGGCC   CCT  CCGCC
                                    CATA  ___
GAM676  ATP6V0C  3'  CGGGCCCGGCGGTGAGGGCGG  44555        CG   AA
                                CGGGCCCGGCG  GAG  GGCGG
                                ||||||||||  |||  |||||
                                GCCCGGGCCGC  CTC  CCGCC
                                     CA  __
GAM676  CACNA1A  5'  TCGGGTCGGGGGGCTCAGAAGGC 35743     CC   C_  GG
            GG                    TCGGG  CGG  GC  AGAAGGCGG
                                |||||  |||  ||  |||||||||
                                AGCCC  GCC  CG  TCTTCCGCC
                                  A_   CC  AG
GAM676  CIAO1    5'  GGCCCGACGCAGGGGGAGGTGG 43684         AGA_   C
                                GGCCCGGCGCGG   AGG GG
                                ||||||||||||   ||| ||
```

```
                                CCGGGCTGCGTC   TCC CC
                                      CCCC  A
GAM676  DES     5'  CGGGCGCACGGAGGAGGCGG  43562      CCG      A
                                CGGGC  GCGCGGAG AGGCGG
                                |||||  |||||||| ||||||
                                GCCCG  CGTGCCTC TCCGCC
                                  ___      C
GAM676  FES     5'  TCAGGCCCGGTGCGGACCCCGG 12821          C    GAAGG
                                TCGGGCCCGG GCGGA    CGG
                                |||||||||| |||||    |||
                                AGTCCGGGCC CGCCT    GCC
                                      A    GGG__
GAM676  GRB14   5'  GCAAGGCGCGGAGGGGGCG   21037   CC       AA
                                GC  GGCGCGGAG  GGCG
                                ||  |||||||||  ||||
                                CG  CCGCGCCTC  CCGC
                                 TT        CC
GAM676  GUCY1A2  5'  TCGCGCCCGGCGGGGC     9224     G      C  AGAAG
                                TCG GCCCGGCG GG    GC
                                ||| ||||||||  ||    ||
                                AGC CGGGCCGC CC    CG
                                  G      _ _____
GAM676  GUK1    5'  GGGCCCGGCCCAGGGCG     9231          G   AGAA
                                GGGCCCGGC CGG   GGCG
                                |||||||||  |||   ||||
                                CCCGGGCCG GTC   CCGC
                                      G  ____
GAM676  HSF4    5'  TCGGGCCCGGCCGCTGCG    40772          G  GAGAAG
                                TCGGGCCCGGC CG     GCG
                                ||||||||||  ||     |||
                                AGCCCGGGCCG GC     CGC
                                      _  GA____
GAM676  IGF2    5'  GGTTCGGCGAAGGCGAGAGGGC 8315    GCC    CG___   A
            GG                    GG   CGGCG    GAGA GGCGG
                                ||   |||||    |||| |||||
                                CC   GCCGC    CTCT CCGCC
                                 AA_    TTCCG   C
GAM676  LFNG    3'  GGGCCCAGCGGGGAGGTGG   45217         C  A  A  C
                                GGGCCCGGCG GG GA GG GG
                                |||||||||| || || || ||
                                CCCGGGTCGC CC CT CC CC
                                      _ _ _ A
GAM676  MAPK8IP1  5'  CGGAGCGCGGCGCGGAGGAGGC 24155    _ C       A
            GG                    CGG GC CGGCGCGGAG AGGCGG
                                ||| || |||||||||| ||||||
                                GCC CG GCCGCGCCTC TCCGCC
                                  T  C        C
GAM676  MMP15   3'  GGGCCCAAGGGGAGGTGG    14562        CGC   AA
                                GGGCCCGG   GGAG  GG
                                ||||||||   ||||  ||
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```
                                CCCGGGTT  CCTC  CC
                                    CC_   CA
GAM676  MPP1    5' GCGGGGCTGCGGAGAAGGCGG 14624   CC  _
                                GC  GGC GCGGAGAAGGCGG
                                ||  ||| |||||||||||||
                                CG  CCG CGCCTCTTCCGCC
                                 CC  A
GAM676  RNMT    3' GGGCTGCTAAAGAAGGTGG  19153    CCG  GC     C
                                GGGC  GC  GGAGAAGG GG
                                ||||  ||  |||||||| ||
                                CCCG  CG  TTTCTTCC CC
                                  A__ A_     A
GAM676  RNPEPL1  5' CCGGGCGCCTCGGGGAAGGCGG 32877      _ GG  C  A
                                TCGGGC CC  CG GG GAAGGCGG
                                |||||| ||  || || ||||||||
                                GGCCCG GG  GC CC CTTCCGCC
                                   C  A_  _  _
GAM676  SH3GL1  3' TCGGGTCAGGACGGAGGTGG  16676    CC  C    AA
                                TCGGG  CGG GCGGAG  GG
                                |||||  ||| ||||||  ||
                                AGCCC  GTC TGCCTC  CC
                                   A_  C    CA
GAM676  TPX1    5' GGGCCGGCGCGTTGCG    17666     C    GAGAAG
                                GGGCC GGCGCG    GCG
                                ||||| ||||||    |||
                                CCCGG CCGCGC    CGC
                                   _    AA____
GAM676  YWHAG   5' GGCGGCTGCGCGGAGGAGGCGG 29796   CCG_     A
                                GGC   GCGCGGAG AGGCGG
                                |||   |||||||| ||||||
                                CCG   CGCGCCTC TCCGCC
                                  CCGA      C
GAM676  ZNF42   5' GGGCCTGGAGAAGGCG     18291     CGGCGC
                                GGGCC    GGAGAAGGCG
                                |||||    ||||||||||
                                CCCGG    CCTCTTCCGC
                                   A_____
GAM677  CENPC1  3' TACATATATACATACATATA  12235     T     _
                                TACAT ATATACAT TATATA
                                ||||| |||||||| ||||||
                                ATGTA TATATGTA GTATAT
                                   _      T
GAM677  CRIM1   3' TATATATATTATATACAC   32381      C
                                TATATA ATTATATACAT
                                |||||| ||||||||||
                                ATATAT TAATATATGTG
                                   A
GAM677  PCDH8   3' CATTATATACAAACATTACATT 15114         TT  _
                                CATTATATACA  ATAT ACATT
                                ||||||||||  |||| |||||
```

```
                                GTAATATATGT  TGTA TGTAA
                                      T_   A
GAM677  PDE4B   3'  TACAAAACATTACATTATATAC 15150     TT   _
          ATT                   TACA  ATAT ACATTATATACATT
                                |||| |||| ||||||||||||||
                                ATGT  TGTA TGTAATATATGTAA
                                  TT   A
GAM677  PDE4B   5'  TACAAAACATTACATTATATAC 15150     TT   _
          ATT                   TACA  ATAT ACATTATATACATT
                                |||| |||| ||||||||||||||
                                ATGT  TGTA TGTAATATATGTAA
                                  TT   A
GAM677  RNTRE   3'  CATTATATACATAAAATATA  31251          T__
                                CATTATATACAT   ATATA
                                ||||||||||||   |||||
                                GTAATATATGTA   TATAT
                                      TTT
GAM677  CENPC1  3'  TACATATATACATACATATA  12235     T     _
                                TACAT ATATACAT TATATA
                                |||||| |||||||| ||||||
                                ATGTA TATATGTA GTATAT
                                  _      T
GAM677  CRIM1   3'  TATATATATTATATACAC    32381      C
                                TATATA ATTATATACAT
                                |||||| ||||||||||
                                ATATAT TAATATATGTG
                                   A
GAM677  PCDH8   3'  CATTATATACAAACATTACATT 15114         TT   _
                                CATTATATACA  ATAT ACATT
                                ||||||||||  |||| |||||
                                GTAATATATGT  TGTA TGTAA
                                      T_   A
GAM677  PDE4B   5'  TACAAAACATTACATTATATAC 15150     TT   _
          ATT                   TACA  ATAT ACATTATATACATT
                                |||| |||| ||||||||||||||
                                ATGT  TGTA TGTAATATATGTAA
                                  TT   A
GAM677  PDE4B   3'  TACAAAACATTACATTATATAC 15150     TT   _
          ATT                   TACA  ATAT ACATTATATACATT
                                |||| |||| ||||||||||||||
                                ATGT  TGTA TGTAATATATGTAA
                                  TT   A
GAM677  RNTRE   3'  CATTATATACATAAAATATA  31251          T__
                                CATTATATACAT   ATATA
                                ||||||||||||   |||||
                                GTAATATATGTA   TATAT
                                      TTT
GAM678  ANXA5   3'  GAAGGAAGGCAGTGGGGT    10101         ___
                                GAAGGGGGGT   GGGGT
                                |||||||||   |||||
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                                CTTCCTTCCG  CCCCA
                                     TCA
GAM678  ASIC4   3'  TAGAAGGGACTCTAGGGGT  33067       GGT__
                                TAGAAGGGG   GGGGT
                                |||||||||   |||||
                                ATCTTCCCT   CCCCA
                                     GAGAT
GAM678  CACNG3  3'  TAGAGAGGATGGAGGGGT   27240     AG  _ T
                                TAGA  GGG GG GGGGT
                                ||||  ||| || |||||
                                ATCT  CCT CC CCCCA
                                  CT   A  T
GAM678  CHRM1   5'  AAGAGGGGTCTGTAGGGT   45420       ____
                                AAGGGGGGT   GGGGT
                                |||||||||   |||||
                                TTCTCCCCA   TCCCA
                                     GACA
GAM678  CLCN5   5'  GAAGGGAGACAAAAGGGT   6357        T___
                                GAAGGGGGG   GGGGT
                                |||||||||   |||||
                                CTTCCCTCT   TCCCA
                                     GTTT
GAM678  CRSP8   3'  GAAGGTGCTGGGTGGGGT   44339     G___
                                GAAGG   GGGTGGGGT
                                |||||   |||||||||
                                CTTCC   CCCACCCCA
                                   ACGA
GAM678  CYP11B1 3'  AGAGGGGTGGCCTGGGGT   41627     A  _  __
                                AGA GGGG GGT  GGGGT
                                ||| |||| |||  |||||
                                TCT CCCC CCG  CCCCA
                                  _   A  GA
GAM678  DNASE1L1 3' GACGGGGGAGGCTGGGGT   27495    A    ___
                                GA GGGGGG   TGGGGT
                                || ||||||   ||||||
                                CT CCCCCT   ACCCCA
                                 G     CCG
GAM678  ELAVL3  5'  GAGGGGGGCTCCGGGGGT   10884    A     _____
                                GA GGGGGGT   GGGGT
                                || |||||||   |||||
                                CT CCCCCCG   CCCCA
                                 _      AGGC
GAM678  EPB41   3'  AGAAGGGCAGAGTTGGGGT   20763      G ___
                                AGAAGGG GG   TGGGGT
                                ||||||| ||   ||||||
                                TCTTCCC TC   ACCCCA
                                    G  TCA
GAM678  GUCY2D  3'  AAGGGGGGTGCCTGGGGT   6762        _____
                                AAGGGGGGT   GGGGT
                                |||||||||   |||||
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                                TTCCCCCCA   CCCCA
                                     CGGA
GAM678  H3FT    3'  TAAAAGAGCCTTTGGGGT   18577       GGG_
                                TAGAAGGG   TGGGGT
                                ||||||||   ||||||
                                ATTTTCTC   ACCCCA
                                     GGAA
GAM678  HOXC10  3'  TAGATGGGGGATGTGGGG   41492    A   __
                                TAGA GGGGG  GTGGGG
                                |||| |||||  ||||||
                                ATCT CCCCC  CACCCC
                                  A    TA
GAM678  HSF4    5'  GGAGGGGTGGGGTAC      40766   _       III
                                GG GGGGTGGGGT  AC
                                || ||||||||||  ||
                                CC CCCCACCCCA  TG
                                 T        III
GAM678  KCNC3   3'  CAGGCAGGGGGGTGGGGTA   22498    AA        III
                                TAG  GGGGGGTGGGGT  A
                                |||  ||||||||||||  |
                                GTC  TCCCCCACCCCA  T
                                  CG         III
GAM678  KCNQ3   5'  AGAAGGGGCGCTCGGGGT   21125       G  __
                                AGAAGGGG GT  GGGGT
                                |||||||| ||  |||||
                                TCTTCCCC CG  CCCCA
                                     G  AG
GAM678  KLK10   3'  TAGGTGGGGGAATGAGGT   15773    AA    _
                                TAG  GGGGGG TGGGGT
                                |||  |||||| ||||||
                                ATC  CCCCCT ACTCCA
                                  CA     T
GAM678  MST1R   3'  CAGAGGCAGCCTTGGGGT   14666    A  G  G__
                                TAGA GG GG   TGGGGT
                                |||| || ||   ||||||
                                GTCT CC TC   ACCCCA
                                  _  G  GGA
GAM678  PLTP    3'  AAGAGGGGCTGAGAGGGGT   26345       _____
                                AAGGGGGGT    GGGGT
                                |||||||||    |||||
                                TTCTCCCCG    CCCCA
                                     ACTCT
GAM678  PPP2CA  3'  TAGAAGGGAGGCCTTGGT    15516         GG_
                                TAGAAGGGGGGT  GGT
                                ||||||||||||  |||
                                ATCTTCCCTCCG  CCA
                                       GAA
GAM678  PSD     3'  CAGAGGGGGACTGATGGT    15778    A    G  _
                                TAGA GGGGG TGG GGT
                                |||| ||||| ||| |||
```

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                                GTCT CCCCT ACT CCA
                                  C    G  A
GAM678  RAC2     3'  TAGGTGGGAGCGCTGGGGT   16131     AA   _ _
                                TAG  GGGGG G TGGGGT
                                |||  ||||| | ||||||
                                ATC  CCCTC C ACCCCA
                                  CA    G G
GAM678  RFX1     3'  AGAAGGGGAAGCAGTGGGGT   16288       ____
                                AGAAGGGG   GGTGGGGT
                                ||||||||   ||||||||
                                TCTTCCCC   TCACCCCA
                                     TTCG
GAM678  RHCG     3'  GAAGGGGAGGGCAGGGGT    32241       __  _
                                GAAGGGG  GGT GGGGT
                                |||||||  ||| |||||
                                CTTCCCC  CCG CCCCA
                                    TC  T
GAM678  SELL     3'  TAAAAGAAGTGGTGGGGT    8512        _
                                TAGAAGGGG GGTGGGGT
                                |||||||| ||||||||
                                ATTTTCTTC CCACCCCA
                                     A
GAM678  SERPINB2 3'  CAGAAGGGCATGGAGGGT    15079       G__  T
                                TAGAAGGG   GG GGGGT
                                ||||||||   || |||||
                                GTCTTCCC   CC TCCCA
                                     GTA  _
GAM678  SLC9A3R1 3'  AGAAGGAAAAAGGTGGGGT   43245       ___
                                AGAAGGG   GGGTGGGGT
                                |||||||   |||||||||
                                TCTTCCT   TCCACCCCA
                                    TTT
GAM678  SMARCB1  3'  AGGGAGGGTGGGGTA       42310     _       III
                                AGGG GGGTGGGGT   A
                                |||| |||||||||   |
                                TCCC CCCACCCCA   T
                                  T        III
GAM678  SOD3     3'  CAGAGGGGGGCCTCGGGGGT   16953     A     ____
                                TAGA GGGGGGT    GGGGT
                                |||| |||||||    |||||
                                GTCT CCCCCCG    CCCCA
                                  _      GAGC
GAM678  STAT1    5'  TAGGCGGGGGCGCGGCGGT   40217     AA   _   _
                                TAG  GGGGG GTGG GGT
                                |||  ||||| |||| |||
                                ATC  CCCCC CGCC CCA
                                  CG    G   G
GAM678  UBE2I    5'  CAGAAATCGGGGGTGGGGT    17814       __
                                TAGAAG  GGGGGTGGGGT
                                ||||||  ||||||||||
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                                GTCTTT  CCCCCACCCCA
                                   AG
GAM678  USF2     3'  CAGAAACAAGAGGTGGGGT   17894       __
                                TAGAAG  GGGGGTGGGGT
                                ||||||  ||||||||||
                                GTCTTT  TCTCCACCCCA
                                   GT
GAM678  VASP     3'  AAGGGGAGTCCCTGGGGT    17911        ____
                                AAGGGGGGT   GGGGT
                                |||||||||   |||||
                                TTCCCCTCA   CCCCA
                                     GGGA
GAM678  ZNF278   3'  AAGGAGTTGGAGTGGGGT    36783      ____
                                AAGG   GGGGTGGGGT
                                ||||   ||||||||||
                                TTCC   CCTCACCCCA
                                  TCAA
GAM679  COL4A2   3'  GATGCAAATTCCTTTGGT    12316     AG  GC
                                GAT  AGA  TCCTTTGGT
                                |||  |||  |||||||||
                                CTA  TTT  AGGAAACCA
                                  CG  A_
GAM679  SLA      3'  ACCAGGGAGGGGTTCCTTTGGT 27562      A ATA  AGC_
                                ACCA G  GAG   TCCTTTGGT
                                |||| |  |||   |||||||||
                                TGGT C  CTC   AGGAAACCA
                                  _ C__  CCCA
GAM679  APG5L    3'  AATTTCCATTCCAGAATATCT  22129        CT ____
                                AATTTCCAT  C   TATCT
                                |||||||||  |   |||||
                                TTAAAGGTA  G   ATAGA
                                     AG TCTT
GAM679  ARHGEF12 3'  TCTAAAATTTTTAATCCCATTC 31651         CC_   TA
          T                      TCTAAAATTT  ATCTC  TCT
                                |||||||||   |||||  |||
                                AGATTTTAAA  TAGGG  AGA
                                     AAT    TA
GAM679  FLRT2    3'  TCTATAGCCCTTCTCTATCTAA 29856     AAATT  A
                                TCTA    TCC TCTCTATCTAA
                                ||||    ||| ||||||||||||
                                AGAT    GGG AGAGATAGATT
                                  ATC__  A
GAM679  GCMB     3'  AAATTTCCCATATTATCTAA   21909       ATCTC
                                AAATTTCC    TATCTAA
                                ||||||||    |||||||
                                TTTAAAGG    ATAGATT
                                     GTATA
GAM679  PSG1     3'  TCTAAAATTTTCTTTTCTCTA  27914        _ CA_
                                TCTAAAATTT C  TCTCTA
                                ||||||||||  |  ||||||
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                                AGATTTTAAA G   AGAGAT
                                      A AAA
GAM679  RPN2     3'  TCAGAATTTCCATCTTTCTTCT 16394    TAA        __   A
                                TC   AATTTCCATC  TCT TCT
                                ||   ||||||||||  ||| |||
                                AG   TTAAAGGTAG  AGA AGA
                                 TC_         AA   _
GAM680  ARHGAP6  3'  CAGGTTTGTGACTCCCAGTATA 30209     C     A  GC  TG
                                CAG GTTTGT AC  TT  GTATA
                                ||| |||||| ||  ||  |||||
                                GTC CAAACA TG  GG  CATAT
                                  _     C  A_  GT
GAM681  ILVBL    3'  TCAGGGAGGTTGTGGAGTC    27770     A C       A  C
                                TCA G GAGGTTGT GA GTT
                                ||| | |||||||| || |||
                                AGT C CTCCAACA CT CAG
                                  _ C       C  _
GAM681  PCLO     3'  TCAGTGAGGTTGCATTGCC    45306     A C       GAC
                                TCA G GAGGTTGTA   GTT
                                ||| | |||||||||   |||
                                AGT C CTCCAACGT   CGG
                                  _ A       AA_
GAM682  ALG6     5'  AGGGAGGGGAAGAAAACA    30032    C  A    CACT
                                AG GA GGGGA    AGAAAACA
                                || || |||||    ||||||||
                                TC CT CCCCT    TCTTTTGT
                                 C  _    _____
GAM682  AP2M1    3'  AGCAGGAGGGAGGAGACAC    19817     __  ___
                                AGC  GA   AGGGGACAC
                                |||  ||   |||||||||
                                TCG  CT   TCCTCTGTG
                                  TC  CCC
GAM682  CDKN1B   5'  GAGGGGGAGAAAAACAC     19797    A    CACTA
                                GA GGGGA    GAAAACAC
                                || |||||    ||||||||
                                CT CCCCT    TTTTTGTG
                                 C    C_____
GAM682  CHRNA3   3'  GAGGACACAGCTAGAAGGCAC  8836         ___    AA
                                GGGGACAC   TAGAA  CAC
                                ||||||||   |||||  |||
                                CTCCTGTG   ATCTT  GTG
                                     TCG    CC
GAM682  CRMP1    3'  AGGAAGGGGGAATGAAAACAC  10592    C      ACACTA
                                AG GAAGGGG     GAAAACAC
                                || |||||||     ||||||||
                                TC CTTCCCC     CTTTTGTG
                                  _      CTTA__
GAM682  DDX11    3'  AGGGAGGGGCCGAAAACA    36165    C  A    ACACTA
                                AG GA GGGG     GAAAACA
                                || || ||||     |||||||
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                                TC CT CCCC     CTTTTGT
                                 C  _   GG____
GAM682  DPYSL2   3'  GCAAGGGAGGAAAAC      10752     A   ACACTA
                                GCGA GGGG     GAAAAC
                                |||| ||||     ||||||
                                CGTT CCTC     CTTTTG
                                  C  _______
GAM682  HDAC4    3'  ACGGAGGGGAAAAAC      25742     A    CACTAG
                                GCG AGGGGA     AAAAC
                                ||| ||||||     |||||
                                TGC TCCCCT     TTTTG
                                 C     _______
GAM682  HMGA1    3'  AGTGAAGGAGCAGAGA      44159    C      A  CT
                                AG GAAGGGG CA  AGA
                                || ||||||| ||  |||
                                TC CTTCCTC GT  TCT
                                 A      _  C_
GAM682  IGJ      3'  AGCGGGGGGGAATGCGAGGAAC 40341      AA    CACTA  A_
            A                    AGCG  GGGGA    GA  AACA
                                ||||  |||||    ||  ||||
                                TCGC  CCCCT    CT  TTGT
                                  CC    TACG_  CC
GAM682  INSR     3'  GGGGAACGAAAAAACAC     43378      C  T
                                GGGGA AC AGAAAACAC
                                ||||| || |||||||||
                                CCCCT TG TTTTTTGTG
                                   _  C
GAM682  JDP1     3'  AGTCAAGGGTAAGAAAACA   34758    CG    GACACT
                                AG  AAGGG     AGAAAACA
                                ||  |||||     ||||||||
                                TC  TTCCC     TCTTTTGT
                                 AG    AT____
GAM682  MADH7    3'  AGGGAAGGGGACTGCTAA    25360    C       A_
                                AG GAAGGGGAC  CTAG
                                || |||||||||  ||||
                                TC CTTCCCCTG  GATT
                                 C        AC
GAM682  MPP2     3'  AGGGAGGGAACAGAGGAA    40792    C  A      CTA
                                AG GA GGGGACA   GAA
                                || || |||||||   |||
                                TC CT CCCTTGT   CTT
                                 C  _      CTC
GAM682  NAP1L3   3'  AGTGAAAGGGAAGGTAGAACAC 21209    C       CAC    A
                                AG GAAGGGGA   TAGAA AC
                                || ||||||||   ||||| ||
                                TC CTTTCCCT   ATCTT TG
                                 A       TCC    G
GAM682  NCOA3    3'  AGGAGGGGGGGAAAAAC      27211    C  A   ACACTA
                                AG GA GGGG     GAAAAC
                                || || ||||     ||||||
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                                TC CT CCCC     TTTTTG
                                 _ C   C_____
GAM682  NR2F2   5' AGCGAGTGGGAGCAGAA    34230      AG   CAC
                                AGCGA GGGA  TAGAA
                                ||||| |||| |||||
                                TCGCT CCCT  GTCTT
                                   CA   C__
GAM682  PTP4A2  3' AGGGGGCAGTTTGGAAAACAC 38620      A CTA__
                                AGGGG CA    GAAAACAC
                                ||||| ||    ||||||||
                                TCCCC GT    CTTTTGTG
                                   C  CAAAC
GAM682  PXN     3' ACGGAGGAAGTGACTAGAAAAC 16024    A   AC_
           A                     GCG AGGGG  ACTAGAAAACA
                                ||| |||||  ||||||||||
                                TGC TCCTT  TGATCTTTTGT
                                  C    CAC
GAM682  RNASE6  5' AGGGAAGGGGAAGAAA     24721    C      CACT
                                AG GAAGGGGA   AGAAA
                                || ||||||||   |||||
                                TC CTTCCCCT   TCTTT
                                 C      ____
GAM682  SCD     3' AGTGAAGGGGCACAAC     22819    C     A  TAGAA
                                AG GAAGGGG CAC    AAC
                                || ||||||| |||    |||
                                TC CTTCCCC GTG    TTG
                                 A     _  _____
GAM682  SLC29A1 3' GAGGGGGACATGGAAAAAACAC 22413    A     CT_
                                GA GGGGACA  AGAAAACAC
                                || |||||||  |||||||||
                                CT CCCCTGT  TTTTTTGTG
                                 C      ACC
GAM682  SMT3H1  3' AGGAGGGGGGGAAAAC     40992    C A   ACACTA
                                AG GA GGGG     GAAAAC
                                || || ||||     ||||||
                                TC CT CCCC     CTTTTG
                                 _ C   C_____
GAM682  SSX2    3' AGTGAGGGGAGCTTGACCAG  45529    C A   C____
                                AG GA GGGGA    ACTAG
                                || || |||||    |||||
                                TC CT CCCCT    TGGTC
                                 A _    CGAAC
GAM682  TEK     3' AGTGAAAGGGAAACAGA    7850    C      C T
                                AG GAAGGGGA AC AGA
                                || |||||||| || |||
                                TC CTTTCCCT TG TCT
                                 A      T _
GAM682  TNFSF4  3' AGTTAAGGGGACATTTCAACTA 17747    CG      _______
           AA                    AG  AAGGGGAC     ACTAGA
                                ||  ||||||||     ||||||
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                                TC  TTCCCCTG     TGATTT
                                 AA       TAAAGT
GAM682  WASF1    3'  GAAGGGGATACTGCTAAACA  19445        C   AGA
                                GAAGGGGA ACT   AAACA
                                |||||||| |||   |||||
                                CTTCCCCT TGA   TTTGT
                                     A   CGA
GAM683  MTF1     3'  TAACCTTAGTTTCCAAGT    25544      G   C_
                                TAACC TAG  TCTAAGT
                                ||||| |||  |||||||
                                ATTGG ATC  AGGTTCA
                                   A   AA
GAM683  RFC3     3'  ACTCTAAAGTCTCTAAGTT   16283    C    CCGT  _
                                AC CTAA    AG CTCTAAGTT
                                || ||||    || |||||||||
                                TG GATT    TC GAGATTCAA
                                 A   _____  A
GAM683  SVIL     5'  CCTCGTTCCTCTAAGTT     34725     AAC   AG
                                CCT   CGT  CTCTAAGTT
                                |||   |||  |||||||||
                                GGA   GCA  GAGATTCAA
                                  ___   AG
GAM683  TFRC     3'  CAACCCTAACTGTAGAAAAG  17426         C    CTCT
                                TAACCCTAAC GTAG    AAG
                                |||||||||| ||||    |||
                                GTTGGGATTG CATC    TTC
                                      A    TT__
GAM683  ZNF10    3'  CTAACCATCATTTCTAGGTT   31734        AGC_    A
                                CTAACCGT    TCTA GTT
                                ||||||||    |||| |||
                                GATTGGTA    AGAT CAA
                                     GTAA    C
GAM684  ADCY8    5'  ACGCAGCGGCAGTGGC      9994       CAGA  GAA    C
                                GCGCA    GC   GGCAG GGC
                                |||||    ||   ||||| |||
                                TGCGT    CG   CCGTC CCG
                                  _____ ___     A
GAM684  DVL3     5'  GCGCGGCGCGGCCCAGCGGCT  20684     ACAGA   AA  __
                                GCGC    GCG  GGC  AGCGGCT
                                ||||    |||  |||  |||||||
                                CGCG    CGC  CCG  TCGCCGA
                                  C_____  G_   GG
GAM684  FMR2     5'  GCGGCGGCGGCAGCGG      12968     CACAGA   AA
                                GCG     GCG  GGCAGCGG
                                |||     |||  ||||||||
                                CGC     CGC  CCGTCGCC
                                  _______  CG
GAM684  HAP1     3'  GCTGCAGAGCGAGGGCCGG   19501    GCA       A   AG
                                GC   CAGAGCGA GGC  CGG
                                ||   |||||||| |||  |||
```

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                                CG  GTCTCGCT CCG  GCC
                                 AC_      C  __
GAM684  KCNF1   5'  GCAGAGAGCGAACTTGGGCT  13833    C      GGCAGC
                                GCA AGAGCGAA    GGCT
                                ||| ||||||||    ||||
                                CGT TCTCGCTT    CCGA
                                  C      GAAC__
GAM684  KRTHB6  3'  GCAGGCAGCGGGCGGCGGCT  14034    CAG   AA  A
                                GCA  AGCG  GGC GCGGCT
                                |||  ||||  ||| ||||||
                                CGT  TCGC  CCG CGCCGA
                                  CCG   __  C
GAM684  LMCD1   5'  GCGCAGCGGGGACAGCGGC  31045     CAGA  AA
                                GCGCA   GCG  GGCAGCGGC
                                |||||   |||  |||||||||
                                CGCGT   CGC  CTGTCGCCG
                                   _____  CC
GAM684  MYO6    5'  GCGGGAGCGAAGGCAG     22664    CACA
                                GCG   GAGCGAAGGCAG
                                |||   ||||||||||||
                                CGC   CTCGCTTCCGTC
                                  C___
GAM684  NEUROD2 5'  CAGGGAGCGGGGGCAGCGGCT  26057   CA    AA
                                CA  GAGCG  GGCAGCGGCT
                                ||  |||||  ||||||||||
                                GT  CTCGC  CCGTCGCCGA
                                 CC    CC
GAM684  PK428   5'  GCGCACAGAGGCGGAGGC    18806         _  A
                                GCGCACAGAG CG AGGC
                                |||||||||| || ||||
                                CGCGTGTCTC GC TCCG
                                      C  C
GAM684  PLD1    5'  GCTGCAGGGCGAAGGGGCCGCT 15375   GCA   A     CA  G
                                GC   CAG GCGAAGG  GC GCT
                                ||   ||| |||||||  || |||
                                CG   GTC CGCTTCC  CG CGA
                                 AC_   C      C_  G
GAM684  PPIL1   3'  GCACAGAGTTAAGAGGGCT   31998       CG   GC  C
                                GCACAGAG  AAG  AG GGCT
                                ||||||||  |||  || ||||
                                CGTGTCTC  TTC  TC CCGA
                                    AA  __  _
GAM684  PTAFR   5'  GCCTGTAGCAGGGGCAGCGGCT 9629    ACAG   AA
                                GC   AGCG  GGCAGCGGCT
                                ||   ||||  ||||||||||
                                CG   TCGT  CCGTCGCCGA
                                 GACA   CC
GAM684  RFX2    5'  GCGGCGGCGGCAGCGG     8452     CACAGA  AA
                                GCG    GCG  GGCAGCGG
                                |||    |||  ||||||||
```

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                                CGC     CGC  CCGTCGCC
                                  _______  CG
GAM684  SNX9     5'  GCAAGGGCGAGGGCGGCGGCT  32156     C  A    A   A
                                GCA AG GCGA GGC GCGGCT
                                ||| || |||| ||| ||||||
                                CGT TC CGCT CCG CGCCGA
                                  _ C    C   C
GAM684  WNT4     5'  GCGCCCGGCCCGGGGCAGCGGC 36256      ACAGA  GAA_
           T                     GCGC    GC   GGCAGCGGCT
                                ||||    ||   ||||||||||
                                CGCG    CG   CCGTCGCCGA
                                  GGC__  GGCC
GAM684  YWHAG    5'  GCGAGCAGCTGAGGCGGCGGCT 29794     CAC  _   GA   A
                                GCG   AG AGC  AGGC GCGGCT
                                |||   || |||  |||| ||||||
                                CGC   TC TCG  TCCG CGCCGA
                                  ___  G   AC   C
GAM685  EEF1A2   3'  GCCCGGGGTTCGGAGCGC    41519       TC   T_
                                GCCCGGG  TCGG  CGT
                                |||||||  ||||  |||
                                CGGGCCC  AGCC  GCG
                                    CA   TC
GAM685  SERPINE2 5'  GCCTGGTCTCGGCGGCGC    44004     CG      T  TTCA
                                GCC  GGTCTCGG CG   CGC
                                |||  |||||||| ||   |||
                                CGG  CCAGAGCC GC   GCG
                                  A_       _ C___
GAM686  ADAMTS1  3'  TGGCAAGATACGCTGGAT    28115        _ _  C
                                TGGCGAGG GC CT GGAT
                                |||||||| || || ||||
                                ACCGTTCT TG GA CCTA
                                    A  C  _
GAM686  DNA2L    3'  TAGCAAAATGGGCTTTGGAT   45037       ___   CTC
                                TGGCGA   GGGC   GGAT
                                ||||||   ||||   ||||
                                ATCGTT   CCCG   CCTA
                                   TTA    AAA
GAM686  MEN1     3'  TGGCAAGGATTTCTTGGAT   39238        C__  C
                                TGGCGAGGG   CT GGAT
                                |||||||||   || ||||
                                ACCGTTCCT   GA CCTA
                                     AAA  A
GAM687  GPX3     3'  GAGCTGGTTTTTCCTTTGG   13278     CA      AGA
                                GAGC  GTTTTTTC   TGG
                                ||||  ||||||||   |||
                                CTCG  CAAAAAGG   ACC
                                  AC       AA_
GAM687  MECP2    3'  TGGCTAGTTTGGCACTGATGGA 22619    A  C    TTTCA_
           TT                    TG GC AGTTT     GATGGATT
                                || || |||||     ||||||||
```

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                                AC CG TCAAA     CTACCTAA
                                 _ A    CCGTGA
GAM688  ABCD2    5'  TCTCTTCCACTGTTGTGTT   23152     G    TTTC_
                                TCT CTTCT    TGTGTT
                                ||| |||||    ||||||
                                AGA GAAGG    ACACAA
                                  _    TGACA
GAM688  ADD2     3'  TCTCCTTCTTTTTGCTCT    32737     G      CTG
                                TCT CTTCTTTT   TGTTCT
                                ||| ||||||||   ||||||
                                AGA GAAGAAAA   ACGAGA
                                  G      ___
GAM688  ANKRA2   5'  TCTCTCCTTTTTTTTAATATT  35757      G  C   CT
                                TCTCT CTT TTTT  GTGTT
                                ||||| ||| ||||  |||||
                                AGAGA GAA AAAA  TATAA
                                   G   A    AT
GAM688  BACH1    3'  TCTGCTTCTTTTATAATC    10152         TC   T
                                TCTGCTTCTTT  TGTG TC
                                ||||||||||  |||| ||
                                AGACGAAGAAA  ATAT AG
                                      __   T
GAM688  BICD1    3'  TCTGTGCTTCGTGTTC     11840     C     TTTTCT
                                TCT TGCTTC     GTGTTC
                                ||| ||||||     ||||||
                                AGA ACGAAG     CACAAG
                                  C     _______
GAM688  CA14     5'  TCTCTGCTTTTCTTGCTGTCTC 29061        C   _   G
                                TCTCTGCTT TTTT CTGT TTC
                                ||||||||| |||| |||| |||
                                AGAGACGAA AGAA GACA GAG
                                     A   C   _
GAM688  CALD1    3'  TCTCTCTTCTTTTCAATACTTT 37630      G       TGTG__
                C                TCTCT CTTCTTTTC     TTC
                                 ||||| |||||||||     |||
                                 AGAGA GAAGAAAAG     AAG
                                   _       TTATGA
GAM688  CBFA2T1  3'  TCTCTGCTCTCTTTTCAGTTCT 20310        _     TGT
                C                TCTCTGCT TCTTTTC   GTTCTC
                                 ||||||| |||||||   ||||||
                                 AGAGACGA AGAAAAG   CAAGAG
                                    G      T__
GAM688  CKTSF1B1 3'  TCAGCTTCTTTCCCTTTTC   30089    T       GTG
                                TC GCTTCTTTTCT   TTC
                                || ||||||||||   |||
                                AG CGAAGAAAGGG   AAG
                                 T         AA_
GAM688  CPD      3'  TCTCTCTTCTTAATGCAGTGTT 10561      G     TTCT__
                CTC                TCTCT CTTCTT     GTGTTCTC
                                   ||||| ||||||     ||||||||
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                                AGAGA GAAGAA     CACAAGAG
                                  _     TTACGT
GAM688  CREBL2   3'  TCTCTACTCCTGTGTT     10587         CTTTT
                                TCTCTGCTT    CTGTGTT
                                |||||||||    |||||||
                                AGAGATGAG    GACACAA
                                     _____
GAM688  CYP1B1   3'  TCTTTCCTTCTTTTCAGTGTT  6455     CTG       T
                                TCT   CTTCTTTTC GTGTT
                                |||   ||||||||| |||||
                                AGA   GAAGAAAAG CACAA
                                  AAG       T
GAM688  CYP4F3   3'  TCTTTTCTTTTCTTTCT    9458     GC       GTG
                                TCT  TTCTTTTCT   TTCT
                                |||  |||||||||   ||||
                                AGA  AAGAAAAGA   AAGA
                                  A_       ___
GAM688  DSG1     5'  TCTCTGTTCTTTTCCTTTCTC  12603       C       GTG
                                TCTCTG TTCTTTTCT   TTCTC
                                ||||||| |||||||||   |||||
                                AGAGAC AAGAAAAGG   AAGAG
                                   _       A__
GAM688  DYRK1A   3'  CTGCTTCTTTTCTAGGCTTCT  38992           T  _
                                CTGCTTCTTTTCTG GTT CT
                                |||||||||||||| ||| ||
                                GACGAAGAAAAGAT CGA GA
                                      C  A
GAM688  EGFL6    3'  TCTGTGCTTTTTTTTCTATTTT 31778     C    C_      G
            C                    TCT TGCTT  TTTTCTGT TTC
                                ||| |||||  |||||||| |||
                                AGA ACGAA  AAAAGATA AAG
                                  C    AA       A
GAM688  FBXW7    3'  TCTCTTCTTCTTTTCCTTCT   37969      G       GTG
                                TCTCT CTTCTTTTCT   TTCT
                                ||||| ||||||||||   ||||
                                AGAGA GAAGAAAAGG   AAGA
                                   A        ___
GAM688  GPC6     3'  TCTCTGTTTGCTTTTTTGT    25045       C  _    C
                                TCTCTG TT CTTTT TGT
                                |||||| || ||||| |||
                                AGAGAC AA GAAAA ACA
                                    A  C    A
GAM688  HUNK     3'  TCTCTGATTTCTCTGTGTTCT  31084       CTTC
                                TCTCTG   TTTTCTGTGTTCT
                                ||||||   ||||||||||||||
                                AGAGAC   AAGAGACACAAGA
                                   TA__
GAM688  MBP      3'  TCTGTTTTCATGTTCT     44896     CTTC    T
                                TCTG   TTTTC GTGTTCT
                                ||||   ||||| |||||||
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                              AGAC    AAAAG TACAAGA
                                ____    _
GAM688  MEIS2    5'  TCTCTTTTTTCCTCTTCT    33545      GC__
                              TCTCT    TTCTTTTCT
                              |||||    |||||||||
                              AGAGA    AGGAGAAGA
                                 AAAA
GAM688  MOX2     3'  TCTCTGTATTCTTTCTTCT    42525      C_     CTGTG
                              TCTCTG  TTCTTTT    TTCT
                              ||||||  |||||||    ||||
                              AGAGAC  AAGAAAG    AAGA
                                 AT      _____
GAM688  MTMR6    3'  TCTCTTTTTTTTTCTATATT   45282      GC  C
                              TCTCT  TT TTTTCTGTGTT
                              |||||  || ||||||||||
                              AGAGA  AA AAAAGATATAA
                                 A_  A
GAM688  PSG1     5'  TCTCTGCTGCTTGTGTGTTCTC 27915       T   TTC
                              TCTCTGCT CTT   TGTGTTCTC
                              |||||||| |||   |||||||||
                              AGAGACGA GAA   ACACAAGAG
                                   C   C__
GAM688  PSG2     5'  TCTCTGCTGCCTGTGTGTTCTC 36312       T   TTC
                              TCTCTGCT CTT   TGTGTTCTC
                              |||||||| |||   |||||||||
                              AGAGACGA GGA   ACACAAGAG
                                   C   C__
GAM688  PSG4     5'  TCTCTGCTGCTTGTGTGTTCTC 15800       T   TTC
                              TCTCTGCT CTT   TGTGTTCTC
                              |||||||| |||   |||||||||
                              AGAGACGA GAA   ACACAAGAG
                                   C   C__
GAM688  PSG6     5'  TCTCTGCTGTCTGTGTGTTCTC 15805       _   TTTC
                              TCTCTGCT TCT    TGTGTTCTC
                              |||||||| |||    |||||||||
                              AGAGACGA AGA    ACACAAGAG
                                   C   C___
GAM688  PSG9     5'  TCTCTGCTGCCTGTGTGTTCTC 15812       T   TTC
                              TCTCTGCT CTT   TGTGTTCTC
                              |||||||| |||   |||||||||
                              AGAGACGA GGA   ACACAAGAG
                                   C   C__
GAM688  RAP1     3'  TTCTTTTCTTTTTATCCCC    33270       G__
                              TTCTTTTCT   TGTTCTC
                              |||||||||   |||||||
                              AAGAAAAGA   ATAGGGG
                                   AAA
GAM688  SALL2    5'  TCTCTGATTCTCTGTTCT    41903      C    TTCTG
                              TCTCTG TTCTT    TGTTCT
                              |||||| |||||    ||||||
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                                AGAGAC AAGAG    ACAAGA
                                   T   _____
GAM688  SHOX2    3'  TGCTCCTTGGTTCT       27842       TTTC  T
                                TGCTTCT   TG GTTCT
                                |||||||   || |||||
                                ACGAGGA   AC CAAGA
                                    ____ _
GAM688  SLC6A3   3'  TCTTCTGCTTTGTTGTTTGTGT 9815     _     CTTTTC_
           T                     TCT CTGCTT      TGTGTT
                                |||  ||||||      ||||||
                                AGA GACGAA      ACACAA
                                  A     ACAACAA
GAM688  TMPRSS3  3'  CTGCTTCTTTTGTTCT      37062         TCTG
                                CTGCTTCTTT   TGTTCT
                                ||||||||||   ||||||
                                GACGAAGAAA   ACAAGA
                                    _____
GAM689  EPHB6    3'  TCCAGGGCTGAGTCACGGGTAT 20802         CTG__  A
           C                     TCCAGGGCT    AC GGTATC
                                |||||||||    || ||||||
                                AGGTCCCGA    TG CCATAG
                                     CTCAG  C
GAM689  LHX5     5'  TTCCGGGCTTCCCCAGGTATC  35326     A    _ GA
                                TTCC GGGCT CT  CAGGTATC
                                |||| ||||| ||  ||||||||
                                AAGG CCCGA GG  GTCCATAG
                                  _    A  G_
GAM689  PUNC     3'  CTCCAACTCCTGATGGGT    44880       GG T   CA
                                TTCCAG  C CTGA  GGT
                                ||||||  | ||||  |||
                                GAGGTT  G GACT  CCA
                                   GA _   AC
GAM690  CTGF     3'  TAATATACATTCTGGTGCTGTG 12504        CGCCA  C  C
                                TAATATAC    TGG GC GTG
                                ||||||||    ||| || |||
                                ATTATATG    ACC CG CAC
                                     TAAG_  A  A
GAM691  ABCD2    5'  CCCCAGCAAATGTTTTA     23149      T
                                CCCCA GCAAATGTTTTA
                                ||||| ||||||||||||
                                GGGGT CGTTTACAAAAT
                                  _
GAM691  FBLN1    3'  CCCCGTGGGGCCAGGGT     27048     A  CAAAT  TT
                                CCCC TG    GT  TAGGGT
                                |||| ||    ||  ||||||
                                GGGG AC    CG  GTCCCA
                                  C  CC___  __
GAM691  FLRT2    3'  CCCATGCAGCTGGAATGGTA  29843        AA  TTTTAG
                                CCCATGCA  TG     GGTA
                                ||||||||  ||     ||||
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                                GGGTACGT  AC     CCAT
                                    CG  CTTA__
GAM691  HSPA8   3'  CCCCTGTGCATATGTTCCA   27324     CA   A
                                CCCC  TGCA ATGTTTTA
                                ||||  |||| ||||||||
                                GGGG  ACGT TACAAGGT
                                  AC   A
GAM691  KCNA6   5'  CCCGTGCGCCCTCTTTAGGGT  13809     A   AAATG
                                CCC TGC    TTTTAGGGT
                                ||| |||    |||||||||
                                GGG ACG    GAAATCCCA
                                 C   CGGGA
GAM691  KIF3C   5'  CCGCATGCAGCCTCCTAGGGT  13949    C     AATG
                                CC CATGCA   TTTTAGGGT
                                || ||||||   |||||||||
                                GG GTACGT   AGGATCCCA
                                 C     CGG_
GAM691  NEFH    3'  CCCATGCAGTCTGGGGT     34345        AAT   TA
                                CCCATGCA   GTTT  GGGT
                                ||||||||   ||||  ||||
                                GGGTACGT   CAGA  CCCA
                                    ____   C_
GAM691  SFRP1   3'  CCCTGCAGGCTGCCTAGGGT   16570     A   AA_    T
                                CCC TGCA   TGTTT AGGGT
                                ||| ||||   ||||| |||||
                                GGG ACGT   ACGGA TCCCA
                                  _   CCG    _
GAM691  SH3BP5  3'  CCCATACAAACTGAGGGT    22122          GTTTT
                                CCCATGCAAAT    AGGGT
                                ||||||||||     |||||
                                GGGTATGTTTG    TCCCA
                                      AC___
GAM692  ADAM19  3'  GGAGATTTTTGGAGATGTGG  37770        C  C    GCA
                                GGAGATTT TG AGGT   GTGG
                                |||||||| || ||||   ||||
                                CCTCTAAA AC TCTA   CACC
                                    A  C   ____
GAM692  CDH1    3'  GGAGCTGGGCAGGTGCAGTGG  20367     ATTTCT
                                GGAG     GCAGGTGCAGTGG
                                ||||     ||||||||||||||
                                CCTC     CGTCCACGTCACC
                                  GACC__
GAM692  CRACC   3'  AGGAGATTTCTCAGCAGTG   34515          G  GGT
                                AGGAGATTTCT CA   GCAGTG
                                |||||||||| ||   ||||||
                                TCCTCTAAAGA GT   CGTCAC
                                      _  ____
GAM692  EIF2C1  3'  AGAGATTTCTGGCTGGTG    29165          _ A
                                GGAGATTTCTG C GGTG
                                |||||||||| | ||||
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                                TCTCTAAAGAC G CCAC
                                      C A
GAM692  GAPD    3'  GGAGATTCAGTGTGGTG    13052       CTGCA   CA
                                GGAGATTT    GGTG  GTG
                                ||||||||    ||||  |||
                                CCTCTAAG    TCAC  CAC
                                    _____   AC
GAM692  GPR44   3'  GAGACGGGGTGCAGTGG    21954     TTCTGCA
                                GAGAT     GGTGCAGTGG
                                |||||     ||||||||||
                                CTCTG     CCACGTCACC
                                  CC_____
GAM692  GRB14   5'  GAGCGCTCTGCAGGTGTGGTGG 21033    AT        CA
                                GAG  TTCTGCAGGTG  GTGG
                                |||  ||||||||||  ||||
                                CTC  GAGACGTCCAC  CACC
                                  GC        AC
GAM692  SECTM1  3'  AAGAGGCTCGGCAGGTGCGGTG 16533     AT   T      A
          G                      AGGAG  TTC GCAGGTGC GTGG
                                |||||  ||| ||||||||  ||||
                                TTCTC  GAG CGTCCACG CACC
                                  C_  C       C
GAM692  SLC7A1  3'  AGGTGGTTTCTGTTGCACTGG  16806    AGA    CAGG   G
                                AGG   TTTCTG    TGCA TGG
                                |||   ||||||    |||| |||
                                TCC   AAAGAC    ACGT ACC
                                  ACC     A___    G
GAM693  AKAP2   3'  AACATAATAGAGCTT      28490       TACTC
                                AACATA    ATAGAGCTT
                                ||||||    |||||||||
                                TTGTAT    TATCTCGAA
                                    _____
GAM693  LILRB4  3'  AACAACACACACTGGGGCTT  27772          CATAGA
                                AACAACATATACT     GCTT
                                ||||||||||||      ||||
                                TTGTTGTGTGTGA     CGAA
                                      CCC___
GAM693  NCKAP1  3'  AACAACATATGCTGCTGCTC  30249         A  CATAGA
                                AACAACATAT CT     GCTT
                                ||||||||||  ||      ||||
                                TTGTTGTATA GA     CGAG
                                     C  CGA___
GAM693  NEBL    3'  AACATGTACTACAAAAGCTTA  26893      A   _  T
                                AACAT TACT CA AGAGCTTA
                                ||||| |||| || ||||||||
                                TTGTA ATGA GT TTTCGAAT
                                  C    T  _
GAM693  SOX9    3'  ATATATCATAAAGCTTA     7372       C
                                ATATA TCATAGAGCTTA
                                ||||| ||||||||||||
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                                TATAT AGTATTTCGAAT
                                  _
GAM693  WARS     3'  AACATACACAGGCTT      42619        TCAT  A
                                AACATATAC    AG GCTT
                                |||||||||    || ||||
                                TTGTATGTG    TC CGAA
                                     _____  _
GAM693  ABCF1    3'  GTGCCTGAATGGTTGCCAG   9908       CATCTA
                                GTGCC     GGTTGCCAG
                                |||||     |||||||||
                                CACGG     CCAACGGTC
                                   ACTTA_
GAM693  ATP1A2   3'  GTGCCTTCTAAGCCAG     8709       CA    GTT
                                GTGCC  TCTAG   GCCAG
                                |||||  |||||   |||||
                                CACGG  AGATT   CGGTC
                                   A_    ____
GAM693  BLAME    3'  GTGCCCATCTCAACCA      33493         AGGTT
                                GTGCCCATCT    GCCA
                                ||||||||||    ||||
                                CACGGGTAGA    TGGT
                                      GT____
GAM693  CDS1     5'  GCCTCCGGTTGCCAG       10399     CA   A
                                GCC  TCT GGTTGCCAG
                                |||  ||| |||||||||
                                CGG  AGG CCAACGGTC
                                  __  _
GAM693  CEACAM5  3'  TGCTCTGTTGCCAGAC      20379     CCA   AG
                                TGC   TCT  GTTGCCAGAC
                                |||   |||  ||||||||||
                                ACG   AGA  CAACGGTCTG
                                  ____  __
GAM693  CRACC    3'  ATGTTCATCTTACGTGCCAGAC 34517     CC    _ G  T
                                GTG  CATCT A GT GCCAGAC
                                |||  ||||| | || |||||||
                                TAC  GTAGA T CA CGGTCTG
                                  AA     A G  _
GAM693  DTX1     5'  CCCTGTTCCCCGCCAGAC    20648     A__   AGG
                                CCC   TCT   TTGCCAGAC
                                |||   |||   |||||||||
                                GGG   AGG   GGCGGTCTG
                                  ACA   ____
GAM693  ESR1     3'  GTGCCCACTGGAACAG      6532         T  A  TTGC
                                GTGCCCA CT GG    CAG
                                ||||||| || ||    |||
                                CACGGGT GA CC    GTC
                                    _ _  TT__
GAM693  GAC1     5'  TGCTCAGTCATTGCCAG     26797     C  _  TAG
                                TGC CA TC   GTTGCCAG
                                ||| || ||   ||||||||
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                              ACG GT AG   TAACGGTC
                                A  C ___
GAM693  GNAI2    3'  GCCCATCCCGCCAG       42650        AGGT
                              GCCCATCT   TGCCAG
                              ||||||||   ||||||
                              CGGGTAGG   GCGGTC
                                   ____
GAM693  GNAT1    3'  GTGCCCCGGCCTTGCCAGAC  6741       ATCTA  __
                              GTGCCC    GGT  TGCCAGAC
                              ||||||    |||  ||||||||
                              CACGGG    CCG  ACGGTCTG
                                 G____  GA
GAM693  GNL1     5'  TGCGTCCAGGTTGCTGGAC   45566    CCA       CA
                              TGC   TCTAGGTTGC  GAC
                              |||   ||||||||||  |||
                              ACG   AGGTCCAACG  CTG
                                C__        AC
GAM693  IDH3A    3'  GTGCCCATTTAGTTTGTCTGGA 24375        C  _______  GCCA
                              GTGCCCAT TAG     GTT   G
                              |||||||| |||     |||   |
                              CACGGGTA ATC     CAG   T
                                   A  AAAIII  ACCG
GAM693  IGFBP3   3'  GCCTGACTTTGCCAGAC    8264     CAT  AGG
                              GCC   CT   TTGCCAGAC
                              |||   ||   |||||||||
                              CGG   GA   AACGGTCTG
                                ACT  ___
GAM693  IL1F5    3'  GTGCCCACTAAGTCAGA    29355       T     TGC
                              GTGCCCA CTAGGT   CAGA
                              ||||||| ||||||   ||||
                              CACGGGT GATTCA   GTCT
                                   _    ___
GAM693  IL1R1    3'  TGCTCTGTTGCCAG       9373     CCA   AG
                              TGC   TCT  GTTGCCAG
                              |||   |||  ||||||||
                              ACG   AGA  CAACGGTC
                                   ___  __
GAM693  IL8RA    3'  GTGCCTGTCCAGAGCCAGA   8442      CA     TT
                              GTGCC  TCTAGG  GCCAGA
                              |||||  ||||||  ||||||
                              CACGG  AGGTCT  CGGTCT
                                AC     __
GAM693  ITIH3    3'  GTGCCCATGTTCCAGA     13634        CTAG   G
                              GTGCCCAT    GTT CCAGA
                              ||||||||    ||| |||||
                              CACGGGTA    CAA GGTCT
                                   _____  _
GAM693  KIF3B    3'  GTGCCCACCTGGGGCC      22039         A  TT
                              GTGCCCATCT GG  GCC
                              |||||||||| ||  |||
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                                CACGGGTGGA CC  CGG
                                      _  C_
GAM693  MPO     3'  GCTCATCTAGGGCAAG      7003     C       TT  C
                                GC CATCTAGG  GC AG
                                || ||||||||  || ||
                                CG GTAGATCC  CG TC
                                 A       __  T
GAM693  NDUFAB1  3'  GTGTCCTCACTGCCAGA     22671     _ _   CTAGGT
                                GTG CC CAT     TGCCAGA
                                ||| || |||     |||||||
                                CAC GG GTG     ACGGTCT
                                  A  A  _______
GAM693  PACE4    3'  GTGTTGTCCAGGCTAGA     15057     CCCA       GCC
                                GTG    TCTAGGTT   AGA
                                |||    ||||||||   |||
                                CAC    AGGTCCGA   TCT
                                  AAC_       ___
GAM693  PIK3R3   3'  GTGCCATCTAAGGCCAG     41446      C      TT
                                GTGCC ATCTAGG  GCCAG
                                ||||| |||||||  |||||
                                CACGG TAGATTC  CGGTC
                                   _      __
GAM693  PRNP     3'  GTGCCCATCAGTGCCAA     7185          TA   T
                                GTGCCCATC  GGT GCCAG
                                |||||||||  ||| |||||
                                CACGGGTAG  TCA CGGTT
                                      __  _
GAM693  SLC22A5  3'  GTGCCCATCCAGGAGCAAGTCA 16863           TT  ____
           GAC                    GTGCCCATCTAGG  GC    CAGAC
                                ||||||||||||||  ||    |||||
                                CACGGGTAGGTCC  CG    GTCTG
                                       T_  TTCA
GAM693  SLC6A12  5'  GCCCATCTGCCCAG       16799        AG  TG
                                GCCCATCT  GT  CCAG
                                ||||||||  ||  ||||
                                CGGGTAGA  CG  GGTC
                                      __  __
GAM693  SOX13    3'  GTGCCCATCGAGTTGGGAC   25015         TA    CCA
                                GTGCCCATC  GGTTG   GAC
                                |||||||||  |||||   |||
                                CACGGGTAG  TCAAC   CTG
                                     C_    C__
GAM693  ZNF214   5'  GTACCCATCTACACGGGT    29911          ____
                                GTGCCCATCTA    GGT
                                ||||||||||||   |||
                                CATGGGTAGAT    CCA
                                       GTGC
GAM694  CA3      3'  TGTGAAATTTTAGATAACAGAA 23222           TACCAA
           AA                     TGTGAAATTTTG     AGAAAA
                                ||||||||||||     ||||||
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                                ACACTTTAAAAT     TCTTTT
                                      CTATTG
GAM694  FZD1    3'  TGTGGAGTTCTGTACCTTAAGA 18620      AAA       A_
                                TGTG   TTTTGTACC  AAGA
                                ||||   |||||||||  ||||
                                ACAC   AAGACATGG  TTCT
                                  CTC        AA
GAM694  IGFBP4  3'  TGTGTAACACCAAAGA     11411      A   TTTGT
                                TGTG AAT    ACCAAAGA
                                |||| |||    ||||||||
                                ACAC TTG    TGGTTTCT
                                  A  _____
GAM694  MTMR7   3'  TGTGAAATATTTGTATTGCACT 42906        _     C__  AA
           GAA                    TGTGAAAT TTTGTA   CA  GAA
                                |||||||| ||||||   ||  |||
                                ACACTTTA AAACAT   GT  CTT
                                     T     AAC  GA
GAM694  NPPB    3'  TGGAAATTTTGTGCTCAAAG  14827    T       AC_
                                TG GAAATTTTGT   CAAAG
                                || ||||||||||   |||||
                                AC CTTTAAAACA   GTTTC
                                 _        CGA
GAM694  PODXL   3'  TGGAAATGGAAGCCCAAAGAA  23985    T    TTTGTA
                                TG GAAAT     CCAAAGAA
                                || |||||     ||||||||
                                AC CTTTA     GGTTTCTT
                                 _    CCTTCG
GAM694  PRKAR1A 3'  TGTGAAATTTTGTTTAAAAAA  15616          ACC
                                TGTGAAATTTTGT   AAAGAA
                                ||||||||||||   ||||||
                                ACACTTTAAAACA   TTTTTT
                                       AA_
GAM694  RPL30   3'  GTGAAATTTTGTAGGTGAAAA  9741           CCAAA
                                GTGAAATTTTGTA    GAAAA
                                ||||||||||||    |||||
                                CACTTTAAAACAT    CTTTT
                                       CCA__
GAM694  TAPBP   3'  TGTGAGATTTTATAACAAAA  17309      A      C
                                TGTGA ATTTTGTA CAAAG
                                ||||| ||||||| |||||
                                ACACT TAAAATAT GTTTT
                                   C       T
GAM694  TGM4    3'  GTGGATGGAATACCAAAGAAA  17465     AAATTTT
                                GTG      GTACCAAAGAAA
                                |||      ||||||||||||
                                CAC      TATGGTTTCTTT
                                  CTACCT_
GAM694  TNFSF15 3'  TGTGAAATTTTGGCCCCAAA  23054          TA_
                                TGTGAAATTTTG   CCAAA
                                ||||||||||||   |||||
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                                ACACTTTAAAAC  GGTTT
                                      CGG
GAM694  TP53BP2  3'  TGTGAAATTTTTGCCAAAA  24065        GTA
                                TGTGAAATTTT  CCAAAG
                                ||||||||||  ||||||
                                ACACTTTAAAA  GGTTTT
                                      AC_
GAM694  TRPM8    3'  TGTAAAATTTTGAAAGA    35864        TACC
                                TGTGAAATTTTG   AAAGA
                                ||||||||||||   |||||
                                ACATTTTAAAAC   TTTCT
                                      ____
GAM694  WNT11    3'  TGAGAAGTGCCACCCCAAAGAA 21543   T  ATT TG A
          AA                     TG GAA  T  T CCAAAGAAAA
                                || |||  |  | ||||||||||
                                AC CTT  G  G GGTTTCTTTT
                                 T  CAC GT G
GAM695  BCL11B   3'  AGAAAAGGTAATAAAAATATTT 39743      AG_
          T                     AGAAAG  AATAAAAATATTTT
                                ||||||  ||||||||||||||
                                TCTTTT  TTATTTTTATAAAA
                                   CCA
GAM695  NRG2     3'  AGAAAATAAAAATATTTT   30361
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM695  SDPR     3'  AGAAAATAAAAATATTTT   21649
                                AGAGAATAAAAATATTTT
                                ||||||||||||||||||
                                TCTTTTATTTTTATAAAA

GAM695  STMN1    3'  AGAAAAAGAGTAAAACACTTT  24515        ATA
                                AGAAAGAGA  AAAATATTTT
                                |||||||||  ||||||||||
                                TCTTTTTCT  TTTTGTGAAA
                                      CA_
GAM696  ITGAV    3'  CATAAAAATTTTACATTTCA  13630         TA
                                CATAAAAATTTT  ATTTCA
                                ||||||||||||  ||||||
                                GTATTTTTAAAA  TAAAGT
                                      TG
GAM697  AOX1     3'  AGCATATCTATCAAATCTAAAT 10106       C   TTT
                                AGCATATC ATCA  TTTAAAT
                                |||||||| ||||  |||||||
                                TCGTATAG TAGT  AGATTTA
                                     A   TT_
GAM697  EMX2     3'  CATCATCATCATTTTTTAA   44678    ATC
                                CAT  CATCATTTTTTAA
                                |||  ||||||||||||
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                                GTA  GTAGTAAAAAATT
                                  GTA
GAM697  HDAC4    5'  TAGCAATGTCCACTCCTTTAA 25780      TA_   CA
                                TAGCA  TCCAT  TTTTTTAA
                                |||||  |||||  ||||||||
                                ATCGT  AGGTG  AGGAAATT
                                   TAC   __
GAM697  THBS1    3'  TAGCATATCTACACAATCT   17513       CAT  TT
                                TAGCATATC  CAT  TTT
                                |||||||||  |||  |||
                                ATCGTATAG  GTG  AGA
                                     AT_  TT
GAM697  UBL3     3'  TAGCATATCAATCTTTAAA   28268       C  ATTT
                                TAGCATATC ATC   TTTAAA
                                |||||||||| |||   ||||||
                                ATCGTATAG TAG   AAATTT
                                     T  ____
GAM697  VNN1     3'  CATCCATCATTTTTTAAAT   21684
                                TATCCATCATTTTTTAAAT
                                ||||||||||||||||||
                                GTAGGTAGTAAAAAATTTA

GAM697  ZNF6     3'  TAGCATATCATATCTCCTAAAT 35091        C  C
                                TAGCATATC AT ATTTTTTAAAT
                                |||||||||  || ||||||||||
                                ATCGTATAG TA TAGAGGATTTA
                                     _  _
GAM697  CA14     3'  TTAAAGTCAGAAACTTTA    29064      A
                                TTAGA TCAGAAACTTTA
                                |||||  ||||||||||||
                                AATTT AGTCTTTGAAAT
                                   C
GAM697  ZFX      3'  TAGAATCAGGGATTACTTTA  18216        AA___
                                TAGAATCAG    ACTTTA
                                |||||||||    ||||||
                                ATCTTAGTC    TGAAAT
                                     CCTAA
GAM698  ACP1     5'  GCGGGGCTGCAGGTTGTC    28238     CTT  C    ACC
                                GCG  GGC TGCAG  GTC
                                |||  ||| |||||  |||
                                CGC  CCG ACGTC  CAG
                                  C__  _    CAA
GAM698  ADAM19   3'  GCTTTGCAAAAACCGTC     37769      G  CTGC
                                GCTT GC   AGACCGTC
                                ||||  ||   ||||||||
                                CGAA CG   TTTGGCAG
                                  A  TT__
GAM698  AXUD1    5'  GCGCTCGGCCCGGCAGCCGTC  37489          _  A
                                GCGCTTGGCCTG CAG CCGTC
                                ||||||||||| ||| |||||
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                                CGCGAGCCGGGC GTC GGCAG
                                       C  _
GAM698  BTRC    3'  GTGCTGAGTAGACCGTC    19479   C  T  CCTGC
                                G GCT GG    AGACCGTC
                                | ||| ||    ||||||||
                                C CGA TC    TCTGGCAG
                                 A  C  A____
GAM698  CASP10  3'  GCTGGCCTGTAGATTGAGTC  37386    T    C  CC__
                                GCT GGCCTG AGA   GTC
                                ||| |||||| |||   |||
                                CGA CCGGAC TCT   CAG
                                  _    A  AACT
GAM698  CCR9    3'  GGCAAGACCTGCAGATCGT   36298   C  TT       C
                                G GC  GGCCTGCAGA CGT
                                | ||  |||||||||| |||
                                C CG  CTGGACGTCT GCA
                                _ TT        A
GAM698  CNP     3'  GCTTGGCCCAGCCTCGTC    37558        _  AGAC
                                GCTTGGCCT GC   CGTC
                                ||||||||| ||   ||||
                                CGAACCGGG CG   GCAG
                                      T  GA__
GAM698  CTMP    3'  GCGCCTGGCCCGAGAGTTGTC  38199          C  CC_
                                GCGCTTGGCCTG AGA  GTC
                                |||||||||||| |||  |||
                                CGCGGACCGGGC TCT  CAG
                                       _  CAA
GAM698  EGR4    3'  GCCTTGGCCTGCCCCAGCCTGT 12675   G       ___  A  _
          C                      GC CTTGGCCTGC  AG CC GTC
                                || ||||||||||  || || |||
                                CG GAACCGGACG  TC GG CAG
                                 _       GGG  _  A
GAM698  EN1     5'  GCGTCTGGCCTGGATCGC    10915    CT     CA  C
                                GCG  TGGCCTG  GA CGT
                                |||  |||||||  || |||
                                CGC  ACCGGAC  CT GCG
                                  AG      __  A
GAM698  KCNK4   3'  CGCAGCGGTGCAGACCGT    37827    T_  CC
                                CGC  TGG  TGCAGACCGT
                                |||  |||  ||||||||||
                                GCG  GCC  ACGTCTGGCA
                                  TC  __
GAM698  KLK10   3'  GCACTTGGCTTGCCCAAAGTC  15771        C  AGACC
                                GCGCTTGGC TGC    GTC
                                ||||||||| |||    |||
                                CGTGAACCG ACG    CAG
                                      A  GGTTT
GAM698  MGAT2   5'  GCCTTGGCCTGTCACGGTC   14449   G       CAG  C
                                GC CTTGGCCTG   AC GTC
                                || |||||||||  || |||
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                                CG GAACCGGAC   TG CAG
                                 _       AG_  C
GAM698  NGFR     3'  GCACTTGGCCTCCCCGT     14777          GCAGA
                                GCGCTTGGCCT    CCGT
                                ||||||||||    ||||
                                CGTGAACCGGA    GGCA
                                      GG___
GAM698  PCDH9    3'  GCTTGGCCAGGTCAGGACTGT  44401        TG__  _  C
                                GCTTGGCC   CAG AC GT
                                ||||||||   ||| || ||
                                CGAACCGG   GTC TG CA
                                     TCCA  C  A
GAM698  SUDD     3'  GCCTGGCCCCCAAATTGT    19260         G   CC
                                GCTTGGCCT CAGA  GT
                                |||||||| ||||  ||
                                CGGACCGGG GTTT  CA
                                      G   AA
GAM699  CACNA2D2 3'  GAGGTGGGAGTGGAGGTGGG  25715     C  CTCGAC
                                GAG GT     GGAGGTGGG
                                ||| ||     |||||||||
                                CTC CA     CCTCCACCC
                                 _  CCCTCA
GAM699  DES      3'  AGGGCGTGGGGAGGTGG     43560    A   CTCGAC
                                AG GCGT     GGAGGTGG
                                || ||||     ||||||||
                                TC CGCA     CCTCCACC
                                 C   CC_____
GAM699  HDGF     3'  AAGGGTGTCAGGAGGTGG    21057     C  C   AC
                                GAG GT TCG  GGAGGTGG
                                ||| || |||  ||||||||
                                TTC CA AGT  CCTCCACC
                                  C  C  __
GAM699  IGFBP5   5'  GTGGAGATGGCGTTGGGGGTGG 8275     A   C  CT  AC  A
           G                     GT GAG GT  CG  GG GGTGGG
                                || ||| ||  ||  || ||||||
                                CA CTC TA  GC  CC CCACCC
                                 C  _  CC  AA  C
GAM699  SELPLG   3'  GAGAGCCCGTGGAGGTGG    40674     C   T  AC
                                GAG GTC CG  GGAGGTGG
                                ||| ||| ||  ||||||||
                                CTC CGG GC  CCTCCACC
                                  T  _  A_
GAM699  SP4      5'  ATAGAGGTGGGTGGGGGGTGGG  17046       C  CTCGAC  A
                                GTAGAG GT     GG GGTGGG
                                |||||| ||     || ||||||
                                TATCTC CA     CC CCACCC
                                   _  CCCAC_  _
GAM699  SSPN     3'  GCTGATGACTGGAGGTGGG   22936    GTCTC  _
                                GC    GAC GGAGGTGGG
                                ||    ||| |||||||||
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                                CG    CTG CCTCCACCC
                                 ACTA_  A
GAM699  SYN3    3' GTCTGCGTTTGATGGAGGTGGG 18566   AGA   CTC  C
                                GT  GCGT  GA GGAGGTGGG
                                ||  ||||  || |||||||||
                                CA  CGCA  CT CCTCCACCC
                                 GA_   AA_ A
GAM699  ZFP36L1 3' GTGGAATGTCTTGAGATGG   22292   A  C   CGACG
                                GT GAG GTCT    GAGGTGG
                                || ||| ||||    |||||||
                                CA CTT CAGA    CTCTACC
                                 C  A   A____
GAM700  ESRRG   5' ACACAAATGTTCTCCTAG    42442     TTAT
                                ACACG   ATGTTCTCCTAG
                                |||||   ||||||||||||
                                TGTGT   TACAAGAGGATC
                                   T___
GAM700  ITGBL1  3' TTCGCATTTATATGTTCT    21990    A  CG
                                TTC CA  TTATATGTTCT
                                ||| ||  ||||||||||||
                                AAG GT  AATATACAAGA
                                 C  A_
GAM700  RGS16   3' TCCACACTTTGTTCTCCT    16327      GTTATA
                                TTCACAC     TGTTCTCCT
                                |||||||     |||||||||
                                AGGTGTG     ACAAGAGGA
                                    AA____
GAM701  DCTN1   3' TGAAGTCCTCAATCA      35704     G     ATGCC
                                TGAAG TCCTCA    ATCA
                                ||||| ||||||    ||||
                                ACTTC AGGAGT    TAGT
                                  _    ______
GAM701  GALNT1  3' TGAAAGTCCTTGATAATCAAA 33842        CA   CC
                                TGAAGGTCCT  ATG  ATCAAG
                                ||||||||||  |||  ||||||
                                ACTTTCAGGA  TAT  TAGTTT
                                      AC  __
GAM701  LANCL1  3' ATGAAGGTTTTTGATGCCA   25849       CCTCA
                                ATGAAGGT    ATGCCA
                                ||||||||    ||||||
                                TACTTCCA    TACGGT
                                    AAAAC
GAM701  PLXNA1  3' ATGAAGGTCCTTGGCCA    43617         CAAT
                                ATGAAGGTCCT   GCCA
                                ||||||||||   ||||
                                TACTTCCAGGA   CGGT
                                      AC__
GAM701  TSSC4   5' ATGAAGGTCCTCAGCGGCAC  25037          A  C
                                ATGAAGGTCCTCA TG CAT
                                |||||||||||| || |||
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                                TACTTCCAGGAGT GC GTG
                                      C  C
GAM701  UBE3A    3'  ACGAAGGTCCCTTTCATCAAG  7858          CAATGC
                                ATGAAGGTCCT     CATCAAG
                                ||||||||||      |||||||
                                TGCTTCCAGGG     GTAGTTC
                                      AAA___
GAM702  ANGPT1   3'  TAATGAAGTTACATGTAT    40243   C    TTTA
                                A GTGA    TTACATGTAT
                                | ||||    ||||||||||
                                A TACT    AATGTACATA
                                 T    TC__
GAM703  CDKN1C   3'  TTGCACAGTTTTCAAAATT    6339           TGT
                                TTGCACAGTTTTT   ATT
                                ||||||||||||   |||
                                AACGTGTCAAAAG   TAA
                                      TTT
GAM703  MKNK2    3'  TTGCAAGTTTTTTGACTT    32764      C       TATT
                                TTGCA AGTTTTTTG    ACTT
                                ||||| |||||||||    ||||
                                AACGT TCAAAAAAC    TGAA
                                   _       _____
GAM703  NFYC     3'  GCACAGTTTTTAATGCATT    30594          __
                                GCACAGTTTTT  TGTATT
                                ||||||||||  ||||||
                                CGTGTCAAAAA  ACGTAA
                                      TT
GAM703  SEDL     3'  GCACAGGCTGTATTACTT    31008       TTTT
                                GCACAG    TTGTATTACTT
                                ||||||    ||||||||||
                                CGTGTC    GACATAATGAA
                                   C___
GAM703  SLC3A2   3'  TTGCAACAGTTTGTTTGT    14403      _     _
                                TTGCA CAGTTT TTTGT
                                ||||| |||||| |||||
                                AACGT GTCAAA AAACA
                                   T     C
GAM703  ZFX      3'  TTGCCAGTTTTCCCTATT    18217      A       G
                                TTGC CAGTTTTTT TATT
                                |||| ||||||||| ||||
                                AACG GTCAAAAGG ATAA
                                   _       G
GAM703  PDGFRA   3'  CCTTTTAAGGTTCAAAAATGGT 26286     C    C   TGT
          T                     CCT TTAAG TTT   GGATGGTT
                                ||| ||||| |||   ||||||||
                                GGA AATTC AAG   TTTACCAA
                                  A    C   TT_
GAM704  CALCRL   3'  TGTGTCAGCAAATGAGTAGA   25129     A        TACAT
                                TGT TCAGCGAATG    GA
                                ||| ||||||||||    ||
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                                ACA AGTCGTTTAC    CT
                                  C        TCAT_
GAM704  CHN2    3'  TGTATCAAGTACCTGTATGAAT 19814       CGAA_   CA
                                TGTATCAG    TGTA  TGAAT
                                ||||||||    ||||  |||||
                                ACATAGTT    ACAT  ACTTA
                                    CATGG   __
GAM704  CREBBP  3'  TGTTAATACCATGTACATGAAT 20431    ATCA  GA
                                TGT   GC  ATGTACATGAAT
                                |||   ||  ||||||||||||
                                ACA   TG  TACATGTACTTA
                                  ATTA  G_
GAM704  GAS2    3'  TATGTCAGCTCATGTATGAAT  23535    A    GA    CA
                                TGT TCAGC  ATGTA  TGAAT
                                ||| |||||  |||||  |||||
                                ATA AGTCG  TACAT  ACTTA
                                  C    AG    __
GAM705  ITGA1   3'  GGATAGATTATTGAATAATTGT 41847   A    C__   T
            TA                    A GTAGAT   TGA TAATTGTTA
                                | ||||||   ||| |||||||||
                                C TATCTA   ACT ATTAACAAT
                                 C     ATA   T
GAM706  ANGPT2  5'  CAAACTTGAGGGCAAAC    10085         AC
                                CAAACTTGAGG  CAAAT
                                ||||||||||  |||||
                                GTTTGAACTCC  GTTTG
                                      C_
GAM706  FKBP1A  3'  AAACTTGAGACTCATAAATG  38272         AC  AAT
                                AAACTTGAGG  CA   AATG
                                ||||||||||  ||   ||||
                                TTTGAACTCT  GT   TTAC
                                     GA  AT_
GAM706  GPR85   3'  AAACTACCAAATAATGC    33254      TGAGG
                                AAACT    ACCAAATAATGC
                                |||||    ||||||||||||
                                TTTGA    TGGTTTATTACG
                                  _____
GAM706  MPP6    5'  CAAACTTCAAATAAT      32390       GAGGAC
                                CAAACTT     CAAATAAT
                                |||||||     ||||||||
                                GTTTGAA     GTTTATTA
                                   _______
GAM706  NELL2   3'  CAGACTTGAGGTCTAATTTTGC 26046    A      ACCA   AA
                                CA ACTTGAGG    AAT  TGC
                                || ||||||||    |||  |||
                                GT TGAACTCC    TTA  ACG
                                 C       AGA_   AA
GAM706  NOL3    3'  CTGAGGACTGGATGATGC    19490        CAA  A
                                TTGAGGAC   AT ATGC
                                ||||||||   || ||||
```

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                                GACTCCTG  TA TACG
                                    ACC  C
GAM706  PROML1   3' CAAATTTAGGGACCAAAC   25684     C  A
                                CAAA TTG GGACCAAAT
                                |||| ||| |||||||||
                                GTTT AAT CCTGGTTTG
                                  A  C
GAM706  UBE2I    5' ACTTGAGGACTCACCATGC   17810        _ AATA
                                ACTTGAGGAC CA   ATGC
                                |||||||||| ||   ||||
                                TGAACTCCTG GT   TACG
                                     A  GG__
GAM706  XK       3' AAACTCACATCCAAATAATGC 34352      AGGA
                                AAACTTG   CCAAATAATGC
                                |||||||   ||||||||||
                                TTTGAGT   GGTTTATTACG
                                    GTA_
GAM707  POH1     5' TTTGTTGAGTTTGACAAATGT 25139       CC  AGAC
                                TTTGTTGAG  TGG   GTGT
                                |||||||||  |||   ||||
                                AAACAACTC  ACT   TACA
                                     AA  GTT_
GAM707  SLC31A1  3' TCTGTTGAGCAGGGGTGTGT  12398       CT  AGAC
                                TTTGTTGAGC  GG   GTGT
                                |||||||||  ||   ||||
                                AGACAACTCG  CC   CACA
                                     T_  CCA_
GAM708  TH1L     3' GCACGAAGTCAGAGGTATA   32308   _
                                GT CGAAGTCAGAGGTATA
                                || ||||||||||||||||
                                CG GCTTCAGTCTCCATAT
                                 T
GAM708  ALOX5AP  3' ACATGACATCATTTTGTTCC  11570       CC___
                                ACATGATATC    GTTCC
                                ||||||||||    |||||
                                TGTACTGTAG    CAAGG
                                     TAAAA
GAM708  ATF7     3' TACATGACAGCCTCC      27793       T  CGT
                                TACATGATA CC   TCC
                                |||||||| ||   |||
                                ATGTACTGT GG   AGG
                                     C  ___
GAM708  DACH     3' TACATAATACCTTCC      38880        CCG
                                TACATGATATC   TTCC
                                ||||||||||   ||||
                                ATGTATTATGG   AAGG
                                       ___
GAM708  GAN      3' TACATGATAGCAATTCC    35149        TCCC
                                TACATGATA   GTTCC
                                |||||||||   |||||
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                                ATGTACTAT   TAAGG
                                     CGT_
GAM708  HDAC5   3'  CACCGACTTCCCGTTCC    40160    A   A
                                TAC TGAT TCCCGTTCC
                                ||| |||| |||||||||
                                GTG GCTG AGGGCAAGG
                                  _   A
GAM708  MLH3    3'  TGAACATCCCTTTGTTCC    30781   T     ___
                                A GATATCCC   GTTCC
                                | ||||||||   |||||
                                A TTGTAGGG   CAAGG
                                 C       AAA
GAM709  MMP8    3'  TATAATCCTTACTTCTAACCAA 14546        CC    ___   T
          AATCT                     TATAATCC  GCTTC   CTA AATCT
                                ||||||||  |||||   ||| |||||
                                ATATTAGG  TGAAG   GGT TTAGA
                                     AA    ATT   T
GAM709  REGL    3'  TCTCCTCCTCTATAATCT    27124    C  G   C
                                TC CC CTTC TATAATCT
                                || || |||| ||||||||
                                AG GG GGAG ATATTAGA
                                 A  A   _
GAM709  FCMD    3'  TAATTAAATGAAATTAAG    27522          TGGGT
                                TAATTAAATGA    AATTAAG
                                ||||||||||    |||||||
                                ATTAATTTACT    TTAATTC
                                      _____
GAM710  ALDH1A3  3'  TACAGCAGTCTTTCCAGTTG   8679     _      C
                                TGC GTAGTCTT CCAGTTG
                                ||| |||||||| |||||||
                                ATG CGTCAGAA GGTCAAC
                                  T       A
GAM710  CSNK1A1  3'  CTGAAGACTGTTCATGCC    12462         ATC  C
                                TTGAAGACT   CA GTC
                                |||||||||   || |||
                                GACTTCTGA   GT CGG
                                     CAA  A
GAM711  EGR4    3'  TGCCTATTCACTGGGTGGTCT  12678        _  GAT  A
                                TGCCTAT TAT   GT GTCT
                                ||||||| |||   || ||||
                                ACGGATA GTG   CA CAGA
                                    A   ACC  C
GAM711  MAK     3'  TTAATGCCTATTCAGAGT    25382          AT  T
                                TTAATGCCTATT  GA GT
                                ||||||||||||  || ||
                                AATTACGGATAA  CT CA
                                       GT  _
GAM712  CHD2    3'  TAAAATGCAAAGTACACTGGA  10448       A    A    AC
                                TAGAAT CAAA TGCGC  GGA
                                |||||| |||| |||||  |||
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                                ATTTTA GTTT ATGTG  CCT
                                   C   C    A_
GAM712  EZH1    3'  GAATACAAACCACGGCGGA   12784        AT   CA
                                GAATACAAA  GCG  CGGA
                                |||||||||  |||  ||||
                                CTTATGTTT  TGC  GCCT
                                     GG   C_
GAM713  ADAM19  3'  CACAGCTCAGGATT      37762       ACGG
                                CACAGCT   CGGGATT
                                |||||||   |||||||
                                GTGTCGA   GTCCTAA
                                    ____
GAM713  CACNA2D2 3'  ACAGCTACCTGATGGGGATT  25701        GGC___
                                ACAGCTAC    GGGATT
                                ||||||||    ||||||
                                TGTCGATG    CCCTAA
                                     GACTAC
GAM713  DGKI    3'  CACAGTTCCCACACAGGATT  21782      ___    G
                                CACAG  CTACG CGGGATT
                                |||||  ||||| |||||||
                                GTGTC  GGTGT GTCCTAA
                                   AAG   _
GAM713  EHD4    3'  CACACTAGGACAGGATT    40206     G  C
                                CACA CTA GGCGGGATT
                                |||| ||| |||||||||
                                GTGT GAT CTGTCCTAA
                                   _  C
GAM713  KCNC3   3'  CACAGCTAATGGGACT     22497       CGGC
                                CACAGCTA   GGGATT
                                ||||||||   ||||||
                                GTGTCGAT   CCCTGA
                                     TA__
GAM713  MYO7A   3'  CACAGCAAACTAGGATT    7026       TAC  _
                                CACAGC  GGC GGGATT
                                ||||||  ||| ||||||
                                GTGTCG  TTG TCCTAA
                                   T__  A
GAM713  PTGS1   3'  CACAGCCACACCTAGATT   38730        GCG
                                CACAGCTACG  GGATT
                                ||||||||||  |||||
                                GTGTCGGTGT  TCTAA
                                     GGA
GAM713  RNMT    5'  CACAGCCAAACGCGATT    19148       C   G
                                CACAGCTA GGCG GATT
                                |||||||| |||| ||||
                                GTGTCGGT TTGC CTAA
                                     _   G
GAM713  SLC6A4  3'  CACAGCAGCACATGGATT   9819       TAC   ___
                                CACAGC  GGCG  GGATT
                                ||||||  ||||  |||||
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                                GTGTCG  TCGT  CCTAA
                                   ___   GTA
GAM713  TACC1   3' CACAGCAGCAAAAAGATT   26590      TA  CG
                                CACAGC  CGG  GGATT
                                ||||||  |||  |||||
                                GTGTCG  GTT  TCTAA
                                   TC   TT
GAM713  TRHDE   3' CACAACTACTAAGAGATT   30103       GGC
                                CACAGCTAC  GGGATT
                                |||||||||  ||||||
                                GTGTTGATG  CTCTAA
                                     ATT
GAM713  USP9Y   5' CACAGCCACCAGAATT     41956       GG
                                CACAGCTAC  CGGGATT
                                |||||||||  |||||||
                                GTGTCGGTG  GTCTTAA

                                   __
GAM714  FABP3   3' GCTCTGCTTTATTGACCTCA  43430   C       A  AA
                                GC CTGTTTTATT AC  CA
                                || ||||||||||  ||  ||
                                CG GACGAAATAA TG  GT
                                 A        C  GA
GAM714  MAP3K7IP2 3' GCCTTGTTTTATAAATACACAT 31521    C      TAACA_
                                GCC TGTTTTAT     ACAT
                                ||| ||||||||     ||||
                                CGG ACAAAATA     TGTA
                                  A      TTTATG
GAM714  DRD1    3' TGTGTGTTTGCTTCATTGGC  9010    _      AA  A
                                TGT TGTTTGCTT  TAT GGC
                                ||| |||||||||  ||| |||
                                ACA ACAAACGAA  GTA CCG
                                  C       __  A
GAM714  RABIF   3' TGTTGTTTGTTTGAGACAGG  16129       CTTAAT
                                TGTTGTTTG     ATAGG
                                |||||||||     |||||
                                ACAACAAAC     TGTCC
                                     AAACTC
GAM714  SEL1L   3' TGTGTTTTTCATTTATAGGCC  22851    T   GCTTAA
                                TGT GTTT     TATAGGCC
                                ||| ||||     ||||||||
                                ACA CAAA     ATATCCGG
                                  _   AAGTAA
GAM714  SHANK2  3' TACGTTGTGCATTGATATGGGC 29467       TT _ A  A
                                TATGTTGT  GC TT ATAT GGC
                                ||||||||  || || |||| |||
                                ATGCAACA  CG AA TATA CCG
                                     __ T C   C
GAM714  WISP2   3' TGCATGTTTGATATAGGC    19310    _    CTTA
                                TGT TGTTTG   ATATAGGC
                                ||| ||||||   ||||||||
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                                ACG ACAAAC    TATATCCG
                                  T     _____
GAM715  CGB      5'  TTTATACCTCGGGGTT      8827          ATG    A
                                TTTGTGCT   TCGG GTT
                                ||||||||   |||| |||
                                AAATATGG   AGCC CAA
                                     ___    C
GAM715  EIF2C1   3'  TTTGTGCTACGTTTTGTGAG   29190           CG___
                                TTTGTGCTATGT    GAG
                                ||||||||||||    |||
                                AAACACGATGCA    CTC
                                      AAACA
GAM715  HMGB1    3'  TTTGTGCTGTGCACCAACAA   13406         A   CGGAGTT
                                TTTGTGCT TGT      ACAA
                                |||||||| |||      ||||
                                AAACACGA ACG      TGTT
                                    C   TGGT___
GAM715  OGT      5'  TGCTGTGGCAGTTACAAA    18789      AT  C  _
                                TGCT  GT GG AGTTACAAA
                                ||||  || || |||||||||
                                ACGA  CA CC TCAATGTTT
                                  __  _  G
GAM715  OGT      3'  TTTGTTAGTTGAGTTACA    18795      GCTAT  CG
                                TTTGT    GT  GAGTTACA
                                |||||    ||  ||||||||
                                AAACA    CA  CTCAATGT
                                   AT___  A_
GAM715  PUM2     3'  TTGTGCTATGGGGTT      31668          TC  A
                                TTGTGCTATG  GG GTT
                                ||||||||||  || |||
                                AACACGATAC  CC CAA
                                      __  _
GAM715  SP100    3'  TTTGTGCTGTGCACTAACAA   17057         A   CGGAGTT
                                TTTGTGCT TGT      ACAA
                                |||||||| |||      ||||
                                AAACACGA ACG      TGTT
                                    C   TGAT___
GAM715  ALDH1B1  3'  TTTGCCTACTCCTTCCCACAAA 8676        CA_   ACA
                                TTTGCC   TCCT   TTTACAAA
                                ||||||   ||||   ||||||||
                                AAACGG   AGGA   GGGTGTTT
                                   ATG    A__
GAM715  CRYM     3'  TTTGCTTTCCAACTACAAA   12458      CCA   TACAT
                                TTTGC   TCC    TTACAAA
                                |||||   |||    |||||||
                                AAACG   AGG    GATGTTT
                                   AA_   TT___
GAM715  GATA6    3'  TTTGCTACCCTGTTTACAAA   23540      CC    ACA
                                TTTGC  ATCCT   TTTACAAA
                                |||||  |||||   ||||||||
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                                AAACG  TGGGA   AAATGTTT
                                  A_    C__
GAM715  MS4A3    3'  TTTGCCCATGTTCATACA    26011        ___  C
                                TTTGCCCA   TC TACA
                                ||||||||   || ||||
                                AAACGGGT   AG ATGT
                                     ACA  T
GAM715  MVK      3'  TTTGCCATCTTTTCCACAAAC  41343       C   CTACA
                                TTTGCC ATC    TTTACAAAC
                                ||||||| |||    |||||||||
                                AAACGG TAG    AGGTGTTTG
                                   _  AAA__
GAM715  PIGN     3'  TTTGCCCATTAGAATTTGTTTA 29557         CCTACA___
             CAAA                   TTTGCCCAT       TTTACAAA
                                ||||||||||       ||||||||
                                AAACGGGTA       AAATGTTT
                                     ATCTTAAAC
GAM715  RNF12    3'  TTTGCCCATCACTATATC    32042         _  C
                                TTTGCCCATC CTA ATT
                                |||||||||| ||| |||
                                AAACGGGTAG GAT TAG
                                     T   A
GAM715  SLC10A2  3'  TTTGCCCATGTTATATTACAAA 7823         CCTACAT
                                TTTGCCCAT      TTACAAA
                                |||||||||      |||||||
                                AAACGGGTA      AATGTTT
                                     CAATAT_
GAM715  SOX13    3'  TTTGCCCATCTCTGGGGCACGA 25018         _ A___   TT
             AC                   TTTGCCCATC CT    CAT  AC
                                |||||||||| ||    |||  ||
                                AAACGGGTAG GA    GTG  TG
                                     A  CCCC   CT
GAM715  TEX15    3'  CCTACCACATTTACAAAC    36324    ATC
                                CC   CTACATTTACAAAC
                                ||   ||||||||||||||
                                GG   GGTGTAAATGTTTG
                                 AT_
GAM715  ZNF138   3'  TTTGCCACATTCTTCACATTT  44346       _  C __
                                TTTGCC CAT CT  ACATTT
                                |||||| ||| ||  ||||||
                                AAACGG GTA GA  TGTAAA
                                   T   A  AG
GAM716  ABCF1    5'  ACTGTGGCGGCGCCCG      9905          A  TGAA
                                ACTGTGGCGG CG    CCCG
                                |||||||||| ||    ||||
                                TGACACCGCC GC    GGGC
                                          _ _____
GAM716  BMP4     5'  GGACTGTGGCGCTGCAGGCTCG 39299    C        GAC  GAACC
             A                    A ACTGTGGCG   GT    CGA
                                | |||||||||   ||    |||
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                                C TGACACCGC  CG    GCT
                                 C       GA_ TCCGA
GAM716  CDK2    3' ACATTGTGGCAGCAGGA    12199    C      A T
                                ACA TGTGGCGG CG GA
                                ||| |||||||| || ||
                                TGT ACACCGTC GT CT
                                  A       _ C
GAM716  EEF1A2  3' CTGGGCGCGGAAGCC      41517    T   GA T  C
                                CTG GGCG  CG GAA CC
                                ||| ||||  || ||| ||
                                GAC CCGC  GC CTT GG
                                  _   __ _  C
GAM716  HADHA   3' ACACCGTGGTGAGAAGCC    6764        C ACGT  C
                                ACACTGTGG GG   GAA CC
                                ||||||||| ||   ||| ||
                                TGTGGCACC CT   CTT GG
                                     A ____  C
GAM716  INHBB   5' CTGCGGCGGGCGCTGCG     13556       A  GAACC
                                CTGTGGCGG CGT    CG
                                ||||||||| |||    ||
                                GACGCCGCC GCG    GC
                                     C  AC___
GAM716  ISL1    5' CTGCGGCGGCGGCAGACTCG  13595       AC  GA  C
                                CTGTGGCGG  GT  AC CG
                                |||||||||  ||  || ||
                                GACGCCGCC  CG  TG GC
                                     GC  TC  A
GAM716  PRX     3' ACACGTGGCAAGCGGACCCG  34099    T    GA  T  A
                                ACAC GTGGCG  CG GA CCCG
                                |||| ||||||  || || ||||
                                TGTG CACCGT  GC CT GGGC
                                  _     TC  _ _
GAM716  SLC25A1 5' CTGTGGCGGCTTCGGGTCCGA 25601       ACG  AAC
                                CTGTGGCGG   TG   CCGA
                                |||||||||   ||   ||||
                                GACACCGCC   GC   GGCT
                                     GAA  CCA
GAM716  SLC30A3 5' CGACTGTGGCGCGCGGAGTCCG 18429   C      GA  T  AC
           A                     A ACTGTGGCG  CG GA  CCGA
                                 | |||||||||  || ||  ||||
                                 G TGACACCGC  GC CT  GGCT
                                  C       GC  _  CA
GAM716  ZNF20   5' TGTGGCAGAGGGACCCG    41822       CGT  A
                                TGTGGCGGA   GA CCCG
                                |||||||||   || ||||
                                ACACCGTCT   CT GGGC
                                     CC_  _
GAM716  ZNF267  5' CTGTGGCGAGGAGACCCGA   18258       ACGT  A
                                CTGTGGCGG   GA CCCGA
                                |||||||||   || |||||
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                                GACACCGCT    CT GGGCT
                                     CCT_  _
GAM717  GFPT2    3'  GACACAGAGAAACAGTATC    23041        AAT  T
                                GACACAGA   AC GTATC
                                ||||||||   || |||||
                                CTGTGTCT   TG CATAG
                                     CTT  T
GAM717  LDHB     5'  AGGCACAGAAACTTGGTGTGTC 14115    A       AC__   A
                                AG CACAGAAAT    TGT TC
                                || |||||||||    ||| ||
                                TC GTGTCTTTG    ACA AG
                                 C        AACC   C
GAM717  LIPA     3'  TAAGACACAAAATGAATCC    6938           ATAC  T
                                TAAGACACAGAA    TG ATCC
                                ||||||||||||    || ||||
                                ATTCTGTGTTTT    AC TAGG
                                      _____  T
GAM717  MAP3K9   3'  GACACAGAAAAGCTCCTATCTC 41354         TA  G_   _
             G                   GACACAGAAA  CT  TATC CG
                                 ||||||||||  ||  |||| ||
                                 CTGTGTCTTT  GA  ATAG GC
                                       TC  GG    A
GAM717  OLFM1    3'  TAAGACACAGGCATAGCC     26779          AA   _
                                 TAAGACACAG  ATA CT
                                 ||||||||||  ||| ||
                                 ATTCTGTGTC  TAT GG
                                       CG   C
GAM717  UBQLN1   3'  CAAGATACAGAAATGCTG     30276      C       A
                                 TAAGA ACAGAAAT CTG
                                 ||||| |||||||| |||
                                 GTTCT TGTCTTTA GAC
                                    A       C
GAM717  CSNK1G3  3'  TAATATGACTTATGAATA     20476          CTT
                                 TAGTATGACTTA   GTA
                                 ||||||||||||   |||
                                 ATTATACTGAAT   TAT
                                        ACT
GAM717  NLGN1    3'  TAGTATACAATTTTTTGTATAA 31388        ACTTAC_
             TAA                   TAGTATG      TTGTATAATAA
                                   |||||||      ||||||||||||
                                   ATCATAT      AACATATTATT
                                      GTTAAAA
GAM718  ARCN1    3'  TGAGTGCTCTGCTTCAAG    11658    _     ATTACG
                                 TG GTGCTC     TTCAAG
                                 || ||||||     ||||||
                                 AC CACGAG     AAGTTC
                                  T     ACG___
GAM719  ADSS     3'  GTTATGCCTAATTGTCAAAAT  43478      C
                                 GTTAT TCTGATTGTCAAAAT
                                 ||||| ||||||||||||||
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                                CAATA GGATTAACAGTTTTA
                                   C
GAM719  PLCB4    5'  GTTTTCTCTGATGCAAA     9585      A       T T
                                GTT TCTCTGAT G CAAA
                                ||| |||||||| | ||||
                                CAA AGAGACTA C GTTT
                                  A       _ _
GAM720  ALDH3B2  3'  TGAGGACACCTGGCATGTTC   8685       G   AGAGTA
                                TGAGG ATA     GCATGTTC
                                ||||| |||     ||||||||
                                ACTCC TGT     CGTACAAG
                                   _  GGAC__
GAM720  ARHGAP6  3'  TGAAAATTAAGAGTAGCATGTT 25965       A
                                TGAGGG TAAGAGTAGCATGTT
                                |||||| ||||||||||||||
                                ACTTTT ATTCTCATCGTACAA
                                    A
GAM720  CHC1     3'  TGAGGGGCAAGAGTATGC    10428       A       _
                                TGAGGG TAAGAGTA GC
                                |||||| |||||||| ||
                                ACTCCC GTTCTCAT CG
                                    C       A
GAM720  GPX3     3'  TGAGGGGTGAGGGCACGTCC   13280       ATAA   TA
                                TGAGGG   GAG  GCATGTTC
                                ||||||   |||  ||||||||
                                ACTCCC   CTC  CGTGCAGG
                                    CA__   C_
GAM720  KIR2DL4  3'  GGGATAAGCAAAGGAGTGTGTT 13962        ___  T  CA
                                GGGATAAG   AG AG  TGTT
                                ||||||||   || ||  ||||
                                CCCTATTC   TC TC  ACAA
                                     GTT  C  AC
GAM720  TFE3     3'  TGAGGGACAAGGGTGGGGC   27174         A  A__
                                TGAGGGATAAG GT   GC
                                |||||||||| ||   ||
                                ACTCCCTGTTC CA   CG
                                       C  CCC
GAM721  ATP8A2   3'  CTCTCTCCCTCTTTCCGGCCTT 45256       AGGGG  ___
                                CTTTCT    CTC   CCGGCCTT
                                ||||||    |||   ||||||||
                                GAGAGA    GAG   GGCCGGAA
                                    GG___   AAA
GAM721  C18orf1  3'  TTTCTAGGGGCTTCCAAAGC   41238         _  C_
                                TTTCTAGGGGCT CC  GGC
                                |||||||||||| ||  |||
                                AAAGATCCCCGA GG  TCG
                                       A  TT
GAM721  DEC1     5'  ACTTTCTAGCGGCCT      32643         GGGCTCC
                                ACTTTCTAG     CGGCCT
                                |||||||||     ||||||
```

```
                                TGAAAGATC      GCCGGA
                                        _______
GAM721  KRTHB1   3' CTTTCTAGGGTGGCCTT     14026          GCTCCC
                                CTTTCTAGGG     GGCCTT
                                ||||||||||     ||||||
                                GAAAGATCCC     CCGGAA
                                     A_____
GAM721  MEN1     3' TTTCTAGGGGCTGGGCCTT   39244           CCC
                                TTTCTAGGGGCT   GGCCTT
                                ||||||||||||   ||||||
                                AAAGATCCCCGA   CCGGAA
                                      C__
GAM721  OPHN1    3' CTTTCTAGGGCTCTCAATAATC 14964          G   C   C___
           TTC                    CTTTCTAGGG CTC CGG    CTTC
                                ||||||||||| ||| |||    ||||
                                GAAAGATCCC GAG GTT    GAAG
                                     _  A   ATTA
GAM721  SELP     3' CCTTCTAGCTTGATTCTTGGCC 16549         G__ GC  CC
           TTC                    CTTTCTAG   G  TC  GGCCTTC
                                ||||||||   |  ||  |||||||
                                GGAAGATC   C  AG  CCGGAAG
                                    GAA TA  AA
GAM721  TP63     3' ACTTTCTAGTGGTTTCTATGC  18991          _  GC  CCG
                                ACTTTCTAG GG  TC   GC
                                |||||||| ||  ||   ||
                                TGAAAGATC CC  AG   CG
                                     A  AA  ATA
GAM721  USP4     3' CTTTCTAGGTAAACGGTCTTC  17889         GGCTCC   C
                                CTTTCTAGG     CGG CTTC
                                |||||||||     ||| ||||
                                GAAAGATCC     GCC GAAG
                                     ATTT__   A
GAM722  CD2AP    3' TAGTGACCTCATTAGAAG    29073     CAC    AAAG
                                TAG   ACCTT    ATTAGAAG
                                |||   |||||    ||||||||
                                ATC   TGGAG    TAATCTTC
                                  AC_    _____
GAM722  CLN5     3' GCATACCCCGGTTAGAAG    27082     C    AAAGA
                                GCA ACCTT    TTAGAAG
                                ||| |||||    |||||||
                                CGT TGGGG    AATCTTC
                                  A    CC___
GAM722  CPD      3' TAGCTCATCTTAAATTAAAAAG 10560      A  C     GATT
           A                     TAGC CA CTTAAA    AGAAGA
                                |||| || ||||||    ||||||
                                ATCG GT GAATTT    TTTTCT
                                  A A     AAT_
GAM722  DBY      3' TAGCATGCATTAAAGACCAGA  21661       CACC
                                TAGCA    TTAAAGATTAGA
                                |||||    ||||||||||||
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                                ATCGT   AATTTCTGGTCT
                                  ACGT
GAM722  IRF2    3'  AGCATAGCAGATTAGAAG   13585    CACCTTAA
                                AGCA      AGATTAGAAG
                                ||||      ||||||||||
                                TCGT      TCTAATCTTC
                                  ATCG____
GAM722  ITGB1   3'  ACATTAAAAGATTAGAAG   38041    CCTT
                                ACA   AAAGATTAGAAG
                                |||   ||||||||||||
                                TGT   TTTCTAATCTTC
                                  AAT_
GAM722  MEN1    3'  CAGCACACTTTGAGATGGCTAG 39162       C  AA   ___
                                TAGCACAC TT  AGAT   TAG
                                |||||||| ||  ||||   |||
                                GTCGTGTG AA  TCTA   ATC
                                     _ AC    CCG
GAM722  SLC6A4  3'  CAGCACATGGATTAGAAG   9820       CCTTAAA
                                TAGCACA     GATTAGAAG
                                |||||||     |||||||||
                                GTCGTGT     CTAATCTTC
                                    AC_____
GAM722  CRY1    3'  CAAAGAGTGCAAAGTTAGAT  19832      C   TTA
                                CAAAGGG GTG   TTAGAT
                                ||||||| |||   ||||||
                                GTTTCTC CGT   AATCTA
                                    A   TTC
GAM722  DFNA5   3'  GGGTGTGTTACTGTTAGAT   20584    C     ___
                                GGG GTGTTAT   TAGAT
                                ||| |||||||   |||||
                                CCC CACAATG   ATCTA
                                  A      ACA
GAM722  LAMC1   3'  AAGAGACACTTTATTAGAT   14076    _   TG
                                AAG GGCG  TTATTAGAT
                                ||| ||||  |||||||||
                                TTC CTGT  AATAATCTA
                                  T   GA
GAM722  SERPINB2 3' AAAGGCATTTATTAGAT    15078       G
                                AAGGGCGT TTATTAGAT
                                |||||||| |||||||||
                                TTTCCGTA AATAATCTA
                                     _
GAM722  SOX12   3'  GGAAGGGCGTGGTCTCAG   28043   A      TTA
                                C AAGGGCGTG   TTAG
                                | |||||||||   ||||
                                C TTCCCGCAC   AGTC
                                 C       CAG
GAM722  SURF5   3'  CAAAGGGCTGCCTCAG     39500       G   A
                                CAAAGGGC TGTT TTAG
                                |||||||| |||| ||||
```

```
                                GTTTCCCG ACGG AGTC
                                      _  _
GAM722  XBP1    3'  AAAGGGCAACAGTATTGGAT  22924       TGT_  A
                                AAAGGGCG   TATT GAT
                                ||||||||   |||| |||
                                TTTCCCGT   ATAA CTA
                                    TGTC   C
GAM723  CHML    5'  GTGATTATGCTGTAATAAAATC 12243       A  A  GTT_
           TG                    GTGATTAT TT TAA   ATCTG
                                ||||||||  || |||   |||||
                                CACTAATA GA ATT   TAGAC
                                    C  C  ATTT
GAM723  OCLN    3'  GTGATTATAAATAACAGTTATC 14906       TTATA_
           TG                    GTGATTATA    AGTTATCTG
                                |||||||||    |||||||||
                                CACTAATAT    TCAATAGAC
                                     TTATTG
GAM724  ENC1    3'  TCACAATGTAAAAGGTT    18865      GAT
                                TCACGG  TAAAAGGTT
                                ||||||  |||||||||
                                AGTGTT  ATTTTCCAA
                                   AC_
GAM724  RAB18   3'  TATCACAGGATTAAAACTCCAG 34575           ____
           TTA                   TATCACGGGATTAAAA   GGTTA
                                ||||||||||||||||   |||||
                                ATAGTGTCCTAATTTT   TCAAT
                                       GAGG
GAM724  ILF1    3'  TCTGTCTTTAAGGAGTG    21120    AA      T
                                TCT  TCTTTAAGG GTG
                                |||  ||||||||| |||
                                AGA  AGAAATTCC CAC
                                  C_       T
GAM724  MFAP3   3'  TCTAATCTTATTTCAGGTTAGT 25455       TA___  __
           G                     TCTAATCTT    AGGT  GTG
                                |||||||||    ||||  |||
                                AGATTAGAA    TCCA  CAC
                                     TAAAG   AT
GAM724  TEM7    3'  CAATATTCGGGGTGTGCTGACG 33803     C  AA     A
                                TAAT TTT  GGTGTGCT ACG
                                |||| |||  |||||||| |||
                                GTTA AAG  CCACACGA TGC
                                  T  CC      C
GAM725  CLN2    3'  GGCCATTGTTTCTGGATGTCAG 7555        CA  AGTGT
                                GGCCATTGT  TC    TGTCAG
                                |||||||||  ||    ||||||
                                CCGGTAACA  AG    ACAGTC
                                     A_  ACCT_
GAM725  DXYS155E 3' GGCTGTTGGTTGTTGTCA   22959    CAT  CATCAG
                                GGC  TGT    TGTTGTCA
                                |||  |||    ||||||||
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```
                                CCG   ACA     ACAACAGT
                                  ___   ACCA__
GAM725  NT5E     3'  GGTCATTTCATCAGCAT     14863    C    G
                                GG CATT TCATCAGTGT
                                || |||| ||||||||||
                                CC GTAA AGTAGTCGTA
                                 A   _
GAM725  DBY      3'  ATGTGGACCTTCCTATCAGTGT 21656          ATTG  _
              T                  ATGTGGGCC    TC ATCAGTGTT
                                |||||||||    || |||||||||
                                TACACCTGG    GG TAGTCACAA
                                     AA__  A
GAM726  HSPG2    3'  GCCAGGGGCTGGGTGGAGGTG  24363      A        AA
                                GTTA GGGCTGGGT  AGGTG
                                |||| |||||||||  |||||
                                CGGT CCCGACCCA  TCCAC
                                   C        CC
GAM726  ATP6V0A4  5'  TCTGGCAGCCCTCCGTGCTTGC 39291        AC    GG_  C
              T                  TCTGGCA  GCCC   GT CTTGCT
                                |||||||  ||||   || ||||||
                                AGACCGT  CGGG   CA GAACGA
                                   __    AGG  C
GAM726  BCL11B   5'  TCTGGCATCGCCCGGAGAGCT  39758        A       TCCTT
                                TCTGGCA CGCCCGGG    GCT
                                ||||||| ||||||||    |||
                                AGACCGT GCGGGCCT    CGA
                                    A       CT___
GAM726  BMP1     3'  GGCAATGTCCCCCTTGCT    25983       CG_   GGGT
                                GGCAA   CCC    CCTTGCT
                                |||||   |||    |||||||
                                CCGTT   GGG    GGAACGA
                                  ACA   _____
GAM726  MIPOL1   5'  TCTGGCAATGTCTCTGGTTTTT 44200        CGCCCG_   CC
              GCT                  TCTGGCAA      GGT  TTGCT
                                |||||||      |||  |||||
                                AGACCGTT      CCA  AACGA
                                    ACAGAGA   AA
GAM726  NPR2L    3'  TCTAGCAGTGCCCGGGCC    27252        AC
                                TCTGGCA  GCCCGGGTC
                                |||||||  |||||||||
                                AGATCGT  CGGGCCCGG
                                    CA
GAM726  P4HB     3'  CGGCAGCGCCCGGGTCTGGCT  9545       A        CTT
                                TGGCA CGCCCGGGTC   GCT
                                ||||| ||||||||||   |||
                                GCCGT GCGGGCCCAG   CGA
                                  C        AC_
GAM726  RUNX1    3'  TCTGGTGGCCCTTAAATTGCT  12030      CAAC    GGGTCC
                                TCTGG    GCCC     TTGCT
                                |||||    ||||     |||||
```

```
                                AGACC   CGGG    AACGA
                                  AC__   AATTT_
GAM727  ANXA9   5' GGTAGAGGAAAGTGGGGG   18692   GTT_   A
                                GG   GGAAA GTGGGGG
                                ||   ||||| |||||||
                                CC   CCTTT CACCCCC
                                 ATCT   _
GAM727  EMX2    5' TGTTTGGGGTGGGGGTGGGGGT 44707    A  T  AAAA
                                TGTT GGG TGG   GTGGGGGT
                                |||| ||| |||   ||||||||
                                ACAA CCC ACC   CACCCCCA
                                  A  C  CC__
GAM727  HNF3B   3' GGTGTTGGGGTGGGGGT    34743   _    AAAA
                                GG GTTGG   GTGGGGGT
                                || |||||   ||||||||
                                CC CAACC   CACCCCCA
                                 A   C___
GAM727  PKIG    3' TGTTGGTGTTGGGACAGGG   28194    A _    AAAA TG
                                TGTT GG GTTGG   G  GGG
                                |||| || |||||   |  |||
                                ACAA CC CAACC   T  CCC
                                  _ A   C___ GT
GAM727  POU4F1  3' TGTAGGGTTGGGGAG      26399    T      AAAAGT
                                TGT AGGGTTGG    GGGG
                                ||| ||||||||    ||||
                                ACA TCCCAACC    CCTC
                                  _     _______
GAM727  RTN4    5' TGTGGGGGTTGGGGAGG    42495    TA     AAAAGT
                                TGT  GGGTTGG    GGGGG
                                |||  |||||||    |||||
                                ACA  CCCAACC    CCTCC
                                  CC     _______
GAM727  SIRT2   3' TGCTGGGGTTGGGGGCCAGGGT 36148     A      AAAA  G
                                TGTT GGGTTGG   GT GGGGT
                                |||| |||||||   || |||||
                                ACGA CCCAACC   CG TCCCA
                                  C      CC__  G
GAM727  SOX12   3' TGTCGGGGAAGGGGTGGGGGT  28063    TA   TT  AAAA
                                TGT  GGG  GG   GTGGGGGT
                                |||  |||  ||   ||||||||
                                ACA  CCC  CC   CACCCCCA
                                  GC   TT  C___
GAM728  SLC1A4  3' TTTCGAAGATTAACA      16766       A  GTTA
                                TTTCGAA GA   TTAACA
                                ||||||| ||   ||||||
                                AAAGCTT CT   AATTGT
                                   _ ____
GAM729  FOXO1A  3' TAAGATTTTAACAGTGATTTT  12890        __   AC
                                TAAGATTT  ACAG  GATTTT
                                ||||||||  ||||  ||||||
```

```
                                ATTCTAAA  TGTC  CTAAAA
                                    AT   A_
GAM730  ARHA    3'  AGGGGTAATATGGCCATT   43313   T      ACCA    G
                                AG GGTAATATG   GCCGT T
                                || |||||||||   ||||| |
                                TC CCATTATAC   CGGTA A
                                 C       ____    G
GAM731  CLN5    5'  TGGGGGTTTTGCGGAG     27089        AA   T
                                TGGGGGTTT  TGT GAG
                                |||||||||  ||| |||
                                ACCCCCAAA  ACG CTC
                                    __  C
GAM731  PURA    3'  TGGGGGTTTCATTCAG     25211        AA   G
                                TGGGGGTTT  TGTT AG
                                |||||||||  |||| ||
                                ACCCCCAAA  GTAA TC
                                    __   G
GAM731  COL19A1  3'  CAACATCCTCATGCCCAG   12372      T    A__
                                CAACAT CCTCAT   CAG
                                ||||||| |||||||   |||
                                GTTGTA GGAGTA   GTC
                                   _     CGG
GAM731  EPS8    3'  CAACATTCTTACATAACATCTG 20809        CT_   _ GAGA
          T                      CAACATTC   CATA CA    CTGT
                                ||||||||   |||| ||    ||||
                                GTTGTAAG   GTAT GT    GACA
                                    AAT    T  A___
GAM731  GCSH    3'  TTCCTCATCTGACACTGT    21019        ACA  G
                                TTCCTCAT   GA ACTGT
                                ||||||||   || |||||
                                AAGGAGTA   CT TGACA
                                    GA_  G
GAM731  JPH2    3'  CATTCCTCATGAGGGTGT    45375        ACA   AC
                                CATTCCTCAT   GAG  TGT
                                ||||||||||   |||  |||
                                GTAAGGAGTA   CTC  ACA
                                    ___   CC
GAM731  LPIN1   3'  CATTCCTCGATTGACCCTGT  42634        ATACA  GA
                                CATTCCTC    GA  CTGT
                                ||||||||    ||  ||||
                                GTAAGGAG    CT  GACA
                                    CTAA_  GG
GAM731  PPP3CB  3'  TTCTTCAGAGAGACTGT    34453     C   TAC
                                TTC TCA   AGAGACTGT
                                ||| |||   |||||||||
                                AAG AGT   TCTCTGACA
                                  A   C__
GAM731  PTGER3  3'  CAAAATTCCTCATCTGCTG   9642      C       ACAGAGA
                                CAA ATTCCTCAT      CTG
                                ||| |||||||||      |||
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                                GTT TAAGGAGTA      GAC
                                  T       GAC____
GAM731  RANBP2L1  3'  TGACATTCGTAAGTGGAGACTG 37028   A     CTCATACA
              T                   C ACATTC       GAGACTGT
                                  | ||||||       ||||||||
                                  A TGTAAG       CTCTGACA
                                   C     CATTCAC_
GAM731  RANBP3    5'  CAACAGTCAAGTGGAGACTGT  28751      TTCC   TACA
                                  CAACA   TCA   GAGACTGT
                                  |||||   |||   ||||||||
                                  GTTGT   AGT   CTCTGACA
                                     C___   TCAC
GAM731  SMP1      3'  TCACAGCGTAGAGACTGT    30718      C___
                                  TCATA   AGAGACTGT
                                  |||||   |||||||||
                                  AGTGT   TCTCTGACA
                                     CGCA
GAM731  WHSC1     3'  CAACATTCTTCAGACAGA    39354        C   T
                                  CAACATTC TCA ACAGA
                                  |||||||| ||| |||||
                                  GTTGTAAG AGT TGTCT
                                       A   C
GAM732  ATP8A2    3'  AGCGACAGGTGTGTTCCT    45251       _    A_
                                  AGCGAC GGTGT  TCCT
                                  |||||| |||||  ||||
                                  TCGCTG CCACA  AGGA
                                     T    CA
GAM732  PABPN1    5'  GGCGGTTCCTATTTATATTCG  21608     TA    _____
                                  GGTG  TCCTA   TATTCG
                                  ||||  |||||   ||||||
                                  CCGC  AGGAT   ATAAGC
                                    CA    AAAT
GAM732  RORB      3'  AACACCCAGTGTCCTATATT   27919     A_    TA
                                  AGCG  CGGTG  TCCTATATT
                                  ||||  |||||  |||||||||
                                  TTGT  GTCAC  AGGATATAA
                                    GG    __
GAM733  CARKL     3'  GGACGTGGGGAACACAGGGACG 29997        A  T__   C_
              GT                    GGACGTGG GA   CAG  ACGGT
                                  |||||||| ||   |||  |||||
                                  CCTGCACC CT   GTC  TGCCA
                                       C  TGT   CC
GAM733  CRYAA     3'  GGGTTGGAGGAAGACGGTC   7566     ACG    ATC  C
                                  GG   TGGAG   AG ACGGTC
                                  ||   |||||   || ||||||
                                  CC   ACCTC   TC TGCCAG
                                   CA_    CT_  _
GAM733  FCER1G    5'  GGCTGGAGATCGGCCG      19953    ACG      A  A
                                  GG   TGGAGATC GC CG
                                  ||   |||||||| || ||
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                                CC   ACCTCTAG CG GC
                                 G__       C  _
GAM733  MLF2     5'  GAACGTGGGGATTGGTCC    24143         A   CAGCAC
                                GGACGTGG GAT     GGTCC
                                |||||||| |||     |||||
                                CTTGCACC CTA     CCAGG
                                    C   A_____
GAM733  MUC3B    3'  GGACGTGAGGATTGGAGGATCC 45340        GA   CAGCAC
              G                  GGACGTG  GAT     GGTCCG
                                |||||||  |||     ||||||
                                CCTGCAC  CTA     CTAGGC
                                   TC   ACCTC_
GAM733  RPS6KA2  3'  GGACGTGGGTGTCGGGAGTC   34467        AGA  AGCAC
                                GGACGTGG   TC    GGTC
                                ||||||||   ||    ||||
                                CCTGCACC   AG    TCAG
                                    CAC  CCC__
GAM733  TRPV1    5'  GGACGTGGGGAACACAGGGACG 38807         A  T__   C_
              GT                  GGACGTGG GA   CAG  ACGGT
                                |||||||| ||   |||  |||||
                                CCTGCACC CT   GTC  TGCCA
                                    C  TGT   CC
GAM734  8D6A     3'  TCAATCTCCAGGGCCACT    32448    T    A TGG
                                TC ATCT C   CAGGGCCACT
                                || |||| |   ||||||||||
                                AG TAGA G   GTCCCGGTGA
                                 T   _ ___
GAM734  DYRK2    3'  TATCCACTAAAAGCTGCT    27042         GC    CA
                                TATCTACTG  AGGGC  CT
                                |||||||||  |||||  ||
                                ATAGGTGAT  TTTCG  GA
                                     __    AC
GAM734  OPRD1    3'  CCTATCTACTGGCCCCACTCC  9513           AGGG
                                TCTATCTACTGGC    CCACTCC
                                ||||||||||||    |||||||
                                GGATAGATGACCG    GGTGAGG
                                      G___
GAM734  POLR2C   3'  TCTATCTATGACCCACT     15454         C    AGGG
                                TCTATCTA TGGC    CCACT
                                |||||||| ||||    |||||
                                AGATAGAT ACTG    GGTGA
                                    _    _____
GAM734  POU5F1   3'  TCTATCTACTGTGTCCCAGGC  15477          GCA___
                                TCTATCTACTG     GGGC
                                ||||||||||     ||||
                                AGATAGATGAC     TCCG
                                      ACAGGG
GAM734  POU5F1   3'  TCTATCTACTGTGTCCCAAGC  15476          GCA___
                                TCTATCTACTG     GGGC
                                ||||||||||     ||||
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                                AGATAGATGAC     TTCG
                                      ACAGGG
GAM734  RAB26    3'  TCTGTCCACTTGCCGCTC    30750     A     GGCAGG   A
                                TCT TCTACT     GCC CTC
                                ||| ||||||     ||| |||
                                AGA AGGTGA     CGG GAG
                                  C     A_____   C
GAM734  TCAP     3'  CTGGATCAGGGCCACTCC    18949      __
                                CTGG  CAGGGCCACTCC
                                ||||  ||||||||||||
                                GACC  GTCCCGGTGAGG
                                   TA
GAM734  ZNF76    3'  TCTATGTACAGGGCCACTC    18312      CTG
                                TCTA   GCAGGGCCACTC
                                ||||   ||||||||||||
                                AGAT   TGTCCCGGTGAG
                                   ACA
GAM735  ANK1     3'  CGAGGAACTGCCAGC       33858        G  G AT
                                CGAGGAAC TG T  GGC
                                |||||||| || |  |||
                                GCTCCTTG AC G  TCG
                                     _  G __
GAM735  CDH11    5'  AAGGAATGTCACAGGGCCG    38028       C  GG  T
                                GAGGAA GT  TA GGCCG
                                |||||| ||  || |||||
                                TTCCTT CA  GT CCGGC
                                    A  GT  C
GAM735  COL4A4   5'  CGGGGAACGCGGACC       6398     A       TATG
                                CG GGAACGTGG    GCC
                                || |||||||||    |||
                                GC CCTTGCGCC    TGG
                                 C       _____
GAM735  FGF4     5'  CGGGAGCGCACGGCCG      12852    A  AC   G
                                CG GGA  GTG TATGGCCG
                                || |||  ||| ||||||||
                                GC CCT  CGC GTGCCGGC
                                  _   __   _
GAM735  GLS      3'  AAGGAACATTGGCC        31372          GGTA
                                GAGGAACGT    TGGCC
                                |||||||||    |||||
                                TTCCTTGTA    ACCGG
                                      _____
GAM735  HTR2C    5'  CGAGAAACGGACTCGGC     9282          T  TA
                                CGAGGAACG GG  TGGC
                                ||||||||| ||  ||||
                                GCTCTTTGC CT  GCCG
                                     _  GA
GAM735  KCNQ2    5'  CGGGAGCCGCATGGCCG     41508    A  AC  G
                                CG GGA  GT GTATGGCCG
                                || |||  || |||||||||
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                                GC CCT  CG CGTACCGGC
                                 _  __ G
GAM735  MARK3    5'  GGGTGGTGGTGCATGGCCG   14362    AAC   __
                                GG  GTGGT  ATGGCCG
                                ||  |||||  |||||||
                                CC  CACCA  TACCGGC
                                 CAC    CG
GAM735  PFKL     3'  GAGGGGCGTGGGCATGGC    15236     AA   _
                                GAGG  CGTGG TATGGC
                                ||||  ||||| ||||||
                                CTCC  GCACC GTACCG
                                  CC    C
GAM735  SERPINE2 5'  CGAGGAGGGTCACAGCCG    44002       ACGT  _
                                CGAGGA   GGT ATGGCCG
                                ||||||   ||| |||||||
                                GCTCCT   CCA TGTCGGC
                                   C___  G
GAM735  USP18    3'  CGAGCAGCCACATGGCCG    41867     GAAC  GG
                                CGAG   GT  TATGGCCG
                                ||||   ||  ||||||||
                                GCTC   CG  GTACCGGC
                                  GT__  GT
GAM735  VDR      3'  CGAGGAACTGTGAGCTTG    7517        _  _ A
                                CGAGGAAC GTG GT TG
                                |||||||| ||| || ||
                                GCTCCTTG CAC CG AC
                                    A  T  A
GAM735  WHSC1L1  5'  GAGGAGGGCCACGGCCG     35712      ACGT  _
                                GAGGA   GGT ATGGCCG
                                |||||   ||| |||||||
                                CTCCT   CCG TGCCGGC
                                  C___  G
GAM736  CENTD1   5'  CCGGTTTCACTACAGCAGCA  40136      ___
                                TCGGT  GCTACAGCAGCA
                                |||||  ||||||||||||
                                GGCCA  TGATGTCGTCGT
                                  AAG
GAM736  COG3     3'  TGCAGTCAGCACTGAGCAGCA  36419     A   TG  AC
                                TGCA TCGG  CT  AGCAGCA
                                |||| ||||  ||  |||||||
                                ACGT AGTC  GA  TCGTCGT
                                  C   GT  C_
GAM736  D1S155E  3'  TGCAGTGATCTAAGCAGCAGCA 28392     ATC  G  __
                                TGCA  GGT CTA  CAGCAGCA
                                ||||  ||| |||  ||||||||
                                ACGT  CTA GAT  GTCGTCGT
                                  CA_  _  TC
GAM736  DACH     3'  TACAATTGTCCAGCAGC     38879      CGG  CTA
                                TGCAAT  TG  CAGCAGC
                                ||||||  ||  |||||||
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                                ATGTTA  AC  GTCGTCG
                                   ___  AG_
GAM736  DDX24   5'  ACCTCAGCTGCAGCAGCA   33825    GGT  A
                                ATC  GCT CAGCAGCA
                                |||  ||| ||||||||
                                TGG  CGA GTCGTCGT
                                  AGT  C
GAM736  DLK1    3'  TGCGTTTGTCACACAGCAGCA 19267    AATCG  GC
                                TGC   GT  TACAGCAGCA
                                |||   ||  ||||||||||
                                ACG   CA  GTGTCGTCGT
                                  CAAA_  GT
GAM736  DUSP7   5'  GCAGTCGAGCAGCAGC     42272    A   T  TAC
                                GCA TCGG GC  AGCAGC
                                ||| |||| ||  ||||||
                                CGT AGCT CG  TCGTCG
                                  C   _ ___
GAM736  FVT1    3'  TACAAAAATATTACAGCAG   13032     TC   C
                                TGCAA  GGTG TACAGCAG
                                |||||  |||| ||||||||
                                ATGTT  TTAT ATGTCGTC
                                   T_   A
GAM736  GLUD1   3'  GCAATTTTATTACAGCAGCA  23588     CGG  C
                                GCAAT  TG TACAGCAGCA
                                |||||  || ||||||||||
                                CGTTA  AT ATGTCGTCGT
                                   AA_  A
GAM736  GRN     5'  CGGTCCTTGGGCAGCAGCA   13292     G  A___
                                CGGT CT   CAGCAGCA
                                |||| ||   ||||||||
                                GCCA GA   GTCGTCGT
                                  G  ACCC
GAM736  HERC2   3'  TACAGTCTACACAGCAGC    21694     A  GG  T
                                TGCA TC  TGC ACAGCAGC
                                |||| ||  ||| ||||||||
                                ATGT AG  ATG TGTCGTCG
                                  C  __  _
GAM736  ITGA1   3'  TCAGCAAACTTTACAGCAG   41855      __  __
                                TCGGT  GCT  ACAGCAG
                                |||||  |||  |||||||
                                AGTCG  TGA  TGTCGTC
                                   TT  AA
GAM736  ITGB3   3'  GCAAATGTCTACAGCAG     6839      TCG  G
                                GCAA  GT CTACAGCAG
                                ||||  || |||||||||
                                CGTT  CA GATGTCGTC
                                  TA_ _
GAM736  LIPE    3'  TGCGGCGGTCGCCGCAGCAGCA 23814     AAT  _  TA
                                TGC  CGGT GC  CAGCAGCA
                                |||  |||| ||  ||||||||
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                                ACG   GCCA CG  GTCGTCGT
                                  CC_   G  GC
GAM736  LMO4     5'  TGCAATCGCTGCTGCA      27663         G    ACA
                                TGCAATCG TGCT   GCA
                                |||||||| ||||   |||
                                ACGTTAGC ACGA   CGT
                                    G   ___
GAM736  NDP      3'  TGAAATCGGTAACCTTTAGCAG 7053     C       _ AC_
              CA                  TG AATCGGTG CT   AGCAGCA
                                || |||||||| ||   |||||||
                                AC TTAGCCAT GG   TCGTCGT
                                 T       T  AAA
GAM736  NRXN2    3'  TGCACGTCGCCCGGCGGCA   31492      AT  G    ACA  A
                                TGCA  CG TGCT   GC GCA
                                ||||  || ||||   || |||
                                ACGT  GC GCGG   CG CGT
                                  __ A   GC_  C
GAM736  PPP1R12B 3'  TGCGGTCAGTGCTGGCA    36983     AA       ACA
                                TGC  TCGGTGCT   GCA
                                |||  ||||||||   |||
                                ACG  AGTCACGA   CGT
                                  CC       C__
GAM736  PRKWNK3  3'  TGAAATCGTAAAACAGCAGCA  41540    C    GTGCT
                                TG AATCG    ACAGCAGCA
                                || |||||    |||||||||
                                AC TTAGC    TGTCGTCGT
                                 T    ATTT_
GAM736  RAD9     3'  TGAATCAATAGCAG       21376    C      GCTAC
                                TG AATCGGT    AGCAG
                                || |||||||    |||||
                                AC TTAGTTA    TCGTC
                                 _     ______
GAM736  TMEFF2   5'  TGCAACTCTGCAGCAGCA    32108       CGGTG  A
                                TGCAAT    CT CAGCAGCA
                                ||||||    || ||||||||
                                ACGTTG    GA GTCGTCGT
                                    A____  C
GAM736  TSN      3'  TGTAACCATTACACAGCAG   21500    C    G   T
                                TG AATCG TGC ACAGCAG
                                || ||||| ||| |||||||
                                AC TTGGT ATG TGTCGTC
                                 A    A  _
GAM736  WHSC1    3'  CCGAGACCTGCAGCAGCA    39401     GT   A_
                                TCG  GCT  CAGCAGCA
                                |||  |||  ||||||||
                                GGC  TGG  GTCGTCGT
                                  TC   AC
GAM737  AGRN     3'  ACTGGGCTGGGGCTGGGGGTG  44245     TC_     A  AGA
                                ACT   CTGGGG CT   GGTG
                                |||   |||||| ||   ||||
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                                TGA  GACCCC GA  CCAC
                                  CCC     _ CCC
GAM737  B3GNT3   3' CTTCCTGGGAGGAAGGTG   30678        ACTA
                                CTTCCTGGGG   GAGGTG
                                ||||||||||   ||||||
                                GAAGGACCCT   TTCCAC
                                     CC__
GAM737  C5R1     3' TCCTGGGGATCCCTGTG    11925        _ AGAG
                                TCCTGGGGA CT   GTG
                                ||||||||| ||   |||
                                AGGACCCCT GG   CAC
                                     A  GA__
GAM737  CLDN3    3' CTTCCTGGCTTCTGGGGGTG  10567       GGA  AGA
                                CTTCCTGG  CT  GGTG
                                ||||||||  ||  ||||
                                GAAGGACC  GA  CCAC
                                     GAA  CCC
GAM737  GCNT3    3' AACTACTAGGGTTAGGGGTG  21904     TC    AC  A
                                AACT  CTGGGG  TAG GGTG
                                ||||  ||||||  ||| ||||
                                TTGA  GATCCC  ATC CCAC
                                  T_    A_  C
GAM737  MEN1     3' CTCCCCGGGCTGGAGGTG    39178       GA  A
                                CTTCCTGGG  CT GAGGTG
                                |||||||||  || ||||||
                                GAGGGGCCC  GA CTCCAC
                                     __  C
GAM737  PAEP     3' CTTCCTGGAGGCGGAGGTG   15068        ACTA
                                CTTCCTGGGG   GAGGTG
                                ||||||||||   ||||||
                                GAAGGACCTC   CTCCAC
                                     CGC_
GAM737  RABIF    3' CCTCCTGAATAGTAGAGGTG  16124       GAC
                                CTTCCTGGG   TAGAGGTG
                                |||||||||   ||||||||
                                GGAGGACTT   ATCTCCAC
                                     ATC
GAM737  RAD54L   5' TTCCCAGGGCTGGAGGTG   18717     TG  A  A
                                TTCC  GGG CT GAGGTG
                                ||||  ||| || ||||||
                                AAGG  CCC GA CTCCAC
                                  GT   _  C
GAM738  NRXN1    3' TGATGCTGTAGTACTCCTTT  39851       AC    GA
                                TGATGCTG  AGTAT  TTTT
                                ||||||||  |||||  ||||
                                ACTACGAC  TCATG  GAAA
                                     A_    AG
GAM738  GSK3B    3' AAGTAACTGGTGGTTTTTCC  13301       TT_  GA
                                AAGTAACTG   GTT  TCC
                                |||||||||   |||  |||
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                                TTCATTGAC  CAA  AGG
                                     CAC  AA
GAM738  HIP1    3'  AAGTAGTGTTGTTGATC    23746      AC
                                AAGTA  TGTTGTTGATC
                                |||||  ||||||||||
                                TTCAT  ACAACAACTAG
                                  C_
GAM738  PVT1    3'  GCAACTGTTGTCCCCC     42308          GA
                                GTAACTGTTGTT  TCCC
                                ||||||||||||  ||||
                                CGTTGACAACAG  GGGG
                                       __
GAM738  XPO1    3'  AACTAACTGTGTTCCCATA   18159   G      T  TGA
                                AA TAACTGT GT   TCCCATA
                                || ||||||| ||   |||||||
                                TT ATTGACA CA   AGGGTAT
                                 G     _ ___
GAM739  B4GALT5  3'  TGCTATAGCTTACCG      21943        AAGGC
                                TGCTATAG    TTTACCG
                                ||||||||    |||||||
                                ACGATATC    GAATGGC
                                      _____
GAM739  CDS2    3'  TGCATAGAAGGCTTACC     19217    T        T
                                TGC ATAGAAGGCTT ACC
                                ||| ||||||||||| |||
                                ACG TATCTTCCGAA TGG
                                  _       _
GAM739  LIMD1   3'  TGCTAGGGGCTCCACTGAC   30637      TAGAA      C
                                TGCTA    GGCTTTAC GAC
                                |||||    |||||||| |||
                                ACGAT    CCGAGGTG CTG
                                   CC___       A
GAM739  MUCDHL  3'  TGCGTAGAAGGCTCCCG    36322    TA       TA
                                TGC  TAGAAGGCTT  CCG
                                |||  ||||||||||  |||
                                ACG  ATCTTCCGAG  GGC
                                  C_        __
GAM739  PCDH11X  5'  TGCTGTAGCGGGCTCTAC   37314     A   AA
                                TGCT TAG  GGCTTTAC
                                |||| |||  ||||||||
                                ACGA ATC  CCGAGATG
                                  C   GC
GAM739  PCDH11Y  5'  TGCTGTAGCGGGCTCTAC   37354     A   AA
                                TGCT TAG  GGCTTTAC
                                |||| |||  ||||||||
                                ACGA ATC  CCGAGATG
                                  C   GC
GAM739  PUM2    3'  TGTTATAAAAGGTTTCAC    31666    C       C
                                TG TATAGAAGG TTTAC
                                || |||||||| |||||
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```
                                AC ATATTTTCC AAGTG
                                 A       A
GAM739  TEM7    3'  TGCTACAGAGCAGACCATTGAC 33817        __    TTACC
                                TGCTATAGA  AGGCT    GAC
                                |||||||||  |||||    |||
                                ACGATGTCT  TCTGG    CTG
                                     CG    TAA__
GAM740  CRLF1   5'  CGGGCTGCGGCTCGGCGGCG  21898    A  C  A  C
                                CG GC GC GC CGGCGGTG
                                || || || || ||||||||
                                GC CG CG CG GCCGCCGC
                                 C  A  C  A
GAM741  B3GALT2 5'  TGCCTCCTGCGATTGCTT    19115       CTA   CC
                                TGTCTCC   CGA  GCTT
                                |||||||   |||  ||||
                                ACGGAGG   GCT  CGAA
                                    AC_   AA
GAM741  LFG     3'  AGCTGTGTCCCCTACCCCC   44130    C    T    GA
                                AGC GTGTC CCCTAC  CC
                                ||| ||||| ||||||  ||
                                TCG CACAG GGGATG  GG
                                  A    _     GG
GAM742  BLAME   3'  TCCTGCAAAACGGTGCCCATCT 33496    GG  C  _      C
                                TCC  GCG GA GGTGCCCA CT
                                |||  ||| || |||||||| ||
                                AGG  CGT TT CCACGGGT GA
                                  A_   T  G       A
GAM742  CCNG1   5'  TCCCCGGGCCTGCTCACC    19769        GCGAGG   C
                                TCTCCGGGC     TGC CACC
                                |||||||||     ||| ||||
                                AGGGGCCCG     ACG GTGG
                                     G_____   A
GAM742  CPNE7   3'  TCTCGGGCGTGGGGGGACTGCC 30872     C    CGA  ____
                                TCTC GGGCG   GG    TGCC
                                |||| |||||   ||    ||||
                                AGAG CCCGC   CC    ACGG
                                  _    ACC  CCTG
GAM742  FDFT1   5'  CCCGGGCGCGACTCTCTCACCT 20895          GGTGCC
                                TCCGGGCGCGA     CACCT
                                ||||||||||     |||||
                                GGGCCCGCGCT     GTGGA
                                      GAGAGA
GAM742  GADD45G 3'  TCTCCAGGCGCCCCCCCCGCCT 27462          GAGGTG   A
                                TCTCCGGGCGC     CCC CCT
                                ||||||||||     ||| |||
                                AGAGGTCCGCG     GGG GGA
                                      GGGG__   C
GAM742  HDAC5   3'  TCTGGGCCCCCGTGCCCACCT  40174    C   GCGAG
                                TC GGGC    GTGCCCACCT
                                || ||||    ||||||||||
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```
                                AG CCCG    CACGGGTGGA
                                 A   GGGG_
GAM742  IGFBP3   3'  TCTCTGGGCGTGAGCTCC    8265      C    C  GTG
                                TCTC GGGCG GAG   CC
                                |||| ||||| |||   ||
                                AGAG CCCGC CTC   GG
                                  A    A  GA_
GAM742  ITGAL    3'  TCCGGGCCCGTGCCC      13622       G GAG
                                TCCGGGC C   GTGCCC
                                |||||||| |   ||||||
                                AGGCCCG G   CACGGG
                                    G ___
GAM742  KRTHB6   3'  TCTCCTGGCGCGAGGTAC    14038      G
                                TCTCC GGCGCGAGGTGC
                                ||||| ||||||||||||
                                AGAGG CCGCGCTCCATG
                                   A
GAM742  LRP1     3'  TCCTGGGTGTGGCCCACC    14227    _  CGCGAG  _
                                TCC GGG     GTG CCCACC
                                ||| |||     ||| ||||||
                                AGG CCC     CAC GGGTGG
                                 A  A_____   C
GAM742  P3       3'  TCTGGGCAGCGCCCACC     33385    C   GCGA
                                TC GGGC    GGTGCCCACC
                                || ||||    ||||||||||
                                AG CCCG    TCGCGGGTGG
                                 A   _____
GAM742  PRDM16   3'  TCTCCGGGGCCCCGCCCGCCT  35249        C  GAGG    A
                                TCTCCGGG GC    TGCCC CCT
                                |||||||| ||    ||||| |||
                                AGAGGCCC CG    GCGGG GGA
                                    _ GG__     C
GAM743  FACL5    3'  CATAGACCCAATTTTTAA    42012           CC
                                TATAGACCCAAT  TTAA
                                ||||||||||||  ||||
                                GTATCTGGGTTA  AATT
                                      AA
GAM743  AGL      5'  AAGAGGGTCTTTTCCAGTTTCT 8484         T  C    A  C
          C                      AAGAGGGT CT TTCTA TT CTC
                                |||||||| || ||||| || |||
                                TTCTCCCA GA AAGGT AA GAG
                                    _ A    C  A
GAM743  ATP1A2   3'  GGGTAACCCTTAATTCCTC   8708      TCT  TC
                                GGGT   CT  TAATTCCTC
                                ||||   ||  |||||||||
                                CCCA   GG  ATTAAGGAG
                                  TT_  GA
GAM743  EBAF     3'  GAAGGTTTTAATTCC       42259        CTCTTC
                                GAGGGTT     TAATTCC
                                |||||||     |||||||
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                                CTTCCAA     ATTAAGG
                                   A_____
GAM743  EHF     3'  AAGAGGATTTTCCCTGGAAATT 29112        __    TCT
              C                    AAGAGGGT  TCTCT   AATTC
                                   ||||||||  |||||   |||||
                                   TTCTCCTA  AGGGA   TTAAG
                                      AA     CCT
GAM743  FHL1    3'  AGGGTTCTTTTCCTGCTC    11091        C    AA
                                   AGGGTTCT TTCT  TTC
                                   ||||||||  ||||  |||
                                   TCCCAAGA AAGG  GAG
                                      A    AC
GAM743  IL10    3'  AAGGGGCTCCCTGGTTTCT   8191      A       ____
                                   AAG GGGTTCTCT    TCT
                                   |||  |||||||||    |||
                                   TTC CCCGAGGGA    AGA
                                     _       CCAA
GAM743  PDYN    3'  AAGAGGGCTTTTTCTCTT    35919        ____
                                   AAGAGGGT    TCTCTT
                                   ||||||||    ||||||
                                   TTCTCCCG    AGAGAA
                                      AAAA
GAM743  RING1   3'  GAGGGTTCTTCACCTTCT    16334         ____
                                   GAGGGTTCT    CTTCT
                                   |||||||||    |||||
                                   CTCCCAAGA    GAAGA
                                      AGTG
GAM743  SH3BP5  3'  AAGAGGGTTGCTTTTTTCT   22121         _  C__
                                   AAGAGGGTT CT   TTCT
                                   |||||||||  ||   ||||
                                   TTCTCCCAA GA   AAGA
                                      C  AAA
GAM743  VIL2    3'  AGAGGGTTTTTCATATGTAATT 17998         C_  TTC__
              C                    AGAGGGTT  TC     TAATTC
                                   ||||||||  ||     ||||||
                                   TCTCCCAA  AG     ATTAAG
                                      AA  TATAC
GAM744  FACL5   3'  ATTGATTTATTTGGGAACTA   42011       A       T
                                   ATTGA TTATTTGG AACTA
                                   |||||  ||||||||  |||||
                                   TAACT AATAAACC TTGAT
                                      A       C
GAM744  PCDH11X 3'  ATTGCAATTTTTTGGTTAACTA 37295      _   A     _
                                   ATTG AATT TTTGGT AACTA
                                   ||||  ||||  ||||||  |||||
                                   TAAC TTAA AAACCA TTGAT
                                     G   A     A
GAM744  PCDH11Y 3'  ATTGCAATTTTTTGGTTAACTA 37334      _   A     _
                                   ATTG AATT TTTGGT AACTA
                                   ||||  ||||  ||||||  |||||
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                                TAAC TTAA AAACCA TTGAT
                                  G   A     A
GAM744  SLC11A3  3'  ACTGAATTCACGTGACTAACCA 31049        ATT  GTA
                                ATTGAATT   TG   ACTAACCA
                                ||||||||   ||  ||||||||
                                TGACTTAA   GC   TGATTGGT
                                    GT_  AC_
GAM745  DIO1     3'  CCGTGTGCAGGGAATGT     9001      CACA       T
                                CCG   GCAGGGAAT GT
                                |||   ||||||||| ||
                                GGC   CGTCCCTTA CA
                                 ACA_       _
GAM745  EPHA2    3'  GCACAGCAGGGAGGCCAC    20738          ATT  A
                                GCACAGCAGGGA   GT GC
                                ||||||||||||   || ||
                                CGTGTCGTCCCT   CG TG
                                       C__  G
GAM745  FRAT2    3'  GCACAGCAATTGTAGCAC    28972        GGGA
                                GCACAGCA   ATTGTAGCAC
                                ||||||||   ||||||||||
                                CGTGTCGT   TAACATCGTG
                                           _____
GAM745  FZD7     3'  CCTGCAGCAGGGGGATCGC   18631    GCA      A_
                                CC   CAGCAGGG  ATTGT
                                ||   ||||||||  |||||
                                GG   GTCGTCCC  TAGCG
                                 AC_       CC
GAM745  GATA4    3'  CCGGCAGCAGGGGGAAGGCAC  13107    CA      AATTGTA
                                CCG  CAGCAGGG      GCAC
                                |||  ||||||||      ||||
                                GGC  GTCGTCCC      CGTG
                                 C_       CCTTC__
GAM745  GPM6A    3'  ACAGCATTCTTGTAGCA     23612       GGGAA
                                ACAGCA    TTGTAGCA
                                ||||||    ||||||||
                                TGTCGT    AACATCGT
                                   AAG__
GAM745  INHBB    5'  CCGCGCGGCAGGGAAGGGGCGC 13550      ACA      TTGTA
                                CCGC   GCAGGGAA    GC
                                ||||   ||||||||    ||
                                GGCG   CGTCCCTT    CG
                                  CGC       CCCCG
GAM745  JAG2     3'  GCGCAGCAGGAAGGGCA     13724    A       ATTGTA
                                GC CAGCAGGGA     GCA
                                || |||||||||     |||
                                CG GTCGTCCTT     CGT
                                 C        CC____
GAM745  KLK10    3'  CACACAGCGGGGAGTGGC    15770        A   ATT  A
                                CGCACAGC GGGA   GT GC
                                |||||||| ||||   || ||
```

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                                GTGTGTCG CCCT   CA CG
                                    C    ___  C
GAM745  LENG4   3'  CGCAGCAGGGCCGACAGTGC  35883     CA     AATT__  A
                                CGCA  GCAGGG     GT GC
                                ||||  ||||||     || ||
                                GCGT  CGTCCC     CA CG
                                  __     GGCTGT  _
GAM745  MCCC2   3'  GCACAGCAGTGTGAGGGCAC  35251        GGAAT  TA_
                                GCACAGCAG    TG   GCAC
                                |||||||||    ||   ||||
                                CGTGTCGTC    AC   CGTG
                                     AC___  TCC
GAM745  PSEN1   3'  ACAGCAGGGCTGACAGCAC   28736         AA  _
                                ACAGCAGGG  TTG TAGCAC
                                |||||||||  ||| ||||||
                                TGTCGTCCC  GAC GTCGTG
                                    __   T
GAM745  SLC9A6  3'  GCATAGCAGGAAAGTCGC    26829     C       TT  A
                                GCA AGCAGGGAA  GT GC
                                ||| |||||||||  || ||
                                CGT TCGTCCTTT  CA CG
                                  A        __ G
GAM745  TRIM14  3'  AGCAGGGATTACAGGCAC    37694        A     _
                                AGCAGGGA TTGTAG CAC
                                |||||||| |||||| |||
                                TCGTCCCT AATGTC GTG
                                    _     C
GAM745  ZNF157  3'  CACAGCACACTGTGGTGC    18352       GGGA    A__
                                CACAGCA    ATTGT   GC
                                |||||||    |||||   ||
                                GTGTCGT    TGACA   CG
                                   G___     CCA
GAM745  CYP7A1  3'  GCTACCACACCTGGCTGTAATG 8938     C   _   A_  CGC
                                GC ACCA ACCT  CTG   ATG
                                || |||| ||||  |||   |||
                                CG TGGT TGGA  GAC   TAC
                                 A   G    CC   AT_
GAM745  DPH2L1  5'  CGCCATCACCTGCCTGCGCATG 10726      CCA   A_
                                CGCCA   ACCT  CTGCGCATG
                                |||||   ||||  |||||||||
                                GCGGT   TGGA  GACGCGTAC
                                  AG_   CG
GAM745  FBXL5   5'  CGCCCCCTTGCGCATGC     37946      A  AACCTAC
                                CGCC CC      TGCGCATGC
                                |||| ||      |||||||||
                                GCGG GG      ACGCGTACG
                                  _ GA_____
GAM745  GCN1L1  3'  GCCATTTGCTGAGGCGCATGCG 43068      CCAAC  ACT
                                GCCA    CT   GCGCATGCG
                                ||||    ||   |||||||||
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                                CGGT    GA  CGCGTACGC
                                  AAAC_ CTC
GAM745  NAP1    3'  CGCGACCACCCGCTGCGCATGC 22136    C   A  TA
          G                      CGC ACCA CC  CTGCGCATGCG
                                 ||| |||| ||  ||||||||||
                                 GCG TGGT GG  GACGCGTACGC
                                   C   _  GC
GAM745  SORCS3  3'  CCCCACCAACCTACTTCCTGCG 31415   G         GCGCA
                                 C CCACCAACCTACT    TGCG
                                 | ||||||||||||    ||||
                                 G GGTGGTTGGATGA    ACGC
                                  G          AGG__
GAM746  HNRPH3  3'  TGTCAAGCTCTATTCCA    29193       CGGTACG
                                 TGTCAAGT     TATTCCA
                                 ||||||||     |||||||
                                 ACAGTTCG     ATAAGGT
                                      AG_____
GAM746  PIGN    3'  TGTCAATTCGGAATTCCAA   29553      G   TACGT
                                 TGTCAA TCGG    ATTCCAA
                                 |||||| ||||    |||||||
                                 ACAGTT AGCC    TAAGGTT
                                    A   T____
GAM746  AP2B1   3'  AACTTCTGTCAGCTTT     10478     A  ACC
                                 AACT CT   GTCAGCTTT
                                 |||| ||   |||||||||
                                 TTGA GA   CAGTCGAAA
                                   A ___
GAM746  GBP1    3'  ACTATCATAAGCTTTAAC    13114     C  C
                                 ACTA CGT AGCTTTAAC
                                 |||| ||| |||||||||
                                 TGAT GTA TCGAAATTG
                                   A  T
GAM746  SFRP1   3'  AAAACTACTGCCTTCTCAGC  16565       A  G__
                                 AAAACTACT CC   TCAGC
                                 ||||||||| ||   |||||
                                 TTTTGATGA GG   AGTCG
                                      C  AAG
GAM746  SLC26A2  3'  AAAACTACTGCCATCTGGGGAG 6470        A   _____
          C                      AAAACTACT CCGTC    AGC
                                 |||||||| |||||    |||
                                 TTTTGATGA GGTAG    TCG
                                      C    ACCCC
GAM746  SOX11   3'  AAAACTACTCATTTCACTTTAA 16997        ACCG  G
          C                      AAAACTACT   TCA CTTTAAC
                                 |||||||||   ||| |||||||
                                 TTTTGATGA   AGT GAAATTG
                                      GTAA  _
GAM747  ITPKB   3'  TGTCTTGTAGTGCAGTTCAGGA 13661         ACAAACG  T
                                 TGTCTTGTAG     CA GA
                                 ||||||||||     || ||
```

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                                ACAGAACATC      GT CT
                                      ACGTCAA  C
GAM747  NFKB1    3'  TGTCTTGTGGACAACGCAGTG  19656        A    A   _
                                TGTCTTGT GACAA CGCA TG
                                |||||||| ||||| |||| ||
                                ACAGAACA CTGTT GCGT AC
                                     C    _   C
GAM747  ARNT2    3'  TATCTACATCTGTAAAGAA   31363     A      CTTGC
                                TATC TACATCTG    AAGAA
                                |||| ||||||||    |||||
                                ATAG ATGTAGAC    TTCTT
                                  _      AT___
GAM747  GJA1     3'  TGACATGCATGCAAGA     6732    T   TC   T
                                A ACA  TGC TGCAAGA
                                | |||  ||| |||||||
                                A TGT  ACG ACGTTCT
                                 C  __  T
GAM747  GSBS     3'  CATACATCTCCTGGGGA     44997         G    CAA
                                CATACATCT CTTG   GA
                                ||||||||| ||||   ||
                                GTATGTAGA GGAC   CT
                                      _   CC_
GAM747  MEN1     3'  TATCATATACTCACAACAGGAA 39227        CATC    TG  ___
          G                      TATCATA    TGCT  CAA   GAAG
                                |||||||    ||||  |||   ||||
                                ATAGTAT    ATGA  GTT   CTTC
                                     _____   GT   GTC
GAM747  PXF      3'  TATCACACAGCATTGTAGGAAG 16012         TCT  _   CAA
                                TATCATACA   GC TTG   GAAG
                                |||||||||   || |||   ||||
                                ATAGTGTGT   CG AAC   CTTC
                                      ___  T   ATC
GAM748  ATM      3'  GAGGATGCAGTGAGCCGTG   39634    A       _
                                GA GATGCAGTG GTTGTG
                                || ||||||||| ||||||
                                CT CTACGTCAC CGGCAC
                                 C        T
GAM748  GPR44    3'  ACGGGGTGCAGTGGAAGTG   21950     AAGA      TT
                                ACG    TGCAGTGG  GTG
                                |||    ||||||||  |||
                                TGC    ACGTCACC  CAC
                                  CCC_       TT
GAM748  GRIN2A   5'  CGAGGATGCAGTGGGGCGCG   9108      A        TTGT
                                CGA GATGCAGTGG    GCGCG
                                ||| ||||||||||    |||||
                                GCT CTACGTCACC    CGCGC
                                  C         C___
GAM748  KCNS2    5'  CGCGGGTGCGAGTGTGTGCG   42823    AAGA  _   GT
                                CG    TGC AGTG  TGTGCG
                                ||    ||| ||||  ||||||
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                                GC    ACG TCAC  ACACGC
                                 GCCC   C   __
GAM748  LAMP1    5'  CGGAGAGCGGGGTCGCGTGCGC 24505    A   T  AGT   __
              G                  CG AGA GC   GGTT  GTGCGCG
                                 || ||| ||   ||||  |||||||
                                 GC TCT CG   CCAG  CACGCGC
                                  C   _  CC_   CG
GAM748  OTX1     3'  CGGGATGCGGCTCTGTGCGCG  30986    AA    A  GG
                                 CG  GATGC GT  TTGTGCGCG
                                 ||  ||||| ||  |||||||||
                                 GC  CTACG CG  GACACGCGC
                                  C_    C  A_
GAM748  TMEPAI   3'  CGGGGACGTGGGTGCGC    33606    AA   GCA   TT
                                 CG  GAT   GTGG  GTGCGC
                                 ||  |||   ||||  ||||||
                                 GC  CTG   CACC  CACGCG
                                  CC   ____   __
GAM748  TNXB     5'  GAGGAGCAGTGGCAGTG     37156    A  T      T
                                 GA GA GCAGTGGT GTG
                                 || || |||||||| |||
                                 CT CT CGTCACCG CAC
                                  C  _       T
GAM748  DNAH9    5'  TTTCACTTCAGTCACCTTGGC  21672          ___    T
                                 TTTTACTTCA   ATCTT GC
                                 ||||||||||   ||||| ||
                                 AAAGTGAAGT   TGGAA CG
                                       CAG    C
GAM748  NCAM1    3'  TTTTATTTTGATCTTTGCTCGG 8321       C  CA      G
                                 TTTTA TT  ATCTTTGC TCGG
                                 ||||| ||  |||||||| ||||
                                 AAAAT AA  TAGAAACG AGCC
                                    A  AC      _
GAM748  SIP      3'  TTTTACTCAATTTTTACACTGG 30849        T   C     TC
                                 TTTTACT CAAT TTTGCG  GG
                                 ||||||| |||| ||||||  ||
                                 AAAATGA GTTA AAATGT  CC
                                     _   A     GA
GAM749  ACPT     3'  CAGCAGCTCGTGGTATCGGGGA 38885        GCTCG___  CAGA
              CAG                   CAGCAGCT       CG    GACAG
                                 ||||||||       ||    |||||
                                 GTCGTCGA       GC    CTGTC
                                      GCACCATA  CC__
GAM749  ACTA2    3'  ACAGTTGTGTGCTAGAGACAG  11516     C  CTC  GC
                                 GCAG TG   GC  AGAGACAG
                                 |||| ||   ||  ||||||||
                                 TGTC AC   CG  TCTCTGTC
                                   A  ACA  A_
GAM749  ADARB1   3'  CAGTGCTGCCAGAGAC      31872     C    C  G
                                 CAG TGCT GC CAGAGAC
                                 ||| |||| || |||||||
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                                GTC ACGA CG GTCTCTG
                                  _   _ _
GAM749  ALDOB    5'  CAGCAGCTGCCAAATAAGACAG 42769          CGCGCA
                                CAGCAGCTGCT     GAGACAG
                                ||||||||||      |||||||
                                GTCGTCGACGG     TTCTGTC
                                    TTTA__
GAM749  ARF3     5'  CAGCAGCTGCTTTCTGGGGACA 11667          CGCGCAGA
          G                      CAGCAGCTGCT       GACAG
                                ||||||||||        |||||
                                GTCGTCGACGA       CTGTC
                                    AAGACCC_
GAM749  CASP8    5'  CAGGGGCTGCTCAGACAG    37869     CA       C
                                CAG  GCTGCTCG GCAG
                                |||  |||||||| ||||
                                GTC  CGACGAGT TGTC
                                  CC       C
GAM749  CAST     5'  GCGGCCGCTCGCGATCTAG    11982     A        CAG_
                                GC GCTGCTCGCG    AG
                                || ||||||||||    ||
                                CG CGGCGAGCGC    TC
                                 C         TAGA
GAM749  CD164    3'  CAGCAGCTATTTAAAATAAGAC 25680          CTCGCGCA
          AG                     CAGCAGCTG       GAGACAG
                                |||||||||       |||||||
                                GTCGTCGAT       TTCTGTC
                                    AAATTTTA
GAM749  CD22     3'  CAGCAGCTCCGGGTGGAGA    12099         G T  CGCA
                                CAGCAGCT C CG    GAGA
                                |||||||| | ||    ||||
                                GTCGTCGA G GC    CTCT
                                   _ _  CCAC
GAM749  DAP      3'  GCAGCTGCTCACGACACAG    43690           _  G
                                GCAGCTGCTCGCG CA AG
                                |||||||||||| || ||
                                CGTCGACGAGTGC GT TC
                                      T  G
GAM749  DES      3'  ACAGCTGGGGTCCGCAGAG    43558         C__  G
                                GCAGCTG   TC CGCAGAG
                                |||||||   || |||||||
                                TGTCGAC   AG GCGTCTC
                                   CCC  _
GAM749  DXYS155E 3'  CAGCAGCCGCTCGCGCAG    22943
                                CAGCAGCTGCTCGCGCAG
                                ||||||||||||||||||
                                GTCGTCGGCGAGCGCGTC

GAM749  JAM3     3'  CAGCAGCTCCTTGCTTTACAG  37260         G  C  ___
                                CAGCAGCT CT GC   GCAG
                                |||||||| || ||   ||||
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                                GTCGTCGA GA CG   TGTC
                                     G  A  AAA
GAM749  KCNQ1    3'  CAGCAGCTGGCAAGGGGAG   6882         CTC   CA__
                                CAGCAGCTG   GCG    GAG
                                |||||||||   |||    |||
                                GTCGTCGAC   CGT    CTC
                                     ___   TCCC
GAM749  LAMP1    5'  GCGCTGGCGTTAGAGACAG   24508    A   CTC   C_
                                GC GCTG   GCG  AGAGACAG
                                || ||||   |||  ||||||||
                                CG CGAC   CGC  TCTCTGTC
                                 _   ___   AA
GAM749  MGAT4B   5'  GCTGCTCAAGGACA       38268        CGC  A
                                GCTGCTCG   AG GACA
                                ||||||||   || ||||
                                CGACGAGT   TC CTGT
                                     ___  _
GAM749  RALBP1   3'  CAGGAGCTGCTCAGACAG    27698     C       C
                                CAG AGCTGCTCG GCAG
                                ||| ||||||||| ||||
                                GTC TCGACGAGT TGTC
                                  C        C
GAM749  RET      3'  CAGTGGCTGCTCGCCAG     33928     CA       G
                                CAG  GCTGCTCGC CAG
                                |||  ||||||||| |||
                                GTC  CGACGAGCG GTC
                                  AC        _
GAM749  SUV39H2  3'  ACAGCTGCTCTCCAGGCAG   36007         GC___
                                GCAGCTGCTC    GCAG
                                ||||||||||    ||||
                                TGTCGACGAG    CGTC
                                     AGGTC
GAM749  TJP1     5'  AGTGGCCGCGCAGAGACA    17534    CT  T
                                AG  GC CGCGCAGAGACA
                                ||  || ||||||||||||
                                TC  CG GCGCGTCTCTGT
                                 AC  _
GAM749  TNFRSF8  3'  GCCGCTGCAGCAGAGACAG   10321       C  _
                                GCTGCT GC GCAGAGACAG
                                |||||| || ||||||||||
                                CGGCGA CG CGTCTCTGTC
                                   _  T
GAM749  ABCC1    5'  GGCGCGGGCGGCGGCG      33411          AGA
                                GGCGCGGGCGGC   GCG
                                ||||||||||||   |||
                                CCGCGCCCGCCG   CGC
                                       C__
GAM749  ABCC1    5'  GGCGCGGGCGGCGGCG      33405          AGA
                                GGCGCGGGCGGC   GCG
                                ||||||||||||   |||
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                                CCGCGCCCGCCG  CGC
                                      C__
GAM749  ACTN2   5'  CGGGCGCGGGGTGACCTTCGCG 9941          C_  AGAG
          CG                    CGGGCGCGGG  GGC   CGCGCG
                                |||||||||  |||   ||||||
                                GCCCGCGCCC  CTG   GCGCGC
                                     CA  GAA_
GAM749  ACTN2   5'  CGGGCGGCGGGCGGCGGGCGCG 9943        _       AGA
                                CGGGCG CGGGCGGC  GCGCG
                                ||||||  ||||||||  |||||
                                GCCCGC GCCCGCCG  CGCGC
                                   C      CC_
GAM749  ALPL    5'  CGGGCGCGGAGTGGCGGGAGCG 7886          _ C  A_
                                CGGGCGCGG G GGC  GAGCG
                                |||||||| | |||  |||||
                                GCCCGCGCC C CCG  CTCGC
                                     T A  CC
GAM749  ANKH    5'  CGGGCGCGGCGGCGGCG    38314         G   AGA
                                CGGGCGCGG CGGC  GCG
                                |||||||| ||||  |||
                                GCCCGCGCC GCCG  CGC
                                     _   C__
GAM749  BCL11A  5'  CGGGGCGGGCGGCGGCG    39710     C       AGA
                                CGGG GCGGGCGGC  GCG
                                |||| |||||||||  |||
                                GCCC CGCCCGCCG  CGC
                                   _       C__
GAM749  BCR     5'  GGGCGCGGGCTGCGCGC    34641         GGCAGA
                                GGGCGCGGGC    GCGCGC
                                ||||||||||    ||||||
                                CCCGCGCCCG    CGCGCG
                                     A_____
GAM749  BMP8    5'  CGGGCGGCGGGCGGCGGGGCG  11878       _      AGA
                                CGGGCG CGGGCGGC  GCG
                                ||||||  ||||||||  |||
                                GCCCGC GCCCGCCG  CGC
                                   C      CCC
GAM749  CACNA2D2  5'  GGGCGCGGGCGGCGGGCG    25719          AGA
                                GGGCGCGGGCGGC  GCG
                                ||||||||||||  |||
                                CCCGCGCCCGCCG  CGC
                                      CC_
GAM749  CALB1   5'  GGGCGCGGGCGCTGCCGGGCG  22312         __  AGA
                                GGGCGCGGGCG  GC  GCG
                                ||||||||||  ||  |||
                                CCCGCGCCCGC  CG  CGC
                                     GA  GCC
GAM749  CAPON   5'  GGGCGCGGCGACGCG      41928         G   AGA
                                GGGCGCGG CGGC  GCG
                                ||||||| ||||  |||
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                                CCCGCGCC GCTG   CGC
                                   _   ____
GAM749  CD81    5'  GGCGCGGGCGGCGGGCG     20344          AGA
                                GGCGCGGGCGGC   GCG
                                ||||||||||||  |||
                                CCGCGCCCGCCG   CGC
                                      CC_
GAM749  CD81    5'  CGGGCGGCGGGCGGCCTGCG  20342      _      AGA
                                CGGGCG CGGGCGGC   GCG
                                ||||||| ||||||||  |||
                                GCCCGC GCCCGCCG   CGC
                                   C       GA_
GAM749  CDC6    3'  GGGCGCGGTGGTGGGCAC    10363        GC  CAGA
                                GGGCGCGG  GG    GCGC
                                ||||||||  ||    ||||
                                CCCGCGCC  CC    CGTG
                                     A_  ACC_
GAM749  CRLF1   5'  CGGGCGCGGGAGGGCGCG    21897          C  CAGA
                                CGGGCGCGGG GG    GCGCG
                                ||||||||||  ||    |||||
                                GCCCGCGCCC CC    CGCGC
                                      T  _____
GAM749  DAG1    5'  GAGCGCAAGGGCGGGGCGCGCG 20521        __     CAGA
                                GGGCGC  GGGCGG    GCGCGCG
                                ||||||  ||||||    |||||||
                                CTCGCG  CCCGCC    CGCGCGC
                                   TT     C___
GAM749  DDEF2   5'  CGGGCGCGGGAGCCGCGC    19317          C   AGAG
                                CGGGCGCGGG GGC    CGCGC
                                ||||||||||  |||    |||||
                                GCCCGCGCCC TCG    GCGCG
                                   _  _____
GAM749  EGR1    5'  GGGCGCGGGCGGGCG       12664          CAGA
                                GGGCGCGGGCGG    GCG
                                ||||||||||||    |||
                                CCCGCGCCCGCC    CGC
                                      _____
GAM749  ELOVL4  5'  CGGGCGCTGGCGGCAGGAGAAA 35540        G       _  CGC
          GCG                     CGGGCGC GGCGGCAG AG   GCG
                                ||||||| |||||||  ||   |||
                                GCCCGCG CCGCCGTC TC   CGC
                                   A       C  TTT
GAM749  FABP5   5'  GGGTGCGGGCGGGCTGGCG   11066     C       CAGA  GC
                                GGG GCGGGCGG    GC  GCG
                                |||  ||||||||    ||  |||
                                CCC CGCCCGCC    CG  CGC
                                  A       _____  AC
GAM749  FACL4   5'  CGGGCGGAGCGGGGGCGCGCG  35677       C     CAGA
                                CGGGCG GGGCGG    GCGCGCG
                                ||||||  ||||||    |||||||
```

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                                GCCCGC CTCGCC    CGCGCGC
                                   _     CC__
GAM749  FASN    5'  GGTGCGGGCGGCGGAGAGCG  19943    C       A  C
                                GG GCGGGCGGC GAG GCG
                                || ||||||||| ||| |||
                                CC CGCCCGCCG CTC CGC
                                 A       C  T
GAM749  FASN    5'  GGGCGCGGGCGGCGGTGCG   19941           AGA
                                GGGCGCGGGCGGC  GCG
                                ||||||||||||  |||
                                CCCGCGCCCGCCG  CGC
                                       CCA
GAM749  FBP1    5'  CAGGTGCGGGCGGCAGGTGCG 8000      C        A_
                                CGGG GCGGGCGGCAG  GCG
                                |||| ||||||||||  |||
                                GTCC CGCCCGCCGTC  CGC
                                  A         CA
GAM749  FOXG1B  5'  CGGGAGCGGGACAGCGGCGCGC 23504     C   _   AGA
          G                      CGGG GCGGG CGGC   GCGCGCG
                                |||| ||||| ||||   |||||||
                                GCCC CGCCC GTCG   CGCGCGC
                                  T    T   C__
GAM749  GALR1   5'  GCGAGCGGCGGGGCGCGCG   11202         AGA
                                GCGGGCGGC   GCGCGCG
                                |||||||||   |||||||
                                CGCTCGCCG   CGCGCGC
                                     CCC
GAM749  GTF2I   5'  CGGCCGCGGCTGGAGAGCGCG 37436    G    GC  C
                                CGG CGCGG  GG AGAGCGCG
                                ||| |||||  || ||||||||
                                GCC GCGCC  CC TCTCGCGC
                                  G    GA  _
GAM749  HAGH    5'  CGGGCGCAGGCGGCTCCCAGCG 23710           AG__
          CG                     CGGGCGCGGGCGGC   AGCGCG
                                ||||||||||||||   ||||||
                                GCCCGCGTCCGCCG   TCGCGC
                                       AGGG
GAM749  HDAC4   5'  CGGGCTCGGGCGGCGGCG   25765      G      AGA
                                CGGGC CGGGCGGC   GCG
                                ||||| ||||||||   |||
                                GCCCG GCCCGCCG   CGC
                                   A       C__
GAM749  HDAC4   5'  GGCGCGGGCGGGTGCGCG   25775          CAGA
                                GGCGCGGGCGG   GCGCG
                                ||||||||||   |||||
                                CCGCGCCCGCC   CGCGC
                                      CA__
GAM749  HIC1    5'  CGGGCGCGGGGGCAGCTCGCG 44565         C    AG
                                CGGGCGCGGG GGCAG  CGCG
                                |||||||||| |||||  ||||
```

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                                GCCCGCGCCC CCGTC  GCGC
                                      _    GA
GAM749  HR      5'  GGCGCGGGCGGTGGCG     32928          CAGA
                                GGCGCGGGCGG   GCG
                                ||||||||||   |||
                                CCGCGCCCGCC   CGC
                                      AC__
GAM749  HSF4    5'  CAGGCGCGGGCAGTGCGCG   40763           CAGA
                                CGGGCGCGGGCGG   GCGCG
                                ||||||||||||   |||||
                                GTCCGCGCCCGTC   CGCGC
                                       A___
GAM749  IGF2R   5'  CGGGCGCGAGGCTAACGGCGCG 9335        _  GGCAGA
           CG                     CGGGCGCG GGC     GCGCGCG
                                ||||||||| |||     |||||||
                                GCCCGCGC CCG     CGCGCGC
                                     T   ATTGC_
GAM749  IGFBP4  5'  GGGCGCAGGCGGGGAGCGCGCG 11405          CA
                                GGGCGCGGGCGG  GAGCGCGCG
                                ||||||||||||  |||||||||
                                CCCGCGTCCGCC  CTCGCGCGC
                                       C_
GAM749  INSM1   5'  CGGGCGCGGCGGCTGCG     13576        G   AGA
                                CGGGCGCGG CGGC   GCG
                                |||||||| ||||   |||
                                GCCCGCGCC GCCG   CGC
                                      _   A__
GAM749  IRS2    5'  GGCGCGGGCGGTGGCCG     40708          CAGA  G
                                GGCGCGGGCGG   GC CG
                                ||||||||||   || ||
                                CCGCGCCCGCC   CG GC
                                      AC__  _
GAM749  ISGF3G  5'  GGCGCGGGCAGCGCGCG     25883          AGA
                                GGCGCGGGCGGC  GCGCG
                                ||||||||||||  |||||
                                CCGCGCCCGTCG  CGCGC
                                       ____
GAM749  JAG2    5'  CGGGCCTGGGCGGCGGGCG   13717      GC     AGA
                                CGGGC  GGGCGGC  GCG
                                |||||  |||||||  |||
                                GCCCG  CCCGCCG  CGC
                                   GA     CC_
GAM749  JPH3    5'  CGGGCGCGGGCGGCCGCG    34017          AGAG
                                CGGGCGCGGGCGGC   CGCG
                                ||||||||||||||   ||||
                                GCCCGCGCCCGCCG   GCGC
                                       _____
GAM749  LAMC1   5'  GGCGCGGGCGGTGGCG      14087          CAGA
                                GGCGCGGGCGG   GCG
                                ||||||||||   |||
```

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                                CCGCGCCCGCC   CGC
                                      AC__
GAM749  LNK     3'  GGGCGCGGTGGCTCGCG    24206       GC  AGAG
                                GGGCGCGG GGC   CGCG
                                |||||||| |||   ||||
                                CCCGCGCC CCG   GCGC
                                    A_  A___
GAM749  MAFK    5'  CGGGCGCGCGGCGGCTCCTCGC 14317       _    AGAG
              G                  CGGGCGCG GGCGGC   CGCG
                                |||||||| ||||||   ||||
                                GCCCGCGC CCGCCG   GCGC
                                    G    AGGA
GAM749  MEN1    5'  CGGGCGGTGGGCGGCGGCG   39177      C_    AGA
                                CGGGCG GGGCGGC  GCG
                                ||||||  |||||||  |||
                                GCCCGC  CCCGCCG  CGC
                                   CA     C__
GAM749  MEN1    5'  CGGGCGGTGGGCGGCGGC    39248      C_    AGA
                                CGGGCG GGGCGGC  GC
                                ||||||  |||||||  ||
                                GCCCGC  CCCGCCG  CG
                                   CA     C__
GAM749  MEN1    5'  CGGGCGGTGGGCGGCGGCCTCC 39176      C_    AGA G__
              GCG                 CGGGCG GGGCGGC  GC  CGCG
                                ||||||  |||||||  ||  ||||
                                GCCCGC  CCCGCCG  CG  GCGC
                                   CA     C__ GAG
GAM749  MEN1    5'  CGGGCGGTGGGCGGCGGCTAC  39249      C_    AGA GC
                                CGGGCG GGGCGGC  GC GC
                                ||||||  |||||||  || ||
                                GCCCGC  CCCGCCG  CG TG
                                   CA     C__ A_
GAM749  MSL3L1  5'  CGGGGCGGGCGGAGCGCGC   38583    C     CAG
                                CGGG GCGGGCGG  AGCGCGC
                                |||| ||||||||  |||||||
                                GCCC CGCCCGCC  TCGCGCG
                                  _     ____
GAM749  NFYC    5'  GCGTCACGGAGCGCGC     30595    G_   CAG
                                GCG GCGG  AGCGCGC
                                |||  ||||  |||||||
                                CGC TGCC  TCGCGCG
                                  AG  ____
GAM749  NR2F2   5'  GGCTGCGGGCGGCGGCG    34238    _      AGA
                                GGC GCGGGCGGC  GCG
                                ||| |||||||||  |||
                                CCG CGCCCGCCG  CGC
                                  A       C__
GAM749  NRG2    3'  CGGGCGGGGCGGAGGGGCGCGC 30364      C    C  A_
              G                  CGGGCG GGGCGG AG  GCGCGCG
                                |||||| |||||| ||  |||||||
```

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                                GCCCGC CCCGCC TC  CGCGCGC
                                   _     _ CC
GAM749  NRIP1    5'  CGCGCGCGGGTGGCGGGCG   40959    G     C  AGA
                                CG GCGCGGG GGC   GCG
                                || ||||||| |||   |||
                                GC CGCGCCC CCG   CGC
                                 G      A   CC_
GAM749  NRIP1    5'  CGGGTGGCGGGCGGGCG    40960     C_      CAGA
                                CGGG  GCGGGCGG   GCG
                                ||||  ||||||||   |||
                                GCCC  CGCCCGCC   CGC
                                  AC       _____
GAM749  PDGFB    5'  CGGGCCCGGGCGGCGGGCACG  15176      G       AGA
                                CGGGC CGGGCGGC   GCGCG
                                ||||| ||||||||   |||||
                                GCCCG GCCCGCCG   CGTGC
                                   G       CC_
GAM749  PPP1CB   5'  CGGGTAGCGAGAGCGCGC    15502     CG  _
                                CGGG  GC AGAGCGCGC
                                ||||  || |||||||||
                                GCCC  CG TCTCGCGCG
                                  AT  C
GAM749  PPP2R5E  5'  CGGGGGCGGGCGGCGGGACCG  26469     C       A_  G
                                CGGG GCGGGCGGC  GA CG
                                |||| |||||||||  || ||
                                GCCC CGCCCGCCG  CT GC
                                  C        CC  G
GAM749  PRKAR1A  5'  CGGGTGCGAGGCGGCGGCG   15607     C  _     AGA
                                CGGG GCG GGCGGC   GCG
                                |||| ||| ||||||   |||
                                GCCC CGC CCGCCG   CGC
                                  A  T     C__
GAM749  PTGER3   5'  CGCGGCGCGGGCGGCGGCG   9645     _         AGA
                                CG GGCGCGGGCGGC   GCG
                                || ||||||||||||   |||
                                GC CCGCGCCCGCCG   CGC
                                 G          C__
GAM749  PTMA     3'  GGGTGGTGGAGAGCGCG     15873     CGCG  C  C
                                GGG    GG GG AGAGCGCG
                                |||    || || ||||||||
                                CCC    CC CC TCTCGCGC
                                  A___  A  _
GAM749  RAC3     5'  CGGGCCGGGCGGCGGCG     22788      G       AGA
                                CGGGC CGGGCGGC   GCG
                                ||||| ||||||||   |||
                                GCCCG GCCCGCCG   CGC
                                   _       C__
GAM749  REV3L    5'  CGGGCGGGGCGGTGTAGGCG   16264       C     CAG  C
                                CGGGCG GGGCGG   AG GCG
                                |||||| ||||||   || |||
```

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                                GCCCGC CCCGCC   TC CGC
                                  _     ACA  _
GAM749  SFRP1    5'  CGGGGCGGCGGGCGCG      16571      C    G   CAGA
                                CGGG GCGG CGG    GCGCG
                                |||| |||| |||    |||||
                                GCCC CGCC GCC    CGCGC
                                  _   _  ____
GAM749  SHOX     3'  GGTGCAGGCGGGGTGCGCG   27826    C       CAGA
                                GG GCGGGCGG    GCGCG
                                || ||||||||    |||||
                                CC CGTCCGCC    CGCGC
                                 A       CCA_
GAM749  SLC21A3  5'  GGGCGCAGGTCAGTGGGTGCGC 39575          _   CAGA_
           G                     GGGCGCGGG CGG     GCGCG
                                |||||||| |||     |||||
                                CCCGCGTCC GTC     CGCGC
                                     A   ACCCA
GAM749  TAPBP    3'  CGGGCGCGGTGGCTCACGCG   17299         GC   AGA
                                CGGGCGCGG  GGC   GCGCG
                                |||||||||  |||   |||||
                                GCCCGCGCC  CCG   TGCGC
                                     A_   AG_
GAM749  TBL1X    5'  CGGGCGCGGCGGCGGCG     24880         G    AGA
                                CGGGCGCGG CGGC   GCG
                                |||||||| ||||   |||
                                GCCCGCGCC GCCG   CGC
                                     _    C__
GAM749  UBTF     5'  CGGGGCGGGCGGAGCGCGGCGC 30612      C       C  A   _
           G                     CGGG GCGGGCGG AG GCG CGCG
                                |||| |||||||| || ||| ||||
                                GCCC CGCCCGCC TC CGC GCGC
                                  _      _ G   C
GAM749  USF2     3'  GGCGTGGGCGGCGGCG      17903      C      AGA
                                GGCG GGGCGGC   GCG
                                |||| |||||||   |||
                                CCGC CCCGCCG   CGC
                                  A      C__
GAM749  VIM      5'  GGGTGTGGGTGGTGGGAGCGCG 45227     CGC   C  CA_
                                GGG   GGG GG   GAGCGCG
                                |||   ||| ||   |||||||
                                CCC   CCC CC   CTCGCGC
                                  ACA   A  ACC
GAM749  YWHAG    5'  CGGGCGCGAGGCGGCTGCG   29793         _     AGA
                                CGGGCGCG GGCGGC   GCG
                                |||||||| ||||||   |||
                                GCCCGCGC CCGCCG   CGC
                                     T     A__
GAM750  ARSB     3'  GTGCAGGCATTTTGCTGTTG   6252     A   A  CG_
                                GT CAG CA   TGCTGTTG
                                || ||| ||   ||||||||
```

```
                                CA GTC GT   ACGACAAC
                                 C   C  AAA
GAM750  BACH2    3'  TGTACAAATGCTATT      34812       ACAC
                                TGTACAG    GTGCTGTT
                                |||||||    ||||||||
                                ACATGTT    TACGATAA
                                      _____
GAM750  CARKL    3'  TGCACAGACATGCTCCTG    30004         CG    G
                                TGTACAGACA  TGCT TTG
                                ||||||||||  |||| |||
                                ACGTGTCTGT  ACGA GAC
                                      __    G
GAM750  CPSF6    3'  TGTGCAGACACGGTTTATCTG  28134     A       TG_____
                                TGT CAGACACG     CTG
                                ||| ||||||||     |||
                                ACA GTCTGTGC     GAC
                                  C       CAAATA
GAM750  ETV5     3'  CACAAATGTGCTGTTG      20843       CAC
                                TACAGA   GTGCTGTTG
                                ||||||   |||||||||
                                GTGTTT   CACGACAAC
                                   A__
GAM750  GFPT2    3'  TGTAGCATCCCTGCTGTTG   23044      _  GACACG
                                TGTA CA     TGCTGTTG
                                |||| ||     ||||||||
                                ACAT GT     ACGACAAC
                                  C  AGGG__
GAM750  GYG      3'  TGTACAGGGTGCCACTG     19971       ACAC    TG
                                TGTACAG    GTGC  TTG
                                |||||||    ||||  |||
                                ACATGTC    CACG  GAC
                                   C___    GT
GAM750  HGF      3'  TGTACAGTACCATT       45325       GACAC
                                TGTACA    GTGCTGTT
                                ||||||    ||||||||
                                ACATGT    CATGGTAA
                                      _____
GAM750  IL1RAP   3'  TGTACAGACACAAAATTG    13510           TGCT
                                TGTACAGACACG   GTTG
                                ||||||||||||   ||||
                                ACATGTCTGTGT   TAAC
                                       TT__
GAM750  KIR2DS1  3'  TGTACATGCTGGTATCTGTTG  30955       GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM750  KIR2DS2  3'  TGTACATGCTGGTATCTGTTG  29481       GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
```

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                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM750  KIR2DS4  3'  TGTACATGCTGGTATCTGTTG  29486      GACAC  _
                                TGTACA    GTG CTGTTG
                                ||||||    ||| ||||||
                                ACATGT    CAT GACAAC
                                   ACGAC   A
GAM750  KLHL3    3'  TGACAGATATGCCACTG    44650    T    CAC    TG
                                TG ACAGA   GTGC  TTG
                                || |||||   ||||  |||
                                AC TGTCT   TACG  GAC
                                 _    A__    GT
GAM750  LFNG     3'  TACAGACACGCCCACTG     45219         G TG
                                TACAGACACGT C  TTG
                                |||||||||||| |  |||
                                ATGTCTGTGCG G  GAC
                                      _ GT
GAM750  MAP3K7IP2 3'  TGTAGGTACTGCTGCTGTTG  31526     CAG  ACG
                                TGTA   AC   TGCTGTTG
                                ||||   ||   ||||||||
                                ACAT   TG   ACGACAAC
                                  CCA  ACG
GAM750  MEF2D    3'  TGCACTGAGTGTGCTGTTG   25425      A  CAC
                                TGTAC GA   GTGCTGTTG
                                ||||| ||   |||||||||
                                ACGTG CT   CACGACAAC
                                   A  CA_
GAM750  MPP1     3'  TGCACAGATGTGTCATT     14626       CAC   CT
                                TGTACAGA   GTG  GTT
                                ||||||||   |||  |||
                                ACGTGTCT   CAC  TAA
                                     A__   AG
GAM750  NR3C1    3'  TGACAGACTCACTGTTG     6756     T     A GT
                                TG ACAGAC C  GCTGTTG
                                || |||||| |  |||||||
                                AC TGTCTG G  TGACAAC
                                 _     A __
GAM750  PCDH7    3'  TGTAAAGAACTTTGCTGTTG   37123     C   CACG
                                TGTA AGA    TGCTGTTG
                                |||| |||    ||||||||
                                ACAT TCT    ACGACAAC
                                  T   TGAA
GAM750  PDHB     3'  TGTACAAAAATACCTGCTGTTG 44609        C__  G
                                TGTACAGA   AC TGCTGTTG
                                ||||||||   || ||||||||
                                ACATGTTT   TG ACGACAAC
                                     TTA  G
GAM750  PDLIM1   3'  TGTCAGACACGTTATATT    34197     A       GC
                                TGT CAGACACGT  TGTT
                                ||| |||||||||  ||||
```

```
                                ACA GTCTGTGCA  ATAA
                                  _       AT
GAM750  PKLR    3'  TGTACAATTGGTGCTGTTG   7149        ACAC
                                TGTACAG   GTGCTGTTG
                                |||||||   |||||||||
                                ACATGTT   CACGACAAC
                                    AAC_
GAM750  RNMT    3'  TGTACAGACCATTAAATGTTG  19160         A  GC__
                                TGTACAGAC CGT   TGTTG
                                ||||||||| |||   |||||
                                ACATGTCTG GTA   ACAAC
                                      _  ATTT
GAM750  RRM2B   3'  TGTACAGACAGTGACGATG   42729         C  C  T
                                TGTACAGACA GTG TG TG
                                |||||||||| ||| || ||
                                ACATGTCTGT CAC GC AC
                                      _  T  T
GAM750  TAL1    3'  TGTACAGATGCTATT      17294        CACG
                                TGTACAGA   TGCTGTT
                                ||||||||   |||||||
                                ACATGTCT   ACGATAA
                                     ____
GAM750  WHSC1   3'  GTGCAGATGATGCTGTTG   39374   A   CAC
                                GT CAGA   GTGCTGTTG
                                || ||||   |||||||||
                                CA GTCT   TACGACAAC
                                 C   AC_
GAM750  WTAP    3'  TATACAGACATCATTGTGTTG  22228         _  GC
                                TGTACAGACA CGT  TGTTG
                                |||||||||| |||  |||||
                                ATATGTCTGT GTA  ACAAC
                                      A  AC
GAM751  AMHR2   5'  TGGAGGATGGCAGCAGCA   33925   AG     TC  _
                                TG  GGATGGC  GTA CA
                                ||  |||||||  ||| ||
                                AC  CCTACCG  CGT GT
                                 CT      T_  C
GAM751  ATP11A  3'  TGAAGGATGGCAATTAACAA  44188         TCGT_
                                TGAGGGATGGC    ACAA
                                ||||||||||    ||||
                                ACTTCCTACCG    TGTT
                                      TTAAT
GAM751  BARHL1  3'  TGGGGATGGCTCCCGGACA   33474   A       GTACA
                                TG GGGATGGCTC    ACA
                                || ||||||||||    |||
                                AC CCCTACCGAG    TGT
                                 _       GGCC_
GAM751  CD5L    3'  AGGGATGGACAACAA      25316        CTCGT
                                AGGGATGG    ACAACAA
                                ||||||||    |||||||
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```
                                TCCCTACC    TGTTGTT
                                   _____
GAM751  EGLN3   3'  TGAAGGATGCAAGAAGTAGCA  35212        G TC___  _
                                TGAGGGATG C    GTA CA
                                ||||||||| |    ||| ||
                                ACTTCCTAC G    CAT GT
                                    _ TTCTT   C
GAM751  GPR4    5'  GAGGGATGGAATTATGACA   40884        CTCG  CA
                                GAGGGATGG   TA  ACA
                                |||||||||   ||  |||
                                CTCCCTACC   AT  TGT
                                    TTA_  AC
GAM751  HD      3'  TGAGGGTGGACAGTAACAAA   13365       A  CTC  CA
                                TGAGGG TGG   GTA  ACAAA
                                |||||| |||   |||  |||||
                                ACTCCC ACC   CAT  TGTTT
                                   _   TGT   __
GAM751  HLF     3'  TGAGGGAAGGGGAACAACAAAA 13398       T  CTCGT
                                TGAGGGA GG    ACAACAAAA
                                ||||||| ||    |||||||||
                                ACTCCCT CC    TGTTGTTTT
                                    T  CCT__
GAM751  KNG     5'  TGAGGGATGGTTTCAAC    9445          CTCGTA
                                TGAGGGATGG     CAAC
                                ||||||||||     ||||
                                ACTCCCTACC     GTTG
                                    AAA___
GAM751  TRPV1   5'  TGAGGATGGCTCAGTCCA    38802       G     _  A
                                TGAGG ATGGCTC GT CA
                                ||||| ||||||| || ||
                                ACTCC TACCGAG CA GT
                                   _      T  G
GAM751  VDAC1   3'  TGAGTGGTGAGAATACAACA   17933      _  A   CTC
                                TGAG GG TGG   GTACAACA
                                |||| || |||   ||||||||
                                ACTC CC ACT   TATGTTGT
                                  A  _   CT_
GAM752  ACADM   3'  TAAAAACCAAACCTGCTTAAGA 6149       T   TG G  A
            GA                    TAAA ACC  G CT CTTAAGAGA
                                |||| |||  | || |||||||||
                                ATTT TGG  T GA GAATTCTCT
                                  T   TT G  C
GAM752  DPYSL2  3'  CAAATACAACATTGCTTAAGAG 10744       CTG   TA__
            A                    TAAATAC   GGC   CTTAAGAGA
                                |||||||   |||   |||||||||
                                GTTTATG   TTG   GAATTCTCT
                                   ___  TAAC
GAM752  MAFF    3'  ACCTGGGCACAGAG       29509        T  TTA
                                ACCTGGGC AC   AGAG
                                |||||||| ||   ||||
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```
                                TGGACCCG TG   TCTC
                                   _ ____
GAM752  NUP98    3'  TAACTAACCAATTACTTAAGAG 32233     AT_   TGGGC
              A                   TAA   ACC    TACTTAAGAGA
                                  |||   |||    ||||||||||
                                  ATT   TGG    ATGAATTCTCT
                                    GAT   TTA__
GAM752  PTPN7    3'  CACCTGGGCCACCGGAG     38710           TAA
                                  TACCTGGGCTACT   GAG
                                  ||||||||||||   |||
                                  GTGGACCCGGTGG   CTC
                                         C__
GAM752  SOX11    3'  TAAAAATAAGACTTACTTAAGA 17035      TACCT    _
              GA                    TAAA    GGGCT ACTTAAGAGA
                                  ||||    ||||| ||||||||||
                                  ATTT    TCTGA TGAATTCTCT
                                    TTAT_    A
GAM753  AIM1     3'  AGAAGATCAGCATTTTAGAAT  45074    T     A  CTA
                                  AG AGATCA CA   TTTGGAAT
                                  || ||||||| ||   ||||||||
                                  TC TCTAGT GT   AAATCTTA
                                   T     C  A__
GAM753  D10S170  3'  AAGTAGATTAACATTAAGGA   24131        C    CTATTT
                                  AAGTAGAT AACA     GGA
                                  |||||||| ||||     |||
                                  TTCATCTA TTGT     CCT
                                       A    AATT__
GAM753  EIF2B1   3'  GCAGATCAGTCTGGA      40645         ACACTA
                                  GTAGATCA     TTTGGA
                                  ||||||||     ||||||
                                  CGTCTAGT     AGACCT
                                       C_____
GAM753  ZNF42    5'  AAGTGATCAACACAGGG     18287      A        TATTT
                                  AAGT GATCAACAC    GG
                                  |||| |||||||||    ||
                                  TTCA CTAGTTGTG    CC
                                    _        TC___
GAM753  HEBP1    3'  TTAGTATATGGAACATGC    31994          AT    A
                                  TTAGTATATG  ACAT GC
                                  |||||||||  |||| ||
                                  AATCATATAC  TGTA CG
                                        CT    _
GAM753  JJAZ1    3'  TATAAACCAACATAGCATT    31694      TGAT_
                                  TATA     ACATAGCATT
                                  ||||     ||||||||||
                                  ATAT     TGTATCGTAA
                                    TTGGT
GAM753  MTAP     3'  GTATATTTACATAGCATT     14676       GA
                                  GTATAT  TACATAGCATT
                                  ||||||  ||||||||||
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                                CATATA  ATGTATCGTAA
                                   A_
GAM754  ATRN    3'  CAAGGCATAGGACTAACA    40266        TACATT
                                CAAGGCGTA     CTAACA
                                |||||||||     ||||||
                                GTTCCGTAT     GATTGT
                                    CCT___
GAM754  CYR61   3'  CCCCAAAAGCTACATT      11416        C  A
                                TCCCAAGG GT TACATT
                                |||||||| || ||||||
                                GGGGTTTT CG ATGTAA
                                   _ _
GAM754  DGAT2   3'  CAAGGCATATACAAAAGTCTGA 37194          T___   A
          CA                      CAAGGCGTATACA    TCT ACA
                                |||||||||||||    ||| |||
                                GTTCCGTATATGT    AGA TGT
                                      TTTC   C
GAM754  FANCC   3'  TCCCAAGATGTGTACAGCTC   43280       GC  A   _
                                TCCCAAG  GT TACA TTC
                                |||||||  || |||| |||
                                AGGGTTC  CA ATGT GAG
                                    TA  C    C
GAM754  MYO1C   3'  TCCCAAGGCCTGGACTCT    41473        GTATAC
                                TCCCAAGGC     ATTCT
                                |||||||||     |||||
                                AGGGTTCCG     TGAGA
                                    GACC__
GAM754  PTGIS   3'  AAGGCAATTCTAAC       9667        TATAC
                                AAGGCG    ATTCTAAC
                                ||||||    ||||||||
                                TTCCGT    TAAGATTG
                                   _____
GAM754  TDE1    5'  TCCTGAGGCTGCTTTCTAACA  27720     CA   GTATACA
                                TCC  AGGC      TTCTAACA
                                |||  ||||      ||||||||
                                AGG  TCCG      AAGATTGT
                                  AC    ACGA___
GAM754  ZNF146  3'  TCCCAAGGTCATATGCATT    28359        _    A
                                TCCCAAGG CGTAT CATT
                                |||||||| ||||| ||||
                                AGGGTTCC GTATA GTAA
                                    A    C
GAM755  CD80    5'  GCAAAACAGGCAGGGCTGATGA 23279         __   TTACCA
          C                      GCAAAACA  TAG     ATGAC
                                |||||||  |||     |||||
                                CGTTTTGT  GTC     TACTG
                                    CC   CCGAC_
GAM755  FNTB    3'  AGGTAATACATAGCCCAATA   13000     C  A      TA
                                AGG AA ACATAGT  CCAATG
                                ||| || |||||||  ||||||
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                                TCC TT TGTATCG  GGTTAT
                                  A  A      __
GAM755  HD      3'  AGACAAAACACAGCTCAGTGAC 13341             AC  A
                                AGGCAAAACATAGTT  CA TGAC
                                |||||||||||||||  || ||||
                                TCTGTTTTGTGTCGA  GT ACTG
                                         __  C
GAM755  MME     3'  AGGCAAAGCTAGTGAATGA   28593        ACA   TACC
                                AGGCAAA   TAGT   AATGA
                                |||||||   ||||   |||||
                                TCCGTTT   ATCA   TTACT
                                    CG_   C___
GAM755  PPP1CC   5'  AGGCAGATCGTCTCCAATGAC  43917      AAACATA   A
                                AGGCA      GTT CCAATGAC
                                |||||      ||| ||||||||
                                TCCGT      CAG GGTTACTG
                                   CTAG___   A
GAM755  SRGAP2   3'  AGGCAAGAGCAAACACCAATGA 43975       AA_  TAGT
            C                    AGGCAA   CA   TACCAATGAC
                                |||||||  ||   ||||||||||
                                TCCGTT   GT   GTGGTTACTG
                                   CTC  TT__
GAM755  TRIM9    3'  GGCAAAACTGGCACATGA    31575        ATA  TACCA
                                GGCAAAAC   GT    ATGA
                                ||||||||   ||    ||||
                                CCGTTTTG   CG    TACT
                                     AC_  TG___
GAM755  MYBL1    3'  AGTATTATGTATGTGTAG    41971          C   CC
                                GGTATTATGTA GTG  GG
                                |||||||||||  |||  ||
                                TCATAATACAT CAC  TC
                                      A   A_
GAM756  ATF6     3'  CTCAGTTTTCCAGCATAGCTGC 41915      A         CCCA__
            AGG                    CTCA TTTTCCAGTAT     AGG
                                |||| ||||||||||     |||
                                GAGT AAAAGGTCGTA     TCC
                                  C         TCGACG
GAM756  CDH6     3'  CCAATTTTCCTCTTCCAAGG   22323          AGTATC
                                TCAATTTTCC     CCAAGG
                                |||||||||      ||||||
                                GGTTAAAAGG     GGTTCC
                                     AGAA__
GAM756  CLECSF5  3'  CTCAGTTTCCCAAATGGGCAAG 29926      A       TATCC
            G                    CTCA TTTTCCAG    CAAGG
                                |||| ||||||||    |||||
                                GAGT AAAGGGTT    GTTCC
                                  C       TACCC
GAM756  CYP51    3'  CCAATTTTATTACTCCCAAGG  8957          CCAGTA
                                TCAATTTT     TCCCAAGG
                                ||||||||     ||||||||
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                                GGTTAAAA     AGGGTTCC
                                    TAATG_
GAM756  EGFL5    3'  TCAATTTTTCAATACCTTTTAA 44535        C      CC__
             GG                   TCAATTTT CAGTATC    AAGG
                                  |||||||| |||||||    ||||
                                  AGTTAAAA GTTATGG    TTCC
                                      A      AAAA
GAM756  IL4R     3'  TCAATTTCTCATCGATTTCCCA 7676         TC  GTA___
             AGG                   TCAATTT  CA     TCCCAAGG
                                  |||||||  ||     ||||||||
                                  AGTTAAA  GT     AGGGTTCC
                                      GA  AGCTAA
GAM756  IL7      5'  ACTGCAGTTTCATCCATCCCAA 9399      _  A   __    GTA
             GG                   ACT CA TTT  TCCA   TCCCAAGG
                                  ||| || |||  ||||   ||||||||
                                  TGA GT AAA  AGGT   AGGGTTCC
                                    C  C   GT   ___
GAM756  PLXNA2   3'  CTCAGTTTCCAGCCAGCCAGGG 36077      AT       ATC   A
                                  CTCA  TTTCCAGT   CCA GG
                                  ||||  ||||||||   ||| ||
                                  GAGT  AAAGGTCG   GGT CC
                                    C_       GTC   C
GAM756  RAB30    5'  TCAATTTTCTCTCGTCCTCAGG 30936         CAGTA   CA
                                  TCAATTTTC    TCC  AGG
                                  |||||||||    |||  |||
                                  AGTTAAAAG    AGG  TCC
                                       AGAGC   AG
GAM756  ZNF179   3'  CTTAACTTTCCTACAATCCAGG 28376    C       AG  TC   A
             G                    CT AATTTTCC  TA  CCA GG
                                  || ||||||||  ||  ||| ||
                                  GA TTGAAAGG  GT  GGT CC
                                   A       AT  TA   C
GAM757  COL19A1  3'  GTTACGGTTAGAAGTAATGGT  12378    G  AA       CC
                                  GT AC  TTAGAAGTA  GGT
                                  || ||  |||||||||  |||
                                  CA TG  AATCTTCAT  CCA
                                   A  CC        TA
GAM757  DXS1283E 3'  CGTGACAATTGAAGAC      43353          A   T
                                  CGTGACAATT GAAG AC
                                  |||||||||| |||| ||
                                  GCACTGTTAA CTTC TG
                                        _   _
GAM757  PPARA    3'  ATGCTCTTAGAAGTACTGGT   22764     ACAA       C
                                  GTG    TTAGAAGTAC GGT
                                  |||    |||||||||| |||
                                  TAC    AATCTTCATG CCA
                                    GAG_         A
GAM757  XRCC5    3'  GTGGTAACTAGAAGGCC     34492     AC       TA
                                  GTG  AATTAGAAG  CC
                                  |||  |||||||||  ||
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                                CAC  TTGATCTTC  GG
                                  CA       C_
GAM758  DYT1    3'  CACTTGGAATTAAAACATAAT  6473     C_    CGAG
                                CAC  GGAAT   TAAAACATAAT
                                |||  |||||   ||||||||||
                                GTG  CCTTA   ATTTTGTATTA
                                  AA   ____
GAM758  FOXO1A  3'  GGAAAGTAATAAAACATAAT  12889     TCG
                                GGAA  AGTAAAACATAAT
                                ||||  ||||||||||||
                                CCTT  TTATTTTGTATTA
                                  TCA
GAM758  GPR44   3'  GGAGAGAAAACATAA      21956     ATC  T
                                GGA  GAG AAAACATAA
                                |||  ||| |||||||||
                                CCT  CTC TTTTGTATT
                                  ___  _
GAM758  KCND2   3'  GGAATCAAAAGACATA      29366        TAAA
                                GGAATCGAG   ACATA
                                |||||||||   |||||
                                CCTTAGTTT   TGTAT
                                     TC__
GAM759  PLAC1   3'  TCAGACATTTGTACACT     34751     A       G
                                TCG ACATTTGTA CATT
                                ||| ||||||||| ||||
                                AGT TGTAAACAT GTGA
                                  C       _
GAM759  POU4F1  3'  TCAACATTTCTATAATTTCAT  26397    G     G  GC
                                TC AACATTT TA  ATTTCAT
                                || ||||||| ||  |||||||
                                AG TTGTAAA AT  TAAAGTA
                                  _     G  AT
GAM759  DSC3    3'  TGGCATGCGGTCTTC      35949        AAT   GA
                                TGGCATGC   GTT  TTC
                                ||||||||   |||  |||
                                ACCGTACG   CAG  AAG
                                     C__   __
GAM759  GHR     3'  TGGCATCAACCAAGATT     6720       G   GTT
                                TGGCAT CAAT   GATT
                                |||||| ||||   ||||
                                ACCGTA GTTG   CTAA
                                   _   GTT
GAM759  NESG1   5'  TGGGATGCCCATTTGATTCG  29584     C   AATG
                                TGG ATGC    TTGATTCG
                                ||| ||||    ||||||||
                                ACC TACG    AACTAAGC
                                  C   GGTA
GAM760  COG7    3'  TGGTGGTCCGGTGTGT      42664     C    CGCGTC  _  C
                                TGG GGTCC     GG GT GT
                                ||| |||||     || || ||
```

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                                ACC CCAGG     CC CA CA
                                  A    _______ A  _
GAM760  NRG1    5'  TGGCGGCTCGCGTCCTGG    30350        CC     G_
                                TGGCGGT  CGCGTC  GG
                                |||||||  ||||||  ||
                                ACCGCCG  GCGCAG  CC
                                    A_     GA
GAM760  RAD54B  3'  TGGTGATTCTTATCTGGTCGTG 39588     C   CCCGC   G
          G                      TGG GGT    GTC GGTCGTGG
                                ||| |||    ||| ||||||||
                                ACC CTA    TAG CCAGCACC
                                  A  AGAA_  A
GAM760  ADD1    5'  CCCCGGCGCGGCGGGCGAGACG 30515           A   TCT
                                TCCCGGCGCGGCG GCG   GACG
                                |||||||||||| |||   ||||
                                GGGGCCGCGCCGC CGC   CTGC
                                        C   T__
GAM760  CCNF    3'  TCCCGGCACGGGGCTCTG    12077          CGA  G
                                TCCCGGCGCGG   GC TCTG
                                ||||||||||   || ||||
                                AGGGCCGTGCC   CG AGAC
                                      C__  _
GAM760  CEBPA   5'  TCCCGGCATGGCGAGCCTC   20399        C      G
                                TCCCGGCG GGCGAGC TC
                                |||||||| ||||||| ||
                                AGGGCCGT CCGCTCG AG
                                    A      G
GAM760  FLI1    5'  CCCGGCGCGGCCTCCCTGGCG  44117          GAGCG    A
                                CCCGGCGCGGC    TCTG CG
                                ||||||||||     |||| ||
                                GGGCCGCGCCG    GGAC GC
                                      GAG__    C
GAM760  FZD10   5'  TCCCGGCGCAGCGGCCCGGCG  28460           AGC    A
                                TCCCGGCGCGGCG   GTCTG CG
                                ||||||||||||   ||||| ||
                                AGGGCCGCGTCGC   CGGGC GC
                                       ___     C
GAM760  GYS1    3'  CGGCGCGGCCACTCTG      44785         GA  G
                                CGGCGCGGC  GC TCTG
                                |||||||||  || ||||
                                GCCGCGCCG  TG AGAC
                                     G_  _
GAM760  HAGH    5'  TCCCAGCGCGGCGAGGCTGCG  23715           C T   A
                                TCCCGGCGCGGCGAG G CTG CG
                                |||||||||||||| | ||| ||
                                AGGGTCGCGCCGCTC C GAC GC
                                        _ _  _
GAM760  ITGB1   5'  CCCGGCGCGGTGGGCTC     38044          CGA  G
                                CCCGGCGCGG   GC TC
                                |||||||||   || ||
```

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                                GGGCCGCGCC  CG AG
                                     ACC  _
GAM760  MLLT2   5'  TCCCGGCGCGGCGCCCCGA  25509          GA  G
                                TCCCGGCGCGGC  GC TCTGA
                                ||||||||||||  || |||||
                                AGGGCCGCGCCG  CG GGGCT
                                     __  _
GAM760  PITX2   3'  TCCCGGCGCTGTGGGTGCG  7255          ___  CGA
                                TCCCGGCGC  GG  GCG
                                |||||||||  ||  |||
                                AGGGCCGCG  CC  CGC
                                     ACA  CA_
GAM760  RTN1    5'  CCCCGGCGCGGCGACGGCG  34472           __
                                TCCCGGCGCGGCGA  GCG
                                ||||||||||||||  |||
                                GGGGCCGCGCCGCT  CGC
                                       GC
GAM761  CD1D    3'  TTCGTTTATTAATTACACCAAG 44301       TCAAT  G
                                TTCGTTT    ATT ATACCAAG
                                |||||||    ||| ||||||||
                                AAGCAAA    TAA TGTGGTTC
                                    TAAT_  _
GAM762  C18orf1 3'  TATTGTACATATTTTAAA   41228
                                TATTGTATATATTTTAAA
                                ||||||||||||||||||
                                ATAACATGTATAAAATTT

GAM762  AXL     3'  GATATACAAAGTTTTAT    34886       TG  A
                                GATATG  AA GTTTTAT
                                ||||||  || |||||||
                                CTATAT  TT CAAAATA
                                   GT  _
GAM762  MSR1    3'  AATACATGAAAAGTTTTAT   14652          _
                                GATATGTGAAA GTTTTAT
                                |||||||||| |||||||
                                TTATGTACTTT CAAAATA
                                       T
GAM762  MYO1C   3'  TAAGACATGATGTGGGTTTTAT 41472        _  AAA
                                TAAGATATG TG  GTTTTAT
                                |||||||| ||  |||||||
                                ATTCTGTAC AC  CAAAATA
                                     T  ACC
GAM762  SLC16A1 3'  AAGATGTTGCCAAAGTTTTAT  16812     A_  G
                                AAGAT  TGT AAAGTTTTAT
                                |||||  ||| ||||||||||
                                TTCTA  ACG TTTCAAAATA
                                   CA  G
GAM762  WRN     3'  AATATATGAATATTTTAT    8129          A
                                GATATGTGAA GTTTTAT
                                |||||||||| |||||||
```

```
                                TTATATACTT TAAAATA
                                      A
GAM763  EDNRA    3'  TAATAGATTTGACTGCTA    41996         AA   T
                                TAATAGGTTT  GACT CTA
                                ||||||||||  |||| |||
                                ATTATCTAAA  CTGA GAT
                                      __    C
GAM763  PDZK1    3'  TAATAGGCTTATCTGCTA    15214         AGACT  A
                                TAATAGGTTTA    TCT CTA
                                ||||||||||     ||| |||
                                ATTATCCGAAT    AGA GAT
                                      _____   C
GAM763  FGA      3'  TTTGTATTTTCTCTCCAC    8007          C
                                TTTGTATT TTTCTCCAT
                                |||||||| |||||||||
                                AAACATAA AGAGAGGTG
                                      A
GAM763  GYPA     3'  TTTGTGTTCTTTCCACAT    44634       A     TC
                                TTTGT TTCTTTC  CAT
                                ||||| |||||||  |||
                                AAACA AAGAAAG  GTA
                                   C      GT
GAM763  MOX2     3'  TCTGTATTCTTTCTTCTC    42526           CCA
                                TTTGTATTCTTTCT   TC
                                ||||||||||||||   ||
                                AGACATAAGAAAGA   AG
                                         AG_
GAM763  ZNF75    3'  TTTGTATTCTTTCACCAC    28327           T
                                TTTGTATTCTTTC CCAT
                                |||||||||||| ||||
                                AAACATAAGAAAG GGTG
                                         T
GAM764  C8A      3'  TAACATCCTGTAAGTTCTCCCT 8159         CA   AAAA__
            GG                    TAGCATCC  TAAG     CTGG
                                ||||||||  ||||     ||||
                                ATTGTAGG  ATTC     GACC
                                      AC    AAGAGG
GAM764  CD79B    3'  TAGCACCCCCAGAAGGCTGG   8424          ATA   AA
                                TAGCATCCC   AGAA  CTGG
                                |||||||||   ||||  ||||
                                ATCGTGGGG   TCTT  GACC
                                      G__    CC
GAM764  CLASP2   3'  TAGCCTTTCACCAAAACTGG   42081     ATCC   AAG
                                TAGC    CAT   AAAACTGG
                                ||||    |||   ||||||||
                                ATCG    GTG   TTTTGACC
                                  GAAA   G__
GAM764  CTNND2   3'  CATCATAAAGAAAACTGG    10633     CCAT
                                CATC    AAGAAAACTGG
                                ||||    ||||||||||
```

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                                GTAG   TTCTTTTGACC
                                  TAT_
GAM764  DGKI    3'  GCATCCCATAAATCTGG    21784          AAAA
                                GCATCCCATAAG   CTGG
                                ||||||||||||  ||||
                                CGTAGGGTATTT   GACC
                                       A___
GAM764  DIAPH2  3'  GCAGCCACAAGAAACTGG   28673    TC       A
                                GCA  CCATAAGAAA CTGG
                                |||  |||||||||| ||||
                                CGT  GGTGTTCTTT GACC
                                 C_       _
GAM764  GPR48   3'  ACATCCCAGCAAATTGG    32979       TAAGA  C
                                GCATCCCA    AAA TGG
                                ||||||||    ||| |||
                                TGTAGGGT    TTT ACC
                                     CG___  A
GAM764  GRB7    3'  AGCAGAGGAGAAAACTGG   23638    TCCCATA
                                AGCA     AGAAAACTGG
                                ||||     ||||||||||
                                TCGT     TCTTTTGACC
                                  CTCC___
GAM764  HMG20A  3'  CAGCTAGGTAAGAAAACTGG  32867    ATCCCA
                                TAGC     TAAGAAAACTGG
                                ||||     ||||||||||||
                                GTCG     ATTCTTTTGACC
                                  ATCC__
GAM764  PLA2G4A 3'  AACACACATAAGAAAGTTGG  43687     CC       AC
                                AGCAT  CATAAGAAA  TGG
                                |||||  |||||||||  |||
                                TTGTG  GTATTCTTT  ACC
                                   T_       CA
GAM764  RABIF   3'  CAGTGTCCCAAAACTG     16122    CA    TAAGA
                                TAG  TCCCA    AAACTG
                                |||  |||||    ||||||
                                GTC  AGGGT    TTTGAC
                                  AC    _____
GAM764  SMARCD2 3'  GCATCCCAGGAGATGATGG   16917       TA  AAAC
                                GCATCCCA  AGA    TGG
                                ||||||||  |||    |||
                                CGTAGGGT  TCT    ACC
                                     CC   ACT_
GAM764  TGFBR3  3'  CAGCATTTTAAAAACTG     17487      CCCATAA
                                TAGCAT      GAAAACTG
                                ||||||      ||||||||
                                GTCGTA      TTTTTGAC
                                   AAA____
GAM764  COL19A1 3'  ACTTTGTAATATGCATCA    12368       CA    C
                                ACTTTGTAA  GTGCA CA
                                |||||||||  ||||| ||
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                                TGAAACATT  TACGT GT
                                     A_    A
GAM765  G22P1    5'  TCTTGTGAGATCTGTTCTAAA  11176    G   ACTAC
                                TC TTGT    CTGTTCTAAA
                                || ||||    ||||||||||
                                AG AACA    GACAAGATTT
                                 _   CTCTA
GAM765  JAG1     3'  GATCGTTGCTGTGGTTCT    6855         ACTACCT
                                GATCGTTGT      GTTCT
                                |||||||||      |||||
                                CTAGCAACG      CAAGA
                                     ACAC___
GAM765  RANBP3   3'  TTGTGAGACTGCCTGTTCT   28776     ___   A
                                TTGT   ACT CCTGTTCT
                                ||||   ||| ||||||||
                                AACA   TGA GGACAAGA
                                  CTC   C
GAM766  ITGA3    3'  GAGCTGTTTATTGGTCGCG   24260     A  CC  CACCC
                                GAGC GT  GT    GGTCGCG
                                |||| ||  ||    |||||||
                                CTCG CA  TA    CCAGCGC
                                  A  AA  A____
GAM766  MN1      5'  GCGGTTGTCACAGCCGCGG   14584    A  CC    CC
                                GC GT  GTCAC  GGTCGCGG
                                || ||  |||||  ||||||||
                                CG CA  CAGTG  TCGGCGCC
                                 C  A_    __
GAM766  PCTK1    5'  GAGCGGTCTGATCGCGG     37472     A   CGTCACCC
                                GAGC GTC       GGTCGCGG
                                |||| |||       ||||||||
                                CTCG CAG       CTAGCGCC
                                  C   A_______
GAM766  PIGB     5'  GAGCAGTCGTCGCTCGCA    22141        C   ACCC G
                                GAGCAGTC GTC    G TCGCG
                                |||||||| |||    | |||||
                                CTCGTCAG CAG    C AGCGT
                                     _   ____ G
GAM766  EN1      3'  CGGGGGCAGCGAGGCGGTG   10909      T  TC    A
                                CGGGG CG  TGAG CGGTG
                                |||||  ||  |||| |||||
                                GCCCC GT  GCTC GCCAC
                                  C  C_    C
GAM766  PAX2     3'  GATGGGGTGAGGCTGGGGCGGT 19607    C    CGT_  AGA
          G                      GA GGGGT    CTG   CGGTG
                                || |||||    |||   |||||
                                CT CCCCA    GAC   GCCAC
                                 A    CTCC   CCC
GAM766  STAR     5'  GGGGTCGCTGCCGCTG      7391         T   AGA  G
                                GGGGTCG CTG   CG TG
                                ||||||| |||   || ||
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```
                                CCCCAGC GAC   GC AC
                                   _  G__  G
GAM767  CROT     3'  TGTAATTCATACCCTT     34499         CCCAAC
                                TGTGATTCA     GCCCTT
                                |||||||||     ||||||
                                ACATTAAGT     TGGGAA
                                   A_____
GAM767  FLI1     3'  GTGATTCACCCGTCTTG     44119          AACGCC
                                GTGATTCACCC     CTTG
                                ||||||||||     ||||
                                CACTAAGTGGG     GAAC
                                   CA____
GAM767  FLRT2    3'  TGTGATTCAACCTGATATATGA 29865         C  AACGCCCT
                                TGTGATTCA CC       TGA
                                ||||||||| ||       |||
                                ACACTAAGT GG       ACT
                                   T  ACTATAT_
GAM767  HSPA5    3'  TGTGATCCACCCGCCTTG    23791          AAC   C
                                TGTGATTCACCC   GCC TTG
                                ||||||||||||   ||| |||
                                ACACTAGGTGGG   CGG AAC
                                   ___   _
GAM767  LUZP1    3'  TGTGATCCGCCTGCCTTG    37967        A  CAAC   C
                                TGTGATTC CC    GCC TTG
                                |||||||| ||    ||| |||
                                ACACTAGG GG    CGG AAC
                                   C  A___   _
GAM767  RAB7L1   3'  TGTGATCCGCCTGCCTTG    19440        A  CAAC   C
                                TGTGATTC CC    GCC TTG
                                |||||||| ||    ||| |||
                                ACACTAGG GG    CGG AAC
                                   C  A___   _
GAM767  RUNX1    5'  TGTGATTCGTCCTGCCTGCTGA 12033        AC  AAC   C_
            C                    TGTGATTC  CC   GCC  TTGAC
                                |||||||  ||   |||  |||||
                                ACACTAAG  GG   CGG  GACTG
                                   CA  A__   AC
GAM767  SS18     3'  TGTATCACAGTGCCCTTGA   24842      AT   CCAAC
                                TGTG  TCAC    GCCCTTGA
                                ||||  ||||    ||||||||
                                ACAT  AGTG    CGGGAACT
                                  __    TCA__
GAM767  TMEM2    3'  TGTGATTCACCAGCAGGAGAC  30156          CAAC  CCTT
                                TGTGATTCACC   GC   GAC
                                ||||||||||   ||   |||
                                ACACTAAGTGG   CG   CTG
                                   T___  TCCT
GAM767  SQSTM1   3'  CGGTGAGGTGGAAGGCATTTAT 19376        CTTT___   C
            TT                   CGGTGAGG      CAT TATTT
                                ||||||||      ||| |||||
```

```
                                GCCACTCC      GTA ATAAA
                                    ACCTTCC   A
GAM767  TLX1     3'  GGCTTTTGAGGCTTTTATTTAT 24342     ____       C  C
              TT                  GGT    GAGGCTTT AT TATTT
                                  |||    |||||||| || |||||
                                  CCG    CTCCGAAA TA ATAAA
                                    AAAA       A  A
GAM768  AMMECR1  5'  AGGCTGGCGGGGCGCGCGCGC  31696     __   TT   A
                                  AGG  GGC  GGC CGCGCGC
                                  |||  |||  ||| |||||||
                                  TCC  CCG  CCG GCGCGCG
                                    GA   CC   C
GAM768  GPR4     3'  TGACCAGGGGCTTTGCAAAC   40892           G   C
                                  TGACCAGGGGCTT GCA GC
                                  |||||||||||||| ||| ||
                                  ACTGGTCCCCGAA CGT TG
                                           A   T
GAM768  MARK3    5'  CCGGGGCTGCACGCGCGC    14353    A     TG
                                  CC GGGGCT  GCACGCGCGC
                                  || ||||||  ||||||||||
                                  GG CCCCGA  CGTGCGCGCG
                                   _     __
GAM768  MIC2     3'  ACCAGGGGTTTCAGACGTGC   14499        C_ TG C   C
                                  ACCAGGGG  T  G ACG GC
                                  ||||||||  |  | ||| ||
                                  TGGTCCCC  A  C TGC CG
                                       AA GT _   A
GAM768  NPR1     3'  TGGCCGTGGGCTTGGCTCAGC  44590    A  AG       A  C
                                  TG CC  GGGCTTGGC CG GC
                                  || ||  |||||||||| || ||
                                  AC GG  CCCGAACCG GT CG
                                    C  CA        A  _
GAM768  TEM6     3'  TGGCCAGGGGCCTGCGGTGC   35565    A         GCAC
                                  TG CCAGGGGCTTG    GC
                                  || ||||||||||    ||
                                  AC GGTCCCCGGAC    CG
                                    C          GCCA
GAM768  USP21    3'  TGGGCAGGGGCTTGGTGAGC   32446    AC         CAC
                                  TG  CAGGGGCTTGG   GC
                                  ||  ||||||||||   ||
                                  AC  GTCCCCGAACC   CG
                                    CC          ACT
GAM768  A2M      3'  GCAAAGCACTTTTCAGCCTTGT 6142     TGCCGT  C       C
                                  GC     CT TTCAGCCT GT
                                  ||     || ||||||| ||
                                  CG     GA AAGTCGGA CA
                                    TTTCGT  A       A
GAM768  ATP1A1   5'  CTGCGCCCCAGCCTCGT     8695       C    CTT
                                  CTGC GTCT   CAGCCTCGT
                                  |||| ||||   |||||||||
```

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                              GACG CGGG  GTCGGAGCA
                                _  ___
GAM768  CACNA1A  3' CCGCTGCCCGGGCCATCGGCCT 35727       _ TC  T  A
           CGT                 CCGCTGCC G  TC TC GCCTCGT
                               |||||||| |  || || |||||||
                               GGCGACGG C  GG AG CGGAGCA
                                  G CC  T  C
GAM768  FASN    5' CCGCTGCCGTCTCTCTGGC   19931           CA
                               CCGCTGCCGTCTCTT  GC
                               ||||||||||||||  ||
                               GGCGACGGCAGAGAG  CG
                                        AC
GAM768  MAGOH   5' GCCGCCGTCTGCCTCG     14329        CTTCA
                               GCTGCCGTCT   GCCTCG
                               ||||||||||   ||||||
                               CGGCGGCAGA   CGGAGC
                                           _____
GAM768  OPRD1   5' CCGCTGTCTCTGCGCCTCG  9512      GCC    TCA
                               CCGCT  GTCTCT  GCCTCG
                               |||||  ||||||  ||||||
                               GGCGA  CAGAGA  CGGAGC
                                  ___   CG_
GAM769  GABRE   3' TAGTGGGCTTCTGGAAAA   35078    CA  C
                               TAG  GGC TTCTGGAAAG
                               |||  ||| ||||||||||
                               ATC  CCG AAGACCTTTT
                                 AC  _
GAM769  HSPA1A  5' AGGTTCGCTCTGGGAAGCCTTG 23781    CC__    A
                               AGG   TTCTGG AAGCCTTG
                               |||   |||||| ||||||||
                               TCC   GAGACC TTCGGAAC
                                 AAGC    C
GAM769  HSPA1B  5' AGGTTCGCTCTGGAAAGCCTTG 23782    CC__
                               AGG   TTCTGGAAAGCCTTG
                               |||   ||||||||||||||||
                               TCC   GAGACCTTTCGGAAC
                                 AAGC
GAM769  KCNK5   3' GGCCCACAGAAAGCCTTG   19038     TCT
                               GGCCT  GGAAAGCCTTG
                               |||||  ||||||||||
                               CCGGG  TCTTTCGGAAC
                                  TG_
GAM769  RAPSN   3' GCAGGCCCCAAGGCCTT    37215       CT  AAA
                               GCAGGCCTT  GG  GCCTT
                               |||||||||  ||  |||||
                               CGTCCGGGG  TC  CGGAA
                                     T_  ___
GAM769  S100A10 5' GGTCCGTTGAAGCCTTG    40398   CCT   GA_
                               GG  TCTG  AAGCCTTG
                               ||  ||||  ||||||||
```

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                                CC   AGGC   TTCGGAAC
                                 ___    AAC
GAM769  SYNGR1   3'  CAGTGGGCCTTCTGGAAGGCC  21753     CA          A
                                TAG  GGCCTTCTGGAA GCC
                                |||  |||||||||||| |||
                                GTC  CCGGAAGACCTT CGG
                                  AC          C
GAM770  CNTNAP2  3'  TGCTGTTGCTTTTAGAGA    30497    A        CTT
                                TG TGTTGCTTTT   GGA
                                || ||||||||||   |||
                                AC ACAACGAAAA   TCT
                                 G         TC_
GAM770  EFNB2    3'  TGATGTTGTTTTTCCCAGAA   19886        C     TG
                                TGATGTTG TTTTCT  GAA
                                |||||||| ||||||  |||
                                ACTACAAC AAAAGG  CTT
                                     A     GT
GAM770  EGLN1    3'  TGATGTTATTTTGAGGAA    35181         C    CTT
                                TGATGTTG TTTT   GGAA
                                |||||||| ||||   ||||
                                ACTACAAT AAAA   CCTT
                                    _    CT_
GAM770  GATA3    5'  TGATTTGCTTTCGGTGG     13100      G       CT
                                TGAT TTGCTTTT  TGG
                                |||| ||||||||  |||
                                ACTA AACGAAAG  ACC
                                  _       CC
GAM770  GCLM     3'  TAATGAATTTTTTTTGGAAATA 13134       TTGC    C
           A                     TGATG    TTTT TTGGAAATAA
                                |||||    |||| ||||||||||
                                ATTAC    AAAA AACCTTTATT
                                   TTA_    A
GAM770  GRIN2A   3'  GATGTGTCTTGGAAAT      9110        T CTTT
                                GATGT G    TCTTGGAAAT
                                ||||| |    ||||||||||
                                CTACA C    AGAACCTTTA
                                  _ _____
GAM770  MKPX     3'  ATGTTGCTTTTCTTTTTGG   33634            ___
                                ATGTTGCTTTTCT   TGG
                                ||||||||||||   |||
                                TACAACGAAAAGA   ACC
                                       AAA
GAM770  PKIA     5'  GATCTCTTTTTTCTTGGA    27741     G  GC
                                GAT TT  TTTTCTTGGA
                                ||| ||  ||||||||||
                                CTA AG  AAAAGAACCT
                                  G  AA
GAM770  SFRP1    3'  TGTGTTGCTGTTGGAAAT    16579    A      TTTC
                                TG TGTTGCT    TTGGAAAT
                                || |||||||    ||||||||
```

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                                AC ACAACGA   AACCTTTA
                                 _     C___
GAM770  SLC6A6   3'  GATGTTGCTTGGGGAA     16790        TTCTT
                                GATGTTGCTT    GGAA
                                ||||||||||    ||||
                                CTACAACGAA    CCTT
                                      CC___
GAM770  TEM6     3'  TGATGTTGTTTGTTCTTG    35563       C _
                                TGATGTTG TT TTCTTG
                                |||||||| || ||||||
                                ACTACAAC AA AAGAAC
                                     A  C
GAM771  MMP16    3'  TAGTAGTGTTTTGTTGTT    35440       C_
                                TGGTGGT  TTTGTTGTT
                                |||||||  |||||||||
                                ATCATCA  AAACAACAA
                                    CA
GAM772  ACHE     3'  GTGGGGATGGGCAGAGTCT   31864     TC  CCGTA
                                GTGG  GT    GGCAGAGTCT
                                ||||  ||    ||||||||||
                                CACC  TA    CCGTCTCAGA
                                  CC  C_____
GAM772  MAPRE3   3'  TGGGGTCCAGGCAGAGT     29542     TC    GT
                                TGG  GTCC  AGGCAGAGT
                                |||  ||||  |||||||||
                                ACC  CAGG  TCCGTCTCA
                                  C_   __
GAM772  TM4SF4   3'  TGTAGTCGTCATGCTGTAGAGT 21458          CGTAG ___
           CT                     TGTGGTCGTC    GC   AGAGTCT
                                ||||||||||    ||  |||||||
                                ACATCAGCAG    CG   TCTCAGA
                                      TA___  ACA
GAM773  ABL1     3'  CTGTGAAATACGTGAGGC    28712     GC   C
                                TTG  GAA ACGTGAGGC
                                |||  ||| |||||||||
                                GAC  TTT TGCACTCCG
                                  AC   A
GAM773  CAPN10   3'  ACCCTCTGGGTGTGAGGC    35759     C    CGAACAC
                                ACCC TTGG      GTGAGGC
                                |||| ||||      |||||||
                                TGGG GACC      CACTCCG
                                  A   CA_____
GAM773  CELL     3'  CCCCTTGGTGATTGTGAA     12223       C  ACAC
                                CCCCTTGG GA    GTGAG
                                |||||||| ||    |||||
                                GGGGAACC CT    CACTT
                                     A  AA__
GAM773  CKAP1    5'  TTGGCGAAGCACCTAGGCC    43888        _   G G
                                TTGGCGAA CAC T AGGCC
                                |||||||| ||| | |||||
```

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                                AACCGCTT GTG A TCCGG
                                    C   G _
GAM773  CLC     3'  CCTTGGCAACATGAAG      12269        AAC
                                CCTTGGCG   ACGTGAGG
                                ||||||||   ||||||||
                                GGAACCGT   TGTACTTC
                                    ___
GAM773  DNM2    3'  CCTGCGCCGCGGGTGCGTGAGG 22379     _  G  AACA__
          CC                      CCT TG CG     CGTGAGGCC
                                  ||| || ||     |||||||||
                                  GGA GC GC     GCACTCCGG
                                    C  G  GCCCAC
GAM773  EGLN2   5'  ACCCCTTGGTGACCAGCGC   38811         C  A  _
                                ACCCCTTGG GA CA CGT
                                ||||||||| || || |||
                                TGGGGAACC CT GT GCG
                                     A  G  C
GAM773  EPAS1   5'  CCCTGGCGGGTGGGGGGC    11001        AACAC   A__
                                CCTTGGCG    GTG   GGC
                                ||||||||    |||   |||
                                GGGACCGC    CAC   CCG
                                    C____   CCC
GAM773  EPHB2   3'  CCTCCTGGCGAGTGG       32665    C       ACAC  GA
                                CC CTTGGCGA    GT  GG
                                || ||||||||    ||  ||
                                GG GGACCGCT    CA  CC
                                 A      _____  __
GAM773  F9      3'  CCATGGTGAACACGAAACC   6573     T   C     GT
                                CC TGG GAACAC  GAGGCC
                                || ||| ||||||  ||||||
                                GG ACC CTTGTG  CTTTGG
                                 T   A     __
GAM773  GCK     3'  CCCCTTGGGGCAGAGGC     37924        CGAA  CGT
                                CCCCTTGG    CA   GAGGC
                                ||||||||    ||   |||||
                                GGGGAACC    GT   CTCCG
                                    CC__   ___
GAM773  GOLGA4  3'  TTGGCTACATGAGGGGCC    41062      GAAC     __
                                TTGGC    ACGTGA  GGCC
                                |||||    ||||||  ||||
                                AACCG    TGTACT  CCGG
                                   A___     CC
GAM773  HOXC4   5'  CCCCTTGGGGGCCAGAGG    31150        CGAACA  T
                                CCCCTTGG     CG GAGG
                                ||||||||     || ||||
                                GGGGAACC     GT CTCC
                                    CCCG__  _
GAM773  KCNN3   5'  CCTCTAGGAGCGTGTGAGGCC  13918      _____   AACAC
                                CCTT    GGCG    GTGAGGCC
                                ||||    ||||    ||||||||
```

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                                GGAG   TCGC    CACTCCGG
                                  ATCC   A____
GAM773  LOXL1    3'  CCCCTCGGCGGGAGG      41182         AACACGT
                                CCCCTTGGCG     GAGG
                                ||||||||||     ||||
                                GGGGAGCCGC     CTCC
                                    C_______
GAM773  MAT1A    3'  CCCCTTGGGAGCAGACC     44904        C  ACAC  G
                                CCCCTTGG GA   GT AGGCC
                                |||||||| ||   || |||||
                                GGGGAACC CT   CG TCTGG
                                   _ _____ _
GAM773  PACSIN3  5'  CCCCTCGGCGGGTGGGG     32140         AACAC   A
                                CCCCTTGGCG    GTG GG
                                ||||||||||    ||| ||
                                GGGGAGCCGC    CAC CC
                                    C_____   C
GAM773  PDGFB    3'  CCCCTTGGTGGAGCAGAC    15171        C_  ACAC  G
                                CCCCTTGG  GA   GT AGGC
                                ||||||||  ||   || ||||
                                GGGGAACC  CT   CG TCTG
                                   AC  _____ _
GAM773  RALBP1   3'  ACCCCTTGAGTGTGTGTGGGG  27695        CGAACAC   A
                                ACCCCTTGG      GTG GG
                                |||||||||      ||| ||
                                TGGGGAACT      CAC CC
                                    CACACA_   C
GAM773  RGS6     3'  CCTCTTAGCGAGTGGAG     20189    C      ACAC   AG
                                CC CTTGGCGA   GTG  G
                                || ||||||||   |||  |
                                GG GAATCGCT   CAC  C
                                 A       _____  CT
GAM773  SCA1     3'  CCCCTTACCCCATGTGGGGCC  7275        G GAA  C   A
                                CCCCTTG C   CA GTG GGCC
                                ||||||| |   || ||| ||||
                                GGGGAAT G   GT CAC CCGG
                                   _ GG_  A   C
GAM773  SECTM1   3'  CCCCCTGGCGGTGGGGC     16536         AACAC   A
                                CCCCTTGGCG    GTG GGC
                                ||||||||||    ||| |||
                                GGGGGACCGC    CAC CCG
                                    _____  C
GAM773  SHC1     3'  ACCCCTTGGGGTGAGGGGC   16693         CGAACAC   __
                                ACCCCTTGG      GTGA  GGC
                                |||||||||      ||||  |||
                                TGGGGAACC      CACT  CCG
                                    C_______   CC
GAM773  SLC7A8   3'  CCCTGGTGAACAGATAGGG   29284       C    C   A
                                CCTTGG GAACA GTG GG
                                |||||| ||||| ||| ||
```

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                                GGGACC CTTGT TAT CC
                                   A    C  C
GAM773  TEM5    3'  CCTTGGTGATGAGGC      37232       C  ACACG
                                CCTTGG GA    TGAGGC
                                |||||| ||    ||||||
                                GGAACC CT    ACTCCG
                                   A ______
GAM773  TMPRSS2  3'  ACCCCTTGCGGACAAGG    24926        G  A   CGTG
                                ACCCCTTG CG ACA   AGG
                                |||||||| || |||   |||
                                TGGGGAAC GC TGT   TCC
                                    _ C  _____
GAM773  WWOX    3'  TTGGCGGGGATGAGGCC    39117       AACAC
                                TTGGCG    GTGAGGCC
                                ||||||    ||||||||
                                AACCGC    TACTCCGG
                                   CCC__
GAM773  ADPRT   5'  GCCGCACCGGCCACCGCC    11519    A  __  T
                                GCC CA  GG CCACCGCC
                                ||| ||  || ||||||||
                                CGG GT  CC GGTGGCGG
                                  C  GG  _
GAM773  ARF4L   3'  TGCTGCAGGCCCAGACCG    43076    CA     __
                                TGC  CAGGTCC  ACCG
                                |||  |||||||  ||||
                                ACG  GTCCGGG  TGGC
                                  AC      TC
GAM773  ARNT    5'  GCCGCAGATGCCACCGCC    11695    A    _
                                GCC CAGGT CCACCGCC
                                ||| ||||| ||||||||
                                CGG GTCTA GGTGGCGG
                                  C    C
GAM773  ATP4A   3'  TGTCAGAGCCCCACCGCC    8720    C  C  G
                                TG CA AG TCCACCGCC
                                || || || |||||||||
                                AC GT TC GGGTGGCGG
                                 A  C  G
GAM773  ATRX    5'  TACCACTGCCACCGCC      39610       AG T
                                TGCCAC  G CCACCGCC
                                ||||||  | ||||||||
                                ATGGTG  C GGTGGCGG
                                   A_ _
GAM773  B3GAT1  3'  TGCCCACCACCCACCGCC    38305     _  AGG
                                TGCC AC   TCCACCGCC
                                ||||  ||   |||||||||
                                ACGG TG   GGGTGGCGG
                                  G  GT_
GAM773  BACE    3'  TACCACAGGGACACACGCC    39969        TC  _
                                TGCCACAGG  CAC CGCC
                                |||||||||  ||| ||||
```

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                                ATGGTGTCC  GTG GCGG
                                     CT   T
GAM773  BSN     3'  TGCCACAGGTCAAACATGCC   18418          C_  C_
                                TGCCACAGGTC  AC  GCC
                                ||||||||||  ||  |||
                                ACGGTGTCCAG  TG  CGG
                                      TT  TA
GAM773  CCND1   3'  TGCACAGACCCAGCCGCC    38225    C   GT  _
                                TGC ACAG  CCA CCGCC
                                ||| ||||  ||| |||||
                                ACG TGTC  GGT GGCGG
                                  _   TG  C
GAM773  CELSR3  5'  TGCACGGCCTCCACCGCC    10841    C  A  __
                                TGC AC GGT  CCACCGCC
                                ||| || |||  ||||||||
                                ACG TG CCG  GGTGGCGG
                                  _ _  GA
GAM773  CYFIP2  3'  TGCACAGGCCCCGCC       43916    C    T  A
                                TGC ACAGG CC CCGCC
                                ||| ||||| || |||||
                                ACG TGTCC GG GGCGG
                                  _    _ _
GAM773  FZD1    3'  CGCAATCCACCGCC         18612    CACA
                                TGC   GGTCCACCGCC
                                |||   ||||||||||
                                GCG   TTAGGTGGCGG
                                  _____
GAM773  GRLF1   3'  TGCCACAGTCCCTGCC      44235        G  ACC
                                TGCCACAG TCC  GCC
                                |||||||| |||  |||
                                ACGGTGTC AGG  CGG
                                     _  GA_
GAM773  GUCY2D  3'  TGTCACAAATCCCTGCC     6763    C       ACC
                                TG CACAGGTCC  GCC
                                || |||||||||  |||
                                AC GTGTTTAGG  CGG
                                 A       GA_
GAM773  HSPA5   3'  TGACACAAACCATTGCC     23789    C    T  CC
                                TG CACAGG CCA  GCC
                                || |||||| |||  |||
                                AC GTGTTT GGT  CGG
                                 T     _  AA
GAM773  IHPK3   5'  TGCCATATGGCCACCGCC    38376      CA_  T
                                TGCCA  GG CCACCGCC
                                |||||  || ||||||||
                                ACGGT  CC GGTGGCGG
                                   ATA  _
GAM773  ITGAL   3'  TGACACAGGTCACATTTGC   13625    C      _  CC_
                                TG CACAGGTC CA  GC
                                || |||||||| ||  ||
```

```
                                AC GTGTCCAG GT   CG
                                 T       T  AAA
GAM773  ITK      3'  TGCCACAGGCCAGGCTGCC   24448         T   CC__
                                TGCCACAGG CCA    GCC
                                ||||||||| |||    |||
                                ACGGTGTCC GGT    CGG
                                      _  CCGA
GAM773  KRT16    5'  TGCCGAAGCCACCGCC      45453      AC   T
                                TGCC  AGG CCACCGCC
                                ||||  ||| ||||||||
                                ACGG  TTC GGTGGCGG
                                  C_  _
GAM773  MAPK8IP1 3'  TGCCACAGGCCAGCATGCC   24162         T   CC__
                                TGCCACAGG CCA    GCC
                                ||||||||| |||    |||
                                ACGGTGTCC GGT    CGG
                                      _  CGTA
GAM773  NDST2    3'  GCCACAGGTAGATCCCACTGCC 18878         _____   C   III
              G                  GCCACAGGT    CCAC GCC   G
                                |||||||||    |||| |||   |
                                CGGTGTCCA    GGTG CGG   C
                                     TCTAG    A   III
GAM773  PHLDA3   5'  GCCGTGAGCCCCACCGCC    29613     AC_  G
                                GCC   AG TCCACCGCC
                                |||   || |||||||||
                                CGG   TC GGGTGGCGG
                                  CAC  G
GAM773  POLD1    5'  GCCACAGCCTACGCCGCC    15440       G  CA__
                                GCCACAG TC    CCGCC
                                ||||||| ||    |||||
                                CGGTGTC GG    GGCGG
                                    _  ATGC
GAM773  POU2F2   3'  TGCCACAGCCGCAGCCGC    15464        G  _  _
                                TGCCACAG TC CA CCGC
                                |||||||| || || ||||
                                ACGGTGTC GG GT GGCG
                                     _  C  C
GAM773  RECQL5   3'  TGCCACAGCCCCGCC      20173        GT  A
                                TGCCACAG  CC CCGCC
                                ||||||||  || |||||
                                ACGGTGTC  GG GGCGG
                                      __  _
GAM773  REPS2    5'  CGCCACAGCCACCGCC      21811        GT
                                TGCCACAG  CCACCGCC
                                ||||||||  ||||||||
                                GCGGTGTC  GGTGGCGG
                                      __
GAM773  REPS2    5'  CGCCGCCACCACCGCC      21812      A_  GGT
                                TGCC  CA   CCACCGCC
                                ||||  ||   ||||||||
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```
                                GCGG  GT   GGTGGCGG
                                  CG  ___
GAM773  RNF26    3'  TGCCACAGGGCACGTGGCC   36757        TC   C__
                                TGCCACAGG  CAC   GCC
                                |||||||||  |||   |||
                                ACGGTGTCC  GTG   CGG
                                     C_   CAC
GAM773  ROCK2    5'  GCCGCGGCCCGGACCGCC    42358     ACA    __
                                GCC   GGTCC  ACCGCC
                                |||   |||||  ||||||
                                CGG   CCGGG  TGGCGG
                                  CG_    CC
GAM773  SLC35A3  5'  CGCCGTAGCCACCGCC     29276     ACA  T
                                TGCC   GG CCACCGCC
                                ||||   ||  ||||||||
                                GCGG   TC GGTGGCGG
                                  CA_  _
GAM773  TCF3     3'  TGCCACAGTGACCACTGCC   43331        GT_   C
                                TGCCACAG   CCAC GCC
                                ||||||||   |||| |||
                                ACGGTGTC   GGTG CGG
                                     ACT    A
GAM773  TPST1    5'  GCCGCTGGTCCCACCGCC    18762     ACA    _
                                GCC   GGTCC ACCGCC
                                |||   ||||| ||||||
                                CGG   CCAGG TGGCGG
                                  CGA    G
GAM773  UBE2L3   3'  TGCCACAAGCGAACGCC     17833         CCAC
                                TGCCACAGGT    CGCC
                                ||||||||||    ||||
                                ACGGTGTTCG    GCGG
                                     CTT_
GAM773  WNT6     3'  CCACAGGTGCGAGCCACCGC   27178        _____
                                CCACAGGT    CCACCGC
                                ||||||||    |||||||
                                GGTGTCCA    GGTGGCG
                                     CGCTC
GAM774  RAB5A    3'  TTGAATATACATAATTGTTAGT 20016          CG  ACAA
           G                     TTGAATATACA  AT   TGGTG
                                ||||||||||  ||   |||||
                                AACTTATATGT  TA   ATCAC
                                      AT  ACA_
GAM774  BDKRB2   3'  GTGGTGGGAATGACA       8406         T   CAAATCA
                                GTGGTGGG AAT      GACA
                                |||||||| |||      ||||
                                CACCACCC TTA      CTGT
                                     _  _______
GAM774  DLEC1    5'  GTGGTGGGTGGTCACCAG    28849         AA   AA
                                GTGGTGGGT  TCA  TCAG
                                |||||||||  |||  ||||
```

```
                                CACCACCCA  AGT  GGTC
                                     CC   __
GAM774  DLEC1   3'  GTGGTGGGTGGTCACCAG    28837        AA   AA
                                GTGGTGGGT  TCA  TCAG
                                |||||||||  |||  ||||
                                CACCACCCA  AGT  GGTC
                                     CC   __
GAM774  DSG1    3'  GTGGTGGGAATTGGATC     12601        T   CAA
                                GTGGTGGG AAT   ATC
                                |||||||| |||   |||
                                CACCACCC TTA   TAG
                                     _  ACC
GAM774  LARS2   3'  GTGGTGGGGACACAGGCA    31680        TAAT  AAT   A
                                GTGGTGGG   CA   CAG CA
                                ||||||||   ||   ||| ||
                                CACCACCC   GT   GTC GT
                                     CT__  ___   C
GAM775  RGL     5'  TAGCAGCGCACAGTCTGA    31543        G   A  CC
                                TAGCAGCG ACA TC  GA
                                |||||||| ||| ||  ||
                                ATCGTCGC TGT AG  CT
                                     G   C  A_
GAM776  COL15A1 3'  AAGAAAACATGAAGGAC     12348       CATT      A
                                AAGAAA   GCATGAA GAC
                                ||||||   ||||||| |||
                                TTCTTT   TGTACTT CTG
                                    ____      C
GAM776  CRI1    3'  TACAGCAAACAAATATGAAAGA 30735      AG    TTGC
                                TACA  AAACA   ATGAAAGA
                                ||||  |||||   ||||||||
                                ATGT  TTTGT   TACTTTCT
                                  CG    TTA_
GAM776  DIAPH2  3'  CACAAGAAACTGGAAG      28668        ATTGCA  A
                                TACAAGAAAC     TG AAG
                                ||||||||||     || |||
                                GTGTTCTTTG     AC TTC
                                     _______ C
GAM776  DLEU1   3'  AGAAACATGCTGGAAAGA    25256        T  AT
                                AGAAACAT GC  GAAAGA
                                |||||||| ||  ||||||
                                TCTTTGTA CG  CTTTCT
                                     _  AC
GAM776  FLG     3'  TACGCAGAATCTTGTGAAAGAC 43363     A_   ACA   CA
                                TAC  AGAA   TTG  TGAAAGAC
                                |||  ||||   |||  ||||||||
                                ATG  TCTT   AAC  ACTTTCTG
                                  CG    AG_   __
GAM776  FMR2    3'  TACAGAAACATCTGAAGA    12978      A      GCA   A
                                TACA GAAACATT   TGAA GA
                                |||| ||||||||   |||| ||
```

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                                ATGT CTTTGTAG   ACTT CT
                                  _     ___   _
GAM776  HEBP1    3'  AAGAATCACAGATGAAAGA   31989      A   TGC
                                AAGAA CAT   ATGAAAGA
                                ||||| |||   ||||||||
                                TTCTT GTG   TACTTTCT
                                   A   TC_
GAM776  IRF6     3'  TACAAGAACAATGCAGAAGGA  26038       A  T    T   A
                                TACAAGAA CA TGCA GAA GA
                                |||||||| || |||| ||| ||
                                ATGTTCTT GT ACGT CTT CT
                                     _ T   _   C
GAM776  LRRC2    3'  GAAACACTGAAAGA       35997       TGCA
                                GAAACAT    TGAAAGA
                                |||||||    |||||||
                                CTTTGTG    ACTTTCT

                                  ____
GAM776  PPP1R8   3'  CAGGAGACATTCTGAAAGAC   39727    A  A    GCA
                                CA GA ACATT   TGAAAGAC
                                || || |||||   ||||||||
                                GT CT TGTAA   ACTTTCTG
                                 C  C    G__
GAM776  TCEA1    3'  TACAAGAAATTACAAGA     44329        AC     T
                                TACAAGAA  ATTGCA GA
                                ||||||||  |||||| ||
                                ATGTTCTT  TAATGT CT
                                     __     T
GAM776  TCERG1   3'  TACAAGAAACACCCAGAAAG  27463           G  T
                                TACAAGAAACATT CA GAAAG
                                |||||||||||| || |||||
                                ATGTTCTTTGTGG GT CTTTC

                                      _ _
GAM776  CA3      3'  TCTGGCTTATGTTTAATTGTT  23218     TACC
                                TCT    TATGTTTAATTGTT
                                |||    ||||||||||||||
                                AGA    ATACAAATTAACAA
                                  CCGA
GAM777  BMP3     5'  CCGGGACGCGGCCGG       10188      TCTTGT
                                CCGGG     CGCGGCCGG
                                |||||     |||||||||
                                GGCCC     GCGCCGGCC
                                   T_____
GAM777  CDH1     5'  CGCCGGGTGCGGTCGGG     20361        CTTGTC   C
                                CGCCGGGT     GCGG CGGG
                                ||||||||     |||| ||||
                                GCGGCCCA     CGCC GCCC
                                     _______   A
GAM777  CDH16    3'  GCTGGATCTTGGGTGCTGGGC  19788    C      TCGCG  C
                                GC GGGTCTTG     GC GGGC
                                || ||||||||     || ||||
```

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                                CG CCTAGAAC    CG CCCG
                                 A      CCA__  A
GAM777  CKB     3'  CGGGTGTGGGCCGGG      12251      CTT  CGC
                                CGGGT  GT  GGCCGGG
                                |||||  ||  |||||||
                                GCCCA  CA  CCGGCCC
                                   ___  C__
GAM777  FASN    3'  CGCTGGGTGTGGCCGGG    19933    C   CTT  CGC
                                CGC GGGT  GT  GGCCGGG
                                ||| ||||  ||  |||||||
                                GCG CCCA  CA  CCGGCCC
                                 A   ___  ___
GAM777  GNAS    5'  CGGCGGGGCGCGGCCGGG   38659   C   TCTT T
                                CG CGGG   G CGCGGCCGGG
                                || ||||   | ||||||||||
                                GC GCCC   C GCGCCGGCCC
                                 C   _____ _
GAM777  HMX1    5'  CGCCGGGCTGGGCTGG     33210       CT  TCGC  C
                                CGCCGGGT  TG   GGC GG
                                ||||||||  ||   ||| ||
                                GCGGCCCG  AC   CCG CC
                                    __  _____  A
GAM777  MADH1   5'  CCGGGTCCGGACGGCCGGGC  25338       TGTC
                                CCGGGTCT   GCGGCCGGGC
                                ||||||||   ||||||||||
                                GGCCCAGG   TGCCGGCCCG
                                    CC__
GAM777  MAN1A1  5'  CGCCGGGTCTTCTCCCCGGG  45096        G  GCGG
                                CGCCGGGTCTT TC   CCGGG
                                |||||||||| ||   |||||
                                GCGGCCCAGAA AG   GGCCC
                                      G  G___
GAM777  MARK1   5'  GCCGGGGTCTAGACCGGCCGGG 33010      _  TGTCG
            C                    GCCGGG TCT    CGGCCGGGC
                                ||||| |||    |||||||||
                                CGGCCC AGA    GCCGGCCCG
                                   C  TCTG_
GAM777  MGAT1   5'  CGCCGGGGCCGGACGGCCGGGC 14431       TCTT   __
                                CGCCGGG   GTCG  CGGCCGGGC
                                |||||||   ||||  |||||||||
                                GCGGCCC   CGGC  GCCGGCCCG
                                    ____   CT
GAM777  MMP14   5'  GGGCTCCGCGGCCGGG    22643    T  GT
                                GGG CTT  CGCGGCCGGG
                                ||| |||  ||||||||||
                                CCC GAG  GCGCCGGCCC
                                  _  __
GAM777  NTN2L   5'  GCGGGTCAGCCAGTGGCCGGGC 26150   C    TT   C_
                                GC GGGTC  GTCG  GGCCGGGC
                                || |||||  ||||  ||||||||
```

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                                CG CCCAG  CGGT  CCGGCCCG
                                 _    T_   CA
GAM777  NUP50    5'  CGCTGGGTCTTGGTTGCGGC  28407    C      TC_
                                CGC GGGTCTTG   GCGGC
                                ||| ||||||||   |||||
                                GCG CCCAGAACC   CGCCG
                                  A       CAA
GAM777  PAX2     5'  CGGGGCTCGGGGCTGGGC   19626     T   TCGC   C
                                CGGG CTTG   GGC GGGC
                                |||| ||||   ||| ||||
                                GCCC GAGC   CCG CCCG
                                  C   C___   A
GAM777  PFKFB3   5'  CGCCGGCGCGCGGCCGGG   44434      GTCT  T
                                CGCCGG   TG CGCGGCCGGG
                                ||||||   || ||||||||||
                                GCGGCC   GC GCGCCGGCCC
                                   _____  _
GAM777  RPIP8    5'  CGCTGGATCACGGCTGGG   27450    C    TTGTC    C
                                CGC GGGTC    GCGGC GGG
                                ||| |||||    ||||| |||
                                GCG CCTAG    TGCCG CCC
                                  A    ______    A
GAM777  SLC6A8   5'  CGTCGGGGCCCGGCCGGG   24765    C   TCTT   G
                                CG CGGG   GTC CGGCCGGG
                                || ||||   ||| ||||||||
                                GC GCCC   CGG GCCGGCCC
                                 A   _____  _
GAM777  ACADS    3'  GCCGGGGTTGGGGTGGA    6154         CCC  C  C
                                GCCGGGGTT   GG GG GGA
                                |||||||||   || || |||
                                CGGCCCCAA   CC CC CCT
                                     ___  _  A
GAM777  ACHE     3'  ACGTCGGGGTGGGGTGG    8556     C     TCCC  C  C
                                ACG CGGGGT   GG GG GG
                                ||| ||||||   || || ||
                                TGC GCCCCA   CC CC CC
                                  A    _____  _  A
GAM777  ACTN2    5'  GCCGGGGCTGCGGCGG     9945         CCCG
                                GCCGGGGTT   GCGGCGG
                                |||||||||   |||||||
                                CGGCCCCGA   CGCCGCC
                                     _____
GAM777  ADRA2A   5'  CGGCGGCGGCGGCGG      8633     _  TTCC
                                CGG GG   CGGCGGCGG
                                ||| ||   |||||||||
                                GCC CC   GCCGCCGCC
                                  G _____
GAM777  AF5Q31   5'  CCGGGAGGCGGCGG       30854       TTCCC
                                CCGGGG   GGCGGCGG
                                ||||||   ||||||||
```

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                                GGCCCT    CCGCCGCC
                                      _____
GAM777  AGTPBP1  5' CGCTGGAGGCGGCGG      31585    C  GTTCCC
                                CGC GGG     GGCGGCGG
                                ||| |||     ||||||||
                                GCG CCT     CCGCCGCC
                                  A  _______
GAM777  ARHGAP6  5' CCGGGGTTTGCCCAGGGCGGTG 30211        __  __    C
           GA                     CCGGGGTT  CCC  GGCGG GGA
                                ||||||||  |||  ||||| |||
                                GGCCCCAA  GGG  CCGCC CCT
                                    AC   TC    A
GAM777  AXUD1    5' CGGCGGCGGCGGCGG      37487    _ TTCC
                                CGG GG    CGGCGGCGG
                                ||| ||    |||||||||
                                GCC CC    GCCGCCGCC
                                  G  ____
GAM777  B3GNT4   5' GCCGGGCGGCGGCGGCGGCGG  42456      GTTCC_
                                GCCGGG     CGGCGGCGG
                                ||||||     |||||||||
                                CGGCCC     GCCGCCGCC
                                   GCCGCC
GAM777  BACE2    5' CACCGGGACCGGCGGCGG    39987       TTC
                                CGCCGGGG   CCGGCGGCGG
                                ||||||||   ||||||||||
                                GTGGCCCT   GGCCGCCGCC
                                      ___
GAM777  C21orf2  3' ACGCTGGGGTCCCCGTGGAG   22298     C       GC  C
                                ACGC GGGGTTCCCG  GG GG
                                |||| ||||||||||  || ||
                                TGCG CCCCAGGGGC  CC TC
                                  A        A_ _
GAM777  CACNA2D2 5' CGGCGGCGGCGGCGGCGG    25711     _  TCC
                                CGG GGT   CGGCGGCGG
                                ||| |||   |||||||||
                                GCC CCG   GCCGCCGCC
                                  G   CC_
GAM777  CDH2     5' CGGCGGCGGCGGCGGCGGA    12169     _  TCC
                                CGG GGT   CGGCGGCGGA
                                ||| |||   ||||||||||
                                GCC CCG   GCCGCCGCCT
                                  G   CC_
GAM777  CDK5R2   5' CCGGGGGACCCGGCGGTGG   19469      TT      C
                                CCGGGG  CCCGGCGG GG
                                ||||||  |||||||| ||
                                GGCCCC  GGGCCGCC CC
                                   CT       A
GAM777  CFTR     5' CGCTGGGGTCCCTGCTAGGG   7950     C    T   G  _  C
                                CGC GGGGT CCC GC GG GG
                                ||| ||||| ||| || || ||
```

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                                GCG CCCCA GGG CG TC CC
                                  A    _  A A _
GAM777  COL11A2  5' ACGCCGGGGTCCCAGGG    38774        T    C
                                ACGCCGGGGT CCCGG GG
                                |||||||||| ||||| ||
                                TGCGGCCCCA GGGTC CC
                                          _    _
GAM777  CPT1A    5' CGGCGGCGGCGGCGGTGGA   12423    _  TCC    C
                                CGG GGT   CGGCGG GGA
                                ||| |||   |||||| |||
                                GCC CCG   GCCGCC CCT
                                  G  CC_    A
GAM777  DAPK1    5' GCCGGGGCGGCGGCGG     22357       TTCC
                                GCCGGGG   CGGCGGCGG
                                |||||||   |||||||||
                                CGGCCCC   GCCGCCGCC
                                     _____
GAM777  DDEF2    5' GCGCGGGGCCTGGCGGCGGA  19320   _    TT  C
                                GC CGGGG  CC GGCGGCGGA
                                || |||||  || |||||||||
                                CG GCCCC  GG CCGCCGCCT
                                 C    __ A
GAM777  DDX26    5' ACACCGGGGCCCGAGGTGGTGG 29083          CC  C  C
          A                      ACGCCGGGGTTC  GG GG GGA
                                ||||||||||||  || || |||
                                TGTGGCCCCGGG  CC CC CCT
                                       CT  A  A
GAM777  DRIL1    5' CGCTAGGGGTGGGCGGCGG   23366    C_    TCCC
                                CGC  GGGGT   GGCGGCGG
                                |||  |||||   ||||||||
                                GCG  CCCCA   CCGCCGCC
                                  AT    C___
GAM777  ELOVL4   5' CGCCGCGGCGGCGG       35539      GGGTTCC
                                CGCCG     CGGCGGCGG
                                |||||     |||||||||
                                GCGGC     GCCGCCGCC
                                     _______
GAM777  FBXO7    5' CGACGGGGACGGCGGCGG    29138   C    TTCC
                                CG CGGGG   CGGCGGCGG
                                || |||||   |||||||||
                                GC GCCCC   GCCGCCGCC
                                 T    T___
GAM777  FMNL     5' CGGCGGCGGCGGCGGCGGA   25296    _  TCC
                                CGG GGT   CGGCGGCGGA
                                ||| |||   ||||||||||
                                GCC CCG   GCCGCCGCCT
                                  G  CC_
GAM777  FMR2     5' CGGCGGCAGCGGCGGCGG    12959    _  TCC
                                CGG GGT   CGGCGGCGG
                                ||| |||   |||||||||
```

```
                                GCC CCG   GCCGCCGCC
                                  G   TC_
GAM777  FOXD1    5'  GCGCGGCGGCGGCGG      20928    _   GGTTCC
                                GC CGG     CGGCGGCGG
                                || |||     |||||||||
                                CG GCC     GCCGCCGCC
                                 C  _______
GAM777  FOXD1    5'  CGCCGGGGCTGCCGGGTGGCGG 20926          _  C___
             CGGA                  CGCCGGGGTT CC    GGCGGCGGA
                                |||||||||| ||    |||||||||
                                GCGGCCCCGA GG    CCGCCGCCT
                                      C  CCCA
GAM777  FTH1     5'  CGCTGGAGCGGCGGCGG     42786     C    TTCC
                                CGC GGGG    CGGCGGCGG
                                ||| ||||    |||||||||
                                GCG CCTC    GCCGCCGCC
                                  A   _____
GAM777  FXYD1    3'  GCTGGGGAAGGGGCGGCGGA   34862    C    TTCCC
                                GC GGGG     GGCGGCGGA
                                || ||||     |||||||||
                                CG CCCC     CCGCCGCCT
                                 A    TTCC_
GAM777  FZD10    5'  GGGGGCCGCGGCGGA       28458      TTC   G
                                GGGG   CCG CGGCGGA
                                ||||   ||| |||||||
                                CCCC   GGC GCCGCCT
                                  C__   _
GAM777  G6PD     3'  ACTCGGGGTCGGGCGGCGG    7594     _      CCC
                                GC CGGGGTT   GGCGGCGG
                                || |||||||   ||||||||
                                TG GCCCCAG   CCGCCGCC
                                 A      C__
GAM777  GCLM     5'  CGGCGGCTGGGCGGCGGCGG   13131     _    CC_
                                CGG GGTT   CGGCGGCGG
                                ||| ||||   |||||||||
                                GCC CCGA   GCCGCCGCC
                                  G    CCC
GAM777  GNAS     5'  CGGCGGCGGCGGCGGCGG     38658     _   TCC
                                CGG GGT   CGGCGGCGG
                                ||| |||   |||||||||
                                GCC CCG   GCCGCCGCC
                                  G   CC_
GAM777  HDAC4    5'  GCTCGGGCTCGGGCGGCGGCGG 25773    CG     C__
                                GC  GGGTTC   CGGCGGCGG
                                ||  ||||||   |||||||||
                                CG  CCCGAG   GCCGCCGCC
                                 AG     CCC
GAM777  HHIP     5'  CGACGGCGGCGGCGG       35407    C   GGTTCC
                                CG CGG     CGGCGGCGG
                                || |||     |||||||||
```

```
                                GC GCC     GCCGCCGCC
                                 T  ______
GAM777  KCNJ5    3'  GCTGGGGTTCCCCCTTGGTGG  9437     C       GGC_  C
                                GC GGGGTTCCC    GG GG
                                || |||||||||    || ||
                                CG CCCCAAGGG    CC CC
                                 A        GGAA  A
GAM777  KIF3B    5'  CGGCGGCGGCGGCGGCGG    22032     _   TCC
                                CGG GGT   CGGCGGCGG
                                ||| |||   |||||||||
                                GCC CCG   GCCGCCGCC
                                  G   CC_
GAM777  LIF      3'  GCCGGGATTGAGGTGGGG    14147         CCC  C  C
                                GCCGGGGTT   GG GG GG
                                |||||||||   || || ||
                                CGGCCCTAA   CC CC CC
                                     CT_  A  _
GAM777  LRP8     5'  CGGTGACGCTCGGCGGCGG   37792    CC  G    CC
                                CG  GG GTTC  GGCGGCGG
                                ||  || ||||  ||||||||
                                GC  CT CGAG  CCGCCGCC
                                 CA  G   __
GAM777  MDM2     5'  CCGGGGTTTTCGCGCTTGGA   27807        CC  _  GGC
                                CCGGGGTT  CG GC   GGA
                                ||||||||  || ||   |||
                                GGCCCCAA  GC CG   CCT
                                     AA  G  AA_
GAM777  ME1      5'  CGCCGGGTTCGGCGGCGG    14405       GTTCC
                                CGCCGGG    CGGCGGCGG
                                |||||||    |||||||||
                                GCGGCCC    GCCGCCGCC
                                   AA___
GAM777  NF1      5'  GCCGGGGGGCGGCGGA      7057        TTCCC
                                GCCGGGG    GGCGGCGGA
                                |||||||    |||||||||
                                CGGCCCC    CCGCCGCCT
                                           _____
GAM777  NFATC1   5'  GCGCGGCGGCGGCGG       26077    _  GGTTCC
                                GC CGG     CGGCGGCGG
                                || |||     |||||||||
                                CG GCC     GCCGCCGCC
                                 C  _______
GAM777  NIPSNAP1 5'  CCCAAGCCCTGGTGGCGGA   18869    G   T  C  C
                                CC GGGT CC GG GGCGGA
                                || |||| || || ||||||
                                GG TTCG GG CC CCGCCT
                                 G   _  A  A
GAM777  NMB      5'  GCCCGGCCCCGGCGGCGGA   43951     G  GT
                                GCC GG  TCCCGGCGGCGGA
                                ||| ||  ||||||||||||
```

```
                                CGG CC  GGGGCCGCCGCCT
                                  G __
GAM777  NSEP1    5'  GCCGGCGGCGGCGG       43997      GGTTCC
                                GCCGG     CGGCGGCGG
                                |||||     |||||||||
                                CGGCC     GCCGCCGCC
                                  _______
GAM777  PEPD     3'  CGCTGGGATTTCTGGCTGG   40897     C     CCC  _
                                CGC GGGGTT   GGC GG
                                ||| ||||||   ||| ||
                                GCG CCCTAA   CCG CC
                                  A     AGA   A
GAM777  PIM1     5'  GCCGGGACTGGCGGCGG     44968       GT CCC
                                GCCGGG  T   GGCGGCGG
                                ||||||  |   ||||||||
                                CGGCCC  A   CCGCCGCC
                                   TG ____
GAM777  PKIG     3'  GCCAGGGTTCCCCCTCTGGGA  28193           GGCGGC
                                GCCGGGGTTCCC     GGA
                                ||||||||||||     |||
                                CGGTCCCAAGGG     CCT
                                      GGAGAC
GAM777  PPM1D    5'  CGCCGAATCCGGCGGCGG    18837       GTTC
                                CGCCGGG    CCGGCGGCGG
                                |||||||    ||||||||||
                                GCGGCTT    GGCCGCCGCC
                                   A____
GAM777  PPP1CB   5'  GGGCTTCTCGGCGGCGGA    15504     G   C
                                GGG TTC CGGCGGCGGA
                                ||| ||| ||||||||||
                                CCC AAG GCCGCCGCCT
                                  G   A
GAM777  PTGER3   5'  GCGCGGGCGGCGGCGG      9647     _    GTTCC
                                GC CGGG    CGGCGGCGG
                                || ||||    |||||||||
                                CG GCCC    GCCGCCGCC
                                 C   ______
GAM777  PTPRF    3'  ACGGCGGGGGTGGCGG      39027     C    TTCCCG C
                                ACG CGGGG     G GGCGG
                                ||| |||||     | |||||
                                TGC GCCCC     C CCGCC
                                  C     _______ A
GAM777  PTPRG    5'  GCCGGCGGGCGGCGGCGG    15936      _  TTCC
                                GCCGG GG    CGGCGGCGG
                                ||||| ||    |||||||||
                                CGGCC CC    GCCGCCGCC
                                   G  C____
GAM777  RAB23    5'  CGCCGGGGGTGGTGGGG     32217        TTCCC  C  C
                                CGCCGGGG    GG GG GG
                                ||||||||    || || ||
```

```
                                GCGGCCCC    CC CC CC
                                    CA___  A  _
GAM777  SDC1    5'  GCCCGGACCGGCGGCGG    16505    G  TTC
                                GCC GGG  CCGGCGGCGG
                                ||| |||  ||||||||||
                                CGG CCT  GGCCGCCGCC
                                  G  ___
GAM777  SF1     5'  GCCGGGGGCGGCGGGG     21564       TTCC    C
                                GCCGGGG   CGGCGG GG
                                |||||||   |||||| ||
                                CGGCCCC   GCCGCC CC
                                    C___    _
GAM777  SHOX    3'  CCGGGGGAGCGGTGGA     27817       TTCCC   C
                                CCGGGG    GGCGG GGA
                                ||||||    ||||| |||
                                GGCCCC    TCGCC CCT
                                   C____    A
GAM777  SIM2    3'  CCGCAAGTCGGCGGCGG    22873    _  TCC
                                CCG GGGT  CGGCGGCGG
                                ||| ||||  |||||||||
                                GGC TTCA  GCCGCCGCC
                                  G  ___
GAM777  SLC7A1  5'  GCCGGCGGCGGCGG       16807      GGTTCC
                                GCCGG     CGGCGGCGG
                                |||||     |||||||||
                                CGGCC     GCCGCCGCC
                                  _____
GAM777  SLIT3   5'  GCCTGGGGAGCGGGCGGCGGA  16868    _  TTCCC
                                GCC GGGG    GGCGGCGGA
                                ||| ||||    |||||||||
                                CGG CCCC    CCGCCGCCT
                                  A   TCGC_
GAM777  SMURF1  5'  CGCCGGGGTCCGAGCCGG    45192       T  C  GG
                                CGCCGGGGT CC GGC  CGG
                                ||||||||| || |||  |||
                                GCGGCCCCA GG TCG  GCC
                                     _ C  __
GAM777  SPF30   5'  GCTGGGGGCGGGGCGGCGG   25237   C   TTCCC
                                GC GGGG    GGCGGCGG
                                || ||||    ||||||||
                                CG CCCC    CCGCCGCC
                                 A   CGCC_
GAM777  ST14    5'  GCGCGGGGCGCAGGCGGCGG  35063   _    TCCC
                                GC CGGGGT   GGCGGCGG
                                || ||||||   ||||||||
                                CG GCCCCG   CCGCCGCC
                                 C     CGT_
GAM777  TBL1X   5'  CGCTGCGGCGGCGGCGG    24879    __  GGTTCC
                                CGC  CGG    CGGCGGCGG
                                |||  |||    |||||||||
```

```
                                GCG  GCC     GCCGCCGCC
                                  AC  ______
GAM777  TESK1    3'  GCTGGGGCTCCCCTACACGG   26615    C       G_  G
                                GC GGGGTTCCC  GCG CGG
                                || |||||||||  ||| |||
                                CG CCCCGAGGG  TGT GCC
                                 A       GA  _
GAM777  USP7     5'  CGGCGGCGGCGGCGGCGG    18453    _  TCC
                                CGG GGT   CGGCGGCGG
                                ||| |||   |||||||||
                                GCC CCG   GCCGCCGCC
                                  G  CC_
GAM777  YY1      5'  CGCCGCGGCGGCGGCGG     18169      G  TTCC
                                CGCCG GG    CGGCGGCGG
                                ||||| ||    |||||||||
                                GCGGC CC    GCCGCCGCC
                                   G  ____
GAM777  ZNF219   5'  CCCGGGCGGGCGGCGGCGGA   32318    G    TCC
                                CC GGGT   CGGCGGCGGA
                                || ||||   ||||||||||
                                GG CCCG   GCCGCCGCCT
                                 G   CCC
GAM778  ACAT1    5'  CAGAGGGCTGAGTATCGG     6160      AGT      TGCT
                                CAGA   CTGAGTA    TCGG
                                ||||   |||||||    ||||
                                GTCT   GACTCAT    AGCC
                                  CCC      ____
GAM778  CELSR3   3'  CAGAAGTTTGGCCTTTGG     10825       C  A  ATG   C
                                CAGAAGT TG GT   CTT GG
                                ||||||| || ||   ||| ||
                                GTCTTCA AC CG   GAA CC
                                    A  _  ___   A
GAM778  FGR      3'  ACAAGGTCTGAGCACTTTTGGG 23495      AA        GC  C
                                ACAG  GTCTGAGTAT  TT GG
                                ||||  ||||||||||  || ||
                                TGTT  CAGACTCGTG  AA CC
                                  C_        AA  C
GAM778  FXR2     5'  CAGCAGTCTGAGTGCGGG    22158     A       AT  TTC
                                CAG AGTCTGAGT  GC   GG
                                ||| |||||||||  ||   ||
                                GTC TCAGACTCA  CG   CC
                                  G        __  C__
GAM778  KCNA6    3'  ACAGAAGCTGGGCATGATTGGG 13803        T   A    C  C
                                ACAGAAG CTG GTATG TT GG
                                ||||||| ||| ||||| || ||
                                TGTCTTC GAC CGTAC AA CC
                                    _  C    T  C
GAM778  PDE1A    3'  ACAGAAGTCTTTAAGGTGTTTC 22707          GAGTA_  C
            GG                    ACAGAAGTCT     TG TTCGG
                                ||||||||||     || |||||
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                                TGTCTTCAGA     AC AAGCC
                                      AATTCC  A
GAM778  PMM2     3'  AAAGTCTGGGTGAAGGCCTGGG 43547        A  AT__   C
                                GAAGTCTG GT    GCTT GG
                                |||||||| ||    |||| ||
                                TTTCAGAC CA    CGGA CC
                                     C  CTTC    C
GAM778  PPP1R12B  3'  AGAAGTCTTACATGTTTGGA   36961        GAG    C  C
                                AGAAGTCT   TATG TT GGA
                                ||||||||   |||| || |||
                                TCTTCAGA   GTAC AA CCT
                                     AT_    _  A
GAM778  SHANK2   3'  GAAGTCTGAGAAACAAGTTTGG 29457         TAT  TTC___
             A                   GAAGTCTGAG   GC     GGA
                                ||||||||||   ||     |||
                                CTTCAGACTC   TG     CCT
                                      TT_  TTCAAA
GAM778  CDH13    3'  TCGGAGCAAAAGTGACAGCT   10372    T  A      CAAAAGA
                                TC GA GCAAAAG      GGCT
                                || || |||||||      ||||
                                AG CT CGTTTTC      TCGA
                                 C  _      ACTG___
GAM778  CEACAM1   3'  TCAGAGGCTGTTAAAAGAGGCT 11834    T  A  AAAAGC
                                TC GA GC     AAAAGAGGCT
                                || || ||     ||||||||||
                                AG CT CG     TTTTCTCCGA
                                 T  C  ACAA__
GAM778  DAZ      3'  CCTGAAAGACTAGTAAAAGAGG 44364        CAAA  C
             CT                   TCTGAAG    AG AAAAGAGGCT
                                |||||||    || ||||||||||
                                GGACTTT    TC TTTTCTCCGA
                                     CTGA  A
GAM778  ENTPD6   3'  CTGAAGCAGCTCAAGGGGCT   10337        AAA  AA   A
                                CTGAAGCA   GC  AAG GGCT
                                ||||||||   ||  ||| ||||
                                GACTTCGT   CG  TTC CCGA
                                     ___  AG   C
GAM778  EPHB6    5'  TCTGAAACCTAGAAGAGAGGCT 20805        AAA  C  A
                                TCTGAAGC   AG AA AGAGGCT
                                ||||||||   || || |||||||
                                AGACTTTG   TC TT TCTCCGA
                                     GA_  _  C
GAM778  HLCS     3'  TCTGAAGCAGTGCGGGGAGGCT 7648         AAA  AAAA
                                TCTGAAGCA   GC    GAGGCT
                                |||||||||   ||    ||||||
                                AGACTTCGT   CG    CTCCGA
                                     CA_  CCC_
GAM778  IGHMBP2  3'  TCTGAAACAAAACCCTGAGGCT 13494          G AAAA
                                TCTGAAGCAAAA C    GAGGCT
                                |||||||||||| |    ||||||
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                                AGACTTTGTTTT G    CTCCGA
                                      _ GGA_
GAM778  KRT17    3'  CTGAAGCAGGGGGCTGAGGCT  7682         AAA_  AAAA
                                CTGAAGCA    GC    GAGGCT
                                ||||||||    ||    ||||||
                                GACTTCGT    CG    CTCCGA
                                     CCCC  A___
GAM778  LEP      3'  TGAAGCAAAGCATCAGC     6919          A   AAAGA
                                TGAAGCAAA GCA     GGC
                                ||||||||| |||     |||
                                ACTTCGTTT CGT     TCG
                                      _  AG___
GAM778  MLLT7    3'  TCTGAAGCAGGGGACAAAGCT  25534         AAAGCAAAA
                                TCTGAAGCA       GAGGCT
                                |||||||||       ||||||
                                AGACTTCGT       TTTCGA
                                     CCCCTG___
GAM778  SFPQ     5'  CGAGGCAAAAGCGAAGA     22858     A       AA
                                TGA GCAAAAGC  AAGA
                                ||| ||||||||  ||||
                                GCT CGTTTTCG  TTCT
                                  C       C_
GAM778  SLC19A2  3'  TGAGGTGGAACAAAGAGGCT   42895     AGCAAA     A
                                TGA     AGCAAA GAGGCT
                                |||     |||||| ||||||
                                ACT     TTGTTT CTCCGA
                                  CCACC_     _
GAM778  SLC21A2  3'  TCTGGAGGCAGAGAAGAGGCT  24805      A  CAAAA   A__
                                TCTG AG    GCA   AAGAGGCT
                                |||| ||    |||   ||||||||
                                AGAC TC    CGT   TTCTCCGA
                                  C _____   CTC
GAM778  SYT4     3'  TAAAGCACAAAAAAGAGG    41660        AAAGC
                                TGAAGCA    AAAAGAGG
                                |||||||    ||||||||
                                ATTTCGT    TTTTCTCC
                                     GTT__
GAM778  UTY      3'  CCTGAAGCAGAGGC        28311         AAAGCAAAA
                                TCTGAAGCA       GAGGC
                                |||||||||       |||||
                                GGACTTCGT       CTCCG
                                     _________
GAM779  SERPINB6 5'  ACTTCCTGCTCGAGACCCG   21300    A   G  TT
                                AC TCT GT  TCGAGACCCG
                                || ||| ||  ||||||||||
                                TG AGG CG  AGCTCTGGGC
                                 A   A __
GAM780  AQP6     5'  TCCTCCACTCCACCC       38257         CTCCC
                                TCCTCCAC    CCACCC
                                ||||||||    ||||||
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                                AGGAGGTG    GGTGGG
                                    A____
GAM780  ASL     5'  TCCTCCACGCCCGTCCC     43533        CT   CCA
                                TCCTCCAC  CCC   CCC
                                ||||||||  |||   |||
                                AGGAGGTG  GGG   GGG
                                    C_   CA_
GAM780  ASTN    3'  ACCATCCTAAGATTTTCCCCTG 42938        CCACC__    CA
            CCC                   ATCATCCT      TCCCC  CCC
                                ||||||||      |||||  |||
                                TGGTAGGA      AGGGG  GGG
                                    TTCTAAA    AC
GAM780  B4GALT2  3'  ATCATCCTCGCCACCCC     36135         CA  T
                                ATCATCCTC  CC CCCC
                                |||||||||  || ||||
                                TAGTAGGAG  GG GGGG
                                    C_  T
GAM780  BCL2    3'  TCCTCCCTCCCACCCC      8525        ACCTCC
                                TCCTCC     CCCACCCC
                                ||||||     ||||||||
                                AGGAGG     GGGTGGGG
                                   GA____
GAM780  C1orf6   3'  TCAGGCTGTCTCCCCCATTCC  33534     TC  CCAC       CC
                                TCA  CT    CTCCCCCA  CC
                                |||  ||    |||||||  ||
                                AGT  GA    GAGGGGGT  GG
                                  CC  CA__       AA
GAM780  CD79B    3'  ACCAGTCTCTGCCTCCCCCATC 8420      TC   CA       _
            CC                    ATCA  CTC  CCTCCCCCA CCC
                                ||||  |||  ||||||||| |||
                                TGGT  GAG  GGAGGGGGT GGG
                                  CA   AC       A
GAM780  CFTR     3'  ATCACCCTAGGTTCTCCCCTGT 7948         CCAC_     CA_
            CCC                   ATCATCCT    CTCCCC   CCC
                                ||||||||    ||||||   |||
                                TAGTGGGA    GAGGGG   GGG
                                    TCCAA     ACA
GAM780  CHST1    5'  CATCCTCCGCCTCCCGCGCCC  18904         A     CCA
                                CATCCTCC CCTCCC   CCC
                                |||||||| ||||||   |||
                                GTAGGAGG GGAGGG   GGG
                                    C     CGC
GAM780  CTNS     3'  TCCTGGGACCCCCACCCC    22349      CCACCT
                                TCCT     CCCCCACCCC
                                ||||     ||||||||||
                                AGGA     GGGGGTGGGG
                                  CCCT__
GAM780  DBN1     5'  CATCCTTCCACCTCACTCC   38924       _      CC_
                                CATCCT CCACCTC   CC
                                ||||||| |||||||   ||
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                                GTAGGA GGTGGAG   GG
                                   A      TGA
GAM780  DLEC1    3'  ACCATTTTCCACCTCCAGCTCC 28813      CC       CCCA
                                ATCAT  TCCACCTCC    CC
                                |||||  |||||||||    ||
                                TGGTA  AGGTGGAGG    GG
                                   AA        TCGA
GAM780  DNMT2    3'  ACCATCCTCCCCATCCACC    20627          A  TCCC
                                ATCATCCTCC CC    CCACC
                                |||||||||| ||    |||||
                                TGGTAGGAGG GG    GGTGG
                                      _  TA__
GAM780  DYSF     5'  TCATCTTCCACCCCCGCCGCCC 18583      C       C  A
                                TCATC TCCACCTCC CC CCC
                                ||||| ||||||||| || |||
                                AGTAG AGGTGGGGG GG GGG
                                   A        C  C
GAM780  E2F1     3'  TCCCCCACTCACCTCTCCCA   44491       ____    C
                                TCCTCC    ACCTC CCCA
                                ||||||    ||||| ||||
                                AGGGGG    TGGAG GGGT
                                   TGAG    A
GAM780  ELAVL3   3'  TCTTCCCCTCCCACCCC     10889    C   A     CC
                                TC TCC CCTCCC  ACCCC
                                || ||| ||||||  |||||
                                AG AGG GGAGGG  TGGGG
                                 A  _     __
GAM780  EPHA1    3'  ATCATCCTTTTACTTCTACCCC 23431        CC_  C  __
                                ATCATCCT   AC TC  CCCC
                                ||||||||   || ||  ||||
                                TAGTAGGA   TG AG  GGGG
                                     AAA  A  AT
GAM780  ESPN     3'  TCATCCTCTATTCACTCC    36448        ____  C
                                TCATCCTC    CAC TCC
                                ||||||||    ||| |||
                                AGTAGGAG    GTG AGG
                                     ATAA  _
GAM780  GABRP    5'  TCATCCTCAGCCCTGTCCC   30560        CA_  CC
                                TCATCCTC   CCT  CCC
                                ||||||||   |||  |||
                                AGTAGGAG   GGA  GGG
                                     TCG   CA
GAM780  GP1BA    3'  ATCACCCTGTGTTCCTTACCCC 6743         CCACC   CCC
                                ATCATCCT    TCC   ACCCC
                                ||||||||    |||   |||||
                                TAGTGGGA    AGG   TGGGG
                                     CACA_   AA_
GAM780  HAO1     3'  TCACCCTCTGCACAGTGTCTC  32761        __  _____
                                TCATCCTC  CAC    CTC
                                ||||||||  |||    |||
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                                AGTGGGAG  GTG    GAG
                                    AC   TCACA
GAM780  HR      5'  CCATCTTCCACCCCAAAGCCGT 32912      C      C___  CAC
             TCC                   TCATC TCCACCTC   CC   CC
                                |||||  ||||||||   ||   ||
                                GGTAG AGGTGGGG   GG   GG
                                   A       TTTC  CAA
GAM780  IL1F5   3'  TCTCCTCCACTCACCCC     29358    A      C  _
                                TC TCCTCCAC TC CCCC
                                || ||||||||  || ||||
                                AG AGGAGGTG AG GGGG
                                 _       _  T
GAM780  INHBB   3'  TCATTCCCACCCGTCCC     13566     C T     CC
                                TCAT C CCACCT  CCC
                                ||||  |  ||||||  |||
                                AGTA G GGTGGG  GGG
                                  A _     CA
GAM780  ISLR    3'  ATCCTCCTCTCCCATTCC    24431       AC    CCA
                                ATCCTCC  CTCCC   CC
                                |||||||  |||||   ||
                                TAGGAGG  GAGGG   GG
                                    A_    TAA
GAM780  JRK     3'  TCACCTCCCAAAGGCCCCACC  44501    T    ACCTC_
                                TCA CCTCC     CCCCACC
                                |||  |||||     |||||||
                                AGT GGAGG     GGGGTGG
                                  _    GTTTCC
GAM780  MAPK8IP1  3'  CCCCACCCTCCCCTACCC    24154       TC    _
                                CTCCACC  CCCC ACCC
                                |||||||  ||||  ||||
                                GGGGTGG  GGGG TGGG
                                    GA   A
GAM780  MBL2    3'  TCATCCTCTACCAGTTCCACTC 6964        C   TCCC   _
             C                   TCATCCTC ACC    CCAC CC
                                |||||||| |||    ||||  ||
                                AGTAGGAG TGG    GGTG GG
                                    A   TCAA    A
GAM780  MLC1    3'  TCGTCCCTGTGGCTCCCACCCC 40154    A    CCACCTCC
                                TC TCCT       CCCACCCC
                                || ||||       ||||||||
                                AG AGGG       GGGTGGGG
                                 C    ACACCGA_
GAM780  MPZ     3'  TCATTTGCCCCCTCCCCCACTC 8038       CC_   A        _
             C                   TCAT   TCC CCTCCCCCAC CC
                                ||||   ||| ||||||||||  ||
                                AGTA   GGG GGAGGGGGTG GG
                                  AAC   _         A
GAM780  MYBL1   5'  ATCATCCTCGTCCCTTGTCCA  41976        CA_   CCC
                                ATCATCCTC   CCT   CCA
                                |||||||||   |||   |||
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                                TAGTAGGAG  GGA  GGT
                                     CAG  ACA
GAM780  NEFH    3'  CATCCAGACCTCCCCTGCCC  34344     TCC      CA
                                CATCC  ACCTCCCC  CCC
                                |||||  ||||||||  |||
                                GTAGG  TGGAGGGG  GGG
                                   TC_      AC
GAM780  NOL3    3'  TCACCCTCCCCTTGCTCC    19492       A  CCC_
                                TCATCCTCC CCT   CC
                                |||||||||  |||   ||
                                AGTGGGAGG GGA   GG
                                     _  ACGA
GAM780  PDE7A   3'  TCTTCCCCTCCCACCCC    42290   C  A    CC
                                TC TCC CCTCCC  ACCCC
                                || ||| ||||||  |||||
                                AG AGG GGAGGG  TGGGG
                                 A  _    __
GAM780  PPP1R8  3'  ATCACCCTTCCACCCCATTCC  39726       _     CC_
                                ATCATCCT CCACCTC  CC
                                ||||||||  |||||||  ||
                                TAGTGGGA GGTGGGG  GG
                                     A      TAA
GAM780  PRX     3'  ATCATCCCCACTTCTTGCC   34104       T   C  CC_
                                ATCATCC CCAC TC   CC
                                |||||||  ||||  ||   ||
                                TAGTAGG GGTG AG   GG
                                     _   A  AAC
GAM780  PYGO2   3'  CATGCCTGCCTTCCCCACCCC  41947    _  CCA  C
                                CAT CCT   CCT CCCCACCCC
                                |||  |||   |||  |||||||||
                                GTA GGA   GGA GGGGTGGGG
                                  C  C__   A
GAM780  RAB5A   3'  ACCATTAATACTCTTCCCCACC  20009      CCTCC  _  C
           CC                     ATCAT    AC CT CCCCACCCC
                                |||||    ||  ||  |||||||||
                                TGGTA    TG GA GGGGTGGGG
                                   ATTA_  A  A
GAM780  RASD1   3'  CATCCCTCCCCCACC      32007      TCCAC
                                CATCC    CTCCCCCACC
                                |||||    ||||||||||
                                GTAGG    GAGGGGGTGG
                                     _____
GAM780  REGL    3'  ATCATCCTTCCATTTCTTGAAT  27118       _  CC  CCCCAC
           CC                     ATCATCCT CCA  TC     CC
                                |||||||  |||  ||     ||
                                TAGTAGGA GGT  AG     GG
                                     A  AA  AACTTA
GAM780  RRM2B   5'  CCCGGCCCCGCCTCCCCCGCC  42716    ATC   A      A
                                TC   CTCC CCTCCCCC CC
                                ||   |||| ||||||||  ||
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                                GG   GGGG GGAGGGGG GG
                                 GCC    C       C
GAM780   SCD      3'  ATCCTCCACTCAGGCCCC    22821         C ___
                                ATCCTCCAC TC   CCCC
                                ||||||||| ||   ||||
                                TAGGAGGTG AG   GGGG
                                     _ TCC
GAM780   SDC4     3'  TCATCAGCCCTCCCCCATTCC  16530      CTCCA       CC
                                TCATC    CCTCCCCCA  CC
                                |||||    |||||||||  ||
                                AGTAG    GGAGGGGGT  GG
                                   TCG__       AA
GAM780   SHOC2    5'  CCATCCTCCTCGCTCGCCC   28892        AC_   C
                                TCATCCTCC   CTC CCC
                                |||||||||   ||| |||
                                GGTAGGAGG   GAG GGG
                                     AGC   C
GAM780   TCAP     3'  ACCATCCTTGCCTCTGCCC   18944        CCA    C_
                                ATCATCCT   CCTC  CCC
                                ||||||||   ||||  |||
                                TGGTAGGA   GGAG  GGG
                                     AC_    AC
GAM780   TCL1A    3'  TCATCCTCTGTCTGTCCATTCC 35030        CAC  CCC   CC
                                TCATCCTC   CT   CCA  CC
                                ||||||||   ||   |||  ||
                                AGTAGGAG   GA   GGT  GG
                                     ACA  CA_   AA
GAM780   TFE3     3'  TCATCCTCACTTCTGTTCC   27171        C  C  CC__
                                TCATCCTC AC TC    CC
                                |||||||| || ||    ||
                                AGTAGGAG TG AG    GG
                                     _ A  ACAA
GAM780   TGFB3    3'  ACCATCCCTTTCCTCTATCCC  17455        CCA    C__
                                ATCATCCT   CCTC   CCC
                                ||||||||   ||||   |||
                                TGGTAGGG   GGAG   GGG
                                     AAA    ATA
GAM780   THBD     3'  CATCCTCCAGGATCCATTCC   7423         CC_   C__
                                CATCCTCCA   TCC   CC
                                |||||||||   |||   ||
                                GTAGGAGGT   AGG   GG
                                     CCT   TAA
GAM780   TIMP3    3'  TCACATCCACCTCCCCTAC    7467      CC         C
                                TCAT  TCCACCTCCCC AC
                                ||||  |||||||||| ||
                                AGTG  AGGTGGAGGGG TG
                                   T_         A
GAM780   TLL2     3'  ATCATCCTCTACACTTCTC    29745         __   __
                                ATCATCCTC  CAC  CTC
                                |||||||||  |||  |||
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                                TAGTAGGAG  GTG  GAG
                                     AT   AA
GAM780  TNFRSF6B  5'  CATGCCACCTCCTTTGCCCC  37281     CCT      CCCA
                                CAT   CCACCTCC    CCCC
                                |||   ||||||||    ||||
                                GTA   GGTGGAGG    GGGG
                                  C__       AAAC
GAM780  VANGL2    3'  ATCCTTTCCCTCTCCCCCACCC 43452      __   AC
           C                     ATCC  TCC  CTCCCCCACCCC
                                ||||  |||  ||||||||||||
                                TAGG  AGG  GAGGGGGTGGGG
                                  AA   GA
GAM780  WHSC1     3'  TCACCCTCTGCCTTTCAC    39381        CA   CCCC
                                TCATCCTC  CCT    CAC
                                ||||||||  |||    |||
                                AGTGGGAG  GGA    GTG
                                     AC   AA__
GAM780  XRCC5     3'  CTCCCCTTCCCACCCC      34489      A   CC
                                CTCC CCT  CCCACCCC
                                |||| |||  ||||||||
                                GAGG GGA  GGGTGGGG
                                  _   A_
GAM780  APOL1     3'  GGTAAGAGCGATGGGAC     18939       GGGA    CGA
                                GGTAGG    AGCGA   GAC
                                ||||||    |||||   |||
                                CCATTC    TCGCT   CTG
                                    _____     ACC
GAM780  EN2       3'  CGGCAGGACTGCGGTGGGAC   10944        GGAA   ACGA
                                CGGTAGGG    GCG    GAC
                                ||||||||    |||    |||
                                GCCGTCCT    CGC    CTG
                                     GA__   CACC
GAM780  FGF1      3'  GGCAGGGGGAGAAACAAGA   37572          A C
                                GGTAGGGGGA G GACGAGA
                                |||||||||| | |||||||
                                CCGTCCCCCT C TTGTTCT
                                      _ T
GAM780  FGF18     5'  CGGTGCGGGGAAGCTCG     19303      AG       GA
                                CGGT  GGGGAAGC  CG
                                ||||  ||||||||  ||
                                GCCA  CCCCTTCG  GC
                                  CG       A_
GAM780  HCFC1     3'  CGGTAGGGGAGGGCTGGAAAGA 43389          AA  GAC_
                                CGGTAGGGGGG  GC   GAGA
                                ||||||||||  ||   ||||
                                GCCATCCCCT  CG   TTCT
                                      CC  ACCT
GAM780  PIK3R3    3'  GTGGGGGGAAGAGAGAC     41447    A       CGAC
                                GT GGGGGAAG    GAGAC
                                || ||||||||    |||||
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                                CA CCCCCTTC   CTCTG
                                 C      T___
GAM780  VDR     3'  GGCAGGGGGAGGACGAG    7523          A C
                                GGTAGGGGGA G GACGAG
                                |||||||||| | ||||||
                                CCGTCCCCCT C CTGCTC
                                      _ _
GAM781  APPL    3'  GCATTGTAGAAGTAGGCAGGC  29008    C _ CGTC
                                GCA TG AG   TAGGCAGGC
                                ||| || ||   |||||||||
                                CGT AC TC   ATCCGTCCG
                                 A  A  TTC_
GAM781  CTGF    3'  CACTGGGGCTACAGGCAGG   12500      A_ GTC
                                CACTG  GC   TAGGCAGG
                                |||||  ||   ||||||||
                                GTGAC  CG   GTCCGTCC
                                   CC  AT_
GAM781  DRPLA   3'  GCTCTGGGTGGCAGGC     12587    A  AGC  CTA
                                GC CTG   GT   GGCAGGC
                                || |||   ||   |||||||
                                CG GAC   CA   CCGTCCG
                                 A   C__  ___
GAM781  FBXL7   5'  GCGCTGAGCCGGGCAGGCC   29404    A     GTCTA
                                GC CTGAGC    GGCAGGCC
                                || ||||||    ||||||||
                                CG GACTCG    CCGTCCGG
                                 C     GC___
GAM781  MSF     3'  ACATTGAGGCTGGGCAGGCC  44718    C   C T  A
                                GCA TGAG G CT GGCAGGCC
                                ||| |||| | || ||||||||
                                TGT ACTC C GA CCGTCCGG
                                 A   _ _  C
GAM781  MUC4    3'  GCGTTGAACGTCTCCTGGCC  39669    AC       AGGCA
                                GC  TGAGCGTCT    GGCC
                                ||  |||||||||    ||||
                                CG  ACTTGCAGA    CCGG
                                 CA       GGA__
GAM781  P53AIP1  3'  ACACTGAGACTCAGGCAGGCC  35228        CG  T
                                GCACTGAG  TC AGGCAGGCC
                                ||||||||  || |||||||||
                                TGTGACTC  AG TCCGTCCGG
                                     TG  _
GAM781  PHF1    3'  CTGAGCGTCTAGGAAGACC   15269          C
                                CTGAGCGTCTAGG AGGCC
                                |||||||||||| |||||
                                GACTCGCAGATCC TCTGG
                                       T
GAM781  RGS3    5'  GCACTGAGTGGGGAGCGGGCC  39568        CGTCTA   A
                                GCACTGAG     GGC GGCC
                                ||||||||     ||| ||||
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                                CGTGACTC     TCG CCGG
                                     ACCCC_  C
GAM781  SCA1    3'  GCCTAGAGTTTAGGCAGG    7280     A  G  C  C
                                GC CT AG GT TAGGCAGG
                                || || || || ||||||||
                                CG GA TC CA ATCCGTCC
                                 _ _ T  A
GAM781  SORCS3  3'  GCATTGAGCAGGCCTGGCGGG  31419     C    __    A   A
                                GCA TGAGC  GTCT GGC GG
                                ||| |||||  |||| ||| ||
                                CGT ACTCG  CGGA CCG CC
                                  A    TC    _  C
GAM781  ABCA1   3'  CAGAACTGTCACAGCTTTA   24269       GC    T
                                CAGAAT  TCAT AGCTTTA
                                ||||||  |||| |||||||
                                GTCTTG  AGTG TCGAAAT
                                    AC   _
GAM781  ANGPT1  3'  CAGAGTACTTGCTTTTACTTC  40238      A    CATTA    _
                                CAGA TGCT    GCTTT ACTTC
                                |||| ||||    ||||| |||||
                                GTCT ATGA    CGAAA TGAAG
                                  C   A____    A
GAM781  CYR61   3'  GAATGCCCTCCCATTTACTT   11417        A  AGC
                                GAATGCTC TT   TTTACTT
                                |||||||| ||   |||||||
                                CTTACGGG AG   AAATGAA
                                     _ GGT
GAM781  GNAS    3'  CAGGATCCTCATCTGCTTC   38655     A  G     A
                                CAG AT CTCATT GCTTT
                                ||| || |||||| |||||
                                GTC TA GAGTAG CGAAG
                                  C  G     A
GAM781  LTB4R   5'  CAGAATGCCAATTACTTC    8879          C    G
                                CAGAATGCT ATTA CTTT
                                ||||||||| |||| ||||
                                GTCTTACGG TAAT GAAG
                                      T   _
GAM781  MPP5    3'  GAATGCTCTGTTGAAAGCTTC  35397         ATT____
                                GAATGCTC      AGCTTT
                                ||||||||      ||||||
                                CTTACGAG      TCGAAG
                                     ACAACTT
GAM781  VHL     3'  GAGTGTCTCATTCACTTC    8109     A  _     A
                                GA TG CTCATT GCTTT
                                || || |||||| |||||
                                CT AC GAGTAA TGAAG
                                 C  A     G
GAM782  ABAT    5'  TCTCCGATCTGCGGGATC    40777      T    AGGACCA
                                TCTC CGGT      CGGGATC
                                |||| ||||      |||||||
```

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                                AGAG GCTA      GCCCTAG
                                  _   GAC____
GAM782  ITGAM    3'  TCTCTCGGTGGTGCAGTGGTTC 43519         A  AC  CG  A
                                TCTCTCGGT GG  CA  GG TC
                                ||||||||| ||  ||  || ||
                                AGAGAGCCA CC  GT  CC AG
                                     _ AC  CA  A
GAM782  LFG      5'  TCTCTCGGGGAAGGGGTC    44150         TA   CCAC   A
                                TCTCTCGG  GGA   GGG TC
                                ||||||||  |||   ||| ||
                                AGAGAGCC  CCT   CCC AG
                                     __  T___  C
GAM782  RANBP3   3'  TCTCTCGGGAGGGCCTCTGGTT 28768         T   A  ACG  A
            C                    TCTCTCGG AGG CC   GG TC
                                ||||||||| ||| ||   || ||
                                AGAGAGCC TCC GG   CC AG
                                     C   C  AGA  A
GAM782  ATRN     3'  TGCCACTCACTAGCTCGTGCGT 40286         C  AG   CCA
                                TGTCACTCAC AG  CGT   CGT
                                |||||||||| ||  |||   |||
                                ACGGTGAGTG TC  GCA   GCA
                                     A  GA   C__
GAM782  IHPK3    5'  TGCTGTTCACCAGAGCCC    38378     CAC        GT
                                TGT   TCACCAGAGC  CC
                                |||   ||||||||||  ||
                                ACG   AGTGGTCTCG  GG
                                  ACA         __
GAM782  NPHS1    3'  TGTCACTCAGCCCCCTCCATGT 21619         _  AGAGCG   C
                                TGTCACTCA CC     TCCA GT
                                ||||||||| ||     |||| ||
                                ACAGTGAGT GG     AGGT CA
                                     C  GGG___    A
GAM782  OSR1     3'  GTCACTCACTAGGTTACGT    23038         C  A__
                                GTCACTCAC AG   GCGT
                                ||||||||| ||   ||||
                                CAGTGAGTG TC   TGCA
                                     A  CAA
GAM782  UQCRC1   5'  TGTTTCTCACCAGCCGCGCTGC 17892     CA      A_   CCA
            GT                    TGT  CTCACCAG  GCGT   CGT
                                |||  ||||||||  ||||   |||
                                ACA  GAGTGGTC  CGCG   GCA
                                  AA       GG    AC_
GAM783  AFP      5'  TTGTTATTGGCAGTG       10069          CGGGACGA
                                TTGTTATTGGC       AGTG
                                ||||||||||        ||||
                                AACAATAACCG       TCAC
                                          _________
GAM783  LASS2    3'  TTGTTATTGAGGATGGGGTGG  42683         GCC    CGAA
                                TTGTTATTG   GGGA   GTGG
                                |||||||||   ||||   ||||
```

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                                AACAATAAC  TCCT   CACC
                                    ___    ACCC
GAM783  SLC22A11  3'  TCGTTATTGGTTGGGCATG   32964        CC   A GAA
                                TTGTTATTGG  GGG C   GTG
                                ||||||||||  ||| |   |||
                                AGCAATAACC  CCC G   TAC
                                     AA   _ ___
GAM784  NPTX2     3'  GATTCCTGGGGAATGAGC    45206     G   TAAA
                                GATT TTTG   GAATGAGC
                                |||| ||||   ||||||||
                                CTAA GGAC   CTTACTCG
                                  _   CC__
GAM784  SLC4A5    5'  GATTGTTTGTGCCAAGC     39430        AAAGAA
                                GATTGTTTGT     TGAGC
                                ||||||||||     |||||
                                CTAACAAACA     GTTCG
                                     CG____
GAM784  SRGAP2    3'  TTGTTTGCAGTGAGC       43993        AAGAA
                                TTGTTTGTA    TGAGC
                                |||||||||    |||||
                                AACAAACGT    ACTCG
                                     C____
GAM784  ALPL      3'  GCGGGGAGGGAGCAAAGGCT  7889       A   C  TTT  A
                                GCGGG AGGG GC   AG CT
                                ||||| |||| ||   || ||
                                CGCCC TCCC CG   TC GA
                                   C   T  TT_  C
GAM784  CDH4      3'  TGGGGGTGGGTGCTCATGCTA  12182    C   AA   C   TAGA
                                TG GGG  GGG GCTT   CTA
                                || |||  ||| ||||   |||
                                AC CCC  CCC CGAG   GAT
                                 _   CA   A   TAC_
GAM784  LMO4      3'  TGCGGGAAGGGCAATCAAGACT 27665          C  T
            AA                    TGCGGGAAGGGCG TT AGACTAA
                                |||||||||||| || |||||||
                                ACGCCCTTCCCGT AG TCTGATT
                                       T  T
GAM784  MYCL2     3'  TGCGGGAAAGGGTGCTGTAG   23913        _  C   T
                                TGCGGGAA GGG GCT TAG
                                |||||||| ||| ||| |||
                                ACGCCCTT CCC CGA ATC
                                     T   A   C
GAM784  TCF7      3'  TGGGGAGGGGTGCACACT     17326    C    A   C  TTT G
                                TG GGGA GGG GC   A ACT
                                || |||| ||| ||   | |||
                                AC CCCT CCC CG   T TGA
                                 _   C   A  ___ G
GAM784  TNFSF5    3'  TGGGGGAGGGAAGAGACT    6334     C   A    CGCTTT
                                TG GGG AGGG     AGACT
                                || ||| ||||     |||||
```

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                                AC CCC TCCC     TCTGA
                                 _  C   TTC___
GAM785  ROCK2   3'  ATGGCTTTATACAAGT     42351      CGCGGA
                                GTGGC     TATACAAGT
                                |||||     |||||||||
                                TACCG     ATATGTTCA
                                  AA____
GAM785  RTN1    3'  AGTGGTTGACACAAGT     34471      CCGCG  AT
                                AGTGG    GAT  ACAAGT
                                |||||    |||  ||||||
                                TCACC    CTG  TGTTCA
                                  AA___  __
GAM785  BRCA1   5'  TCTGGAACTCCTGACCTCATGA 28649        AC     GA  _
                                TCTGGAAC  CCTGAC  CTT TGA
                                ||||||||  ||||||  ||| |||
                                AGACCTTG  GGACTG  GAG ACT
                                    A_     __   T
GAM785  C5R1    3'  TCTGGAACTCTTGACCTCA   11926        ACC  GAC
                                TCTGGAAC   CT   GACTTTG
                                ||||||||   ||   |||||||
                                AGACCTTG   GA   CTGGAGT
                                    A__  A__
GAM785  DMRT2   3'  TCTGGGACAGCCTGATGA    27268      A  C    C
                                TCTGG ACA CCTGA GA
                                ||||| ||| ||||| ||
                                AGACC TGT GGACT CT
                                  C   C    A
GAM785  FGFR2   3'  TCTGGAACTCCTGACCTCATGA 35669        AC     GA  _
                                TCTGGAAC  CCTGAC  CTT TGA
                                ||||||||  ||||||  ||| |||
                                AGACCTTG  GGACTG  GAG ACT
                                    A_     __   T
GAM785  FLRT2   5'  TCTGGAACTCCTGGGCTAAATG 29857        AC   ACGACTT
          A                      TCTGGAAC  CCTG      TGA
                                ||||||||  ||||      |||
                                AGACCTTG  GGAC      ACT
                                    A_    CCGATTT
GAM785  LZTR1   3'  TCTGGGCACCCTGACCCTTG   27644      AA       GA
                                TCTGG  CACCCTGAC  CTTTG
                                |||||  |||||||||  |||||
                                AGACC  GTGGGACTG  GGAAC
                                  C_       __
GAM785  MAGEC1  5'  TCTGGGAACCTTGACTCCT   24167      AAC   C    GA
                                TCTGG   ACC TGAC  CT
                                |||||   ||| ||||  ||
                                AGACC   TGG ACTG  GA
                                  CT_   A    AG
GAM785  NEDD4   3'  TCTGGAACTTCTGACAATCTG  43102        ACC      C
                                TCTGGAAC   CTGACGA TTTG
                                ||||||||   ||||||| ||||
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                                AGACCTTG  GACTGTT AGAC
                                   AA_     _
GAM785  PCBP2    5'  TCTGGGGAGCTGGACTTTG   36714      AACACC  AC
                                TCTGG    CTG  GACTTTG
                                |||||    |||  |||||||
                                AGACC    GAC  CTGAAAC
                                  CCTC__  __
GAM785  PITPNB   3'  TGGAACACCAAAAAATTTTGA  29629        CT  C  C
                                TGGAACACC  GA GA TTTGA
                                |||||||||  || || |||||
                                ACCTTGTGG  TT TT AAACT
                                     T_  T  A
GAM785  SLC16A2  3'  TGGAACACCTGGAGCTTTGA   27161        C  AC  _
                                TGGAACACC TG  GA CTTTGA
                                |||||||||  ||  || ||||||
                                ACCTTGTGG AC  CT GAAACT
                                     _  __  C
GAM786  BECN1    3'  TGGTATTGTAAACATGTA    19071      CAAC
                                TGGTA   AAACATGTA
                                |||||   |||||||||
                                ACCAT   TTTGTACAT
                                  AACA
GAM786  CD36     3'  TATTGTGCTATTGTTACA    6314        TA   A
                                TATTGTG  CTAT GTTATA
                                |||||||  |||| ||||||
                                ATAACAC  GATA CAATGT
                                    __   A
GAM786  PTN      3'  TATTGTGTACTTAGCTATA   44390         A
                                TATTGTGTACT TAGTTATA
                                |||||||||||  ||||||||
                                ATAACACATGA ATCGATAT
                                          _
GAM786  TM4SF2   3'  TATTATGTACTGTGCTCTAAC  21451         ATA  AT_
                                TATTGTGTACT   GTT   AC
                                ||||||||||   |||   ||
                                ATAATACATGA   CGA   TG
                                     CA_   GAT
GAM787  F2RL3    3'  GTTTGATCCTGTTTCAGATTC  19529      TA   ___
                                GTTTG  ATCT   TTCAGATTC
                                |||||  ||||   |||||||||
                                CAAAC  TAGG   AAGTCTAAG
                                  __   ACA
GAM787  NLGN3    3'  TGTCTGTGGTCAGATT      33290       AATCTT
                                TGTTTGT     TCAGATT
                                |||||||     |||||||
                                ACAGACA     AGTCTAA
                                   CC____
GAM787  PHKB     3'  AAATGTTTGATAAGGTACAGAT 7121          TAATCTTT
          T                     AAATGTTTG       CAGATT
                                |||||||||       ||||||
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                                TTTACAAAC       GTCTAA
                                     TATTCCAT
GAM787  SECTM1   3'  ACGTTTCTTTCAGATT      16534       TGTAA
                                ATGTT    TCTTTCAGATT
                                |||||    ||||||||||
                                TGCAA    AGAAAGTCTAA
                                  _____
GAM787  ATP6V1G2 3'  GGAATTATAAGAGAGGGGC   39627         AATTTAT
                                GGAGTTATAA      GGGC
                                ||||||||||      ||||
                                CCTTAATATT      CCCG
                                     CTCTC__
GAM787  LUM      3'  GGATTATAAAACTTGGC     14270     G         ATG
                                GGA TTATAAAATTT   GGC
                                ||| ||||||||||   |||
                                CCT AATATTTTGAA   CCG
                                  _       ___
GAM787  MTCP1    5'  GAAGTTATGAGGCGCGGGCC   30577        AAAATTTA
                                GGAGTTAT       TGGGCC
                                ||||||||       ||||||
                                CTTCAATA       GCCCGG
                                     CTCCGC__
GAM787  SMPX     3'  GGTGTTGAATTTATGGGC    30728    A   ATAA
                                GG GTT    AATTTATGGGC
                                || |||    ||||||||||
                                CC CAA    TTAAATACCCG
                                 A  C___
GAM787  SNX5     3'  GGGTTTGTAGGGACATGGGCCA 30865    A   ATAAAATT
                                GG GTT       TATGGGCCA
                                || |||       |||||||||
                                CC CAA       GTACCCGGT
                                 _  ACATCCCT
GAM787  XPR1     3'  GGAGTTACGACAGGGATGGGTC 21852         AAAATTT    C
           AA                     GGAGTTAT      ATGGG CAA
                                |||||||       ||||| |||
                                CCTCAATG      TACCC GTT
                                     CTGTCCC     A
GAM788  ELOVL4   3'  CAAGTTTAAGTGTATACACATT 35538         CATAAT_
           T                     CAAGTTTAA      CACATTT
                                |||||||||      |||||||
                                GTTCAAATT      GTGTAAA
                                     CACATAT
GAM788  FGF7     3'  CAAGACATAGTCACATTT    12856      TTTA    A
                                CAAG    ACATA TCACATTT
                                ||||    ||||| ||||||||
                                GTTC    TGTAT AGTGTAAA
                                  _____    C
GAM788  IGSF8    3'  ACAAGTTTATTCACATT     38078          ACATAA
                                ACAAGTTTA     TCACATT
                                |||||||||     |||||||
```

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                                TGTTCAAAT     AGTGTAA
                                    A_____
GAM788  NOV     3'  CAAGTTTACAGTTAATTACATT 14807        ACA_   C
            T                    CAAGTTTA   TAAT ACATTT
                                 ||||||||   |||| ||||||
                                 GTTCAAAT   ATTA TGTAAA
                                     GTCA   A
GAM788  RPL10   3'  GTTAACTATAATCACATT    25671     T  _
                                 GTT AAC ATAATCACATT
                                 ||| ||| ||||||||||
                                 CAA TTG TATTAGTGTAA
                                   _  A
GAM788  SLC4A7  3'  TACAGGCTTAACAACATT    18823     A      TAATC
                                 TACA GTTTAACA    ACATT
                                 |||| ||||||||    |||||
                                 ATGT CGAATTGT    TGTAA
                                   C      _____
GAM788  TRAM    3'  GTATAACATAAAGCACATT    30702    T      T_
                                 GT TAACATAA  CACATT
                                 || ||||||||  ||||||
                                 CA ATTGTATT  GTGTAA
                                  T       TC
GAM788  ADRBK2  3'  ACGTGGATTTGTAAAATT    23127        _  TC
                                 ACGTGGATT GTG  ATT
                                 ||||||||| |||  |||
                                 TGCACCTAA CAT  TAA
                                     A   TT
GAM788  BPAG1   3'  GTGGGTGTGTTTGTCTTTTT  31782     AT    CATTA
                                 GTGG  TGTGT    CTTTTT
                                 ||||  |||||    ||||||
                                 CACC  ACACA    GAAAAA
                                   C_    AACA_
GAM789  GPR61   3'  TCCTGTCCAGTTTGCA      44266         CA
                                 TCCTGTCCAG  TTTGCA
                                 ||||||||||  ||||||
                                 AGGACAGGTC  AAACGT
                                     __
GAM789  RFP     3'  ACATCCTGTCTCCCACTGCA  27127         CAG   T
                                 ACATCCTGTC   CATT GCA
                                 ||||||||||   |||| |||
                                 TGTAGGACAG   GTGA CGT
                                     AGG   _
GAM789  STAT3   3'  ACACATCCTTATTTG       40230         GTCCAGC
                                 ACACATCCT      ATTTG
                                 |||||||||      |||||
                                 TGTGTAGGA      TAAAC
                                     A_______
GAM789  UBE4A   3'  ACATTCTGGCATTTGC      21967     C   TCCA
                                 ACAT CTG    GCATTTGC
                                 |||| |||    ||||||||
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                                TGTA GAC    CGTAAACG
                                  A  _____
GAM789  CCRL1    3'  ACAATGTGTGTATATAGTT   32426        C    C_
                                GCAATGTG TGTGT  AGTT
                                |||||||| |||||  ||||
                                TGTTACAC ACATA  TCAA
                                    _     TA
GAM789  CHD1     3'  GCAATTACTGTGTTGGTT    10434      G       CA
                                GCAAT TGCTGTGT  GTT
                                ||||| ||||||||  |||
                                CGTTA ATGACACA  CAA
                                  _       AC
GAM789  PCDHB7   5'  TAATAGCAATGTTTGTG     33203          GC
                                TAATAGCAATGT  TGTG
                                ||||||||||||  ||||
                                ATTATCGTTACA  ACAC
                                      A_
GAM790  IDH3A    3'  CCAGTGAAAATGAAGTACT   24373     C       TAAT
                                TCAG GAAAATGAA    TGCT
                                |||| |||||||||    ||||
                                GGTC CTTTTACTT    ATGA
                                  A        C___
GAM790  P53AIP1  3'  TCAGCAAAGTGATGACGCT   35238        AA   ATAAT
                                TCAGCGAA  TGA    TGCT
                                ||||||||  |||    ||||
                                AGTCGTTT  ACT    GCGA
                                    C_   ACT__
GAM790  PTP4A2   5'  TCAGCGAAAATGCTGTGCT   38642          AATAAT
                                TCAGCGAAAATG     TGCT
                                ||||||||||||     ||||
                                AGTCGCTTTTAC     ACGA
                                      GAC___
GAM790  RAP1     3'  AGCAAAATGAATACAGC     33266     G        ATT
                                AGC AAAATGAATA   GC
                                ||| ||||||||||   ||
                                TCG TTTTACTTAT   CG
                                  _        GT_
GAM790  TGFA     3'  TCAGGGGAACAATTGC      17445      CGAAAAT
                                TCAG      GAATAATTGC
                                ||||      ||||||||||
                                AGTC      CTTGTTAACG
                                  CC_____
GAM790  DISC1    3'  CTGCACTGCCTGGCATTGA   33035    T   GGC      CC
                                CT CAT   GCCTGGCA  GA
                                || |||   ||||||||  ||
                                GA GTG   CGGACCGT  CT
                                 C  A__       AA
GAM790  GALR1    3'  ACTTCATGTGACTTACTGA   11192        GC  ___
                                ACTTCATG  GC   CTGG
                                ||||||||  ||   ||||
```

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                                TGAAGTAC  TG   GACT
                                    AC  AAT
GAM791  HOXB2    3'  GGATTAAACGCTAATTCAGTAA 13433          GGGCCAC
              T                  GGATTAGACG      CAGTAAT
                                 ||||||||||      |||||||
                                 CCTAATTTGC      GTCATTA
                                     GATTAA_
GAM791  TTF1     3'  CCATATTATTCTGGGCTTGTCT 28855      TGCG_
                                 CCAT    TCTGGGCTTGTCT
                                 ||||    ||||||||||||||
                                 GGTA    AGACCCGAACAGA
                                   TAATA
GAM792  ADCY8    5'  AAAGACTCAAAGGCGG      9993      AC    AA
                                 AAA  CTCAA  AGGCGG
                                 |||  |||||  ||||||
                                 TTT  GAGTT  TCCGCC
                                   CT    __
GAM792  ARHGEF12 3'  TCAAAACCCTCAATACCAGTGG 31647        _   AAA_  C
                                 TCAAAACC TCAA    GG GG
                                 |||||||| ||||    || ||
                                 AGTTTTGG AGTT    TC CC
                                      G    ATGG  A
GAM792  DIA1     3'  CCAAAACCCTGAGGCGG     28784         CAAAA
                                 TCAAAACCT     AGGCGG
                                 |||||||||     ||||||
                                 GGTTTTGGG     TCCGCC
                                      AC___
GAM792  EPHB2    3'  TCAAGTCCTCAAAAGGTAG   32677      AA       A  CG
                                 TCAA  CCTCAAAA GG  G
                                 ||||  |||||||| ||  |
                                 AGTT  GGAGTTTT CC  C
                                   CA       _  AT
GAM792  FBN2     3'  AAAACCTCAAAATACTGG    12803           AG  _
                                 AAAACCTCAAAA  GC GG
                                 ||||||||||||  || ||
                                 TTTTGGAGTTTT  TG CC
                                       A_  A
GAM792  GRM7     3'  CAAAACCTCAAGACA       9183          AAA
                                 CAAAACCTCA   AGGCG
                                 ||||||||||   |||||
                                 GTTTTGGAGT   TCTGT
                                              ___
GAM792  KNSL4    3'  CAAAAATTTGAAAAGGCGG   28733       CCTCA
                                 CAAAA    AAAAGGCGG
                                 |||||    |||||||||
                                 GTTTT    TTTTCCGCC
                                    TAAAC
GAM792  MBNL     3'  TCCAAACCTCAAAAAAAGG   34322    A          C
                                 TC AAACCTCAAAAAGG GG
                                 || ||||||||||||| ||
```

```
                                AG TTTGGAGTTTTTTT CC
                                 G          _
GAM792  PABPN1   5' TCAAAACCGTAAATCACGG   21610       TCA  AG
                                TCAAAACC  AAA  GCGG
                                ||||||||  |||  ||||
                                AGTTTTGG  TTT  TGCC
                                    CA_  AG
GAM792  SAS      3' CAAAACCTTAAAGACTGG    25586       CAA    _
                                CAAAACCT  AAAGGC GG
                                ||||||||  ||||||  ||
                                GTTTTGGA  TTTCTG CC
                                    A__    A
GAM792  SOST     3' AAAACCCCAGGGCGG      36098       AAAA
                                AAAACCTCA   GGCGG
                                |||||||||   |||||
                                TTTTGGGGT   CCGCC
                                    C___
GAM792  TCF7L2   3' CAAAACCTTTCAAGGTGG   36249       CAAA   C
                                CAAAACCT   AAGG GG
                                ||||||||   ||||  ||
                                GTTTTGGA   TTCC CC
                                    AAG_   A
GAM792  ABCC5    3' CTTGGAACCAACAGGTC    25023    A_   ACA
                                CTT  AACT  GACAGGTC
                                |||  ||||  ||||||||
                                GAA  TTGG  TTGTCCAG
                                  CC   ___
GAM792  BLAME    3' CTCAAACTGCAGGGTC     33487       A  ACA
                                CTTAAACT CAG  GGTC
                                |||||||| |||  ||||
                                GAGTTTGA GTC  CCAG
                                    C  ___
GAM792  BMP6     3' CCTTATGCTACAGACATCC  11862     AA      GG
                                CCTTA  CTACAGACA  TCC
                                |||||  |||||||||  |||
                                GGAAT  GATGTCTGT  AGG
                                   AC       __
GAM792  CALM3    3' CTCAAAGCTGGGCAGGTCCCAG 23233      _  ACAGA
                                CTTAAA CT    CAGGTCCCAG
                                ||||||  ||   ||||||||||
                                GAGTTT GA    GTCCAGGGTC
                                   C  CCC__
GAM792  CASP3    3' CTCAAGTTACAGGCAGCTC   37416     AC   A  G
                                CTTAA  TACAG CAG TC
                                |||||  |||||  |||  ||
                                GAGTT  ATGTC GTC AG
                                   CA   C  G
GAM792  CREBL2   3' CTTAAACTGCCAGTTCAG    10579       A_  A_
                                CTTAAACT  CAG  CAG
                                ||||||||  |||  |||
```

```
                                GAATTTGA  GTC  GTC
                                    CG   AA
GAM792  DDX9     3'  CCTTAAACTACAATGAACCACA 44794          ACA GT  _
            G                    CCTTAAACTACAG   G  CC CAG
                                 ||||||||||||   |  || |||
                                 GGAATTTGATGTT   C  GG GTC
                                       A__ TT  T
GAM792  ESRRBL1  3'  CTTAAACTAAAGAGAGGTC   32839        C   C
                                 CTTAAACTA AGA AGGTC
                                 |||||||| ||| |||||
                                 GAATTTGAT TCT TCCAG
                                     T   C
GAM792  GHRHR    3'  CCTTGGGCTAGAGCCCCA    9065      AAA   CAGACA
                                 CCTT   CTA     GGTCCCA
                                 ||||   |||     |||||||
                                 GGAA   GAT     TCGGGGT
                                   CCC   C_____
GAM792  ICOS     3'  TTAAACTACAACATAATCCCAG 29002          ACA
                                 TTAAACTACAG   GGTCCCAG
                                 ||||||||||   ||||||||
                                 AATTTGATGTT   TTAGGGTC
                                       GTA
GAM792  MOCS1    3'  CCCTGAACATGGAGCGGGTCCC 45122     A   TAC_  ACA
            AG                    CCTT AAC    AG   GGTCCCAG
                                  |||| |||    ||   ||||||||
                                  GGGA TTG    TC   CCAGGGTC
                                    C   TACC  GC_
GAM792  PCTK3    3'  CCTAGGATTCCAGGGTCCCAG  43776    TAAACTA   ACA
                                 CCT      CAG   GGTCCCAG
                                 |||      |||   ||||||||
                                 GGA      GTC   CCAGGGTC
                                   TCCTAAG   ___
GAM792  SACM1L   3'  TTAAACTACAGAGGGTTTTCCA 30429          CA   C__
            G                     TTAAACTACAGA  GGT   CCAG
                                  ||||||||||||  |||   ||||
                                  AATTTGATGTCT  CCA   GGTC
                                        C_   AAA
GAM792  SLC1A4   3'  TTAAACACCTGAGTCCCAG    16764       T  AGACA
                                 TTAAAC AC     GGTCCCAG
                                 ||||||  ||    ||||||||
                                 AATTTG TG     TCAGGGTC
                                    _  GAC__
GAM792  SLC21A3  5'  CCTTGAGCTCAGCAATCCCAG  39571      AAA  A   A   G
                                 CCTT   CT CAG CAG TCCCAG
                                 ||||   || ||| ||| ||||||
                                 GGAA   GA GTC GTT AGGGTC
                                   CTC  _   _   _
GAM792  TAF7L    3'  CTTAAACTCACTATGGCAGGTC 36057         _  AGA__
            C                     CTTAAACT AC     CAGGTCC
                                  |||||||  ||     |||||||
```

```
                                GAATTTGA TG    GTCCAGG
                                    G  ATACC
GAM793  B4GALT1  3'  AGTGGTTTGGGGTCCGACACGA 11278      CCG   C  A   G
            G                    AGTGG   GGGG CC GACG GAG
                                 |||||   |||| || |||| |||
                                 TCACC   CCCC GG CTGT CTC
                                   AAA   A  _   G
GAM793  BAT3    5'  GGCCGGCCTAGGTGGGA    21584     GGG   C  AC
                                 GGCC   GGCC AG  GGGA
                                 ||||   |||| ||  ||||
                                 CCGG   CCGG TC  CCCT
                                   ___    A  CA
GAM793  CDK5    3'  GGCCGGGGGGTCCCGGG     41777        _  AGAC
                                 GGCCGGGGGG CCC   GGG
                                 |||||||| |||   |||
                                 CCGGCCCCC GGG   CCC
                                      A  _____
GAM793  CGTHBA   5'  GGCCGGGGGGCGGAGGGG    28962        CCA  C
                                 GGCCGGGGGC   GA GGG
                                 ||||||||||   || |||
                                 CCGGCCCCCG   CT CCC
                                      C__  C
GAM793  CKB     5'  GCGGCCGGGCGGGGGCGGG   12252        _  CCCAGA
                                 GTGGCCGGG GG     CGGG
                                 |||||||| ||     ||||
                                 CGCCGGCCC CC     GCCC
                                      G  CCC___
GAM793  CLCN6   3'  AGGGCCGGGGGCCCATTGG   34712    T         GACG
                                 AG GGCCGGGGGCCCA   GG
                                 || ||||||||||||   ||
                                 TC CCGGCCCCCGGGT   CC
                                  _         AA__
GAM793  COL6A2   3'  GTGACCGGGGGGCTCGCCGCCAG 38448          _______
                                 GTGGCCGGGGGC     CCAG
                                 ||||||||||||     ||||
                                 CACTGGCCCCCG     GGTC
                                       AGCGGC
GAM793  DRIL1   5'  GTGGCAGGGGGCGGG      23374      C     CCAGAC
                                 GTGGC GGGGGC     GGG
                                 ||||| ||||||     |||
                                 CACCG CCCCCG     CCC
                                   T    _______
GAM793  DYRK1B   3'  AGGGCCCCCAGATGGG     21775    T   GGGGG     C
                                 AG GGCC    CCCAGA GGG
                                 || ||||    |||||| |||
                                 TC CCGG    GGGTCT CCC
                                  _   _____     A
GAM793  ENO1    3'  TGGTCGGGGGCCTCGAG     10972     C       CAGA
                                 TGG CGGGGGCC    CGGG
                                 ||| ||||||||    ||||
```

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                                ACC GCCCCCGG   GCTC
                                  A      A___
GAM793  ESPN    3'  AGGGCTGGGGATACGGG    36438   T  C   CCCAG
                                AG GGC GGGGG   ACGGG
                                || ||| |||||    |||||
                                TC CCG CCCCT   TGCCC
                                 _  A   A____
GAM793  FGD1    5'  GGCCGGGGGCCGCTGGGGAG  20907        CAGAC
                                GGCCGGGGGCC   GGGAG
                                ||||||||||    |||||
                                CCGGCCCCCGG   CCCTC
                                      CGAC_
GAM793  GAMT    3'  GTGGCCGGGCCGGGGTGGG   6684      GG   CAGAC
                                GTGGCC  GGGCC   GGG
                                ||||||  |||||   |||
                                CACCGG  CCCGG   CCC
                                   __   CCCCA
GAM793  HDAC7A  3'  AGTGGCCGAGGGGTCCCAGGGG 32466       _  _   AC
                                AGTGGCCG GGGG CCCAG  GGG
                                |||||||| |||| |||||  |||
                                TCACCGGC CCCC GGGTC  CCC
                                     T   A   __
GAM793  HSPG2   3'  AGGGGCTGGGTGGAGGTGGG  24361   T  C  _ CCC  AC
                                AG GGC GGG GG  AG  GGG
                                || ||| ||| ||  ||  |||
                                TC CCG CCC CC  TC  CCC
                                 C  A  A ___ CA
GAM793  LASS2   5'  GGCTGGGCGTGACGGGAG   42680    CGG   CCA
                                GGC  GGGC  GACGGGAG
                                |||  ||||  ||||||||
                                CCG  CCCG  CTGCCCTC
                                  A__   CA_
GAM793  LDB1    5'  GGCCGGGGGCCAGGGGG    19342         C  AC
                                GGCCGGGGGCC AG  GGG
                                |||||||||| ||  |||
                                CCGGCCCCCGG TC  CCC
                                      _ C_
GAM793  LETM1   5'  GCGGCTGGCCTCGGACGGGAG  29502     CGGG   CA_
                                GTGGC   GGCC   GACGGGAG
                                |||||   ||||   ||||||||
                                CGCCG   CCGG   CTGCCCTC
                                   A___   AGC
GAM793  MAP3K10 5'  AGGGGCCGGGGGGCTGCGGGAG  42753   T       CCAGA
                                AG GGCCGGGGGGC   CGGGAG
                                || ||||||||||    ||||||
                                TC CCGGCCCCCG    GCCCTC
                                 C        AC___
GAM793  MUCDHL  3'  AGTGGCTGGTTGGTGGGA   34928      C  G_  CCCAGAC
                                AGTGGC GG  GG     GGGA
                                |||||| ||  ||     ||||
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                                TCACCG CC  CC      CCCT
                                   A  AA  A_______
GAM793  OTP      3'  GCGGCCGGGAGACGGG      36994          GGCCC
                                GTGGCCGGG    AGACGGG
                                |||||||||    |||||||
                                CGCCGGCCC    TCTGCCC
                                      ______
GAM793  PAX2     3'  GGCTGGGAGGGGATGGGAG   19610     C    CCCA  C
                                GGC GGGGG   GA GGGAG
                                ||| |||||   || |||||
                                CCG CCCTC   CT CCCTC
                                  A    CC__  A
GAM793  PCDH7    5'  TGGCCGGGAATGGGGGTGGGAG 37122          CCCAGAC
                                TGGCCGGGGG      GGGAG
                                ||||||||||      |||||
                                ACCGGCCCTT      CCCTC
                                      ACCCCCA
GAM793  PRG3     3'  AGAGGTTGGGGGACGGGA    25896    T  CCG   CCCA
                                AG GG   GGGG   GACGGGA
                                || ||   ||||   |||||||
                                TC CC   CCCC   CTGCCCT
                                 T  AA_   _____
GAM793  PTPRS    3'  GCGGCCGGGGCCGGTGGGG   39302         G  CAGAC
                                GTGGCCGGGG CC    GGG
                                |||||||||| ||    |||
                                CGCCGGCCCC GG    CCC
                                      _  CCAC_
GAM793  RARA     3'  GTGTCTGGGGGCCCTATGGGG  9713     GCC      AGAC
                                GTG   GGGGGCCC   GGG
                                |||   ||||||||   |||
                                CAC   CCCCCGGG   CCC
                                  AGA      ATAC
GAM793  SHB      3'  AGTGGCTGGGGGCTGGTTGGTG 16686      C     CCAGAC__
            GG                    AGTGGC GGGGGC       GGG
                                |||||| ||||||       |||
                                TCACCG CCCCCG       CCC
                                   A     ACCAACCA
GAM793  SIGLECL1 3'  AGAGGCCGGGGGGCGGGGA    37843    T       CCAGAC
                                AG GGCCGGGGGC     GGGA
                                || ||||||||||     ||||
                                TC CCGGCCCCCG     CCCT
                                 T        C_____
GAM793  SYN3     3'  AGTGGCCGAGTGTGATGGG    18560         GGCCCA  C
                                AGTGGCCGGG     GA GGG
                                ||||||||||     || |||
                                TCACCGGCTC     CT CCC
                                      ACA___  A
GAM793  TEM6     3'  AGTGGCCAGGGGCCTGCGG   35552           CAGA
                                AGTGGCCGGGGGCC   CGG
                                ||||||||||||||   |||
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                                TCACCGGTCCCCGG   GCC
                                      AC__
GAM793  TUFT1    3'  AGTGGCCAGGGGCTTGGG   33507          CCAGAC
                                AGTGGCCGGGGGC    GGG
                                ||||||||||||     |||
                                TCACCGGTCCCCG    CCC
                                      AA____
GAM793  VAT1     3'  GTGGCGGGGCAGGGACGGGAG 26853     CG   CCA
                                GTGGC GGGGC  GACGGGAG
                                ||||| |||||  ||||||||
                                CACCG CCCCG  CTGCCCTC
                                   __   TCC
GAM794  SRGAP2   3'  GAACTACAGAAAATAATAA   43980     ATT
                                GAAT  TAGAAAATAATAA
                                ||||  ||||||||||||
                                CTTG  GTCTTTTATTATT
                                  AT_
GAM794  ANXA4    3'  AAGGCTTTGACTATGAA     41717      A  GATA
                                AAGGCT TTG   ACTATGAA
                                |||||| |||   ||||||||
                                TTCCGA AAC   TGATACTT
                                   _  ____
GAM794  C7orf2   3'  AAAGCCTGAGGACTATGAA   35365      ATT  TAA
                                AAGGCT  GGA  CTATGAA
                                ||||||  |||  |||||||
                                TTTCGG  CCT  GATACTT
                                    ACT  ___
GAM794  EIF4EBP2 3'  GGCTACTTAACTATGA      19894      GGA
                                GGCTATT  TAACTATGA
                                |||||||  |||||||||
                                CCGATGA  ATTGATACT
                                   ___
GAM794  NGB      3'  AGGCTACTGGGGATGA      34579        ATAACT
                                AGGCTATTGG     ATGA
                                ||||||||||     ||||
                                TCCGATGACC     TACT
                                     CC____
GAM794  NT5E     3'  GGCTATTGATAATTATGAA   14862       G   C
                                GGCTATTG ATAA TATGAA
                                |||||||| |||| ||||||
                                CCGATAAC TATT ATACTT
                                   _   A
GAM794  SCA1     3'  AAAGGTTTAAAAACTATGAAA 7267      CTA   T
                                AAAGG  TTGGA AACTATGAAA
                                |||||  ||||| ||||||||||
                                TTTCC  AATTT TTGATACTTT
                                  A__   _
GAM795  ADAM19   3'  CATGCAGTCACTATGGC    37765   C  CC
                                CA GTA  TCACTATGGC
                                || |||  ||||||||||
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                                GT CGT  AGTGATACCG
                                 A  C_
GAM795  MPHOSPH1  3'  TACACGTATTTCACATTGC   32116       CC   TATG
                                TACACGTA  TCAC   GC
                                ||||||||  ||||   ||
                                ATGTGCAT  AGTG   CG
                                    AA   TAA_
GAM795  PPP2R5A   3'  TACAATATACTATGGCCAT   26442     C  CCTC
                                TACA GTA   ACTATGGCCAT
                                |||| |||   ||||||||||
                                ATGT TAT   TGATACCGGTA
                                  _  A___
GAM795  RABL2A    3'  ACGTACCTTGTGGTATGGC   30195       CAC__
                                ACGTACCT    TATGGC
                                ||||||||    ||||||
                                TGCATGGA    ATACCG
                                    ACACC
GAM795  RABL2B    3'  ACGTACCTTGTGGTATGGC   28201       CAC__
                                ACGTACCT    TATGGC
                                ||||||||    ||||||
                                TGCATGGA    ATACCG
                                    ACACC
GAM795  SOX13     3'  TACAGTGTCCCCTGGCCAT   25016     C_ A   ACTA
                                TACA  GT CCTC   TGGCCAT
                                ||||  || ||||   |||||||
                                ATGT  CA GGGG   ACCGGTA
                                  CA  _   _____
GAM795  TAF4B     3'  ATACTGTAGAATATGGCCATA  44548     CTCAC__
                                GTAC      TATGGCCATA
                                ||||      ||||||||||
                                TATG      ATACCGGTAT
                                  ACATCTT
GAM795  B4GALT7   3'  CACGTGAAGGAGGTCAGA    28542        A  ACCC
                                TACGTGAAG AG    GTCGGA
                                ||||||||| ||    ||||||
                                GTGCACTTC TC    CAGTCT
                                    C  _____
GAM795  CHD2      3'  TGAAGAAGATTGTAAAAAT   10452        CCC  CG
                                TGAAGAAGA   GT  GAAT
                                |||||||||   ||  ||||
                                ACTTCTTCT   CA  TTTA
                                    AA_  TT
GAM795  CYLN2     3'  TGAAGAAGGTTCAGAA      18065        ACCCG
                                TGAAGAAG    TCGGAA
                                ||||||||    ||||||
                                ACTTCTTC    AGTCTT
                                    CA___
GAM795  TACC1     3'  GTGGAGAAGACCCCAAAGA   26597     A       GTC
                                GTG AGAAGACCC   GGA
                                ||| |||||||||   |||
```

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                                CAC TCTTCTGGG   TCT
                                  C       GTT
GAM796  CACNG3   5'  TTCTGAGGGTCCCTGGGT    27248        A  G__
                                TTCTGAGG TC   GGGT
                                |||||||| ||   ||||
                                AAGACTCC AG   CCCA
                                     C  GGA
GAM796  CDS2     3'  TACATTCTGCAGGATTTTGGTG 19216         _    CG_ _  A
           TGGAT                   TACATTCTG AGGAT   GG GT GAT
                                |||||||||| |||||   || || |||
                                ATGTAAGAC TCCTA   CC CA CTA
                                     G    AAA  A  C
GAM796  COL10A1  3'  CATTTTGTAGGGTGGGGT    7962       C  _  ATC
                                CATT TG AGG   GGGGT
                                |||| || |||   |||||
                                GTAA AC TCC   CCCCA
                                  A  A   CA_
GAM796  GYG2     3'  TAATTCTGAATAGGGTAG    19391    C       GATC
                                A ATTCTGAG    GGGGTAG
                                | ||||||||    |||||||
                                A TAAGACTT    TCCCATC
                                 T       A___
GAM796  NUP98    3'  TTCTGGAAGGGGTAGA      32239       A   TC
                                TTCTG GGA  GGGGTAGA
                                ||||| |||  ||||||||
                                AAGAC CTT  CCCCATCT
                                     _  __
GAM796  PCDHB7   3'  TTCTGAGACTAGGGTAG     33205        G  CG
                                TTCTGAG AT  GGGTAG
                                ||||||| ||  ||||||
                                AAGACTC TG  CCCATC
                                    _  AT
GAM796  DIAPH2   3'  TCACCTCTCCCTTTAGGTGA   28680        AA     C   C
                                TCACCTT  TCTCTT AGG GA
                                |||||||  |||||| ||| ||
                                AGTGGAG  AGGGAA TCC CT
                                    __     A   A
GAM796  NARS     3'  TATCACTTGATGTTCAGGTGA  21219       CTTAATCTC     C
                                TATCAC        TTCAGG GA
                                ||||||        |||||| ||
                                ATAGTG        AAGTCC CT
                                   AACTAC___      A
GAM797  ACP2     3'  GAGGCCCAACCCAGGATCT    11508        G G     C
                                GGGGCCCG G TTAGGA CT
                                |||||||| | |||||| ||
                                CTCCGGGT T GGTCCT GA
                                    _ G     A
GAM797  ADAMTS9  3'  AGAGGTCACTCCCTGGGGTC   33693      _____  _
                                AGGGG    CCC GGGGTT
                                |||||    ||| ||||||
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                                TCTCC    GGG CCCCAG
                                  AGTGA  A
GAM797  ANK1    5' AGGGGCCCGCCGAAGGGCCT  33850       GGGTT  A
                                AGGGGCCCG    AGG CCT
                                |||||||||    ||| |||
                                TCCCCGGGC    TCC GGA
                                     GGCT_  C
GAM797  ARHGEF7 5' GGGGCTCGGGGTAGACCT   19365     C    TA
                                GGGGC CGGGGT GGACCT
                                ||||| ||||||  ||||||
                                CCCCG GCCCCA  TCTGGA
                                  A     __
GAM797  ATP2B3  3' GGGGCCCGGAGGCGCTCCT  34974       _  TAGGA
                                GGGGCCCGG GGT    CCT
                                ||||||||| |||    |||
                                CCCCGGGCC CCG    GGA
                                     T  CGA__
GAM797  B3GNT3  5' AGGGTCTGGGGTCGGCCT   30677    GCCC    A A
                                AGGG   GGGGTT GG CCT
                                ||||   |||||| || |||
                                TCCC   CCCCAG CC GGA
                                  AGA_    _ _
GAM797  BAT2    5' GGGATCCGGGACCCGGGCCT  21581    GC    GT A  A
                                GGG  CCGGG  T GG CCT
                                |||  |||||  | || |||
                                CCC  GGCCC  G CC GGA
                                  TA    TG G  C
GAM797  BAZ2A   3' AGGGGCTGCCCCAGGACCT  30301     __ GGGG
                                AGGGGC  CC   TTAGGACCT
                                ||||||  ||   |||||||||
                                TCCCCG  GG   GGTCCTGGA
                                  AC  _____
GAM797  BCL2L2  5' AGGAGCCCCCAGCTGGGGCCT 19734       GG   A  A
                                AGGGGCCC  GGTT GG CCT
                                ||||||||  |||| || |||
                                TCCTCGGG  TCGA CC GGA
                                     GG   C  C
GAM797  BDP1    5' GGGGCCCGGGGAGGCAGCCT  32950        TTA_  A
                                GGGGCCCGGGG   GG CCT
                                ||||||||||   || |||
                                CCCCGGGCCCC   TC GGA
                                      TCCG  _
GAM797  BRCA1   3' GGGGCTAGGGAAGACCT    28636     CC   TT
                                GGGGC  GGGG  AGGACCT
                                |||||  ||||  |||||||
                                CCCCG  TCCC  TTCTGGA
                                  A_   __
GAM797  C21orf2 3' AAGGGCCCAGGGACC      22296         TTAGG
                                AGGGGCCCGGGG   ACC
                                ||||||||||||   |||
```

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                                TTCCCGGGTCCC    TGG
                                      _____
GAM797  CACNA1A  3'  GGGACCCGGGGGCCCCT    35740         TTAGGA
                                GGGGCCCGGGG    CCT
                                ||||||||||    |||
                                CCCTGGGCCCC    GGA
                                     CGG___
GAM797  CACNG3   3'  AGGATGGAGGGGTTAGGAC   27229     GCCC
                                AGGG   GGGGTTAGGAC
                                ||||   ||||||||||
                                TCCT   CCCCAATCCTG
                                  ACCT
GAM797  CDK5R2   5'  GGGACCCGGCGGTGGGGGGCCT 19475        _  TA_  A
                                GGGGCCCGG GGT   GG CCT
                                ||||||||| |||   || |||
                                CCCTGGGCC CCA   CC GGA
                                     G   CCC  C
GAM797  CEP2     3'  AGGGCGCCTGGGCTGAC    28432      _ G    AG
                                GGGGC CC GGGTT  GAC
                                ||||| || |||||  |||
                                TCCCG GG CCCGA  CTG
                                  C  A    __
GAM797  CLDN3    5'  AGGGGCCGGGGCCGCTGGGCCT 10563       C    A__  A
                                AGGGGCC GGGGTT   GG CCT
                                ||||||| ||||||   || |||
                                TCCCCGG CCCCGG   CC GGA
                                   _     CGA  C
GAM797  CTSD     3'  AGGGCCCGGGAGGACGGCCT   12526         TTA_  A
                                GGGGCCCGGGG    GG CCT
                                ||||||||||    || |||
                                TCCCGGGCCCT    CC GGA
                                     CCTG  _
GAM797  DGKG     5'  GGTGGCCCGGGGCGCTCCT    10657    _       TAGGA
                                GG GGCCCGGGGT    CCT
                                || ||||||||||    |||
                                CC CCGGGCCCCG    GGA
                                 A        CGA__
GAM797  DTX1     5'  AGGAGGCCTGGGCCACAGCCT  20647    _   CG    _ A
                                AGG GGCC  GGGTTA GG CCT
                                ||| ||||  |||||| || |||
                                TCC CCGG  CCCGGT TC GGA
                                  T   A_     G  _
GAM797  DUSP4    5'  GGTGGCCTAACCAGGACCT    10815   _   CG GG
                                GG GGCC  G  TTAGGACCT
                                || ||||  |  |||||||||
                                CC CCGG  T  GGTCCTGGA
                                 A   AT __
GAM797  FAAH     3'  AGGGGCTGCCCCAGGGTC    11045      _____
                                AGGGGC   CCGGGGTT
                                ||||||   ||||||||
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                                TCCCCG   GGTCCCAG
                                   ACGG
GAM797  FBXO7    5'  GGCGGCCCGAGGGGCC     29140   _      TTA  A
                                GG GGCCCGGGG   GG CC
                                || |||||||||   || ||
                                CC CCGGGCTCC   CC GG
                                 G       ____ _
GAM797  FGR      3'  AGGGGTCCAGCCAAGAC     23497      C  GG
                                AGGGG CC  GGTTAGGAC
                                ||||| ||  |||||||||
                                TCCCC GG  TCGGTTCTG
                                   A  __
GAM797  FXYD7    3'  AGGGGCCAGGGGGACGGATCT  35126       C   TTA   C
                                AGGGGCC GGGG   GGA CT
                                ||||||| ||||   ||| ||
                                TCCCCGG CCCC   CCT GA
                                    T   CTG   A
GAM797  GALR1    5'  GGAGCCCGGAGCTGGACCT   11203          A
                                GGGGCCCGGGGTT GGACCT
                                |||||||||||| ||||||
                                CCTCGGGCCTCGA CCTGGA
                                              _
GAM797  GDF2     3'  AGGGGCATGCAGGACC      32121       CCGGG  T
                                AGGGGC    GT AGGACC
                                ||||||    || ||||||
                                TCCCCG    CG TCCTGG
                                   TA___  _
GAM797  GNAZ     3'  AGGGTCCCAGCAGGGCCT    13178     G    GGT   A
                                AGGG CCCGG   TAGG CCT
                                |||| |||||   |||| |||
                                TCCC GGGTC   GTCC GGA
                                  A    ___   C
GAM797  GYS1     3'  GGTGGCCCGCATGCCGGGCCT  44793   _    GG_  TA  A
                                GG GGCCCG   GT  GG CCT
                                || ||||||   ||  || |||
                                CC CCGGGC   CG  CC GGA
                                 A     GTA  GC  _
GAM797  H4FM     3'  AGGGGCCCTAAAAAGGGCCT  18586       GG  TT   A
                                AGGGGCCC  GG  AGG CCT
                                ||||||||  ||  ||| |||
                                TCCCCGGG  TT  TCC GGA
                                    A_  TT   C
GAM797  HNRPDL   5'  GGGGCGCGGCGGGGCCT    24177      C  _  TTA  A
                                GGGGC CGG GG   GG CCT
                                ||||| ||| ||   || |||
                                CCCCG GCC CC   CC GGA
                                  C  G  ___  _
GAM797  HOXC6    3'  GGGGTCCAGAGCTGAC      21077      C       AG
                                GGGG CCGGGGTT  GAC
                                |||| ||||||||  |||
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                                CCCC GGTCTCGA  CTG
                                  A      __
GAM797  HOXD4    3'  GGGGTCCGACTGGGACCT    31176     C    GGTTA
                                GGGG CCGG    GGACCT
                                |||| ||||    ||||||
                                CCCC GGCT    CCTGGA
                                  A   GAC__
GAM797  HS3ST4   3'  AGGGGTTGTGGGATGAGACCT  43865     CCCG   TTA
                                AGGGG   GGG   GGACCT
                                |||||   |||   ||||||
                                TCCCC   CCC   TCTGGA
                                  AACA   TAC
GAM797  HYAL1    5'  GGGGCCTAAGCAGGGCCT    37644      CG  GT    A
                                GGGGCC  GG  TAGG CCT
                                ||||||  ||  |||| |||
                                CCCCGG  TC  GTCC GGA
                                   AT  __   C
GAM797  IL22RA2  3'  AGGGGCCAGTTTGGA      38132      CGG    A
                                AGGGGCC   GGTT GGA
                                |||||||   |||| |||
                                TCCCCGG   TCAA CCT
                                   ___    A
GAM797  INSM1    3'  AGGGCCCTGGGGACC       13573      GG  TTA
                                GGGGCCC  GG   GGACC
                                |||||||  ||   |||||
                                TCCCGGG  CC   CCTGG
                                   A_  ___
GAM797  JUP      3'  AGGGGTCAGGGGCTCGGTGGAC 13770      CCC     A___
           CT                    AGGGG   GGGGTT    GGACCT
                                |||||   ||||||    ||||||
                                TCCCC   CCCCGA    CCTGGA
                                  AGT     GCCA
GAM797  KCNK4    3'  GGGTGCCCGGGGACC       37838     _      TTAGG
                                GGG GCCCGGGG     ACC
                                ||| ||||||||     |||
                                CCC CGGGCCCC     TGG
                                  A      _____
GAM797  KIAA0857 3'  AGGGGTCAGGGAGCAGCCT   42467      CC    TTA  A
                                AGGGG  CGGGG   GG CCT
                                |||||  |||||   || |||
                                TCCCC  GTCCC   TC GGA
                                  A_    TCG  _
GAM797  KLK10    5'  AGGGGCCCTGGAATACAGG   15769        _    _
                                AGGGGCCC GGGGT TAGG
                                |||||||| ||||| ||||
                                TCCCCGGG CCTTA GTCC
                                   A    T
GAM797  LAMA4    5'  AGGGCTCGGGCGCTGTGG    14059      C   _  A_
                                GGGGC CGGG GTT  GG
                                ||||| |||| |||  ||
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                                TCCCG GCCC CGA  CC
                                   A   G   CA
GAM797  LDB1    5'  GGGGCCAGGGGGCCGGCCT   19345      C   TTA  A
                                GGGGCC GGGG  GG CCT
                                |||||| ||||  || |||
                                CCCCGG CCCC  CC GGA
                                   T   CGG  _
GAM797  LSS     3'  AGGGGCATGGGGCTCCCT    14245      CC    TAGGA
                                AGGGGC  GGGGT    CCT
                                ||||||  |||||    |||
                                TCCCCG  CCCCG    GGA
                                   TA    AG___
GAM797  MAPK10  3'  AGGGGTCCTGCCGAGGCT    39977      _  ___
                                AGGGG CC   CGGGGTT
                                ||||| ||   |||||||
                                TCCCC GG   GCTCCGA
                                   A  ACG
GAM797  MAPK4   3'  GGGGCCAGGAGACTGGGA    15662      C   _  A
                                GGGGCC GGGG TT GGA
                                |||||| |||| || |||
                                CCCCGG CCTC GA CCT
                                   T   T  C
GAM797  MAZ     5'  GGGACCCGGCCGGCCT      43853        GGTTA  A
                                GGGGCCCGG    GG CCT
                                |||||||||    || |||
                                CCCTGGGCC    CC GGA
                                     GG___  _
GAM797  MEOX1   3'  AGGAGGCCTGGCTGACCT    30394    _   CGG   AG
                                AGG GGCC   GGTT  GACCT
                                ||| ||||   ||||  |||||
                                TCC CCGG   CCGA  CTGGA
                                  T   A__   __
GAM797  MMP2    3'  AGGGGTCTGGAGTGGCCACCT  21193      CCC    TA __
                                AGGGG   GGGGT  GG  ACCT
                                |||||   |||||  ||  ||||
                                TCCCC   CCTCA  CC  TGGA
                                   AGA    __  GG
GAM797  MMP25   5'  GGGGTTCGAAGGGGGCCT    35390     CC    TTA  A
                                GGGG  CGGGG   GG CCT
                                ||||  |||||   || |||
                                CCCC  GCTTC   CC GGA
                                   AA    CC_  _
GAM797  MOCS1   3'  AGGGGTCTGGGGGACCC     45120      CCCG   TTA
                                AGGGG   GGG   GGACCT
                                |||||   |||   ||||||
                                TCCCC   CCC   CCTGGG
                                   AGA_  ____
GAM797  MUC4    5'  AGGGGCCAGGGAACC       39661        C   TTAG
                                AGGGGCC GGGG   GACC
                                ||||||| ||||   ||||
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```
                                TCCCCGG TCCC   TTGG
                                   _   ____
GAM797  NOL3    3' GGGGCTAGGTTTGGGATCT   19491     CCG   A_  C
                                GGGGC  GGGTT  GGA CT
                                |||||  |||||  ||| ||
                                CCCCG  TCCAA  CCT GA
                                  A__    AC   A
GAM797  NPAS1   5' GGGGCCAGGGGCAACGCT   40873     C   TAG  _
                                GGGGCC GGGGT  GAC CT
                                |||||| |||||  ||| ||
                                CCCCGG CCCCG  TTG GA
                                  T    ___   C
GAM797  P2RX3   5' GGGGCCCAGTGGTGGCCT   14995       _  TA  A
                                GGGGCCCGG GGT  GG CCT
                                ||||||||| |||  || |||
                                CCCCGGGTC CCA  CC GGA
                                    A  __  _
GAM797  PCOLCE  3' AGGGGCCGGGGCTGGCCT   45236      C    A  A
                                AGGGGCC GGGGTT GG CCT
                                ||||||| |||||| || |||
                                TCCCCGG CCCCGA CC GGA
                                   _    _ _
GAM797  PIGR    3' AGGGACCCATGAGGACCT   43696       GGGTT
                                AGGGGCCCG   AGGACCT
                                |||||||||   |||||||
                                TCCCTGGGT   TCCTGGA
                                    AC___
GAM797  PSAP    3' AGGGGCTAGGGGCTCCCT   42964     CC   TAGGA
                                AGGGGC  GGGGT   CCT
                                ||||||  |||||   |||
                                TCCCCG  CCCCG   GGA
                                  AT    AG___
GAM797  PTBP1   3' GGGGCCCGGCCGTGGGGGCCT 15851       G_  TA  A
                                GGGGCCCGG  GT  GG CCT
                                ||||||||| ||  || |||
                                CCCCGGGCC  CA  CC GGA
                                    GG  CC  C
GAM797  RET     3' AGGGGTCTGGGGGAACCT   33927     CCC   TTA
                                AGGGG  GGGG  GGACCT
                                |||||  ||||  ||||||
                                TCCCC  CCCC  CTTGGA
                                  AGA  ___
GAM797  SLC16A7 3' AGGGGTTTGGGATTCAGA   21837     CCC    A
                                AGGGG  GGGGTT GGA
                                |||||  |||||| |||
                                TCCCC  CCCTAA TCT
                                  AAA    G
GAM797  SLC1A3  3' GGGCTCCCCACAGGACCT   20044     _ GGGGT
                                GGGC CC   TAGGACCT
                                |||| ||   ||||||||
```

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                                CCCG GG    GTCCTGGA
                                  A  GGT__
GAM797  SLC1A4   3' AGGGGACCTGGGAACC     16739      C  G   TTAG
                                AGGGG CC GGG   GACC
                                ||||| || |||   ||||
                                TCCCC GG CCC   TTGG
                                  T  A  ____
GAM797  SLC1A5   5' GGGGCCGGGAAGCGGACCT   24748       C    TTA
                                GGGGCC GGGG   GGACCT
                                |||||| ||||   ||||||
                                CCCCGG CCCT   CCTGGA
                                   _   TCG
GAM797  SLC22A12 3' AGGGGCCAGGCTTACAGGGCT 40328       ________
                                AGGGGCC      CGGGGTT
                                |||||||      |||||||
                                TCCCCGG      GTCCCGA
                                    TCCGAAT
GAM797  SLC22A12 5' GGGGCCAGGGCCGGCCT     40334       C     A  A
                                GGGGCC GGGGTT GG CCT
                                |||||| |||||| || |||
                                CCCCGG TCCCGG CC GGA
                                   _     _ _
GAM797  SLC5A5   5' AGGGGCCGGGGCTCCC      7824        C     TAGGA
                                AGGGGCC GGGGT    CC
                                ||||||| |||||    ||
                                TCCCCGG CCCCG    GG
                                   _    AG___
GAM797  SORCS2   3' GGGGTCTGGGGGGCAGAACCT 34062     CCC_   T
                                GGGG   GGGG TAGGACCT
                                ||||   |||| ||||||||
                                CCCC   CCCC GTCTTGGA
                                  AGAC   C
GAM797  SOX10    3' GGAGCCAAGGGTTAGGGCCT   28004       C       A
                                GGGGCC GGGGTTAGG CCT
                                |||||| ||||||||| |||
                                CCTCGG TCCCAATCC GGA
                                   T       C
GAM797  SOX12    3' AGGGGTCCGGAGGACTCT    28027      C   GGTT    _
                                AGGGG CCGG   AGGAC CT
                                ||||| ||||   ||||| ||
                                TCCCC GGCC   TCCTG GA
                                  A   ____    A
GAM797  TBX3     3' GGAGTCCGGGGCCCC       32437      C       AGGA
                                GGGG CCGGGGTT   CC
                                |||| ||||||||   ||
                                CCTC GGCCCCGG   GG
                                  A      ____
GAM797  TCF7     3' GGGACCCGGGGCAGCCT     17322          TA  A
                                GGGGCCCGGGGT  GG CCT
                                ||||||||||| || |||
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                                CCCTGGGCCCCG  TC GGA
                                          __  _
GAM797  TCIRG1   3'  AGGAGGTCTGGCAGGACCT   25837      CCCGG   T
                                AGGGG    GGT AGGACCT
                                |||||    ||| |||||||
                                TCCTC    CCG TCCTGGA
                                   CAGA_  _
GAM797  THRA     5'  GGGGCCCGGGCCGCCCGCCT  17522         __  AGGA
                                GGGGCCCGGG  GTT   CCT
                                ||||||||||  |||   |||
                                CCCCGGGCCC  CGG   GGA
                                      GG  GC__
GAM797  TM7SF2   5'  GGGGCCCGGGGGCC       17588          TTAG A
                                GGGGCCCGGGG   G CC
                                ||||||||||   | ||
                                CCCCGGGCCCC   C GG
                                          ____ _
GAM797  TNFRSF8  3'  AGGGGCCCCGGGAGCTGGCCT 10310       _  _  A  A
                                AGGGGCCC GGG GTT GG CCT
                                |||||||| ||| ||| || |||
                                TCCCCGGG CCC CGA CC GGA
                                     G  T  _ _
GAM797  VIPR1    3'  GGGGCCGGGGGCAGCCT    21514      C    TA  A
                                GGGGCC GGGGT  GG CCT
                                |||||| |||||  || |||
                                CCCCGG CCCCG  TC GGA
                                   C    __  _
GAM797  VIPR2    3'  AGGGGCCCGCAGGCC      18005       GGGT   A
                                AGGGGCCCG   TAGG CC
                                |||||||||   |||| ||
                                TCCCCGGGC   GTCC GG
                                          ____   _
GAM797  WNT3A    3'  GGAGCCCGGGCAGGGCGGGCCT 37547         GTTA__  A
                                GGGGCCCGGG     GG CCT
                                ||||||||||     || |||
                                CCTCGGGCCC     CC GGA
                                      GTCCCG  C
GAM797  ABCD1    5'  GGCCTTGAGAGGTCTC     6197      C  GTTA
                                GGCCT GGG   GGGTCTC
                                ||||| |||   |||||||
                                CCGGA CTC   TCCAGAG
                                   A  ____
GAM797  ADD1     5'  AGGCCTCGGGATCCCACCTC  30514          AGGG
                                AGGCCTCGGGGTT   TCTC
                                ||||||||||||   ||||
                                TCCGGAGCCCTAG   GGAG
                                       GGT_
GAM797  ARHGAP6  3'  GGCATCGGGGTTGTC      30221     C      AGG
                                GGC TCGGGGTT   GTC
                                ||| ||||||||   |||
```

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                                CCG AGCCCCAA   CAG
                                  T      ___
GAM797  ASH1     3'  AAGGTCTCTGGGGTAGCTCT  32972      C  _    TA  G
                                AAGG CTC GGGGT  GG TCT
                                |||| ||| |||||  || |||
                                TTCC GAG CCCCA  TC AGA
                                  A  A    __ G
GAM797  BAIAP3   3'  AGGGTCGTGGAGCAGGTCTCAG 19453     CC   G  TTA
                                AGG  TCG GG   GGGTCTCAG
                                |||  ||| ||   |||||||||
                                TCC  AGC CC   TCCAGAGTC
                                  C_  A  TCG
GAM797  CLCN7    3'  GGCCTTGGAGGTTTTTCTCAG  10520      C  _   AGGG
                                GGCCT GG GGTT    TCTCAG
                                ||||| || ||||    ||||||
                                CCGGA CC CCAA    AGAGTC
                                   A  T    AA__
GAM797  KCNQ1    3'  GGCGCTTGGGGTAACAACTCAG 6886      _  C     TAGGGT
                                GGC CT GGGGT     CTCAG
                                ||| || |||||     |||||
                                CCG GA CCCCA     GAGTC
                                  C  A    TTGTT_
GAM797  MASP1    3'  GGTCCTGGGGGCTGTCTC    40103    _  C     AGG
                                GG CCT GGGGTT   GTCTC
                                || ||| ||||||   |||||
                                CC GGA CCCCGA   CAGAG
                                 A  C     ___
GAM797  NR1D1    5'  AAGGTCTTGGGGTGGCC     34701      C  C    TAG
                                AAGG CT GGGGT   GGTC
                                |||| || |||||   ||||
                                TTCC GA CCCCA   CCGG
                                  A  A    ___
GAM797  NXF2     5'  GGCCTTGGTGGTGCATTTCAG  35187      C  _   TAGG  C
                                GGCCT GG GGT    GT TCAG
                                ||||| || |||    || ||||
                                CCGGA CC CCA    TA AGTC
                                   A  A   CG__  A
GAM797  PFKFB4   3'  AAGGCCTCGGTGGTCTCACCTC 21283          _    AGGG
          AG                    AAGGCCTCGG GGTT    TCTCAG
                                ||||||||| ||||    ||||||
                                TTCCGGAGCC CCAG    GGAGTC
                                     A    AGT_
GAM797  PTGS1    3'  AGGTCCTGAGAAAAGGGTCTCA 38729     _  C    TT
          G                     AGG CCT GGGG  AGGGTCTCAG
                                ||| ||| ||||  ||||||||||
                                TCC GGA CTCT  TCCCAGAGTC
                                  A  _    TT
GAM797  SLC16A2  3'  GGCCTTGAGGTTAATGCCT   27149      C       G
                                GGCCT GGGGTTAG GTCT
                                ||||| |||||||| ||||
```

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                                CCGGA CTCCAATT CGGA
                                  A       A
GAM797  SOST     3'  GGCCTGGAAGGTCTCA      36109      C   GTTA
                                GGCCT GGG    GGGTCTCA
                                ||||| |||    ||||||||
                                CCGGA CCT    TCCAGAGT
                                  _  _____
GAM797  TM4SF2   3'  GGCCTCGGGGGTGAGGTTC    21447          T   G
                                GGCCTCGGGGGT AGG TC
                                |||||||||||| ||| ||
                                CCGGAGCCCCA TCC AG
                                      C   A
GAM798  GPR17    3'  GCGTGGGGTTACAGCAGGAGA  23620      A_  C   CT  C
                                GTGT  GG TAC  GC GGAGA
                                ||||  || |||  || |||||
                                CGCA  CC ATG  CG CCTCT
                                  CC  A   T_  T
GAM798  B3GALT5  3'  GTACCTCTCGCAGCTGC     37684         TAT
                                GTACCTCTC   GGCTGC
                                |||||||||   ||||||
                                CATGGAGAG   TCGACG
                                     CG_
GAM798  CSNK1G3  3'  ACTACCTCTCCTTAGTG     20474    G       A   C
                                AC TACCTCTCT TGG TG
                                || ||||||||| ||| ||
                                TG ATGGAGAGG ATC AC
                                 _       A   _
GAM798  CYP4F3   3'  CATTCCTTTTTATGGCTG    9452     A   CTC
                                CGT CCT   TATGGCTG
                                ||| |||   ||||||||
                                GTA GGA   ATACCGAC
                                  A   AAA
GAM798  GRIN2B   3'  CGTACCTCCAGAGCTGCA    9120         CTAT
                                CGTACCTCT    GGCTGCA
                                |||||||||    |||||||
                                GCATGGAGG    TCGACGT
                                     TC__
GAM798  PSD      5'  TTCACATATTTCTTTTTCTAC  15794        CC   CTATGG
                                TTCACGTA  TCT     CTGC
                                ||||||||  |||     ||||
                                AAGTGTAT  AGA     GATG
                                    AA   AAAA__
GAM798  REGL     3'  TTCACCTACCTCTCTGTG    27125      G       A
                                TTCAC TACCTCTCT TG
                                ||||| ||||||||| ||
                                AAGTG ATGGAGAGA AC
                                  G       C
GAM799  GABRP    3'  AGAACAATGGTTGGAGCTT   30553     TCC   GC
                                AGA   GTGG  TGGAGCTT
                                |||   ||||  ||||||||
```

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                                TCT  TACC  ACCTCGAA
                                  TGT   A_
GAM799  LLT1    3'  CTAAAGATTAGTTGGGGCT   29973       CC  __
                                TTAAAGAT  GT  GGGCT
                                ||||||||  ||  |||||
                                GATTTCTA  CA  CCCGA
                                    AT  AC
GAM799  RRP22   3'  AGACTGGGTTGGAGCTT    27003     CCG   C
                                AGAT   TGGG TGGAGCTT
                                ||||   |||| ||||||||
                                TCTG   ACCC ACCTCGAA
                                  ___   A
GAM799  AHSG    3'  AGTTCCAATGGTTTTT     11557       GCAAA
                                AGTTCT    AATGGTTTTT
                                ||||||    ||||||||||
                                TCAAGG    TTACCAAAAA

                                _____
GAM799  ALEX2   5'  CAAGTTCTGCTGAGGCTT   31325         AAAAAT
                                CAAGTTCTGC     GGTTT
                                ||||||||||     |||||
                                GTTCAAGACG     CCGAA
                                    ACT___
GAM799  CDC23   3'  CAAGCTCTGTGAGATTATTTTT 21666         CAAAAATG
                                CAAGTTCTG       GTTTTT
                                |||||||||       ||||||
                                GTTCGAGAC       TAAAAA
                                    ACTCTAA_
GAM799  CLECSF5 3'  CAAGTTCTGAAAAATGA    29925         C
                                CAAGTTCTG AAAAATGG
                                ||||||||| ||||||||
                                GTTCAAGAC TTTTTACT

                                _
GAM799  DNAJB1  3'  AGTTCTGCAGGAATAGTTT   26028         AA
                                AGTTCTGCA  AATGGTTT
                                |||||||||  ||||||||
                                TCAAGACGT  TTATCAAA
                                    CC
GAM799  EIF1A   3'  CAGGTTCTGAAAACGGCATTT  44806    A     CA       T
                                CA GTTCTG  AAAATGGT TTT
                                || ||||||  |||||||| |||
                                GT CAAGAC  TTTTGCCG AAA
                                 C     __       T
GAM799  FMO1    3'  TGAGATCTGTGAAAATAGTTT  12922   A  T   CA
                                C AG TCTG  AAAATGGTTT
                                | || ||||  ||||||||||
                                A TC AGAC  TTTTATCAAA
                                 C  T   AC
GAM799  GYG     3'  CAGGCTCTGCAGATTTT     19968    A      AAAAT
                                CA GTTCTGCA    GGTTTT
                                || ||||||||    ||||||
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                                GT CGAGACGT    CTAAAA
                                 C      _____
GAM799  MECP2    3'  CAAGTTCTGCAAGCCTTT    22576          AAAAT
                                CAAGTTCTGCA    GGTTTTT
                                ||||||||||    |||||||
                                GTTCAAGACGT    TCGGAAA
                                      _____
GAM799  NT5E     3'  GGAGCCTGTAAAGATGGTTTTT 14861   A  T  C  A
                                C AGT CTG AAA ATGGTTTTT
                                | ||| ||| ||| |||||||||
                                C TCG GAC TTT TACCAAAAA
                                 C  _  A  C
GAM799  PRKG2    3'  TTCTGCAAACCACCATTTT   26524        A_  G
                                TTCTGCAAA  AT GTTTT
                                |||||||||  || |||||
                                AAGACGTTT  TG TAAAA
                                      GG  G
GAM799  SLC38A2  3'  CAGGTTCTCAAAGGTCTTC   33274   A    G   AAT
                                CA GTTCT CAAA  GGTTTTT
                                || ||||| ||||  |||||||
                                GT CAAGA GTTT  CCAGAAG
                                 C    _   ___
GAM799  TP63     3'  AGTTCTGCAAGCTATAGTTTT  18992         AA_
                                AGTTCTGCAA  ATGGTTTT
                                ||||||||||  ||||||||
                                TCAAGACGTT  TATCAAAA
                                      CGA
GAM800  MMP2     3'  CTTTAGGGGTGGCTCTGAGGGT 21195          A  GTC_
                                CTTTAGGGGT GT   GGGGT
                                |||||||||| ||   |||||
                                GAAATCCCCA CG   TCCCA
                                      C  AGAC
GAM801  IGF1R    3'  GCGCGTGCGCACACGTT     9330      A     AG
                                GCGC TGCGCAC  ACGTT
                                |||| |||||||  |||||
                                CGCG ACGCGTG  TGCAA
                                  C      __
GAM801  ACP1     5'  GCGCCTGCGGAGGCGTCCT   20195        CTATATA  C
                                GCGCTTGCG      CG CCT
                                |||||||||      || |||
                                CGCGGACGC      GC GGA
                                     CTCC___  A
GAM801  IGF2R    3'  GCACGCACGTGTGTGTGCCCT  9337       TT  CTATATAC
                                GCGCGC  GCG      GCCCT
                                ||||||  |||      |||||
                                CGTGCG  TGC      CGGGA
                                   __  ACACACA_
GAM802  ACVR1B   3'  TGCGGGCCAGGGCTCCTGGCCA 33763    ACA    TGAG_
            CA                  TGC  GCCAG    CTGGCCACA
                                |||  |||||    |||||||||
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                                ACG   CGGTC    GACCGGTGT
                                  CC_    CCGAG
GAM802  AIM1     5'  GCCTGCGCGGAGCTGGCC    45084     A ___
                                GCC GT   GAGCTGGCC
                                ||| ||   |||||||||
                                CGG CG   CTCGACCGG
                                  A  CGC
GAM802  ALDOC    5'  TGCGCAGCCAGTTAGCAGCCGC 23160     A      G   T   A
              A                  TGC CAGCCAGT AGC GGCC CA
                                ||| |||||||| ||| |||| ||
                                ACG GTCGGTCA TCG TCGG GT
                                  C       A  _   C
GAM802  CASP3    3'  TGACAGCCAGTGAGACTTGG   37418    C          _ _
                                TG ACAGCCAGTGAG CT GG
                                || ||||||||||||| || ||
                                AC TGTCGGTCACTC GA CC
                                 _          T  A
GAM802  CPSF4    3'  GCAGGCGTGAGCTGGCCACA   27439     CA  CA
                                GCA  GC  GTGAGCTGGCCACA
                                |||  ||  ||||||||||||||
                                CGT  CG  CACTCGACCGGTGT
                                  C_  __
GAM802  DSCAM    5'  TGCGCAGCCAGCGGCCTCCC   10809     A       A   GG
                                TGC CAGCCAGTG GCT  CC
                                ||| |||||||| |||  ||
                                ACG GTCGGTCGC CGG  GG
                                  C        _  AG
GAM802  EGR1     5'  TGCGGCGGCGGAAGCTGGC    12670     ACA  CA   __
                                TGC   GC  GTG  AGCTGGC
                                |||   ||  |||  |||||||
                                ACG   CG  CGC  TCGACCG
                                  C__   C_   CT
GAM802  FOXO1A   3'  TACATGGCCACCCCTGGCCACA 12891      CA    GTGAG
                                TGCA  GCCA    CTGGCCACA
                                ||||  ||||    |||||||||
                                ATGT  CGGT    GACCGGTGT
                                   AC    GGG__
GAM802  HDAC4    3'  GCCAGGCTCGGCTGGCCACA   25767       ___  A
                                GCCAG   TG GCTGGCCACA
                                |||||   || ||||||||||
                                CGGTC   GC CGACCGGTGT
                                   CGA  _
GAM802  KCNK10   3'  TGTACGGCCAGAACCGGCTAC  39684    C  A   GT      C
                                TG AC GCCA  GAGCTGGC AC
                                || || ||||  |||||||| ||
                                AC TG CGGT  CTTGGCCG TG
                                 A  C    __       A
GAM802  MPL      3'  TGCACAGCTAGTAAATG     23882         C     C
                                TGCACAGC AGTGAG TG
                                |||||||| |||||| ||
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```
                                ACGTGTCG TCATTT AC
                                    A    _
GAM802  NGFR    5' TGCCCGCCGGAGCTGGCC   14793    ACA  AGT
                                TGC  GCC  GAGCTGGCC
                                |||  |||  |||||||||
                                ACG  CGG  CTCGACCGG
                                  GG_  C__
GAM802  NPR2L   3' TGCACTGGCCAGTGGGCCGCA 27254     A_    AGCT   A
                                TGCAC  GCCAGTG   GGCC CA
                                |||||  |||||||   |||| ||
                                ACGTG  CGGTCAC   CCGG GT
                                   AC     _____   C
GAM802  NTSR1   3' GCACCCCATCCTGGCCAC   14882    AG  GTGAG
                                GCAC  CCA   CTGGCCAC
                                ||||  |||   ||||||||
                                CGTG  GGT   GACCGGTG
                                  G_  AG___
GAM802  P2RY1   3' TGCACAGCAGTGGGGC     15012       C   AGCT
                                TGCACAGC AGTG   GGC
                                |||||||| ||||   |||
                                ACGTGTCG TCAC   CCG
                                    _   C___
GAM802  PABPN1  5' TGCCAGCTAGTGAGCTG    21613    A   C
                                TGC CAGC AGTGAGCTG
                                ||| |||| |||||||||
                                ACG GTCG TCACTCGAC
                                  _   A
GAM802  PACE4   3' TGCACAGCAGCAGTTGG    15061       C  G  C
                                TGCACAGC AGT AG TGG
                                |||||||| ||| || |||
                                ACGTGTCG TCG TC ACC
                                    _  _ A
GAM802  PGC     5' TGCTGGTCCCCAACTGGCCACA 15244    ACAG  AGTG
                                TGC   CC   AGCTGGCCACA
                                |||   ||   ||||||||||||
                                ACG   GG   TTGACCGGTGT
                                  ACCA  GG__
GAM802  PIK4CB  3' GCATGGCCAGTGGCCAACCACA 15314    CA     A  TG
                                GCA  GCCAGTG GC  GCCACA
                                |||  ||||||| ||  ||||||
                                CGT  CGGTCAC CG  TGGTGT
                                  AC     _  GT
GAM802  PPP1R12B 3' TGCCAGCCAGTGGTAGGCACA  36982    A      AGCT  C
                                TGC CAGCCAGTG   GGC ACA
                                ||| |||||||||   ||| |||
                                ACG GTCGGTCAC   CCG TGT
                                  _       CAT_  _
GAM802  RANBP3  3' TGCAAGCTGGCTCTTGGCCA  28770    C  CA  GAGC
                                TGCA AGC  GT   TGGCCA
                                |||| |||  ||   ||||||
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                                ACGT TCG  CG    ACCGGT
                                  _  AC  AGA_
GAM802  TRPM1    5'  TGCTGGTTGGTGAACTGGCCAC 14541     ACAGCCA
              A                   TGC      GTGAGCTGGCCACA
                                  |||      ||||||||||||||
                                  ACG      CACTTGACCGGTGT
                                    ACCAAC_
GAM802  PTK7     3'  TCATCTGCCAGGCACTTAG   15862     CGA   A__
                                  TCA   CTGT   GCACTTAG
                                  |||   ||||   ||||||||
                                  AGT   GACG   CGTGAATC
                                    A__    GTC
GAM803  ANGPT2   3'  AATCACAATTATGGATGTT   10084      TGGGA   C
                                  GATC    AAT ATGGATGTT
                                  ||||    ||| |||||||||
                                  TTAG    TTA TACCTACAA
                                    TG___   A
GAM803  GASC1    5'  AGATTTGGGAAATTTGG     42028      C       CA
                                  AGAT TGGGAAAT  TGG
                                  |||| ||||||||  |||
                                  TCTA ACCCTTTA  ACC
                                    A       A_
GAM803  PPP2R5C  3'  TCTGGGAAGTCACCATTGTTT  15525         A    GGA
                                  TCTGGGAA TCAT   TGTTT
                                  |||||||| ||||   |||||
                                  AGACCCTT AGTG   ACAAA
                                       C    GTA
GAM803  RP2      3'  AGATTTGGGAAACAGTGCTT   27930      C       CAT  A
                                  AGAT TGGGAAAT   GG TGTTT
                                  |||| ||||||||   || |||||
                                  TCTA ACCCTTTG   TC ACGAA
                                    A       ___  _
GAM803  FCN2     3'  TTCCCTGGGCGGTCAGGGC   31898      ATT       AA
                                  TTTT   GGCGGTCA  GC
                                  ||||   ||||||||  ||
                                  AAGG   CCGCCAGT  CG
                                    GAC       CC
GAM804  BSN      3'  TCCATGGACCAGAGGCCTGC   18414    G         TA_
                                  TC CATGGACCAGG   TTGC
                                  || ||||||||||   ||||
                                  AG GTACCTGGTCT   GACG
                                  _          CCG
GAM804  PTK2B    3'  GCATGGACCAGGCTGGCT     19921           AT  C
                                  GCATGGACCAGGT  TG GCT
                                  ||||||||||||  || |||
                                  CGTACCTGGTCCG  AC CGA
                                                 __  _
GAM804  SMAP     3'  TCGTGTGGCCCAGGTACC     27454     CA   A
                                  TCG  TGG CCAGGTATT
                                  |||  ||| |||||||||
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                                AGC  ACC GGTCCATGG
                                  AC   G
GAM804  TGFBR2   3'  TCGCATGGATGGGGACATC   17484         CCA  _
                                TCGCATGGA   GG TATT
                                |||||||||   || ||||
                                AGCGTACCT   CC GTAG
                                     ACC  T
GAM804  ZFHX1B   5'  TCGCATGGACTCGGCGCCCT  31342          CA   ATT  G
                                TCGCATGGAC  GGT   GC CT
                                ||||||||||  |||   || ||
                                AGCGTACCTG  CCG   CG GA
                                     AG   ___  G
GAM804  ATP6V0D1 3'  GAGGAGCAACATCCCCCCA   21724    A  A  C_
                                GA GA GT  TATCCCCCCA
                                || || ||  ||||||||||
                                CT CT CG  GTAGGGGGGT
                                 C  _  TT
GAM804  BMPR2    5'  CCAAGAAGAAATCCCCC     37856    G     TCT
                                CC AAGAAG   ATCCCCC
                                || ||||||   |||||||
                                GG TTCTTC   TAGGGGG
                                 _     TT_
GAM804  CRTAP    3'  CCAGAGAAGACTGCCCTTCAAA 26839     A    T  AT   CC
                                CCG AGAAG CT  CCC  CAAA
                                ||| ||||| ||  |||  ||||
                                GGT TCTTC GA  GGG  GTTT
                                  C    T  C_   AA
GAM804  FXYD1    5'  AAAGAAGGCCCCCAA       34860        TCTATC
                                GAAGAAG     CCCCCAA
                                |||||||     |||||||
                                TTTCTTC     GGGGGTT
                                    C_____
GAM804  GNE      3'  ACCAAAGAACAGATGTCCTTCC 24213         _____   A
                                ACCGAAGAA    GTCT TCC
                                |||||||||    |||| |||
                                TGGTTTCTT    CAGG AGG
                                     GTCTA   A
GAM804  HOXB2    5'  CGGAAGGGACCCCCCC      13432    AA   TCT
                                CG  GAAG   ATCCCCCC
                                ||  ||||   ||||||||
                                GC  CTTC   TGGGGGGG
                                 __   CC_
GAM804  KCNN3    3'  CGAAGAGCCCATCCCCC     13919       A
                                CGAAGA GTCTATCCCCC
                                |||||| ||||||||||
                                GCTTCT CGGGTAGGGGG
                                    _
GAM804  KIAA0857 3'  CCTGAAGAAGTGGTGGTCCCA  42471    _      CTATCCC
                                CC GAAGAAGT      CCCA
                                || ||||||||      ||||
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                                GG CTTCTTCA      GGGT
                                 A       CCACCA_
GAM804  MBNL    5'  GATGAAAATGTCCCCTCAAA  34313    A   TCTA    C
                                GA GAAG   TCCCC CAAA
                                || ||||   ||||| ||||
                                CT CTTT   AGGGG GTTT
                                 A   TAC_    A
GAM804  MEIS2   3'  GAAGAAGAGTCCCCCAAA    33541        TCTATC
                                GAAGAAG     CCCCCAAA
                                |||||||     ||||||||
                                CTTCTTC     GGGGGTTT
                                    TCA___
GAM804  NKTR    3'  GAGAGAAGCCCCCCAAA     23927    _    TCTAT
                                GA AGAAG    CCCCCCAAA
                                || |||||    |||||||||
                                CT TCTTC    GGGGGGTTT
                                 C    _____
GAM804  OAS3    3'  ACCGGGAAGCCCCCA       26176      AA   TCTATC
                                ACCG  GAAG     CCCCCA
                                ||||  ||||     ||||||
                                TGGC  CTTC     GGGGGT
                                  C_   _______
GAM804  POU4F1  3'  GAGGAAAGCCCCCCAA      26387    A   TCTAT
                                GA GAAG    CCCCCCAA
                                || ||||    ||||||||
                                CT CTTT    GGGGGGTT
                                 C   C____
GAM804  PPIF    3'  ACCAGGAAATGCTTCCCTCC   25058      AA    _ A   C
                                ACCG  GAAGT CT TCCC CC
                                ||||  ||||| || |||| ||
                                TGGT  CTTTA GA AGGG GG
                                  C_    C _    A
GAM804  PRKY    3'  CCGGATATCTTATTCCCCCAAA 15692     AA  A   _ C
                                CCG  GA GTCT AT CCCCCAAA
                                |||  || |||| || ||||||||
                                GGC  CT TAGA TA GGGGGTTT
                                  __ A   A  A
GAM804  RDS     3'  ACGGAAGAAGCTCCC       7240     C       CTA
                                AC GAAGAAGT   TCCC
                                || ||||||||   ||||
                                TG CTTCTTCG   AGGG
                                 C      ___
GAM804  RFP     3'  CCAAGAAGTCAATGAATCCC   27129    G       T____
                                CC AAGAAGTC    ATCCC
                                || ||||||||    |||||
                                GG TTCTTCAG    TAGGG
                                 _      TTACT
GAM804  SECTM1  3'  CCGCGGAAGGGCCCCCAA    16538    AA   TCTATC
                                CCG  GAAG     CCCCCAA
                                |||  ||||     |||||||
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                                GGC  CTTC     GGGGGTT
                                  GC    CC____
GAM804  SPS2     3'  GAACAAATATCCCCCCAAA   29303     G    CT
                                GAA AAGT  ATCCCCCCAAA
                                ||| ||||  ||||||||||
                                CTT TTTA  TAGGGGGGTTT
                                  G   __
GAM804  SURF5    3'  ACCAAAGATTCCCTCA      39499         AGTCTA    CC
                                ACCGAAGA     TCCC  CA
                                ||||||||     ||||  ||
                                TGGTTTCT     AGGG  GT
                                    A_____    A_
GAM804  TNFSF9   3'  CGAAGACCCCCCCCCCCAAA   19194       AGTCTA
                                CGAAGA     TCCCCCCAAA
                                ||||||     ||||||||||
                                GCTTCT     GGGGGGGTTT
                                   GGG___
GAM804  XRCC5    3'  ACCAAGAAGTCTGTACACCAAA 34485     G        ATCCCC
                                ACC AAGAAGTCT     CCAAA
                                ||| |||||||||     |||||
                                TGG TTCTTCAGA     GGTTT
                                  _       CATGT_
GAM805  NXF2     3'  GGGTGGTTATGTCACGTG    32821     C  A   CGC
                                GGG GG TTA   GTTACGTG
                                ||| || |||   ||||||||
                                CCC CC AAT   CAGTGCAC
                                  A  _   A__
GAM805  GNA11    3'  CCGTTGACAAAAGG        44038         CTTTG
                                CCGTTGAC    AAAAGG
                                ||||||||    ||||||
                                GGCAACTG    TTTTCC
                                     _____
GAM805  WBSCR14  3'  TCTTCTTGACCTCCAGGAGG  37289     CCG      TT AAA
                                TCT   TTGACCT  G   AGG
                                |||   |||||||  |   |||
                                AGA   AACTGGA  T   TCC
                                  AG_      GG CC_
GAM806  CSE1L    5'  CCAGAGCGCATGAGCGAGCGGC 41588        AC G        A
                                TCAGAGC  G ATGAGCGAGC GC
                                |||||||  | ||||||||||  ||
                                GGTCTCG  C TACTCGCTCG CG
                                   __ G        C
GAM806  DDX6     3'  CAGTGCGGATGAACTGCAG   20550     A  AC       GA
                                CAG GC  GGATGAGC  GCAG
                                ||| ||  ||||||||  ||||
                                GTC CG  CCTACTTG  CGTC
                                  A  __       A_
GAM806  DVL3     3'  TCGCAGCACCCTGCGAGCAG  20690     AG    GGATGA
                                TC  AGCAC     GCGAGCAG
                                ||  |||||     ||||||||
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                                AG  TCGTG    CGCTCGTC
                                 CG    GGA___
GAM806  ELL     3'  GAGCACAGAAACACAGTGGC  27207        TGA  A__
                                GAGCACGGA  GCG  GC
                                |||||||||  |||  ||
                                CTCGTGTCT  TGT  CG
                                     TTG  CAC
GAM806  EXT1    5'  CCAGGGCGGGCGAGCA     6548      A  AC  ATGA
                                TCAG GC  GG   GCGAGCA
                                ||||  ||  ||   |||||||
                                GGTC CG  CC   CGCTCGT
                                  C  __  _____
GAM806  FTSJ2   3'  TCAGAGCAGGGGTGGAAAGC  30170        C  A  AGC
                                TCAGAGCA GG TG  GAGC
                                ||||||||  ||  ||  ||||
                                AGTCTCGT CC AC  TTCG
                                     C  C  CT_
GAM806  KCNS2   5'  GAGCACGGGTGCCCGCGGC   42826        A  A__  A
                                GAGCACGG TG  GCG GC
                                ||||||||  ||  |||  ||
                                CTCGTGCC AC  CGC CG
                                     C  GGG  _
GAM806  KIFC3   3'  CCAGGCAGGTGAGCGAGCAGC  24455      A  C  A
                                TCAG GCA GG TGAGCGAGCAGC
                                ||||  |||  ||  ||||||||||||
                                GGTC CGT CC ACTCGCTCGTCG
                                  _  _  _
GAM806  PRV1    3'  GAGTGTGGTGGTGAGCAGC   43876     CAC  A  AGC
                                GAG  GG TG  GAGCAGC
                                |||  ||  ||  |||||||
                                CTC  CC AC  CTCGTCG
                                  ACA  _  CA_
GAM806  RXRA    3'  TCCGGGCACGGATGGGTGGGCG 16436    AGA       A____
                                TC  GCACGGATG    GCG
                                ||  |||||||||    |||
                                AG  CGTGCCTAC    CGC
                                 GCC       CCACC
GAM806  VCP     5'  CCAGGCGGTGGGCGAGCAGC  44009     A  AC  A  A
                                TCAG GC  GG TG GCGAGCAGC
                                ||||  ||  || ||  |||||||||
                                GGTC CG  CC AC CGCTCGTCG
                                  _  __  _  C
GAM806  VDAC1   5'  GAGCCGAGCGAGCGGC     17930     A  GA    A
                                GAGC CG  TGAGCG GC
                                ||||  ||  ||||||  ||
                                CTCG GC  GCTCGC CG
                                  _  TC    _
GAM806  CHST5   5'  GGAGCTTTCGTTCCTCTCCTGG 29079      CTA  CG_
          T                      GGAGCT   TC   TCTCTCCTGGT
                                ||||||   ||  ||||||||||
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                                CCTCGA  AG  GGAGAGGACCA
                                   A__  CAA
GAM806  MAGEA9   5' GGGCTCCTGTCCTCCTGG   23850   A   ATCC  T
                                GG GCTCT   GTC CTCCTGG
                                || |||||   ||| |||||||
                                CC CGAGG   CAG GAGGACC
                                 _    A___  _
GAM806  PLAB     5' GGACTTTGTCCGTCTCCGCCT 42318    G  CTA      _
                                GGA CT   TCCGTCTCT CCT
                                ||| ||   ||||||||| |||
                                CCT GA   AGGCAGAGG GGA
                                  _ AAC       C
GAM807  MADH7    5' AGTCGTTTGCCTGCTAAGGAG 25361   C      C  GGTGCC
                                AG CGTTTGCC GT     GGAG
                                || |||||||| ||     ||||
                                TC GCAAACGG CG     CCTC
                                 A       A  ATT___
GAM807  RNF4     3' GCCGTTTGTTTGGCGTGA    16354       CCCG    CCG
                                GCCGTTTG   TGGTG  GA
                                ||||||||   |||||  ||
                                CGGCAAAC   ACCGC  CT
                                     AA__    A__
GAM807  EPS8     3' TGCAGACTTTCCAGCTGAC   20815     C       AACG
                                TGCA GACTTTCCG   GAC
                                |||| |||||||||   |||
                                ACGT CTGAAAGGT   CTG
                                  _       CGA_
GAM807  ETV5     3' CTGTAGACTTTCCACAC     20851     CAC       A
                                CTG  GACTTTCCG AC
                                |||  ||||||||| ||
                                GAC  CTGAAAGGT TG
                                  AT_       G
GAM807  IRAK1    3' CTGCTCGACTTTCTGGAGGA   11473     A      CGAAC
                                CTGC CGACTTTC    GGA
                                |||| ||||||||    |||
                                GACG GCTGAAAG    CCT
                                  A       ACCT_
GAM807  MYEOV    5' CTGCTCCTGAATGGAC      39875     ACGACTT  _  C
                                CTGC      TCC GAA GGAC
                                ||||      ||| ||| ||||
                                GACG      AGG CTT CCTG
                                  ________  A  A
GAM807  SLC22A3  3' CTGTACAACTTTCTCAAA    35049     C       _
                                CTG ACGACTTTC CGAA
                                ||| ||||||||| ||||
                                GAC TGTTGAAAG GTTT
                                  A       A
GAM808  CYFIP2   5' TCAAAGTTAGCCTGGTACA   43914       TC    A
                                TCAAAGTT  TCTGG TACA
                                ||||||||  ||||| ||||
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                                AGTTTCAA  GGACC ATGT
                                    TC    _
GAM808  GCNT3    3'  TCCATCAAAGTTCTCCTCCAC  21908          T   GGA
                                TCCATCAAAGTT CTCT   TAC
                                |||||||||||| ||||  |||
                                AGGTAGTTTCAA GAGG   GTG
                                      _   AG_
GAM808  HUNK     3'  CCTGTCAAGTGCCAGCTGGATA 31064    ATCA   T  T_
          CA                     CC   AAGT TC  CTGGATACA
                                ||   |||| ||  |||||||||
                                GG   TTCA GG  GACCTATGT
                                 ACAG   C  TC
GAM808  LARS     3'  CATCAAAGTATAAAGTACA   33478        TTCTCT  A
                                CATCAAAGT     GG TACA
                                |||||||||     || ||||
                                GTAGTTTCA     TC ATGT
                                     TATT__  _
GAM808  NFYC     3'  TCCATGGCCTCTGGATC     30597      CAAA  TT      A
                                TCCAT   GT  CTCTGGAT C
                                |||||   ||  |||||||| |
                                AGGTA   CG  GAGACCTA G
                                   C___  __       C
GAM808  NKX2E    5'  CCCGTCGGCCAGCTCTGGAT   20493     A  AAA   T_
                                TCC TC   GTT  CTCTGGAT
                                ||| ||   |||  ||||||||
                                GGG AG   CGG  GAGACCTA
                                  C  C__   TC
GAM808  OGN      3'  TCAAAGTTTTTGGAACA     30430         CTC    T
                                TCAAAGTTT   TGGA ACA
                                |||||||||   |||| |||
                                AGTTTCAAA   ACCT TGT
                                     A__   _
GAM808  ZNF131   3'  TCCATTTAAGTTTCCAGAAATA 43149      CA      CT
                                TCCAT  AAGTTTCT  GGATA
                                |||||  ||||||||  |||||
                                AGGTA  TTCAAAGG  TTTAT
                                   AA       TC
GAM809  ACY1     3'  TGTCCTTGTGTTAGTACTTCAG 8570     G   ACA_   CC
            A                    TGT CCT    TTAG  ATTTCAGA
                                ||| |||    ||||  ||||||||
                                ACA GGA    AATC  TGAAGTCT
                                  _   ACAC    A_
GAM809  BTEB1    3'  TATGTTTACACATTTCAG    10219     CC    TTAGC
                                TGTG  TACA    CATTTCAG
                                ||||  ||||    ||||||||
                                ATAC  ATGT    GTAAAGTC
                                  AA   _____
GAM809  DUSP5    3'  GTGTCTACACAACATTTCAG   20660     C     TAGC
                                GTG CTACAT    CATTTCAG
                                ||| ||||||    ||||||||
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                                CAC GATGTG   GTAAAGTC
                                  A     TT__
GAM809  E2F3     3'  TGTGCCTACCATTGGGTCAG  12635       ACATTA     ___
                                TGTGCCT     GCCATT   TCAG
                                |||||||     ||||||   ||||
                                ACACGGA     TGGTAA   AGTC
                                   _______      CCC
GAM809  TRPC6    3'  TGTGTCCACATTAGCCAC    21486     C
                                TGTG CTACATTAGCCAT
                                |||| ||||||||||||
                                ACAC GGTGTAATCGGTG
                                  A
GAM809  D1S155E  3'  AATGGTGTGCTTTGTGGAT   28387        ACACGACT
                                AATGGTGTG       TGGAT
                                |||||||||       |||||
                                TTACCACAC       ACCTA
                                     GAAAC___
GAM809  ELMO1    3'  AATGATGTAAACTTGGAT    39047         CACG
                                AATGGTGTGA   ACTTGGAT
                                ||||||||||   ||||||||
                                TTACTACATT   TGAACCTA
                                   _____
GAM809  MUC4     3'  AATGGCTCCAGCGACTTGG   32903       GTGA _
                                AATGGT   CA CGACTTGG
                                ||||||   || ||||||||
                                TTACCG   GT GCTGAACC
                                   AG__  C
GAM809  SDC1     3'  AATGGTGCGATGCCAGG     16496         CACGA  T
                                AATGGTGTGA    CT GG
                                ||||||||||    || ||
                                TTACCACGCT    GG CC
                                     AC___  T
GAM809  SF3B3    5'  ATGGTGTGGATATCCAACGGAT 29679        ACA___   TT
                                ATGGTGTG     CGAC  GGAT
                                ||||||||     ||||  ||||
                                TACCACAC     GTTG  CCTA
                                     CTATAG   __
GAM810  UNC13    5'  CAGCTCCTCATGGTCCCGGTCG 26860        GA  TAGA
                                CGGCTCC  TC   TCCCGGTCG
                                |||||||  ||   |||||||||
                                GTCGAGG  AG   AGGGCCAGC
                                   __  TACC
GAM810  ABCC3    3'  GGTCCAGGTTCATGCGCAGGGT 33425       A  C  G T  __
          C                      GGTCCA GT CA G CGC  GGTC
                                ||||||  ||  ||  |  |||  ||||
                                CCAGGT CA GT C GCG  CCAG
                                   C  A  A _   TC
GAM810  CLDN5    3'  GAGGTCCAGGCCAAGTCACTGG 17608         A T       _
          TC                     GAGGTCCA G CCAGGTCGC GGTC
                                ||||||||  |  |||||||||  ||||
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                                CTCCAGGT C GGTTCAGTG CCAG
                                    C _       A
GAM810  HCN4     5'  GGCTCCAGGTCCGCCCGCCGGT 24231    _   A   AGG   _
              C                  GG TCCA GTCC   TCGC GGTC
                                 || |||| ||||   |||| ||||
                                 CC AGGT CAGG   GGCG CCAG
                                  G   C   CG_   G
GAM810  IMPDH1   5'  GAGGTCCAATCTAGGGC     9409          G  C   TC
                                 GAGGTCCAA TC AGG  GC
                                 ||||||||| || |||  ||
                                 CTCCAGGTT AG TCC  CG
                                      _ A   __
GAM810  KCNA6    5'  GGGTCCGGCCAAGGTCGCGGT  13818   A    AA   C
                                 G GGTCC  GTC AGGTCGCGGT
                                 | |||||  ||| ||||||||||
                                 C CCAGG  CGG TCCAGCGCCA
                                 _    C_   T
GAM810  NFE2L1   3'  AGGTCCAGGTCCAGGTCCAGGT 17328        A       GC
              C                   AGGTCCA GTCCAGGTC  GGTC
                                  ||||||| |||||||||  ||||
                                  TCCAGGT CAGGTCCAG  CCAG
                                      C        GT
GAM810  PMX1     5'  GAGGCCAAGTCCGGCGCGGTC  35511      T       A  T
                                 GAGG CCAAGTCC GG CGCGGTC
                                 |||| |||||||| || |||||||
                                 CTCC GGTTCAGG CC GCGCCAG
                                       _       _ _
GAM811  ACT      5'  CCTGCATTTCCTCCAAGTC   33885    CC  CC      AAC
                                 CC  CA  TCCTCCA   GGTC
                                 ||  ||  |||||||   ||||
                                 GG  GT  AGGAGGT   TCAG
                                  AC  AA      ____
GAM811  ACTR1B   3'  CCCCCACCCCCTTTTAGGTC   43344           CCAAAC
                                 CCCCCACCTCCT     GGTC
                                 ||||||||||||     ||||
                                 GGGGGTGGGGGA     CCAG
                                        AAAT__
GAM811  ADCY6    3'  CCCCCACCCCCACAGT      34167           TCCAA
                                 CCCCCACCTCC     ACGGT
                                 ||||||||||     |||||
                                 GGGGGTGGGGG     TGTCA
                                                _____
GAM811  ALEX2    5'  CCTCCTCCTCCTCGCCTGGGT  31326    _ A      CAAAC
                                 CC CC CCTCCTC     GGT
                                 || || |||||||     |||
                                 GG GG GGAGGAG     CCA
                                  A  A      CGGAC
GAM811  ANXA6    3'  CCCCTGCCCCTTCCTTAGTC   19712      CA   C   AAAC
                                 CCCC  CCTC TCC    GGTC
                                 ||||  |||| |||    ||||
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                                GGGG  GGGG AGG    TCAG
                                  AC    A   AA__
GAM811  AP2B1    3'  CCCCATTTCTTTCCAGAGTC   10482      CC  C_   AAC
                                CCCCA  TC  TCCA   GGTC
                                |||||  ||  ||||   ||||
                                GGGGT  AG  AGGT   TCAG
                                  AA  AA    C__
GAM811  ATP2A3   3'  CCCTGCCTCCCCCACTGCG   23191     CA       AA_
                                CCC  CCTCCTCCA   CG
                                |||  |||||||||   ||
                                GGG  GGAGGGGGT   GC
                                  AC        GAC
GAM811  BAT1     3'  CCTCTCCTGAAGGACAGACGGT 21588    AC    C_____  A
           C                     CC  CTCCT     CA ACGGTC
                                ||  |||||     || ||||||
                                GG  GAGGA     GT TGCCAG
                                 A_    CTTCCT  C
GAM811  BCAS1    3'  CCTCCACCTCCTGGGTACAAGC 18919    _       C____   A
           GGT                     CC CCACCTCCT     CAA CGGT
                                || |||||||||     ||| ||||
                                GG GGTGGAGGA     GTT GCCA
                                 A        CCCAT   C
GAM811  BMP1     3'  CCCCCACCTCCTATGGACAGTC 25977           CCAA
                                CCCCCACCTCCT    ACGGTC
                                ||||||||||||    ||||||
                                GGGGGTGGAGGA    TGTCAG
                                       TACC
GAM811  CA11     5'  CCCACACCTCCTCTCCG     10236     _       CAAA
                                CCC CACCTCCTC    CG
                                ||| |||||||||    ||
                                GGG GTGGAGGAG    GC
                                  T       AG__
GAM811  CACNA2D2 3'  CCTCCCCCTCCTCCCAGTC    25710    _  A      AAA
                                CC CCC CCTCCTCC   CGGTC
                                || ||| ||||||||   |||||
                                GG GGG GGAGGAGG   GTCAG
                                 A  _      ____
GAM811  CCND1    3'  CCTCACACCTCCTCCCGCCTGT 38202    CC_        AAACG
           C                     CC   CACCTCCTCC    GTC
                                ||   ||||||||||    |||
                                GG   GTGGAGGAGG    CAG
                                 AGT        GCGGA
GAM811  CSNK1G2  3'  CCCCTGCCTTCCCCTTTGGT   10611      CA   C    AAAC
                                CCCC  CCT CTCC    GGT
                                ||||  ||| ||||    |||
                                GGGG  GGA GGGG    CCA
                                  AC   A    AAA_
GAM811  CSRP1    3'  CCCCCCTCCTCATCTTGGTC   19840      A      CAAAC
                                CCCC CCTCCTC     GGTC
                                |||| |||||||     ||||
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                                GGGG GGAGGAG    CCAG
                                  _     TAGAA
GAM811  DLEC1    3'  CCTCCAGCTCCAGGACGGTC  28822    A  TC    A_
                                CC CC  CTCCA  ACGGTC
                                || ||  |||||  ||||||
                                GG GG  GAGGT  TGCCAG
                                 A  TC    CC
GAM811  DYRK1B   3'  CCCCCACCCCCTCCTAGGGTC 21777           AAAC
                                CCCCCACCTCCTCC   GGTC
                                ||||||||||||||   ||||
                                GGGGGTGGGGGAGG   CCAG
                                       ATC_
GAM811  EN1      5'  CCTCCCCCTCCTTCAGGC    10908    _  A    C  AAC
                                CC CCC CCTCCT CA   GGT
                                || ||| |||||| ||   |||
                                GG GGG GGAGGA GT   CCG
                                 A  _     A ___
GAM811  FABP2    3'  CCTCCAACTCTTCCAAGTC   6585    _  C   C   AAC
                                CC CCA CTC TCCA   GGTC
                                || ||| ||| ||||   ||||
                                GG GGT GAG AGGT   TCAG
                                 A  T  A   ___
GAM811  FCN2     3'  CCCCCATCATCTCTGACTGTC 31899      CCTC   CAA  G
                                CCCCCA   CTC   AC GTC
                                ||||||   |||   || |||
                                GGGGGT   GAG   TG CAG
                                   AGTA   AC_  A
GAM811  FN14     3'  CCCCCACCCCCCTTGTGGT   32490         CCAAAC
                                CCCCCACCTCCT     GGT
                                ||||||||||||     |||
                                GGGGGTGGGGGG     CCA
                                       AACA__
GAM811  FOSB     3'  CCTCCTCCTCTTCCAAGTC   27535   _ A   C   AAC
                                CC CC CCTC TCCA   GGTC
                                || || |||| ||||   ||||
                                GG GG GGAG AGGT   TCAG
                                 A  A   A   ___
GAM811  FOSB     3'  CCTCCTCCTCCTCTTCCAAGTC 27534    _ A     CAAAC
                                CC CC CCTCCTC    GGTC
                                || || |||||||    ||||
                                GG GG GGAGGAG    TCAG
                                 A  A      AAGGT
GAM811  FOXD2    5'  CCCCCACCTTCCTGGC     20956        _  CCAAAC
                                CCCCCACCT CCT     GGT
                                |||||||||  |||     |||
                                GGGGGTGGA GGA     CCG
                                      A  _______
GAM811  GABRG2   5'  CCCCCACCTGCCTCTAGTAGGT 9048         _   CAAAC
             C                   CCCCCACCT CCTC    GGTC
                                |||||||||  ||||    ||||
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                                GGGGGTGGA GGAG    CCAG
                                     C   ATCAT
GAM811  GALGT    3'  CCCCACCCCCTCGGT      11178          CAAAC
                                CCCCACCTCCTC    GGT
                                ||||||||||||    |||
                                GGGGTGGGGGAG    CCA
                                      _____
GAM811  GATA2    3'  CCCCACCTGGGCAGCGGTC   13082       CCTC  AA
                                CCCCACCT   CA  CGGTC
                                ||||||||   ||  |||||
                                GGGGTGGA   GT  GCCAG
                                    CCC_  C_
GAM811  GDF2     3'  CCCTTTCCTCCTCCAGGC    32123     CCA       AAC
                                CCC   CCTCCTCCA   GGT
                                |||   |||||||||   |||
                                GGG   GGAGGAGGT   CCG
                                  AAA       ___
GAM811  GLTSCR1  3'  CCCCCACCCCCTCTCCGGT   31834          CAAA
                                CCCCCACCTCCTC    CGGT
                                ||||||||||||    ||||
                                GGGGGTGGGGGAG   GCCA
                                      AG__
GAM811  GNA11    5'  CCCCACCTTCCGAGT      44032        CC   AAAC
                                CCCCACCT  TCC    GGT
                                ||||||||  |||    |||
                                GGGGTGGA  AGG    TCA
                                    __   C___
GAM811  H1F0     3'  CCCCACCCTTCCCCTGAAGT   23698        CC   AAAC
                                CCCCACCT  TCC    GGT
                                ||||||||  |||    |||
                                GGGGTGGG  GGG    TCA
                                    AA   GACT
GAM811  HDGF     5'  CCTCCACCCCCCGCCCGGTC   21060    _       _ AAA
                                CC CCACCTCCT CC   CGGTC
                                || |||||||| ||   |||||
                                GG GGTGGGGGG GG   GCCAG
                                  A        C ___
GAM811  INHBB    3'  CCCCGCCATTTCCTCCTGCGGT 13544      A ___     AAA
              C                  CCCC CC   TCCTCC   CGGTC
                                 |||| ||   ||||||   |||||
                                 GGGG GG   AGGAGG   GCCAG
                                   C  TAA     AC_
GAM811  KCNJ4    3'  CCCCCACCTTCCTCCAGAAGGT 22536         _     AAC
              C                  CCCCCACCT CCTCCA   GGTC
                                 |||||||| ||||||   ||||
                                 GGGGGTGGA GGAGGT   CCAG
                                      A     CTT
GAM811  KCNK5    3'  CCTCCACCCCACTACGGT    19034    _      _ CCAA
                                 CC CCACCTC CT    ACGGT
                                 || ||||||| ||    |||||
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                                GG GGTGGGG GA    TGCCA
                                 A      T _____
GAM811  KIP2     3'  CCACCACCTCCTGTTGGGT   26887    _       CCAAAC
                                CC CCACCTCCT     GGT
                                || |||||||||     |||
                                GG GGTGGAGGA     CCA
                                 T       CAAC__
GAM811  KLF4     5'  CCCCCACCACTGTCGCGGTC  20152        TC  CCAAA
                                CCCCCACC  CT    CGGTC
                                ||||||||  ||    |||||
                                GGGGGTGG  GA    GCCAG
                                     T_  CAGC_
GAM811  LEP      3'  CCCTCACCTCCTTCAAAC    6912     _      C
                                CCC CACCTCCT CAAAC
                                ||| |||||||| |||||
                                GGG GTGGAGGA GTTTG
                                  A       A
GAM811  LRP1     5'  CCCCCTCCTCCTTGACCGTTTG 14209      A    T_______  AAAC
           G                     CCCCC CCTCC      CC    GG
                                ||||| |||||      ||    ||
                                GGGGG GGAGG      GG    CC
                                   A    AAIIICT  CAAA
GAM811  LRRC2    3'  CCCCACCTTGGAACGGT     36029         CCTCCA
                                CCCCACCT     AACGGT
                                ||||||||     ||||||
                                GGGGTGGA     TTGCCA
                                     ACC___
GAM811  MAP3K11  3'  CCTCCCCTCCTCCCTGC     14533    _ A       AAACG
                                CC CC CCTCCTCC     GT
                                || || ||||||||     ||
                                GG GG GGAGGAGG     CG
                                 A  _       GA___
GAM811  MEIS1    3'  CCATGCCTCCTCCTACCAGTC  14415     __       AAA
                                CCA  CCTCCTCC   CGGTC
                                |||  ||||||||   |||||
                                GGT  GGAGGAGG   GTCAG
                                  AC       ATG
GAM811  MEIS2    5'  CCTCCTCCTCCTGATC      33540    A       AAAC
                                CC CCTCCTCC    GGTC
                                || ||||||||    ||||
                                GG GGAGGAGG    CTAG
                                 A       A___
GAM811  MGAT3    5'  CCCCCACTTCCACCCCGTC    14456        C   T  AAACG
                                CCCCCAC TCC CC     GTC
                                ||||||| ||| ||     |||
                                GGGGGTG AGG GG     CAG
                                    A  T  GG___
GAM811  MMP9     3'  CCTCCCTTTCCTCCAGAAC    22628    _  ACC      _
                                CC CCC   TCCTCCA AAC
                                || |||   ||||||| |||
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                                GG GGG   AGGAGGT TTG
                                 A  AA_      C
GAM811  NGB      5'  CCCCCGCCCCCTCCAGGC    34582       A        AAC
                                CCCCC CCTCCTCCA   GGT
                                ||||| |||||||||   |||
                                GGGGG GGGGGAGGT   CCG
                                  C        ___
GAM811  PCSK2    3'  CACCTCCTTCAGGCC       15125         C  AAC
                                CACCTCCT CA   GGTC
                                |||||||| ||   ||||
                                GTGGAGGA GT   CCGG
                                    A  ___
GAM811  PFKFB2   3'  CCTCCTCCTCCAGATC      26306    A        AAC
                                CC CCTCCTCCA   GGTC
                                || |||||||||   ||||
                                GG GGAGGAGGT   CTAG
                                 A        ___
GAM811  PHGDH    5'  CCTCCTCCTCCTCTTACAGTC  42033    _  A      CAA
                                CC CC CCTCCTC   ACGGTC
                                || || |||||||   ||||||
                                GG GG GGAGGAG   TGTCAG
                                 A  A      AA_
GAM811  PIP5K1A  5'  CCCCGCCCCCTCCGGGCC    18651      A       AAAC
                                CCCC CCTCCTCC    GGTC
                                |||| ||||||||    ||||
                                GGGG GGGGGAGG    CCGG
                                  C       C___
GAM811  PPP3CC   5'  CCTCGGCCTCCTCCAGGC    24676    CCCA       AAC
                                CC    CCTCCTCCA   GGT
                                ||    |||||||||   |||
                                GG    GGAGGAGGT   CCG
                                 AGCC        ___
GAM811  PSD      5'  CCCCACCTGCCTCATCG     15780         _   CAAA
                                CCCCACCT CCTC    CG
                                |||||||| ||||    ||
                                GGGGTGGA GGAG    GC
                                    C    TA__
GAM811  PTBP1    3'  CCCCCACCCCTTGGGT      36718         T  CCAAAC
                                CCCCCACC CCT     GGT
                                |||||||| |||     |||
                                GGGGGTGG GGA     CCA
                                    _   AC_____
GAM811  PTPRJ    5'  CCGCTGCCTCCTCCGCGCGTC  15950    CCCA       AAA  _
                                CC    CCTCCTCC   CG GTC
                                ||    ||||||||   || |||
                                GG    GGAGGAGG   GC CAG
                                 CGAC       C__  G
GAM811  RAB5B    3'  CCTCCACCTCCGCCCAGT    16090    _       T  AAA
                                CC CCACCTCC CC   CGGT
                                || |||||||| ||   ||||
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                                GG GGTGGAGG GG   GTCA
                                 A       C ___
GAM811  RENBP    5'  CCTCCCCCTCCTCTTCAGGGT  16243    _  A      CAAAC
                                CC CCC CCTCCTC     GGT
                                || ||| |||||||     |||
                                GG GGG GGAGGAG     CCA
                                 A  _       AAGTC
GAM811  RFC2     3'  CCTCCACCTCCTCCTCCTGGGT 16278    _         AAAC_
                                CC CCACCTCCTCC     GGT
                                || ||||||||||     |||
                                GG GGTGGAGGAGG     CCA
                                 A          AGGAC
GAM811  SLC6A2   3'  CCTCCTTCTCCTCCAGGC    9804     _ AC       AAC
                                CC CC  CTCCTCCA   GGT
                                || ||  ||||||||   |||
                                GG GG  GAGGAGGT   CCG
                                 A  AA       ___
GAM811  SNX15    5'  CCCCACCCCTCCGG        43931         T    AAAC
                                CCCCACC CCTCC    GG
                                ||||||| |||||    ||
                                GGGGTGG GGAGG    CC
                                   _    _____
GAM811  SNX15    5'  CCTCCACCTCCTCGCCG     43933    _        CAAA
                                CC CCACCTCCTC    CG
                                || ||||||||||    ||
                                GG GGTGGAGGAG    GC
                                 A         CG__
GAM811  SP3      5'  CCTCCTCCTCCTCCTGGTC   44374    _ A      AAAC
                                CC CC CCTCCTCC    GGTC
                                || || ||||||||    ||||
                                GG GG GGAGGAGG    CCAG
                                 A  A       A___
GAM811  STARD5   5'  CCCACACCTCCTCTAGTGTC  36124     _       CAAACG
                                CCC CACCTCCTC     GTC
                                ||| |||||||||     |||
                                GGG GTGGAGGAG     CAG
                                  T        ATCA__
GAM811  SURF5    3'  CCCCTCCAGCTCAAACGGTC  39503     A  TC   C
                                CCCC CC  CTC AAACGGTC
                                |||| ||  ||| ||||||||
                                GGGG GG  GAG TTTGCCAG
                                  A  TC  _
GAM811  TEAD3    3'  CCCCACCTCTCTGAGGTC    17370         C  CAAAC
                                CCCCACCTC TC    GGTC
                                ||||||||| ||    ||||
                                GGGGTGGAG AG    CCAG
                                      _ ACT__
GAM811  TMEPAI   3'  CCCTCATGCTCTCCTCTGGTC  33596    _ C___     CAAAC
                                CCC CA    CTCCTC    GGTC
                                ||| ||    ||||||    ||||
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                                GGG GT   GAGGAG    CCAG
                                  A  ACGA     A____
GAM811  USP7    5'  CCTCCTCCTCCTCCCGCGCGTC 18451    _ A       AAA  _
                                CC CC CCTCCTCC   CG GTC
                                || || ||||||||   || |||
                                GG GG GGAGGAGG   GC CAG
                                 A  A       GC_  G
GAM811  VAT1    3'  CCTCCACCTCCCATTGCAATGG 26847    _       CCA__  C
          T                      CC CCACCTCCT     AA GGT
                                || |||||||||     || |||
                                GG GGTGGAGGG     TT CCA
                                 A        TAACG  A
GAM811  VEGF    5'  CCTCCCCCTCCTCCGGC     17950    _  A       AAAC
                                CC CCC CCTCCTCC    GGT
                                || ||| ||||||||    |||
                                GG GGG GGAGGAGG    CCG
                                 A  _       _____
GAM811  ZNF219  5'  CCCCCGCCCCCTCCCCGGTC  32315       A       AAA
                                CCCCC CCTCCTCC   CGGTC
                                ||||| ||||||||   |||||
                                GGGGG GGGGGAGG   GCCAG
                                   C       G__
GAM811  CST2    3'  GGGTGGGAGTAGGAGGTGGTCA 10621     _    C     AGAC
                                GGG GGGAG AGGGGG    GGTCA
                                ||| ||||| ||||||    |||||
                                CCC CCCTC TCCTCC    CCAGT
                                  A    A     A___
GAM811  GPR86   3'  GGGTGGGGCAGGGGGATAGGGG 35795     _  A       GAC_
          T                      GGG GGG GCAGGGGGA    GGT
                                ||| ||| |||||||||    |||
                                CCC CCC CGTCCCCCT    CCA
                                  A  _        ATCC
GAM811  JUND    3'  AGGGGAGGGGGGGGACGGTC    23796        CA    A
                                GGGGGAG  GGGGG GACGGTC
                                |||||||  ||||| |||||||
                                TCCCCTC  CCCCC CTGCCAG
                                     __    _
GAM811  KPNB1   5'  GGTGGGGTGGGGGGCGGGGGTC 13976    _   AGCA    AGAC
          A                      GG GGGG    GGGGG    GGTCA
                                || ||||    |||||    |||||
                                CC CCCC    CCCCC    CCAGT
                                 A    AC__     GCCC
GAM811  MAP4    5'  GGGGCGCAGGGAGGCGGTC    36274      A       AGA
                                GGGG GCAGGGGG   CGGTC
                                |||| ||||||||   |||||
                                CCCC CGTCCCTC   GCCAG
                                  G       C__
GAM811  MMP14   3'  GGAGGGAGGGAGGCGGTC    22638        CA    AGA
                                GGGGGGAG  GGGGG   CGGTC
                                |||||||  |||||   |||||
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                              CCTCCCTC  CCTCC   GCCAG
                                 __    ___
GAM811  MPHOSPH1  3'  AGGGGGAGGTGGGGATGGT   32112       CAG    GAC
                              GGGGGGAG   GGGGA   GGT
                              ||||||||   |||||   |||
                              TCCCCCTC   CCCCT   CCA
                                  CA_    A__
GAM811  OBP2A     3'  GGTGGGAGCAGGGAAGGGTCA 31042    G        G  AC
                              GG GGGAGCAGGGG AG  GGTCA
                              || ||||||||||| ||  |||||
                              CC CCCTCGTCCCT TC  CCAGT
                               A         _ __
GAM811  OBP2B     3'  GGTGGGAGCAGGGAAGGGTCA 31037    G        G  AC
                              GG GGGAGCAGGGG AG  GGTCA
                              || ||||||||||| ||  |||||
                              CC CCCTCGTCCCT TC  CCAGT
                               A         _ __
GAM811  PDE4A     3'  GGGGGGCGGGGGGGGT      26273      A  A    AGAC
                              GGGGG GC GGGGG    GGT
                              ||||| || |||||    |||
                              CCCCC CG CCCCC    CCA
                                _ _    _____
GAM811  RAD23B    5'  GGGGGTGGGGGGCTTGTCA    16140      AGCA    AGACG
                              GGGGG    GGGGG    GTCA
                              |||||    |||||    ||||
                              CCCCC    CCCCC    CAGT
                                 A____    GAA__
GAM811  SMCX      3'  GGAGGGAGGACTGAGGTGGT   20073       CAG_   AGAC
                              GGGGGGGAG   GGGG   GGT
                              ||||||||   ||||   |||
                              CCTCCCTC   CTCC   CCA
                                  CTGA   A___
GAM811  TBL1X     3'  GGGGGGAATGAAAAGGCGGTC  24894       GCAG GG   A
                              GGGGGGA   G  GAG CGGTC
                              |||||||   |  ||| |||||
                              CCCCCCT   C  TTC GCCAG
                                  TA__ TT   C
GAM811  TNFRSF11A 3'  GGGGGGAGTCGGGGGGAGG   19276       CA    A  C
                              GGGGGGAG  GGGGG GA GG
                              ||||||||  ||||| || ||
                              CCCCCCTC  CCCCC CT CC
                                  AG    _ _
GAM811  VAT1      3'  GGGAGGGGCAGGGGAGAGCGGT 26849      A     _  A
          CA                    GGGGGG GCAGGGG GAG CGGTCA
                              |||||| ||||||| ||| ||||||
                              CCCTCC CGTCCCC CTC GCCAGT
                                 C      T  _
GAM811  WT1       5'  GGGGGAGCGGACAGGCGGTC  35966       AG   G  A
                              GGGGGAGC  GGG AG CGGTC
                              ||||||||  ||| || |||||
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                                CCCCCTCG  CCT TC GCCAG
                                    __   G  C
GAM811  YWHAE    3'  GGGAGGAGGGGGTGGT      27596        GCA    AGAC
                                GGGGGGA  GGGGG   GGT
                                |||||||  |||||   |||
                                CCCTCCT  CCCCC   CCA
                                   ___    A___
GAM812  ATP2B4   5'  TGTCACGATGATTGGTGTC   43205    C       CGA
                                TG CATGATGAT  TGTC
                                || |||||||||  ||||
                                AC GTGCTACTA  ACAG
                                 A        ACC
GAM812  REV3L    5'  TGCCATGATGATGATGTCAC   16270           C
                                TGCCATGATGAT GATGTCAT
                                |||||||||||| ||||||||
                                ACGGTACTACTA CTACAGTG

                                          _
GAM812  ZNF157   3'  TGCCCTGGTGATCATATG    18355      A  A    _
                                TGCC TG TGATCG ATG
                                |||| || |||||| |||
                                ACGG AC ACTAGT TAC
                                  G  C     A
GAM812  DUT      3'  GTTCCAGAAGCACTCCATGT   12624    C   A  TT
                                GT CCA GA  TGCTCCATGT
                                || ||| ||  ||||||||||
                                CA GGT CT  GTGAGGTACA
                                 A  _  TC
GAM812  EMX2     3'  GTCTCTTTTGCTCCATG     44696     CCAAGA
                                GTC     TTTGCTCCATG
                                |||     ||||||||||
                                CAG     AAACGAGGTAC
                                  AGA___
GAM812  GPLD1    3'  TACTCCCAGGAGCCCCATG   45115     G    A  TTT
                                TAC TCCCA GA   GCTCCATG
                                ||| ||||| ||   ||||||||
                                ATG AGGGT CT   CGGGGTAC
                                  _     C  ___
GAM813  CPSF6    3'  CTTTTTAAATCACACAGG    28133      CATT   A
                                CTTTT    AAT CACACAGG
                                |||||    ||| ||||||||
                                GAAAA    TTA GTGTGTCC
                                   AT__   _
GAM813  CRK      3'  CCCTTCTGATACACACAG    40826       CATTA
                                CCTTTT    ATACACACAG
                                ||||||    ||||||||||
                                GGGAAG    TATGTGTGTC
                                   AC___
GAM813  CYLN2    3'  TTTCCACCACGCACAGG     18075        TAA   A
                                TTTTCAT   TAC CACAGG
                                |||||||   ||| ||||||
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                                AAAGGTG   GTG GTGTCC
                                   ___  C
GAM813  D1S155E  3'  TTTTCACTTACACAG      28394        AATAC
                                TTTTCATT    ACACAG
                                ||||||||    ||||||
                                AAAAGTGA    TGTGTC
                                   A____
GAM813  MAX      3'  TTTCTTAGAAATACACACGGG  40367     ATT__       A
                                TTTC    AATACACAC GG
                                ||||    ||||||||| ||
                                AAAG    TTATGTGTG CC
                                  AATCT       C
GAM813  TOMM22   3'  CTTTTTTTAAACACACACACAG 33675      CATTA__
           G                     CTTTT      ATACACACAGG
                                |||||      ||||||||||
                                GAAAA      TGTGTGTGTCC
                                   AAATTTG
GAM814  ACVR1    3'  CTGCAGTGTGAACAGTTC    9960       C   AG
                                CTGCAG GTGA  GCAGTTT
                                |||||| ||||  |||||||
                                GACGTC CACT  TGTCAAG
                                   A   __
GAM814  ATP6V0D1 3'  CCTTAGAGAGGGCAGTTT    21723     GC  CGT  A
                                CCT  AG   GA GGCAGTTT
                                |||  ||   || ||||||||
                                GGA  TC   CT CCGTCAAA
                                  A_  T__  C
GAM814  BRCA1    3'  CTGAGCATGGCAGTTT      28629     C    GAA
                                CTG AGCGT   GGCAGTTT
                                ||| |||||   ||||||||
                                GAC TCGTA   CCGTCAAA
                                  _    ____
GAM814  CDH5     3'  CCCTTGCAGTGTGAGGGGC   12185     C    C   A_
                                CCC TGCAG GTGA  GGC
                                ||| ||||| ||||  |||
                                GGG ACGTC CACT  CCG
                                  A    A   CC
GAM814  HMGA2    3'  CCCCTGTGTTTACAGCAGTTT  18504       CAGC  GAA_
                                CCCCTG   GT   GGCAGTTT
                                ||||||   ||   ||||||||
                                GGGGAC   CA   TCGTCAAA
                                   A___  AATG
GAM814  HTRA3    3'  CTCCATGGAAGGCAGTTT    44829    G  GCGT
                                CT CA    GAAGGCAGTTT
                                || ||    ||||||||||
                                GA GT    CTTCCGTCAAA
                                 G  AC__
GAM814  MAP3K11  3'  CCCTTCCAGTGTGAAGGC    14531     G_   C
                                CCCT  CAG GTGAAGGC
                                ||||  ||| ||||||||
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                                GGGA  GTC CACTTCCG
                                  AG   A
GAM814  NKX3A   3'  CCCTGGGGAAGGCAGTTT   26111      CAGCGT
                                CCCTG     GAAGGCAGTTT
                                |||||     ||||||||||
                                GGGAC     CTTCCGTCAAA
                                  CC_____
GAM814  NPAS1   5'  CCTGCAGCGGGAGGGGGC   40871        T  A__
                                CCTGCAGCG GA   GGC
                                ||||||||| ||   |||
                                GGACGTCGC CT   CCG
                                     C  CCC
GAM814  PLAUR   5'  CCTCAGGAAGGAGGCAGTTT  15369     G   CGTGA
                                CCT CAG    AGGCAGTTT
                                ||| |||    |||||||||
                                GGA GTC    TCCGTCAAA
                                  _  CTTCC
GAM814  SEZ6L   5'  CTGCTTGAGCGAAGGCAGTTTC 34421     AGC_
                                CTGC   GTGAAGGCAGTTTC
                                ||||   ||||||||||||||
                                GACG   CGCTTCCGTCAAAG
                                  AACT
GAM814  SNX13   3'  TGCTTGAGATGGGGGCAGTTT  31535     ___  C   AA
                                TGC   AG GTG  GGCAGTTT
                                |||   || |||  ||||||||
                                ACG   TC TAC  CCGTCAAA
                                  AAC  _   CC
GAM814  STXBP1  3'  CTTCAGTGTGTCCAGCAGTTTC 17207    G   C   AA_
                                CT CAG GTG   GGCAGTTTC
                                || ||| |||   |||||||||
                                GA GTC CAC   TCGTCAAAG
                                 A   A   AGG
GAM814  TP73    3'  CCTGCCTCCTGAGGCAGTTT   24068      AGCG   A
                                CCTGC    TGA GGCAGTTT
                                |||||    ||| ||||||||
                                GGACG    ACT CCGTCAAA
                                  GAGG   _
GAM814  ZNF137  3'  CCTGGGAGTAATAGGCAGTTT  18336     CAGC   _
                                CCTG    GTGA AGGCAGTTT
                                ||||    |||| |||||||||
                                GGAC    CATT TCCGTCAAA
                                  CCT_    A
GAM814  ZNF76   3'  CCCTTCAGTTAGGCAGTTT   18305     G   CGTGA
                                CCCT CAG    AGGCAGTTT
                                |||| |||    |||||||||
                                GGGA GTC    TCCGTCAAA
                                  A   AA___
GAM814  FGF12   3'  TCGCAGCATTATCATGAG    34299       A___
                                TCGCAGCA    TATGGG
                                ||||||||    ||||||
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                                AGCGTCGT   GTACTC
                                    AATA
GAM814  GLP1R   3'  TCACAGCAATAAAGAAAA   13142          T
                                TCGCAGCAATA GGGAAA
                                |||||||||| ||||||
                                AGTGTCGTTAT TCTTTT
                                      T
GAM814  PART1   3'  GCACAGGCTGAAGAAAATAAAT 32460    G  ATA  _
                                GCA CA   TGG GAAAATAAAT
                                ||| ||   ||| ||||||||||
                                CGT GT   ACT CTTTTATTTA
                                  _ CCG   T
GAM814  SUV39H2 3'  TCATAGCAATATAATGAA   36020    C       _
                                TCG AGCAATATGG GAA
                                ||| |||||||||| |||
                                AGT TCGTTATATT CTT
                                  A        A
GAM814  TPT     3'  GCAATAAAAAAAAATAAAT   41283       TG
                                GCAATA  GGAAAATAAAT
                                ||||||  ||||||||||
                                CGTTAT  TTTTTTATTTA
                                    TT
GAM815  ARHGEF7 5'  TCCGGGGCTCGGGGTAGACCTG 19369      T  C  TC
                                TCCGG GC TG  GTAGACCTG
                                ||||| || ||  |||||||||
                                AGGCC CG GC  CATCTGGAC
                                   C  A  CC
GAM815  GHR     3'  GGTGCCTGGTAAGTTGATCTG  6714        TC__  A  C
                                GGTGCCTG   GT GA CTG
                                ||||||||   || || |||
                                CCACGGAC   CA CT GAC
                                     CATT  A  A
GAM815  KCNK6   3'  GGTGCCTGAAATGAGGTCTG   22083        TC  _  AC
                                GGTGCCTG  GT AG  CTG
                                ||||||||  || ||  |||
                                CCACGGAC  TA TC  GAC
                                     TT  C  CA
GAM815  MGAT4B  5'  CCTGGTGCCTGTGTCTCTG   38266   _      C  AGAC
                                CC GGTGCCTGT GT   CTG
                                || |||||||| ||   |||
                                GG CCACGGACA CA   GAC
                                 A       _  GA__
GAM815  NEBL    3'  CGGTTTTGTCATAGCTG    26900     GCC      AC
                                CGGT  TGTCGTAG  CTG
                                ||||  ||||||||  |||
                                GCCA  ACAGTATC  GAC
                                  AA_       __
GAM815  UBE2L3  3'  CGGGGCCACCACAGACCTG   17825    T  TGT
                                CGG GCC  CGTAGACCTG
                                ||| |||  ||||||||||
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                                GCC CGG   GTGTCTGGAC
                                  C   TG_
GAM815  UBTF     3'  TCCGGTGCTGGCTTAGTCTG  30618        C  TCG   AC
                                TCCGGTGC TG   TAG  CTG
                                |||||||| ||   |||  |||
                                AGGCCACG AC   ATC  GAC
                                     _  CGA   A_
GAM815  USP6     5'  TCCTGTGCCTGCAAAC     45032     G      CGT
                                TCC GTGCCTGT   AGAC
                                ||| ||||||||   ||||
                                AGG CACGGACG   TTTG
                                  A       ___
GAM815  WEE1     5'  TCCGGTGCTGGGGGATCTG   18100        C  TCGTA  C
                                TCCGGTGC TG    GA CTG
                                |||||||| ||    || |||
                                AGGCCACG AC    CT GAC
                                     _  CCC__  A
GAM815  ZNF278   3'  GGTTCCTGAGCAGACCTG    36806     G    TC
                                GGT CCTG  GTAGACCTG
                                ||| ||||  |||||||||
                                CCA GGAC  CGTCTGGAC
                                  A   T_
GAM816  LAMA3    3'  GTGCATTGGGTAATCAGTGCTT 6904          AGA__    A
           T                     GTGCATTGG    TAGT GCTTT
                                |||||||||    |||| |||||
                                CACGTAACC    GTCA CGAAA
                                     CATTA   _
GAM816  HD       3'  TCCGTAGGCAGGTCCACGT    13361     A      CA    G
                                TCC TAGGCAGG  TCCG CGT
                                ||| ||||||||  |||| |||
                                AGG ATCCGTCC  AGGT GCA
                                  C       __   _
GAM816  SIRPB2   3'  CCTGTGGGCAGGCAGATGTC   38897    ATA_      TCC GC
                                CC   GGCAGGCA  G  GTC
                                ||   ||||||||  |  |||
                                GG   CCGTCCGT  C  CAG
                                 ACAC       ___ TA
GAM816  TMEM5    5'  TCCGAGGCAGGCCCAGC     30672     AT      AT
                                TCC  AGGCAGGC  CCGGC
                                |||  ||||||||  |||||
                                AGG  TCCGTCCG  GGTCG
                                  C_       __
GAM817  IRS1     3'  GCAGACTCATTATTCTGGT    24422         __    C
                                GTAGATTT  TATTC GGT
                                ||||||||  ||||| |||
                                CGTCTGAG  ATAAG CCA
                                     TA    A
GAM817  PHB      3'  TTTCACAGTGATTTCTGGGGT  15266         A     ATTCC
                                TTTCACAGT GATTTT    GGT
                                ||||||||| ||||||    |||
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                                AAAGTGTCA CTAAAG    CCA
                                     _     ACC__
GAM817  C4orf1   3'  TGCCTGTAAAATTATAAA    40493          __
                                TGCCTGTAAAA  ATAAA
                                |||||||||||  |||||
                                ACGGACATTTT  TATTT
                                      AA
GAM817  CDK2     3'  TGCCTGTAGAAGGGACAAACA  12206        A ___
                                TGCCTGTA AA   ATAAACA
                                |||||||| ||   |||||||
                                ACGGACAT TT   TGTTTGT
                                     C  CCC
GAM817  CPSF6    3'  CTGATAAACATCAAC      28132     TAAAA
                                CTG    ATAAACATCAAC
                                |||    ||||||||||||
                                GAC    TATTTGTAGTTG
                                 ______
GAM817  CX3CR1   3'  TGCCTGTAAGAAATAACAACA  43299         _     ACAT
                                TGCCTGTAA AAATAA    CAACA
                                |||||||||| ||||||   |||||
                                ACGGACATT TTTATT    GTTGT
                                     C    _____
GAM817  ETV1     3'  TAAAAATAAATATCAACA    22420          C
                                TAAAAATAAA ATCAACA
                                |||||||||| |||||||
                                ATTTTTATTT TAGTTGT
                                      A
GAM817  FOXO1A   3'  TGTCTGTAAGTACATCAACA   12895    C     AAATAA
                                TG CTGTAA     ACATCAACA
                                || ||||||     |||||||||
                                AC GACATT     TGTAGTTGT
                                 A     CA____
GAM817  IL20RA   3'  TGCCTGTACCAATAATATCAA  30881        AA    AC
                                TGCCTGTA  AATAA  ATCAA
                                ||||||||  |||||  |||||
                                ACGGACAT  TTATT  TAGTT
                                     GG    A_
GAM817  PIGH     3'  TGCTTCACAAACATCAACA   21304     AAAA
                                TGT    ATAAACATCAACA
                                |||    ||||||||||||||
                                ACG    TGTTTGTAGTTGT
                                  AAG_
GAM817  PPARBP   3'  TGCCTATAAACTTATCAA    21934         AATAAAC
                                TGCCTGTAAA      ATCAA
                                ||||||||||      |||||
                                ACGGATATTT      TAGTT
                                      GAA_____
GAM818  COLQ     3'  CTTGAGGTCTGCTGTGGGGGTG 38700         ATAC   TTA_
                                CTTGAGGTC    GTT    GGGTG
                                |||||||||    |||    |||||
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                                GAACTCCAG   CGA   CCCAC
                                     A___   CACC
GAM818  TLX1    5'  TTGGGGTCTGCTGCCAGGGTG  24353    A   ATAC  _
                                TTG GGTC   GTT TTAGGGTG
                                ||| ||||   ||| ||||||||
                                AAC CCAG   CGA GGTCCCAC
                                  C   A___   C
GAM818  CA11    5'  CCTCTCCGTTCTCTTTTCATTA 10237   _  TA   CTCTTG
                                CC CTC  TTCTC     CGTTA
                                || |||  |||||     |||||
                                GG GAG  AAGAG     GTAAT
                                 A  GC    AAAA__
GAM818  CKTSF1B1 3'  CCTCTGTTCACTTGGGTT   30084      A   TCCT   C
                                CCTCT TTC   CTTG GTT
                                ||||| |||   |||| |||
                                GGAGA AAG   GAAC CAA
                                   C   T___   C
GAM818  DLG4    5'  CCCTCCCTTTTGTGTT     10704      TATTCT   C   C
                                CCCTC     CCT TTG GTT
                                |||||     ||| ||| |||
                                GGGAG     GGA AAC CAA
                                   _______  A   A
GAM818  EBP     3'  CCCCTTTATTCCCCTTCTTG   27307      C       _
                                CCCCT TATTCTCCT CTTG
                                ||||| ||||||||| ||||
                                GGGGA ATAAGGGGA GAAC
                                   A        A
GAM818  ELK3    5'  CCTCTTTTTTTTTCCCCTCT   23419      A_____
                                CCTCT     TTCTCCTCT
                                |||||     |||||||||
                                GGAGA     AAGGGGAGA
                                   AAAAAA
GAM818  FOXE3    5'  CCCCTCTAATTTCCTCTCCCA  29142        TTC      G
                                CCCCTCTA   TCCTCTT CG
                                ||||||||   ||||||| ||
                                GGGGAGAT   AGGAGAG GT
                                     TAA      G
GAM818  GNG2    5'  CCCTCTGTCTCTCCTGC     45437       AT   C
                                CCCTCT  TCTC TCTTGC
                                ||||||  |||| ||||||
                                GGGAGA  AGAG AGGACG
                                   C_   _
GAM818  GRIA1    5'  CCCTTTATTCTTTTCGC     9086       C     CCTC
                                CCCT TATTCT    TTGC
                                |||| ||||||    ||||
                                GGGA ATAAGA    AGCG
                                  A     AA__
GAM818  HTN1    3'  TATTCTCCATTGCCTTA     13464        TC   G
                                TATTCTCC  TTGC TTA
                                ||||||||  |||| |||
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                                ATAAGAGG  AACG AAT
                                    T_   G
GAM818  PCDH7   3' CCCCTTATTCTCCTTTTCAT  37112      C       C  G
                                CCCCT TATTCTCCT TT CGT
                                ||||| ||||||||| || |||
                                GGGGA ATAAGAGGA AA GTA
                                  _       A  _
GAM818  PRAME   3' CCCCTTTTTTTCCTCACTG   25919      CTA  C    _
                                CCCCT   TT TCCTC TTG
                                |||||   || ||||| |||
                                GGGGA   AA AGGAG GAC
                                  AA_  A    T
GAM818  RAB13   3' CCTCATTCTCTTTAC      16113      T     CTC
                                CCTC ATTCTC   TTGC
                                |||| ||||||   ||||
                                GGAG TAAGAG   AATG
                                  _     A__
GAM818  RAP1A   5' TCTTTGCTCTTCTCGCGT    16154     ATT   C
                                TCT   CTC TCTTGCGT
                                |||   ||| ||||||||
                                AGA   GAG AGAGCGCA
                                  AAC   A
GAM818  SLC4A4  5' CTCTATTCCTTTGGTT      19063       TC    C   C
                                CTCTAT  TCCT TTG GTT
                                ||||||  |||| ||| |||
                                GAGATA  AGGA AAC CAA
                                   __   _  _
GAM818  SOX9    5' CCCTTCTCTTCTCCTCCTG   7373     C   A
                                CCC TCT TTCTCCTCTTG
                                ||| ||| ||||||||||
                                GGG AGA AAGAGGAGGAC
                                  A   G
GAM818  TGFBR1  3' CCTTCTGTTCCCTCTCAGT   21434    C   A   T     C
                                CC TCT TTC CCTCTTG GT
                                || ||| ||| ||||||| ||
                                GG AGA AAG GGAGAGT CA
                                 A   C   _      _
GAM818  UPF3B   3' CTCTATTCTTTGCCCT      35692         CCTC    G
                                CTCTATTCT    TTGC TT
                                |||||||||    |||| ||
                                GAGATAAGA    AACG GA
                                     _____    G
GAM818  WDR4    5' CCCCTTTATTTTCTTG      38018      C    CTCC
                                CCCCT TATT    TCTTG
                                ||||| ||||    |||||
                                GGGGA ATAA    AGAAC
                                  A    A___
GAM819  CCNF    3' AGAGTAAACAGAAGTGGAT   12069          TTGAC
                                AGAGTAAACA    GGAT
                                ||||||||||    ||||
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                                TCTCATTTGT    CCTA
                                      CTTCA
GAM819  PLA2G1B  3' GGAGAGTACAGTGTGAGAT   9576       AA  T  AC
                                GGAGAGT  ACA TG  GGAT
                                |||||||  ||| ||  ||||
                                CCTCTCA  TGT AC  TCTA
                                   __  C  AC
GAM819  COL1A1   3' CATAACCCAACGGGCA     6366       T  CAT
                                CATAACTC AC   GGCA
                                |||||||| ||   ||||
                                GTATTGGG TG   CCGT
                                     T  C__
GAM819  EMP1     3' CATAACCCTAACATGGCA    10891        C
                                CATAACTCTA CATGGCA
                                |||||||||| |||||||
                                GTATTGGGAT GTACCGT
                                      T
GAM819  EPHA8    3' ATAACTCCAGGTCCTGTGGC  33891        ___ A_
                                ATAACTCTA   CC  TGGC
                                |||||||||   ||  ||||
                                TATTGAGGT   GG  ACCG
                                     CCA  AC
GAM819  G22P1    3' CACCATCACCATGGCA     11173    AAC  T
                                CAT   TC ACCATGGCA
                                |||   || |||||||||
                                GTG   AG TGGTACCGT
                                  GT_  _
GAM819  HEM1     3' CACAGCTTCCACTATGGCA   23737    A  _   C
                                CATA CT CTAC ATGGCA
                                ||||  ||  ||||  ||||||
                                GTGT GA GGTG TACCGT
                                   C  A   A
GAM819  LMO1     5' CATAACCCTGTCTCTGGCA   14179        ACCA_
                                CATAACTCT    TGGCA
                                |||||||||    |||||
                                GTATTGGGA    ACCGT
                                     CAGAG
GAM819  MBP      3' CACAACTCCGCAGGCA      14376        AC  T
                                CATAACTCT  CA GGCA
                                |||||||||  ||  ||||
                                GTGTTGAGG  GT CCGT
                                     C_  _
GAM819  MME      5' CATAACTCCCCAAGGCA     28598        A   T
                                CATAACTCT CCA GGCA
                                ||||||||| |||  ||||
                                GTATTGAGG GGT CCGT
                                     _  T
GAM819  PRKAR2A  3' CATAACCACAGCAATGGCA   20006       C  C  _
                                CATAACT TA CA TGGCA
                                |||||||  ||  ||  |||||
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                                GTATTGG GT GT ACCGT
                                    T  C  T
GAM819  SHANK2   3'  CACAACTCTCACAGGGCA    29450        AC  T
                                CATAACTCT  CA GGCA
                                |||||||||  || ||||
                                GTGTTGAGA  GT CCGT
                                     GT  C
GAM819  SLC25A15 3'  CATAATAGCTCCATGGCA    30665      CT_  A
                                CATAA   CT CCATGGCA
                                |||||   || ||||||||
                                GTATT   GA GGTACCGT
                                   ATC  _
GAM819  YES1     3'  CATATACGCCATGGCA      24117      _  TCTA
                                CATA AC    CCATGGCA
                                |||| ||    ||||||||
                                GTAT TG    GGTACCGT
                                  A  C___
GAM820  NT5C3    3'  TGTAATGATTAGCAACATTGT  32412      A   AAACAT
                                TGTAA GAT     CAACATTGT
                                ||||| |||     |||||||||
                                ACATT CTA     GTTGTAACA
                                   A   ATC___
GAM821  CDH6     3'  TACCGTTTAATTTGCTTC    22330          C   C
                                TGCCGTTTAAT TGC TC
                                |||||||||||| ||| ||
                                ATGGCAAATTA ACG AG
                                      A   A
GAM822  ACAA1    3'  CTTTTGTGGTGTTACTGCC    11493      GA  AC_
                                CTTT  TG   TTACTGCC
                                ||||  ||   ||||||||
                                GAAA  AC   AATGACGG
                                  AC  CAC
GAM822  AF1Q     3'  TTTGTGTTTACTGCCCTG     27731      A  AC
                                TTTG TG  TTACTGCCCTG
                                |||| ||  ||||||||||
                                AAAC AC  AATGACGGGAC
                                  _  A_
GAM822  C14orf1  3'  CCCTTGGTCACAGCTGCTCTG  28411       ATG  TTA   C
                                CCTTTG   AC   CTGC CTG
                                ||||||   ||   |||| |||
                                GGGAAC   TG   GACG GAC
                                   CAG  TC_   A
GAM822  JAG1     3'  CTTGTTCCCTTACTGCTCTG   6853       ATGA      C
                                TTTG    CTTACTGC CTG
                                ||||    |||||||| |||
                                GAAC    GAATGACG GAC
                                  AAGG       A
GAM822  MEN1     5'  ACCCTCTGAAACAGGCTGTCT  39246          T   TTA   CC
                                ACCCTTTGA GAC   CTG  CT
                                |||||||| |||   |||  ||
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                                TGGGAGACT TTG  GAC  GA
                                     _  TCC  A_
GAM822  NHP2L1   3' CTTTGGTATGCTGCTGCCCTG  22678     __  A  TA
                                CTTTG  ATG CT  CTGCCCTG
                                |||||  ||| ||  ||||||||
                                GAAAC  TAC GA  GACGGGAC
                                   CA  _ C_
GAM822  PTGFRN   3' CCCTTCTTACTGCCCT     42588      TGATGA
                                CCCTT     CTTACTGCCCT
                                |||||     ||||||||||
                                GGGAA     GAATGACGGGA
                                     _____
GAM822  ZNF10    5' CTTGATGATACTTCCT      31735        CT   GC
                                TTTGATGA  TACT  CCT
                                ||||||||  ||||  |||
                                GAACTACT  ATGA  GGA
                                     __   A_
GAM822  AKAP2    5' TAGAACCCGGGAGAACGCCCAG 28500       ACTCCCTC
                                TAGAAC       ACGCCCAG
                                ||||||       ||||||||
                                ATCTTG       TGCGGGTC
                                   GGCCCTCT
GAM822  ARHGEF7  3' TAGAACACTTGTTCTACG    19367         CCC  _
                                TAGAACACT   TC ACG
                                |||||||||   || |||
                                ATCTTGTGA   AG TGC
                                     ACA  A
GAM822  CCNDBP1  3' TAGGCACTCCCTTTCAATCCAG 29103     AA      CA  C_
                                TAG  CACTCCCT  CG  CCAG
                                |||  ||||||||  ||  ||||
                                ATC  GTGAGGGA  GT  GGTC
                                  C_       AA  TA
GAM822  CEP2     3' CAGGACACTCCCCGTCCAG   28433     A      TCA  C
                                TAG ACACTCCC   CG CCAG
                                ||| ||||||||   || ||||
                                GTC TGTGAGGG   GC GGTC
                                  C       ___  A
GAM822  CMKLR1   5' GAACACCCCTATCACCC     19827       T   CA
                                GAACAC CCCT  CGCCC
                                |||||| ||||  |||||
                                CTTGTG GGGA  GTGGG
                                   _   TA
GAM822  ENC1     3' TAGAACACATCTAGGAACCAG  18864        TCC  CACGC
                                TAGAACAC  CT    CCAG
                                ||||||||  ||    ||||
                                ATCTTGTG  GA    GGTC
                                     TA_  TCCTT
GAM822  MB       3' AGGGCACTCCCGGTTCCCAG  23855    AA     TCACG
                                AG  CACTCCC    CCCAG
                                ||  |||||||    |||||
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                                TC  GTGAGGG    GGGTC
                                 CC      CCAA_
GAM822  MPO     3'  AAACACTCCCCATGTTCAG   6998          T  CGCC
                                GAACACTCCC CA    CAG
                                |||||||||| ||    |||
                                TTTGTGAGGG GT    GTC
                                      _  ACAA
GAM822  PRKY    3'  AGAACACTCTCACGCC      15682         CC
                                AGAACACTC  TCACGCC
                                |||||||||  |||||||
                                TCTTGTGAG  AGTGCGG
                                      __
GAM822  RGS16   3'  TAGAACACTTCCTTCTCC    16325         C   CACG
                                TAGAACACT CCT    CC
                                ||||||||| |||    ||
                                ATCTTGTGA GGA    GG
                                      A   AGA_
GAM822  SCN2A2  5'  TAGAATCTTTTACACCCAG   34244       CAC  CCTC
                                TAGAA   TC    ACGCCCAG
                                |||||   ||    ||||||||
                                ATCTT   AG    TGTGGGTC
                                   ___  AAAA
GAM822  TEM8    3'  TAGAACACTCCATTCCCACA  38191           ___
                                TAGAACACTCC   CTCACG
                                ||||||||||   ||||||
                                ATCTTGTGAGG   GGGTGT
                                      TAA
GAM823  BRCA1   3'  TGGACACCTGTGCCAAG     28653          CG
                                TGGACACTTG  GTTAGG
                                ||||||||||  ||||||
                                ACCTGTGGAC  CGGTTC
                                      A_
GAM823  CUL3    3'  GGATGGAATGGTTAGGA     18739   A    CACTTGC
                                A ATGGA      GGTTAGGA
                                | |||||      ||||||||
                                C TACCT      CCAATCCT
                                 C    TA_____
GAM823  ITGA3   3'  AAATGGGCCTTAGGA       13605       ACACTT  GG
                                AAATGG     GC  TTAGGA
                                ||||||     ||  ||||||
                                TTTACC     CG  AATCCT
                                   _______  G_
GAM823  LPIN1   5'  TGGCTGCTGTTAGGAC      42642     ACAC    G
                                TGG    TTGC GTTAGGAC
                                |||    |||| ||||||||
                                ACC    GACG CAATCCTG
                                  _____    A
GAM823  MAK     3'  AAATAGACATTTGTAGAC     25378         C   CGGTTA
                                AAATGGACA TTG     GGAC
                                ||||||||| |||     ||||
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                                TTTATCTGT AAC     TCTG
                                     A  A_____
GAM823  MEF2C    3'  ATGGGCAAGTTAGGA      14406     A  CTTGC
                                ATGG CA    GGTTAGGA
                                |||| ||    ||||||||
                                TACC GT    TCAATCCT
                                  C _____
GAM823  PXR1     3'  TGGACACTCACAGGGC      7235        TG  TTA  A
                                TGGACACT  CGG  GG C
                                ||||||||  |||  || |
                                ACCTGTGA  GTC  CC G
                                     GT  ___ _
GAM823  SRGAP2   3'  GGATGGACACTGATCAAG    43984   A       TGC
                                A ATGGACACT  GGTTAGG
                                | |||||||||  |||||||
                                C TACCTGTGA  CTAGTTC
                                 C       ___
GAM823  TBP      3'  TGGGCACTTACAGAAGGGCA  42113    A       TT  A
                                TGG CACTTGCGG  AGG CA
                                ||| |||||||||  ||| ||
                                ACC GTGAATGTC  TCC GT
                                  C       T_  C
GAM823  ITGAM    3'  CAGCCGCACCGGGGCCATGT  43509      ATA___
                                CGGTCG     GGCCATGT
                                ||||||     ||||||||
                                GTCGGC     CCGGTACA
                                   GTGGCC
GAM823  SCN1A    3'  AGCTGGGAGGGCCATGT     44812    _  TC  TA
                                AGC GG  GA  GGCCATGT
                                ||| ||  ||  ||||||||
                                TCG CC  CT  CCGGTACA
                                  A  __  C_
GAM823  SLC9A3   3'  AGCGGCCGGTTAGCGGCGTGT  20048       ATA___  CA
                                AGCGGTCG     GGC  TGT
                                ||||||||     |||  |||
                                TCGCCGGC     CCG  ACA
                                     CAATCG  C_
GAM823  SULT1C1  3'  GCACTCAGGCCATGT      9840     G  GAT
                                GCG TC   AGGCCATGT
                                ||| ||   |||||||||
                                CGT AG   TCCGGTACA
                                  G  ___
GAM823  THRA     3'  CAAGGGAGTCTGGCCATGT   17517     C  TCGATA
                                CAAG GG     GGCCATGT
                                |||| ||     ||||||||
                                GTTC CC     CCGGTACA
                                  _ TCAGA_
GAM824  S100A10  3'  TTATTTTTACATTTGCTAAGTG 40401        AA____   T
            TCC                   TTATTTTTA     TTAA GTGTCC
                                |||||||||     |||| ||||||
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                                AATAAAAAT     GATT CACAGG
                                      GTAAAC   _
GAM825  ADAM12   3'  TGGCTACACCTTAAGATTCC   18481    A      CCCCA
                                TG GCTACACC    GTTCC
                                || ||||||||    |||||
                                AC CGATGTGG    TAAGG
                                 _      AATTC
GAM825  BRF2     3'  GCCAGAATTCCCCAGTTCCCGC 32898     CACC_
                                GCTA    CCCCAGTTCCCGC
                                ||||    ||||||||||||||
                                CGGT    GGGGTCAAGGGCG
                                  CTTAA
GAM825  CDX2     5'  TGGCTGCGCCCCAGCCCG    10410    A  ACACC     TT
                                TG GCT    CCCCAG  CCCG
                                || |||    ||||||  ||||
                                AC CGA    GGGGTC  GGGC
                                 _  CGC__     __
GAM825  CTSZ     3'  AGCCACCCCAGTTCCG      41609      CACC        C
                                AGCTA   CCCCAGTTCC G
                                |||||   |||||||||| |
                                TCGGT   GGGGTCAAGG C
                                   ____        A
GAM825  DDX3     5'  GAGCTACACTTCCCG       35819         CCCCCAG
                                GAGCTACAC      TTCCCG
                                |||||||||      ||||||
                                CTCGATGTG      AAGGGC
                                              _______
GAM825  EN2      3'  TGGGCACACCCCCTGGCT    10965    A  T      CA
                                TG GC ACACCCCC  GTT
                                || || ||||||||  |||
                                AC CG TGTGGGGG  CGA
                                 C  _       AC
GAM825  GPR17    3'  TGAGCTGAGCTCCCG       23622       ACACCCCCC
                                TGAGCT       AGTTCCCG
                                ||||||       ||||||||
                                ACTCGA       TCGAGGGC
                                   C_________
GAM825  HTRA3    3'  TGGGCTGGACCCCACCCCCGC  44837    A  AC    CCA TT
                                TG GCT  ACCCC   G  CCCGC
                                || |||  |||||   |  |||||
                                AC CGA  TGGGG   T  GGGCG
                                 C   CC     ___ GG
GAM825  PHGDH    5'  TGGGCAGTATTCTCCAGCTCCC 42036    A  TACACCCC
             GC                   TG GC       CCAGTTCCCGC
                                || ||       ||||||||||
                                AC CG       GGTCGAGGGCG
                                 C  TCATAAGA
GAM825  TCP10    5'  TGGGCCGTGTCCCCACAGCT   21430    A  ACAC   _
                                TG GCT    CCCC CAGTT
                                || |||    |||| |||||
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                                AC CGG    GGGG GTCGA
                                 C   CACA    T
GAM825  VGF      3'  TGGGCTGGCCCCCGGTCACCCG 17997    A   ACAC     A   _
              C                   TG GCT    CCCCC GTT CCCGC
                                  || |||    ||||| ||| |||||
                                  AC CGA    GGGGG CAG GGGCG
                                   C   CC__    C   T
GAM826  MEN1     3'  TTAGATCAGATTCTTTTG    39242         T   C
                                  TTAGATCAG TTC TTTG
                                  ||||||||| ||| ||||
                                  AATCTAGTC AAG AAAC
                                        T   A
GAM826  TACC1    3'  TTACATCAGTTTCTTTA     26608     G       C
                                  TTA ATCAGTTTC TTTG
                                  ||| ||||||||| ||||
                                  AAT TAGTCAAAG AAAT
                                    G       _
GAM827  ACTN2    3'  CTCCTACTCTAACTCT      9944          CTAG     CC
                                  CTCCTACTC    TGGCTC  T
                                  |||||||||    ||||||  |
                                  GAGGATGAG    ATTGAG  A
                                               ____     __
GAM827  ARHGAP6  5'  CTCCTCCTCCCTCCCT      30213       A    TAGTGG
                                  CTCCT CTCC     CTCCCT
                                  ||||| ||||     ||||||
                                  GAGGA GAGG     GAGGGA
                                     G   _______
GAM827  ASTN     3'  CCTGCTTCACCCTCTCCCTGG  42945     A  _ _  AGTGG
                                  CCT CT C CT    CTCCCTGG
                                  ||| || | ||    ||||||||
                                  GGA GA G GG    GAGGGACC
                                    C  A T  GA___
GAM827  ATP7B    3'  CTCCTTTTCTGAAGCCCCTGG  6276       AC  CTAGT   T
                                  CTCCT  TC     GGC CCCTGG
                                  |||||  ||     ||| ||||||
                                  GAGGA  AG     TCG GGGACC
                                     AA  ACT__   _
GAM827  AVPR1A   5'  CCTACTCCCCGCTCCCTGG   8725          AGTG
                                  CCTACTCCT    GCTCCCTGG
                                  |||||||||    |||||||||
                                  GGATGAGGG    CGAGGGACC
                                       G___
GAM827  B4GALT5  3'  CTCCCTATTTGAGTGCTCCTTG 21938       ACTCCT   G   C
              G                    CTCCT     AGTG CTCC TGG
                                   |||||     |||| |||| |||
                                   GAGGG     TCAC GAGG ACC
                                     ATAAAC    _    A
GAM827  CA14     3'  CTACTCCTACAGTGTTTCTGG  29057         __    GCTCC
                                  CTACTCCT  AGTG    CTGG
                                  ||||||||  ||||    ||||
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                              GATGAGGA TCAC    GACC
                                  TG   AAA__
GAM827  CAPZA1   5' CTACTCCTACAAGTTTTTCTGG 43713        GT CTCC_
                              CTACTCCTA GG    CTGG
                              |||||||||  ||    ||||
                              GATGAGGAT TC    GACC
                                   GT AAAAA
GAM827  CHRNB4   3' CTCCTACTGGGGCTTCCTGG 8870        CCTAGT   C
                              CTCCTACT    GGCT CCTGG
                              ||||||||    |||| |||||
                              GAGGATGA    CCGA GGACC
                                  CC____   A
GAM827  CLECSF5  3' TCCTACTCTTCGTCGGCT   29929       CTA _
                              TCCTACTC  GT GGCT
                              ||||||||  || ||||
                              AGGATGAG  CA CCGA
                                  AAG G
GAM827  DGUOK    3' TCCTTTCTCCTCCTCCCTGG 38964     A_   AGTGG
                              TCCT CTCCT   CTCCCTGG
                              ||||  |||||   ||||||||
                              AGGA GAGGA   GAGGGACC
                                AA   G____
GAM827  DTNB     3' CTCTGGCTCCCCTCTCCCTGG 37602    CTA   AGTGG
                              CTC  CTCCT   CTCCCTGG
                              |||  |||||   ||||||||
                              GAG  GAGGG   GAGGGACC
                                ACC   GA___
GAM827  FGF2     5' CCCCTACTCGCTCGGGTTTTCT 12833       _ AGT CTCC
           GG                   CTCCTACTC CT  GG   CTGG
                              |||||||||  ||  ||   ||||
                              GGGGATGAG GA  CC   GACC
                                   C GC_ AAAA
GAM827  FZD7     3' CCTACTCCACGTCTCCTTGG  18630       TAGTGG   C
                              CCTACTCC    CTCC TGG
                              ||||||||    |||| |||
                              GGATGAGG    GAGG ACC
                                  TGCA__   A
GAM827  HNRPD    5' CTCCTGCGCCTCTCCCTG    36391     A_ GG
                              CTCCT  GT  CTCCCTG
                              |||||  ||  |||||||
                              GAGGA  CG  GAGGGAC
                                 CG  GA
GAM827  KLK3     3' CTTTTCCTAGCAACCCTGG   11613   AC    TG CT
                              CT  TCCTAG  G  CCCTGG
                              ||  ||||||  |  ||||||
                              GA  AGGATC  T  GGGACC
                               AA    GT __
GAM827  MNAT1    3' TACTTTTGCTAGCTCCCTGG  14602     CCTAG
                              TACT    TGGCTCCCTGG
                              ||||    ||||||||||
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                                ATGA    ATCGAGGGACC
                                  AAACG
GAM827  MYOG    3'  CCCCTGCTTTACCTCCCTG   40422      AG__  G
                                CTCCT   TG CTCCCTG
                                |||||   || |||||||
                                GGGGA   AT GAGGGAC
                                  CGAA  G
GAM827  OGDH    3'  TCCTATCCTAGTGGGTGAGACT 45017      C       CTCC__
          GG                      TCCTA TCCTAGTGG     CTGG
                                |||||| |||||||||     ||||
                                AGGAT AGGATCACC     GACC
                                  _       CACTCT
GAM827  PMM2    3'  CTCCTCTTACTGTTCTCTG   43551      A  CC  G  GC  C
                                CTCCT CT  TA TG  TC CTG
                                ||||| ||  || ||  || |||
                                GAGGA GA  AT AC  AG GAC
                                  _ __  G  A_  A
GAM827  RFX5    3'  CCCTGCTCCTAGTTTCCACTTG 7793      A       GGC  _ _
          G                      TCCT CTCCTAGT   TCC CT GG
                                |||| ||||||||   ||| || ||
                                GGGA GAGGATCA   AGG GA CC
                                  C       A__   T  A
GAM828  CDH18   5'  TCCATCAGGGAAAGGTCAGATC 22341        AA      TA___
          ATATT                   TCCATCAG  AGAGGTT    ATATT
                                ||||||||  |||||||    |||||
                                AGGTAGTC  TTTCCAG    TATAA
                                    CC      TCTAG
GAM828  FBXW1B  3'  TCCACGGGAAGAGGTTT    37995      CA   A
                                TCCAT  GAA GAGGTTT
                                |||||  ||| |||||||
                                AGGTG  CTT CTCCAAA
                                  CC  _
GAM828  FBXW1B  3'  TCCACGGGAAGAGGTTT    37999      CA   A
                                TCCAT  GAA GAGGTTT
                                |||||  ||| |||||||
                                AGGTG  CTT CTCCAAA
                                  CC  _
GAM828  FBXW1B  3'  TCCACGGGAAGAGGTTT    37999      CA   A
                                TCCAT  GAA GAGGTTT
                                |||||  ||| |||||||
                                AGGTG  CTT CTCCAAA
                                  CC  _
GAM828  IRTA1   3'  TCCATCAGGAGACCTCTAATAT 36355        AA   GG
          T                      TCCATCAG  AGA  TTTAATATT
                                ||||||||  |||  |||||||||
                                AGGTAGTC  TCT  AGATTATAA
                                    C_  GG
GAM828  KERA    3'  AGAAAGCATTCAATATT    28151       AG
                                AGAAAG  GTTTAATATT
                                ||||||  ||||||||||
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                                TCTTTC  TAAGTTATAA
                                   G_
GAM828  PCMT1    3'  CCATCTTAAGGTTTAATATT  23940      AGAAA
                                CCATC    GAGGTTTAATATT
                                |||||    ||||||||||||||
                                GGTAG    TTCCAAATTATAA
                                  AA___
GAM828  BACH2    3'  TATTTTTGTAAGAAAAGA    34804          CCATC
                                TATTTTTGTGAGA    GAAGA
                                |||||||||||||    |||||
                                ATAAAAACATTCT    TTTCT
                                      _____
GAM828  HADH2    3'  TTTTTGTGAGAAAAAGA     21056          CCATC
                                TTTTTGTGAGA    GAAGA
                                ||||||||||||    |||||
                                AAAAACACTCT    TTTCT
                                      T____
GAM828  IL10     3'  TATTTTTTTGAGACAG      8196        G     CATCGA
                                TATTTTT TGAGAC     AG
                                ||||||| ||||||     ||
                                ATAAAAA ACTCTG     TC
                                   A    _______
GAM829  DKK1     3'  TCAGAAAATAAGCTAGTATTTT 29271        _    TAA
                                TCAGAAAG AGGTT   TATTTT
                                |||||||| |||||   ||||||
                                AGTCTTTT TTCGA   ATAAAA
                                     A    TC_
GAM829  KERA     3'  AGAAAGCATTCAATATTTT   28152       AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM829  PPP1R12A 3'  CCAGAAAGATGTAGTATTTT   14726        G  TTAA
                                TCAGAAAGA GT    TATTTT
                                |||||||||  ||    ||||||
                                GGTCTTTCT CA    ATAAAA
                                     A  TC__
GAM829  S100B    3'  GAAAGAGGTTTTCAATTTT   26568          AAT
                                GAAAGAGGTTT   ATTTT
                                ||||||||||   |||||
                                CTTTCTCCAAA   TAAAA
                                      AGT
GAM830  DKK1     3'  TCAGAAAATAAGCTAGTATTTT 29271        _    TAA
                                TCAGAAAG AGGTT   TATTTT
                                |||||||| |||||   ||||||
                                AGTCTTTT TTCGA   ATAAAA
                                     A    TC_
GAM830  KERA     3'  AGAAAGCATTCAATATTTT   28152       AG
                                AGAAAG  GTTTAATATTTT
                                ||||||  ||||||||||||
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                                TCTTTC  TAAGTTATAAAA
                                   G_
GAM830  PPP1R12A  3'  CCAGAAAGATGTAGTATTTT  14726        G  TTAA
                                TCAGAAAGA GT    TATTTT
                                ||||||||| ||    ||||||
                                GGTCTTTCT CA    ATAAAA
                                     A  TC__
GAM830  S100B    3'  GAAAGAGGTTTTCAATTTT   26568          AAT
                                GAAAGAGGTTT   ATTTT
                                ||||||||||   |||||
                                CTTTCTCCAAA   TAAAA
                                      AGT
GAM831  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 45182        CG  AA
           T                     TGATGGAGT  TA  AAAAGTTTT
                                ||||||||| ||  |||||||||
                                ACTACCTCA  AT  TTTTTAAAA
                                     AA  C_
GAM831  ADAMTS12  5'  GTGAAAAAAGTTTTAGCCCTC  36289    A         T
                                GT AAAAAAGTTTTA CTCTT
                                || ||||||||||||| |||||
                                CA TTTTTTCAAAAT GGGAG
                                 C          C
GAM831  ALDOB    3'  AAAAGTTGCTCCCTTTC     42767       TTA
                                AAAAGTT   TCTCTTTC
                                |||||||   ||||||||
                                TTTTCAA   AGGGAAAG
                                   CG_
GAM831  FGG      3'  AAAAAAGTAAATCTCTTT    34836        TTT
                                AAAAAAGT   ATCTCTTT
                                ||||||||   ||||||||
                                TTTTTTCA   TAGAGAAA
                                     TT_
GAM831  PPP2R2B  3'  AAAAAAAACTTATCTCTTT   21324        T
                                AAAAAAG TTTATCTCTTT
                                ||||||| ||||||||||
                                TTTTTTT GAATAGAGAAA
                                   T
GAM831  TEM8     3'  GTAGGCAAAGTTTTCCTCTTTC 32858     AAA       A
                                GTA   AAAGTTTT TCTCTTTC
                                |||   |||||||| ||||||||
                                CAT   TTTCAAAA GGAGAAAG
                                  CCG       _
GAM832  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 45182        CG  AA
           T                     TGATGGAGT  TA  AAAAGTTTT
                                ||||||||| ||  |||||||||
                                ACTACCTCA  AT  TTTTTAAAA
                                     AA  C_
GAM833  EBF      3'  AGAATAAATATATCCCC     42367      A
                                AGAA TAAATATATCTTT
                                |||| ||||||||||||
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                                TCTT ATTTATATAGGGG
                                   _
GAM833  GBP1     3'  AGAGGTAAATGCATCTTTGTT  13115     AA    A
                                AGA  TAAAT TATCTTTGTT
                                |||  ||||| ||||||||||
                                TCT  ATTTA GTAGAAACAA
                                  CC    C
GAM833  GNA11    3'  GAAATAAAAACCATTTGTTAAA 44042        T  ATC
                                GAAATAAA AT   TTTGTTAAA
                                |||||||| ||   |||||||||
                                CTTTATTT TG   AAACAATTT
                                     T  GT_
GAM834  ABCC5    3'  AGCGGCTGTGGGGAGGCG    25019        C  AA   G
                                AGCGGCTG TGG  GAGG CG
                                |||||||| |||  |||| ||
                                TCGCCGAC ACC  CTCC GC
                                     _  C_   _
GAM834  ALDH3B1  3'  GGCTGCTGTTGGAGAAGGCG  45066        GA__
                                GGCTGCTG   AGAGGGCG
                                ||||||||   ||||||||
                                CCGACGAC   TCTTCCGC
                                     AACC
GAM834  AREG     5'  AGCGGGTGTTGGAAGAGCG   11662      C  C     GG
                                AGCGG TG TGGAAGA  GCG
                                ||||| || |||||||  |||
                                TCGCC AC ACCTTCT  CGC
                                   C  A     __
GAM834  BSN      3'  GCGGCTGTGGGAAGTACG    18403       CT    AGG
                                GCGGCTG  GGAAG   GCG
                                |||||||  |||||   |||
                                CGCCGAC  CCTTC   TGC
                                     AC    A__
GAM834  CAPON    5'  GCGGCTGCAGGAAGGGGC    41923        T    A
                                GCGGCTGC GGAAG GGGC
                                |||||||| ||||| ||||
                                CGCCGACG CCTTC CCCG
                                     T    _
GAM834  CAV1     5'  GGCGCTGGAGGGGGGCG     11994     T     AGA
                                GGC GCTGGA   GGGCG
                                ||| ||||||   |||||
                                CCG CGACCT   CCCGC
                                  _     CCC
GAM834  CCR9     5'  AGGGCTTGTGGAGGGCGA    36294    C   GC   AGA
                                AG GGCT  TGGA   GGGCGA
                                || ||||  ||||   ||||||
                                TC CCGA  ACCT   CCCGCT
                                 _   AC   ____
GAM834  CDK2AP1  5'  GCGGCTGCGGGAGGCCAGGGCG 21600        T   AG__
                                GCGGCTGC GGA    AGGGCG
                                |||||||| |||    ||||||
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                                CGCCGACG CCT   TCCCGC
                                    C  CCGG
GAM834  CHST5   5' AGGGCTGCTGGGAGAGC    29076   C      AA
                                AG GGCTGCTGG  GAGGGC
                                || |||||||||  ||||||
                                TC CCGACGACC  CTCTCG
                                 _       __
GAM834  CHST6   5' AGGGCTGCTGGGAGAGC    34674   C      AA
                                AG GGCTGCTGG  GAGGGC
                                || |||||||||  ||||||
                                TC CCGACGACC  CTCTCG
                                 _       __
GAM834  COL5A3  5' GCGGCTGCGGGGCGCGGCG  31852       T  AAGAG
                                GCGGCTGC GG    GGCG
                                |||||||| ||    ||||
                                CGCCGACG CC    CCGC
                                    C  CGCG_
GAM834  CUL3    5' GCGGCGGCGGGGGCGC     18736     T  T  AAGA   A
                                GCGGC GC GG   GGGCG C
                                ||||| || ||   ||||| |
                                CGCCG CG CC   CCCGC G
                                  C  _ _____   C
GAM834  EN2     3' GCGGCTGCTGGTGAGCA    10957         AAGA
                                GCGGCTGCTGG   GGGCG
                                ||||||||||   |||||
                                CGCCGACGACC   CTCGT
                                      A___
GAM834  ENO2    5' GCGGCTGCGGCTCCCGGGCGGC 12711       T  AAGA_   A
          G                     GCGGCTGC GG    GGGCG CG
                                |||||||| ||    ||||| ||
                                CGCCGACG CC    CCCGC GC
                                    _  GAGGG   C
GAM834  ERBB3   5' GGCTGCTGCGGCGAC      12756       GAAGAG
                                GGCTGCTG     GGCGAC
                                ||||||||     ||||||
                                CCGACGAC     CCGCTG
                                    G_____
GAM834  FXYD7   5' GGCTGCTGGATGCTTTGGCGGC 35130        AGAG__   A
          G                     GGCTGCTGGA     GGCG CG
                                ||||||||||     |||| ||
                                CCGACGACCT     CCGC GC
                                     ACGAAA   C
GAM834  GLUL    5' AGCTTTCTGGGAGAGGGCGA  13150     G_   A
                                GGCT  CTGG AGAGGGCGA
                                ||||  |||| |||||||||
                                TCGA  GACC TCTCCCGCT
                                  AA   C
GAM834  GRM7    5' GCGGCGCTGGAGGGAAC    9187      T    AGA  C
                                GCGGC GCTGGA  GGG GAC
                                ||||| ||||||  ||| |||
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                                CGCCG CGACCT   CCC TTG
                                  _    ____  _
GAM834  HNF4A    3'  GGTGTTGGAGAAGACG      7843     C  C    A
                                GG TG TGGA GAGGGCG
                                || || |||| |||||||
                                CC AC ACCT CTTCTGC
                                 _ A   _
GAM834  HOXB2    5'  GGCTGCTGGGGGGGGGCG     13434          AAGA
                                GGCTGCTGG   GGGCG
                                |||||||||   |||||
                                CCGACGACC   CCCGC
                                     CCC_
GAM834  INSM1    5'  GCGGCTGCGGGACTCGCGTGGC 13579         T   AGAG___
            G                    GCGGCTGC GGA      GGCG
                                |||||||| |||      ||||
                                CGCCGACG CCT      CCGC
                                     C   GAGCGCA
GAM834  IRF1     3'  AGGGCTGCTGGGGCTTGAGGG  42039    C       AA___
                                AG GGCTGCTGG    GAGGG
                                || |||||||||    |||||
                                TC CCGACGACC    CTCCC
                                 _       CCGAA
GAM834  KCNQ1    3'  GCTGGCTGCTGGGACTGGGCG  6885     _       AAGA
                                GC GGCTGCTGG   GGGCG
                                || |||||||||   |||||
                                CG CCGACGACC   CCCGC
                                 A       CTGA
GAM834  MPG      5'  GCTGCTGCTGGGGGCA      14619    G      AAGA
                                GC GCTGCTGG   GGGCG
                                || ||||||||   |||||
                                CG CGACGACC   CCCGT
                                 A      _____
GAM834  NFKB1    5'  GCGGCTGCGGCCTCGGCGGCG  19654         T  AAGAG   A
                                GCGGCTGC GG    GGCG CG
                                |||||||| ||    |||| ||
                                CGCCGACG CC    CCGC GC
                                     _ GGAG_   C
GAM834  PDAP1    5'  GCGGCTGCGGCGGCGGCG    45203         T  AAGAG
                                GCGGCTGC GG    GGCG
                                |||||||| ||    ||||
                                CGCCGACG CC    CCGC
                                     _ GCCG_
GAM834  PODXL    5'  GCGGCTGCGTCCTGGGCGGCG  23978         T GAAGA    A
                                GCGGCTGC G    GGGCG CG
                                |||||||| |    ||||| ||
                                CGCCGACG C    CCCGC GC
                                     _ AGGA_    C
GAM834  PPP2R5B  5'  GGCTGCCCGTAGGGAGGGCGAC 26448         _____  AA
            G                    GGCTGCT   GG  GAGGGCGACG
                                |||||||   ||  ||||||||||
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                                CCGACGG   CC  CTCCCGCTGC
                                    GCAT  __
GAM834  RFNG     3'  GCGGCAGAGAGGGCGC      44772       TGCT   A      A
                                GCGGC   GGA GAGGGCG C
                                |||||   ||| ||||||| |
                                CGCCG   TCT CTCCCGC G
                                  _____  _      C
GAM834  RNF28    3'  AGTGTCTGCTGGACGCAGCG   37196    CGG       AGAG
                                AG   CTGCTGGA   GGCG
                                ||   ||||||||   ||||
                                TC   GACGACCT   TCGC
                                 ACA       GCG_
GAM834  SGT      3'  AGCGGCTGCAGGGCCGCGGCG  16605         T  AAGAG
                                AGCGGCTGC GG    GGCG
                                |||||||||| ||    ||||
                                TCGCCGACG CC    CCGC
                                     T  CGGCG
GAM834  SNL      3'  AGGGCTCCCGGAGGGGGCGACG 16934    C    G     A A
                                AG GGCT CTGGA G GGGCGACG
                                || |||| ||||| | ||||||||
                                TC CCGA GGCCT C CCCGCTGC
                                 _   G    _ C
GAM834  SOX12    3'  GGCTGTGCAGGAGGGGGGCGACG 28046       CT__   A A
                                GGCTG   GGA G GGGCGACG
                                |||||   ||| | ||||||||
                                CCGAC   CCT C CCCGCTGC
                                   ACGT  _ C
GAM834  SPTBN2   3'  AGTGGCAGCTGGAGTTACAGGG 28066    C   T     AG___
                                AG GGC GCTGGA    AGGG
                                || ||| ||||||    ||||
                                TC CCG CGACCT    TCCC
                                 A  T     CAATG
GAM834  TRC8     5'  AGCGATGGCCGAGAGGGCGGCG 28509       CT    GA       A
                                AGCGG  GCTG  AGAGGGCG CG
                                |||||  ||||  |||||||| ||
                                TCGCT  CGGC  TCTCCCGC GC
                                   AC   __       C
GAM835  ZNF236   3'  TGTGGACAGCTGAATCCTTATT 28870         ACAAAC  AA
                                TGTGGACA     AT  TTATT
                                ||||||||     ||  |||||
                                ACACCTGT     TA  AATAA
                                     CGACT_  GG
GAM835  AKT1     3'  TGTGCCTGCCACCCCCAG    23143          G  AG
                                TGTGCCTGTCAT CC  CCAG
                                |||||||||||| ||  ||||
                                ACACGGACGGTG GG  GGTC
                                          _ __
GAM835  DBH      3'  GTGCCTGTCCCAGAAGCCAG   8972          ATGCC
                                GTGCCTGTC    AGCCAG
                                |||||||||    ||||||
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                                CACGGACAG    TCGGTC
                                     GGTCT
GAM835  IL8RA   3'  GTGCCTGTCCAGAGCCAGA   8442        ATGCC
                                GTGCCTGTC    AGCCAGA
                                |||||||||    |||||||
                                CACGGACAG    TCGGTCT
                                     GTC__
GAM835  KCNF1   3'  TGGGCTCTCGTGCCAGCCAG  13840   T  C G  A
                                TG GC T TC TGCCAGCCAG
                                || || | || ||||||||||
                                AC CG A AG ACGGTCGGTC
                                 C  _ G  C
GAM835  NR2E1   5'  TGTGCCTGTCGCTGCGGGC   17582        A_   CA
                                TGTGCCTGTC  TGC  GC
                                ||||||||||  |||  ||
                                ACACGGACAG  ACG  CG
                                      CG   CC
GAM835  NT5C    3'  TGTATTTCCATGCCAGCCAG  31103     CCTG
                                TGTG   TCATGCCAGCCAG
                                ||||   ||||||||||||||
                                ACAT   GGTACGGTCGGTC
                                  AAA_
GAM836  HUNK    3'  GTTCGATCCTTGGAGAAAG   31077     A   GATATC
                                GTTC GTCC    GGAGAAAG
                                |||| ||||    ||||||||
                                CAAG TAGG    CCTCTTTC
                                  C   AA____
GAM836  SYT1    3'  GTTGCTTCAGTTTTCTAG    24855       G   GTGAA
                                GTTGCTTC AGTT    TTAG
                                |||||||| ||||    ||||
                                CAACGAAG TCAA    GATC
                                     _   AA___
GAM837  BRCA1   3'  AAGTTCACTGGTATTTGA    28618        ACTC
                                AAGTTCACTG   TTGA
                                ||||||||||   ||||
                                TTCAAGTGAC   AACT
                                     CATA
GAM837  DAG1    5'  TCCAAGTTTGCTCAAGTCGATA 20526       CAC  A  ___
                                TCCAAGTT  TG CTC  TTGATA
                                ||||||||  || |||  ||||||
                                AGGTTCAA  AC GAG  AGCTAT
                                     ___  _  TTC
GAM837  IL5RA   3'  TCCAAGTTCATGGTTCACTCC  8162        C  ____
                                TCCAAGTTCA TG   ACTCT
                                |||||||||| ||   |||||
                                AGGTTCAAGT AC   TGAGG
                                     _ CAAG
GAM837  KCNJ5   3'  GTTCACTGAAGCCAGTGA    9439        CT  __
                                GTTCACTGA  CT  TGA
                                |||||||||  ||  |||
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                                CAAGTGACT  GG  ACT
                                     TC  TC
GAM837  KCNK2    3'  TCCAAATTCTCTTGAT     30567         ACTGAC
                                TCCAAGTTC     TCTTGAT
                                |||||||||     |||||||
                                AGGTTTAAG     AGAACTA
                                      _______
GAM837  MEOX2    3'  CATAGTTTGCTCTTGATA    25450    _   CAC  A
                                CA AGTT   TG CTCTTGATA
                                || ||||   || |||||||||
                                GT TCAA   AC GAGAACTAT
                                 A   ___ _
GAM837  PLAG1    3'  TCTCAGTTCACTAATTTGAT   15358    CA        CTC
                                TC  AGTTCACTGA   TTGAT
                                ||  ||||||||||   |||||
                                AG  TCAAGTGATT   AACTA
                                 AG         A__
GAM837  TPTE     5'  GTTCACTCCTGATAA       30024       TGAC
                                GTTCAC    TCTTGATAA
                                ||||||    |||||||||
                                CAAGTG    AGGACTATT
                                      _____
GAM837  UBE4A    3'  TCCAAGTTTAGTATTAGCCTCT 21978         CACTGA_____
           TG                     TCCAAGTT         CTCTTG
                                |||||||||         ||||||
                                AGGTTCAA         GAGAAC
                                     ATCATAATCG
GAM837  ZNF35    5'  CCTGAGTTCACTGGCTCT    18283    A_       A
                                CC  AGTTCACTG CTCT
                                ||  ||||||||| ||||
                                GG  TCAAGTGAC GAGA
                                 AC        C
GAM837  ABL1     3'  TGACAGTGACCTGCCACCCTT  28719     G      GTAT
                                TGA AGTGACT    TCACCCTT
                                ||| |||||||    ||||||||
                                ACT TCACTGG    GGTGGGAA
                                  G      AC__
GAM837  CYP39A1  3'  TGAGAGTGATGTTAGATTC    32464         C   ___
                                TGAGAGTGA TGT   ATTC
                                ||||||||| |||   ||||
                                ACTCTCACT ACA   TAAG
                                      _  ATC
GAM837  DNMT3B   3'  TAAGAGTGGCCCCTGCCCTT   27881         ACT  ATTCA
                                TGAGAGTG   GT    CCCTT
                                ||||||||   ||    |||||
                                ATTCTCAC   CG    GGGAA
                                     ___  GGGAC
GAM837  EPHB1    3'  TGAGAGTGGGAGCTGGGTTTAC 20778         A___   TA  C  C
           TCTT                    TGAGAGTG    CTG  TT AC CTT
                                ||||||||    |||  || || |||
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                                ACTCTCAC   GAC  AA TG GAA
                                    CCTC   CC  A  A
GAM837  JUN     3'  TGAGAGTGATTTTATCGAGCAT 13751        CT_______
            TC                   TGAGAGTGA       GTATTC
                                 |||||||||       ||||||
                                 ACTCTCACT       CGTAAG
                                     AAAATAGCT
GAM837  NAV2    3'  GAGTGACCCTCACCCTTA    41142        GTA
                                 GAGTGACT   TTCACCCTTA
                                 ||||||||   ||||||||||
                                 CTCACTGG   GAGTGGGAAT
                                     ___
GAM837  PIP5K1A  3'  GAGGTGGTTAAACACCCTTA  18654    A  ACTG  TT
                                 GAG GTG   TA  CACCCTTA
                                 ||| |||   ||  ||||||||
                                 CTC CAC   AT  GTGGGAAT
                                   _  CA__  TT
GAM838  EPHA8   3'  CCATATGCTACAGGAAGGGGT  33893         AAAGTTAT  A
                                 CCATATGCTA       GG GT
                                 ||||||||||       || ||
                                 GGTATACGAT       CC CA
                                      GTCCTT__  C
GAM838  FGF12   3'  CCAAATGCTAAGAGCAAGT   34297    T     A   TATG
                                 CCA ATGCTAA AGT   GAGT
                                 ||| ||||||| |||   ||||
                                 GGT TACGATT TCG   TTCA
                                   T      C  _____
GAM838  TAF4    3'  CATGTGCCAAAAGTTATG    17259    A
                                 CAT TGCTAAAAGTTATG
                                 ||| ||||||||||||||
                                 GTA ACGGTTTTCAATAC
                                   C
GAM838  TAP2    3'  CCATATGCAAAGGCACAAAG  8081        TA   T  TG
                                 CCATATGC  AAAG TA  GAG
                                 ||||||||  |||| ||  |||
                                 GGTATACG  TTTC GT  TTC
                                      __   C  GT
GAM838  MYB     3'  CATTAAGATATTAACAACTGG  40531    CG T   GAC
                                 CAT  A GTG   AACAACTGG
                                 |||  | |||   |||||||||
                                 GTA  T TAT   TTGTTGACC
                                   AT C   AA_
GAM838  STIM1   5'  GATGTGGACACCTCGG      41128         A AAC
                                 GATGTGGACA C   TGG
                                 |||||||||| |   |||
                                 CTACACCTGT G   GCC
                                      _ GA_
GAM839  ACTN1   3'  TCCCACACCAAAATGGACA   9937          ___
                                 TCTCACACCAG   GGACA
                                 ||||||||||   |||||
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                                AGGGTGTGGTT  CCTGT
                                      TTA
GAM839  BBS2    3'  TCTTTGCCAGGAACTTCAT   36640    CACA      AA
                                TCT   CCAGGGAC  CAT
                                |||   ||||||||  |||
                                AGA   GGTCCTTG  GTA
                                  AAC_      AA
GAM839  C14orf1  3'  CTCTTAGCCTGGACAACATA  28412    ACA_ AG
                                CTC   CC  GGACAACATA
                                |||   ||  ||||||||||
                                GAG   GG  CCTGTTGTAT
                                  AATC  A_
GAM839  DBH     3'  CCCACAGGGACAGCAT     8967       CCA     A
                                CTCACA   GGGACA CAT
                                ||||||   |||||| |||
                                GGGTGT   CCCTGT GTA
                                   ___     C
GAM839  HSPA5   3'  TCCTACACCAGATGCACAT   23788    TC      GACA
                                TC  ACACCAGG   ACAT
                                ||  ||||||||   ||||
                                AG  TGTGGTCT   TGTA
                                 GA       ACG_
GAM839  KIT     3'  TCAACAATTGGACAACATA   6899     _ CCAG
                                TCA CA   GGACAACATA
                                ||| ||   ||||||||||
                                AGT GT   CCTGTTGTAT
                                  T  TAA_
GAM839  LANCL1   3'  TCCCATTAAATGACAACATA  25857      CACCAGG
                                TCTCA      GACAACATA
                                |||||      |||||||||
                                AGGGT      CTGTTGTAT
                                   AATTTA_
GAM839  MAGEA8   3'  CCTCACACCCAACAT      23845        AGGGA
                                TCTCACACC    CAACAT
                                |||||||||    ||||||
                                GGAGTGTGG    GTTGTA
                                      _____
GAM839  MLF1    3'  TCCTAAAAGAGGGACAATATA  35352    CACACC      C
                                TCT     AGGGACAA ATA
                                |||     |||||||| |||
                                AGG     TCCCTGTT TAT
                                  ATTTTC       A
GAM839  MTMR3   3'  TCCCACGGGGGACAACAT    34400      ACCA
                                TCTCAC   GGGACAACAT
                                ||||||   ||||||||||
                                AGGGTG   CCCTGTTGTA
                                   CC__
GAM839  RP42    3'  CTCACATCAACAACATA     33985      C  GGG
                                CTCACA CA   ACAACATA
                                |||||| ||   ||||||||
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                                GAGTGT GT   TGTTGTAT
                                   A ___
GAM839  SDC1     3'  TCTCACACGGGCTTCTCCAAC  16512        CA   A_____
                                TCTCACAC  GGG     CAAC
                                ||||||||  |||     ||||
                                AGAGTGTG  CCC     GTTG
                                    __  GAAGAG
GAM839  SLC19A1  3'  ACAGTGCAGGGACAGCAT    16842     C__       A
                                ACA   CAGGGACA CAT
                                |||   |||||||| |||
                                TGT   GTCCCTGT GTA
                                  CAC       C
GAM839  SLC6A3   3'  CCTCACACAGACAGCAT     9807         CAG     A
                                TCTCACAC   GGACA CAT
                                ||||||||   ||||| |||
                                GGAGTGTG   TCTGT GTA
                                    ___     C
GAM839  SMT3H1   3'  TCTTATACACGACAACATA   41004     C__    CAGG
                                TCT   ACAC   GACAACATA
                                |||   ||||   |||||||||
                                AGA   TGTG   CTGTTGTAT
                                  ATA   _____
GAM839  TMEPAI   3'  TCCCACGCCAGGAACCAAC   33622       A       _
                                TCTCAC CCAGGGAC AAC
                                |||||| |||||||| |||
                                AGGGTG GGTCCTTG TTG
                                   C       G
GAM839  AEGL1    3'  CAGGTGTTGGACTTGACCT   10061           CTGA
                                CAGGTGTTGGATT   TGGCTT
                                ||||||||||||   ||||||
                                GTCCACAACCTGA   ACTGGA
                                        _____
GAM839  BSN      3'  AGGTGTTAGATGATGGCTT   18391         TTC
                                AGGTGTTGGA   TGATGGCTT
                                ||||||||||   |||||||||
                                TCCACAATCT   ACTACCGAA
                                       ___
GAM839  DSG1     3'  AGTGCTTGATGGCT       12599       GGATTC
                                GGTGTT     TGATGGCT
                                ||||||     ||||||||
                                TCACGA     ACTACCGA
                                      _______
GAM839  HADHB    3'  ATGTGAGATTCTGGTGGCT   6767      T       A
                                GTGT GGATTCTG TGGCT
                                |||| |||||||| |||||
                                TACA TCTAAGAC ACCGA
                                  C       C
GAM839  HHLA1    5'  ACAGGGGTTGCGATGGCT    25048      T    GATTC
                                ACAGG GTTG     TGATGGCT
                                ||||| ||||     ||||||||
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                                TGTCC CAAC    GCTACCGA
                                  C  _____
GAM839  LARS2    3'  AGTGTCTCTGATGGCT     31673       GGAT
                                GGTGTT   TCTGATGGCT
                                ||||||   ||||||||||
                                TCACAG   AGACTACCGA
                                  ____
GAM840  IL16     3'  GTTTGTGTCAGCTCTAACT   21099       G  AT   C
                                GTTTGTGT GG  CTC AACT
                                |||||||| ||  ||| ||||
                                CAAACACA TC  GAG TTGA
                                    G  __  A
GAM840  ITPKB    3'  GTTTTGTGCCCCAAC      13652     G   GGAT
                                GTTT TGTG   CTCCAAC
                                |||| ||||   |||||||
                                CAAA ACAC   GGGGTTG
                                  _  _____
GAM840  ATP8A2   3'  TTTCTTTTCTTTCTTTACAGA  45275      ACCCC_
                                TTTCT     TCTTTACAGA
                                |||||     ||||||||||
                                AAAGA     AGAAATGTCT
                                  AAAGAA
GAM840  BLK      5'  TGGCTTTCTGCCGGCAGCAGA  11849        A  CCTCTTTA
                                TGGCTTTCT CC       CAGA
                                ||||||||| ||       ||||
                                ACCGAAAGA GG       GTCT
                                    C  CCGTC___
GAM840  CRTAP    3'  TGGCTTTCTTCCTTTTCC    26843        A  CC_
                                TGGCTTTCT CC   TCT
                                ||||||||| ||   |||
                                ACCGAAAGA GG   AGG
                                    A  AAA
GAM840  DES      3'  TGGCTTTCTCTCTCC       43574        ACCC
                                TGGCTTTCT   CTCTTT
                                |||||||||   ||||||
                                ACCGAAAGA   GAGAGG
                                  ____
GAM840  DGAT2    3'  TGGCTTTCGCCTCTC       37195        TACC
                                TGGCTTTC   CCTCTT
                                ||||||||   ||||||
                                ACCGAAAG   GGAGAG
                                    C___
GAM840  EPB42    5'  GGCTTTCTGTCTTCCAGACAGA 6515        ACCCC  TT
                                GGCTTTCT   TCT  ACAGA
                                ||||||||   |||  |||||
                                CCGAAAGA   AGG  TGTCT
                                    CAGA_  TC
GAM840  F7       3'  TGGCTTTCTCTCCACA      33347        TACCCC
                                TGGCTTTC    TCTTTACA
                                ||||||||    ||||||||
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                                ACCGAAAG     AGAGGTGT
                                        ______
GAM840  F8A     3'  TGTCTTTTTATTCCTCCCCAGA 29111    G   C  CC     TA
                                TG CTTT TA  CCTCTT  CAGA
                                || |||| ||  ||||||  ||||
                                AC GAAA AT  GGAGGG  GTCT
                                 A   A  AA    __
GAM840  FLRT2   3'  GCTTTCTATCCTGGTGCAG   29852       CC   CTTTA
                                GCTTTCTA  CCT    CAG
                                ||||||||  |||    |||
                                CGAAAGAT  GGA    GTC
                                    A_   CCAC_
GAM840  GOLGA4  5'  TGGCTTTCTGTACCTTTTT   41060       ACC   C
                                TGGCTTTCT   CCT TTT
                                |||||||||   ||| |||
                                ACCGAAAGA   GGA AAA
                                     CAT   A
GAM840  GPC4    3'  GCTTTCTATCTTTCAA     11084       CCCC    A
                                GCTTTCTA    TCTTT CAG
                                ||||||||    ||||| |||
                                CGAAAGAT    AGAAA GTT
                                        ____    _
GAM840  GRAF    3'  TGGCCTTCTGTTCCTCCACA  31458       ACC    TT
                                TGGCTTTCT   CCTCT  ACA
                                |||||||||   |||||  |||
                                ACCGGAAGA   GGAGG  TGT
                                     CAA    __
GAM840  HOXB9   3'  TGGCTTTCCTGTCTACAG    35848       CTACC   C
                                TGGCTTT    CCT TTTACAG
                                |||||||    ||| |||||||
                                ACCGAAA    GGA AGATGTC
                                    _____  C
GAM840  IRTA1   3'  TGGCTTCCTATTTCTTT     36358         CCCC
                                TGGCTTTCTA    TCTTT
                                ||||||||||    |||||
                                ACCGAAGGAT    AGAAA
                                     AA__
GAM840  LAIR1   3'  TGACTTTCTACCCTCAGGTGCA 14055          C  TTTA_
          GA                    TGGCTTTCTACCC TC    CAGA
                                ||||||||||||| ||    ||||
                                ACTGAAAGATGGG AG    GTCT
                                      _  TCCAC
GAM840  MYBL1   3'  TAGCTTTCTGCCTACTATATAG 41982       A  CCT  T  C
          A                     TGGCTTTCT CC   CT TA AGA
                                ||||||||| ||   || || |||
                                ATCGAAAGA GG   GA AT TCT
                                     C  AT_  T  A
GAM840  MYO9A   3'  GGCTTTCTGCTTCTGCAG    27905       ACCCC   TTA
                                GGCTTTCT    TCT   CAG
                                ||||||||    |||   |||
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                                CCGAAAGA    AGA  GTC
                                    CGA__   C__
GAM840  PACE4    3'  GCTTTCTACTGGAGATACAGA  39688        CCCTCTT
                                GCTTTCTAC      TACAGA
                                |||||||||      ||||||
                                CGAAAGATG      ATGTCT
                                    ACCTCT_
GAM840  RAB1A    3'  GCTTTCTACCTCTACCACAGA  43187         C  CT
                                GCTTTCTACC CT  TTACAGA
                                |||||||||| ||  |||||||
                                CGAAAGATGG GA  GGTGTCT
                                     A  T_
GAM840  TLE1     3'  TGGACTTGTCGCCTCCTCTTTG 22923     _  _  TA  _      AC
           TAGA                    TGG CTT TC  CC CCTCTTT  AGA
                                ||| ||| ||  || |||||||  |||
                                ACC GAA AG  GG GGAGAAA  TCT
                                  T  C  C_  A      CA
GAM840  UBE2G2   3'  TGACTCTTCTTTACA      42128        CTACCCC
                                TGGCTTT      TCTTTACA
                                |||||||      ||||||||
                                ACTGAGA      AGAAATGT
                                    ________
GAM841  EMX2     3'  TGTCCGTTTCTGTGGGGT    44706      AATTG     A
                                TGTCC    TCTGTG GGT
                                |||||    |||||| |||
                                ACAGG    AGACAC CCA
                                   CAA__     C
GAM841  RRAD     3'  CTGTCCATGACCATGAGGT    20018        AT  T
                                CTGTCCA  TG CTGTGAGGT
                                |||||||  || |||||||||
                                GACAGGT  AC GGTACTCCA
                                    __  T
GAM841  SLC22A12 5'  CCTGCTGGTGTCACTTGGGGT  40331      CCAAT    TG_  A
                                CCTGT    TGTC   TG GGT
                                |||||    ||||   || |||
                                GGACG    ACAG   AC CCA
                                   ACC__    TGA  C
GAM841  IKBKAP   3'  TTAATCTCATGATTACCATAA  43288         CAGAA
                                TTAATCTTA    ATTACCATAA
                                |||||||||    ||||||||||
                                AATTAGAGT    TAATGGTATT
                                     AC___
GAM841  PDGFB    3'  TCTGCCAGAAATTGTCATA    15196     TA      AC
                                TCT  CAGAAATT  CATA
                                |||  ||||||||  ||||
                                AGA  GTCTTTAA  GTAT
                                  CG       CA
GAM842  JUN      3'  GGCGCCGTCAGACCGAAC    13745     AT  ____
                                GGC  GCT    GACCGAAC
                                |||  |||    ||||||||
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                                CCG  CGG   CTGGCTTG
                                  __  CAGT
GAM842  GLRB    3'  CAGCGTGCATATCATTTTATTA 9069        C   AACGAA
              T                  CAGCGTGC ATA     TATTAT
                                 |||||||| |||     ||||||
                                 GTCGCACG TAT     ATAATA
                                      _  AGTAAA
GAM843  ABCC5   3'  ATATAGGCTATGTACAGAATTA 25020    C      __  AG  C
              TAT                  ATA AGGCTATG  CA  GT ATAT
                                 ||| ||||||||  ||  || ||||
                                 TAT TCCGATAC  GT  TA TATA
                                   A       AT  CT  A
GAM843  EGFL5   5'  TGACAGGCTATGTTCACAT   44541   T       CAAGG
                                 A ACAGGCTATG    TCATAT
                                 | ||||||||||    ||||||
                                 A TGTCCGATAC    AGTGTA
                                  C        A____
GAM843  ITGA9   3'  TGACAGGCTAGTGATCAGGTCA 13614   T      _  CA_
              T                   A ACAGGCTA TG   AGGTCAT
                                 | ||||||||  ||   |||||||
                                 A TGTCCGAT AC   TCCAGTA
                                  C       C  TAG
GAM843  MGAM    3'  CATACAGGTTGTGCACGT    43652       CTA   AG
                                 TATACAGG   TGCA  GT
                                 ||||||||   ||||  ||
                                 GTATGTCC   ACGT  CA
                                      AAC    G_
GAM843  MYCN    3'  TATACAGGCAGTGTAAGA    23917       TA  C
                                 TATACAGGC  TG AAGG
                                 |||||||||  || ||||
                                 ATATGTCCG  AC TTCT
                                       TC  A
GAM843  SH3BP5  3'  TATACAGGCTGTGACAGAAT   22124        A  _  AG
                                 TATACAGGCT TG CA  GT
                                 ||||||||||  || ||  ||
                                 ATATGTCCGA AC GT  TA
                                       C  T  CT
GAM843  ZNF8    3'  TACACAGGTGGGTAGGTTATAT 41966       CTATGCA   C
                                 TATACAGG      AGGT ATAT
                                 ||||||||      |||| ||||
                                 ATGTGTCC      TCCA TATA
                                      ACCCA__    A
GAM843  FGFRL1  3'  CTGCACGTGTGTGCATGTCCA  34907      __      ATA
                                 TTGCAC  GTGTGCAT   CCA
                                 ||||||  ||||||||   |||
                                 GACGTG  CACACGTA   GGT
                                    CA       CA_
GAM843  FGFRL1  3'  CTGCACGTGTGTGCGTCCA   34908         CATATA
                                 TTGCACGTGTG     CCA
                                 ||||||||||      |||
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                                GACGTGCACAC     GGT
                                      ACGCA_
GAM843  GRM7     3'  ACCTATCATATACCAAA     9180     G  G
                                AC TGT CATATACCAAA
                                || ||| ||||||||||
                                TG ATA GTATATGGTTT
                                 G  _
GAM843  LAMC1    3'  CCTTGACCAATGCATAT     14083      C  GT
                                TCTTG AC  GTGCATAT
                                ||||| ||  ||||||||
                                GGAAC TG  TACGTATA
                                   _ GT
GAM843  TIMELESS 3'  TCTTACATGTTTAATACCAAA  19398       CG   GCAT
                                TCTTGCA  TGT   ATACCAAA
                                |||||||  |||   ||||||||
                                AGAATGT  ACA   TATGGTTT
                                    __  AAT_
GAM844  CABC1    5'  GAGCGTCTGTTTGTGCTGCTT  33683      ATATAC
                                GAGTG     TTGTGCTGCTT
                                |||||     ||||||||||
                                CTCGC     AACACGACGAA
                                   AGACA_
GAM844  EGLN2    5'  GGGTAATAAACACTGCT     38831    A     T  TTGT
                                GG GTGATA AC    GCTGCT
                                || |||||| ||    ||||||
                                CC CATTAT TG    TGACGA
                                 _     T  _____
GAM844  GCK      3'  GGTGTGCTGAATGCTGCTT   37930    A   ATATACTT
                                GG GTG       GTGCTGCTT
                                || |||       |||||||||
                                CC CAC       TACGACGAA
                                 A  GACT_____
GAM844  BAALC    3'  TGACTTTTGACCTGCA      36044       CGCATT  _
                                TGGCTTT     TG CCTGCA
                                |||||||     || ||||||
                                ACTGAAA     AC GGACGT
                                    _______ T
GAM844  GRLF1    3'  GGCTGCTTTTGCCTGC      44232      TTC  A
                                GGCT   GC TTTGCCTGC
                                ||||   || |||||||||
                                CCGA   CG AAACGGACG
                                   ___  A
GAM844  HDAC4    3'  TGGCTTCCGCGTGTCCGTG   25789         ATT  _  _
                                TGGCTTTCGC   TG CC TG
                                ||||||||||   || || ||
                                ACCGAAGGCG   AC GG AC
                                      C__  A  C
GAM844  LEP      3'  TGGCTTTCAGCCCTTTGC    6921          _  A_
                                TGGCTTTC GC  TTTGC
                                ||||||||  ||  |||||
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                                ACCGAAAG CG  AAACG
                                    T  GG
GAM844  MYO1C    3'  TGGCTTTCCTATTGCTG     41475        GCAT    C
                                TGGCTTTC    TTGC TG
                                ||||||||    |||| ||
                                ACCGAAAG    AACG AC
                                    GAT_   _
GAM844  NR3C2    3'  TGGCTTTCATATTACTG     9473         CAT    C
                                TGGCTTTCG   TTGC TG
                                |||||||||   |||| ||
                                ACCGAAAGT   AATG AC
                                     AT_   _
GAM844  TPO      3'  TGATTTCCGATTTGCCTG    8099     GC     C
                                TG  TTTCG ATTTGCCTG
                                ||  ||||| |||||||||
                                AC  AAGGC TAAACGGAC
                                 TA    _
GAM845  B3GALT2  3'  TTTGGCAGACATGCATCTTA   19117      A       _  G
                                TTTG CAGACATG AT TTG
                                |||| |||||||| || |||
                                AAAC GTCTGTAC TA AAT
                                  C       G  G
GAM845  MAGEL2   3'  TTTGGCAGATACGAAACCAAGT 33302      A    C    TG TG
           T                     TTTG CAGA ATGA  T  GGTT
                                |||| |||| ||||  |  ||||
                                AAAC GTCT TGCT  G  TCAA
                                  C    A    TT GT
GAM845  CLCA1    5'  TGTTTTACTATTGCTC      10508      G     T
                                TGTT TTACT ATTGCTC
                                |||| ||||| |||||||
                                ACAA AATGA TAACGAG

                                  _    _
GAM845  FZD6     3'  ATATTGTTGTCATTAACC     18624           C   TT
                                ATATTGTTGTTA TTA  GCT
                                |||||||||||| |||  |||
                                TATAACAACAGT AAT  TGG

                                        _  __
GAM845  TMOD2    3'  CATAATGTTGTCTTGCT     30967      T      ACTTA
                                CATA TGTTGTT    TTGCT
                                |||| |||||||    |||||
                                GTAT ACAACAG    AACGA
                                  T     _____
GAM846  ARHGEF12 3'  AGGAAAGAAAAATTTTGTAGA  31633    T    CC
                                AG GAAG  GAAAAATTTTGTAGA
                                || ||||  ||||||||||||||
                                TC CTTT  CTTTTTAAAACATCT

                                 _   __
GAM846  AVPR1A   5'  GTGGAGCTGGGAGACTCGCAGA 8731      A   CGAAAAAT
                                GTG AGC       TTTGTAGA
                                ||| |||       ||||||||
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                                CAC TCG       GAGCGTCT
                                  C   ACCCTCT_
GAM846  DCTN1    3'  AGTGAAGCTGAACGGGGCAG  35697        C   AAATTTT
                                AGTGAAGC GAA      GTAG
                                |||||||| |||      ||||
                                TCACTTCG CTT      CGTC
                                    A   GCCC___
GAM846  LFG      3'  AGTGAAGCTAGAAGAGATGTGG 44132        C_   AAATTT   A
              A                  AGTGAAGC  GAA     TGT GA
                                |||||||| |||     ||| ||
                                TCACTTCG  CTT     ACA CT
                                    AT   CTCT__   C
GAM846  MMP19    5'  AGTGGGGCCGGTAGCCCTCGTA 35579     AA    AAAAA
              GA                   AGTG  GCCG    TTTTGTAGA
                                |||| ||||    |||||||||
                                TCAC  CGGC    GGAGCATCT
                                  CC    CATCG
GAM846  SLC38A2  3'  AGTGAAACTGAAAACATTAG   33272        C    ATTTTG
                                AGTGAAGC GAAAA     TAG
                                |||||||| |||||      |||
                                TCACTTTG CTTTT     ATC
                                    A    GTA___
GAM846  NIPSNAP1 3'  AGTGCCACTGTCTGTCGGGGT  18868         AC  T    A
                                AGTGCTACT  TT TCGG GT
                                |||||||||  || |||| ||
                                TCACGGTGA  GA AGCC CA
                                     CA  C    C
GAM846  NOS2A    3'  GTGCTACTTGTTAGGAGGTCA  8418         ACTTTTC   _
                                GTGCTACT      GGAG TCA
                                ||||||||      |||| |||
                                CACGATGA      CCTC AGT
                                    ACAAT__    C
GAM846  PPP3R1   3'  AAGTGCTACACTGAGT      44070         T   TTTCG
                                AAGTGCTAC ACT     GAGT
                                ||||||||| |||     ||||
                                TTCACGATG TGA     CTCA
                                    _  ______
GAM846  SIM2     3'  GTGCTACTCTTGGTGT      22879         A   TTC  A
                                GTGCTACT CTT   GG GT
                                |||||||| |||   || ||
                                CACGATGA GAA   CC CA
                                    _  ___  A
GAM847  CLCN4    3'  TATGCTCCAATAGTTCAT    12290        AA   T
                                TATGCT  AAT AGTTCAT
                                ||||||  ||| |||||||
                                ATACGA  TTA TCAAGTA
                                   GG   _
GAM847  FACL6    3'  TAATATTGCTAGACAGTTCAT  31609        A    AAAT
                                TAATAT TGCTA    TAGTTCAT
                                |||||| |||||    ||||||||
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                                ATTATA ACGAT   GTCAAGTA
                                   _    CT__
GAM847  GABRB3   3'  ATATATGCTGAGAAGTTCAC  34872        AAAATT
                                ATATATGCT     AGTTCAT
                                |||||||||     |||||||
                                TATATACGA     TCAAGTG
                                    CTCT__
GAM847  CDC27    3'  AAAGTGGCACACTCATG     10365      A   ATGTT
                                AAAGT GCAT    ACTCATG
                                ||||| ||||    |||||||
                                TTTCA CGTG    TGAGTAC
                                  C   _____
GAM847  FER      5'  TAAAGTAGCGTGTCCATG    23493        ATA   ACT
                                TAAAGTAGC   TGTT   CATG
                                |||||||||   ||||   ||||
                                ATTTCATCG   ACAG   GTAC
                                    C__    ___
GAM847  GAS2     3'  AGTGCTTTTACTCATG      23534     A  ATATG
                                AGT GC    TTACTCATG
                                ||| ||    |||||||||
                                TCA CG    AATGAGTAC
                                  _ AA___
GAM847  HIP2     3'  TAAAGTAGCATGTTTCTTCCAT 23770         TA   A __
          G                      TAAAGTAGCA  TGTT CT  CATG
                                ||||||||||  |||| ||  ||||
                                ATTTCATCGT  ACAA GA  GTAC
                                    __    A  AG
GAM847  VHL      3'  GCAGCGGCATACTCATGA    8112       ATATGT
                                GTAGC     TACTCATGA
                                |||||     |||||||||
                                CGTCG     ATGAGTACT
                                  CCGT__
GAM848  PRKY     3'  GTGCATCTGCCATAATGAC   15704        _     G
                                GTGCATC GCCATGG TGAC
                                ||||||| ||||||| ||||
                                CACGTAG CGGTATT ACTG
                                    A     _
GAM848  ESRRG    3'  TAATTCTGGCATTTGCCTTAT  42447       GC  ATACG
                                TAATTC  GG    TTGCCTTAT
                                ||||||  ||    |||||||||
                                ATTAAG  CC    AACGGAATA
                                   A_  GTA__
GAM848  LHX5     5'  TAATTCGCGCATCCTT      35324         G  ACGTTG
                                TAATTCGCG AT     CCTT
                                ||||||||| ||     ||||
                                ATTAAGCGC TA     GGAA
                                    G _______
GAM849  BCL6     5'  TCGGACTTTACCACTGCTACG  39910         A   TTCCC
                                TCGGACTTTG CCG    ACG
                                |||||||||| |||    |||
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                                AGCCTGAAAT GGT    TGC
                                      _  GACGA
GAM849  LANCL1   5'  AACCCCGTTCCCACG      25844     TTGA
                                GACT   CCGTTCCCACG
                                ||||   ||||||||||
                                TTGG   GGCAAGGGTGC
                                 ____
GAM849  NPY2R    5'  CCTGGACCTCGCGTT      9491     C      AC
                                CCT GGACTTTG  CGTT
                                ||| ||||||||  ||||
                                GGA CCTGGAGC  GCAA
                                  _     __
GAM850  AIPL1    3'  GATTTAAACAGATTACTT    40818    ___
                                GAT   AGCAGATTACTT
                                |||   ||||||||||||
                                CTA   TTGTCTAATGAA
                                  AAT
GAM850  ESR1     3'  TAATAGAGGCAGCAATTACTTA 6535      T  A    A
                                TAATA AG TAGCAG TTACTTA
                                ||||| || |||||| |||||||
                                ATTAT TC GTCGTT AATGAAT
                                   C  C    _
GAM850  PCDH11X  3'  TAACATAGATAGTAACCA    37306         CA
                                TAATATAGATAG  GATTA
                                ||||||||||||  |||||
                                ATTGTATCTATC  TTGGT
                                      A_
GAM850  PCDH11Y  3'  TAACATAGATAGTAACCA    37346         CA
                                TAATATAGATAG  GATTA
                                ||||||||||||  |||||
                                ATTGTATCTATC  TTGGT
                                      A_
GAM850  VSNL1    3'  ATATAGATAGATATACTTAA   18035        CAGAT
                                ATATAGATAG    TACTTAA
                                ||||||||||    |||||||
                                TATATCTATC    ATGAATT
                                      TAT__
GAM851  HEPH     3'  GCTGGGAGTGCACTACAGA    39858        A  C_
                                GCTGGGAGT CAC  CGGA
                                ||||||||| |||  ||||
                                CGACCCTCA GTG  GTCT
                                     C   AT
GAM851  HIF1A    5'  TCGCCGGGGTCCGGGCCC     11353        A  ACAC   A
                                TCGCTGGG GT   CCGG CCC
                                |||||||| ||   |||| |||
                                AGCGGCCC CA   GGCC GGG
                                     _ _____   C
GAM851  IGFBP4   5'  CCTGGAGGACCCGGACCC     11397    G   TAC
                                CT GGAG   ACCCGGACCC
                                || ||||   ||||||||||
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                                GG CCTC   TGGGCCTGGG
                                 A   C__
GAM851  MIPEP    5'  TCGCTGGGAGCGCGCGCTCCG  45231          ACAC___
                                TCGCTGGGAGT      CCG
                                ||||||||||      |||
                                AGCGACCCTCG      GGC
                                      CGCGCGA
GAM851  PDGFB    5'  TCGCTGGGGGGCAGGGGAGGAC 15195        A_  CACCC
          C                      TCGCTGGG  GTA    GGACC
                                ||||||||  |||    |||||
                                AGCGACCC  CGT    CCTGG
                                    CC   CCCCT
GAM851  PRX      5'  GCTGGGAGGCACCTGCG     34127        TA   _____
                                GCTGGGAG  CACC    CG
                                ||||||||  ||||    ||
                                CGACCCTC  GTGG    GC
                                    C_    ACIII
GAM851  SLIT3    5'  TCGCTGGGAGTGCCCAG     16874          ACA
                                TCGCTGGGAGT   CCCGG
                                ||||||||||   |||||
                                AGCGACCCTCA   GGGTC
                                      C__
GAM851  ZNF76    3'  GCTGGGAGGGCAGGACAGGGCC 18309        TA  CCC   ____
                                GCTGGGAG  CA   GGAC   CC
                                ||||||||  ||   ||||   ||
                                CGACCCTC  GT   CCTG   GG
                                    CC  ___    TCCC
GAM852  TMEM2    3'  TAAGTGAATAAAAATAGCACAT 30153        TTAAT   A
                                TGAGTGAAT    GATA CACAT
                                |||||||||    |||| |||||
                                ATTCACTTA    TTAT GTGTA
                                     TTT__    C
GAM853  ATP8A2   3'  ACAGTGAAGTCTGCATGTGGC  45248        CT   TAAGCA
                                ACAGTGAAG  TGC     GGC
                                |||||||||  |||     |||
                                TGTCACTTC  ACG     CCG
                                     AG   TACA__
GAM853  CACNB1   3'  GCGAGGACAAAGAAGCAGGC   8782      A_  TTGCT
                                GTGA  GC    AAGCAGGC
                                ||||  ||    ||||||||
                                CGCT  TG    TTCGTCCG
                                  CC  TTTC_
GAM853  F7       3'  GTGAAGCTGGGAAGCAGG    33341        T CT
                                GTGAAGCT G  AAGCAGG
                                ||||||||  |  |||||||
                                CACTTCGA C  TTCGTCC
                                    _ CC
GAM853  FANCC    3'  CACATGAAGCCAGCAG      43265      G     TGCTA
                                CACA TGAAGCT    AGCAG
                                ||||  |||||||    |||||
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                              GTGT ACTTCGG    TCGTC
                                _    _____
GAM853  FHIT    5' ATAGAGGGTCTAAGCAGG   12866    A  CTTG
                              GTG AG   CTAAGCAGG
                              ||| ||   |||||||||
                              TAT TC   GATTCGTCC
                                C  CCA_
GAM853  GRB10   3' ACAGTGAAGCCTGCCACCAGG 23644            AG
                              ACAGTGAAGCTTGCTA  CAGG
                              ||||||||||||||||  ||||
                              TGTCACTTCGGACGGT  GTCC
                                        G_
GAM853  HFE     3' CACAGTGAGTCTGCAG     40000       AG  TGCTAA
                              CACAGTGA  CT    GCAG
                              ||||||||  ||    ||||
                              GTGTCACT  GA    CGTC
                                   CA  _______
GAM853  HPS1    3' AGAGAGCTTGCTGGGTGGGC  6800    T  A     AAGCA
                              AG GA GCTTGCT    GGC
                              || || |||||||    |||
                              TC CT CGAACGA    CCG
                               T  _     CCCAC
GAM853  KAI1    3' CAGTGAAGTGGGAGGCAGGC  13786       CT  CTAA
                              CAGTGAAG  TG   GCAGGC
                              ||||||||  ||   ||||||
                              GTCACTTC  AC   CGTCCG
                                   __  CCTC
GAM853  MLLT2   3' AGGAAGCAAGCAGG       25492    T    TTGCT
                              AG GAAGC    AAGCAGG
                              || |||||    |||||||
                              TC CTTCG    TTCGTCC
                                _    _____
GAM853  NGB     3' CAGTGAAGGGACTGGGCAGGC 34580       CTT   AA
                              CAGTGAAG   GCT  GCAGGC
                              ||||||||   |||  ||||||
                              GTCACTTC   TGA  CGTCCG
                                   CC_   CC
GAM853  PAH     3' ATGAAGCTTGAATGAAGCAGG  7091         CT__
                              GTGAAGCTTG    AAGCAGG
                              ||||||||||    |||||||
                              TACTTCGAAC    TTCGTCC
                                    TTAC
GAM853  PBX3    3' ACAGTAAAGCTGTAGATGGTGG 26211          TGCTAAGCA_
          GC                    ACAGTGAAGCT        GGC
                              ||||||||||         |||
                              TGTCATTTCGA        CCG
                                    CATCTACCAC
GAM853  RASGRP1 3' AGTGGGCTTAAGCAGG     25072     AA  TGC
                              AGTG  GCT   TAAGCAGG
                              ||||  |||   ||||||||
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                                TCAC  CGA   ATTCGTCC
                                  C_  ___
GAM853  RRP22    3'  CAGTGAAGCTCCAGGAGCAGGC 27004          GCTA
                                CAGTGAAGCTT    AGCAGGC
                                ||||||||||    |||||||
                                GTCACTTCGAG    TCGTCCG
                                      GTCC
GAM853  SYNGR1   3'  TGAGTGAGTAAGCAG      21772    C     A CTTGC
                                A AGTGA G     TAAGCAG
                                | |||||  |    |||||||
                                A TCACT C     ATTCGTC
                                 C    _ _____
GAM853  TK1      3'  CAGAGGGGAAGAAGCAGGC   17549     T___    CTTGCT
                                CAG    GAAG     AAGCAGGC
                                |||    ||||     ||||||||
                                GTC    CTTC     TTCGTCCG
                                  TCCC   _______
GAM854  GP1BA    3'  TTTGGCTGGGACTGAAATTGTG 6745       A_  A    GTC
                                TTTG  TG GGAC   GAAATTGTG
                                ||||  || ||||   |||||||||
                                AAAC  AC CCTG   CTTTAACAC
                                  CG  _    A__
GAM855  ATP6V1E1 5'  GGCTCGAGTTTAGGTTTG    11787     A   A CC
                                GGT TGA G  TAGGTTTG
                                ||| ||| |  ||||||||
                                CCG GCT C  ATCCAAAC
                                  A  _ AA
GAM855  DISC1    3'  TGGGGTGAATAGGTTTG     33056     TA    GCC
                                TGG  TGAA   TAGGTTTG
                                |||  ||||   ||||||||
                                ACC  ACTT   ATCCAAAC
                                  CC   ____
GAM855  KLK8     3'  TGGTATAGACGCCAGGTTTG   40327       _  A   T
                                TGGTAT GA GCC AGGTTTG
                                |||||| || ||| |||||||
                                ACCATA CT CGG TCCAAAC
                                    T  G  _
GAM855  LAMP1    3'  TGGATGAAGCAGATTTG     24513     T      CT
                                TGG ATGAAGC  AGGTTTG
                                ||| |||||||  |||||||
                                ACC TACTTCG  TCTAAAC
                                  _      ___
GAM855  LARS2    3'  TGGTATGAGTCCATTCCTG   31682        AG  TAGG
                                TGGTATGA  CC    TTTG
                                ||||||||  ||    ||||
                                ACCATACT  GG    GGAC
                                     CA  TAA_
GAM855  MECP2    3'  TGGTGTGGGGCCAGACTTG   22622      A  AA   T  GT
                                TGGT TG  GCC AG  TTG
                                ||||  ||  |||  ||  |||
```

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                                ACCA AC  CGG TC  AAC
                                  C  CC  _  TG
GAM855  MEF2C    3'  TGATATGCCTGCAGGTTTG   14410      GAA   __
                                TGGTAT  GCCT  AGGTTTG
                                ||||||  ||||  |||||||
                                ACTATA  CGGA  TCCAAAC
                                   ___   CG
GAM855  PTPRM    3'  TGGTATGAAAGGGATTGTTTG  15976        CCTAG_
                                TGGTATGAAG    GTTTG
                                ||||||||||    |||||
                                ACCATACTTT    CAAAC
                                      CCCTAA
GAM855  SCO1     3'  TGGTATGAAGGCCATTCTG   21380        _  TAGG
                                TGGTATGAAG CC   TTTG
                                |||||||||| ||   ||||
                                ACCATACTTC GG   AGAC
                                      C  TA__
GAM855  STARD4   3'  GGTATGAAGAACTTTG     40126        CCT  G
                                GGTATGAAG  AG TTTG
                                |||||||||  || ||||
                                CCATACTTC  TT AAAC
                                   ___  G
GAM855  TCL1B    3'  GGTATGAAGGGGATTTG     22255        CCTA
                                GGTATGAAG   GGTTTG
                                |||||||||   ||||||
                                CCATACTTC   CTAAAC
                                      CC__
GAM855  ZNFN1A3  3'  TGGTATGAAAAGAAGTTTG   41202        CCT
                                TGGTATGAAG  AGGTTTG
                                ||||||||||  |||||||
                                ACCATACTTT  TTCAAAC
                                      TC_
GAM855  DISC1    3'  CCGGGTGCGGTGGCTCACACCT 33033        AATA__  G T
          GT                      CCGGGTGC     TCA C CCTGT
                                |||||||     ||| | |||||
                                GGCCCACG     AGT G GGACA
                                   CCACCG  _ T
GAM855  INMT     3'  GGGTGTGGTGGCGAGCTCCTGT 27679      CAATATC_
                                GGGTG       AGCTCCTGT
                                |||||       |||||||||
                                CCCAC       TCGAGGACA
                                  ACCACCGC
GAM855  IRTA2    3'  GGGCTGCATACAGGCTCCTGT  36344    _   A  CA
                                GGG TGCA TAT  GCTCCTGT
                                ||| |||| |||  ||||||||
                                CCC ACGT ATG  CGAGGACA
                                  G   _  TC
GAM855  TAL1     3'  GGGTGCAATGGCTGACACCTGT 17287        ATCA_  T
                                GGGTGCAAT    GC CCTGT
                                |||||||||    || |||||
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                                CCCACGTTA    TG GGACA
                                     CCGAC  T
GAM855  ZNF174   5'  ACCGGGTGCATGTCGCC     18357          ATA  A
                                ACCGGGTGCA   TC GCT
                                ||||||||||  || |||
                                TGGCCCACGT   AG CGG
                                     AC_  _
GAM855  ZNF264   3'  CCGGGTGCAGTGGCTCACACCT 18270         ATA__  G T
          GT                     CCGGGTGCA    TCA C CCTGT
                                ||||||||||    ||| | |||||
                                GGCCCACGT    AGT G GGACA
                                     CACCG  _ T
GAM856  ADRB1    3'  ACGAGGATTGTGGGCTTCGAGT 8655         CGCGA  GG
                                ACGGGGAT    GC  TCGAGT
                                ||||||||    ||  ||||||
                                TGCTCCTA    CG  AGCTCA
                                     ACACC  A_
GAM856  SPON2    5'  CGCGGCCGGCAGCGGTCGGGTC 29712    G  A   CG      A
                                CG GG TCG  AGCGGTCG GTC
                                || || |||  |||||||| |||
                                GC CC GGC  TCGCCAGC CAG
                                 G  _   CG       C
GAM856  APLP2    3'  CGATCGGAATCGTGGGATCTTC 44920     A   CAGCA___
          C                      CGA CGG       GATCTTCC
                                |||  |||       ||||||||
                                GCT GCC       CTAGAAGG
                                  A   TTAGCACC
GAM856  APOBEC1  3'  CCTGAGCTTCGCCAGATCTTCC 25257    GAAC   A__  _
                                CC    GGC   GC AGATCTTCC
                                ||    |||   || ||||||||||
                                GG    TCG   CG TCTAGAAGG
                                 AC__   AAG  G
GAM856  HOXC13   3'  GAGGGCCAGATCTTC      40665    AC   AG
                                GA  GGC  CAGATCTTC
                                ||  |||  |||||||||
                                CT  CCG  GTCTAGAAG
                                 C_   __
GAM856  MAGEA3   5'  GACCCACTGGCAGATCTTC   23843     GA  GGCA
                                GACC  AC    GCAGATCTTC
                                ||||  ||    ||||||||||
                                CTGG  TG    CGTCTAGAAG
                                  G_  AC__
GAM856  RERE     5'  CGGTCGGGCAGATCTT     29027    AA   CA
                                CG  CGG  GCAGATCTT
                                ||  |||  |||||||||
                                GC  GCC  CGTCTAGAA
                                 CA   __
GAM856  SCA1     5'  CCTTGCAGCAGATCTT     7276     GAACG
                                CC    GCAGCAGATCTT
                                ||    ||||||||||||
```

```
                                GG    CGTCGTCTAGAA
                                 AA___
GAM856  SLC12A4  3'  GACTGAGCCAGATCTTC    22896    C  ACG  AG
                                GAC GA   GC  CAGATCTTC
                                ||| ||   ||  |||||||||
                                CTG CT   CG  GTCTAGAAG
                                  A  ___  __
GAM856  TM4SF6   3'  CAACCATTCCAGCAGATTTTC  17585      AACGG      C
                                CGACCG    CAGCAGAT TTC
                                ||||||    |||||||| |||
                                GTTGGT    GTCGTCTA AAG
                                   AAG__      A
GAM856  XRCC3    5'  CCAACGGCAGTCCGGCTCC   24102    G      CAGAT
                                CC AACGGCAG    CTTC
                                || ||||||||    ||||
                                GG TTGCCGTC    GAGG
                                 _      AGGCC
GAM857  HTR4     3'  TTCCCGGGACTTCTGC     9306          TA   C
                                TTCCCGGGACT  TCT GT
                                ||||||||||  ||| ||
                                AAGGGCCCTGA  AGA CG
                                       __   _
GAM857  PIGN     5'  TTCTGGAGCTTATCCCG    29555    CC  GA
                                TTC  GG  CTTATCTCG
                                |||  ||  |||||||||
                                AAG  CC  GAATAGGGC
                                  A_  TC
GAM857  SCNN1G   3'  TCCCGGGATTTATCTCAGCC   9793        C     _
                                TCCCGGGA TTATCTC GTC
                                |||||||| ||||||| |||
                                AGGGCCCT AATAGAG CGG
                                     A      T
GAM857  DMRT2    3'  TGTCAATTTTATTGCTTTTTGA 27273        AC     GATCG
                                TGTCAATT  ATTGCT    TGA
                                ||||||||  ||||||    |||
                                ACAGTTAA  TAACGA    ACT
                                     AA     AAA__
GAM857  MDM1     3'  TGTTAACTACATGCGCATTGTG 33520     C      _   TGATC
                                TGT AATTACAT TGC    GTG
                                ||| |||||||| |||    |||
                                ACA TTGATGTA GCG    CAC
                                  A       C   TAA__
GAM858  ADAM22   3'  TGCCTTAGCCCTGCATGCTCAT 34700     A      _
           T                     TGCC TTAGCTCT TATGCTCATT
                                 |||| |||||||| ||||||||||
                                 ACGG AATCGGGA GTACGAGTAA
                                   _       C
GAM858  PCDHB14  3'  TGACATTAGCTCTTAATACT   33190    C         _
                                TG CATTAGCTCTTA TGCT
                                || ||||||||||| ||||
```

```
                                AC GTAATCGAGAAT ATGA
                                 T          T
GAM858  FGFR1    3'  TGGAATGTTCTATTTGT     31960    A       GTG
                                TG GAATGTTCTA   GT
                                || ||||||||||   ||
                                AC CTTACAAGAT   CA
                                 _        AAA
GAM858  MAPK4    3'  AAGGATGTTGGGTCCCATG   15658    A    CTAGT
                                GAG ATGTT    GGTCCCATG
                                ||| |||||    |||||||||
                                TTC TACAA    CCAGGGTAC
                                  C    C____
GAM858  SLC16A2  3'  TGAGGATTTAAATGTCCCATG 27157     AAT   CT   G
                                TGAG   GTT  AGTG TCCCATG
                                ||||   |||  |||| |||||||
                                ACTC   TAA  TTAC AGGGTAC
                                  C__   AT   _
GAM858  ZNF135   3'  GAGCTTGGTGGTCCCAT     18332     AA  TTCTA
                                GAG  TG    GTGGTCCCAT
                                |||  ||    ||||||||||
                                CTC  AC    CACCAGGGTA
                                 GA  _____
GAM859  GCA      5'  GAGCGAGCGTCACCCTCGAGTC 29163         ACTG
           G                     GAGCGAGCG    TCTCGAGTCG
                                |||||||||    ||||||||||
                                CTCGCTCGC    GGAGCTCAGC
                                     AGTG
GAM859  LIPA     5'  CGGGCCGCTGTCTCGAGTC    6936     A  GA
                                CG GC  CTGTCTCGAGTC
                                || ||  ||||||||||||
                                GC CG  GACAGAGCTCAG
                                 C  GC
GAM859  AKAP1    3'  ACGAACAGGTGCCCGGCA     40221        ATA   G  C
                                ACGAACAG   GCC CG GCA
                                ||||||||   ||| || |||
                                TGCTTGTC   CGG GC CGT
                                     CA_   _ _
GAM859  CRY2     3'  AACAGATGCATGCACAC      43575        A  CGC
                                AACAGAT GC   GCGCAC
                                ||||||| ||   ||||||
                                TTGTCTA CG   CGTGTG
                                    _  TA_
GAM859  FGF7     3'  GAACAGATAGTCTGCTAGGCAC 12859         CC_  GC_
                                GAACAGATAG   GC   GCAC
                                ||||||||||   ||   ||||
                                CTTGTCTATC   CG   CGTG
                                      AGA  ATC
GAM859  G6PD     5'  CGAGGGCAGGTGCGCGCGC    7600      A__   ATA  C
                                CGA   CAG   GC GCGCGC
                                |||   |||   || ||||||
```

```
                                GCT  GTC  CG CGCGCG
                                  CCC  CA_ _
GAM859  IFNAR1   3'  CGAACAGACAGGTGTGGCACA 8431          CCGCGC
                                CGAACAGATAG    GCACA
                                ||||||||||    |||||
                                GCTTGTCTGTC    CGTGT
                                     CACAC_
GAM859  LRP8     3'  GATGGATAGCCACAAAGCA  21572   ACA      C_
                                GA  GATAGCCGCG  GCA
                                ||  ||||||||||  |||
                                CT  CTATCGGTGT  CGT
                                 AC_       TT
GAM859  MYO10    3'  ACGAACAGGCAAGCACGTACAC 29567       A  C   CG
                                ACGAACAG TAG CGCG  CAC
                                |||||||| ||| ||||  |||
                                TGCTTGTC GTT GTGC  GTG
                                     C  C   AT
GAM859  MYO1D    5'  ACGGGGAGGGGGCGCGCACGC  43486    AAC  ATA  _
                                ACG  AG  GC CGCGCGC
                                |||  ||  || |||||||
                                TGC  TC  CG GCGTGCG
                                  CCC  CCC  C
GAM859  PEA15    3'  ACAAACAGCCAGAGCGTGCGCA 19074       A  C_  C
          C                      ACGAACAG TAG  CG GCGCAC
                                ||||||||  |||  ||  ||||||
                                TGTTTGTC GTC  GC CGCGTG
                                     G  TC  A
GAM859  PRKACB   3'  GATGCAGAGTGCGCACAC   15595   A_   TAGCC
                                GA  CAGA   GCGCGCAC
                                ||  ||||   ||||||||
                                CT  GTCT   CGCGTGTG
                                 AC   CA___
GAM859  USP7     5'  CGGCAGGGAGACGCGCAC   18452   AA  AT  C
                                CG  CAG  AG CGCGCGC
                                ||  |||  || |||||||
                                GC  GTC  TC GCGCGTG
                                 C_  CC  T
GAM859  WISP2    5'  ACGAGTACACACGCGCGCGC  19306    __  G  A  C
                                ACGA  ACA AT GC GCGCGC
                                ||||  ||| || || ||||||
                                TGCT  TGT TG CG CGCGCG
                                  CA  G  _ _
GAM860  APAF1    3'  GTATGTATTCACATTTTCATT  10111       GGAGG_
                                GTATGTAT    TTTCATT
                                ||||||||    |||||||
                                CATACATA    AAAGTAA
                                     AGTGTA
GAM860  PURA     3'  GTGTGTGTGGGGGTTTCATT  25210   A  A  A
                                GT TGT TGG GGTTTCATT
                                || ||| ||| |||||||||
```

```
                                CA ACA ACC CCAAAGTAA
                                 C  C  C
GAM860  TERF1   3'  TAAGGTATGTATGACCTTGTT  32744    A       AG__
                                TAA GTATGTATGG   GTT
                                ||| ||||||||||   |||
                                ATT CATACATACT   CAA
                                  C        GGAA
GAM860  TRIM9   3'  AAAGTATGTGTGTGAACTTT  31550        A _  G
                                AAAGTATGT TG GAG TTT
                                ||||||||| || ||| |||
                                TTTCATACA AC CTT AAA
                                     C A  G
GAM860  KIF5C   3'  ATAGGATAGGAGTTTCCACC  21144    TA      GTGA
                                ATA  ATAGGAGT   TTACC
                                |||  ||||||||   |||||
                                TAT  TATCCTCA   GGTGG
                                  CC       AA__
GAM860  MTMR6   3'  ATATAATAGAGGTGTAAC   45276        GA
                                ATATAATAG  GTGTGAT
                                |||||||||  |||||||
                                TATATTATC  CACATTG
                                     TC
GAM860  PCDHA9  3'  ATATGAAGGACTAAATTACCAA 36540     AAT   G  T
                                ATAT   AGGA TG GATTACCAA
                                ||||   |||| || |||||||||
                                TATA   TCCT AT TTAATGGTT
                                  CT_   G  _
GAM860  PPARGC1 3'  ACATAATAGGATTTACTA   29947         GTGTG
                                ATATAATAGGA    ATTA
                                ||||||||||    ||||
                                TGTATTATCCT    TGAT
                                      AAA__
GAM860  UTY     3'  TAATAGGAGTAGTGTTTA   28315         _  A
                                TAATAGGAGT GTG TTA
                                |||||||||| ||| |||
                                ATTATCCTCA CAC AAT
                                     T   A
GAM860  ZNF138  3'  TAATAAGAGTTGAGGACCA   44344        G   TT
                                TAATAGGAGT TGA  ACCA
                                |||||||||| |||  ||||
                                ATTATTCTCA ACT  TGGT
                                     _   CC
GAM861  CDC42   3'  TACTGGATCTACTCAAGGGTG  12160       AA  AG   A
                                TATTGGAT  AC  CAA GGTG
                                ||||||||  ||  ||| ||||
                                ATGACCTA  TG  GTT CCAC
                                    GA  A_   C
GAM861  ITGAL   3'  TATTGGATAAATACATGCA   13621         __  _
                                TATTGGATAA  ACA GCA
                                ||||||||||  ||| |||
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                                ATAACCTATT  TGT CGT
                                      TA   A
GAM861   PON2     3'  TTGGAAGGCAAAGGTGA     7165        TAAACA
                                TTGGA     GCAAAGGTGA
                                |||||     ||||||||||
                                AACCT     CGTTTCCACT
                                   TC____
GAM861   SDC4     3'  TATTGGATAGCACAGCCCTAGA 16528          A_    AA_
                                TATTGGATA  ACAGC   AGG
                                |||||||||  |||||   |||
                                ATAACCTAT  TGTCG   TCT
                                      CG    GGA
GAM861   TRPS1    3'  TTGGATAAGGCAGGCTCTATGA 30478         A_   CAAAG
            A                    TTGGATAA  CAG    GTGAA
                                |||||||||  |||    |||||
                                AACCTATT  GTC    TACTT
                                     CC   CGAGA
GAM861   ANK2     3'  TGAAGAGGTCTGCAGGTGAAGT 34157         C    ____   C
            TCTTC                    TGGAGAGG CTGTA    AAGT CTTC
                                |||||||| |||||    |||| ||||
                                ACTTCTCC GACGT    TTCA GAAG
                                     A    CCAC    A
GAM861   APAF1    3'  TGGGGGGGCCTGCTAAATC    29829     AGA      A
                                TGG   GGCCTGT AAGTC
                                |||   ||||||| |||||
                                ACC   CCGGACG TTTAG
                                  CCC       A
GAM861   BBS4     3'  GGAGAGAAAAGTCCTT      37496        CCTGT
                                GGAGAGG    AAAGTCCTT
                                |||||||    |||||||||
                                CCTCTCT    TTTCAGGAA
                                     _____
GAM861   COG3     3'  GATTTCTGTAAAGTTCTT    36415    GGC       C
                                GA   CTGTAAAGT CTT
                                ||   ||||||||| |||
                                CT   GACATTTCA GAA
                                  AAA        A
GAM861   FECH     3'  TGGAGAGGCTTGCAAGGTCCC  6609          C    A
                                TGGAGAGGC TGTAA GTCCT
                                |||||||||  ||||| |||||
                                ACCTCTCCG ACGTT CAGGG
                                     A    C
GAM861   JUNB     3'  GGGGGGGCTTGTAAACGTC    13762    AGA  C    _
                                GG   GGC TGTAAA GTC
                                ||   ||| |||||| |||
                                CC   CCG ACATTT CAG
                                  CCC   A     G
GAM861   MEOX1    3'  TGGAGAGGCTGTGGAGTCCC   21187         C   AA
                                TGGAGAGGC TGT  AGTCCT
                                |||||||||  |||  ||||||
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                                ACCTCTCCG ACA  TCAGGG
                                      _  CC
GAM861  MLLT2   3'  TGGGGCACAGTGGAGTCCTTC  25514    AGA  CT_  AA
                                TGG  GGC  GT  AGTCCTTC
                                |||  |||  ||  ||||||||
                                ACC  CCG  CA  TCAGGAAG
                                  ___  TGT  CC
GAM861  P2RX3   3'  TGGGGAGGCCTGGAGCCTT   14997    A      TAA  T
                                TGG GAGGCCTG  AG CCTT
                                ||| ||||||||  || ||||
                                ACC CTCCGGAC  TC GGAA
                                  C      C__  _
GAM861  PIAS3   3'  GGAGGGCACAGGGTCCTTC   25910     A  CTGTAAA
                                GGAG GGC     GTCCTTC
                                |||| |||     |||||||
                                CCTC CCG     CAGGAAG
                                  _  TGTCC__
GAM861  PTX3    5'  TGGAGAGACGCAAAGTTCTT  15991       CT     C
                                TGGAGAGGC  GTAAAGT CTT
                                |||||||||  ||||||| |||
                                ACCTCTCTG  CGTTTCA GAA
                                      __     A
GAM861  RPL29   3'  TGGGGGGTCGCACCAGTCCTTC 9743    AGA  CC   A_
                                TGG  GG  TGTA  AGTCCTTC
                                |||  ||  ||||  ||||||||
                                ACC  CC  GCGT  TCAGGAAG
                                  C__  CA   GG
GAM861  SAS     3'  TGGAGAGAGAGGAAGAAAGTTT 25592       CCTGT__   CC
           TTC                  TGGAGAGG     AAAGT  TTC
                                ||||||||     |||||  |||
                                ACCTCTCT     TTTCA  AAG
                                    CTCCTTC    AA
GAM861  SLC22A12 5'  TGGGGAGGCCTAAGTTTTTC  40339    A      TAA  CC
                                TGG GAGGCCTG  AGT  TTC
                                ||| ||||||||  |||  |||
                                ACC CTCCGGAT  TCA  AAG
                                  C       ___  AA
GAM861  TBX6    3'  TGGGGAGGCCTGGTAAGT    38864    A      TA
                                TGG GAGGCCTG  AAGT
                                ||| ||||||||  ||||
                                ACC CTCCGGAC  TTCA
                                  C       CA
GAM861  TRPM7   3'  TGGAGAAGTTTGTAAGTTC   41622       CC    AG
                                TGGAGAGG  TGTAA  TC
                                ||||||||  |||||  ||
                                ACCTCTTC  ACATT  AG
                                    AA    CA
GAM861  VANGL2  3'  TGGTGAGGTGGGAGTCCTTC  43466    A   CC  TAA
                                TGG GAGG  TG   AGTCCTTC
                                ||| ||||  ||   ||||||||
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                                ACC CTCC  AC   TCAGGAAG
                                  A   __  CC_
GAM862  ADRA2A   3'  GTGAAATAAGAGTGCAGGCCTT 8640      TCTT_  CA
            AA                    GTGAA    GG  CAGGCCTTAA
                                  |||||    ||  ||||||||||
                                  CACTT    TC  GTCCGGAATT
                                    TATTC  AC
GAM862  ETV3     3'  TGCGAATCTACTAGGGGTCTTA 23479        TGGCACA  C
                                  TGTGAATCT      GG CTTA
                                  |||||||||      || ||||
                                  ACGCTTAGA      CC GAAT
                                       TGATCC_  A
GAM862  F7       3'  TGAATCTTGGAGTCTC     33344         CAC  GC
                                  TGAATCTTGG   AG  CTT
                                  ||||||||||   ||  |||
                                  ACTTAGAACC   TC  GAG
                                       ___  A_
GAM862  LYAAT1   5'  TGTCAGTCTTGGCACAAG    38531     GAA
                                  TGT   TCTTGGCACAGG
                                  |||   ||||||||||||
                                  ACA   AGAACCGTGTTC
                                    GTC
GAM862  MTF1     3'  TGTGAGCCAGGCCTT      25545      ATCTTG  A
                                  TGTGA     GC CAGGCCTT
                                  |||||     || ||||||||
                                  ACACT     CG GTCCGGAA
                                       _______  _
GAM862  DAPK1    3'  GTTTATAAATCATACAGTGG   22360     CA_  GC
                                  GTT   GA  CATACAGTGG
                                  |||   ||  ||||||||||
                                  CAA   TT  GTATGTCACC
                                    ATA  TA
GAM862  FGF5     3'  TCCCTGTGGATCTATACAGTGG 20918     AC  TCA  GCC
                                  TCC  GT   GA   ATACAGTGG
                                  |||  ||   ||   |||||||||
                                  AGG  CA   CT   TATGTCACC
                                    GA  C__  AGA
GAM862  FREB     3'  CCACGTCCTCATATGGTG    37222        AGAGC   CA
                                  CCACGTTC    CATA  GTG
                                  ||||||||    ||||  |||
                                  GGTGCAGG    GTAT  CAC
                                       A____    AC
GAM862  LZTR1    5'  TCCACGCTCGGGGCTACCTTGG 27642         AGA  CA   AG
                                  TCCACGTTC   GC  TAC  TGG
                                  |||||||||   ||  |||  |||
                                  AGGTGCGAG   CG  ATG  ACC
                                       CCC  __   GA
GAM862  SLC25A1  5'  TCCGCGCTCGGTCCGCGGTGG  25605     A    AGAG  ATACA
                                  TCC CGTTC    CC     GTGG
                                  ||| |||||    ||     ||||
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                                AGG GCGAG   GG    CACC
                                  C    CCA_  CGC__
GAM862  TGFBI   3'  TCCAAGTTTCTGCATGCAGTGG 7413      C  CAGA  C  A
                                TCCA GTT   GC AT CAGTGG
                                |||| |||   || || ||||||
                                AGGT CAA   CG TA GTCACC
                                  T  AGA_  _  C
GAM863  DAZ     5'  GCGCGTGGTATCGGCCTGAGCC 44366       A  CCAGCA
          A                      GCGCGT GG     CCTGAGCCA
                                |||||| ||     |||||||||
                                CGCGCA CC     GGACTCGGT
                                   _ ATAGCC
GAM863  EDN2    3'  GCTGTGGGCCAGCAGC     12646    GC  A      CCTGA
                                GC  GT GGCCAGCA    GC
                                ||  || ||||||||    ||
                                CG  CA CCGGTCGT    CG
                                 A_  C      _____
GAM863  GRB10   3'  GCGCGAGGCCAGCGAGC     23660      T      ACCT
                                GCGCG AGGCCAGC   GAGC
                                ||||| ||||||||   ||||
                                CGCGC TCCGGTCG   CTCG
                                  _      ____
GAM863  MTMR3   5'  GCGCTGGGCAGCGCCTGAGCC  34395     GTA  C  A
                                GCGC   GGC AGC CCTGAGCC
                                ||||   ||| ||| ||||||||
                                CGCG   CCG TCG GGACTCGG
                                  AC_  _  C
GAM863  NRF1    3'  GGCAAGGTCAGCACCTGGGCCA 41095   C  T  C      A
                                G GCG AGG CAGCACCTG GCCA
                                | ||| ||| |||||||||| ||||
                                C CGT TCC GTCGTGGAC CGGT
                                _  _  A       C
GAM863  PCDHA1  3'  GTAGGCTAGCACACC      36399      C    CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA10 3'  GTAGGCTAGCACACC      36566      C    CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA11 3'  GTAGGCTAGCACACC      36578      C    CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA12 3'  GTAGGCTAGCACACC      36598      C    CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
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                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA13  3' GTAGGCTAGCACACC      36606      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA2   3' GTAGGCTAGCACACC      33140      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA3   3' GTAGGCTAGCACACC      36477      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA4   3' GTAGGCTAGCACACC      36490      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA5   3' GTAGGCTAGCACACC      36499      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA6   3' GTAGGCTAGCACACC      36513      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA7   3' GTAGGCTAGCACACC      36521      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA8   3' GTAGGCTAGCACACC      36530      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHA9   3' GTAGGCTAGCACACC      36549      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A    ____
GAM863  PCDHAC1  3' GTAGGCTAGCACACC      36621      C   CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
```

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                                CATCCG TCGTG   TGG
                                   A   ____
GAM863  PCDHAC2  3'  GTAGGCTAGCACACC      36632      C    CTGA
                                GTAGGC AGCAC   GCC
                                |||||| |||||   |||
                                CATCCG TCGTG   TGG
                                   A   ____
GAM863  PIK3CD   3'  CAGAGCTGGCACCTGAGCC   22726    _  CA
                                TAG GC  GCACCTGAGCC
                                ||| ||  ||||||||||
                                GTC CG  CGTGGACTCGG
                                  T  AC
GAM863  RAB2L    5'  GCAGCGTGGGTCCTGAGCC   21919   _   A  CCAGCA
                                GC GCGT GG     CCTGAGCC
                                || |||| ||     ||||||||
                                CG CGCA CC     GGACTCGG
                                 T   C  A_____
GAM863  DNALI1   5'  CCAGCAGCTGCCCTGTCCAGTG 18441        G   GCG__   CGC
           TGG                    CCAGCAGC TGC    CCAG   GG
                                ||||||| |||    ||||  ||
                                GGTCGTCG ACG    GGTC   CC
                                    _  GGACA   ACA
GAM863  ECEL1    5'  CCGGCAGGTGCGCGCCCGAGCC 22093    A   C      __  G
           GG                    CC GCAG GTGCGCGCC  AGC CGG
                                || |||| |||||||||  ||| |||
                                GG CGTC CACGCGCGG  TCG GCC
                                 C   _       GC  _
GAM863  ERCC1    5'  CCAGCACGGCCAGCGTGG    12759      AGCGT   C     C
                                CCAGC    GCG GCCAGCG GG
                                |||||    ||| ||||||| ||
                                GGTCG    TGC CGGTCGC CC
                                  _____  _     A
GAM863  FN1      5'  GCAGCACAGCCGGCGCGG    38336      GT   C   A
                                GCAGC  GCG GCC GCGCGG
                                |||||  ||| ||| ||||||
                                CGTCG  TGT CGG CGCGCC
                                  __  _  C
GAM863  HTRA3    5'  GCGGCGGGTGGCAGCGCGG   44833    T   CGC__
                                GCG GCG    CAGCGCGG
                                ||| |||    ||||||||
                                CGC CGC    GTCGCGCC
                                  _  CCACC
GAM863  KCNH1    5'  GCGGGCGTCCTGGCGCGG    13842    T   CG  A_
                                GCG GCG  CC  GCGCGG
                                ||| |||  ||  ||||||
                                CGC CGC  GG  CGCGCC
                                  C  A_  AC
GAM863  SKIV2L   5'  CAGCGGCCAGCGCG       27969      TGCGC
                                CAGCG    GCCAGCGCG
                                |||||    |||||||||
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                              GTCGC    CGGTCGCGC
                                _____
GAM863  TAPBP    3'  GCAGTGGCTCCAGCGCGG    17304    GC   C  G
                              GCA  GTG GC CCAGCGCGG
                              |||  ||| || |||||||||
                              CGT  CAC CG GGTCGCGCC
                                __  _  A
GAM864  CUGBP1   3'  TACTTCAAAGTTGTCTTTAAAA 27277         CTT  AT
                              TACTTCAGAG   TC  TTTAAAA
                              ||||||||||   ||  |||||||
                              ATGAAGTTTC   AG  AAATTTT
                                    AAC  __
GAM864  GRM6     3'  CTTTAGAGCTCTCATCCCA   9170     C
                              CTT AGAGCTTTCATTTTA
                              ||| ||||||||||||||
                              GAA TCTCGAGAGTAGGGT
                                A
GAM864  ITGAM    3'  TTCAGAACTGTATTTTA     43523        TTC
                              TTCAGAGCT   ATTTTA
                              |||||||||   ||||||
                              AAGTCTTGA   TAAAAT
                                   CA_
GAM864  NEBL     3'  TACTTCAGAGACTTTTATTTTA 26907         _   C
                              TACTTCAGAG CTTT ATTTTA
                              |||||||||| |||| ||||||
                              ATGAAGTCTC GAAA TAAAAT
                                    T   A
GAM864  PTPRK    3'  TTCATCAGCTTTCATTTTA   15968     G_
                              TTCA  AGCTTTCATTTTA
                              ||||  ||||||||||||
                              AAGT  TCGAAAGTAAAAT
                                AG
GAM864  RBM8A    3'  CTTTAGAACTTTCAATTTTA   23012     C       _
                              CTT AGAGCTTTCA TTTTA
                              ||| ||||||||| |||||
                              GAA TCTTGAAAGT AAAAT
                                A        T
GAM864  SCD      3'  CTTCAGAGTTTTTTCCAAA    22827       C   CA
                              CTTCAGAG TTT  TTTTAAA
                              |||||||| |||  |||||||
                              GAAGTCTC AAA  AAGGTTT
                                   A  __
GAM864  ZNF18    3'  CTCTAGAACTCATTTTAA    44202    TC    TT
                              CT  AGAGC  TCATTTTAA
                              ||  |||||  |||||||||
                              GA  TCTTG  AGTAAAATT
                               GA    __
GAM864  CX3CR1   3'  GTCTGAGTTGAATTTTT     43295        GC
                              GTTTGAGT  TGAATTTTT
                              ||||||||  |||||||||
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                                CAGACTCA  ACTTAAAAA
                                    __
GAM864  IRTA1    3'  TAATATTTGGCTGCTGGTTTTT 36354         AG    AA
              G                  TAATGTTTG  TGCTG  TTTTTG
                                 |||||||||  |||||  ||||||
                                 ATTATAAAC  ACGAC  AAAAAC
                                      CG    C_
GAM864  LAPTM5   3'  TGATTTCAGGGCTGAATTTTTG 27608    T   G  T
                                 A GTTT AG GCTGAATTTTTG
                                 | |||| || ||||||||||||
                                 A TAAA TC CGACTTAAAAAC
                                  C   G  C
GAM864  XK       3'  TGTTTGGGTGCTATTTTTG   34375       A    GA
                                 TGTTTG GTGCT  ATTTTTG
                                 ||||||| |||||  |||||||
                                 ACAAAC CACGA  TAAAAAC
                                     C    __
GAM865  ID4      3'  GTGTAAAATGAAGAGTA     11385    A   CC
                                 GT TGAA  TGAAGAGTA
                                 || ||||  |||||||||
                                 CA ATTT  ACTTCTCAT
                                  C   T_
GAM865  PCDH1    5'  AACTGTACTGGGAAGGGT    37106        GAACCT   A
                                 AACTGTAT     GAAG GT
                                 ||||||||     |||| ||
                                 TTGACATG     CTTC CA
                                      ACC___    C
GAM865  PEX10    3'  CAACTGTATGGTTTGGGGAAG  15217          AACCT__
                                 CAACTGTATG      GAAG
                                 ||||||||||      ||||
                                 GTTGACATAC      CTTC
                                       CAAACCC
GAM865  RAG1     3'  ACTGTGTATGAAGAGTA     7783       A  AACC
                                 ACTGT TG    TGAAGAGTA
                                 ||||| ||    |||||||||
                                 TGACA AT    ACTTCTCAT
                                    C  ____
GAM865  SCA7     3'  CAGCCAATCTAACTTGAAGAGT 7305     A   TATG   C
                                 CA CTG    AAC TGAAGAGT
                                 || |||    ||| ||||||||
                                 GT GGT    TTG ACTTCTCA
                                  C   TAGA   A
GAM865  TIRAP    3'  TATATGGAAGAGTA       38093       AACCT
                                 TGTATG    GAAGAGTA
                                 ||||||    ||||||||
                                 ATATAC    CTTCTCAT
                                      _____
GAM865  CST6     5'  GAGCCCTCAGAGCCGTGAGTGC 10622          AAAA   C
                                 GAGCCTTCA    TTG TGAGTGC
                                 |||||||||    ||| |||||||
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                                CTCGGGAGT   GGC ACTCACG
                                     CTC_  _
GAM865  LILRB3   3'  GAGTCTCCTTCTGCTGAGTG  27801    C   AAAAA
                                GAG CTTC    TTGCTGAGTG
                                ||| ||||    ||||||||||
                                CTC GAGG    GACGACTCAC
                                  A   AA___
GAM865  MADH6    5'  GAGCCTTCAAAAGTTGTG    24598          A  C
                                GAGCCTTCAAAA TTG TG
                                |||||||||||| ||| ||
                                CTCGGAAGTTTT AAC AC
                                       C  _
GAM865  OTX1     3'  GAGCCTCCGAAGGCTGCAAGTG 30987        A  AA   T
              C                  GAGCCTTC AA  TTGC GAGTGC
                                |||||||| ||  |||| ||||||
                                CTCGGAGG TT  GACG TTCACG
                                     C  CC   _
GAM865  PCTK3    3'  GAGCCTTCGGGAGCTGAG    43778        AAAAATT
                                GAGCCTTC      GCTGAG
                                ||||||||      ||||||
                                CTCGGAAG      CGACTC
                                     CCCT___
GAM865  TNFAIP2  3'  GAGCCTCCAGAAGGAGTG    26636        AAAATTGCT
                                GAGCCTTCA       GAGTG
                                |||||||||       |||||
                                CTCGGAGGT       CTCAC
                                     CTTC_____
GAM866  CEBPA    3'  ATCGGCTGATAAAGCA      20382      GTACA
                                ATCGG    TGATAAAGCA
                                |||||    ||||||||||
                                TAGCC    ACTATTTCGT
                                   G____
GAM866  PKM2     3'  GGGCCACATGATGGGGCA    15334     _     AAA
                                GGGT ACATGAT   GCA
                                |||| |||||||   |||
                                CCCG TGTACTA   CGT
                                  G      CCC
GAM866  PLAGL1   3'  TTAAATTTGGTACAAAGC    15367      CG     TGATA
                                TTAAAT  GGTACA    AAGC
                                ||||||  ||||||    ||||
                                AATTTA  CCATGT    TTCG
                                   AA    _____
GAM866  APM1     3'  AGTAGTTTGCATAATATTTT  22010        T  CG
                                AGTAGTTT CA  GTATTTT
                                |||||||| ||  |||||||
                                TCATCAAA GT  TATAAAA
                                     C  AT
GAM866  KCNN2    3'  AGAGTTTTCACTCATTTT    34664    T       GG
                                AG AGTTTTCAC  TATTTT
                                || |||||||||  ||||||
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                                TC TCAAAAGTG  GTAAAA
                                 _       A_
GAM867  COIL     3'  TTACTTAAAACTTATTGAG   42738       TAAT
                                TTATTT    AAACTTATTGAG
                                ||||||    ||||||||||||
                                AATGAA    TTTGAATAACTC
                                   T___
GAM867  MBL2     3'  TTAAGAAATAAACTTATTGAG  6968      TTTT
                                TTA    AATAAACTTATTGAG
                                |||    ||||||||||||||||
                                AAT    TTATTTGAATAACTC
                                  TCT_
GAM867  CD2AP    3'  TCCCTCTCAAATAGTATAT   29074     AC    GGTAC
                                TCC  CTCA    AATAGTATAT
                                |||  ||||    ||||||||||
                                AGG  GAGT    TTATCATATA
                                  GA   _____
GAM867  RB1CC1   3'  ACCCTGTTACATAGTATAT   31305     CAGG    A
                                ACCT    TACA TAGTATAT
                                ||||    |||| ||||||||
                                TGGG    ATGT ATCATATA
                                  ACA_   _
GAM867  SHC1     3'  TCTGCCTCAGGTCTCTGGTAT  16709    CA       ACAATA
                                TC  CCTCAGGT     GTAT
                                ||  ||||||||     ||||
                                AG  GGAGTCCA     CATA
                                 AC       GAGAC_
GAM867  SMARCA3  3'  TCAGGCCACAGTATAT      40055       A  A
                                TCAGGT CA TAGTATAT
                                |||||| || ||||||||
                                AGTCCG GT GTCATATA
                                   _ _
GAM867  TCTE1L   3'  CACCTTAGGTACAAAATAT   43373       C       T
                                CACCT AGGTACAA AGTAT
                                ||||| |||||||| |||||
                                GTGGA TCCATGTT TTATA
                                   A       _
GAM868  TIM3     3'  TACCGTCTTGAAATTTAAGTT  37252    G     ATTA
                                TA CGTCTT    AAGTTTAAGTT
                                || ||||||    ||||||||||||
                                AT GCAGAA    TTTAAATTCAA
                                 G     C___
GAM868  ADCY9    3'  CTTTTGTTCTAAAAGTCA    10019      CA
                                CTTT  TTTTAAAAGTCG
                                ||||  ||||||||||||
                                GAAA  AAGATTTTCAGT
                                  AC
GAM868  IAPP     3'  TTTCATTTTAAAAGATAC    7667              TC
                                TTTCATTTTAAAAG  GC
                                ||||||||||||||  ||
```

```
                                AAAGTAAAATTTTC TG
                                       TA
GAM868  ITGA4   3' ACTTTCATTTCAAGATATC  9417          AA_
                                ACTTTCATTTTAA  GTC
                                |||||||||||||  |||
                                TGAAAGTAAAGTT  TAG
                                       CTA
GAM868  RNTRE   3' ACTTCCATTTTAAAAGACA  31245           T
                                ACTTTCATTTTAAAAG CG
                                |||||||||||||||| ||
                                TGAAGGTAAAATTTTC GT
                                       T
GAM868  SLC4A7  3' TTTCATTTTAAAAATGATCT  18829          CGC
                                TTTCATTTTAAAAGT  GTCT
                                |||||||||||||||  ||||
                                AAAGTAAAATTTTTA  TAGA
                                       C__
GAM868  UBL3    3' ACATTCATTTTAAAACTC   28261   T       G
                                AC TTCATTTTAAAA TC
                                || ||||||||||| ||
                                TG AAGTAAAATTTT AG
                                 T         G
GAM869  F8      3' TTGTGTTATTTTCAGCA    6571       TACTTTA
                                TTGTGTT     TTTAGCA
                                |||||||     |||||||
                                AACACAA     AAGTCGT
                                    TAA____
GAM869  M11S1   3' ATTGTTTTACTCCTAAGCAA  25326     G      ATTT
                                ATTGT TTTACTTT   AGCAA
                                ||||| ||||||||   |||||
                                TAACA AAATGAGG   TCGTT
                                   _      AT__
GAM869  MAPK9   3' CATTGTGTTTCTTACATGCA  40077        A  T  TTA
                                CATTGTGTTT CTT AT  GCA
                                |||||||||| ||| ||  |||
                                GTAACACAAA GAA TG  CGT
                                      _  _  TA_
GAM869  NEDD4   3' ATTGTAGTTTACTCAATAG   43099     _      TATT
                                ATTGT GTTTACTT   TAG
                                ||||| ||||||||   |||
                                TAACA CAAATGAG   ATC
                                   T      TT__
GAM869  NFIB    3' TTGTGTTTCTTTTTCCCTCA  24640       A   A  AG
                                TTGTGTTT CTTT TTT  CA
                                |||||||| |||| |||  ||
                                AACACAAA GAAA AGG  GT
                                    _   A  GA
GAM869  PPP2R5C 3' TTGTGTTACTTTATGC     15527       T     TTA
                                TTGTGTT ACTTTAT  GC
                                ||||||| |||||||  ||
```

```
                                AACACAA TGAAATA   CG
                                  _     ___
GAM869  PTGFR    3'  ATTGTGTCTACCTCCCATTGGC 9657            AT_  A
              AA                  ATTGTGTTTACTTT   TT GCAA
                                  ||||||||||||||   || ||||
                                  TAACACAGATGGAG   AA CGTT
                                        GGT  C
GAM869  SLC2A8   3'  TGTGTCAGTCTTTATTTGGCAA 31033       TA_      A
                                  TGTGTT   CTTTATTT GCAA
                                  ||||||   |||||||| ||||
                                  ACACAG   GAAATAAA CGTT
                                     TCA       C
GAM869  TSG101   3'  TATGCAACAAATTTTATTTAGC 26647      TT  ____
              A                    TGTGT  AC    TTTATTTAGCA
                                  |||||  ||    ||||||||||
                                  ATACG  TG    AAATAAATCGT
                                     T_  TTTA
GAM869  MEN1     5'  TATCTGTAAGCCTATTTGGGTG 39228     G        GCG  A
                                  TAT TGTAAGCCTA   TG GTG
                                  ||| ||||||||||   || |||
                                  ATA ACATTCGGAT   AC CAC
                                    G         AA_  C
GAM869  RNF26    3'  TAATGCTGTCCTAGCGTGAGTG 36755    T    AAG
              C                    A GTGT   CCTAGCGTGAGTGC
                                  | ||||   ||||||||||||||
                                  A TACG   GGATCGCACTCACG
                                   T    ACA
GAM869  SLC21A9  3'  ATGTGTAGGAATCAGTGAGTGC 28559        AGCCTAGC
                                  ATGTGTA       GTGAGTGC
                                  |||||||       ||||||||
                                  TACACAT       CACTCACG
                                      CCTTAGT_
GAM870  CX3CR1   3'  TATGTGAAAGGTACCTTA    43297        TAGAT
                                  TATGTGAA    AGGTATTTTA
                                  ||||||||    ||||||||||
                                  ATACACTT    TCCATGGAAT
                                     _____
GAM870  GAD1     3'  TATGTTGGTAGAAGTATTTTAT 9053       GAA    TA
                                  TATGT   TAGA  GGTATTTTAT
                                  |||||   ||||  ||||||||||
                                  ATACA   ATCT  TCATAAAATA
                                     ACC   __
GAM871  OAS3     3'  CCTAGGTCTCGACTCC      26179      A    AATC
                                  CCTA GGTC    CGACTCC
                                  |||| ||||    |||||||
                                  GGAT CCAG    GCTGAGG
                                    _    A___
GAM871  CTSZ     3'  CAGAGCCATGCTGTGCAAGTGT 41611         AC  TTCG
                                  CAGAGCCAT  CT    AAGTGT
                                  |||||||||  ||    ||||||
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                                GTCTCGGTA GA   TTCACA
                                    C_ CACG
GAM871  SLC16A2  3' TCAGAGTCTACCTTTCA    27154      CCA
                                TCAGAG  TACCTTTCG
                                ||||||  |||||||||
                                AGTCTC  ATGGAAAGT
                                   AG_
GAM872  ITPR1    3' TTCATCTTTATATGGATGTATA 13671        TATCACC___
          TAGTT                 TTCATCTTT       ATATAGTT
                                |||||||||       ||||||||
                                AAGTAGAAA       TATATCAA
                                    TATACCTACA
GAM872  KRT12    3' TTCATCTTTTATTACAAT    6902          CACCA
                                TTCATCTTTTAT    TATAGT
                                ||||||||||||    ||||||
                                AAGTAGAAAATA    ATGTTA
                                      _____
GAM872  NRIP1    5' TTCATCTTTTGTTCCCCAT   40991         A_ A
                                TTCATCTTTT  TC CCAT
                                ||||||||||  || ||||
                                AAGTAGAAAA  AG GGTA
                                    CA  G
GAM872  PLAB     3' TTTTATCACCAGAGTT     42320         TAT
                                TTTTATCACCA  AGTT
                                ||||||||||  ||||
                                AAAATAGTGGT  TCAA
                                    C__
GAM872  USH2A    3' TTCATCTTTTATTTTTCC    28306         CA__
                                TTCATCTTTTAT   CC
                                ||||||||||||   ||
                                AAGTAGAAAATA   GG
                                     AAAA
GAM872  ZNF236   3' TTCATCTTTTATTTATAGT   28871         CACCA
                                TTCATCTTTTAT    TATAGT
                                ||||||||||||    ||||||
                                AAGTAGAAAATA    ATATCA
                                    A____
GAM872  PCDH9    5' GGGGGCATTATCATTGGTATCC 44404    AACTACGT   _
          T                      GG       TCAT GGTATCCT
                                 ||       |||| ||||||||
                                 CC       AGTA CCATAGGA
                                  CCCGTAAT    A
GAM872  ZNF216   3' GGAACTACATTTTGTTCCT   25656         CATG  A
                                GGAACTACGTT   GT TCCT
                                ||||||||||   || ||||
                                CCTTGATGTAA   CA AGGA
                                    AA__  _
GAM873  ADORA2B  3' CACCATAAACAAGGCAGACTTT 8611      TGATTT   AA
                                CACC     ACAA  CAGACTTT
                                ||||     ||||  ||||||||
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                                GTGG     TGTT  GTCTGAAA
                                  TATT__   CC
GAM873  ATP7A    3'  CACCTGATTTTAAGACT     6259          ACAAAAC
                                CACCTGATTT      AGACT
                                ||||||||||      |||||
                                GTGGACTAAA      TCTGA
                                     AT_____
GAM873  CELSR1   3'  CACCTGATTTGAAGAACAA   30650         ACAA
                                CACCTGATTT    AACAG
                                ||||||||||    |||||
                                GTGGACTAAA    TTGTT
                                     CTTC
GAM873  EXTL3    5'  CACCCTGGAATCAGACAGACTT 11026       GATTTA  AA
           T                     CACCT     CA  ACAGACTTT
                                |||||     ||  |||||||||
                                GTGGG     GT  TGTCTGAAA
                                   ACCTTA  C_
GAM873  FRK      3'  ACCTATTTCTCAGACTT     13010       A   ACAAAA
                                ACCTG TTT     CAGACTT
                                ||||| |||     |||||||
                                TGGAT AAA     GTCTGAA
                                   _  GA____
GAM873  GDF8     3'  CACTTATTTACAAAACAA    23542     CTG
                                CAC   ATTTACAAAACAG
                                |||   ||||||||||||
                                GTG   TAAATGTTTTGTT
                                  AA_
GAM873  NR5A2    3'  TGTTCTACAGCAGACTTT    19238    A     AAA
                                TG TTTACA   CAGACTTT
                                || ||||||   ||||||||
                                AC AGATGT   GTCTGAAA
                                 A     C__
GAM873  PIK3R3   3'  CCCAATGAAACAGACTTT    41439    TG  TTACA
                                CC  AT    AAACAGACTTT
                                ||  ||    ||||||||||
                                GG  TA    TTTGTCTGAAA
                                 GT  C____
GAM873  PODXL    3'  CACCTGATCTACAAGACAAATA 23958            A   __
             CTTT                  CACCTGATTTACAA ACAG  ACTTT
                                |||||||||||||| ||||  |||||
                                GTGGACTAGATGTT TGTT  TGAAA
                                       C    TA
GAM873  PRKCN    3'  TGATATAAACAGACTTT     25171      TTACA
                                TGAT    AAACAGACTTT
                                ||||    ||||||||||
                                ACTA    TTTGTCTGAAA
                                  TA___
GAM874  EPS8     3'  TCTAAATATTCTTCCAT     20813      A
                                TCTA GATATTCTTCCAT
                                |||| ||||||||||||
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                                AGAT TTATAAGAAGGTA
                                  _
GAM874  RNASE4   3'  TCTCAATTCTTCCATTAACTT  16347     AAGAT        C
                                TCT    ATTCTTCCAT AACTT
                                |||    |||||||||| |||||
                                AGA    TAAGAAGGTA TTGAA
                                  GT___        A
GAM874  RUNX1    3'  TCTGGGATATTCTCTCAT    12029     AA      TC
                                TCT  GATATTCT  CAT
                                |||  ||||||||  |||
                                AGA  CTATAAGA  GTA
                                  CC       GA
GAM874  SOX11    3'  TAAGATATTCTGTCAA      17036          TCCA
                                TAAGATATTCT   TCAA
                                ||||||||||   ||||
                                ATTCTATAAGA   AGTT
                                      C___
GAM874  ARHGDIA  3'  GGGGGGACACATCCGCC     20215     AA      ATGA
                                GGG  GATACATT   CGTC
                                |||  ||||||||   ||||
                                CCC  CTGTGTAG   GCGG
                                  CC      ____
GAM874  CLCN6    3'  GAGAAGAATGACGT       34716       TACATT
                                GGGAAGA     ATGACGT
                                |||||||     |||||||
                                CTCTTCT     TACTGCA
                                   _______
GAM874  HLF      3'  GGGAAAATATCCTACGTC    13392        CA  ATG
                                GGGAAGATA  TT   ACGTC
                                |||||||||  ||   |||||
                                CCCTTTTAT  AG   TGCAG
                                     __ GA_
GAM874  PAG      3'  GGGAAATACACATTCATG    32955       _     _
                                GGGAAG ATACAT TATG
                                |||||| |||||| ||||
                                CCCTTT TGTGTA GTAC
                                   A     A
GAM874  RAB7L1   3'  GAGAAACTTAATTATGACGT  19433       ATAC
                                GGGAAG   ATTATGACGT
                                ||||||   ||||||||||
                                CTCTTT   TAATACTGCA
                                   GAAT
GAM874  RBBP9    3'  GGGAAAATACAAAATATATGTC 43140          TT   AC_
                                GGGAAGATACA  ATG   GTC
                                ||||||||||  |||   |||
                                CCCTTTTATGT  TAT   CAG
                                      TT   ATA
GAM874  TH1L     3'  AGGAGGAGCAATGACGTC    32306      A  TACATT
                                GGGA GA     ATGACGTC
                                ||||  ||     ||||||||
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                                TCCT CT     TACTGCAG
                                  C  CGT___
GAM874  VGF     5'  GGGAAGATCGGGACGCGTC   17994       ACATT   A
                                GGGAAGAT    ATG CGTC
                                ||||||||    ||| ||||
                                CCCTTCTA    TGC GCAG
                                    GCCC_   _
GAM875  ABCC3   3'  CACGAGCTGCCTCTGG     33416       GC    CTGCG
                                CACGAGCTG  CCTC    GG
                                |||||||||  ||||    ||
                                GTGCTCGAC  GGAG    CC
                                    __    A____
GAM875  ARHGAP6  5'  CGGGGCTGGCCCGGGG     25964    A_      TCCT C
                                CG  GCTGGCCC    G GGG
                                ||  ||||||||    | |||
                                GC  CGACCGGG    C CCC
                                 CC       _____ _
GAM875  BRCA1   3'  CACGAGCTGACTCTGGGGC   28621         CCTC   C
                                CACGAGCTGGC    CTG GGGC
                                ||||||||||    ||| ||||
                                GTGCTCGACTG    GAC CCCG
                                     A___   _
GAM875  CAPN10   3'  CACCAGCTGGCCCCCAGGGC   35763     G        CTGC
                                CAC AGCTGGCCCTC    GGGC
                                ||| ||||||||||    ||||
                                GTG TCGACCGGGGG    CCCG
                                  G         T___
GAM875  CCND1   3'  GAGCTGGCTGCAGGGC     38205       CCTCC  _
                                GAGCTGGC    TGC GGGC
                                ||||||||    ||| ||||
                                CTCGACCG    ACG CCCG
                                    ______  T
GAM875  CIT     5'  GAGCTGGCGCTTGAGC     43049       CCTC  GC
                                GAGCTGGC    CT  GGGC
                                ||||||||    ||  ||||
                                CTCGACCG    GA  CTCG
                                    C___  A_
GAM875  CTBP1   5'  CGAGCGGCCGCGGG      42748      T   CTCCT
                                CGAGC GGCC    GCGGG
                                ||||| ||||    |||||
                                GCTCG CCGG    CGCCC
                                  _   ______
GAM875  DHCR24   3'  GAGCTGGCCTTGGGG      31298       CTCC  C
                                GAGCTGGCC    TG GGG
                                |||||||||    || |||
                                CTCGACCGG    AC CCC
                                     A___  _
GAM875  ESPN    5'  CACGTGTTCTTGCGGG     36441     AGC  GCCC  C
                                CACG   TG    TC TGCGGG
                                ||||   ||    || ||||||
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                                GTGC   AC    AG ACGCCC
                                  ___  A___  A
GAM875  FBP1     5'  CGGGCGGCAGGTGCGGGCC   8001     A  T   CCTCC
                                CG GC GGC    TGCGGGCC
                                || || |||    ||||||||
                                GC CG CCG    ACGCCCGG
                                 C  _  TCC__
GAM875  FOXE1    5'  CGGGCTGGCCCCGAGAGCC   20942    A       CCT C
                                CG GCTGGCCCT   G GGGCC
                                || |||||||||   | |||||
                                GC CGACCGGGG   C CTCGG
                                 C        ___ T
GAM875  G6PC     3'  GAGCTGGCCCTACCTGGAAG   6661          _   CG
                                GAGCTGGCCCT CCTG  GG
                                |||||||||| ||||  ||
                                CTCGACCGGGA GGAC  TC
                                       T    CT
GAM875  GYPE     5'  CACGAGCTGGCTCCTGAAG    13330         CC    C
                                CACGAGCTGGC  TCCTG GG
                                ||||||||||  ||||| ||
                                GTGCTCGACCG  AGGAC TC
                                      __     T
GAM875  HSD17B1  5'  CAAGGATAAGCCTTCCTGCGGG 7655      CT__    C
                                CGAG    GGCC TCCTGCGGG
                                ||||    |||| |||||||||
                                GTTC    TCGG AGGACGCCC
                                  CTAT    A
GAM875  KIAA0857 5'  CGGGCTGGGCTGGGCCGGGCC  42472    A    CCCTC  ___
                                CG GCTGG    CTG   CGGGCC
                                || |||||    |||   ||||||
                                GC CGACC    GAC   GCCCGG
                                 C    C____   CCG
GAM875  LTBP2    5'  CGGGCTGTTCTCCCGGC     7694     A   GCC    GCG
                                CG GCTG   CTCCT   GGC
                                || ||||   |||||   |||
                                GC CGAC   GAGGG   CCG
                                 C    AA_    ___
GAM875  MECP2    3'  GAGCTGGCCCCGGATGTGGGCC 22588          CC_  C
                                GAGCTGGCCCT   TG GGGCC
                                ||||||||||   || |||||
                                CTCGACCGGGG   AC CCCGG
                                      CCT  A
GAM875  MEIS2    3'  GCTGACCCTCTGGAC      33542          CTGC
                                GCTGGCCCTC    GGGC
                                ||||||||||    ||||
                                CGACTGGGAG    CCTG
                                      A___
GAM875  MKNK2    3'  GAGCTGGCCTGGGGC       32763         CTCC  C
                                GAGCTGGCC    TG GGGC
                                |||||||||    || ||||
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                              CTCGACCGG   AC CCCG
                                  _____ _
GAM875  MYD88   3'  GAGCTGGCTCTGCTGG     14715       CCTC   G
                              GAGCTGGC   CTGC GG
                              ||||||||   |||| ||
                              CTCGACCG   GACG CC
                                  A___   A
GAM875  PIK4CB  3'  CACAGCTGGCTCTCCCAC   15312    G     C   TG
                              CAC AGCTGGC CTCC  C
                              ||| ||||||| ||||  |
                              GTG TCGACCG GAGG  G
                                _     A   GT
GAM875  PRX2    5'  CGAGCGGCCCCGGGGGGGCC  32229     T    CCTGC
                              CGAGC GGCCCT    GGGCC
                              ||||| ||||||    |||||
                              GCTCG CCGGGG    CCCGG
                                _     CCCC_
GAM875  RANBP3  3'  CAAGCTGGCTCTTGGC     28752       CC  CTGCG
                              CGAGCTGGC  TC    GGC
                              |||||||||  ||    |||
                              GTTCGACCG  AG    CCG
                                   __  AA___
GAM875  RGS14   3'  ACCGGCTCTTCCTGCGGGCC  27014      C  _
                              GCTGGC CT CCTGCGGGCC
                              |||||| || ||||||||||
                              TGGCCG GA GGACGCCCGG
                                 A  A
GAM875  RNPEPL1 3'  CGGGCTGGCCCCAGGGC    32878   A      CCTGC
                              CG GCTGGCCCT    GGGC
                              || |||||||||    ||||
                              GC CGACCGGGG    CCCG
                               C       T_____
GAM875  SDC1    5'  CGGGCCGGCTTCGCGGG    16503   A    CC  CT
                              CG GCTGGC  TC  GCGGG
                              || ||||||  ||  |||||
                              GC CGGCCG  AG  CGCCC
                               C     A_  __
GAM875  SLC6A3  3'  GACTGGCCCTGCACGGCC   9811    G     CCT  _
                              GA CTGGCCCT   GCG GGCC
                              || ||||||||   ||| ||||
                              CT GACCGGGA   CGT CCGG
                               _      ___  G
GAM875  SURF5   5'  CACGGCCTGGCCCTCCCGC  39502    AG
                              CACG  CTGGCCCTCCTGC
                              ||||  ||||||||||||
                              GTGC  GACCGGGAGGGCG
                                CG
GAM875  TCF20   3'  CACGGGTCCCTGTGGG     42531    AGCT  CCC   C
                              CACG   GG   TCCTG GGG
                              ||||   ||   ||||| |||
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                                GTGC   CC  GGGAC CCC
                                  ____ A__   A
GAM875  TCN2    5' GCTGGCCCTGCTGAGGC    7407        C  C
                                GCTGGCCCT CTG GGGC
                                ||||||||| ||| ||||
                                CGACCGGGA GAC TCCG
                                    C  _
GAM875  VIPR2   3' CGCAGCTGGCCTGGGG     18009   _     CTCC  C
                                CG AGCTGGCC   TG GGG
                                || ||||||||   || |||
                                GC TCGACCGG   AC CCC
                                 G     ____ _
GAM876  CAPN10  3' GGGCTCCAGTCACCTGA    35776    TTCACC   AC
                                GGGC    TCCA  CACCTGA
                                ||||    ||||  |||||||
                                CCCG    AGGT  GTGGACT
                                  _______  CA
GAM876  FS      5' GGGCTGCACCTGAGCCTG    35088     T   CCAACCA
                                GGGCT CACCT     CCTG
                                ||||| |||||     ||||
                                CCCGA GTGGA     GGAC
                                  C   CTC____
GAM876  GCH1    5' GGGCTGTGGCCGGAGTCACCTG 6704      TCA_  TCCAAC
           AG                   GGGCT   CC    CACCTGAG
                                |||||   ||    ||||||||
                                CCCGA   GG    GTGGACTC
                                  CACC  CCTCA_
GAM876  MMP14   3' GGGCCTCAGCCCCAGCTGCCTG 22642       C    ACCA
           AG                   GGGCTTCA CTCCA   CCTGAG
                                |||||||| |||||   ||||||
                                CCCGGAGT GGGGT   GGACTC
                                    C    CGAC
GAM876  PPP1R3D 3' GGCCTTCTGGCCACCTGA   26427   G   ACCTCCAA
                                GG CTTC      CCACCTGA
                                || ||||      ||||||||
                                CC GAAG      GGTGGACT
                                 G   ACC_____
GAM877  CX3CR1  3' TATGTGAAAGGTACCTTA   43297       TAGAT
                                TATGTGAA    AGGTATTTTA
                                ||||||||    ||||||||||
                                ATACACTT    TCCATGGAAT
                                   _____
GAM877  GAD1    3' TATGTTGGTAGAAGTATTTTAT 30294     GAA   TA
                                TATGT   TAGA  GGTATTTTAT
                                |||||   ||||  ||||||||||
                                ATACA   ATCT  TCATAAAATA
                                  ACC   __
GAM877  DKK1    3' TCATTCCAAGAGATCC     29272     CGAA
                                TCAT    TTTAAGAGATCC
                                ||||    ||||||||||||
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                                AGTA   AGGTTCTCTAGG
                                  ____
GAM877  IHPK3    3'  TTCCTCATTTTAAGAGAT    38380     A   CGAA
                                TTC TCAT   TTTAAGAGAT
                                ||| ||||   ||||||||||
                                AAG AGTA   AAATTCTCTA
                                  G   ____
GAM878  BTG1     3'  TTAAAAATGCCAAGATAAGAA  11914          ATCT
                                TTAGAAATGCCAA   ATAAGAA
                                ||||||||||||   |||||||
                                AATTTTTACGGTT   TATTCTT
                                       C___
GAM878  CKTSF1B1 3'  TTAGAAATGTTAACCTTTAAG  30095        CCA    A
                                TTAGAAATG   AATCT TAAG
                                |||||||||   ||||| ||||
                                AATCTTTAC   TTGGA ATTC
                                     AA_    A
GAM879  DXS1283E 3'  CGAGTCTCAAGAGATCCG    43352     A_
                                CGA  TTTAAGAGATCCG
                                |||  ||||||||||||
                                GCT  GAGTTCTCTAGGC
                                  CA
GAM879  VHL      3'  CCGGGTTCAAGAGATTCG    8107      AA       C
                                TCG  TTTAAGAGAT CG
                                |||  |||||||||| ||
                                GGC  AAGTTCTCTA GC
                                  CC        A
GAM880  BRPF1    3'  ACGCAGTGTCCTAACT      43814    A   ATAT A
                                AC CAGT    G TCCTAACT
                                || ||||    | ||||||||
                                TG GTCA    C AGGATTGA
                                 C   _____ _
GAM880  DACH     3'  CACAGCACATTTTAACT     38870         GATCC
                                CACAGTATAT    TAACT
                                ||||||||||    |||||
                                GTGTCGTGTA    ATTGA
                                     AA___
GAM880  DLEC1    3'  ACACAGCAGGTCCTGGCT    28812       TATGA   AA
                                ACACAGTA    TCCT  CT
                                ||||||||    ||||  ||
                                TGTGTCGT    AGGA  GA
                                    CC___   CC
GAM880  HCS      3'  CAGTGGCACAATCCTGGCTC  33225     A_  TG    AA
                                CAGT  TA  ATCCT  CTC
                                ||||  ||  |||||  |||
                                GTCA  GT  TAGGA  GAG
                                  CC  GT    CC
GAM880  HLA-E    3'  CAGTCGCACAATCCTGGCTC  44956     A_  TG    AA
                                CAGT  TA  ATCCT  CTC
                                ||||  ||  |||||  |||
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                                GTCA  GT  TAGGA  GAG
                                  GC  GT    CC
GAM880  KCNAB1   3'  ACACAGTATAGTCTCACAA   41397         TGA  C
                                ACACAGTATA   TC TAA
                                ||||||||||   || |||
                                TGTGTCATAT   AG GTT
                                     CAG  T
GAM880  MNT      3'  TAACACAGAGCCCCTGACT   33725        TATATGA   A
                                TAACACAG      TCCT ACT
                                ||||||||      |||| |||
                                ATTGTGTC      GGGA TGA
                                     TCG____    C
GAM880  PPT2     3'  TAACGCGGTACATGGTCC    39925      ACA      A
                                TAAC   GTATATG TCC
                                ||||   ||||||| |||
                                ATTG   CATGTAC AGG
                                  CGC      C
GAM880  USP9Y    3'  TAACATAGTATATATACCT    41959      C       AT
                                TAACA AGTATATG  CCT
                                ||||| ||||||||  |||
                                ATTGT TCATATAT  GGA
                                   A       AT
GAM881  NPHP1    3'  CATGGTATCTTTACTGGGAATA 41679         ____   C
           TTA                    CATGGTATC    CTGG GAATATTA
                                ||||||||    |||| ||||||||
                                GTACCATAG    GACC CTTATAAT
                                     AAAT   _
GAM882  ATP11A   3'  TGTGTGCATGTGTGCAGT    44194          _   T
                                TGTGTGCATGT TGTA GT
                                |||||||||| |||| ||
                                ACACACGTACA ACGT CA
                                     C   _
GAM882  ATP11A   3'  TGTGTGCATGTGTGTAGGAGCC 44195          _   TGT_
           TGT                    TGTGTGCATGT TGTA    TTTGT
                                |||||||||| ||||    |||||
                                ACACACGTACA ACAT    GGACA
                                     C    CCTC
GAM882  ATP8A2   3'  TGTGTGCATGTGTGTGTT    45273          T  A
                                TGTGTGCATGT GT TGTT
                                |||||||||| || ||||
                                ACACACGTACA CA ACAA
                                     _  C
GAM882  CPNE3    3'  TGAGTGCATGCTGTTTTGT    19385    T      TGTA
                                TG GTGCATGT    TGTTTTGT
                                || ||||||||    ||||||||
                                AC CACGTACG    ACAAAACA
                                 T      ____
GAM882  CSF2RB   3'  TGTGTGTGTGTGTGTCTGT    7575       CA   T  A    T
                                TGTGTG  TGT GT TGTTT GT
                                ||||||  ||| || ||||| ||
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                                ACACAC  ACA CA ACAGA CA
                                  __  _ C    _
GAM882  CX3CR1   3'  TGTGTGGCATTTGTTTTGT   43302       _  GTTGTA
                                TGTGTG CAT     TGTTTTGT
                                |||||| |||     ||||||||
                                ACACAC GTA     ACAAAACA
                                   C  A_____
GAM882  DGKG     3'  TGTGTGCATGTGTGAGTGT   10661          _ TA
                                TGTGTGCATGT TG  TGT
                                |||||||||| ||  |||
                                ACACACGTACA AC  ACA
                                      C  TC
GAM882  DIAPH2   3'  TGTGTGCATGTGTGTGCATTTG 28687          T  A  _
          T                      TGTGTGCATGT GT TGT TTTGT
                                |||||||||| || ||| |||||
                                ACACACGTACA CA ACG AAACA
                                      _ C  T
GAM882  DIAPH2   3'  TGTGTGCATTTGTGTATGT   28688        GT_
                                TGTGTGCAT   TGTATGT
                                |||||||||   |||||||
                                ACACACGTA   ACATACA
                                     AAC
GAM882  DMD      3'  TGTGTGTGTGTTTGTTTTG   19699       CA  T  A
                                TGTGTG  TGT GT TGTTTTG
                                ||||||  ||| || |||||||
                                ACACAC  ACA CA ACAAAAC
                                  __  _ A
GAM882  EGR3     3'  TGTGTGTATGTTATGTATATGT 40564       C      A   TT
          A                     TGTGTG ATGTTGT TGT  TGTA
                                |||||| ||||||| |||  ||||
                                ACACAC TACAATA ATA  ACAT
                                   A      C  T_
GAM882  EHD3     3'  TGTGTGCATGTTTGTGTGTGTG 31121          _ A   TT
          T                     TGTGTGCATGTT GT TGT  TGT
                                |||||||||||| || |||  |||
                                ACACACGTACAA CA ACA  ACA
                                      A  C   C_
GAM882  FOSB     3'  TGTGTTTGTTTGTTTTGT    27547      GCATG   A
                                TGTGT    TTGT TGTTTTGT
                                |||||    |||| ||||||||
                                ACACA    AACA ACAAAACA
                                  _____   A
GAM882  GLS      3'  TGTGTGCATGTGTGTGT     31382          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _ C
GAM882  GNAZ     3'  TGTGTGCATGTGTGTGT     13191          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
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                                ACACACGTACA CA ACA
                                      _ C
GAM882  GTF2H1   3'  TGTGTGTGTGTGTATAT    23694       CA   T
                                TGTGTG  TGT GTATGT
                                ||||||  ||| ||||||
                                ACACAC  ACA CATATA
                                   AC  _
GAM882  KIF5A    3'  TGTGTGCGTGTGTGCGTGT   22552       A  _  TA
                                TGTGTGC TGT TG  TGT
                                ||||||| ||| ||  |||
                                ACACACG ACA AC  ACA
                                   C  C  GC
GAM882  KIF5A    3'  TGTGTGCGTGTGTGTATG    22553       A  _
                                TGTGTGC TGT TGTATG
                                ||||||| ||| ||||||
                                ACACACG ACA ACATAC
                                   C  C
GAM882  KIF5A    3'  TGTGTGCATGTTTGTGTGCGTG 22551          _  A  TT
           T                     TGTGTGCATGTT GT TGT  TGT
                                ||||||||||| || |||  |||
                                ACACACGTACAA CA ACG  ACA
                                      A  C  C_
GAM882  MHC2TA   3'  TGTGTGTATGTGTGTGT    6993        C   T  A
                                TGTGTG ATGT GT TGT
                                |||||| |||| || |||
                                ACACAC TACA CA ACA
                                   A  _ C
GAM882  NLGN3    3'  TGTGTGTGTGTGTGTCTGCGTG 33292       CA  _  A  TT
           T                     TGTGTG  TGT TGT TGT  TGT
                                ||||||  ||| ||| |||  |||
                                ACACAC  ACA ACA ACG  ACA
                                   AC  C  G  C_
GAM882  NLGN3    3'  TGTGTGTGTGTGTGTGTCT   33293       CA  T  A
                                TGTGTG  TGT GT TGTTT
                                ||||||  ||| || |||||
                                ACACAC  ACA CA ACAGA
                                   AC  _ C
GAM882  PCDH11Y  3'  TGTGTGTATGTGTGTGT    37356       C   T  A
                                TGTGTG ATGT GT TGT
                                |||||| |||| || |||
                                ACACAC TACA CA ACA
                                   A  _ C
GAM882  PCDH11Y  3'  TGTGTGTGTGTATGTGTGT   37360       CA  T    TT
                                TGTGTG  TGT GTATGT  TGT
                                ||||||  ||| ||||||  |||
                                ACACAC  ACA CATACA  ACA
                                   __  _    C_
GAM882  PCDH11Y  3'  TGTGTGTGTGTGTGTATGT   37361       CA  _
                                TGTGTG  TGT TGTATGT
                                ||||||  ||| |||||||
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                                ACACAC  ACA ACATACA
                                   AC   C
GAM882  PLAG1    3'  TGTGTGCATGTGTGTGT     15362          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _  C
GAM882  RCV1     3'  TGTGTGCATGTGTGTGT     16227          T  A
                                TGTGTGCATGT GT TGT
                                |||||||||| || |||
                                ACACACGTACA CA ACA
                                      _  C
GAM882  SLC1A4   3'  TGTGTGTGTGTTGTGTAT    16763       CA     A
                                TGTGTG  TGTTGT TGT
                                ||||||  |||||| |||
                                ACACAC  ACAACA ATA
                                   AC     C
GAM882  SNAP25   3'  TGTGTGTGTGTTGTCTCATCAG 39263       CA     ATGT  T
          TA                     TGTGTG  TGTTGT    TT GTA
                                ||||||  ||||||    || |||
                                ACACAC  ACAACA    AG CAT
                                   AC     GAGT  T
GAM882  WHSC1    3'  TGTGTGCGTGTGTATAAAAAGT 39407        A   T    TTTT
                                TGTGTGC TGT GTATG    GT
                                ||||||| ||| |||||    ||
                                ACACACG ACA CATAT    CA
                                    C  _    TTTT
GAM882  XKRY     5'  TGTGGGCATGTTTTTGTTTGT  21708      T      GTA    T
                                TGTG GCATGTT   TGTTT GT
                                |||| |||||||   ||||| ||
                                ACAC CGTACAA   ACAAA CA
                                  C      AA_    _
GAM883  CPSF6    3'  TTTGACCCCTTACACAT     28135      T   A
                                TTTG CCTT TTACACAT
                                |||| |||| ||||||||
                                AAAC GGGG AATGTGTA
                                  T   _
GAM883  HAO1     3'  CTCTTTGTCAAGTAATACA   32759         CT_  T
                                TTCTTTGTC   TA TACA
                                |||||||||   || ||||
                                GAGAAACAG   AT ATGT
                                     TTC  T
GAM883  HCS      3'  TCTTTAATATTACACAT     33236       TCCT
                                TCTTTG    TATTACACAT
                                ||||||    ||||||||||
                                AGAAAT    ATAATGTGTA
                                   T___
GAM883  INMT     3'  TTCCTTGTCCTTAACA      27684           TT
                                TTCTTTGTCCTTA  ACA
                                |||||||||||||  |||
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                                AAGGAACAGGAAT  TGT
                                        __
GAM883  NRXN2    3'  TTCTTTTTCCCACACA     31496       G    TATT
                                TTCTTT TCCT    ACACA
                                |||||| ||||    |||||
                                AAGAAA AGGG    TGTGT
                                   A   ____
GAM883  PTPRM    3'  TCTTTGTTCATTACACAT    15975       CC
                                TCTTTGT  TTATTACACAT
                                |||||||  ||||||||||
                                AGAAACA  AGTAATGTGTA
                                    __
GAM883  RAD21    3'  TTCTGTGTCCCCTACACAT   26534     T     TA
                                TTCT TGTCCT  TTACACAT
                                |||| ||||||  ||||||||
                                AAGA ACAGGG  GATGTGTA
                                  C     __
GAM883  RP1      3'  TTCTTGTCCTTAGCACA     26554      T     T
                                TTCTT GTCCTTA TACA
                                ||||| |||||||  ||||
                                AAGAA CAGGAAT GTGT
                                   _      C
GAM883  USP6     5'  TTCCTTGTCCTGATGCCACAT  45034          T  TA
                                TTCTTTGTCCT AT  CACAT
                                |||||||||||  ||  |||||
                                AAGGAACAGGA TA  GTGTA
                                      C  CG
GAM883  WBSCR1   3'  TTCTTTATCTTATCCACAT   35274         C    A
                                TTCTTTGTC TTATT CACAT
                                |||||||||  ||||| |||||
                                AAGAAATAG AATAG GTGTA
                                    _   _
GAM884  ARHGEF7  5'  AGGAACTGAGGACCTTGTT   19358        C  TT   CC
                                AGGAACTG GG  GCC  GTT
                                ||||||||  ||  |||  |||
                                TCCTTGAC CC  TGG  CAA
                                     T  __   AA
GAM884  BMPR2    3'  GGAATGAACTGCCCTGTT    37857      C  C GT    C
                                GGAA TG G  TGCCC GTT
                                ||||  ||  |  |||||  |||
                                CCTT AC T  ACGGG CAA
                                  _  _ TG    A
GAM884  CTNND2   3'  AGAAACTGCTGAATGCCTTGTT 10632         _ GT    CC
                                AGGAACTGC G  TGCC  GTT
                                |||||||||  |  ||||  |||
                                TCTTTGACG C  ACGG  CAA
                                     A TT    AA
GAM884  RAB3A    3'  AGGAACTGGGGGGGCACGTT   16058        C  TT  CC
                                AGGAACTG GG  GC  CGTT
                                ||||||||  ||  ||  ||||
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                                TCCTTGAC CC  CG  GCAA
                                    _ CC  T_
GAM884  RANBP3   5'  GGAGGCTGACCCCGT      28761     ACTGC    _
                                GGA    GGTTG CCCCGT
                                |||    ||||| ||||||
                                CCT    CCGAC GGGGCA
                                 _____    T
GAM884  SCA1     3'  AGGCACTGTGAAGCCCCGTT  7273      A   C  TT
                                AGG ACTG GG  GCCCCGTT
                                ||| |||| ||  ||||||||
                                TCC TGAC CT  CGGGGCAA
                                  G   A  T_
GAM884  SHC1     3'  AGGAACTGCAGGTTTTGCGTT  16694        _   GCCC
                                AGGAACTGC GGTT   CGTT
                                ||||||||| ||||   ||||
                                TCCTTGACG CCAA   GCAA
                                     T   AAC_
GAM884  WNT3A    3'  AGGAGTACTGCCCCGTT    37536     AC   GGT
                                AGGA  TGC   TGCCCCGTT
                                ||||  |||   |||||||||
                                TCCT  ATG   ACGGGGCAA
                                  C_  ___
GAM885  SCN3A    3'  AGTTTAGATGCTTATAG     27949         ATACC
                                AGTTTAGATG    TATAG
                                ||||||||||    |||||
                                TCAAATCTAC    ATATC
                                     GA___
GAM886  COL13A1  5'  CTCCCGGGCCAGTCAGTT    38895        AACCCT  _
                                CTCCCGGGC     TAG CAGTT
                                |||||||||     ||| |||||
                                GAGGGCCCG     GTC GTCAA
                                     _______  A
GAM886  EZH1     3'  TCCTGGGCCCAAGCTTAGCAGT 12787     C    AACC_
           T                     TCC GGGC     CTTAGCAGTT
                                 ||| ||||     ||||||||||
                                 AGG CCCG     GAATCGTCAA
                                   A    GGTTC
GAM886  GAN      3'  CTCCCAGGTAGTTTTTCAACAG 35143        CAACCC_
           TT                     CTCCCGGG      TTAGCAGTT
                                  ||||||||      |||||||||
                                  GAGGGTCC      AGTTGTCAA
                                      ATCAAAA
GAM886  HNRPDL   5'  TCCTGGGGTCAGCAGTT     24179     C   CAACCC
                                TCC GGG     TTAGCAGTT
                                ||| |||     |||||||||
                                AGG CCC     AGTCGTCAA
                                  A  C_____
GAM886  MSF      5'  CTCCCGGGCGGATCAGGTT   44726        AACCC   CA
                                CTCCCGGGC    TTAG  GTT
                                |||||||||    ||||  |||
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                                GAGGGCCCG    AGTC  CAA
                                     CCT__   __
GAM887  ABCD4    5'  AAGAAGGAAACAAAACCTTCAG 33737       C  T GG    C
              T                   AAGAAGG AG T  AACCT CAGT
                                  ||||||| || |  ||||| ||||
                                  TTCTTCC TT G  TTGGA GTCA
                                     _  T TT    A
GAM887  AKAP1    3'  AGAAGGCAGTGCCA       40222          T GAACCT
                                  AGAAGGCAGT G     CCA
                                  |||||||||| |     |||
                                  TCTTCCGTCA C     GGT
                                       _ _______
GAM887  CCND2    3'  AAGAGGCAGAACAGAGCCTCCA 12040     A    T_   A
              GT                   AAGA GGCAG  TGGA CCTCCAGT
                                  |||| |||||  |||| ||||||||
                                  TTCT CCGTC  GTCT GGAGGTCA
                                    _    TT   C
GAM887  CSN2     3'  AAAAGGCATCATATTTCCAGT  12461        GTTGGAACC
                                  AGAAGGCA       TCCAGT
                                  ||||||||       ||||||
                                  TTTTCCGT       AGGTCA
                                       AGTATAA__
GAM887  DDEF2    3'  GAAGGCAGTGGTACACTCAGT  19319        T  A  _   C
                                  GAAGGCAGT GG AC CTC AGT
                                  ||||||||| || || ||| |||
                                  CTTCCGTCA CC TG GAG TCA
                                       _  A  T   _
GAM887  DISC1    3'  AAGAAGGCATTGACCA      33023         G    AACCT
                                  AAGAAGGCA TTGG     CCA
                                  ||||||||| ||||     |||
                                  TTCTTCCGT AACT     GGT
                                       _   _____
GAM887  GATA4    3'  GAAGGGTGGGCTCCCTCCAGT  13111       CA  T  AA_
                                  GAAGG  GT GG   CCTCCAGT
                                  |||||  || ||   ||||||||
                                  CTTCC  CA CC   GGAGGTCA
                                     __  C  GAG
GAM887  MUCDHL   3'  GGGAGCGAGACCTCCAG     34940    C   T   A
                                  GG AGT GGA CCTCCAG
                                  || ||| ||| |||||||
                                  CC TCG TCT GGAGGTC
                                   C   C   _
GAM887  MYO10    3'  GGAAAGGCAGTTCCCTTCAGT  29573    A        GGAA   C
                                  A GAAGGCAGTT    CCT CAGT
                                  | ||||||||||    ||| ||||
                                  C TTTCCGTCAA    GGA GTCA
                                   C         G___   A
GAM887  PSAP     3'  AAGAGGGTTGATGGCCTCCAGT 42963      A  CA    AA_
                                  AAGA GG  GTTGG   CCTCCAGT
                                  |||| ||  |||||   ||||||||
```

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                                TTCT CC  CAACT   GGAGGTCA
                                  _ __     ACC
GAM887  PSAP     3'  GGCAGGCTAAAAGACCTCCAGT 42968      _    __
                                GGCAG TTGGA  ACCTCCAGT
                                ||||| |||||  |||||||||
                                CCGTC GATTT  TGGAGGTCA
                                   C     TC
GAM887  SOST     5'  GAGGGCACGCCACCTTCCAGT  36103    A   _  GGA   _
                                GA GGCA GTT   ACCT CCAGT
                                || |||| |||   |||| |||||
                                CT CCGT CGG   TGGA GGTCA
                                 C   G  ___   A
GAM888  B3GALT2  3'  TTTGGGAAACCTTTTTTG    19118     CCT
                                TTTG   GGACCTTTTTTG
                                ||||   ||||||||||||
                                AAAC   TTTGGAAAAAAC
                                  CC_
GAM888  RAI14    3'  TCACATTTCTTTGGAGCATTTT 31806        GCC    CCT
           TG                    TCACATTT   TGGA   TTTTTG
                                ||||||||   ||||   ||||||
                                AGTGTAAA   ACCT   AAAAAC
                                     GAA    CGT
GAM889  C18orf1  3'  AGCTGAACAAAGTCTTCTGCT  41205       AGTC_
                                AGCTGAA    TCTTCTGCT
                                |||||||    |||||||||
                                TCGACTT    AGAAGACGA
                                    GTTTC
GAM889  CANX     3'  AAGAGCTGAAAGCTG      44658    A       TCTCTT
                                GA AGCTGAAAG     CTG
                                || |||||||||     |||
                                TT TCGACTTTC     GAC
                                 C       _______
GAM889  CD3G     3'  GCTGAAAGTCTCTCTGCT    6315            T
                                GCTGAAAGTCTCT CTGCT
                                |||||||||||| |||||
                                CGACTTTCAGAGA GACGA
                                                _
GAM889  CYP24    5'  GAAAGCTGGGAGTCCTCCTG   8945         AA   T
                                GAAAGCTG  AGTC CTTCTG
                                ||||||||  |||| ||||||
                                CTTTCGAC  TCAG GAGGAC
                                     CC   _
GAM889  DEDD     3'  AAACTGAAGTTCTGC      37424         A  CTCT
                                AAGCTGAA GT    TCTGC
                                |||||||| ||    |||||
                                TTTGACTT CA    AGACG
                                   _ _____
GAM889  DGSI     3'  GAAGGCTGGAGTCCTCTGCT   35531     A   AA    CT
                                GAA GCTG  AGTCT  TCTGCT
                                ||| ||||  |||||  ||||||
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                                CTT CGAC  TCAGG  AGACGA
                                  C   C_    __
GAM889  IRTA1    3'  GAAAGTGAATATCCTTTTGCT  36353      C   A  T  C
                                GAAAG TGAA GTC CTT TGCT
                                ||||| |||| ||| ||| ||||
                                CTTTC ACTT TAG GAA ACGA
                                   _   A  _  A
GAM889  MCC      3'  GAAAGCAGAAACGAGGCTCTGC 14381       T   GTCTC
           T                     GAAAGC GAAA    TTCTGCT
                                ||||||| ||||    |||||||
                                CTTTCG CTTT    GAGACGA
                                   T   GCTCC
GAM889  PCDHA9   3'  GAAAGTGTCTCTTCTGC    30418      CTGAAA
                                GAAAG     GTCTCTTCTGC
                                |||||     ||||||||||
                                CTTTC     CAGAGAAGACG
                                  A_____
GAM889  SCN8A    3'  CGGCAGCCTCTCTTCTG    30530    AA   GAAAG
                                CG  AGCT    TCTCTTCTG
                                ||  ||||    |||||||||
                                GC  TCGG    AGAGAAGAC
                                 CG   _____
GAM890  HS2ST1   3'  TATGTTAAAGATGTTTC    29339       AAAT
                                TATGTTAA   AGGTGTTTT
                                ||||||||   |||||||||
                                ATACAATT   TCTACAAAG
                                           ____
GAM890  ITGA1    3'  TGTTTTGAAAATAGATGTTTC  41861     A__
                                TGTT   AAAATAGGTGTTTT
                                ||||   ||||||||||||||
                                ACAA   TTTTATCTACAAAG
                                  AAC
GAM891  HMGCR    3'  TTCAAGAATTTCATCAAAACT  9239      T       TTT
                                TTCA GAATTTCATT   AGAACT
                                |||| ||||||||||   ||||||
                                AAGT CTTAAAGTAG   TTTTGA
                                  T       ___
GAM891  POLQ     3'  TTCATGAATATTCATTCCTACA 27323        _       GA
           CT                    TTCATGAAT TTCATTTTTA  ACT
                                |||||||| |||||||||  |||
                                AAGTACTTA AAGTAAGGAT  TGA
                                     T       G_
GAM891  SSPN     3'  TTCATGAATTTCCATTTTTAG  22940         _
                                TTCATGAATTTC ATTTTTAG
                                |||||||||||| ||||||||
                                AAGTACTTAAAG TAAAAATC
                                       G
GAM891  VAPA     3'  ATGAATTTCATAAAGGACT   18701          TTTT  A
                                ATGAATTTCAT   AG ACT
                                ||||||||||   || |||
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```
                                TACTTAAAGTA   TC TGA
                                      TT__  C
GAM892  ABCB9   3'  CGGAGGGCAGCTGGGGGC   33353     AA _  C
                                TGGA  GT GTT GGGGGC
                                ||||  || ||| ||||||
                                GCCT  CG CGA CCCCCG
                                  CC  T  _
GAM892  ACY1    3'  TGGAAGCCCCAGGGGC     8569      A  G
                                TGGAA GT TTCGGGGGC
                                ||||| || |||||||||
                                ACCTT CG GGGTCCCCG
                                  _ _
GAM892  ALK     5'  TGGAAGCTCAGGGGC      43839      AGT
                                TGGAA  GTTCGGGGGC
                                |||||  ||||||||||
                                ACCTT  CGAGTCCCCG
                                  ___
GAM892  ARHC    5'  TGGGTGCCCCAGGGGGC    23179    AAA    __
                                TGG  GTGTTC  GGGGGC
                                |||  ||||||  ||||||
                                ACC  CACGGG  CCCCCG
                                  ___    GT
GAM892  ATP6V0C 3'  TGGGGCGCCGGGGGC     44560    AAA   T
                                TGG  GTGT CGGGGGC
                                |||  |||| |||||||
                                ACC  CGCG GCCCCCG
                                  C__  _
GAM892  BACE    5'  GGAGAGGGAGCTTGGGGGC  29045    A  T__  C
                                GGA AG  GTT GGGGGC
                                ||| ||  ||| ||||||
                                CCT TC  CGA CCCCCG
                                  C  CCT  A
GAM892  BCL11B  3'  TGGGAAGTAGCGCTGGGC   39763    A    TT  G_
                                TGG AAGTG  CG  GGGC
                                ||| |||||  ||  ||||
                                ACC TTCAT  GC  CCCG
                                  C    C_  GA
GAM892  CBFA2T3 3'  TGAAAAGTCACAGGGGGC   23269       GTTC
                                TGGAAAGT   GGGGGC
                                ||||||||   ||||||
                                ACTTTTCA   CCCCCG
                                     GTGT
GAM892  CCND2   3'  TAGAAGGACCCAGGGGC    12051     A TG
                                TGGAA G  TTCGGGGGC
                                ||||| |  |||||||||
                                ATCTT C  GGGTCCCCG
                                   _ CT
GAM892  CD44    3'  TGGGAAATGTCCTTAGC    8301     A     GGG
                                TGG AAGTGTTC  GGC
                                ||| ||||||||  |||
```

```
                                ACC TTTACAGG   TCG
                                  C       AA_
GAM892  CDH6     3'  TGGAAAATGAAAAAGGC     22332         TTC
                                TGGAAAGTG   GGGGGC
                                |||||||||   ||||||
                                ACCTTTTAC   TTTCCG
                                     TT_
GAM892  CDKN2B   3'  TGGTGAGTGTCGAGGGC     38555     AA    T
                                TGG  AGTGT CGGGGGC
                                |||  ||||| |||||||
                                ACC  TCACA GCTCCCG
                                  AC    _
GAM892  CHN1     5'  TGGGGTGCCCGATGGGGC     12249     AAA     __
                                TGG   GTGTTCG  GGGGC
                                |||   |||||||  |||||
                                ACC   CACGGGC  CCCCG
                                  C__      TA
GAM892  CHN1     5'  TGGGGCGTGCTGGGGGC     12248     AAA    C
                                TGG   GTGTT GGGGGC
                                |||   ||||| ||||||
                                ACC   CACGA CCCCCG
                                  CCG    _
GAM892  CLCN4    3'  TGGCAGGCTGGGGGC       12293     AA  T   C
                                TGG  AG GTT GGGGGC
                                |||  || ||| ||||||
                                ACC  TC CGA CCCCCG
                                  G_ _  _
GAM892  CRHR2    3'  TGGAGTCCAAGGGC        12446     AAGT
                                TGGA    GTTCGGGGGC
                                ||||    ||||||||||
                                ACCT    CAGGTTCCCG
                                  ____
GAM892  DAG1     3'  TGGAGTTGCTAGGGGC      20530     AAG    C
                                TGGA   TGTT GGGGGC
                                ||||   |||| ||||||
                                ACCT   ACGA TCCCCG
                                  CA_   _
GAM892  DLG5     5'  TGGGGGTGTCAGAGGC      44473     AAA    T
                                TGG   GTGT CGGGGGC
                                |||   |||| |||||||
                                ACC   CACA GTCTCCG
                                  CC_   _
GAM892  DLX2     3'  TGGGGGCTCCGAGGGC      20598     AAA  G
                                TGG   GT TTCGGGGGC
                                |||   || |||||||||
                                ACC   CG AGGCTCCCG
                                  CC_  _
GAM892  DPYSL3   3'  CGGAAGTCCCAAGGGC      10766       A  G
                                TGGAA GT TTCGGGGGC
                                ||||| || |||||||||
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```
                                GCCTT CA GGGTTCCCG
                                  _ _
GAM892  DR1     5' CGGAGAGTGATCCCGGGGG  40440     A   __
                                TGGA AGTG  TTCGGGGG
                                |||| ||||  ||||||||
                                GCCT TCAC  GGGCCCCC
                                  C    TA
GAM892  DRD1    5' TGGAGATTGTTCAAAGGGC  9009      AAG     _
                                TGGA  TGTTCGG GGGC
                                ||||  ||||||| ||||
                                ACCT  ACAAGTT CCCG
                                  CTA      T
GAM892  EFNA3   3' TGGAGAGGCCAAAGGC     22404     A  T  T
                                TGGA AG GT CGGGGGC
                                |||| || || |||||||
                                ACCT TC CG GTTTCCG
                                  C  _  _
GAM892  EIF2C1  3' TGGAAAGGCCAGGGGC     29188       T  T
                                TGGAAAG GT CGGGGGC
                                ||||||| || |||||||
                                ACCTTTC CG GTCCCCG
                                  _  _
GAM892  ESPN    3' TGGGGTCCCGGGGGC      36450     AAA  G
                                TGG  GT TTCGGGGGC
                                |||  || |||||||||
                                ACC  CA GGGCCCCCG
                                 C__  _
GAM892  EXTL3   3' TGGAAAGTGGTAACTCGGG  11041         ____
                                TGGAAAGTG   TTCGGG
                                |||||||||   ||||||
                                ACCTTTCAC   GAGCCC
                                     CATT
GAM892  FANCD2  3' TGGAAAATGAGAGGC      37515        TTC
                                TGGAAAGTG  GGGGGC
                                |||||||||  ||||||
                                ACCTTTTAC  TCTCCG
                                   ___
GAM892  GCSH    3' TAGAAAGTTAAAGGGC     21018       GTTC
                                TGGAAAGT   GGGGGC
                                ||||||||   ||||||
                                ATCTTTCA   TTCCCG
                                    AT__
GAM892  GPX4    3' TGGAAGGCTCCAAGGGC    13284     A  G
                                TGGAA GT TTCGGGGGC
                                ||||| || |||||||||
                                ACCTT CG AGGTTCCCG
                                  C  _
GAM892  HDAC4   5' TGGAAAGGTCCAGAAGGGGC 25788       T   ___
                                TGGAAAG GTTC  GGGGGC
                                ||||||| ||||  ||||||
```

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                                ACCTTTC CAGG   TCCCCG
                                    _   TCT
GAM892  HDAC7A   5'  TGGAAAGTTTGTCCTCGGGGGC 32477        GT____
                                TGGAAAGT     TCGGGGGC
                                ||||||||     ||||||||
                                ACCTTTCA     AGCCCCCG
                                     AACAGG
GAM892  HMOX2    3'  TAGAGCTGGGTCGGGGGC    42173     AA  GT__
                                TGGA  GT    TCGGGGGC
                                ||||  ||    ||||||||
                                ATCT  CG    AGCCCCCG
                                  __ ACCC
GAM892  ITGA11   3'  CGGGAGCCCCAGGGGC     29198     AA   G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                GCC  TCG GGGTCCCCG
                                  C_  _
GAM892  JAK2     5'  TGGGCCCTCGGGGGC      22479     AAA  G
                                TGG   GT TTCGGGGGC
                                |||   || |||||||||
                                ACC   CG GAGCCCCCG
                                  ___  G
GAM892  JPH3     3'  TGGAAGGCCGGGGGC      34028      A T  T
                                TGGAA G GT CGGGGGC
                                ||||| | || |||||||
                                ACCTT C CG GCCCCCG
                                   _ _  _
GAM892  KLF8     5'  TGGAAAATGAGGAGGGGG    28540        TTC_
                                TGGAAAGTG    GGGGG
                                |||||||||    |||||
                                ACCTTTTAC    CCCCC
                                     TCCT
GAM892  MAF      5'  TGGAAGGCGCGGCGGGC     23841      A   TT   _
                                TGGAA GTG  CGG GGGC
                                ||||| |||  ||| ||||
                                ACCTT CGC  GCC CCCG
                                   C   __   G
GAM892  MAP3K12  5'  TGGGCCCTCGGGGGC      26696     AAA  G
                                TGG   GT TTCGGGGGC
                                |||   || |||||||||
                                ACC   CG GAGCCCCCG
                                  ___  G
GAM892  MAP3K14  3'  TGCAAAGTGCCGTCGGC     19545    G     T  GG
                                TG AAAGTGT CG  GGC
                                || ||||||| ||  |||
                                AC TTTCACG GC  CCG
                                 G      _  AG
GAM892  MAPK4    3'  TAGGGAGTGCTGAGGGGG    15666     AA    C_
                                TGG  AGTGTT  GGGGG
                                |||  ||||||  |||||
```

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                                ATC  TCACGA  CCCCC
                                  CC     CT
GAM892  MATK    5'  CGGAGGAAGCGGGGGC     40308     __  TGTT
                                TGGA  AAG   CGGGGGC
                                ||||  |||   |||||||
                                GCCT  TTC   GCCCCCG
                                  CC  ____
GAM892  MEN1    5'  TGGAAAGTTTCTAAGC     39237       G  GG
                                TGGAAAGT TTC  GGGC
                                |||||||| |||  ||||
                                ACCTTTCA AAG  TTCG
                                    _  A_
GAM892  MGAT5   5'  TGGATGCCCCCTTGGGGG   14479     AA  G  __
                                TGGA  GT TTC  GGGGG
                                ||||  || |||  |||||
                                ACCT  CG GGG  CCCCC
                                  A_  G   AA
GAM892  MMP19   3'  CGGAAGTGTTAGAGGC     35583     A    C
                                TGGAA GTGTT GGGGGC
                                ||||| ||||| ||||||
                                GCCTT CACAA TCTCCG
                                  _    _
GAM892  NAGA    5'  TGGGAGTCCCGAGGGC     7046     AA   G
                                TGG  AGT TTCGGGGGC
                                |||  ||| |||||||||
                                ACC  TCA GGGCTCCCG
                                  C_  _
GAM892  NFATC1  5'  GGAAAGTCATCGAGGGGC   26078       GT  _
                                GGAAAGT  TCG GGGGC
                                |||||||  ||| |||||
                                CCTTTCA  AGC CCCCG
                                    GT   T
GAM892  NGFB    3'  GGAGAGTGTAGAAGGGGC   14771    A    TC_
                                GGA AGTGT   GGGGGC
                                ||| |||||   ||||||
                                CCT TCACA   TCCCCG
                                  C    TCT
GAM892  NPTX1   3'  TGGGAAGGTCGAGGGC     14844    A  T  T
                                TGG AAG GT CGGGGGC
                                ||| ||| || |||||||
                                ACC TTC CA GCTCCCG
                                  C  _ _
GAM892  ORC2L   3'  CGGGGAGTGTTAAAAGGC   26192    AA    CG
                                TGG  AGTGTT  GGGGC
                                |||  ||||||  |||||
                                GCC  TCACAA  TTCCG
                                  CC     TT
GAM892  OTC     5'  TGGAAGCTATTTTGGGGG   8045      AG   C_
                                TGGAA  TGTT  GGGGG
                                |||||  ||||  |||||
```

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                                ACCTT  ATAA  CCCCC
                                  CG    AA
GAM892  OTOF     3'  TGAAAAGTGGACGCTGGGC   22065        TT  G_
                                TGGAAAGTG  CG  GGGC
                                |||||||||  ||  ||||
                                ACTTTTCAC  GC  CCCG
                                     CT  GA
GAM892  PDE1B    3'  GGGGAGGTCCCAGGGGGC   9565     AA  T   __
                                GG  AG GTTC  GGGGGC
                                ||  || ||||  ||||||
                                CC  TC CAGG  CCCCCG
                                 CC  _   GT
GAM892  PLS3     3'  TGGGAAATGTCAAGGGC    22762     A     T
                                TGG AAGTGT CGGGGGC
                                ||| |||||| |||||||
                                ACC TTTACA GTTCCCG
                                  C     _
GAM892  PPP1R14B 3'  TGGAAAACTGAGGGGGC    39797        _  TTC
                                TGGAAAG TG   GGGGGC
                                |||||||  ||   ||||||
                                ACCTTTT AC   CCCCCG
                                    G  T__
GAM892  PRKY     3'  TGGAAATGTCCTCAGGC    15712       G    GG
                                TGGAAA TGTTC  GGGC
                                ||||||  |||||  ||||
                                ACCTTT ACAGG  TCCG
                                   _    AG
GAM892  PRSS8    5'  TGGGGTGGTGTCGAAGGC   15763     AAA_   T
                                TGG    GTGT CGGGGGC
                                |||    |||| |||||||
                                ACC    CACA GCTTCCG
                                  CCAC   _
GAM892  PVRL2    3'  TGGTCAGGTCGGGGGC     16004     AA  T  T
                                TGG  AG GT CGGGGGC
                                |||  ||  || |||||||
                                ACC  TC CA GCCCCCG
                                  AG  _  _
GAM892  RAB36    3'  TGGAGGCCCGAAGGGGC    22248      AA T    __
                                TGGA  G GTTCG  GGGGC
                                ||||  |  |||||  |||||
                                ACCT  C CGGGC  CCCCG
                                   __ _    TT
GAM892  RASGRP2  5'  TGGAGGTCGGGGGGC      25176      AA T  T
                                TGGA  G GT CGGGGGC
                                ||||  |  ||  |||||||
                                ACCT  C CA GCCCCCG
                                   __ _  _
GAM892  RGS19IP1 3'  TGGAAAGTGGTGGAGGCGGGGG 41700          TT_____
                                TGGAAAGTG      CGGGGG
                                |||||||||      ||||||
```

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                                ACCTTTCAC      GCCCCC
                                     CACCTCC
GAM892  SLC19A1  5'  TGGAGATGTGCCAGGGGC    16851      AA_   T
                                TGGA   GTGT CGGGGGC
                                ||||   |||| |||||||
                                ACCT   CACG GTCCCCG
                                  CTA   _
GAM892  SPI1     5'  TGGACGGTCGTGGGGC      17085      AAG  T  _
                                TGGA   TG TCG GGGGC
                                ||||   || ||| |||||
                                ACCT   GC AGC CCCCG
                                  ___  C   A
GAM892  TBL1X    5'  TGGAAAGTTTCGGTGGC     24899        G    G
                                TGGAAAGT TTCGG GGC
                                |||||||| ||||| |||
                                ACCTTTCA AAGCC CCG
                                     _    A
GAM892  TCF15    3'  TGGAGATGTCCCGAGGGC    21424      AA     _
                                TGGA  GTGTTC GGGGGC
                                ||||  |||||| ||||||
                                ACCT  TACAGG CTCCCG
                                  C_     G
GAM892  TCTA     3'  TGGGTGGGCCAGGGGC      35284     AAA   T_
                                TGG   GTG  TCGGGGGC
                                |||   |||  ||||||||
                                ACC   CAC  GGTCCCCG
                                  ____   CC
GAM892  TGIF     5'  TGGCAGCCGGCCGGGGGC    17503     AA   _ TT
                                TGG  AGT G  CGGGGGC
                                |||  ||| |  |||||||
                                ACC  TCG C  GCCCCCG
                                  G_   G CG
GAM892  XPNPEP2  3'  TGGAAAGTTCAAAGGGC     18157        G  CG
                                TGGAAAGT TT  GGGGC
                                |||||||| ||  |||||
                                ACCTTTCA AG  TCCCG
                                     _ TT
GAM892  ZNF144   3'  TGGAAGGAGTGGAGAGGC    28346       __   TTC
                                TGGAA  AGTG   GGGGGC
                                |||||  ||||   ||||||
                                ACCTT  TCAC   TCTCCG
                                   CC    C__
GAM893  CLCA3    3'  TAGATGCCATCATTCTTGA   22264        C  GCTAG
                                TAGATGCCG CA    TTGA
                                |||||||||  ||    ||||
                                ATCTACGGT GT    AACT
                                     A  AAG__
GAM893  CLTCL1   3'  TAGATGCCCTTAAGCCCTGA  41885        GCC_   AG
                                TAGATGCC   AGCT  TTGA
                                ||||||||   ||||  ||||
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                                ATCTACGG   TCGG  GACT
                                    GAAT   __
GAM893  ESR1    3'  TAAATGGAGCTAGTTG     6534       CCGCC
                                TAGATG    AGCTAGTTG
                                ||||||    |||||||||
                                ATTTAC    TCGATCAAC
                                   C____
GAM893  FOSB    5'  GATGCCGCTGTACCTCTTGA  27539        CA_  AG
                                GATGCCGC  GCT  TTGA
                                ||||||||  |||  ||||
                                CTACGGCG  TGG  AACT
                                    ACA  AG
GAM893  GEMIN5  5'  TAGATACCAGCTGTGTTG    44843      GCC     A_
                                TAGAT  GCCAGCT  GTTG
                                |||||  |||||||  ||||
                                ATCTA  TGGTCGA  CAAC
                                  ___     CA
GAM893  IL1RAP  3'  TAGATGCCGTCAGGCTAG    13506        C  _
                                TAGATGCCG CAG CTAG
                                ||||||||| ||| ||||
                                ATCTACGGC GTC GATC
                                    A  C
GAM893  PIR51   3'  GATCAGAAGCTAGTTGA     27013     GC  CC
                                GAT  CG  AGCTAGTTGA
                                |||  ||  ||||||||||
                                CTA  GT  TCGATCAACT
                                 __  CT
GAM893  STAC    3'  TAGATGATGCTAATTG      17138      CCGCCA
                                TAGATG    GCTAGTTG
                                ||||||    ||||||||
                                ATCTAC    CGATTAAC
                                   TA____
GAM893  TPS1    3'  TAGATGCCAGGCCGGTTG    41307        CCA  TA
                                TAGATGCCG  GC  GTTG
                                |||||||||  ||  ||||
                                ATCTACGGT  CG  CAAC
                                    C__  GC
GAM894  IL10RA  3'  GGGGGTCATGGCTGGATTC   40624        CAA  AA
                                GGGGGTTA  CT  ATTC
                                ||||||||  ||  ||||
                                CCCCCAGT  GA  TAAG
                                    ACC  CC
GAM895  GABPA   3'  GTATGAAATATTTATAAAAA  13037      T_
                                GTATG  ATATTTATAAAAA
                                |||||  ||||||||||||
                                CATAC  TATAAATATTTTT
                                  TT
GAM895  HYAL4   3'  GTATGTACATTCATGAAAA   29343           A
                                GTATGTATATTTAT AAAA
                                |||||||||||||| ||||
```

```
                                CATACATGTAAGTA TTTT
                                        C
GAM896  DAF     3'  TGTGTGTATTTTCTTCT    8208         CCC
                                TGTGTGTATT  CTTCT
                                ||||||||||  |||||
                                ACACACATAA  GAAGA
                                     AA_
GAM896  SMAC    3'  TGCACCCCTTCTCTTAG    39899    TT      CC
                                TGTA  CCCCTTCTC  AG
                                ||||  |||||||||  ||
                                ACGT  GGGGAAGAG  TC
                                  __       AA
GAM897  GRM1    3'  TACGTAGGAGAAATAAT    9141       TA
                                TACGTAG  AGAAATAAT
                                |||||||  |||||||||
                                ATGCATC  TCTTTATTA
                                    C_
GAM898  BMP1    3'  GAAAGCAGTTCAGG       25979      TTTT
                                GAAAGT   AGTTCAGG
                                ||||||   ||||||||
                                CTTTCG   TCAAGTCC
                                  ____
GAM898  CHRNB1  3'  TCAGGGGCAGACAGTTCAGG  41312    AAA  TTT
                                TCG  GT  TAGTTCAGG
                                |||  ||  |||||||||
                                AGT  CG  GTCAAGTCC
                                  CCC  TCT
GAM898  CRI1    3'  GAAACTTTTTAATTAAGG    30733    G      C
                                GAAA TTTTTAGTT AGG
                                |||| ||||||||| |||
                                CTTT AAAAATTAA TCC
                                  G       T
GAM898  GRB10   3'  GAAAGTTTACAATTAGG    23656       T    C
                                GAAAGTTT TAGTT AGG
                                |||||||| ||||| |||
                                CTTTCAAA GTTAA TCC
                                     T    _
GAM898  IGF2R   3'  GAAAGTTTCTGTTAAAGG   9336         A  C_
                                GAAAGTTTTT GTT  AGG
                                |||||||||| |||  |||
                                CTTTCAAAGA CAA  TCC
                                     _  TT
GAM898  ITSN1   3'  GAAAGTTTCTAACTACAGG  16656         GT _
                                GAAAGTTTTTA  T CAGG
                                ||||||||||  | ||||
                                CTTTCAAAGAT  A GTCC
                                       TG T
GAM898  KIAA0442 3' GAAGCTTTCTTTCAGG     31789    A    AG
                                GAA GTTTTT  TTCAGG
                                ||| ||||||  ||||||
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                                CTT CGAAAG  AAGTCC
                                  _     A_
GAM898  LTB4R    5'  GAAGTCAGAGTTCAGG      8884      A   TTT
                                GAA GTT   AGTTCAGG
                                ||| |||   ||||||||
                                CTT CAG   TCAAGTCC
                                  _  TC_
GAM898  MTERF    3'  TCCAAAGTAATTCAG       28097    G    TTTT
                                TC AAAGT    AGTTCAG
                                || |||||    |||||||
                                AG TTTCA    TTAAGTC
                                 G    ____
GAM898  P23      3'  GAGGTTTTCAGCCCGGG     27343    AA         A
                                GA  GTTTTTAGTTC GG
                                ||  ||||||||||| ||
                                CT  CAAAAGTCGGG CC
                                 C_         C
GAM898  TEM7     3'  TCCAAAGTTTAGAGCAGG    33813    G     TT   TT
                                TC AAAGTT  TAG  CAGG
                                || ||||||  |||  ||||
                                AG TTTCAA  ATC  GTCC
                                 G     __   TC
GAM898  TM7SF3   3'  CCGAAAGTTTAGACAGG     40653         TT   TT
                                TCGAAAGTT  TAG  CAGG
                                |||||||||  |||  ||||
                                GGCTTTCAA  ATC  GTCC
                                     __   T_
GAM899  ADD2     3'  TGTCAGCACTGGTGGTCAT   32735          A  A
                                TGTCAGCACTG TG TTAT
                                |||||||||||  || ||||
                                ACAGTCGTGAC AC AGTA
                                      C  C
GAM899  CHRNA3   3'  TGTCAGTGGTGATGATCACGT  8842        CAC
                                TGTCAG   TGATGATTATGT
                                ||||||   ||||||||||||
                                ACAGTC   ACTACTAGTGCA
                                   ACC
GAM899  LAPTM5   3'  TCAGCAGAACAATTGTGTGT   27607       CT  TG   A
                                TCAGCA  GA  ATT TGTGT
                                ||||||  ||  ||| |||||
                                AGTCGT  TT  TAA ACACA
                                   C_  GT   C
GAM900  IL8      3'  GTATATTCTCCCGTGCAATA   45390         TA   A
                                GTATATTTT  CGT CAATA
                                |||||||||  ||| |||||
                                CATATAAGA  GCA GTTAT
                                      GG   C
GAM901  BAK1     3'  AGGGGATTGCACAGTTTATTT  45105     AATTT   _
                                AGG    GATT TGCAGTTTATTT
                                |||    |||| ||||||||||||
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                                TCC    CTAA GTGTCAAATAAA
                                  C____   C
GAM901  NCOA3   5'  AGGATGTTCAAGCAGTTTATTT 27212     A_  TG TTT
                                AGGA  TT  A   GCAGTTTATTT
                                ||||  ||  |   ||||||||||
                                TCCT  AA  T   CGTCAAATAAA
                                  AC  GT ___
GAM902  COL9A2  3'  GCATAGACCTCAGTATTG    12339       GT   _
                                GCATAG  TTTA TATTG
                                ||||||  |||| |||||
                                CGTATC  GAGT ATAAC
                                   TG   C
GAM902  PAWR    3'  CAGCATAGGAATATTG      15096         TTTT
                                TAGCATAGG   ATATTG
                                |||||||||   ||||||
                                GTCGTATCC   TATAAC
                                     T___
GAM902  TUBA3   3'  AGCATAGGTCAGTAATTG    25663         TTAT
                                AGCATAGGTT   ATTG
                                ||||||||||   ||||
                                TCGTATCCAG   TAAC
                                     TCAT
GAM903  PRG4    5'  GTTTTCAGGTACCGAAT     25150      A     AC
                                GTTT TCAGGT  GCCGAGT
                                |||| ||||||  |||||||
                                CAAA AGTCCA  TGGCTTA
                                  _     __
GAM903  ZNF278  5'  GTCTCGCAGGTGCGCCGAGT  36807      AT    A
                                GTTT  CAGGT CGCCGAGT
                                ||||  ||||| ||||||||
                                CAGA  GTCCA GCGGCTCA
                                  GC    C
GAM904  DMXL1   3'  CACCTTTAACACTATGACA   24289          AGAC
                                TACCTTTAACA   GACA
                                ||||||||||   ||||
                                GTGGAAATTGT   CTGT
                                     GATA
GAM904  ITGB2   3'  CACCTTTAATCAGACTGA    6836          CA   _
                                TACCTTTAA  AGAC GA
                                |||||||||  |||| ||
                                GTGGAAATT  TCTG CT
                                     AG   A
GAM905  COL4A3  3'  TTAATCTGTAATATTAATC   36388           GTCGAT
                                TTAGTCTGTAATAT     ATC
                                ||||||||||||||     |||
                                AATTAGACATTATA     TAG
                                     AT____
GAM905  GPM6B   3'  TTAGTCTGGAGTGTCAGTGATA 42545        TAATA   ___
            T                    TTAGTCTG    TGTC   GATAT
                                ||||||||    ||||   |||||
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                                AATCAGAC    ACAG   CTATA
                                    CTC__    TCA
GAM905  NRXN2    3'  GTCTGTAATATATATC      31490          CGAT
                                GTCTGTAATATGT    ATC
                                ||||||||||||    |||
                                CAGACATTATATA    TAG
                                      ____
GAM905  TSG      3'  AGTCTGTAATATAAATAT    33999          TC
                                AGTCTGTAATATG  GATAT
                                ||||||||||||  |||||
                                TCAGACATTATAT  TTATA
                                      __
GAM906  ACCN2    3'  CAGAGGGATGTGTGACACAACG 33432       __________    GTT
           TG                    CAGAGGG       GACAC   GTG
                                |||||||       |||||   |||
                                GTCTCCC       CTGTG   CAC
                                    TACACAIII    TTG
GAM906  ACP1     3'  GAGGGGACTACTGTC      28237        _ GTTG
                                GAGGGGAC AC    TGTC
                                |||||||| ||    ||||
                                CTCCCCTG TG    ACAG
                                    A  ____
GAM906  ADAM15   3'  CCAGAGGGCACGCCCGCCTC  19211        GA     _  G
                                CCAGAGGG  CACGTT GT TC
                                ||||||||  |||||| || ||
                                GGTCTCCC  GTGCGG CG AG
                                    __     G  G
GAM906  ADAM19   3'  GAGGGGACGTGGCTTGTC    35751        AC_   G
                                GAGGGGAC   GTT TGTC
                                ||||||||   ||| ||||
                                CTCCCCTG   CGA ACAG
                                    CAC  _
GAM906  ADAMTS7  3'  GAGGGGGAGCTGTGTC      30696       ACAC
                                GAGGGG    GTTGTGTC
                                ||||||    ||||||||
                                CTCCCC    CGACACAG
                                   CT__
GAM906  ALPL     3'  CCAGAGGGGAGCGAGGT     7885          CA  TT
                                CCAGAGGGGA  CG  GT
                                ||||||||||  ||  ||
                                GGTCTCCCCT  GC  CA
                                     C_  TC
GAM906  ANKRD3   3'  GAGGGGACACTCCGGTC     33966         G   T
                                GAGGGGACAC TTG GTC
                                |||||||||| ||| |||
                                CTCCCCTGTG GGC CAG
                                     A  _
GAM906  B3GALT5  3'  CAGAAGGGATGTCCTGC     37678         CAC   G
                                CAGAGGGGA   GTT TGT
                                |||||||||   ||| |||
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                                GTCTTCCCT  CAG ACG
                                     A__  G
GAM906  CA12    3'  CAGAGGGAGATGCCCCGTC  10241      _ CAC  G
                                CAGAGGG GA  GTT TGTC
                                ||||||| ||  ||| ||||
                                GTCTCCC CT  CGG GCAG
                                    T A__  G
GAM906  CACNG1  3'  CCAGAGAGGGTGTGT     8802        ACAC  T
                                CCAGAGGGG   GT GTGT
                                |||||||||   || ||||
                                GGTCTCTCC   CA CACA
                                     _____ _
GAM906  CAPN1   3'  CAGAGGGGGCGTTGGC    23248       ACA   T
                                CAGAGGGG  CGTTG GT
                                ||||||||  ||||| ||
                                GTCTCCCC  GCAAC CG
                                     C__   _
GAM906  CDH23   3'  CCGGAGGGAACATCAGTC   38073   A      _ _
                                CC GAGGGGACA C GTT
                                || |||||||||  | |||
                                GG CTCCCTTGT G CAG
                                 C       A T
GAM906  CDK10   3'  TGAGAGGGGATACGAAGGTC  18951  C      C  TTGT
                                C AGAGGGGA ACG   GTC
                                | |||||||| |||   |||
                                A TCTCCCCT TGC   CAG
                                 C      A  TTC_
GAM906  CSPG3   3'  CCAGAGGAGGCATGGGAAAGGT 20484       A  CGTT____
          GT                     CCAGAGGGG CA      GTGT
                                |||||||||  ||       ||||
                                GGTCTCCTC GT      CACA
                                     C  ACCCTTTC
GAM906  D1S155E 5'  CAGATCAAGTGTTGTGTC   28388    G_  ACAC
                                CAGA  GGG   GTTGTGTC
                                ||||  |||   ||||||||
                                GTCT  TTC   CAACACAG
                                  AG  A___
GAM906  DAG1    3'  CCAGAGAGGGCGGGCTTGTC  20518       ACAC  G
                                CCAGAGGGG   GTT TGTC
                                |||||||||   ||| ||||
                                GGTCTCTCC   CGA ACAG
                                     CGCC  _
GAM906  DISC1   3'  CCAGAGAGGGTACTCCTTTGT  33031       AC  GTTG_
                                CCAGAGGGG  AC    TGT
                                |||||||||  ||    |||
                                GGTCTCTCC  TG    ACA
                                     CA  AGGAA
GAM906  DPH2L1  3'  TGAGAGGGGATGACTTTGT   10731   C      C_  G
                                C AGAGGGGA  AC TTGT
                                | ||||||||  || ||||
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                                A TCTCCCCT  TG AACA
                                 C       AC  A
GAM906  DR1      5'  CAGAGGGGCGGGCGCTGT    40439        ACA_
                                CAGAGGGG   CGTTGT
                                ||||||||   ||||||
                                GTCTCCCC   GCGACA
                                    GCCC
GAM906  DUSP2    3'  CCAGAGGGGAGCCCACCAGTC  20658         CA_  TT T
                                CCAGAGGGGA  CG  G GTC
                                ||||||||||  ||  | |||
                                GGTCTCCCCT  GT  T CAG
                                     CGG  GG _
GAM906  EGFL4    3'  CAGAGGGACATGCGACACAACG 41559        __________    GTT
           TG                    CAGAGGG       GACAC   GTG
                                 |||||||       |||||   |||
                                 GTCTCCC       CTGTG   CAC
                                    TGTACGIII    TTG
GAM906  EVA1     3'  CCAGAGGGGTGTTGCTTGTC  25131        ACAC    __
                                 CCAGAGGGG   GTTGT  GTC
                                 |||||||||   |||||  |||
                                 GGTCTCCCC   CAACG  CAG
                                      A___    AA
GAM906  FBXL7    5'  GAGGGGGTGCTGCGTC     29402       ACAC
                                 GAGGGG   GTTGTGTC
                                 ||||||   ||||||||
                                 CTCCCC   CGACGCAG
                                    CA__
GAM906  FNTB     3'  CAGAGGGGGTTTTGACACAACG 13002        __________    GTT
           TG                    CAGAGGG       GACAC   GTG
                                 |||||||       |||||   |||
                                 GTCTCCC       CTGTG   CAC
                                    CCAAAAIII    TTG
GAM906  FOXE3    3'  CAAAGGGGACGCTTCTGTC   29141         ACG  G
                                 CAGAGGGGAC   TT TGTC
                                 ||||||||||   || ||||
                                 GTTTCCCCTG   AA ACAG
                                      CG_  G
GAM906  G6PT1    5'  CCAAGGGGACCCAGTGTC    11159     G      ACGTT
                                 CCA AGGGGAC    GTGTC
                                 ||| |||||||    |||||
                                 GGT TCCCCTG    CACAG
                                   _      GGT__
GAM906  GBA      3'  AGAGGGGAAAGTGAGTC     44066        CAC  T T
                                 AGAGGGGA   GT G GTC
                                 ||||||||   || | |||
                                 TCTCCCCT   CA C CAG
                                      TT_  _ T
GAM906  GRINL1A  3'  CAGAGGGGAAATGGTG      42996         CAC  T
                                 CAGAGGGGA   GT GTG
                                 |||||||||   || |||
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                                GTCTCCCCT   TA CAC
                                     T__  C
GAM906  HPCA     3'  CCAGGGGGACCGTGT      13421      A     ACGT
                                CCAG GGGGAC    TGTGT
                                |||| ||||||    |||||
                                GGTC CCCCTG    GCACA
                                  _     _____
GAM906  INHBB    3'  GAGGGGACACCCCCCATC    13557          G  G
                                GAGGGGACAC TT TGTC
                                |||||||||| || ||||
                                CTCCCCTGTG GG GTAG
                                     G  G
GAM906  KCNJ5    3'  CAGAGGGGCTGTCGACACAACG 9431          __________     GTT
           TG                     CAGAGGG       GACAC   GTG
                                |||||||        |||||   |||
                                GTCTCCC       CTGTG   CAC
                                   CGACAGIII    TTG
GAM906  KIAA0857 3'  CCAGAGGGCACGTGT      42468         G  ACGTT
                                CCAGAGGG AC    GTGT
                                |||||||| ||    ||||
                                GGTCTCCC TG    CACA
                                   G  _____
GAM906  KLHL2    5'  CCGGAGGGGGCGCCGCGC    28527    A     ACA
                                CC GAGGGG   CGTTGTGT
                                || ||||||   ||||||||
                                GG CTCCCC   GCGGCGCG
                                 C     C__
GAM906  LFG      3'  GAGGGGGTACACTGTGTC    44136       AC
                                GAGGGG  ACGTTGTGTC
                                ||||||  ||||||||||
                                CTCCCC  TGTGACACAG
                                   CA
GAM906  MAN2A2   3'  CCAGAGGGTACAGTAACGTC  25942        G   C  TG
                                CCAGAGGG ACA GT  TGTC
                                |||||||| ||| ||  ||||
                                GGTCTCCC TGT CA  GCAG
                                   A   _  TT
GAM906  NR1I2    5'  CCAGAGGGGAGCTGAAGAGTC  35100         CAC    T___
                                CCAGAGGGGA   GTTG    GTC
                                ||||||||||   ||||    |||
                                GGTCTCCCCT   CGAC    CAG
                                     ___     TTCT
GAM906  ODF2     5'  CCAGAGGGGCAGGCTTGTC    14927         A  C   G
                                CCAGAGGGG CA GTT TGTC
                                ||||||||| || ||| ||||
                                GGTCTCCCC GT CGA ACAG
                                     _  C   _
GAM906  PCTK1    5'  CCAGAGGAGGATGCG       37466         _   CACGT
                                CCAGAGG GGA    TGTG
                                ||||||| |||    ||||
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                                GGTCTCC CCT    ACGC
                                   T  _____
GAM906  PDGFRB   5'  CCAGAGGGGCCGCCCTG    42335       ACA   G
                                CCAGAGGGG  CGTT TG
                                |||||||||  |||| ||
                                GGTCTCCCC  GCGG AC
                                     G__   G
GAM906  PML      3'  CCAGGGGGAACACCTGC    37724     A     G
                                CCAG GGGGACAC TTGT
                                |||| |||||||| ||||
                                GGTC CCCTTGTG GACG
                                  C      _
GAM906  PXF      3'  CAGAGAGGAAAACGTGTTGTGT 16006       C_   __
                                CAGAGGGGA  ACGT  TGTGT
                                |||||||||  ||||  |||||
                                GTCTCTCCT  TGCA  ACACA
                                     TT    CA
GAM906  PYCS     3'  CACGGGGGACACAGCATC    16037    GA      TT
                                CA  GGGGACACG  GTGTC
                                ||  |||||||||  |||||
                                GT  CCCCTGTGT  CGTAG
                                 GC       __
GAM906  RAB36    3'  CCAGAGGAGGGCAGTGCCATGT 22236       _  A  C_  TG
                                CCAGAGG GG CA  GT  TGT
                                ||||||| || ||  ||  |||
                                GGTCTCC CC GT  CG  ACA
                                    T  C  CA  GT
GAM906  RAB5B    3'  CCGTAGGGGTTGTGTGTC    16089    AG    ACAC  T
                                CC  AGGGG   GT GTGTC
                                ||  |||||   || |||||
                                GG  TCCCC   CA CACAG
                                 CA    AA__  _
GAM906  RANBP2L1 5'  CCAGTGGCCAGTTGTGTC    37021     AG  GA  C
                                CCAG  GG  CA GTTGTGTC
                                ||||  ||  || ||||||||
                                GGTC  CC  GT CAACACAG
                                  A_  G_  _
GAM906  RAP1GA1  3'  CAGAGGGGGTGGCGACACAACG 16163       __________    GTT
           TG                    CAGAGGG       GACAC   GTG
                                 |||||||       |||||  |||
                                 GTCTCCC       CTGTG   CAC
                                    CCACCGIII    TTG
GAM906  S100A6   5'  GAGGGGATGGGCTATGTC    31198       CAC
                                GAGGGGA   GTTGTGTC
                                |||||||   ||||||||
                                CTCCCCT   CGATACAG
                                    ACC
GAM906  SERPINA5 3'  CCAGAGAGGGAAAGTGT     8411        _   CACGTT
                                CCAGAG GGGA     GTGT
                                |||||| ||||     ||||
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                                GGTCTC CCCT     CACA
                                   T   TT____
GAM906  SHANK2   3'  CCAGAGGAGACGCTGT     29453          AC
                                CCAGAGGGGAC  GTTGT
                                ||||||||||  |||||
                                GGTCTCCTCTG  CGACA
                                      __
GAM906  SLC4A7   3'  AGAGGAGGACATTACAT     18820      _    CG   TG
                                AGAGG GGACA  TTG  T
                                ||||| |||||  |||  |
                                TCTCC CCTGT  AAT  A
                                   T    __  GT
GAM906  SLC7A8   5'  CCAGGGGAGACATACATT    29283      A     __
                                CCAG GGGGAC  ACGTT
                                |||| ||||||  |||||
                                GGTC CCTCTG  TGTAA
                                  C     TA
GAM906  SMCX     3'  CCGAGGGGGGTCTCTGTC    20067    A     ACACG  G
                                CC GAGGGG    TT TGTC
                                || ||||||    || ||||
                                GG CTCCCC    GA ACAG
                                 _     CCA__  G
GAM906  SORCS2   3'  CAGAGGGGGTGGTGCC      34046        ACAC  T
                                CAGAGGGG    GT GTGTC
                                ||||||||    || |||||
                                GTCTCCCC    CA CACGG
                                     _____  C
GAM906  SOST     5'  CCAGAGGAGGGCACGCCAC   36101        _ A    TG
                                CCAGAGG GG CACGT  T
                                ||||||| || |||||  |
                                GGTCTCC CC GTGCG  G
                                    T  C    GT
GAM906  SRGAP2   3'  AGAGGGGAGTGTGC        43974        CAC  T
                                AGAGGGGA   GT GTGT
                                ||||||||   || ||||
                                TCTCCCCT   CA CACG
                                     ___  _
GAM906  STX1A    3'  CCAGAGGGACACCTGGGGTC  21411         G   G   T_
                                CCAGAGGG ACAC TTG  GTC
                                |||||||| |||| |||  |||
                                GGTCTCCC TGTG GAC  CAG
                                     _   _  CC
GAM906  TAF6     5'  AGAGGGGGTCGTGT       24857        ACAC
                                AGAGGGG    GTTGTGT
                                |||||||    |||||||
                                TCTCCCC    CAGCACA
                                     _____
GAM906  THOP1    3'  CCAGAGAGGAGACGTGT     43828          C    T
                                CCAGAGGGGA ACGT GT
                                |||||||||| |||| ||
```

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                                GGTCTCTCCT TGCA CA
                                      C   _
GAM906  TYRO3    3'  AGAGGGGAAGTTGACACAACGT 26648        _________    GTT
                G                    AGAGGG       GACAC   GTG
                                     ||||||       |||||   |||
                                     TCTCCC       CTGTG   CAC
                                        CTTCAAIII    TTG
GAM906  USF2     3'  GAGGGGCATGTGTC       17896       A  CGT
                                     GAGGGG CA   TGTGTC
                                     |||||| ||   ||||||
                                     CTCCCC GT   ACACAG
                                       _ ___
GAM906  VNN3     3'  CAGGGGGACACTGAGAGTC   38557     A      GTTGT
                                     CAG GGGGACAC    GTC
                                     ||| ||||||||    |||
                                     GTC CCCCTGTG    CAG
                                       _      ACTCT
GAM907  FGFR2    3'  GTGGATACTGAGGAAGGC    35666       _    TC
                                     GTGGATAC GAGGA  GT
                                     |||||||| |||||  ||
                                     CACCTATG CTCCT  CG
                                          A    TC
GAM908  GALE     3'  TGCTGCTTTTCCTGGTCCTT   41801        C   ACGAA
                                     TGTTGCTTT CCTG    CCTT
                                     ||||||||| ||||    ||||
                                     ACGACGAAA GGAC    GGAA
                                          A   CA___
GAM908  LY64     3'  TTGCTTTCTCTGGAAACCTTC  24572       C  AC
                                     TTGCTTTC CTG  GAACCTTC
                                     |||||||| |||  ||||||||
                                     AACGAAAG GAC  TTTGGAAG
                                          A  C_
GAM908  PABPN1   5'  TGTTGTTTCCTTCCACTCTTC  21615     C    C GA  AAC
                                     TGTTG TTTCC T  CG   CTTC
                                     ||||| ||||| |  ||   ||||
                                     ACAAC AAAGG A  GT   GAAG
                                       _    _ AG  GA_
GAM908  PCSK2    3'  TGTGCTTTCCTCACAGAGGTCT 15138    T     C G  _  AC_
                TC                     TGT GCTTTCC T AC GA   CTTC
                                     ||| ||||||| | || ||   ||||
                                     ACA CGAAAGG A TG CT   GAAG
                                       _      _ G  T  CCA
GAM908  SLC22A12 3'  TTGCTTTCCTCCTGCCTT    40340        _ GACGAA
                                     TTGCTTTCC CT     CCTT
                                     ||||||||| ||     ||||
                                     AACGAAAGG GG     GGAA
                                          A  AC____
GAM908  TIRAP    3'  TGTTGCTTTCTCCTGATGCCCA 38094         _    CGAA  _
                TTC                    TGTTGCTTTC CCTGA    CC TTC
                                     |||||||||| |||||    || |||
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                                ACAACGAAAG GGACT   GG AAG
                                     A    ACG_ T
GAM908  ABR     3'  TGCCAGGGAGCTCCTGGC   35018     CAG     G  CA
                                TGTC  GGGGAGC TCC  GC
                                ||||  ||||||| |||  ||
                                ACGG  TCCCTCG AGG  CG
                                  ___     _  AC
GAM908  CLTCL1  3'  TGTCCAGGTGTGGTCCAGCCG  41889       GGGAGC   C
                                TGTCCAGG    GTCC AGCCG
                                ||||||||    |||| |||||
                                ACAGGTCC    CAGG TCGGC
                                     ACAC__   _
GAM908  DTNB    3'  TGTGCAGGGGGAGGCCCACTAG 37610    C       C   C__
            C                    TGT CAGGGGGAG GTCC  AGC
                                ||| |||||||| ||||  |||
                                ACA GTCCCCCTC CGGG  TCG
                                  C       _   TGA
GAM908  FXYD1   3'  TGCCAGGGGAGTCCTGGCC   34867   T     AGC   CA
                                TG CCAGGGGG  GTCC  GCC
                                || ||||||||  ||||  |||
                                AC GGTCCCCT  CAGG  CGG
                                 _     ___   AC
GAM908  KLHL3   3'  TATCCAAGTGGCGTCTCGGC  44646       GGGA   CCA
                                TGTCCAGG   GCGTC  GC
                                ||||||||   |||||  ||
                                ATAGGTTC   CGCAG  CG
                                     AC__    AGC
GAM908  NFKBIL2  5'  TGTCCAGGTGGGTGCGGCC   30242       _  A  TCCCA
                                TGTCCAGG GGG GCG    GCC
                                |||||||| ||| |||    |||
                                ACAGGTCC CCC CGC    CGG
                                     A  A  _____
GAM908  NOL3    5'  TGTCGGGGCTCGATCCCAGCCG 19494     CAG   AG  _
                                TGTC  GGGG  CG TCCCAGCCG
                                ||||  ||||  || |||||||||
                                ACAG  CCCC  GC AGGGTCGGC
                                  ___   GA  T
GAM908  NPY2R   5'  TGTCCAGGGTCTCTCAGCC   9503        GGAGCG  C
                                TGTCCAGGG    TC CAGCC
                                |||||||||    || |||||
                                ACAGGTCCC    AG GTCGG
                                     AG____  A
GAM908  SERPINF2 3'  GTCGGGGTGTCCCAGC     9593     CAG   AGC
                                GTC  GGGG  GTCCCAGC
                                |||  ||||  ||||||||
                                CAG  CCCC  CAGGGTCG
                                  ___   A__
GAM908  TTC3    3'  TCCAGGGGGAAAAAGTCTTAGT 17717         C__  CC  C
            CG                   TCCAGGGGGAG  GTC  AG CG
                                ||||||||||  |||  || ||
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                                AGGTCCCCCTT  CAG  TC GC
                                     TTT  AA  A
GAM908  WNT3A   3'  GTCCAGGGGGAGCCGCGGCCG  37550          _  CCCA
                                GTCCAGGGGGAGC GT   GCCG
                                |||||||||||| ||   ||||
                                CAGGTCCCCCTCG CG   CGGC
                                   G  C___
GAM908  ZNF85   5'  TCCAGGGGGTCCCGGCGTCTTA 18315        A____   CC
          GC                    TCCAGGGGG   GCGTC  AGC
                                |||||||||   |||||  |||
                                AGGTCCCCC   CGCAG  TCG
                                    AGGGC   AA
GAM909  CLECSF5  3'  GGAGTTAGGAGGGGCAT    29928        AAAAA  A_
                                GGGGTTAG   GAG  GCGT
                                ||||||||   |||  ||||
                                CCTCAATC   CTC  CGTA
                                    _____  CC
GAM909  COX10   5'  CGGGCTCCGAAAGGAGAGCGT  10549     G  A   AA
                                CGGG TT GAAA  GAGAGCGT
                                |||| || ||||  ||||||||
                                GCCC AG CTTT  CTCTCGCA
                                  G  G   C_
GAM909  ESPN    3'  CACGGGGCTGGGGAGAGC    36440        AGAAAAA
                                CACGGGGTT     GAGAGC
                                |||||||||     ||||||
                                GTGCCCCGA     CTCTCG
                                    CCC____
GAM909  ITPKB   3'  GGGGCCAGGGAGGGCG      13650        AAAAA  A
                                GGGGTTAG   GAG GCG
                                ||||||||   ||| |||
                                CCCCGGTC   CTC CGC
                                    C____  C
GAM909  LIMK1   3'  CACGGGGTGGGAGAAGGCA   32526        TA  AAAA  A
                                CACGGGGT  GA   GAG GCG
                                ||||||||  ||   ||| |||
                                GTGCCCCA  CT   TTC CGT
                                    CC  C___  _
GAM909  MX1     3'  ACGGGGCTGGACAGAGG     14687        A  AAAAG   C
                                ACGGGGTT GA    AGAG G
                                |||||||| ||    |||| |
                                TGCCCCGA CT    TCTC C
                                    C  G____   A
GAM909  MYO3A   3'  CGGGAGTTCCGAGAGAGAGCGT 41113     _  A_  AAA
                                CGGG GTT  GA  AGAGAGCGT
                                |||| |||  ||  |||||||||
                                GCCC CAA  CT  TCTCTCGCA
                                  T  GG  C__
GAM909  NLGN3   3'  GGGTTGGAAAAGCAT      33286      A  AAAGA
                                GGGTT GAA    GAGCGT
                                ||||| |||    ||||||
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                                CCCAA CTT    TTCGTA
                                  C  _____
GAM909  PAX2    3'  CGGCGGTCCCGGGAGAGCGT  19624    _   AGAAAAA
                                CGG GGTT     GAGAGCGT
                                ||| ||||     ||||||||
                                GCC CCAG     CTCTCGCA
                                  G   GGCC___
GAM909  ACK1    3'  CTGGCACCCTTTCTCCGCTT  25114   C  T   CTC
                                CT GC TTCTT  TCTCCGCTT
                                || || |||||  |||||||||
                                GA CG GGGAA  AGAGGCGAA
                                 C  T   ____
GAM909  BMP4    5'  CCTCGCTTTCTTTCTTTCC   10191          C  C
                                CCTCGCTTTCTT TCT TCC
                                |||||||||||| ||| |||
                                GGAGCGAAAGAA AGA AGG
                                       _  A
GAM909  CSNK1D  3'  CTCTGCAATTCTCTCTCTGCTT 40066    _ TTTC       C
                                CTC GC   TTCTCTCTC GCTT
                                ||| ||   ||||||||| ||||
                                GAG CG   AAGAGAGAG CGAA
                                  A  TT__       A
GAM909  DDX11   3'  CTTTCTTCTTCTCTGCT    36174        C   C
                                CTTTCTTCT TCTC GCT
                                ||||||||| |||| |||
                                GAAAGAAGA AGAG CGA
                                      _   A
GAM909  EDAR    5'  CCCCGCTTCCTTTCCG     35302          CTCTC
                                CCTCGCTTTCTT    TCCG
                                ||||||||||||    ||||
                                GGGGCGAAGGAA    AGGC
                                       _____
GAM909  EHD4    3'  TCTCTTTCTTCTCAACCC   40209   G       TC
                                TC CTTTCTTCTC  TCC
                                || ||||||||||  |||
                                AG GAAAGAAGAG  GGG
                                 A        TT
GAM909  ERBB2IP 3'  CTTGCTGTCTTCCCCGCT   33097   C  T  TCTC
                                CT GCT TCT   TCTCCGCT
                                || ||| |||   ||||||||
                                GA CGA AGA   AGGGGCGA
                                 A  C  ____
GAM909  GPR85   5'  CCTCTTTTCTTCCACTT    33260     GC    TCTCTC
                                CCTC  TTTCT    TCCGCTT
                                ||||  |||||    |||||||
                                GGAG  AAAGA    AGGTGAA
                                  A_   _______
GAM909  GRB2    3'  TCACTTTCTTTAAATAATTGCT 13288         CTCTCTCC_
            T                    TCGCTTTCTT       GCTT
                                ||||||||||       ||||
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                                AGTGAAAGAA        CGAA
                                     ATTTATTAA
GAM909  HHIP     5'  CCTCTTTTCTTCTTCT      35406      GC       C
                                CCTC  TTTCTTCT TCT
                                ||||  |||||||| |||
                                GGAG  AAAGAAGA AGA
                                  A_       _
GAM909  IRTA1    3'  TCTTTTCTTCTCTCTCCCTT   36357    GC           G
                                TC  TTTCTTCTCTCTCC CTT
                                ||  |||||||||||||| |||
                                AG  AAAGAAGAGAGAGG GAA
                                 A_           _
GAM909  MBTPS1   5'  GCTTTCATTTCTTTCTCCGCTT 19133        __    C
                                GCTTTC  TTCT TCTCCGCTT
                                ||||||  |||| |||||||||
                                CGAAAG  AAGA AGAGGCGAA
                                    TA    A
GAM909  NLGN1    5'  CTTCCTTTTCTCTTTTTTTGCT 31384        C     CC____
              T                  CTTTCTT TCTCT      GCTT
                                 ||||||| |||||      ||||
                                 GAAGGAA AGAGA      CGAA
                                    A     AAAAAA
GAM909  NT5C2    3'  TCCCTTTCTTTTCTGGGGGCTT 29235    G      C   CTCC
                                TC CTTTCTT TCT    GCTT
                                || ||||||| |||    ||||
                                AG GAAAGAA AGA    CGAA
                                 G      A   CCCC
GAM909  RGL      3'  CGCTTTCTTTTCTGGCTT    31539         C   CTCC
                                CGCTTTCTT TCT    GCTT
                                |||||||||| |||    ||||
                                GCGAAAGAA AGA    CGAA
                                     A   C___
GAM909  RGS1     3'  CCTCCTTCTGCGGTCTCTCT   16307      G    CT___
                                CCTC CTTT     TCTCTCT
                                |||| ||||     |||||||
                                GGAG GAAG     AGAGAGA
                                  _    ACGCC
GAM909  SMN1     3'  CCTTTTTTCTTTCCCAACACTT 7365      CGC     C    TC
                                CCT   TTTCTT TCTC  CGCTT
                                |||   |||||| ||||  |||||
                                GGA   AAAGAA AGGG  GTGAA
                                  AA_     _    TT
GAM909  SYCP1    5'  CCTCGTTTCCTTCTCCCT     17229       C
                                CCTCG TTTCTTCTCTCT
                                ||||| ||||||||||||
                                GGAGC AAGGAAGAGGGA
                                   A
GAM909  TRHDE    5'  CCTCTTTTTCTTCTTCT      30104      GC       C
                                CCTC  TTTCTTCT TCT
                                ||||  |||||||| |||
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                                GGAG  AAAGAAGA AGA
                                  AA       _
GAM909  TRIM9    5'  CTTGCTTTCTTTCTTTCT    31565    C       _ C
                                CT GCTTTCTT CT TCT
                                || |||||||| || |||
                                GA CGAAAGAA GA AGA
                                 A       A  A
GAM909  TRPS1    3'  CTTGCTTTCTCTTTTCTCT   30461    C       C__
                                CT GCTTTCTT   TCTCT
                                || ||||||||   |||||
                                GA CGAAAGAG   AGAGA
                                 A       AAA
GAM909  WHSC1    3'  CCTCGTTTTCTTCTTGGTCT  39360      C       C__
                                CCTCG TTTCTTCT   TCT
                                ||||| ||||||||   |||
                                GGAGC AAAGAAGA   AGA
                                   A       ACC
GAM909  ZIC1     5'  CTCCGTTTTTCCCTCTCTGCTT 18235     GC   C       C
                                CTC  TTT TTCTCTCTC GCTT
                                |||  ||| |||||||||| ||||
                                GAG  AAA AAGGGAGAG CGAA
                                  GC  _       A
GAM910  ABCA2    3'  TCTGTGCGCTATGTACAG    45527         A    C
                                TCTGTGCGT GTGT CAG
                                ||||||||| |||| |||
                                AGACACGCG TACA GTC
                                      A    T
GAM910  ABCC5    3'  TCTGTGCAGTGGCCAG      25025        GT    T
                                TCTGTGC  AGTG CCAG
                                |||||||  |||| ||||
                                AGACACG  TCAC GGTC
                                    __    C
GAM910  ADAM19   3'  CCTCTGCAGTGTCCAG      37767     G   GT
                                TCT TGC  AGTGTCCAG
                                ||| |||  |||||||||
                                GGA ACG  TCACAGGTC
                                  G  __
GAM910  ALDOC    5'  CCTGTGCGCAGCCAG       23157          TGT
                                TCTGTGCGTAG   CCAG
                                ||||||||||   ||||
                                GGACACGCGTC   GGTC
                                             ___
GAM910  ALPP     3'  TCTATGCCCAGTGTCCAG    42872        G
                                TCTGTGC TAGTGTCCAG
                                ||||||| ||||||||||
                                AGATACG GTCACAGGTC
                                    G
GAM910  ALX3     3'  TCCGTGGTGTCCAG        27068        CGTA
                                TCTGTG    GTGTCCAG
                                ||||||    ||||||||
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                                AGGCAC    CACAGGTC
                                      ____
GAM910  BHLHB3   5'  TCTGTGCGTCTCCAG       36261         AGTG
                                TCTGTGCGT    TCCAG
                                |||||||||    |||||
                                AGACACGCA    AGGTC
                                     G___
GAM910  CHST6    3'  TCTGTGGCCACACCCAG     34683       C  A TG
                                TCTGTG GT G  TCCAG
                                ||||||  || |  |||||
                                AGACAC CG T  GGGTC
                                   _  G GT
GAM910  DLX2     3'  TCTGTGTCCAAGTCCAG     20596       CG   T
                                TCTGTG  TAG GTCCAG
                                ||||||  |||  ||||||
                                AGACAC  GTT CAGGTC
                                   AG   _
GAM910  DNM2     3'  TGCGCAGTGCGGTGTCCAG   22388       ___ TA
                                TGTGC   G  GTGTCCAG
                                |||||   |  ||||||||
                                ACGCG   C  CACAGGTC
                                   TCA GC
GAM910  DRD5     3'  TCTGTGCGGTTATGCAG     9027         TAG   C
                                TCTGTGCG   TGT CAG
                                ||||||||   ||| |||
                                AGACACGC   ATA GTC
                                     CA_   C
GAM910  EBAF     3'  TCTATGCACACGTTCAG     42260         G   C
                                TCTGTGCGTA TGT CAG
                                |||||||||| ||| |||
                                AGATACGTGT GCA GTC
                                      _   A
GAM910  EFNB1    3'  CTGTCCATCAGTGTCCAG    20717      G   _
                                CTGT CGT AGTGTCCAG
                                ||||  ||| |||||||||
                                GACA GTA TCACAGGTC
                                  G   G
GAM910  EMS1     3'  CTGTGCGTCCCAATCCAG    23426         AGT_
                                CTGTGCGT    GTCCAG
                                ||||||||    ||||||
                                GACACGCA    TAGGTC
                                     GGGT
GAM910  EPHB6    3'  TCTCGGACCAGTGTCCAG    20803     _ TG G
                                TCT G  C TAGTGTCCAG
                                |||  |  | ||||||||||
                                AGA C  G GTCACAGGTC
                                  G CT _
GAM910  FADD     3'  CCTGACCCTAGTGTCCAG    19244      TGCG
                                TCTG    TAGTGTCCAG
                                ||||    ||||||||||
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                                GGAC   ATCACAGGTC
                                  TGGG
GAM910  FGF5    3'  TCTGTGATTTATGTCCAG   37593      CGTA
                                TCTGTG   GTGTCCAG
                                ||||||   ||||||||
                                AGACAC   TACAGGTC
                                   TAAA
GAM910  FGFRL1  3'  CTGTGTGTGTGTGTCCAG   34909     C  A_
                                CTGTG GT  GTGTCCAG
                                ||||| ||  ||||||||
                                GACAC CA  CACAGGTC
                                  A  CA
GAM910  FGFRL1  3'  TCTGGAAGTGTGTGTCCAG  34918     TGC  A_
                                TCTG   GT  GTGTCCAG
                                ||||   ||  ||||||||
                                AGAC   CA  CACAGGTC
                                  CTT  CA
GAM910  FGFRL1  3'  TCTGTGCACGTGTGTGTCC  34920       TA___
                                TCTGTGCG    GTGTCC
                                ||||||||    ||||||
                                AGACACGT    CACAGG
                                    GCACA
GAM910  FGFRL1  3'  TCTGTGTGTGTGTCCAG    34921      C  A
                                TCTGTG GT GTGTCCAG
                                |||||| || ||||||||
                                AGACAC CA CACAGGTC
                                   A  _
GAM910  FMN2    5'  TCTGTAGTAATTCCAG     44287      C    G
                                TCTGTG GTAGT TCCAG
                                |||||| ||||| |||||
                                AGACAT CATTA AGGTC
                                  _    _
GAM910  FRAP1   3'  TCTGTGCATCTGCTCAG    22439       AG  TC
                                TCTGTGCGT  TG  CAG
                                |||||||||  ||  |||
                                AGACACGTA  AC  GTC
                                    G_  GA
GAM910  FTSJ2   3'  TCTGTGCGTGGTGCTCTCAG  30172       A  _ _
                                TCTGTGCGT GTG TC CAG
                                ||||||||| ||| || |||
                                AGACACGCA CAC AG GTC
                                    C   G  A
GAM910  HF1     5'  TCTGTTCACAACGTCCAG   6780      G
                                TCTGT CGTAGTGTCCAG
                                ||||| ||||||||||||
                                AGACA GTGTTGCAGGTC
                                  A
GAM910  HPCA    3'  TCTGTGTGTATCCAA      13427      CGTA
                                TCTGTG   GTGTCCAG
                                ||||||   ||||||||
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                                AGACAC    CATAGGTT
                                   A___
GAM910  INSRR    5'  TCTGAGCGAATATCCAG     42849      T   T
                                TCTG GCG AGTGTCCAG
                                |||| ||| |||||||||
                                AGAC CGC TTATAGGTC
                                  T   _
GAM910  IRS1     3'  TCTGCTGTGATGTCCAG     24430      GC  A
                                TCTGT  GT GTGTCCAG
                                |||||  || ||||||||
                                AGACG  CA TACAGGTC
                                   A_  C
GAM910  JAM3     3'  TCTGTGCGCTCTCAG       37266         AGTG  _
                                TCTGTGCGT    TC CAG
                                |||||||||    || |||
                                AGACACGCG    AG GTC
                                     _____  A
GAM910  LPP      5'  TCTGATGAGCGTCCAG      24560      _  CGT
                                TCTG TG   AGTGTCCAG
                                |||| ||   |||||||||
                                AGAC AC   TCGCAGGTC
                                  T  ____
GAM910  LRPAP1   3'  TCTGTGCATGGTATTTCC    14235         A  __
                                TCTGTGCGT GTG  TCC
                                ||||||||| |||  |||
                                AGACACGTA CAT  AGG
                                     C   AA
GAM910  MAPK1    3'  TCTGAGCACGTCCAG       15655      T   TAG
                                TCTG GCG   TGTCCAG
                                |||| |||   |||||||
                                AGAC CGT   GCAGGTC
                                  T   ____
GAM910  MEL      3'  TCTTGGCCATGTCCAG      23874      G  C  A
                                TCT TG GT GTGTCCAG
                                ||| || || ||||||||
                                AGA AC CG TACAGGTC
                                  _ _  G
GAM910  MSR1     3'  TCCGTGCATGAGAGGTGTCCAG 14663          A_____
                                TCTGTGCGT    GTGTCCAG
                                |||||||||    ||||||||
                                AGGCACGTA    CACAGGTC
                                     CTCTC
GAM910  MYLK2    3'  CTGTGTGGCTGCGTCCAG    37521       C_  A
                                CTGTG  GT GTGTCCAG
                                |||||  || ||||||||
                                GACAC  CG CGCAGGTC
                                   AC  A
GAM910  NRIP1    3'  TCTATACATTTGTCCAG     40988         AG
                                TCTGTGCGT  TGTCCAG
                                |||||||||  |||||||
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                                AGATATGTA  ACAGGTC
                                     A_
GAM910  NUMA1    5'  TCTGTGCAGATACCAG      45245        TA   T
                                TCTGTGCG  GTG CCAG
                                ||||||||  ||| ||||
                                AGACACGT  TAT GGTC
                                     C_   _
GAM910  OCA2     3'  TCTGTAGCATCTCCAG      41193       C   G G
                                TCTGTG GTA T TCCAG
                                ||||||| ||| | |||||
                                AGACAT CGT A AGGTC
                                   _   _ G
GAM910  PBX3     3'  TCTGTGCAGCACCCAG      26216        GT  TG
                                TCTGTGC  AG  TCCAG
                                |||||||  ||  |||||
                                AGACACG  TC  GGGTC
                                     __  GT
GAM910  PML      3'  CTGTCAGCAGGTGTCCAG    37753      GC   _
                                CTGT  GTAG TGTCCAG
                                ||||  |||| |||||||
                                GACA  CGTC ACAGGTC
                                  GT    C
GAM910  PPFIA3   3'  TCTGTACAGATGGTCCAG    41426         TAGT
                                TCTGTGCG    GTCCAG
                                ||||||||    ||||||
                                AGACATGT    CAGGTC
                                     CTAC
GAM910  PPP1R8   5'  TCTTTGAATGTCCAG       39733     G  CGT
                                TCT TG   AGTGTCCAG
                                ||| ||   |||||||||
                                AGA AC   TTACAGGTC
                                  A  ____
GAM910  RALBP1   3'  TCTGTGGATGCACCAG      27702       CGTA   _
                                TCTGTG    GTGT CCAG
                                ||||||    |||| ||||
                                AGACAC    TACG GGTC
                                     C___    T
GAM910  RPS6KA2  3'  CCTGTGTGCACACCCAG     34458       C   G GT
                                TCTGTG GTA T  CCAG
                                |||||| ||| |  ||||
                                GGACAC CGT G  GGTC
                                     A   _ TG
GAM910  SLC12A7  3'  TCTGGCCACGTCCAG       27333      T  G  G
                                TCTG GC TA TGTCCAG
                                |||| || || |||||||
                                AGAC CG GT GCAGGTC
                                  _  _  _
GAM910  SLC4A5   5'  TCTGAACCATGTCCAG      39431      T  GTA
                                TCTG GC   GTGTCCAG
                                |||| ||   ||||||||
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                                AGAC TG   TACAGGTC
                                  T  G__
GAM910  TGFA     3'  TCTGTGGCACACCCAG      17447       C   G GT
                                TCTGTG GTA T  CCAG
                                |||||| ||| |  ||||
                                AGACAC CGT G  GGTC
                                   _   _ TG
GAM910  TNFRSF8  3'  TCTGGCCAATGTCCAG      10323      T  G
                                TCTG GC TAGTGTCCAG
                                |||| || ||||||||||
                                AGAC CG GTTACAGGTC
                                  _ _
GAM910  TRIM9    3'  TCTGTGCAGTAACAG       38140       GT    TC
                                TCTGTGC  AGTG  CAG
                                |||||||  ||||  |||
                                AGACACG  TCAT  GTC
                                   __    T_
GAM910  UBE2G2   3'  CCTGTGCGAGGCCAG       42120        T  T T
                                TCTGTGCG AG G CCAG
                                |||||||| || | ||||
                                GGACACGC TC C GGTC
                                   _ _ _
GAM910  WFDC1    5'  TCATGTGTCCGCGTCCAG    34525    _   CGTA
                                TC TGTG    GTGTCCAG
                                || ||||    ||||||||
                                AG ACAC    CGCAGGTC
                                 T    AGG_
GAM910  ZNF26    5'  TCTGTGTAGAATCCAG      43805      GC    T
                                TCTGT  GTAG GTCCAG
                                |||||  |||| ||||||
                                AGACA  CATC TAGGTC
                                   __    T
GAM911  FOXG1B   5'  ACCGGTGGGTGCCGAACG    23499      A        TTTG
                                GCCG TGGGTGCCGG    GCG
                                |||| ||||||||||    |||
                                TGGC ACCCACGGCT    TGC
                                  C         ____
GAM911  HMGA2    5'  TGGGTGCCGGAGGTGG      18534          TTT  C
                                TGGGTGCCGG   GG GG
                                ||||||||||   || ||
                                ACCCACGGCC   CC CC
                                     T__  A
GAM912  DBCCR1   5'  GCTCTCGCTCTCGCTGTT    31146       G GC_  _
                                GCTCTCG C   CGC GTT
                                ||||||| |   ||| |||
                                CGAGAGC G   GCG CAA
                                   _ AGA   A
GAM912  TNFRSF6B 5'  GCTCCCGGCGGAAACTGTT   32357          CC_ _
                                GCTCTCGGCG   GC GTT
                                ||||||||||   || |||
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                                CGAGGGCCGC   TG CAA
                                     CTT  A
GAM913  PKNOX1   3'  CTAGAAATTTTATCCTCAATAT 21307       C    TGA_
            AG                    CTAGAA ATTTT   TTAATATAG
                                  |||||| |||||   |||||||||
                                  GATCTT TAAAA   AGTTATATC
                                     _    TAGG
GAM913  AP3B2    3'  GGTATAGATGGGAGCCAAACA  21616    A      TTTTA
                                  GG TATAGATG    CAAACA
                                  || ||||||||    ||||||
                                  CC ATATCTAC    GTTTGT
                                   _      CCTCG
GAM913  ARHGEF12 3'  AGATATAGATATATGTTTGTAA 31632          TTTAC___
            ACAAA                   GGATATAGATGT      AAACAAA
                                  ||||||||||||      |||||||
                                  TCTATATCTATA      TTTGTTT
                                        TACAAACA
GAM913  CLCA2    3'  GGAGTAGAAACTTACAAACAAA 27224    TA   TGT
                                  GGA  TAGA   TTTACAAACAAA
                                  |||  ||||   ||||||||||||
                                  CCT  ATCT   GAATGTTTGTTT
                                    C_   TT_
GAM913  FGFR2    3'  GGAAATAGATGCCAGGAACA   35665    T      TT__
                                  GGA ATAGATGTT    ACA
                                  ||| |||||||||    |||
                                  CCT TATCTACGG    TGT
                                    T       TCCT
GAM913  MOG      3'  GGATGAGATGTCCCCAAGGACA 14613     AT      A  __
            AA                    GGAT  AGATGTTTT CAA  ACAAA
                                  ||||  ||||||||| |||  |||||
                                  CCTA  TCTACAGGG GTT  TGTTT
                                    C_       _  CC
GAM913  NCF2     3'  GGTGCTAAATCTTACAAACAA  7727     ATA   AT
                                  GG   TAG  GTTTTACAAACAA
                                  ||   |||  ||||||||||||||
                                  CC   ATT  TAGAATGTTTGTT
                                   ACG   __
GAM913  PDLIM1   3'  GGACTCAATGTTTTACAAGCA  34194      ATA         A
                                  GGAT   GATGTTTTACAA CA
                                  ||||   |||||||||||| ||
                                  CCTG   TTACAAAATGTT GT
                                    AG_          C
GAM913  WHSC1    3'  GGTTTAGATGTCAAGACAGACA 39373    ATA      TT_  A
            AA                    GG   TAGATGTT   ACA ACAAA
                                  ||   ||||||||   ||| |||||
                                  CC   ATCTACAG   TGT TGTTT
                                   AA_       TTC   C
GAM913  WNT1     3'  GGATAGGGGACACCACAAACAA 24085      TA_  TG TT
                                  GGATA   GA  T  TACAAACAA
                                  |||||   ||  |  |||||||||
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                                CCTAT  CT  G  GTGTTTGTT
                                   CCC  GT __
GAM914  MGA     3'  GTGATTCAAATACTGCC     41726    ACTT       C
                                GT   TTCAAATAC GCC
                                ||   ||||||||| |||
                                CA   AAGTTTATG CGG
                                 CT__       A
GAM914  RANBP3   5'  GCACCTGTTTTTCAAAACAGCC 28757      ____      T  C
                                GTACT   TTTCAAA AC GCC
                                |||||   ||||||| || |||
                                CGTGG   AAAGTTT TG CGG
                                   ACAA      _ T
GAM914  LRAT    3'  TCAGAGTACATTAGTAA     41084          C  TAC
                                TCAGAGTACG TA   GTAA
                                |||||||||| ||   ||||
                                AGTCTCATGT AT   CATT
                                      A ___
GAM914  NELL2    3'  TCAGAGTGTACTGTACATAA   26050        AC   A
                                TCAGAGT  GCT TACGTAA
                                |||||||  ||| |||||||
                                AGTCTCA  TGA ATGTATT
                                    CA   C
GAM914  RAI14    3'  CCAGAGTACTCGTAATAA    31800         GCTATA
                                TCAGAGTAC     CGTAATAA
                                |||||||||     ||||||||
                                GGTCTCATG     GCATTATT
                                      A_____
GAM915  AKAP4    5'  GTTTTCTTGTTGATTTGGAT   40234      TC  C
                                GTTTT  TG TGATTTGGAT
                                |||||  || ||||||||||
                                CAAAA  AC ACTAAACCTA
                                   GA  A
GAM915  MECP2    3'  GTTTTTCTTTTGGA       22608         GCTGA
                                GTTTTTCT    TTTGGA
                                ||||||||    ||||||
                                CAAAAAGA    AAACCT
                                     _____
GAM915  SLC4A7   3'  ACGGTTTTTCTGGCACTGGAT  18818    A       CTGAT
                                AC GTTTTTCTG    TTGGAT
                                || |||||||||    ||||||
                                TG CAAAAAGAC    GACCTA
                                 C       CGT__
GAM916  ALX3     3'  TGGCTGCTTCGAAGCC      27072      ACCA  _
                                TGGC   GCT CGAAGCC
                                ||||   ||| |||||||
                                ACCG   CGA GCTTCGG
                                  A___  A
GAM916  ARF5     3'  TAGCACCACCCGAAGCC     11683         G
                                TGGCACCA CTCGAAGCC
                                |||||||| |||||||||
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                                ATCGTGGT GGGCTTCGG
                                       _
GAM916  ATP2B2   5'  TGGCACCAGGCGGCC      11765        CT  AA
                                TGGCACCAG  CG  GCC
                                |||||||||  ||  |||
                                ACCGTGGTC  GC  CGG
                                     C_  __
GAM916  B4GALT7  3'  TGGCCCAGCCCAAGCC     28551     A     G
                                TGGC CCAGCTC AAGCC
                                |||| ||||||| |||||
                                ACCG GGTCGGG TTCGG
                                  _     _
GAM916  BCLG     3'  TGGCCCATCAAAGCC       39824     A  GC
                                TGGC CCA  TCGAAGCC
                                |||| |||  ||||||||
                                ACCG GGT  AGTTTCGG
                                  _  __
GAM916  CACNA2D2 3'  TGGCACCAGTGCGTGTGGCC  25728        CT  AA__
                                TGGCACCAG  CG   GCC
                                |||||||||  ||   |||
                                ACCGTGGTC  GC   CGG
                                     AC  ACAC
GAM916  CDC25B   5'  GGCACCAGCCAGGGAAGCC   34853         C__
                                GGCACCAGCT   GAAGCC
                                ||||||||||   ||||||
                                CCGTGGTCGG   CTTCGG
                                      TCC
GAM916  CKAP1    5'  TGGGCCAGCCCAGCC      43886     CA     GA
                                TGG  CCAGCTC  AGCC
                                |||  |||||||  ||||
                                ACC  GGTCGGG  TCGG
                                  C_     __
GAM916  CNP      5'  TGGCACAACCCGAGCC      37563       C     A
                                TGGCAC AGCTCGA GCC
                                |||||| ||||||| |||
                                ACCGTG TTGGGCT CGG
                                       _     _
GAM916  CNP      5'  GGCACCAGCGCTCCGGGGCC  37559         ___  AA
                                GGCACCAGC   TCG  GCC
                                |||||||||   |||  |||
                                CCGTGGTCG   GGC  CGG
                                     CGA   CC
GAM916  CYP4F3   3'  TGGCACCACCCCAGCC     9459         G  GA
                                TGGCACCA CTC  AGCC
                                |||||||| |||  ||||
                                ACCGTGGT GGG  TCGG
                                     G  __
GAM916  DCK      3'  GGCACCAGGGAAAAAAGCC   8979         CTC__
                                GGCACCAG    GAAGCC
                                ||||||||    ||||||
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                                CCGTGGTC    TTTCGG
                                    CCTTT
GAM916  DUSP7   3'  TGGACGCCCAAAGCC      42278    C  CA
                                TGG AC  GCTCGAAGCC
                                ||| ||  ||||||||||
                                ACC TG  CGGGTTTCGG
                                 _ __
GAM916  EGFL3   3'  TAGCACCAAAAAGCC      41709        CTC
                                TGGCACCAG   GAAGCC
                                |||||||||   ||||||
                                ATCGTGGTT   TTTCGG
                                    ____
GAM916  EGFL4   5'  TGGGCCAGCCCAGCC      41585    CA     GA
                                TGG  CCAGCTC  AGCC
                                |||  |||||||  ||||
                                ACC  GGTCGGG  TCGG
                                  C_     __
GAM916  GGT2    5'  TGTGCCAGCTCATAGCC     43928    GCA      A
                                TG   CCAGCTCG AGCC
                                ||   |||||||| ||||
                                AC   GGTCGAGT TCGG
                                 AC_      A
GAM916  HSPG2   3'  GGCACCAGCCCACAAGCC    24364          _
                                GGCACCAGCTCG AAGCC
                                |||||||||||| |||||
                                CCGTGGTCGGGT TTCGG
                                       G
GAM916  LNK     3'  TGGCACCAGATTCCCAGC    24209        C_  GA
                                TGGCACCAG  TC  AGC
                                |||||||||  ||  |||
                                ACCGTGGTC  AG  TCG
                                     TA  GG
GAM916  MCM3    3'  TGGAACCACCCAAAGCC     14384    C   G
                                TGG ACCA CTCGAAGCC
                                ||| |||| |||||||||
                                ACC TGGT GGGTTTCGG
                                  T   _
GAM916  MLC1    3'  TGGCACTACCCAAAGCC     31584      CA
                                TGGCAC  GCTCGAAGCC
                                ||||||  ||||||||||
                                ACCGTG  TGGGTTTCGG
                                   A_
GAM916  MPP2    3'  TGGCACCACCACCCGGGCC   40802        __    AA
                                TGGCACCA  GCTCG  GCC
                                ||||||||  |||||  |||
                                ACCGTGGT  TGGGC  CGG
                                     GG    C_
GAM916  MYOG    5'  TGCCACCAGCCCCCAAGC    40424    G      _ G
                                TG CACCAGCT C AAGC
                                || |||||||| | ||||
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```
                                AC GTGGTCGG G TTCG
                                 G       G G
GAM916  PAX2     3'  TGACGCCCCCAAAGCC      19612      A  AG
                                TGGC CC  CTCGAAGCC
                                |||| ||  |||||||||
                                ACTG GG  GGGTTTCGG
                                  C  __
GAM916  PCMT1    3'  TGACACCACATCAAAAGC    23943        GC    _
                                TGGCACCA  TCGAA GC
                                ||||||||  ||||| ||
                                ACTGTGGT  AGTTT CG
                                     GT    T
GAM916  PIP5K1A  5'  TGGACCAGCTCAAGGCC     18661     C        A
                                TGG ACCAGCTCGA GCC
                                ||| ||||||||| |||
                                ACC TGGTCGAGTT CGG
                                  _        C
GAM916  PPP2R4   3'  GGCACCAGCCAGGACAGC    41329          C_ _
                                GGCACCAGCT  GA AGC
                                ||||||||||  || |||
                                CCGTGGTCGG  CT TCG
                                      TC  G
GAM916  PRKCSH   3'  TGGACCAGCCCCGCC       15647     C       GAA
                                TGG ACCAGCTC   GCC
                                ||| ||||||||   |||
                                ACC TGGTCGGG   CGG
                                  _      G__
GAM916  RPA2     5'  TGGCACCACAAACGCC      16378        GCT   _
                                TGGCACCA   CGAA GCC
                                ||||||||   |||| |||
                                ACCGTGGT   GTTT CGG
                                     ___   G
GAM916  SDHC     3'  TGGCACCCAAAGCC        42981        AGCT
                                TGGCACC    CGAAGCC
                                |||||||    |||||||
                                ACCGTGG    GTTTCGG
                                     ____
GAM916  SHOX     3'  TGGCACCACCGTGCC       27834        G T  AA
                                TGGCACCA C CG  GCC
                                |||||||| | ||  |||
                                ACCGTGGT G GC  CGG
                                     _ _  A_
GAM916  SLC7A4   3'  TGGCACCAGCACCAGCC     42188          TCGA
                                TGGCACCAGC    AGCC
                                ||||||||||    ||||
                                ACCGTGGTCG    TCGG
                                      TGG_
GAM916  SNX9     3'  TGACACCAACTGGCC       32160          CGAA
                                TGGCACCAGCT    GCC
                                ||||||||||    |||
```

```
                                ACTGTGGTTGA   CGG
                                      C___
GAM916  TCF2    3'  TGACACACGGAAGCC      27031      CA  TC
                                TGGCAC  GC  GAAGCC
                                ||||||  ||  ||||||
                                ACTGTG  TG  CTTCGG
                                   __  C_
GAM916  TNFRSF6B 3'  TGGCACCACTCACAGGCC    32364       G   AA_
                                TGGCACCA CTCG   GCC
                                |||||||| ||||   |||
                                ACCGTGGT GAGT   CGG
                                     _   GTC
GAM916  WDR4    5'  TGTGCCAGCCCAGAGCC    38025    GCA      A
                                TG   CCAGCTCG AGCC
                                ||   |||||||| ||||
                                AC   GGTCGGGT TCGG
                                 AC_      C
GAM916  WNT1    3'  TGACACCATCAGGAGCC     24087       GC   A_
                                TGGCACCA  TCG  AGCC
                                ||||||||  |||  ||||
                                ACTGTGGT  AGT  TCGG
                                     __  CC
GAM917  DMRT2   3'  GTTGTGGTTGTTATGGATTT  27265    _   GCC_
                                GTT TGGT    ATGGATTT
                                ||| ||||    ||||||||
                                CAA ACCA    TACCTAAA
                                  C   ACAA
GAM917  TBXA2R  5'  TATTGGGTTTGGAGGAATT   9859          TGCCAT
                                TATTGGGTTTGG     GGATT
                                ||||||||||||     |||||
                                ATAACCCAAACC     CTTAA
                                       TC____
GAM918  COL4A2  3'  TAAGTGCTGCTGCTGGA     12320       ATC   TTCG
                                TAAGTGCT   GCT   GGA
                                ||||||||   |||   |||
                                ATTCACGA   CGA   CCT
                                     ___  CGA_
GAM918  AGA     3'  TTAGTAAAATTACAGTAC    6188         AT
                                TTAGTAAAAT  TATAGTAC
                                |||||||||  ||||||||
                                AATCATTTTA  ATGTCATG
                                           __
GAM918  CLCN3   3'  CTCAGTAAAATCACAGTAC   12271        AT
                                CTTAGTAAA  ATTATAGTAC
                                |||||||||  ||||||||||
                                GAGTCATTT  TAGTGTCATG
                                           __
GAM918  COL4A4  3'  CTCAGTAAAATAAGAGTA    6399          TTAT
                                CTTAGTAAAATA   AGTA
                                ||||||||||||   ||||
```

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                                GAGTCATTTTAT   TCAT
                                      TC__
GAM918  SEPP1    3'  TTAGCAAAATATTCACGT   24001          ATA
                                TTAGTAAAATATT  GT
                                ||||||||||||  ||
                                AATCGTTTTATAA  CA
                                     GTG
GAM919  C1orf6   3'  AGGAAAATTACCACCT     33523     CTATG
                                AGGA    AAATTACCACCT
                                ||||    ||||||||||||
                                TCCT    TTTAATGGTGGA
                                 _____
GAM919  IQGAP2   3'  GGACTATGCTCACTATCTA   27371       AAA   CAC
                                GGACTATG  TTAC  CTA
                                ||||||||  ||||  |||
                                CCTGATAC  AGTG  GAT
                                    G__   ATA
GAM919  NFATC1   3'  GACTATGAACAAGCCTAC    26075       ATTACCA
                                GACTATGAA     CCTAC
                                |||||||||     |||||
                                CTGATACTT     GGATG
                                    GTTC___
GAM919  PIN4     3'  GGAGCTAATACCACCT     26328    _  TGAAAT
                                GGA CTA     TACCACCT
                                ||| |||     ||||||||
                                CCT GAT     ATGGTGGA
                                  C  T_____
GAM919  TPM4     3'  AGGATCAATTAATTACCATCTA 17645     C  TGA      C
                                AGGA TA   AATTACCA CTA
                                |||| ||   |||||||| |||
                                TCCT GT   TTAATGGT GAT
                                  A  TAA      A
GAM919  ABCD4    3'  TCTTTAGCAAACATGATCT   33750       G   GTTG
                                TCTTTAG AAAT   ATGATCT
                                ||||||| ||||   |||||||
                                AGAAATC TTTG   TACTAGA
                                    G   _____
GAM919  ICA1     5'  TCTTCTATTGTTGATGAT    22471      AGGAAA
                                TCTTT     TGTTGATGAT
                                |||||     ||||||||||
                                AGAAG     ACAACTACTA
                                   ATA___
GAM919  IFNAR1   3'  TTTAGGACCTATGATCT     8435       AATGTTG
                                TTTAGGA     ATGATCT
                                |||||||     |||||||
                                AAATCCT     TACTAGA
                                    GGA____
GAM919  SLC21A3  3'  TCTTTAGGGGGCTGTTATTG  39580       AAA_   A
                                TCTTTAGG   TGTTG TG
                                ||||||||   ||||| ||
```

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                                AGAAATCC   ACAAT AC
                                    CCCG   A
GAM919  TOP2A    3'  TCTTTGGCCTCTGATGAT   9884      A  AAATG
                                TCTTT GG   TTGATGAT
                                ||||| ||   ||||||||
                                AGAAA CC   GACTACTA
                                  _ GGA__
GAM920  GABRE    5'  GCCGCGTTTGCCTAGTGTTGG  35076   T A       C
                                GC C CGTTTGCTTG TGTTGG
                                || | |||||||||| ||||||
                                CG G GCAAACGGAT ACAACC
                                 _ C       C
GAM920  HMGCR    3'  CAGCTTATATTTGCTTTCAGAG 9235      CAC      GCTGTT
          G                      CAGCT  GTTTGCTT    GG
                                |||||  ||||||||    ||
                                GTCGA  TAAACGAA    CC
                                   ATA     AGTCT_
GAM920  RB1CC1   5'  GCTTATGTTTGCTTTGCT   31315    CAC      _
                                GCT  GTTTGCTT GCT
                                |||  |||||||| |||
                                CGA  CAAACGAA CGA
                                  ATA     A
GAM920  SLC35A1  3'  AGCTTCGTTTGTTTGTTGTT  26946    CA    C  C
                                AGCT  CGTTTG TTG TGTT
                                ||||  |||||| ||| ||||
                                TCGA  GCAAAC AAC ACAA
                                  A_    A  A
GAM921  ABCB4    5'  CTTTGCCCTGCACCTCCAG   7770       AATT  _
                                TTTTGCCC   TC CCAG
                                ||||||||   || ||||
                                GAAACGGG   GG GGTC
                                    ACGT  A
GAM921  ACK1     3'  TTCTGCCCGACACCCCAG   25122       A  T
                                TTTTGCCC AT TCCCAG
                                |||||||| || ||||||
                                AAGACGGG TG GGGGTC
                                    C  T
GAM921  ALS2     3'  TTTTGCTTATTTCCCAG    34098      CCA
                                TTTTGC  ATTTCCCAG
                                ||||||  |||||||||
                                AAAACG  TAAAGGGTC
                                   AA_
GAM921  AQP6     5'  TCTTGGCCTTTCCCAG     38258     C  AA
                                TTTTG CC  TTTCCCAG
                                ||||| ||  ||||||||
                                AGAAC GG  AAAGGGTC
                                  C __
GAM921  ARHGEF12 3'  TTTTCCCAGACCCCAG     31656     G   ATT
                                TTTT CCCA  TCCCAG
                                |||| ||||  ||||||
```

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                                AAAA GGGT   GGGGTC
                                  _   CT_
GAM921   ARNT2    3'  TTTTCCCAGCATTCCCCCAG  31369     G   A___ TT
                                TTTT CCCA   T  CCCAG
                                |||| ||||   |  |||||
                                AAAA GGGT   A  GGGTC
                                  _   CGTA GG
GAM921   ATP5B    5'  TTCTGCCCAAAGTCTCAG   40651         TT  C
                                TTTTGCCCAA  TC CAG
                                ||||||||||  || |||
                                AAGACGGGTT  AG GTC
                                      TC  A
GAM921   BARX2    3'  TTTTCCCTTCTCCCCAG    18930     G   AA
                                TTTT CCC  TTTCCCAG
                                |||| |||  ||||||||
                                AAAA GGG  GAGGGGTC
                                  _   AA
GAM921   C1orf1   3'  TTTTGCCATGTTTCCCAG   10231       CAA
                                TTTTGCC   TTTCCCAG
                                |||||||   ||||||||
                                AAAACGG   AAAGGGTC
                                    TAC
GAM921   CALM3    3'  TCTTGTCCCTCCCAG      23247      _   AATT
                                TTTTG CCC   TCCCAG
                                ||||| |||   ||||||
                                AGAAC GGG   AGGGTC
                                  A  _____
GAM921   CD5L     3'  TCTTGACCTTTTCCCAG    25319      C  AA
                                TTTTG CC  TTTCCCAG
                                ||||| ||  ||||||||
                                AGAAC GG  AAAGGGTC
                                  T  A_
GAM921   CDH1     3'  TTCTGCATTTCCCAG      20372      CCA
                                TTTTGC   ATTTCCCAG
                                ||||||   |||||||||
                                AAGACG   TAAAGGGTC
                                   ___
GAM921   CDK3     3'  CTTTGCTCTCCCCAG      10379      CCAA
                                TTTTGC   TTTCCCAG
                                ||||||   ||||||||
                                GAAACG   GAGGGGTC
                                  A___
GAM921   CHEK1    5'  TTCTGCCCTCCTCAG      10463       AATT  _
                                TTTTGCCC   TCC CAG
                                ||||||||   ||| |||
                                AAGACGGG   AGG GTC
                                    _____  A
GAM921   CRP      3'  TTTTGGACCGTTTCCCAG   43450      C_  AA
                                TTTTG  CC  TTTCCCAG
                                |||||  ||  ||||||||
```

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                                AAAAC  GG  AAAGGGTC
                                   CT  C_
GAM921   CYBB    3'  TTCTGCCCTTCCCCCAG     44105        AA TT
                                TTTTGCCC  T  CCCAG
                                ||||||||  |  |||||
                                AAGACGGG  A  GGGTC
                                    A_ GG
GAM921   DEDD    3'  CTTTGCCCAAGCCAG       37427          TTTC
                                TTTTGCCCAA    CCAG
                                ||||||||||    ||||
                                GAAACGGGTT    GGTC
                                      C___
GAM921   DGKI    3'  CTTTGCCCGAATACCAG     21783         _   TTC
                                TTTTGCCC AAT   CCAG
                                |||||||| |||   ||||
                                GAAACGGG TTA   GGTC
                                    C   T__
GAM921   DLG4    3'  TTTTCCCCAAAAAAATTCCCAG 10710      G     T____
                                TTTT CCCAA     TTCCCAG
                                |||| |||||     |||||||
                                AAAA GGGTT     AAGGGTC
                                  G     TTTTT
GAM921   ESR1    3'  TTTTGCCCTCCCAG        6544          AATT
                                TTTTGCCC    TCCCAG
                                ||||||||    ||||||
                                AAAACGGG    AGGGTC
                                     ____
GAM921   FEN1    3'  TTCTGCCCATCTTCTCTCAG   19962         A__    C
                                TTTTGCCCA   TTTC CAG
                                |||||||||   |||| |||
                                AAGACGGGT   AGAG GTC
                                     AGA    A
GAM921   FMR2    3'  TTTGCCCAGATTTCATTCC    12991         _     ___
                                TTTGCCCA ATTTC   CC
                                |||||||| |||||   ||
                                AAACGGGT TAAAG   GG
                                    C     TAA
GAM921   GTF2I   5'  CTCTGCTCTCCCAG        37437        CCAA
                                TTTTGC    TTTCCCAG
                                ||||||    ||||||||
                                GAGACG    AGAGGGTC
                                    ____
GAM921   H4F2    3'  TTTTCCCCGGTTTCCCAG    18643      G   AA
                                TTTT CCC  TTTCCCAG
                                |||| |||  ||||||||
                                AAAA GGG  AAAGGGTC
                                  G   CC
GAM921   HP      3'  CTTTGCCCTCTTCCAG      23108         AA   C
                                TTTTGCCC  TTT CCAG
                                ||||||||  ||| ||||
```

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                                GAAACGGG  AGA GGTC
                                   __   A
GAM921  IRF1    3'  TTTTCCCAAGCCCCTCAG    42046     G    T   _
                                TTTT CCCAA TTCC CAG
                                |||| ||||| |||| |||
                                AAAA GGGTT GGGG GTC
                                  _    C    A
GAM921  KCNK3   3'  TCTTGCCCTGTCACCCAG    13915       AA  T
                                TTTTGCCC  TT CCCAG
                                ||||||||  || |||||
                                AGAACGGG  AG GGGTC
                                     AC  T
GAM921  KLRG1   3'  TCTTGCTCTATCTCCCAG    25155      CCA
                                TTTTGC   ATTTCCCAG
                                ||||||   |||||||||
                                AGAACG   TAGAGGGTC
                                   AGA
GAM921  LASS2   3'  CTTTGCTCCTCCCCCAG     42673      _  AA TT
                                TTTTGC CC  T  CCCAG
                                |||||| ||  |  |||||
                                GAAACG GG  A  GGGTC
                                   A  __ GG
GAM921  LFG     3'  TTCTGCCCGGCTTCCCCAG   44158       AA_
                                TTTTGCCC   TTTCCCAG
                                ||||||||   ||||||||
                                AAGACGGG   AAGGGGTC
                                     CCG
GAM921  MADD    3'  TCTTGCCCATACCCAG      39070       ATTT
                                TTTTGCCCA    CCCAG
                                |||||||||    |||||
                                AGAACGGGT    GGGTC
                                     AT__
GAM921  MAPK4   3'  TTTTACCCACAGACCCCAG   15675       ATT_
                                TTTTGCCCA    TCCCAG
                                |||||||||    ||||||
                                AAAATGGGT    GGGGTC
                                     GTCT
GAM921  MGAM    3'  CTTTGCCCATCATCCCAG    43655       ATT
                                TTTTGCCCA   TCCCAG
                                |||||||||   ||||||
                                GAAACGGGT   AGGGTC
                                     AGT
GAM921  MOG     3'  TTTTGCTTCCCCAG       14617      CCAA
                                TTTTGC    TTTCCCAG
                                ||||||    ||||||||
                                AAAACG    AAGGGGTC
                                     ____
GAM921  MTMR8   3'  TCTTGCCCTTTCGCCCAG   31757       AA  T
                                TTTTGCCC  TT CCCAG
                                ||||||||  || |||||
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                                AGAACGGG  AG GGGTC
                                    AA  C
GAM921  MYO9A    3'  TTTTGCTTTCCCCAG      27907      CCAA
                                TTTTGC   TTTCCCAG
                                ||||||   ||||||||
                                AAAACG   AAGGGGTC
                                   A___
GAM921  P2RY1    3'  TTCTGCCCACCCCAG      15013       ATT
                                TTTTGCCCA  TCCCAG
                                |||||||||  ||||||
                                AAGACGGGT  GGGGTC
                                    ___
GAM921  PDGFRB   3'  TTTTGCCCAGGATACCCCC   42347       AT___
                                TTTTGCCCA   TTCCC
                                |||||||||   |||||
                                AAAACGGGT   GGGGG
                                     CCTAT
GAM921  PHLDA3   3'  TTCTGCCCTCCTCCCAG    29617       AA
                                TTTTGCCC TTTCCCAG
                                |||||||| ||||||||
                                AAGACGGG GGAGGGTC
                                    A_
GAM921  PKIB     5'  TTCTGCTTCTCCCAG      37166      CCAA
                                TTTTGC   TTTCCCAG
                                ||||||   ||||||||
                                AAGACG   AGAGGGTC
                                   A___
GAM921  POU4F1   3'  TTTCGCCCAACATGCAG    26400         TTCC
                                TTTTGCCCAAT   CAG
                                ||||||||||   |||
                                AAAGCGGGTTG   GTC
                                      TAC_
GAM921  PPARA    5'  TCTTGAACTTCCCAG      22770      CCC
                                TTTTG  AATTTCCCAG
                                |||||  ||||||||||
                                AGAAC  TTGAAGGGTC
                                   ___
GAM921  PSEN1    3'  CTTTGTCCTCCCCAG      28738      C  AAT
                                TTTTG CC  TTCCCAG
                                ||||| ||  |||||||
                                GAAAC GG  AGGGGTC
                                   A ___
GAM921  SCA1     3'  TTTCGCCCTGACTAATTTC   7304         _____
                                TTTTGCCC    AATTTC
                                ||||||||    ||||||
                                AAAGCGGG    TTAAAG
                                     ACTGA
GAM921  SCN3A    5'  CTTTGCTCCTTTCCCAG     27951       _  AA
                                TTTTGC CC  TTTCCCAG
                                |||||| ||  ||||||||
```

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                                GAAACG GG  AAAGGGTC
                                   A  __
GAM921  SELP     5'  TTCTGCCCAACCCAG       16554          TTT
                                TTTTGCCCAA   CCCAG
                                ||||||||||   |||||
                                AAGACGGGTT   GGGTC
                                    ____
GAM921  SH3BP2   3'  TTTTCCCAAGCCCCAG      16648      G    TT
                                TTTT CCCAA  TCCCAG
                                |||| |||||  ||||||
                                AAAA GGGTT  GGGGTC
                                  _    C_
GAM921  SLC39A1  3'  TTCTGCCCCACCCCAG      30891         AATT
                                TTTTGCCC    TCCCAG
                                ||||||||    ||||||
                                AAGACGGG    GGGGTC
                                    GT__
GAM921  SLC9A1   3'  TTCTGCCCAATCCACCAG    43244           TC
                                TTTTGCCCAATT  CCAG
                                ||||||||||||  ||||
                                AAGACGGGTTAG  GGTC
                                     GT
GAM921  TACC1    3'  TTTTACCCAGCCCAG       26609         ATTT
                                TTTTGCCCA    CCCAG
                                |||||||||    |||||
                                AAAATGGGT    GGGTC
                                    C___
GAM921  TCAP     3'  TCTTGCCCTCACCAG       18950         AATT  _
                                TTTTGCCC    TC CCAG
                                ||||||||    || ||||
                                AGAACGGG    AG GGTC
                                    _____  T
GAM921  TNFRSF1B 3'  TCTTGCCCAGGCCACAG     9877          ATTT  _
                                TTTTGCCCA    CC CAG
                                |||||||||    || |||
                                AGAACGGGT    GG GTC
                                     CC__  T
GAM921  TNS      3'  TTTTCCCAACTGTCCAG      35484      G      TC
                                TTTT CCCAATT  CCAG
                                |||| |||||||  ||||
                                AAAA GGGTTGA  GGTC
                                  _      CA
GAM921  TRAM     5'  TTCTGCTCTTCCCAG       30707        CCAA
                                TTTTGC    TTTCCCAG
                                ||||||    ||||||||
                                AAGACG    GAAGGGTC
                                   A___
GAM921  VAT1     3'  TTTTGCCCTGCCTCCCCAG   26857         AA_
                                TTTTGCCC   TTTCCCAG
                                ||||||||   ||||||||
```

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                                AAAACGGG  GAGGGGTC
                                    ACG
GAM921  VEGFB   3'  TCTTGCTGCCTCCCAG     17981      CCAA
                                TTTTGC   TTTCCCAG
                                ||||||   ||||||||
                                AGAACG   GGAGGGTC
                                   AC__
GAM921  YWHAZ   3'  TTCTGCCCTTATCCAG     18208      AA  TC
                                TTTTGCCC  TT  CCAG
                                ||||||||  ||  ||||
                                AAGACGGG  AA  GGTC
                                    __  TA
GAM921  ZIC3    3'  TCTTGCCCAAAACCTTCC    18255        ___
                                TTTTGCCCAA  TTTCC
                                ||||||||||  |||||
                                AGAACGGGTT  GAAGG
                                     TTG
GAM921  ZNF24   3'  TTTTACATTTCCCAG      28090      CCA
                                TTTTGC  ATTTCCCAG
                                ||||||  |||||||||
                                AAAATG  TAAAGGGTC
                                  ___
GAM921  ZNF264  3'  TTTTGCCCAACTGCAG      18279        TCC
                                TTTTGCCCAATT  CAG
                                ||||||||||||  |||
                                AAAACGGGTTGA  GTC
                                     C__
GAM921  ZNF268  3'  TTTTGCCGTACTTCCCAG    41767      CA
                                TTTTGCC  ATTTCCCAG
                                |||||||  |||||||||
                                AAAACGG  TGAAGGGTC
                                   CA
GAM922  BCS1L   5'  GACAATAAGATCCGCC      20250      CCCGC
                                GACAATAA    TCCGCC
                                ||||||||    ||||||
                                CTGTTATT    AGGCGG
                                    CT___
GAM922  CLDN3   5'  CGGCAAGGCCCGCTCCACC   10565   A  TAA
                                CG CAA  CCCGCTCCGCC
                                || |||  ||||||||||
                                GC GTT  GGGCGAGGTGG
                                 C  CC_
GAM922  SNCAIP  5'  CGAAACCCGCTTCAC      45503    CAAT     C
                                CGA   AACCCGCT CGC
                                |||   |||||||| |||
                                GCT   TTGGGCGA GTG
                                  _____      A
GAM922  TMEPAI  5'  CGCGGGACCGCGCTCCGCTGCG 33600   ACAATA  _     CA
                                CG    ACC CGCTCCGC  CG
                                ||    ||| ||||||||  ||
```

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                                GC     TGG GCGAGGCG  GC
                                 GCCC__   C       AC
GAM922  ZNF26    5'  GACAATAATCCCCAGCACG   43800        CCCG    C
                                GACAATAA    CTCCG CACG
                                ||||||||    ||||| ||||
                                CTGTTATT    GGGGT GTGC
                                    A___     C
GAM923  ANK1     3'  TGTGTGTGTGTGTGTGTGTG    33878      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___ A
GAM923  APBA1    3'  TGTGTGTGTGTGTGTGTGTG    43092      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___ A
GAM923  ASTN     3'  TGTGCACACGTGTGTGTGTGT  42957       TT
                                TGTGC  TGCGTGTGTGTGTGT
                                |||||  ||||||||||||||
                                ACACG  GTGCACACACACACA
                                  T_
GAM923  ASTN     3'  TGTGCACACGTGTGTGTGTGT  42957       TT
                                TGTGC  TGCGTGTGTGTGTGT
                                |||||  ||||||||||||||
                                ACACG  GTGCACACACACACA
                                  T_
GAM923  BMP4     3'  TGTGGTGTGTGTGT       10198      CTTTGC
                                TGTG     GTGTGTGTGT
                                ||||     ||||||||||
                                ACAC     CACACACACA

                                  _______
GAM923  CACNA2D2 3'  TGTGTGTGTGTGTGTGTGTG    25730      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___ A
GAM923  CACNG3   5'  TGTGTGTGTGTGTGTGTGTG    27246      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___ A
GAM923  CACNG3   5'  TCTGTGTGAGTGTGTGTGTGTG 27243       CTT_  C
           TGT                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACAC    AC CACACACACACA
                                   ACTC  A
GAM923  CARPX    3'  TTGTAAGAGTGTGTGTGTGTGT 33584       CTTTGC
                                TTGTG     GTGTGTGTGTGT
                                |||||     ||||||||||||
```

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                                AACAT     CACACACACACA
                                  TCTCA_
GAM923  CBFA2T1  3'  TGTGTGTGTGTGTGTGTG    20314     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  CBFA2T1  3'  TGTGCGTGTGTGTGTGTGTGT  20313      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||
                                ACACG  AC CACACACACACA
                                  C_  A
GAM923  CBFA2T1  3'  TATGTGCGTGTGTGTGTGT   20308     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ATAC   ACGCACACACACACA
                                  ___
GAM923  CCND1    3'  TTTGTGTGTGTGTGTGTGTGTG 38231       CTT  C
            T                    TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM923  CCND1    3'  TGTGTGTGTGTGTGTGTG    38227     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  CD22     3'  TGTGTGTGCGTGTGTGTGTGT  12104     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACACA
                                  AC_
GAM923  CD22     3'  TGTGCGTGTGTGTGTGTGTGT  12103      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||
                                ACACG  AC CACACACACACA
                                  C_  A
GAM923  CDH12    3'  TGTGTGTGTGTGTGTGTG    19780     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  CDH12    3'  TGTGTTTGTGTGTGTGTGTA 19783     C   C         III
                                TGTG TTTG GTGTGTGTGTGT   A
                                |||| |||| ||||||||||   |
                                ACAC AAAC CACACACACACA   T
                                  _   A          III
GAM923  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    38556     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  CENTD2   5'  TCTGTGTGTATGTGTGTGTGT  31605      CTT  CG
                                TTTGTG   TG  TGTGTGTGTGT
                                ||||||   ||  ||||||||||
                                AGACAC   AC  ACACACACACA
                                   ___   AT
GAM923  CHES1    3'  TGTGTGTGTGTGTGTGTG    23289     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  COLQ     5'  TGTGTTTGTGTGTGTGTGTGT  38699     C    C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM923  CRHBP    3'  TGTGTATGTGTGTGTGTGTGT  40512     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM923  CRTL1    5'  TGTGTGTGTGTGTGTGTG    12455     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || |||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  CRTL1    5'  TGTGAGAGTGTGTGTGTGTGTG 12453     CTT_ C
           T                     TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||
                                ACAC   AC CACACACACACA
                                  TCTC  A
GAM923  CSF2RB   3'  TGTGCATGTACGTGTGTGTGTG 7574      TT_
           T                     TGTGC  TGCGTGTGTGTGTGT
                                |||||  ||||||||||||||
                                ACACG  ATGCACACACACACA
                                   TAC
GAM923  CSF2RB   3'  TGTACGTGTGTGTGTGTGTGT  7572      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||
                                ACATG  AC CACACACACACA
                                  C_   A
GAM923  DGKA     3'  TGTGTTTTGGGGTGTGTGT   10648     C   CGT
                                TGTG TTTG  GTGTGTGT
                                |||| ||||  ||||||||
                                ACAC AAAC  CACACACA
                                  A   CC_
GAM923  DGKG     3'  TGTGTATGTGTGTGTGTGTGT  10660     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||
```

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                                ACAC   AC CACACACACACA
                                  AT_  A
GAM923  DMD     3'  TGTGTATGTGTGTGTGTGTGT  19698     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM923  DMD     3'  TATGTGTGTGTGTGTGTG    19693     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM923  EFNB1   3'  TGTGTGTGTGTGTGTGTG    20730     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  EFNB1   3'  TTTGTGTGTGTGTGTGTGTGTG 20732       CTT  C
              T                  TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
                                 AAACAC   AC CACACACACACA
                                    AC_  A
GAM923  EHD3    3'  TGTGTGTGTGTGTGTGTG    31122     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  EHD3    3'  TTTGTGTGTGTGTGTGTGTGTG 31126       CTT  C
              T                  TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
                                 AAACAC   AC CACACACACACA
                                    AC_  A
GAM923  EN2     3'  TGTGTGTGTGTGTGTGTG    10967     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  F7      3'  TGTGCATTGGCGTGTGTGTGTG 33348      _  T
              T                  TGTGC TT GCGTGTGTGTGTGT
                                 |||||  || ||||||||||||||
                                 ACACG AA CGCACACACACACA
                                    T  C
GAM923  FGFR2   3'  TTTGTGCTCTGTAAGTGTGT   35673         CGT
                                TTTGTGCTTTG   GTGTGT
                                ||||||||||   ||||||
                                AAACACGAGAC   CACACA
                                      ATT
GAM923  FGFRL1  3'  CCGTGTGTGTGTGTGTGT    34904    T  C
                                CT TG GTGTGTGTGTGT
                                ||  ||  ||||||||||||
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                                GG AC CACACACACACA
                                 C  A
GAM923  FGFRL1   3'  TCTGTGCACGCGTGTGTGTGTG 34919        TT
             T                   TTTGTGC  TGCGTGTGTGTGTGT
                                 |||||||  ||||||||||||||
                                 AGACACG  GCGCACACACACACA
                                    T_
GAM923  FGFRL1   3'  TGTGTCTGTGTGTGTGTGT   34924     C   C
                                 TGTG TTTG GTGTGTGTGT
                                 |||| |||| ||||||||||
                                 ACAC AGAC CACACACACA
                                   _   A
GAM923  FLRT2    3'  TGTTTGTGTGTGTGTGTG    29868    C   C
                                 TG TTTG GTGTGTGTGTG
                                 || |||| ||||||||||
                                 AC AAAC CACACACACAC
                                  _   A
GAM923  FLRT2    3'  TTTGTGTGTGTGTGTGTGTGTG 29871       CTT  C
             T                   TTTGTG   TG GTGTGTGTGTGT
                                 ||||||   || ||||||||||||
                                 AAACAC   AC CACACACACACA
                                    AC_  A
GAM923  FLRT2    3'  TGTGTGTGTGTGTGTGTG    29866     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM923  FMR2     3'  TGTGTGTGAGTGTGTGTGTGT  12988     CTT  C
                                 TGTG   TG GTGTGTGTGTGT
                                 ||||   || ||||||||||||
                                 ACAC   AC CACACACACACA
                                   AC_  T
GAM923  FMR2     3'  TGTGAGTGTGTGTGTGTGTGT  12987     CTT  C
                                 TGTG   TG GTGTGTGTGTGT
                                 ||||   || ||||||||||||
                                 ACAC   AC CACACACACACA
                                   TC_  A
GAM923  GFRA2    3'  TTTGCAAGGTGTGTGTGTGT   11271      ___
                                 TTTGC   GTGTGTGTGTGT
                                 |||||   ||||||||||||
                                 AAACG   CACACACACACA
                                    TTC
GAM923  GLP1R    3'  TGTGTGTGTGTGTGTGTG    13146     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
                                 ACAC   AC CACACACACAC
                                   ___  A
GAM923  GLP1R    3'  TATGTGTGTGTGTGTGTG    13141     CTT  C
                                 TGTG   TG GTGTGTGTGTG
                                 ||||   || ||||||||||
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                                ATAC   AC CACACACACAC
                                  ___  A
GAM923  GLP1R    3'  TGTATGTGTGTGTGTGTG    13145     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAT   AC CACACACACAC
                                  ___  A
GAM923  GLS      3'  TTTGTGTGCATGTGTGTGTGT  31383       CTT
                                TTTGTG   TGCGTGTGTGTGTGT
                                ||||||   ||||||||||||||
                                AAACAC   ACGTACACACACACA
                                   ___
GAM923  GNAZ     3'  TGTGTGTGCATGTGTGTGTGT  13192      CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGTACACACACACA
                                  AC_
GAM923  GRLF1    3'  TGTGAAGTTTTGTGTGTGTGTG 44238      C___    C
           TGT                    TGTG    TTTG GTGTGTGTGTGT
                                ||||    |||| ||||||||||||
                                ACAC    AAAC CACACACACACA
                                  TTCA    A
GAM923  GRLF1    3'  TGTGTGTGTGTGTGTGTGTG    44240     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  GRLF1    3'  TTTGTGTGTGTGTGTGTGTGTG 44242       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM923  GYPA     3'  TTTGTGTGTGTGTGTGTGTGTG 44633       CTT  C
           T                     TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AAACAC   AC CACACACACACA
                                   AC_  A
GAM923  GYPA     3'  TGTGTTTGTGTGTGTGTGTGT  44630     C   C
                                TGTG TTTG GTGTGTGTGTGT
                                |||| |||| ||||||||||||
                                ACAC AAAC CACACACACACA
                                  _    A
GAM923  GYPA     3'  TGTGTGTGTGTGTGTGTG    44628     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  HCN4     3'  TTTGTTTTTCTGGTGTGTGT   24233      GC_   C
                                TTTGT   TTTG GTGTGTGT
                                |||||   |||| ||||||||
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                                AAACA  AGAC CACACACA
                                  AAA  _
GAM923  HPS3    3'  TGTGTGTGTGTGTGTGTG   37043    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  HPS3    3'  TATGTGTGTGTGTGTGTG   37041    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ATAC  AC CACACACACAC
                                  ___ A
GAM923  IGF1    3'  TGTGTGTGTGTGTGTGTG   8360     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  IGF1    3'  GTGAATGTGTGTGTGTGT   8346     CTT  C
                                GTG  TG GTGTGTGTGTGT
                                |||  || ||||||||||||
                                CAC  AC CACACACACACA
                                 TT_ A
GAM923  ITGA11  3'  TGTGTGTGTGTGTGTGTG   29208    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  KCNJ5   5'  TGTGTGTGTGTGTGTGTG   9444     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  KCNJ5   5'  CTCTGTGTGTGTGTGTGT   9435     C
                                CTTTG GTGTGTGTGTGT
                                ||||| ||||||||||||
                                GAGAC CACACACACACA
                                  A
GAM923  KIF1B   3'  TATGTGTGTGTGTGTGTG   31466    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ATAC  AC CACACACACAC
                                  ___ A
GAM923  KIF1B   3'  TGTGTGTGTGTGTGTGTG   31468    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  KIF1B   3'  TTTGTGTTTTTGTCTGTGT  31469     C  GC  G
                                TTTGTG TTT  GT TGTGT
                                |||||| |||  || |||||
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                                AAACAC AAA  CA ACACA
                                   A  A_  G
GAM923  KIF1B    3'  TCTGTGTATGTGTGTGTGTGTG 31467       CTT  C
                T                   TTTGTG  TG GTGTGTGTGTGT
                                    ||||||  || ||||||||||||
                                    AGACAC  AC CACACACACACA
                                      AT_  A
GAM923  KLF7     3'  TGTGTATATGTGTGTGTGTGTG 18983      CTT_  C
                T                   TGTG   TG GTGTGTGTGTGT
                                    ||||   || ||||||||||||
                                    ACAC   AC CACACACACACA
                                      ATAT  A
GAM923  KLF7     3'  TATGTGTGTGTGTGTGTGTG    18982      CTT  C
                                    TGTG  TG GTGTGTGTGTG
                                    ||||  || ||||||||||
                                    ATAC  AC CACACACACAC
                                      ___  A
GAM923  KLF7     3'  TGTGTGTGTGTGTGTGTGTG    18984      CTT  C
                                    TGTG  TG GTGTGTGTGTG
                                    ||||  || ||||||||||
                                    ACAC  AC CACACACACAC
                                      ___  A
GAM923  LDHB     5'  TGAATTTGTGTGTGTGTGTGT  14123    TGC   C
                                    TG  TTTG GTGTGTGTGTGT
                                    ||  |||| ||||||||||||
                                    AC  AAAC CACACACACACA
                                     TT_   A
GAM923  LILRB4   3'  TATGCAAGTTTGTGTGTGTGTG 27780       ___   C
                TGT                   TGTGC  TTTG GTGTGTGTGTGT
                                    |||||  |||| ||||||||||||
                                    ATACG  AAAC CACACACACACA
                                       TTC   A
GAM923  MAPK10   3'  TGTGTCTGCATTTGTGTGTGTG 39976      C   ____
                TGT                   TGTG TTTGC   GTGTGTGTGTGT
                                    |||| |||||   ||||||||||||
                                    ACAC AGACG   CACACACACACA
                                      _    TAAA
GAM923  MAPK10   3'  TGTGTCTGCGTGTGTGTGTGT  39983      C
                                    TGTG TTTGCGTGTGTGTGTGT
                                    |||| ||||||||||||||||
                                    ACAC AGACGCACACACACACA
                                      _
GAM923  MNT      3'  TGTGTGTGTGTGTGTGTGTG    33732      CTT  C
                                    TGTG  TG GTGTGTGTGTG
                                    ||||  || ||||||||||
                                    ACAC  AC CACACACACAC
                                      ___  A
GAM923  MNT      3'  TGTGCGTGCGTGTGTGTGTGT  33731      TT
                                    TGTGC  TGCGTGTGTGTGT
                                    |||||  ||||||||||||||
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                                ACACG  ACGCACACACACACA
                                  C_
GAM923  MUC4    3'  TGTGTGTGTGTGTGTGTGTG    32906     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  NAPB    3'  CTTGTGATATGTGTGTGTGTGT 43174       CTT  C
                                TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                GAACAC   AT CACACACACACA
                                   T__  A
GAM923  NLGN3   3'  TATGTGTGTGTGTGTGTGTG    33287     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM923  NLGN3   3'  TGTGTGTGTGTGTGTGTGTG    33294     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  NLGN3   3'  TGTGTCTGCGTGTGTGTGTGT  33291      C
                                TGTG TTTGCGTGTGTGTGTGT
                                |||| ||||||||||||||||
                                ACAC AGACGCACACACACACA
                                  _
GAM923  NR2E1   3'  TGTGTGTGTGTGTGTGTGTG    17583     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  NR4A2   3'  TGTGTCTCTGTGTGTGTGTGTG 26170     _    C
          T                      TGTG CTTTG GTGTGTGTGTGT
                                |||| ||||| ||||||||||||
                                ACAC GAGAC CACACACACACA
                                  A    A
GAM923  NR4A2   3'  TGTGTGTGTGTGTGTGTGTG    26172     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  NR4A2   3'  TGTGTGTGTATGTGTGTGTGT  26171     CTT  CG
                                TGTG   TG  TGTGTGTGTGT
                                ||||   ||  ||||||||||
                                ACAC   AC  ACACACACACA
                                  AC_  AT
GAM923  NRXN1   3'  TGTGTGTGTGTGTGTGTGTG    39852     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  OLR1    3'  TGTGTGTGTGTGTGTGTG    14945     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  OXTR    3'  TGTGCGTGTGTGTGTGTGTGT  9533      TT  C
                                TGTGC  TG GTGTGTGTGTGT
                                |||||  || ||||||||||||
                                ACACG  AC CACACACACACA
                                   C_  A
GAM923  OXTR    3'  TGTGTGCGTGTGTGTGTG    9534      CTT
                                TGTG   TGCGTGTGTGTGTG
                                ||||   ||||||||||||||
                                ACAC   ACGCACACACACAC

                                ___
GAM923  OXTR    3'  TGTGTGTGTGTGTGTGTG    9535      CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  PACSIN3  3'  TTTGGTTTTGTGTGTGGGTGTG 32144     TGC   C    T
          T                      TTTG   TTTG GTGTG GTGTGT
                                ||||   |||| ||||| ||||||
                                AAAC   AAAC CACAC CACACA
                                  CA_   A    C
GAM923  PATE    3'  TGTGTGTGTGTGTGTGTG    39649     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  PATE    3'  TCTGTAGTGTGTGTGTGTGTGT 39645      CTT  C
                                TTTGTG   TG GTGTGTGTGTGT
                                ||||||   || ||||||||||||
                                AGACAT   AC CACACACACACA
                                   C__  A
GAM923  PCDH11X  3'  TGTGCACGTGTGTGTGTGT   37315     TTT
                                TGTGC   GCGTGTGTGTGTGT
                                |||||   ||||||||||||||
                                ACACG   TGCACACACACACA

                                ___
GAM923  PCDH11X  3'  TGTGTGTGTGTGTGTGTG    37327     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  PCDH11X  3'  TGTGCACGTGTGTGTGTGT   37315     TTT
                                TGTGC   GCGTGTGTGTGTGT
                                |||||   |||||||||||||||
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                          ACACG  TGCACACACACACA
                                 ___
GAM923  PCDH11X  3' TGTGCACGTGTGTGTGTGT  37315    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||||
                          ACACG  TGCACACACACACA
                                 ___
GAM923  PCDH11Y  3' TGTGCACGTGTGTGTGTGT  37355    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||||
                          ACACG  TGCACACACACACA
                                 ___
GAM923  PCDH11Y  3' TGTGCACGTGTGTGTGTGT  37355    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||||
                          ACACG  TGCACACACACACA
                                 ___
GAM923  PCDH11Y  3' TGTGTGTGTGTGTGTGTG   37362    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                                ___ A
GAM923  PCDH11Y  3' TGTGTGTGTATGTGTGTGTGT 37358    CTT CG
                          TGTG  TG  TGTGTGTGTGT
                          ||||  ||  ||||||||||
                          ACAC  AC  ACACACACACA
                                AC_ AT
GAM923  PCDH11Y  3' TGTGCACGTGTGTGTGTGT  37355    TTT
                          TGTGC  GCGTGTGTGTGTGT
                          |||||  ||||||||||||||
                          ACACG  TGCACACACACACA
                                 ___
GAM923  PCDHB16  5' TGTGTGTGTGTGTGTGTG   34148    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ACAC  AC CACACACACAC
                                ___ A
GAM923  PCDHB16  5' TATGTGTGTGTGTGTGTG   34144    CTT C
                          TGTG  TG GTGTGTGTGTG
                          ||||  || ||||||||||
                          ATAC  AC CACACACACAC
                                ___ A
GAM923  PIM1    3' TTTGTGCATTTTTTGTGTGTGT 44976     _  GCG
                          TTTGTGC TTT  TGTGTGTGT
                          ||||||| |||  |||||||||
                          AAACACG AAA  ACACACACA
                              T  AA_
GAM923  PLAG1   3' TGTGCATGTGTGTGTGTGTGT  15361    TT C
                          TGTGC  TG GTGTGTGTGTGT
                          |||||  || ||||||||||||
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                                ACACG  AC CACACACACACA
                                  T_  A
GAM923  PURA    3'  TGTGGCTGTGTGTGTGTGTGT  25212     CT   C
                                TGTG  TTG GTGTGTGTGTGT
                                ||||  ||| ||||||||||||
                                ACAC  GAC CACACACACACA
                                  C_  A
GAM923  PURA    3'  TGTGTATGCATGTGTGTGTGT  25213     CTT
                                TGTG  TGCGTGTGTGTGTGT
                                ||||  ||||||||||||||
                                ACAC  ACGTACACACACACA
                                  AT_
GAM923  RAB33A  5'  TGTGCGCGCGTGTGTGTGTGT  22002      TT
                                TGTGC  TGCGTGTGTGTGTGT
                                |||||  |||||||||||||||
                                ACACG  GCGCACACACACACA
                                  C_
GAM923  RBBP9   3'  TATGTGTGTGTGTGTGTG    43142     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ATAC  AC CACACACACAC
                                  ___ A
GAM923  RBBP9   3'  TGTGTATGTGTGTGTGTGTGT  43145     CTT  C
                                TGTG  TG GTGTGTGTGTGT
                                ||||  || ||||||||||||
                                ACAC  AC CACACACACACA
                                  AT_ A
GAM923  RBBP9   3'  TGTGTGTGTGTGTGTGTG    43146     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  RCV1    3'  TGTGTGTGCATGTGTGTGTGT  16228     CTT
                                TGTG  TGCGTGTGTGTGTGT
                                ||||  |||||||||||||||
                                ACAC  ACGTACACACACACA
                                  AC_
GAM923  SCN8A   3'  TGTGAGTGTGTGTGTGTG    30536     CTTTGC
                                TGTG    GTGTGTGTGTG
                                ||||    ||||||||||
                                ACAC    CACACACACAC
                                  TCA___
GAM923  SLC31A1 3'  TGTGTGTGTGTGTGTGTG    12399     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  SNAI2   3'  TCTGTGGGTGTGTGTGTGTGTG 16886       CTT  C
          T                      TTTGTG  TG GTGTGTGTGTGT
                                ||||||  || ||||||||||||
```

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                                AGACAC   AC CACACACACACA
                                   CC_  A
GAM923  SNAI2    3'  TGTGTGTGCATATGTGTGTGT  16888     CTT
                                TGTG   TGCGTGTGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACGTATACACACACA
                                  AC_
GAM923  SNX2     3'  TGTGTGTGTGTGTGTGTG    40515     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  SRGAP2   3'  TGTGTAAAATGTGTGTGTGTGT 43988     CTTTGC
                                TGTG     GTGTGTGTGTGT
                                ||||     ||||||||||||
                                ACAC     CACACACACACA
                                  ATTTTA
GAM923  SRGAP2   3'  TATGTGTGTGTGTGTGTG    43985     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ATAC   AC CACACACACAC
                                  ___  A
GAM923  SRGAP2   3'  TGTGTGTGTGTGTGTGTG    43990     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  SSX2     3'  TTTGTGTGCGTGTGTGTGT   45536      CTT
                                TTTGTG   TGCGTGTGTGTGT
                                ||||||   ||||||||||||
                                AAACAC   ACGCACACACACA
                                   ___
GAM923  SSX2     3'  TGTGTGTGTGTGTGTGTG    45533     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  SSX3     3'  TGTGTGTGTGTGTGTGTG    34251     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
                                ACAC   AC CACACACACAC
                                  ___  A
GAM923  TFAP4    5'  TGTGTATGTGTGTGTGTGTGT  17420     CTT  C
                                TGTG   TG GTGTGTGTGTGT
                                ||||   || ||||||||||||
                                ACAC   AC CACACACACACA
                                  AT_  A
GAM923  TFAP4    5'  TATGTGTGTGTGTGTGTG    17415     CTT  C
                                TGTG   TG GTGTGTGTGTG
                                ||||   || ||||||||||
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                                ATAC  AC CACACACACAC
                                  ___ A
GAM923  TFAP4   5'  TGTGTGTGTGTGTGTGTG   17421    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  TNFSF5  3'  TGTGTGTGTGTGTGTGTG   6335     CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  TTC1    3'  TGCTGGGCTGTGTGTGTGT   17710    TT  G
                                TGCT  GC TGTGTGTGTGT
                                ||||  || ||||||||||
                                ACGA  CG ACACACACACA
                                  CC  _
GAM923  VSNL1   3'  TGTGTGTGTGTGTGTGTG   18040    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  VSNL1   3'  TTTGTGTGTGTGTGTGTGTG 18043      CTT  C
          T                      TTTGTG  TG GTGTGTGTGTGT
                                ||||||  || ||||||||||||
                                AAACAC  AC CACACACACACA
                                   AC_  A
GAM923  XRCC1   3'  TGTGTGTGTGTGTGTGTG   26670    CTT  C
                                TGTG  TG GTGTGTGTGTG
                                ||||  || ||||||||||
                                ACAC  AC CACACACACAC
                                  ___ A
GAM923  EGR3    3'  TAACACACGTATGTAGATATAA 40557      C  A  CC
          TC                     TAACACAC TAT TA  TGTAATC
                                |||||||| ||| ||  |||||||
                                ATTGTGTG ATA AT  ATATTAG
                                    C  C  CT
GAM923  FGF5    3'  ACATCATTGTACCTGTAATC  37576    CCTATA
                                ACA     TACCTGTAATC
                                |||     ||||||||||
                                TGT     ATGGACATTAG
                                  AGTAAC
GAM923  HK2     3'  CACATCTATATACATAAC   6785     C      CT
                                CACA CTATATAC  GTAAT
                                |||| ||||||||  |||||
                                GTGT GATATATG  TATTG
                                  A      __
GAM923  NPR2L   3'  TGACCCATGCCTGTAA     27253   C     ATA
                                A ACCTAT   CCTGTAA
                                | ||||||   |||||||
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                                A TGGGTA   GGACATT
                                 C     C__
GAM923  SNAP23   3'  ACACACGCCTGTAATC      19249       CTATATA
                                ACACAC      CCTGTAATC
                                ||||||      |||||||||
                                TGTGTG      GGACATTAG
                                   C_______
GAM924  ADAR     3'  GGGGGTGAGTGGGGGT      31906     AT  A  AT  T
                                GGG  GGT GGG  TGG GGGT
                                |||  ||| |||  ||| ||||
                                CCC  CCA CTC  ACC CCCA
                                  __  _  __  _
GAM924  ASNS     5'  GGGGACTGGTGGGGATGGCGGG 11718       _   A    T
                                GGGGA TGGT GGGAT GGTGGG
                                ||||| |||| ||||| ||||||
                                CCCCT ACCA CCCTA CCGCCC
                                   G   C    _
GAM924  GAP43    3'  GGGGAGGGTGGGGATGTG    13047      T  A    TG
                                GGGGA GGT GGGAT  GTG
                                ||||| ||| |||||  |||
                                CCCCT CCA CCCTA  CAC
                                   C  C    __
GAM924  GAS7     3'  GGGGTGGTGCGGGGGCAGGTG  25278     A   A_  ATT  TG
                                GGGG TGGT  GGG   GG  GGTG
                                |||| ||||  |||   ||  ||||
                                CCCC ACCA  CCC   CC  CCAC
                                   _   CG   ___  GT
GAM924  HCN2     3'  GGGGTGTGGGGGTTAATG    10172     A  GTA   A
                                GGGG TG   GGG TTGGTG
                                |||| ||   ||| ||||||
                                CCCC AC   CCC AATTAC
                                   _ AC_   C
GAM924  JAM2     5'  GGGGTGGGGGGATTGGGT    34549     A   TA    TGG
                                GGGG TGG  GGGAT   TGGGT
                                |||| |||  |||||   |||||
                                CCCC ACC  CCCTA   ACCCA
                                   _  C_    ___
GAM924  KCNK3    3'  GGGGTGCTGGGGGAGAGTGGTG 13910      A__   TA   T
                                GGGG   TGG  GGGA TGGTG
                                ||||   |||  |||| |||||
                                CCCC   ACC  CTCT ACCAC
                                   ACG   CC   C
GAM924  KLK10    3'  GGGGATAGGTGGGGGGAATGAGG 15772       _  A_   T  GT
           TG                    GGGGAT GGT  GGGA TG  GGGTG
                                ||||||| |||  |||| ||  |||||
                                CCCCTA CCA  CCCT AC  TCCAC
                                   T   CC    T  __
GAM924  LCN1     3'  GGGGTGGTAGGAAGGGGTG   42021      A       TT
                                GGGG TGGTAGGGA  GGTG
                                |||| |||||||||  ||||
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                                CCCC ACCATCCTT  CCAC
                                  _       CC
GAM924  LHX5    5'  GGGGTGGTGGGGGGCGGGTG  35322     A   A  ATT
                                GGGG TGGT GGG  GGTGGGTG
                                |||| |||| |||  ||||||||
                                CCCC ACCA CCC  CCGCCCAC
                                  _   C  ___
GAM924  MSR1    3'  GGGGTGATAGGGGAGAGAGGTG 14660     A      ATT GT
                                GGGG TGGTAGGG  G  GGGTG
                                |||| ||||||||  |  |||||
                                CCCC ACTATCCC  C  TCCAC
                                  _      CT_ TC
GAM924  RPA1    3'  GGGGATGGGGGGGGGGG     16370       TA  ATT  T
                                GGGGATGG  GGG  GG GGG
                                ||||||||  |||  || |||
                                CCCCTACC  CCC  CC CCC
                                   __  ___ _
GAM924  SHOX    3'  GGGGTGGTGGTGGCAGGT   27825     A   A  GAT  TG
                                GGGG TGGT GG  TGG  GGT
                                |||| |||| ||  |||  |||
                                CCCC ACCA CC  ACC  CCA
                                  _   _ ___  GT
GAM924  SYNGR1  3'  GGGGATGGGGGGGATGGTG   21766       TA   T
                                GGGGATGG  GGGAT GGTG
                                ||||||||  ||||| ||||
                                CCCCTACC  CCCTA CCAC
                                    C_   _
GAM924  SYNGR1  3'  GGGGATGGTAGGAGGTGGGTG  21767          ATT
                                GGGGATGGTAGGG  GGTGGGTG
                                ||||||||||||  ||||||||
                                CCCCTACCATCCT  CCACCCAC
                                      ___
GAM924  TBX6    3'  GGGGGGTGGGGATTGA     38860     AT  A
                                GGGG  GGT GGGATTGG
                                ||||  ||| ||||||||
                                CCCC  CCA CCCTAACT
                                  __  C
GAM925  ANGPT1  3'  TGGAGTTCTAAAAATATTTTT  40248      CG
                                TGGAGT  TAAAAATATTTTT
                                ||||||  |||||||||||||
                                ACCTCA  ATTTTTATAAAAA
                                   AG
GAM925  DAAM2   3'  TGATGGAGTTTTAGAAAAATTT 45182       CG  A  T
          T                     TGATGGAGT  TA AAA ATTTT
                                |||||||||  || ||| |||||
                                ACTACCTCA  AT TTT TAAAA
                                     AA  C  T
GAM925  NKTR    3'  TGTGGCATAAAAATATTTT   23929    A  AGT
                                TG TGG  CGTAAAAATATTTT
                                || |||  ||||||||||||||
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                                AC ACC   GTATTTTTATAAAA
                                 _  ___
GAM925  NUP153   3'  TGCTGGATCATAAAATATTTTT 23059    A   G      A
                                TG TGGA TCGTAAAA TATTTTT
                                || |||| |||||||| |||||||
                                AC ACCT AGTATTTT ATAAAAA
                                 G   _      _
GAM926  ANXA6    3'  GGCAGAAGTGCCCGCCAAA   19715   __    TA  A
                                GG  GGAGTG  CCC CCAAA
                                ||  ||||||  ||| |||||
                                CC  CTTCAC  GGG GGTTT
                                 GT     __  C
GAM926  BAPX1    3'  AGGGGAGTCCCGGGCCA     10158       GTA  A__
                                AGGGGAGT   CCC   CCA
                                ||||||||   |||   |||
                                TCCCCTCA   GGG   GGT
                                     ___  CCC
GAM926  CSNK1D   3'  TACAGGGCGGCCACCA     40069       GA TGTAC
                                TACAGGG  G    CCACCA
                                |||||||  |    ||||||
                                ATGTCCC  C    GGTGGT
                                    GC _____
GAM926  EFNB2    3'  CAGGGAGCGTGTGTGTTCACCA 19877      A_   ACC__
          A                      CAGGGG  GTGT    CACCAA
                                ||||||  ||||    ||||||
                                GTCCCT  CACA    GTGGTT
                                   CG    CACAA
GAM926  GPM6A    3'  TACAGAGGTGCAATCCA     23614       A   TAC
                                TACAGGGG GTG   CCA
                                |||||||| |||   |||
                                ATGTCTCC CGT   GGT
                                     A   TA_
GAM926  IGFBP4   3'  TACAGGGAGCGAGCCAC     11406       G    TAC
                                TACAGGG AGTG   CCAC
                                ||||||| ||||   ||||
                                ATGTCCC TCGC   GGTG
                                    _   TC_
GAM926  MCL1     3'  AAGGAATACTTACCAAA     34993      GT   CC
                                GGGGA  GTAC  ACCAAA
                                |||||  ||||  ||||||
                                TTCCT  TATG  TGGTTT
                                   __   AA
GAM926  PPP1CB   3'  CAGGTGAAGGTGTTACCA    15501     _   _  AC
                                CAGG GGAG TGT  CCA
                                |||| |||| |||  |||
                                GTCC CTTC ACA  GGT
                                  A   C   AT
GAM926  RNH      5'  CACAGCTCAGGTACCCGCCA  40601      GGG  T     A
                                TACAG   AG GTACCC CCA
                                |||||   || |||||| |||
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                                GTGTC   TC CATGGG GGT
                                   GAG _     C
GAM926  SMURF1   3'  GGGAACGCGTGTGTCCACC   45197      ___    AC
                                GGGGA   GTGT  CCACC
                                |||||   ||||  |||||
                                CCCTT   CACA  GGTGG
                                   GCG    CA
GAM926  TEAD3    3'  TAAGGGAACAGTGCCCACCAA  17378   C     GT  A
                                A AGGGGA  GT CCCACCAA
                                | ||||||  || ||||||||
                                A TCCCTT  CA GGGTGGTT
                                 T     GT  C
GAM926  UBTF     3'  CAGGGGAGAGGGCCACCA    30608        TGTAC
                                CAGGGGAG    CCACCA
                                ||||||||    ||||||
                                GTCCCCTC    GGTGGT
                                     TCCC_
GAM926  UNC13    3'  GGAGAGGTGTCTACCAA     26865       _   ACCC
                                GGGGAG TGT    ACCAA
                                ||||||| |||    |||||
                                CCTCTC ACA    TGGTT
                                   C   GA__
GAM926  VIPR2    3'  TACAGGGGAGGAACAGCC    18027         TGT  CCA
                                TACAGGGGAG   AC   CC
                                ||||||||||   ||   ||
                                ATGTCCCCTC   TG   GG
                                      CT_  TC_
GAM927  ADCY6    3'  TCTTTGTACAAAATATTGTACA 34180       G       TTCAC
           A                     TCTTTG TACAAAAT    ACAA
                                ||||||| ||||||||    ||||
                                AGAAAC ATGTTTTA    TGTT
                                   _       TAACA
GAM927  ALDOB    5'  TCTTTGGTAGCACAC       42771         CAAAATTT
                                TCTTTGGTA       CACAC
                                |||||||||       |||||
                                AGAAACCAT       GTGTG
                                     C________
GAM927  APBB2    5'  TCTTTGGTACAAAGCTCA    43679           AT
                                TCTTTGGTACAAA  TTCA
                                ||||||||||||  ||||
                                AGAAACCATGTTT  GAGT
                                      C_
GAM927  ATP8B2   3'  TCTTTGGTATAAAAATCA    42217         C    TT
                                TCTTTGGTA AAAA  TCA
                                ||||||||| ||||  |||
                                AGAAACCAT TTTT  AGT
                                     A   T_
GAM927  CEACAM1  3'  TCTTTGCTAGTTCACACA    11835       G  CAAAAT
                                TCTTTG TA     TTCACACA
                                |||||| ||     ||||||||
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                                AGAAAC AT     AAGTGTGT
                                   G  C_____
GAM927  CHST1    3'  TTTGGCACAAAGAAATATCACA 18917          ___  T
                                TTTGGTACAAA   AT TCACA
                                ||||||||||   || |||||
                                AAACCGTGTTT   TA AGTGT
                                      CTT  T
GAM927  DACH     3'  TCTCTGGTATGAACCACA    38881         CAAAATT
                                TCTTTGGTA      TCACA
                                |||||||||      |||||
                                AGAGACCAT      GGTGT
                                     ACTT___
GAM927  FBXL7    3'  TCTTTGGTGGAAAACACGCA  29414        AC   TTT   A
                                TCTTTGGT  AAAA   CAC CA
                                ||||||||  ||||   ||| ||
                                AGAAACCA  TTTT   GTG GT
                                     CC   ___   C
GAM927  HOXC9    3'  GTACAAAATCTGCACGCA    41482          _  A
                                GTACAAAATTT CAC CA
                                |||||||||| ||| ||
                                CATGTTTTAGA GTG GT
                                      C   C
GAM927  IGF1     3'  TTTGGTACAAATGCCACA    8364           ATT
                                TTTGGTACAAA   TCACA
                                ||||||||||   |||||
                                AAACCATGTTT   GGTGT
                                      AC_
GAM927  ITGAL    3'  TTTGGACAGAATTTCACA    13628      T   A
                                TTTGG ACA AATTTCACA
                                ||||| ||| |||||||||
                                AAACC TGT TTAAAGTGT
                                   _  C
GAM927  LBR      3'  TCCTTGGTGCAATCCAGTACA  40431        A  AAT   C_
                                TCTTTGGT CAA   TTCA  ACA
                                |||||||| |||   ||||  |||
                                AGGAACCA GTT   AGGT  TGT
                                     C   ___   CA
GAM927  MIP      3'  CTTGAAAGATTTCACACA    28933      TACAAA
                                TTTGG     ATTTCACACA
                                |||||     ||||||||||
                                GAACT     TAAAGTGTGT
                                   TTC___
GAM927  RLN2     3'  TTTGGTACAACCAACA      22808          AATT  C
                                TTTGGTACAA    TCA ACA
                                ||||||||||    ||| |||
                                AAACCATGTT    GGT TGT
                                      ____  _
GAM927  SART2    3'  TCTTTGGTATGAAAATCA    30039         CA  TT
                                TCTTTGGTA  AAA  TCA
                                |||||||||  |||  |||
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                                AGAAACCAT  TTT  AGT
                                     AC   T_
GAM927  TPK1     3'  TCTTTGGTAGCAAAATTT    35357          _
                                TCTTTGGTA CAAAATTT
                                ||||||||| ||||||||
                                AGAAACCAT GTTTTAAA
                                     C
GAM927  TRIP12   3'  CCTTTTTTAAATTTCACACA  20160      GGTACA
                                TCTTT     AAATTTCACACA
                                |||||     ||||||||||||
                                GGAAA     TTTAAAGTGTGT
                                   AAA___
GAM928  ANGPT1   3'  TGGAGTTCTAAAAATATTTT  40247       CG
                                TGGAGT  TAAAAATATTTT
                                ||||||  ||||||||||||
                                ACCTCA  ATTTTTATAAAA
                                    AG
GAM928  DMD      3'  GGAGTTGTAAAACATTT     19686       C     A
                                GGAGT GTAAAA TATTT
                                ||||| |||||| |||||
                                CCTCA CATTTT GTAAA
                                   A     _
GAM929  LTB4R    5'  TCAGATTGGAGGCTACAA    8889         TTA  CA
                                TCAGATTG   GA  GCTACAA
                                ||||||||   ||  |||||||
                                AGTCTAAC   CT  CGATGTT
                                     ____  C_
GAM929  SAFB     3'  TCACATTGTATTGAGCTACAA  16451     G    TAGAC
                                TCA ATTGT    AGCTACAA
                                ||| |||||    ||||||||
                                AGT TAACA    TCGATGTT
                                  G    TAAC_
GAM929  HRB      3'  TATGTACAGTACTGCAGCA   21090           __
                                TATGTGCAGTAC  CAGTG
                                ||||||||||||  |||||
                                ATACATGTCATG  GTCGT
                                       AC
GAM929  LAMP1    5'  TGCGCAGTGCGCGCGAGAC   24512         ACCA   C
                                TGTGCAGT    GTGA GAC
                                ||||||||    |||| |||
                                ACGCGTCA    CGCT CTG
                                     CGCG   _
GAM929  RORA     3'  ATGTGCAGTGTGTGGCG     39515         ACCA   A
                                ATGTGCAGT    GTG CG
                                |||||||||    ||| ||
                                TACACGTCA    CAC GC
                                     CA__   C
GAM929  SNX3     3'  TGTGCAGTATTGGAAACCAATG 19139         ________
                                TGTGCAGT      ACCAGTG
                                ||||||||      |||||||
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                                ACACGTCA      TGGTTAC
                                    TAACCTT
GAM929  WHSC1    3'  TATGTGCACTACCTGAAGA   39379        G   AG  C
                                TATGTGCA TACC  TGA GA
                                |||||||| ||||  ||| ||
                                ATACACGT ATGG  ACT CT
                                    G   __  T
GAM930  ARHI     3'  CATTTTGTTCTCCTCTTC    21699       A    TTTCT
                                TATTTT TTCTC    CTCTTC
                                |||||| |||||    ||||||
                                GTAAAA AAGAG    GAGAAG
                                  C   _____
GAM930  CBFA2T1  3'  TATTCTCTGCTCTCTTTTCA  20309        _    C
                                TATTCTCT TTCTCT TTCA
                                |||||||| |||||| ||||
                                ATAAGAGA GAGAGA AAGT
                                    C    A
GAM930  CDH18    5'  TTCTGTTCTTGCTCCTCTTCA  22344     A   CT  T
                                TTTT TTCT  TTC CTCTTCA
                                |||| ||||  ||| |||||||
                                AAGA AAGA  GAG GAGAAGT
                                  C   AC  _
GAM930  CREBL2   3'  TATTTTCCCCCTTTTCTTTCTT 10584       A      _ C
                                TATTTT TTCTCTTT CT TCTT
                                |||||| |||||||| || ||||
                                ATAAAA GGGGGAAA GA AGAA
                                   _      A  A
GAM930  ENC1     3'  TCTTTTCCTTTTTTTCTCTTCA 18866     A   C  C
                                TTTT TTCT TTT TCTCTTCA
                                |||| |||| ||| ||||||||
                                AGAA AGGA AAA AGAGAAGT
                                  A   A  A
GAM930  GOLGA4   5'  TTTTGTTCAGCTTTTCTCTTCA 41064     A  T_  C
                                TTTT TTC  CTTT TCTCTTCA
                                |||| |||  |||| ||||||||
                                AAAA AAG  GAAA AGAGAAGT
                                  C  TC  _
GAM930  IL6R     3'  TATTTTTTCTCTTCCTCCTTTT 8185       A        C__
            TCA                   TATTTT TTCTCTTTCTCT   TTCA
                                |||||| ||||||||||||   ||||
                                ATAAAA AAGAGAAGGAGG   AAGT
                                   _         AAA
GAM930  KERA     3'  TATTTTATTTTCTCATTTTCTT 28157        C   TCTC
            CA                   TATTTTATT TCTT   TCTTCA
                                |||||||| ||||   ||||||
                                ATAAAATAA AGAG   AGAAGT
                                    A   TAAA
GAM930  NPAT     3'  TTTACAAAATTCTCTCTT    42618      TCTCT
                                TTTAT    TTCTCTCTT
                                |||||    |||||||||
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                                AAATG    AAGAGAGAA
                                  TTTT_
GAM930  POH1     5'  TATTTTATTTTTTCTTTCTCTC 25138        C__
           CT                    TATTTTATT   TCTTTCTCTCTT
                                 |||||||||   ||||||||||||
                                 ATAAAATAA   AGAAAGAGAGGA
                                    AAA
GAM930  PURA     3'  TTTTATTTTCTCTCTTTCTT   25215       C     C
                                 TTTTATT TCTTTCT TCTT
                                 ||||||| ||||||| ||||
                                 AAAATAA AGAGAGA AGAA
                                    A      A
GAM930  TPD52L2  3'  TATTTTATGCTTAGAACTCTTC 17640        T  CTTTCT
           A                     TATTTTAT CT     CTCTTCA
                                 |||||||| ||     |||||||
                                 ATAAAATA GA     GAGAAGT
                                    C  ATCTT_
GAM930  VIP      3'  CTTTATTTTCTCTCTT      18003        CTCT
                                 TTTTATT    TTCTCTCTT
                                 |||||||    |||||||||
                                 GAAATAA    AAGAGAGAA
                                            ____
GAM931  ARHGEF12 3'  TCATAAAAGAGCTATTTTACAA 31649        A  ___
           A                     TCATAAAA AGT   TTTACAAA
                                 |||||||| |||   ||||||||
                                 AGTATTTT TCG   AAATGTTT
                                    C   ATA
GAM931  IL12A    3'  TCATTTCAAAGTTTTATAAAAA 9404       AAA       C
           T                     TCAT   AAAGTTTTA AAAAAT
                                 ||||   ||||||||| ||||||
                                 AGTA   TTTCAAAAT TTTTTA
                                   AAG        A
GAM931  MADH2    3'  TAAAAAAGACACACAAAAATA  25345        TTT
                                 TAAAAAAG   TACAAAAATA
                                 ||||||||   ||||||||||
                                 ATTTTTTC   GTGTTTTTAT
                                    TGT
GAM931  MPHOSPH1 3'  ATAAAAAAGCCTTATAAAAATA 32113            C
                                 ATAAAAAAGTTTTA AAAAATA
                                 |||||||||||||| |||||||
                                 TATTTTTTCGGAAT TTTTTAT
                                       A
GAM931  MYH8     3'  TCATAAAGCAAGTGACCAAAAA 40814        A_   TTTA
           TA                    TCATAAA  AAGT   CAAAAATA
                                 |||||||  ||||   ||||||||
                                 AGTATTT  TTCA   GTTTTTAT
                                    CG   CTG_
GAM931  PMP2     3'  AAAAAGTCTTGTACAAAAATA  15416        __
                                 AAAAAGTTT  TACAAAAATA
                                 |||||||||  ||||||||||
```

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                                TTTTTCAGA  ATGTTTTTAT
                                     AC
GAM931  PROML1   3'  TAAAAAAGTAAAAAACAAAAAT 25687        TTT__
            A                  TAAAAAAGT    ACAAAAATA
                               |||||||||    |||||||||
                               ATTTTTTCA    TGTTTTTAT
                                    TTTTT
GAM932  CDH19    3'  TATTTTTACTCTTTCC      34503        TT
                               TATTTTTA  CTCTTTCT
                               ||||||||  ||||||||
                               ATAAAAAT  GAGAAAGG
                                     __
GAM932  CLTC     3'  AATATTTTGTTTGAATTTCTCT 22146       TATTCTC
            CT                   AATATTTT      TTTCTCTCT
                               ||||||||      |||||||||
                               TTATAAAA      AAAGAGAGA
                                    CAAACTT
GAM932  CRH      5'  TTCCCACTCTCTTTTTCT    8896            C
                               TTTTTATTCTCTTT TCT
                               |||||||||||||| |||
                               AAGGGTGAGAGAAA AGA
                                        A
GAM932  DYRK2    3'  GGATTTTCAACCCTCTTTCT   27039   T     _
                               A ATTTTTA TTCTCTTTCT
                               | ||||||| ||||||||||
                               C TAAAAGT GGGAGAAAGA
                                C      T
GAM932  DYRK2    3'  GGATTTTCAACCCTCTTTCT   27039   T     _
                               A ATTTTTA TTCTCTTTCT
                               | ||||||| ||||||||||
                               C TAAAAGT GGGAGAAAGA
                                C      T
GAM932  MEIS2    5'  ATATTTCTTCTTTTTCTCT    33536       TA   C
                               ATATTTT  TTCT TTTCTCT
                               |||||||  |||| |||||||
                               TATAAAG  AAGA AAAGAGA
                                    __   A
GAM932  NOTCH2   3'  AATATTTTAATTCTCAGACTCT 35903       T    TTT
            CT                   AATATTTT ATTCTC   CTCTCT
                               |||||||| ||||||   ||||||
                               TTATAAAA TAAGAG   GAGAGA
                                    T     TCT
GAM932  PTP4A2   3'  ATTCCTTTTCTCTTTCTCT   38621       A
                               ATTTTT TTCTCTTTCTCT
                               |||||| ||||||||||||
                               TAAGGA AAGAGAAAGAGA
                                  A
GAM932  PTP4A2   3'  ATTCCTTTTCTCTTTCTCT   38621       A
                               ATTTTT TTCTCTTTCTCT
                               |||||| ||||||||||||
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                                TAAGGA AAGAGAAAGAGA
                                   A
GAM932  RTN3    3'  TTCTTTCATTTTCTCTCT    43962     A   TC
                                TTT TTC  TTTCTCTCT
                                ||| |||  |||||||||
                                AAG AAG  AAAGAGAGA
                                  A   TA
GAM933  CDH10   3'  TAATGTACAGAACAGGATA   27488         T   TG
                                TAATGTACAG ACAG  TA
                                |||||||||| ||||  ||
                                ATTACATGTC TGTC  AT
                                      T   CT
GAM933  CDK8    3'  TGTACAGTACATTCTCAT    10386         GTGTAA
                                TGTACAGTACA     CAT
                                ||||||||||      |||
                                ACATGTCATGT     GTA
                                      AAGA__
GAM933  EGFL4   3'  TGTACAGTATGGACGCCAGTG  41586         _______
                                TGTACAGTA      CAGTG
                                |||||||||      |||||
                                ACATGTCAT      GTCAC
                                     ACCTGCG
GAM933  HRB     3'  ATGTACAGTACTGCAGCATA   21082          AG   A
                                ATGTACAGTAC  TGTA CATA
                                ||||||||||  |||| ||||
                                TACATGTCATG  ACGT GTAT
                                     __   C
GAM933  KLHL1   3'  TAATGTACAGATCAATGTA   34081          TA
                                TAATGTACAG  CAGTGTA
                                ||||||||||  |||||||
                                ATTACATGTC  GTTACAT
                                      TA
GAM933  LDHA    3'  TAATGTACACTACTGATATA   24520         G   A_
                                TAATGTACA TAC  GTGTA
                                |||||||| |||  |||||
                                ATTACATGT ATG  TATAT
                                     G   AC
GAM933  SUV39H2 3'  TAATGTACATTACAGTAT    36017         G
                                TAATGTACA TACAGTGT
                                |||||||| ||||||||
                                ATTACATGT ATGTCATA
                                     A
GAM933  TRHDE   3'  TACATGTGCAGTGTACAACATA 30110     _ A     __
                                TACA GT CAGTGTA  ACATA
                                |||| || |||||||  |||||
                                ATGT CA GTCACAT  TGTAT
                                  A C      GT
GAM933  IFI16   3'  TGTGTATGTATAGTGTTGTATT 43411     A   C   T
            T                    TGTG TGTG ATG TGTTGTATTT
                                |||| |||| ||| ||||||||||
```

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                                ACAC ATAC TAT ACAACATAAA
                                  _   A   C
GAM933  LFG     3'  TGTGATGCGTGTGTGACACTGT 44157        CA  __ GT
                                TGTGATGTG  TGT  T  TGT
                                |||||||||  |||  |  |||
                                ACACTACGC  ACA  G  ACA
                                     AC   CT TG
GAM933  NR4A2   3'  TGTGTGTGTGTGTTACATT   26173     A   CA   T
                                TGTG TGTG  TGT GTTGTATT
                                |||| ||||  ||| ||||||||
                                ACAC ACAC  ACA CAATGTAA
                                  _   __  _
GAM933  SCN8A   3'  TGTGAGTGTGTGTGTGTGTT  30538      _   CA  _
                                TGTGA TGTG  TGT TGTT
                                ||||| ||||  ||| ||||
                                ACACT ACAC  ACA ACAA
                                   C   AC  C
GAM933  SLC1A4  3'  TGTGTGTGTGTGTTGTGT    16762     A   CA    T
                                TGTG TGTG  TGTTGT GT
                                |||| ||||  |||||| ||
                                ACAC ACAC  ACAACA CA
                                  _   AC    _
GAM934  CDH19   3'  TATTTTTACTCTTTCC     34503        TT
                                TATTTTTA  CTCTTTCT
                                ||||||||  ||||||||
                                ATAAAAAT  GAGAAAGG
                                          __
GAM934  SHOX2   3'  AATATTTTCTCTTTTCTTGCT  27838       TTAT     _ C
                                AATATTT   TCTCTTT CT GCT
                                |||||||   ||||||| || |||
                                TTATAAA   AGAGAAA GA CGA
                                   ____     A  A
GAM934  TRPS1   3'  AATATTTTCATTTCCTTCT   30453          C
                                AATATTTTTATT TCTTTCT
                                |||||||||||| |||||||
                                TTATAAAAGTAA AGGAAGA
                                          _
GAM935  B4GALT1 3'  GTCATCTCATCCCAGGTGGC  11286    CCA        C
                                GTC  CTCATCCCAGG GGC
                                |||  |||||||||| |||
                                CAG  GAGTAGGGTCC CCG
                                  TA_        A
GAM935  FGFR1   5'  TCGGTCCCGTCCGGACG    31955       ACTCA  CA
                                TCGGTCCC   TCC  GGCG
                                ||||||||   |||  ||||
                                AGCCAGGG   AGG  CTGC
                                    C____  C_
GAM935  HNRPM   5'  GGCCCCACTCGCCCGCGGC  25570         AT  AG
                                GGTCCCACTC  CCC  GCGGC
                                ||||||||||  |||  |||||
```

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                                CCGGGGTGAG  GGG  CGCCG
                                     C_  __
GAM935  IER3    3'  TCGGTCCCGCCTCAAGCACCGG 19354        A_   TC__  A  C
            GTGGC                   TCGGTCCC  CTCA   CC GG GGC
                                |||||||| ||||   || || |||
                                AGCCAGGG  GAGT   GG CC CCG
                                     CG   TCGT  C  A
GAM935  VCP     5'  TCGGCTCTTCCAGGCG     44011     TCCCA   ATC
                                TCGG    CTC   CCAGGCG
                                ||||    |||   |||||||
                                AGCC    GAG   GGTCCGC
                                  _____  AA_
GAM936  CALD1   3'  TGAGCTCGTCCTGCGTCTTGAG 37631          ___  AA_   C
            CTTG                    TGAGCTCGTCT   GT   GAGC TG
                                |||||||||||  ||   |||| ||
                                ACTCGAGCAGG   CA   CTCG AC
                                      ACG  GAA   A
GAM936  DHFR    3'  AGCTACTTGGGAGCCTGA    8987      C TC  TAA
                                AGCT G  TG   GAGCCTGA
                                |||| |  ||   ||||||||
                                TCGA T  AC   CTCGGACT
                                  _ GA  C__
GAM936  HCFC1   3'  TGGGCCGGGGGAGCCTGA    43400    A  T  TCTGTAA
                                TG GC CG      GAGCCTGA
                                || || ||      ||||||||
                                AC CG GC      CTCGGACT
                                 C  _  CCC____
GAM936  LOXL2   3'  TGAGCTCGGTGGCTTG      14199        TC  TAAGA  C
                                TGAGCTCG  TG    GC TG
                                ||||||||  ||    || ||
                                ACTCGAGC  AC    CG AC
                                     C_  _____  A
GAM936  OLFM1   3'  TGGCTCTCAAAGAGCCTG    26784    A    G  TGT
                                TG GCTC TC   AAGAGCCTG
                                || |||| ||   |||||||||
                                AC CGAG AG   TTCTCGGAC
                                 _   _  T__
GAM936  PHEMX   3'  TGACTTGTCAACAGCCTGA   40023     G  C   TGT  G
                                TGA CT GTC   AA AGCCTGA
                                ||| || |||   || |||||||
                                ACT GA CAG   TT TCGGACT
                                  _  A   ___  G
GAM936  PRIM2A  3'  TGAGCCCAGGAGTCTG      9622         TCTGTAA   C
                                TGAGCTCG      GAG CTG
                                ||||||||      ||| |||
                                ACTCGGGT      CTC GAC
                                     C_______  A
GAM936  SMARCD1 3'  GCTCGCAGGAGCCTGA      40086       CTGTAA
                                GCTCGT     GAGCCTGA
                                ||||||     ||||||||
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                                CGAGCG     CTCGGACT
                                   TC____
GAM936  T       3'  TCATCTGTAAGCCACCTG    17250          A_
                                TCGTCTGTAAG  GCCTG
                                ||||||||||  |||||
                                AGTAGACATTC  TGGAC
                                      GG
GAM936  TACC1    3'  TGAGTCCAGTAAGAGCTTGA  26606     CT  TCT      C
                                TGAG  CG   GTAAGAGC TGA
                                ||||  ||   |||||||| |||
                                ACTC  GT   CATTCTCG ACT
                                  AG  ___      A
GAM937  BCR     5'  TCTGGCCACGGCCCGCGCGCTC 34642       G   C   __
            CT                    TCTGGC CAC GGT  GCGCGCTCCT
                                ||||||| ||| |||  ||||||||||
                                AGACCG GTG CCG  CGCGCGAGGA
                                   _  _  GG
GAM937  EGR3     3'  TCTGCGCTTTGGTGCGCTCCT  40560     G   ACC    GC
                                TCTG CGC   GGTGC  GCTCCT
                                |||| |||   |||||  ||||||
                                AGAC GCG   CCACG  CGAGGA
                                  _   AAA    __
GAM937  TSG     3'  TCTGCGCACCTGCTTCT    34010     G     GG   GCG
                                TCTG CGCACC  TGC   CT
                                |||| ||||||  |||   ||
                                AGAC GCGTGG  ACG   GA
                                  _     ___  AA_
GAM937  ALDH3B2  5'  CGGAACTCGGCCGGCCGCG   8681     C   CC  C  A
                                CGG AAC  CG GC CGGCCGCG
                                ||| |||  || || ||||||||
                                GCC TTG  GC CG GCCGGCGC
                                  _  A_ _ _
GAM937  DBN1     5'  CGGGACCCCGCGCCTCCGGGCC 38930     CA       AC___
            GCGT                   CGG  ACCCCGCGC    GGCCGCGT
                                |||  |||||||||    ||||||||
                                GCC  TGGGGCGCG    CCGGCGCA
                                  C_       GAGGC
GAM937  FOXD2    5'  GCCGGCCGCTGTGGCCGCGT  20967    AACC   GCAC
                                GC   CCGC   GGCCGCGT
                                ||   ||||   ||||||||
                                CG   GGCG   CCGGCGCA
                                  GCC_   ACA_
GAM937  HOXA3    5'  GGCCGCCCCGCGCAGACCG   36195     AA       C
                                GGC  CCCCGCGCA GGCCG
                                |||  ||||||||| |||||
                                CCG  GGGGCGCGT CTGGC
                                  GC       _
GAM937  ICMT     3'  GGCTCCTCACAGGCCGCGT   29656     AACC  G   C
                                GGC   CC CGCA GGCCGCGT
                                |||   || |||| ||||||||
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                                CCG   GG GTGT CCGGCGCA
                                  A___  A   _
GAM937  LASS1    3'  CGGCTCCCGGGGCGGCCGCGT  34600     AAC   CGCA
                                CGGC  CCCG   CGGCCGCGT
                                ||||  ||||   |||||||||
                                GCCG  GGGC   GCCGGCGCA
                                  A__   CCC_
GAM937  LEF1     5'  CGGCCACCCCGCGACCCCGCGT 32205     A      C  GG
                                CGGC ACCCCGCG AC  CCGCGT
                                |||| |||||||| ||  ||||||
                                GCCG TGGGGCGC TG  GGCGCA
                                  G       _  G_
GAM938  MYD88    3'  TGAGAGTACATGTCT      14721         AGCTC
                                TGAGAGTATG    GTCT
                                ||||||||||    ||||
                                ACTCTCATGT    CAGA
                                      A____
GAM939  CAPZA1   5'  TTCCAACCCCGGGGGGG     43725      ACGGAC      A
                                TTTCA     GCCCCGGG GG
                                |||||     |||||||| ||
                                AAGGT     TGGGGCCC CC
                                  _______       C
GAM939  DDEF1    3'  TTTCAACGGTTGCTGGAG    40572        AC  CCCG
                                TTTCAACGG  GC   GGAG
                                |||||||||  ||   ||||
                                AAAGTTGCC  CG   CCTC
                                     AA  A___
GAM939  FECH     3'  CAAGGTCCCGGGAGGA     6607     C  ACGC
                                CAA GG   CCCGGGAGGA
                                ||| ||   ||||||||||
                                GTT CC   GGGCCCTCCT
                                  _  A___
GAM939  PK428    5'  TTTCAACGGATTCCGGG     18811         CGCC
                                TTTCAACGGA   CCGGG
                                ||||||||||   |||||
                                AAAGTTGCCT   GGCCC
                                     AA__
GAM940  C18orf1  3'  CATTCTTCCGTCATTATT    41216       A TA
                                CATTCTT T  TCATTATT
                                ||||||| |  ||||||||
                                GTAAGAA G  AGTAATAA
                                   _ GC
GAM941  LHX2     5'  CTAATGATACATGCTACA    21982         CA
                                TTAATGATACA  CTACA
                                ||||||||||  |||||
                                GATTACTATGT  GATGT
                                      AC
GAM941  MS4A1    3'  TTAATGATACAATACTGC    6605          CACTAC
                                TTAATGATACA     ACTGT
                                ||||||||||      |||||
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                                AATTACTATGT     TGACG
                                      TA____
GAM942  AGL     3'  TTTTATTTTCTTAACACACA  8493       GACCC
                                TTTTAT    TAACACACA
                                ||||||    |||||||||
                                AAAATA    ATTGTGTGT
                                   AAAGA
GAM942  APLP2   3'  ACTTTTATGGAGACACACA   44915        ACCCTA
                                ACTTTTATG     ACACACA
                                |||||||||     |||||||
                                TGAAAATAC     TGTGTGT
                                     CTC___
GAM942  CLECSF2  3'  CTTTTATGTGTAGCCTGACAC  23061        AC___   A
                                CTTTTATG    CCT ACAC
                                ||||||||    ||| ||||
                                GAAAATAC    GGA TGTG
                                     ACATC   C
GAM942  CUL3    3'  TAACCTTTATGACCTAA     18744           C
                                TAACTTTTATGACC TAA
                                |||||||||||||| |||
                                ATTGGAAATACTGG ATT
                                      _
GAM942  HPRT1   3'  ACTTTTCTAACACA       6797       ATGACC
                                ACTTTT     CTAACACA
                                ||||||     ||||||||
                                TGAAAA     GATTGTGT
                                     _______
GAM942  JRK     3'  CTTTTATAATCTTCACACA   44499        CC  AA
                                CTTTTATGA  CT  CACACA
                                |||||||||  ||  ||||||
                                GAAAATATT  GA  GTGTGT
                                     A_  A_
GAM942  MFI2    3'  TTTTATGACCTTAAGACA    25474         C   C
                                TTTTATGACC TAA ACA
                                |||||||||| ||| |||
                                AAAATACTGG ATT TGT
                                     A   C
GAM942  NT5C2   3'  TTTTAATACCCTAACATACA  29236      TG       C
                                TTTTA  ACCCTAACA ACA
                                |||||  ||||||||| |||
                                AAAAT  TGGGATTGT TGT
                                   TA       A
GAM942  PCDHB13  3'  TTTTACACATTAACACACA   33188       G  CC
                                TTTTAT AC  TAACACACA
                                |||||| ||  |||||||||
                                AAAATG TG  ATTGTGTGT
                                   _ TA
GAM942  PLOD2   3'  TTTTATAATTTTCTAACACA  9597         CC__
                                TTTTATGA   CTAACACA
                                ||||||||   ||||||||
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```
                                AAAATATT   GATTGTGT
                                    AAAA
GAM942  RFXAP    3'  TAACTTTATGACTTCCACA   8054        T    CCTAA
                                TAACTTT ATGAC    CACA
                                ||||||| |||||    ||||
                                ATTGAAA TACTG    GTGT
                                   _    AAG__
GAM942  SCN1A    3'  TAACATTTATGACTCCAAACA  44815     T      _ T
                                TAAC TTTATGAC CC AACA
                                |||| |||||||| || ||||
                                ATTG AAATACTG GG TTGT
                                  T       A  T
GAM942  AKT1     3'  CGTGGAGGGGCCCAGGGATGGC 23138        T  GG  T   CA
           C                     CGTGGAGG GG  CG GGA  GCC
                                 |||||||| ||  || |||  |||
                                 GCACCTCC CC  GT CCT  CGG
                                    _ GG  C   AC
GAM942  AMT      5'  GAAGGGGGCGTGGGCAGCC    7907       T       A
                                 GAGG GGGGCGTGG CAGCC
                                 |||| ||||||||| |||||
                                 CTTC CCCCGCACC GTCGG
                                   _        C
GAM942  ARHGEF1  3'  TGGGGGTGGGGGTGGAGGGGTG 21739     A      C    CA____
           GCC                    TGG GGTGGGG GTGGA     GCC
                                  ||| ||||||| |||||      |||
                                  ACC CCACCCC CACCT     CGG
                                    C      _    CCCCAC
GAM942  ARVCF    5'  CCTGGAGCGCAGCGTGGGCGGC 11702    G    G  G      ACA
           C                      C TGGAG TG GGCGTGG   GCC
                                  | ||||| || |||||||   |||
                                  G ACCTC GC TCGCACC   CGG
                                   G    _ G      CGC
GAM942  ARVCF    3'  GGAGGTGGGGCACCTGTAGCC  11704           TGGAC
                                 GGAGGTGGGGCG    AGCC
                                 ||||||||||||    ||||
                                 CCTCCACCCCGT    TCGG
                                        GGACA
GAM942  C2       3'  CGGGAGGTGGGGCAGCGAGGCA 6297     T        _  _ A
           G                      CG GGAGGTGGGGC GTG G CAG
                                  || |||||||||| ||| | |||
                                  GC CCTCCACCCCG CGC C GTC
                                   _         T   T C
GAM942  CDH4     3'  GTGGGGGTGGGTGCTCATG    12181      A    _ __
                                 GTGG GGTGGG GC  GTG
                                 |||| |||||| ||  |||
                                 CACC CCACCC CG  TAC
                                   C     A  AG
GAM942  CHAC     3'  GTGGAGATGAATTATGGGCAGC 37815          GC    A
           C                      GTGGAGGTGGG  GTGG CAGCC
                                  ||||||||||  |||| |||||
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                                CACCTCTACTT  TACC GTCGG
                                      AA   C
GAM942  CRMP1    3'  GTGGAGGTGGGGCGAGC     10599            TGGAC
                                GTGGAGGTGGGGCG    AGC
                                ||||||||||||||    |||
                                CACCTCCACCCCGC    TCG
                                      _____
GAM942  DMPK     3'  CGTGGAGGATGGAACACGGACG 20611         _          A
           GCC                    CGTGGAGG TGGGGCGTGGAC GCC
                                ||||||||| |||||||||||| |||
                                GCACCTCC ACCTTGTGCCTG CGG
                                     T          C
GAM942  DSC3     3'  CGTGGTGGTGGGCGCCTG    35943      A     _ G
                                CGTGG GGTGGG GC TG
                                ||||| |||||| || ||
                                GCACC CCACCC CG AC
                                   A     G  G
GAM942  EDG6     3'  CGGGGAGGTGGGGTGG      19094    T        CG
                                CG GGAGGTGGGG  TGG
                                || ||||||||||  |||
                                GC CCTCCACCCC  ACC
                                 C        __
GAM942  F7       3'  CGTGCAGGTGGGGCTTGG    6557       G        G
                                CGTG AGGTGGGGC TGG
                                |||| ||||||||| |||
                                GCAC TCCACCCCG ACC
                                  G        A
GAM942  GALGT    3'  GTGGGGGTGGGGCTGGAGC   11190      A       G    CA
                                GTGG GGTGGGGC TGGA  GC
                                |||| |||||||| ||||  ||
                                CACC CCACCCCG ACCT  CG
                                  C       _   __
GAM942  GJA4     5'  GTGGAGGTGGGGACGATGG   40438            _ _
                                GTGGAGGTGGGG CG TGG
                                |||||||||||| || |||
                                CACCTCCACCCC GC ACC
                                       T  T
GAM942  GNA11    5'  CGTGGGGTTGGAAGGACAGCC  44041       A   GG  CGT
                                CGTGG GGT  GG   GGACAGCC
                                ||||| |||  ||   ||||||||
                                GCACC CCA  CC   CCTGTCGG
                                  _   A_  TT_
GAM942  GPR81    3'  CGTGGTGGTGGGGCGCCCGCAG 37189       A        GGA
                                CGTGG GGTGGGGCGT   CAG
                                ||||| ||||||||||   |||
                                GCACC CCACCCCGCG   GTC
                                   A         GGC
GAM942  HRMT1L1  5'  CGCGGAGGGGTGGAC       42181        GGTG   C
                                CGTGGA    GGG GTGGAC
                                ||||||    ||| ||||||
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                                GCGCCT   CCC CACCTG
                                   ____  _
GAM942  LLGL1    3'  CGTGGTGGTGGGCGCCTG    42503      A    _ G
                                CGTGG GGTGGG GC TG
                                ||||| |||||| || ||
                                GCACC CCACCC CG AC
                                   A     G  G
GAM942  MAP4K2   3'  CGTGGGGTGGGGCGGGGAGCC  21350      A       T  AC
                                CGTGG GGTGGGGCG GG  AGCC
                                ||||| ||||||||| ||  ||||
                                GCACC CCACCCCGC CC  TCGG
                                   _       _ C_
GAM942  MEF2D    3'  GTGGGGGTGGGGCACCTCCATG 25421     A       TGGA __
           GCC                    GTGG GGTGGGGCG   CA  GCC
                                ||||| |||||||||   ||  |||
                                CACC CCACCCCGT   GT  CGG
                                  C       GGAG  AC
GAM942  NLGN2    3'  GTGCAGGTGGGGCACGAGC   44761    G        GAC
                                GTG AGGTGGGGCGTG   AGC
                                ||| ||||||||||||  |||
                                CAC TCCACCCCGTGC   TCG
                                 G         ___
GAM942  RHBDL    3'  CGTGAAGGCCCCTGGTGGGCGG 19553        ____ _ C
                                CGTGGAGGT   GG GG GTGG
                                |||||||||   || || ||||
                                GCACTTCCG   CC CC CGCC
                                     GGGA  A  _
GAM942  SIAT7D   3'  CCTGGAGGTGGGGTGAGC   30830   G       CG  GAC
                                C TGGAGGTGGGG  TG   AGC
                                | ||||||||||  ||   |||
                                G ACCTCCACCCC  AC   TCG
                                 G        __ ___
GAM942  SYNGR1   3'  CGTGGGGATGGTAGGAGGTGGG 21756     A___     C   ACA
           TGGCC                  CGTGG   GGTGGGG GTGG   GCC
                                |||||   ||||||| ||||   |||
                                GCACC   CCATCCT CACC   CGG
                                   CCTA     C   CAC
GAM942  TAPBP    3'  CCTGGAGGTGGGCGGGAGGC  17298   G       G  T   CA
                                C TGGAGGTGGG CG GGA  GC
                                | |||||||||| || |||  ||
                                G ACCTCCACCC GC CCT  CG
                                 G        _ _  C_
GAM942  TNFRSF8  5'  CGTGAGGTGGCCTGGCGGC   10318     G   GG   G   ACA
                                CGTG AGGT  GGC TGG   GC
                                |||| ||||  ||| |||   ||
                                GCAC TCCA  CCG ACC   CG
                                  _   __   G   GC_
GAM942  TPI1     5'  GTGGGCGTGGAGCCGGCAGCC  7476      AG      G   A
                                GTGG  GTGGGGC TGG CAGCC
                                ||||  ||||||| ||| |||||
```

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                                CACC  CACCTCG GCC GTCGG
                                  CG     _  _
GAM942  UCP3    3'  CATGGGGGTGGGGCTCCTGTGG 17852      A      ____
                                CGTGG GGTGGGGC   GTGG
                                ||||| ||||||||   ||||
                                GTACC CCACCCCG   CACC
                                   C       AGGA
GAM942  YES1    3'  CGTGGTGGTGGGCACCTG    24118      A    _ G
                                CGTGG GGTGGG GC TG
                                ||||| |||||| || ||
                                GCACC CCACCC TG AC
                                   A     G  G
GAM943  GTF2I   3'  GCTACCATGTCATATAAT    37441       CAC
                                GTTACTA   CATATAAT
                                |||||||   ||||||||
                                CGATGGT   GTATATTA
                                    ACA
GAM943  HOXD4    3'  CAGTAGCTCCTGCCATATAAT  31168     TA  ACA_
                                CAGT  CT    CCATATAAT
                                ||||  ||    |||||||||
                                GTCA  GA    GGTATATTA
                                  TC  GGAC
GAM943  USP9Y    3'  TCCACATCAACCATATAA    41961      G   CTAC
                                TCCACA TTA    ACCATATAA
                                |||||| |||    |||||||||
                                AGGTGT AGT    TGGTATATT
                                  _   ____
GAM944  CHRNA10  5'  TGCAAGAGCGGGGGCAGG    33793      A      __
                                TGCAA AGCGGGGG  GG
                                ||||| ||||||||  ||
                                ACGTT TCGCCCCC  CC
                                   C       GT
GAM944  DGCR2    3'  GCAGAAGGCGGGCTGTGGT    23093     AAA C   G   A   C
                                GCA   G GGG GGG CTG GGT
                                |||   | ||| ||| ||| |||
                                CGT   C TCC CCC GAC CCA
                                  ___ T   G   _   A
GAM944  GRLF1    3'  AGCGGGAGTGGGGGCAGC    44220        _  ACT
                                AGCGGGGG GG   GCGGT
                                ||||||||  ||   |||||
                                TCGCCCTC CC   CGTCG
                                    A  CC_
GAM944  ITM2B    5'  GCAGAGGCGGCTACTGCGGT   35093       _  __
                                GCGGGGG GG  ACTGCGGT
                                ||||||| ||  ||||||||
                                CGTCTCC CC  TGACGCCA
                                    G  GA
GAM944  MGAT1    3'  GCAGCCTGGGGACTGTGG    14433      G__      C
                                GCGG   GGGGACTG GG
                                ||||   |||||||| ||
```

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                                CGTC   CCCCTGAC CC
                                  GGA       A
GAM944  PACE    3'  TGCAAGAGAGGGGAGGGTGGT  15039      A  C      ACTGC
                                TGCAA AG GGGGGGG    GGT
                                ||||| || |||||||    |||
                                ACGTT TC CCCCTCC    CCA
                                   C  T      CA___
GAM944  PRDM2   5'  TGTAAGAGTGGAGGGAAGG   29250    C  A  C      CTGC
                                TG AA AG GGGGGGGA   GG
                                || || || ||||||||   ||
                                AC TT TC CCTCCCTT   CC
                                 A  C  A      _____
GAM944  SCN8A   5'  TGCGGCGGGCGGGACTGCGGT  30534     AAAA    G
                                TGC   GCGGG GGGACTGCGGT
                                |||   ||||| ||||||||||
                                ACG   CGCCC CCCTGACGCCA
                                  C___    G
GAM944  EPB49   5'  CGCCCGCCGGGTCACTCG    12727        ACA  T
                                CGCCCGCC   TC TTCG
                                ||||||||   || ||||
                                GCGGGCGG   AG GAGC
                                     CCC  T
GAM944  SMARCD2  5'  GGAACCCGCCCGCGCCTC    16919   A        CACA
                                A AACCCGCCCGC    TCTT
                                | ||||||||||    ||||
                                C TTGGGCGGGCG    GGAG
                                 C         C___
GAM944  WBSCR1   3'  AAACCCGCTGGCCATTCAC   35264        CC   __
                                AAACCCGC  GCCA  CAT
                                ||||||||  ||||  |||
                                TTTGGGCG  CGGT  GTG
                                     AC    AA
GAM944  ZNF217   3'  AAAACCCCCCCCGCCACTGAATC 27187        G       ATCTT
           G                     AAAACCC CCCGCCAC    TCG
                                |||||||  ||||||||    |||
                                TTTTGGG GGGCGGTG    AGC
                                     G       ACTT_
GAM945  FTSJ2   3'  GTTGCTATGTTGCC       30169       TATATTT
                                GTTGCT      ATGTTGTT
                                ||||||      ||||||||
                                CAACGA      TACAACGG
                                          ________
GAM945  PIP5K1B  3'  GTTGCTTATGTATAATCACTG  18667         ATTTAT  TG
                                GTTGCTTAT     GT  TTG
                                |||||||||     ||  |||
                                CAACGAATA     TA  GAC
                                     CATAT_  GT
GAM945  ALCAM   3'  TTATGTATGTGTGTCTAT    11567           CA
                                TTATGTATGTGTG  TGT
                                ||||||||||||  |||
```

```
                                AATACATACACAC  ATA
                                      AG
GAM945  AOX1    3'  ATTTATGCATGTGATATT    10108          TGC
                                ATTTATGTATGTG  ATGTT
                                ||||||||||||  |||||
                                TAAATACGTACAC  TATAA
                                      ___
GAM945  DRD5    3'  ATTTGCGTGTGTGTGCGTGCT  9025      A  A     A
                                ATTT TGT TGTGTGC TGTT
                                |||| ||| ||||||| ||||
                                TAAA GCA ACACACG ACGA
                                  C  C      C
GAM945  EHD3    3'  TATGTGTGTGTGCATGTT    31114      A
                                TATGT TGTGTGCATGTT
                                ||||| ||||||||||||
                                ATACA ACACACGTACAA
                                   C
GAM945  ESRRBL1  3'  ATCTGTGTATGTGAGCATGTTG 32837     A      T
                                ATTT TGTATGTG GCATGTTG
                                |||| |||||||| ||||||||
                                TAGA ACATACAC CGTACAAC
                                  C       T
GAM945  GABRB3   3'  ATATATGTGTGTGTCTGCT   34873         CA__
                                ATGTATGTGTG   TGTT
                                ||||||||||   ||||
                                TATATACACAC   ACGA
                                      ACAG
GAM945  GALNT1   3'  ATTTGTGTGTGTGTGCACAT  33837     A  A
                                ATTT TGT TGTGTGCATGT
                                |||| ||| ||||||||||
                                TAAA ACA ACACACGTGTA
                                  C  C
GAM945  IARS    3'  TTCATGTGTGTGTCTATG    30202       A    GC
                                TTTATGT TGTGT  ATG
                                ||||||| |||||  |||
                                AAGTACA ACACA  TAC
                                    C    GA
GAM945  IGF2R    3'  TATGTGTGTGTGTGCT     9340       A     CA
                                TATGT TGTGTG  TGTT
                                ||||| ||||||  ||||
                                ATACA ACACAC  ACGA
                                   C     __
GAM945  PPAT    3'  ATTTATGTGTATGTGTACATG  15481      __
                                ATTTA  TGTATGTGTGCATG
                                |||||  ||||||||||||||
                                TAAAT  ACATACACATGTAC
                                   AC
GAM945  RARA    3'  TTTGTGTGTGTGCGCACG    9717     A  A
                                TTT TGT TGTGTGCATG
                                ||| ||| ||||||||||
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                                AAA ACA ACACGCGTGC
                                  C   C
GAM945  SLC1A4   3'  TACATATGTGTGTGTGTTG  16756          CA__
                                TATGTATGTGTG   TGTTG
                                ||||||||||||  |||||
                                ATGTATACACAC   ACAAC
                                      ACAC
GAM945  ZNF138   3'  CTTATGTATAGTAAGTGTTG  44343         T   CA
                                TTTATGTATG GTG  TGTTG
                                |||||||||| |||  |||||
                                GAATACATAT CAT  ACAAC
                                      _  TC
GAM946  AP2B1    3'  AACACTGCTAAACAGGCTG   10477          TCCT_
                                AACACTGCTAA    CTG
                                ||||||||||    |||
                                TTGTGACGATT    GAC
                                      TGTCC
GAM946  ARNT2    3'  AACCAGGATAATTAAATCCTCT 31350      CAACACTGCT
              G                  AACCA        AATCCTCTG
                                |||||        |||||||||
                                TTGGT        TTAGGAGAC
                                   CCTATTAAT_
GAM946  BDKRB2   3'  CAGCACTGTGATCCTCTG   8400    A    CTA
                                CA CACTG   ATCCTCTG
                                || |||||   ||||||||
                                GT GTGAC   TAGGAGAC
                                 C    AC_
GAM946  CKN1     3'  CCTCCACTTGCTGATCCTCTG  6349    ACAA   _   A
                                CC    CACT GCT ATCCTCTG
                                ||    |||| ||| ||||||||
                                GG    GTGA CGA TAGGAGAC
                                 AG__    A   C
GAM946  CYB561   3'  CACAGAAAAGGCATCCTCTG   12540     ACACT_  TA
                                CACA     GC  ATCCTCTG
                                ||||     ||  ||||||||
                                GTGT     CG  TAGGAGAC
                                   CTTTTC  __
GAM946  FBXL3A   3'  AACACTGCCTCCCTTCTG    29123         AA   _
                                AACACTGCT  TCCT CTG
                                |||||||||  |||| |||
                                TTGTGACGG  GGGA GAC
                                     A_   A
GAM946  HSD17B8  3'  AACCATACACTGCCACCCCT   30621      CA       AT
                                AACCA  ACACTGCTA  CCTCT
                                |||||  |||||||||  |||||
                                TTGGT  TGTGACGGT  GGGGA
                                   A_        __
GAM946  PDE4D    3'  CATCACAGTACTAACCCTCTG  43893    CA   C
                                CA  ACA TGCTAATCCTCTG
                                ||  ||| ||||||||||||
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                              GT  TGT ATGATTGGGAGAC
                               AG   C
GAM946  PRKAB1   3' CCAGGGCTGCAGATCCTCTG  26502    CAACA   TA
                              CCA    CTGC  ATCCTCTG
                              |||    ||||  ||||||||
                              GGT    GACG  TAGGAGAC
                                CCC__   TC
GAM946  SCD      3' CACAGAAAAGGCATCCTCTG  22822    ACACT_  TA
                              CACA    GC  ATCCTCTG
                              ||||    ||  ||||||||
                              GTGT    CG  TAGGAGAC
                                CTTTTC __
GAM946  SNAP23   3' AACCATGATACTACTAAT   19248     CAAC
                              AACCA   ACTGCTAAT
                              |||||   |||||||||
                              TTGGT   TGATGATTA
                                 ACTA
GAM946  TAF12    3' AACCACAAATAAAATCTTCTCT 24865       CACTGCT   __
           G                   AACCACAA     AATC  CTCTG
                              ||||||||     ||||  |||||
                              TTGGTGTT     TTAG  GAGAC
                                   TATT___   AA
GAM946  TRPC5    3' AACCACAAGCTGACAATTCT  29762       CA  C   CC
                              AACCACAA  CTG TAAT  TCT
                              ||||||||  ||| ||||  |||
                              TTGGTGTT  GAC GTTA  AGA
                                   C_  T   __
GAM946  WBSCR5   3' CACAACACTGTTTAATCAGCTC 37124        C_    __
           TG                   CACAACACTG  TAATC  CTCTG
                              ||||||||||  |||||  |||||
                              GTGTTGTGAC  ATTAG  GAGAC
                                   AA    TC
GAM946  YES1     3' AACCACTAATGCTGCTATTCAA 24113      _ CA     A  C__
           ATCTG                AACCAC AA  CTGCTA TC   TCTG
                              ||||||  ||  ||||||  ||   ||||
                              TTGGTG TT  GACGAT AG   AGAC
                                 A  AC     A  TTT
GAM946  ENTPD6   3' CCCTCAGTGTGTGCCTGTGGTT 10335     AC_  C  CATA
                              TCCT   TG TG   CCTGTGGTT
                              ||||   || ||   |||||||||
                              GGGA   AC AC   GGACACCAA
                                GTC  _  AC__
GAM946  FOXO1A   3' CTGCCCCAAATACCTGTGGTT  12887     G  __
                              CTGCT CA  TACCTGTGGTT
                              |||||  ||  ||||||||||
                              GACGG GT  ATGGACACCAA
                                 G  TT
GAM946  IL1F5    3' CTATTGCTGCATAACAAGT   29349     C       _ CT
                              CTA TGCTGCATA C  GT
                              |||  |||||||||  |  ||
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                                GAT ACGACGTAT G  CA
                                  A       T TT
GAM946  PPARGC1  3'  CTATGGAACCTGTGGT     29951     C  CAT
                                CTG TG   ACCTGTGGT
                                ||| ||   |||||||||
                                GAT AC   TGGACACCA
                                  _ CT_
GAM946  PRKR     5'  CTATGCTTGTCGTGCCTGTGGT 15678     C    GCATA__
           T                     CTA TGCT      CCTGTGGTT
                                ||| ||||      |||||||||
                                GAT ACGA      GGACACCAA
                                  _   ACAGCAC
GAM946  SDC2     5'  CTTCTTGCTCTGCTGTGGTT   42565    A  GC   ATAC
                                CT CT  TGC    CTGTGGTT
                                || ||  |||    ||||||||
                                GA GA  ACG    GACACCAA
                                 A  __   AGAC
GAM946  STAC     3'  TCCTACTGCTGCTGCCAAGC   17140          ATA  TGT
                                TCCTACTGCTGC   CC   GGT
                                ||||||||||||   ||   |||
                                AGGATGACGACG   GG   TCG
                                       AC_  T__
GAM947  CELSR3   3'  TACTGTAAACAAAGTGTA    10840     CC        A
                                TAC  GTAAACGGGG TGTA
                                |||  |||||||||| ||||
                                ATG  CATTTGTTTC ACAT
                                  A_        _
GAM947  KIF5B    3'  CACCTGTGGGTATGTATAA    21138     C  AAAC   G
                                TACC GT    GGG ATGTATAA
                                ||||  ||    |||  ||||||||
                                GTGG CA    CCC TACATATT
                                  A  _____   A
GAM947  FEZ1     3'  GTCCCTCCTGAAAGAGTA     35422        C   T  C
                                GTCCCTCC GAA GG GTA
                                |||||||| ||| || |||
                                CAGGGAGG CTT TC CAT
                                     A   _  T
GAM947  LPL      3'  CGTCCCTCTCCAAGTTACAT   6940         _    ATG
                                CGTCCCTC CCGA   GCGT
                                |||||||| ||||   ||||
                                GCAGGGAG GGTT   TGTA
                                     A    CAA
GAM947  MAML1    3'  CCTGTCCCTTTTTGGCATA    31281    C     CCCGAA
                                CC GTCCCT     TGGCGTA
                                || ||||||     |||||||
                                GG CAGGGA     ACCGTAT
                                 A     AAA____
GAM947  PAG      3'  CCTGCTTTTCTGAATGGCA    32952    C  CCC  CC
                                CC GT   TC  GAATGGCG
                                || ||   ||  ||||||||
```

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                                GG CG   AG  CTTACCGT
                                 A  AAA  A_
GAM947  SET7     5'  CCCGTCCCTCTGGGT      36154          CCGAA   C
                                CCCGTCCCTC     TGG GT
                                ||||||||||     ||| ||
                                GGGCAGGGAG     ACC CA
                                      _____  _
GAM947  TRPM7    3'  CCGTCCCTCTTGAAAATG    41617         CC__
                                CCGTCCCTC    GAATG
                                |||||||||    |||||
                                GGCAGGGAG    TTTAC
                                     AACT
GAM947  ZFP103   5'  CCCGTCCCGCTCGGATGGGCA  24957         TCC  A    C
                                CCCGTCCC   CG ATGG GTA
                                ||||||||   || |||| |||
                                GGGCAGGG   GC TACC CGT
                                     CGA  C   _
GAM948  PCDHB16  5'  TGCATCCGCCATCACAATTT   34147      A_   GC
                                TGCAT  GTTG  CACAATTT
                                |||||  ||||  ||||||||
                                ACGTA  CGGT  GTGTTAAA
                                   GG    A_
GAM948  RBMX     3'  TTACATAGGCATGTGATTTCAG 42813        GTT   CACA_
                                TTGCATA   GGC    ATTTCAG
                                |||||||   |||    |||||||
                                AATGTAT   CCG    TAAAGTC
                                    ____  TACAC
GAM948  SNAI1    3'  TTGCATAGTTAGTCACACCTC  25611          C    A
                                TTGCATAGTTGG CACA TTTC
                                |||||||||||| |||| ||||
                                AACGTATCAATC GTGT GGAG
                                       A    _
GAM948  GHR      3'  TACAAAATGCTTCTTGTAC    6717           GGCA
                                TACAAAATGCTTTT    GTAC
                                ||||||||||||||    ||||
                                ATGTTTTACGAAGA    CATG
                                       A___
GAM948  LZTFL1   3'  ACAAAATGCTTTTCAAAATACA 33767           GGC
              T                  ACAAAATGCTTTT   AGTACAT
                                 ||||||||||||   |||||||
                                 TGTTTTACGAAAA   TTATGTA
                                       GTT
GAM948  MTERF    3'  CAAAATTCTTTTGGAAT     28096       G      C
                                CAAAAT CTTTTGG AGT
                                |||||| ||||||| |||
                                GTTTTA GAAAACC TTA
                                   A      _
GAM949  ANXA9    5'  AGCAAGAGTTCTTGCAA     18688     C   TATCTG
                                AGC AAG     TCTTGCAA
                                |||  |||     ||||||||
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                                TCG TTC     AGAACGTT
                                  _  TCA___
GAM949  BMP1    3' GCCTGTGCTGTCTTGCA    25981    AA  AT
                                GCC  GT  CTGTCTTGCA
                                |||  ||  ||||||||||
                                CGG  CA  GACAGAACGT
                                  A_  C_
GAM949  CALCR   3' AAGCCGCTTTGTCTTGCA   11942     AA  ATC
                                AAGCC  GT   TGTCTTGCA
                                |||||  ||   |||||||||
                                TTCGG  CG   ACAGAACGT
                                   __  AA_
GAM949  FUT6    5' GCCAAGGGATCTTGCA     6652       TATCT
                                GCCAAG    GTCTTGCA
                                ||||||    ||||||||
                                CGGTTC    TAGAACGT
                                   CC___
GAM949  GRM7    5' AGCCAAGTGTTTGCCCCATAA 9181        ATC    GC
                                AGCCAAGT   TGTCTT  AA
                                ||||||||   ||||||  ||
                                TCGGTTCA   ACGGGG  TT
                                     CAA     TA
GAM949  HLCS    3' AGCTGCACAGTCTTGCA    7634     CAA   CT
                                AGC   GTAT  GTCTTGCA
                                |||   ||||  ||||||||
                                TCG   CGTG  CAGAACGT
                                  A__    T_
GAM949  LAD1    3' AGCTGGCTGAGTCTTGCAAA  24481    CAA  ATCT
                                AGC   GT   GTCTTGCAAA
                                |||   ||   ||||||||||
                                TCG   CG   CAGAACGTTT
                                  AC_  ACT_
GAM949  PITPN   3' TGACCACTGTCTTGCA     26341   A   AGTAT
                                A GCCA    CTGTCTTGCA
                                | ||||    ||||||||||
                                A TGGT    GACAGAACGT
                                 C   _____
GAM949  PRX     3' CAAGTATCTTGTTCCCCAAA  34105        _  CT G
                                CAAGTATCT GT  T CAAA
                                ||||||||| ||  | ||||
                                GTTCATAGA CA  G GTTT
                                     A  AG G
GAM949  PTGFRN  3' AAGTCAGTCAGTCTTGCAA  42581    CCA  ATCT
                                AAG   AGT   GTCTTGCAA
                                |||   |||   |||||||||
                                TTC   TCA   CAGAACGTT
                                  AG_   GT__
GAM949  SCGB2A2 3' AGCCAAAGGTCTTGCA     14483       TATCT
                                AGCCAAG    GTCTTGCA
                                |||||||    ||||||||
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                                TCGGTTT    CAGAACGT
                                   C____
GAM949  WHSC1    3'  TAAGTTAATATCTGCTCCCCAA 39376     CCA      TC  G
            A                   TAAG   AGTATCTG  TT CAAA
                                ||||   ||||||||  || ||||
                                ATTC   TTATAGAC  GG GTTT
                                  AA_       GA  G
GAM949  ZNF215   5'  TAAGCCAAGTTATTTCAC    29918         ATC   C TG
                                TAAGCCAAGT   TGT T  C
                                ||||||||||   ||| |  |
                                ATTCGGTTCA   ATA A  G
                                     ___   A GT
GAM950  NELL2    3'  CTTCTACATGGTGATGT     26048         TATTAT
                                CTTCTATAT     TGATGT
                                |||||||||     ||||||
                                GAAGATGTA     ACTACA
                                     CC____
GAM950  TRIM9    3'  CCCTTCTATTTGTTATTCTTG  31556         A__     A
                                CCCTTCTAT   TTATT TTG
                                |||||||||   ||||| |||
                                GGGAAGATA   AATAA AAC
                                     AAC     G
GAM950  EGR2     3'  TGTAGAAAACGTCTTAGATCA  7584          TATTA     C
                                TGTAGAAAAC    CTTAGA CA
                                ||||||||||    |||||| ||
                                ACATCTTTTG    GAATCT GT
                                     CA___     A
GAM950  HIF1A    3'  TGTAGAAAATATAAATAGAC   11355         C   TACT
                                TGTAGAAAA TAT    TAGAC
                                ||||||||| |||    |||||
                                ACATCTTTT ATA    ATCTG
                                     _  TTT_
GAM950  INHBB    3'  TGTAGAAAAATATCTCAGGCC  13567         C   TA    A
                                TGTAGAAAA TAT  CTTAG CC
                                ||||||||| |||  ||||| ||
                                ACATCTTTT ATA  GAGTC GG
                                     T  __    C
GAM950  LDOC1    3'  GTAGAAAACTAACCA       29493          TTACTTAG
                                GTAGAAAACTA       ACCA
                                ||||||||||        ||||
                                CATCTTTTGAT       TGGT
                                          _________
GAM951  ENTPD5   5'  TTTCTTTGTTGACCAGGA    10353       ATAATCC
                                TTTCT      TGACCAGGA
                                |||||      |||||||||
                                AAAGA      ACTGGTCCT
                                   AACA___
GAM951  FBXL5    3'  TTCTATAATCCTAAAGAA    37951            CC
                                TTCTATAATCCTGA  AGGA
                                ||||||||||||||  ||||
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                                AAGATATTAGGATT  TCTT
                                    __
GAM951  RNMT    3'  TTTCTATGATCCTGACCAA   19161       A
                                TTTCTAT ATCCTGACCAG
                                ||||||| ||||||||||
                                AAAGATA TAGGACTGGTT
                                    C
GAM952  CA7     3'  AGGTGGCTTTGGTGACTGGGTG 41195     A   CCCTC
                                AGGT GCT    GACTGGGTG
                                |||| |||    |||||||||
                                TCCA CGA    CTGACCCAC
                                  C   AACCA
GAM952  MBP     3'  AGGTGGCCCCCTCTCTG    44884     A      GA
                                AGGT GCTCCCTC  CTG
                                |||| ||||||||  |||
                                TCCA CGGGGGAG  GAC
                                  C       A_
GAM952  AF3P21  3'  TCAGGTTCCTTCTG       32404      AAGTGC
                                TCAGG     TTCCTTCTG
                                |||||     |||||||||
                                AGTCC     AAGGAAGAC
                                  _______
GAM952  AICDA   3'  AGGATCTACCTTCTGC     34036     AGTG  T
                                AGGA   CT CCTTCTGC
                                ||||   || ||||||||
                                TCCT   GA GGAAGACG
                                  A___  T
GAM952  AK2     3'  CAGGAAGCAGATATCTTTCTG  30187        CT__  C
                                CAGGAAGTG   TC TTCTG
                                |||||||||   || |||||
                                GTCCTTCGT   AG AAGAC
                                     CTAT  A
GAM952  CA11    3'  CAGGAAGTATTCTG       10235        CTTCC
                                CAGGAAGTG    TTCTG
                                |||||||||    |||||
                                GTCCTTCAT    AAGAC
                                   _____
GAM952  CD83    3'  TCGTGAAGTCCCTTCTGC   20141   AG    GCT
                                TC  GAAGT   TCCTTCTGC
                                ||  |||||   |||||||||
                                AG  CTTCA   GGGAAGACG
                                 CA    ___
GAM952  CDH12   3'  TCAGAAAGTGTTCTTCT    19778        C   C
                                TCAGGAAGTG TTC TTCT
                                |||||||||| ||| ||||
                                AGTCTTTCAC AAG AAGA
                                   _   _
GAM952  COX11   3'  TCAGAAAGCGTTCTTCTG   20421        C   C
                                TCAGGAAGTG TTC TTCTG
                                |||||||||| ||| |||||
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                                AGTCTTTCGC AAG AAGAC
                                      _  _
GAM952  CTMP     3'  CAGGAAGTGTTTCTG      38198        CTTCC
                                CAGGAAGTG    TTCTG
                                |||||||||    |||||
                                GTCCTTCAC    AAGAC
                                     A____
GAM952  CYP21A2  3'  TCAGGAAGGGAGCTCTGC    7985        T__  TTCCT
                                TCAGGAAG  GC    TCTGC
                                ||||||||  ||    |||||
                                AGTCCTTC  CG    AGACG
                                     CCT  _____
GAM952  DNAJB1   3'  TCAGGAAGGCCCCTTG     26034       T  T  TC
                                TCAGGAAG GCT CCT  TG
                                |||||||| ||| |||  ||
                                AGTCCTTC CGG GGA  AC
                                      _  _  __
GAM952  GATA2    3'  TCGGGAAATGCTGGGCTGC   13092    A       TCCTT
                                TC GGAAGTGCT    CTGC
                                || |||||||||    ||||
                                AG CCTTTACGA    GACG
                                 C       CCC__
GAM952  GNAI1    3'  AGAAAGGTCCTTCTG      13164       TGCT
                                AGGAAG   TCCTTCTG
                                ||||||   ||||||||
                                TCTTTC   AGGAAGAC
                                   C___
GAM952  GRB10    5'  TCAGAAATTTCCTTCTGC    23667       GTGC
                                TCAGGAA   TTCCTTCTGC
                                |||||||   ||||||||||
                                AGTCTTT   AAGGAAGACG
                                    A___
GAM952  HMGCL    3'  CAGGAGGTCCTTCTG       6790       A TGCT
                                CAGGA G   TCCTTCTG
                                ||||| |   ||||||||
                                GTCCT C   AGGAAGAC
                                   C _____
GAM952  IL1RAPL2 5'  CCAGACTCTTCCTTTTGC    32639      AAGTG     C
                                TCAGG    CTTCCTT TGC
                                |||||    ||||||| |||
                                GGTCT    GAAGGAA ACG
                                   GA___      A
GAM952  ITGA1    3'  TCAGGAGGTTCTTCGCTG    41856      A  G   CTT
                                TCAGGA GT CTTC   CTG
                                |||||| || ||||  |||
                                AGTCCT CA GAAG   GAC
                                   C  A   C__
GAM952  LMO2     3'  TCAAGGGCTGGTCCTTCTG   24549      AAGT  __
                                TCAGG   GCT  TCCTTCTG
                                |||||   |||  ||||||||
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                                AGTTC   CGA  AGGAAGAC
                                  C___   CC
GAM952  MECP2   3'  GGAAATGCCTTTTGC      22596       TTC   C
                                GGAAGTGC   CTT TGC
                                ||||||||   ||| |||
                                CCTTTACG   GAA ACG
                                     ___   A
GAM952  MECP2   3'  TCACACCTGCTTCCTTCTGC  22610    GGAAG
                                TCA    TGCTTCCTTCTGC
                                |||    ||||||||||||
                                AGT    ACGAAGGAAGACG
                                 GTGG_
GAM952  MME     3'  GGAAGTGCTCCTCTTTTG    28600         _  C
                                GGAAGTGCTTC CTT TG
                                |||||||||| ||| ||
                                CCTTCACGAGG GAA AC
                                      A   A
GAM952  MMP11   3'  TCAGGAAGTGGCCCTG     25540        CTT  TT
                                TCAGGAAGTG   CC  CTG
                                |||||||||   ||  |||
                                AGTCCTTCAC   GG  GAC
                                     C__  __
GAM952  MSH3    3'  TCATGACCTTATTCCTTCTG  14632    G  AGTGC
                                TCA GA    TTCCTTCTG
                                ||| ||    |||||||||
                                AGT CT    AAGGAAGAC
                                 A  GGAAT
GAM952  NFATC1  3'  CAGGCCGTTCCTTCTGC    26070    AA  GCT
                                CAGG  GT   TCCTTCTGC
                                ||||  ||   |||||||||
                                GTCC  CA   AGGAAGACG
                                  GG  ___
GAM952  NT5M    3'  CAGGGAACCCCCTTCTGC    33645    AAGT
                                CAGG   GCTTCCTTCTGC
                                ||||   ||||||||||||
                                GTCC   TGGGGGAAGACG
                                  CT__
GAM952  P53AIP1 3'  TCAGAAAACCTTTCTG     35237       TGCTT   _
                                TCAGGAAG    CCTT CTG
                                ||||||||    |||| |||
                                AGTCTTTT    GGAA GAC
                                     _____   A
GAM952  PLN     3'  TCAGGAAGTGGTCTG      15407        CTTCCT
                                TCAGGAAGTG     TCTG
                                ||||||||||     ||||
                                AGTCCTTCAC     AGAC
                                     C_____
GAM952  PNN     3'  TCAAGAAATCTTCTG      43403        GCTTC
                                TCAGGAAGT    CTTCTG
                                |||||||||    ||||||
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                                AGTTCTTTA    GAAGAC
                                      _____
GAM952  RAB3B    3'  TCAGGAAGGTGGGCCTTGC   16085       _ CTT   TC
                                TCAGGAAG TG   CCT  TGC
                                |||||||| ||   |||  |||
                                AGTCCTTC AC   GGA  ACG
                                     C  CC_   __
GAM952  S100A2   3'  CAGGAAGTCAAGAGTTCTGC  25583       GCTTCC
                                CAGGAAGT     TTCTGC
                                ||||||||     ||||||
                                GTCCTTCA     AAGACG
                                     GTTCTC
GAM952  SFRP2    3'  TCAGGAAATGCTGGGGATGC  43545         TCCTTC
                                TCAGGAAGTGCT     TGC
                                ||||||||||||     |||
                                AGTCCTTTACGA     ACG
                                       CCCCT_
GAM952  SLC18A1  3'  TCAAGGAGCACCTTCTGC    16823     AAGT  TT
                                TCAGG   GC  CCTTCTGC
                                |||||   ||  ||||||||
                                AGTTC   CG  GGAAGACG
                                   CT__  T_
GAM952  SNRPN    5'  TCAGTGAGGCAGTCCTTCTGC 35612     GA  T  T_
                                TCAG  AG GC  TCCTTCTGC
                                ||||  || ||  |||||||||
                                AGTC  TC CG  AGGAAGACG
                                  AC  _  TC
GAM952  SNX9     3'  TCAGGAAGGGCGCTGGTCTG  32158       T  TTCCT
                                TCAGGAAG GC    TCTG
                                |||||||| ||    ||||
                                AGTCCTTC CG    AGAC
                                     C  CGACC
GAM952  TFDP2    3'  TCAGAAAGCATGCTTTCTG   26620       __   CCT
                                TCAGGAAGT  GCTT   TCTG
                                |||||||||  ||||   ||||
                                AGTCTTTCG  CGAA   AGAC
                                     TA   ____
GAM952  TNP1     3'  GGCAGTTCCCCTTCTGC    40475    A   GC
                                GG AGT  TTCCTTCTGC
                                || |||  ||||||||||
                                CC TCA  GGGGAAGACG
                                 G   A_
GAM952  UNC13    3'  TCAGGAAGTCCAGGAGGCTGC 26866       G  TCCTT_
                                TCAGGAAGT CT     CTGC
                                |||||||||  ||     ||||
                                AGTCCTTCA GG     GACG
                                     _  TCCTCC
GAM952  XBP1     3'  TCAGCAGGTGTTCCCGTTGC  22925     GAA  C    TC
                                TCAG   GTG TTCCT  TGC
                                ||||   ||| |||||  |||
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                                AGTC   CAC AAGGG  ACG
                                  GTC  _    CA
GAM953  GFPT2    3'  TGGGCCACACACGAGAA     23043      ATCT
                                TGGGC    TGCACGAGAA
                                |||||    ||||||||||
                                ACCCG    GTGTGCTCTT
                                   GT__
GAM953  NT5E     3'  GCACATGGGTGTTGCAAGAGA  14860         CATC    C
                                GTACATGGG    TTGCA GAGA
                                |||||||||    ||||| ||||
                                CGTGTACCC    AACGT CTCT
                                      AC__     T
GAM953  RNMT     3'  GTACATGGCATCAGATGGTGAG 19154         G    TTGCAC_
          AA                      GTACATGG CATC      GAGAA
                                |||||||| ||||       |||||
                                CATGTACC GTAG      CTCTT
                                    _    TCTACCA
GAM953  SHC1     3'  GTACATAGGCATGCAACATGGG 16705           CTT   C__
          AG                      GTACATGGGCAT   GCA   GAG
                                ||||||||||||   |||   |||
                                CATGTATCCGTA   TGT   CTC
                                       CGT   ACC
GAM953  CLK1     3'  TGTAAGATCTCTTCGAGAGAGC 45382    C       CAA  T_
          TG                      TG AAGATCTC   CG  GGAGCTG
                                || ||||||||   ||  |||||||
                                AC TTCTAGAG   GC  TCTCGAC
                                 A       AA_  TC
GAM953  GPD1     3'  CAGGATCTCCAGGTGCGTAGCT 40657    A       AC_   G
          G                       CA GATCTCCA   GTG AGCTG
                                || ||||||||   ||| |||||
                                GT CTAGAGGT   CGC TCGAC
                                 C       CCA   A
GAM953  MKI67    3'  GCAAGATTTCTGGTTAGAGCTG 14523        C  CAACG
                                GCAAGAT TC     TGGAGCTG
                                ||||||| ||     ||||||||
                                CGTTCTA AG     ATCTCGAC
                                    A  ACCA_
GAM954  DNMT2    3'  TTATGCCTGTTATGACACT    20634           TT   G
                                TTATGTCTGTTA  TGA ATT
                                ||||||||||||  ||| |||
                                AATACGGACAAT  ACT TGA
                                       __   G
GAM954  HEM1     5'  TATCAACTTGTTTGAGATTC   23741      TG_  A
                                TGTC   TT TTTGAGATTC
                                ||||   || ||||||||||
                                ATAG   AA AAACTCTAAG
                                  TTG  C
GAM954  C1D      3'  TCACAATGTTAAAATCC     26762          AACC
                                TCACAATGT    AATCT
                                |||||||||    |||||
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                                AGTGTTACA   TTAGG
                                     ATT_
GAM954  CA12    3'  TCACAATGTATATCT      10250        ACCA
                                TCACAATGTA   ATCT
                                ||||||||||   ||||
                                AGTGTTACAT   TAGA
                                     A___
GAM954  COG3    3'  TCAGAAGCAACCAATCT    36417    C  T
                                TCA AA GTAACCAATCT
                                ||| || ||||||||||
                                AGT TT CGTTGGTTAGA
                                  C  _
GAM954  DMBT1   3'  CACAATGTAGGGCTCAATCT  20599       AC___
                                CACAATGTA    CAATCT
                                |||||||||    ||||||
                                GTGTTACAT    GTTAGA
                                     CCCGA
GAM954  GALC    3'  CACAACATGGACCAATCT    6670       A_
                                CACAATGT  ACCAATCT
                                ||||||||  ||||||||
                                GTGTTGTA  TGGTTAGA
                                     CC
GAM954  GSBS    3'  CCACAGGGAACCAATCT    44998     ATGT
                                TCACA   AACCAATCT
                                |||||   |||||||||
                                GGTGT   TTGGTTAGA
                                   CCC_
GAM954  OGT     5'  TCACAATGCCCCGTCT     18786       AA  AA
                                TCACAATGT  CC  TCT
                                |||||||||  ||  |||
                                AGTGTTACG  GG  AGA
                                     __  GC
GAM954  RAB27A  3'  CACAATGCCCATTAATCT   21359       AA  ___
                                CACAATGT  CCA  ATCT
                                ||||||||  |||  ||||
                                GTGTTACG  GGT  TAGA
                                     __  AAT
GAM954  SNAP23  3'  ACATATGAAAACCAATCT   19250    _  T_
                                ACA ATG  AACCAATCT
                                ||| |||  |||||||||
                                TGT TAC  TTGGTTAGA
                                  A  TT
GAM954  TCP11   5'  CACAAGAAAAACCAATCT   33070     TGT_
                                CACAA   AACCAATCT
                                |||||   |||||||||
                                GTGTT   TTGGTTAGA
                                   CTTT
GAM954  TP63    3'  CCACAGGAAAACCAATCT   18995     ATGT
                                TCACA   AACCAATCT
                                |||||   |||||||||
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                                GGTGT   TTGGTTAGA
                                  CCTT
GAM955  BRCA1    3'  GTACAATCAAGTCTTC     28658         CCCA
                                GTACAATCAAG   TTC
                                ||||||||||   |||
                                CATGTTAGTTC   AAG
                                      AG__
GAM955  DNASE1L1 3'  ATACAACATCTTCATTCCTC  27489       CAAGCC
                                GTACAAT    CATTCCTC
                                |||||||    ||||||||
                                TATGTTG    GTAAGGAG
                                   TAGAA_
GAM955  DPH2L1   3'  TCAGTACAGGCAGGGCCC    10729       AT  A_
                                TCAGTACA  CA  GCCC
                                ||||||||  ||  ||||
                                AGTCATGT  GT  CGGG
                                     CC  CC
GAM955  HOXA7    3'  AGTACAATCAAGTCATCCCTC  45213         CC
                                AGTACAATCAAG  CATTCCTC
                                ||||||||||||  ||||||||
                                TCATGTTAGTTC  GTAGGGAG
                                      A_
GAM955  LDB3     3'  TCAGTACAGTCAGCAACCTCCT 44111        A   A  CCA
                                TCAGTACA TCA GC   TTCCT
                                |||||||| ||| ||   |||||
                                AGTCATGT AGT CG   GAGGA
                                     C   _  TTG
GAM955  MAP7     3'  TCATGCCTAGTCAGCCCATTTC 19573     _  ACAA   A      C
           T                     TCA GT    TCA GCCCATT CT
                                ||| ||    ||| ||||||| ||
                                AGT CG    AGT CGGGTAA GA
                                  A  GATC   _      A
GAM955  SLC24A1  3'  TCAGTGAATCATTCC      21824       AC    AGCCCA
                                TCAGT  AATCA     TTCC
                                |||||  |||||     ||||
                                AGTCA  TTAGT     AAGG
                                   C_    _______
GAM955  ATF7     3'  AGGAAGTGGCATGCTGGTAAG  27791      T    TA
                                AGGAG GTGGC  ATGCTGGTAAG
                                |||||| |||||  ||||||||||
                                TCCTT CACCG  TACGACCATTC
                                      _    __
GAM955  B3GALT5  5'  AGGAGTGTGGCTCAGTCCAA   37674          AATG TG
                                AGGAGTGTGGCT    C  G
                                ||||||||||||   |  |
                                TCCTCACACCGA    G  T
                                       GTCA GT
GAM955  F2RL3    3'  AGGGGCGTGGCTGGGGGAGTGG 19509     A       AATGC__
           TAAG                    AGG GTGTGGCT      TGGTAAG
                                ||| ||||||||      |||||||
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                                TCC CGCACCGA      ACCATTC
                                  C       CCCCCTC
GAM955  FCN1    3'  GGAGTGTGTCTGGCTGG     12818        G  AAT
                                GGAGTGTG CT   GCTGG
                                |||||||| ||   |||||
                                CCTCACAC GA   CGACC
                                     A  C__
GAM955  IL1R1   3'  GGAGTGACATGCTGGT      9363        TGGCTA
                                GGAGTG     ATGCTGGT
                                ||||||     ||||||||
                                CCTCAC     TACGACCA
                                   TG____
GAM955  LFG     3'  GGGGTGTGGCAGCTGGC     44144    A      TAAT
                                GG GTGTGGC    GCTGGT
                                || |||||||    ||||||
                                CC CACACCG    CGACCG
                                 C      T___
GAM955  MEF2D   3'  AGGAGTGTGGGTGATTGTCAG  25416         CTAA_  CT
                                AGGAGTGTGG    TG  GG
                                ||||||||||    ||  ||
                                TCCTCACACC    AC  TC
                                      CACTA  AG
GAM955  SELENBP1 3'  GGAGTGTGGGTGATGA      19483         CTAA  C
                                GGAGTGTGG    TG TGG
                                |||||||||    || |||
                                CCTCACACC    AC ACT
                                      C___  T
GAM955  SFRP5   3'  GGGGTGTGGCTGGAGGCACTGA 16596    A       AAT___
                                GG GTGTGGCT     GCTGG
                                || ||||||||     |||||
                                CC CACACCGA     TGACT
                                 C       CCTCCG
GAM955  SLC9A1  3'  AGGAGTGTGAGACCTTGGT   43229         CTA  GC
                                AGGAGTGTGG   AT  TGGT
                                ||||||||||   ||  ||||
                                TCCTCACACT   TG  ACCA
                                      C__  GA
GAM955  SOX10   5'  GGAGGTGACGCTGGT      28005      T    TAAT
                                GGAG GTGGC    GCTGGT
                                |||| |||||    ||||||
                                CCTC CACTG    CGACCA
                                  _    _____
GAM955  TCF20   3'  AGGGTGTGGCTGCACGGTA   42530     A       AAT  _
                                AGG GTGTGGCT   GC TGGTA
                                ||| ||||||||   || |||||
                                TCC CACACCGA   CG GCCAT
                                  _       ___  T
GAM955  VANGL2  3'  AGGAATGTGGCTGGGCCTGA  43451           AATG
                                AGGAGTGTGGCT    CTGG
                                ||||||||||||    ||||
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                                TCCTTACACCGA   GACT
                                      CCCG
GAM956  ACVR1B   3'  TAGCACTGGCAACACCTC    33762     G  A__
                                TAG AC   CAACACCTC
                                ||| ||   |||||||||
                                ATC TG   GTTGTGGAG
                                  G  ACC
GAM956  DKK1     3'  AATAGGCAGTGCAGCACCT   29268       A  ___  A
                                AATAGG CA   CA CACCT
                                |||||| ||   || |||||
                                TTATCC GT   GT GTGGA
                                   _  CAC  C
GAM956  EGLN1    5'  AATAGAACACTTGCAACAC   35157         _____
                                AATAGGACAC    AACAC
                                ||||||||||    |||||
                                TTATCTTGTG    TTGTG
                                      AACG
GAM956  KPNB2    3'  CAGTGACGGCAACACCTC    13999     _   A_
                                TAG GAC  CAACACCTC
                                ||| |||  |||||||||
                                GTC CTG  GTTGTGGAG
                                  A   CC
GAM956  MCM6     3'  CAATAGGACAGCACATACCT  25406          _  AC_
                                TAATAGGACA CA   ACCT
                                |||||||||| ||   ||||
                                GTTATCCTGT GT   TGGA
                                      C  GTA
GAM956  PCDHB2   3'  TAAAAGGAGACACCTC     33194     T    CACA
                                TAA AGGA    ACACCTC
                                ||| ||||    |||||||
                                ATT TCCT    TGTGGAG
                                  T    C___
GAM956  SMN1     3'  TAAGACACTCTAACACTTC   7366         ___     C
                                TAGGACAC   AACAC TC
                                ||||||||   ||||| ||
                                ATTCTGTG   TTGTG AG
                                     AGA     A
GAM956  SP4      5'  TAACAGGACAAACCCTC     17052          C   A
                                TAATAGGACA AAC CCTC
                                |||||||||| ||| ||||
                                ATTGTCCTGT TTG GGAG
                                      _   _
GAM956  CBFA2T2  3'  TGTGGCTCAGCAGGTGCCAAAT 22984           C__  A
           G                     TGTGGCTCAGCA   GT GAGTG
                                ||||||||||||   || |||||
                                ACACCGAGTCGT   CG TTTAC
                                      CCA  G
GAM956  CDC25A   3'  TGTGGCTCAGAGCAGCTTGACA 12153          CAC    AG
                                TGTGGCTCAG   GTAG  TGACA
                                ||||||||||   ||||  |||||
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                                ACACCGAGTC  CGTC  ACTGT
                                     T__   GA
GAM956  CRLF1    5'  TGCGGCTCGGCGGCGGTGGCG  21902       A  A_  TAGA
                                TGTGGCTC GC  CG   GTG
                                |||||||| ||  ||   |||
                                ACGCCGAG CG  GC   CGC
                                    C  CC  CAC_
GAM956  ENTPD6   3'  TGTGGCTCAGCTGACCCGTGGC 10346         ACGTAGA  A
          A                  TGTGGCTCAGC     GTG CA
                             ||||||||||     ||| ||
                             ACACCGAGTCG     CAC GT
                                  ACTGGG_  C
GAM956  FSTL3    3'  TGTGGTTTACACGCAGGCA   25225     CTCA      A
                                TGTGG   GCACGTAG GTG
                                |||||   |||||||| |||
                                ACACC   TGTGCGTC CGT
                                  AAA_      _
GAM956  GAPD     5'  TGTGGCTCGGCTGGCGAC    13053       A  ACGTAGA
                                TGTGGCTC GC     GTGAC
                                |||||||| ||     |||||
                                ACACCGAG CG     CGCTG
                                    C  AC_____
GAM956  MOCS1    3'  TGTGGCTCAGGGCCACGTGGTG 45128         ___    AGA
                                TGTGGCTCAG  CACGT  GTG
                                |||||||||  |||||  |||
                                ACACCGAGTC  GTGCA  CAC
                                     CCG    C__
GAM956  NDST1    3'  TGGCTCAGCGTGTGGTG    11373       AC  AGA
                                TGGCTCAGC  GT  GTG
                                |||||||||  ||  |||
                                ACCGAGTCG  CA  CAC
                                    CA  C__
GAM956  PML      3'  TGAGGCTCAGCATCGGGGGTGG 37739    T      _  TAGA  A
          CA                    TG GGCTCAGCA CG   GTG CA
                                || |||||||| ||   ||| ||
                                AC CCGAGTCGT GC   CAC GT
                                 T       A  CCC_  C
GAM956  PML      3'  TGTGGCTCGGCGGTCTCCATG  37748       A  AC  AGA_
                                TGTGGCTC GC  GT   GTG
                                |||||||| ||  ||   |||
                                ACACCGAG CG  CA   TAC
                                    C  C_  GAGG
GAM956  SLC16A2  3'  TGTGGCTCAGCCTGAGATG   27163         ACGTA  _
                                TGTGGCTCAGC    GAG TG
                                ||||||||||    ||| ||
                                ACACCGAGTCG    CTC AC
                                     GA___   T
GAM956  SLC7A7   5'  TGGCTCAGCACTTTCTGTGA  19581         GTAGA
                                TGGCTCAGCAC    GTGA
                                ||||||||||    ||||
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                                ACCGAGTCGTG    CACT
                                     AAAGA
GAM956  SOX15    5'  TGGGCTCAGCGTTTGTGC    28022    T      AC  AGA   A
                                TG GGCTCAGC  GT   GTG C
                                || ||||||||  ||   ||| |
                                AC CCGAGTCG  CA   CAC G
                                 _      __  AA_   C
GAM957  CDH11    5'  AACTGTACGGTGGTCTTGCTGA 38027        ATTAGC     A
          GG                      AATTGTAT     CTTGCT AGG
                                |||||||||     |||||| |||
                                TTGACATG     GAACGA TCC
                                    CCACCA     C
GAM957  DACH     3'  TTAAGTGTTGTAATCCT     38883      A      C
                                TTAA TGTTGTAA TCCT
                                |||| |||||||| ||||
                                AATT ACAACATT AGGA
                                  C      _
GAM957  PPP3CA   3'  GTTGCCACTTTTTTTAGGAT   9615       A   CC__
                                GTTGT ACT    TTAGGAT
                                ||||| |||    |||||||
                                CAACG TGA    AATCCTA
                                   G   AAAA
GAM958  ABCC3    3'  CACCAGGTCTAGGCCCGGC    33415      AGCA   _
                                CATCA    TCT GGCCCGGC
                                |||||    ||| ||||||||
                                GTGGT    AGA CCGGGCCG
                                   CC__   T
GAM958  AKAP13   3'  CATCAAGCCTTCTCTCACTGG  28475        A___   G  CC
                                CATCAAGC    TCT GC  GG
                                ||||||||    ||| ||  ||
                                GTAGTTCG    AGA TG  CC
                                     GAAG   G  A_
GAM958  AKT1     5'  ACCCAGGCTGGCTCGGC     23134     A  CAT     C
                                ATC AG   CTGGC CGGC
                                ||| ||   ||||| ||||
                                TGG TC   GACCG GCCG
                                  G  C__     A
GAM958  ALPPL2   3'  TCGAACATCTGAGTGGC     42877    A       CCC
                                TC AGCATCTGG   GGC
                                || |||||||||   |||
                                AG TTGTAGACT   CCG
                                 C        CA_
GAM958  AMD1     3'  CATCGACATCTAGAAAGC    11587      AA       CCC
                                CATC  GCATCTGG   GGC
                                ||||  ||||||||   |||
                                GTAG  TGTAGATC   TCG
                                  C_       TT_
GAM958  ANXA7    5'  TCACAGCCCAACCCGGC     19717     _   AT TG
                                TCA AGC  C  GCCCGGC
                                ||| |||  |  |||||||
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                                AGT TCG  G  TGGGCCG
                                  G  __ GT
GAM958  APBA2    3'  TCAAGTCTGCGGCCCGGC    24281      CATC
                                TCAAG   TGGCCCGGC
                                |||||   |||||||||
                                AGTTC   GCCGGGCCG
                                   AGAC
GAM958  APXL     3'  CATCCAGCAGAGCCTGG     11619     A   TCT   C
                                CATC AGCA   GGCC GG
                                |||| ||||   |||| ||
                                GTAG TCGT   TCGG CC
                                  G   C__   A
GAM958  ARHGEF7  5'  CATCAAACGTCTCCAGC     19361       A  GGC
                                CATCAAGC TCT   CCGGC
                                |||||||| |||   |||||
                                GTAGTTTG AGA   GGTCG
                                    C  ___
GAM958  AVP      5'  TCAGGCATCTGGGGAC      7941      A      CCC
                                TCA GCATCTGG   GGC
                                ||| ||||||||   |||
                                AGT CGTAGACC   CTG
                                  C       C__
GAM958  B4GALT2  5'  CATCCGGCTGCTGGCCCGGC  36137     AA  AT
                                CATC  GC  CTGGCCCGGC
                                ||||  ||  ||||||||||
                                GTAG  CG  GACCGGGCCG
                                  GC  AC
GAM958  BACH1    3'  CATCAAACATTGAGAAGGC   10145        C   CCC
                                CATCAAGCAT TGG   GGC
                                |||||||||| |||   |||
                                GTAGTTTGTA ACT   CCG
                                     _  CTT
GAM958  CASP6    5'  CAGGCTCCCGGGCCCGGC    37420    A  AT   _
                                CA GC  CTGG CCCGGC
                                || ||  |||| ||||||
                                GT CG  GGCC GGGCCG
                                 C  AG   C
GAM958  CDC25B   3'  CAGCAGGCCCTCAGCCCGGC  34846    T  A  A  _
                                CA CA GC TCT GGCCCGGC
                                || || || ||| ||||||||
                                GT GT CG GGA TCGGGCCG
                                 C  C  _   G
GAM958  CYP1A1   3'  CATCAGCATCTATGTGGC    7973       A      GCCC
                                CATCA GCATCTG    GGC
                                ||||| |||||||    |||
                                GTAGT CGTAGAT    CCG
                                   _      ACA_
GAM958  DDX6     3'  CATCAAGCATGTTGGGAGGGGC 20551          C_   CCC_
                                CATCAAGCAT  TGG    GGC
                                |||||||||  |||    |||
```

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                                GTAGTTCGTA ACC   CCG
                                     CA  CTCC
GAM958  ESR1    3' CATCAAACACAATTTGGC   6526        C___
                                CATCAAGCAT   TGGC
                                ||||||||||   ||||
                                GTAGTTTGTG   ACCG
                                     TTAA
GAM958  FLRT2   3' CATCAAGCTCTTTATTGGC  29842       A  GGCCC
                                CATCAAGC TCT   GGC
                                |||||||| |||   |||
                                GTAGTTCG AGA   CCG
                                   _  AATAA
GAM958  FMR2    3' CATCAAGATCTAGAGGC    12954       C    CCC
                                CATCAAG ATCTGG  GGC
                                ||||||| ||||||  |||
                                GTAGTTC TAGATC  CCG
                                   _    T__
GAM958  FZD3    3' CATCAAGCATGTTCCAGC   32627       TC  GC
                                CATCAAGCA  TG  CCGGC
                                |||||||||  ||  |||||
                                GTAGTTCGT  AC  GGTCG
                                     __ AA
GAM958  GRAF    3' CATCAAATGTGGTCGGC    31441       CATC  CC
                                CATCAAG   TGG  CGGC
                                |||||||   |||  ||||
                                GTAGTTT   ACC  GCCG
                                   AC__  A_
GAM958  GRAF    3' TCGAGATCAGCCCGGC     31456   A C  T
                                TC AG ATC GGCCCGGC
                                || || ||| ||||||||
                                AG TC TAG TCGGGCCG
                                 C _  _
GAM958  HD      3' CATCAGCAGCAGCCCGGC   13344     A  TC
                                CATCA GCA  TGGCCCGGC
                                ||||| |||  |||||||||
                                GTAGT CGT  GTCGGGCCG
                                   _  C_
GAM958  KIFC3   5' TCGGGCTCCGGGGCCCGGC  24466   AA A  __
                                TC  GC TCT  GGCCCGGC
                                ||  || |||  ||||||||
                                AG  CG AGG  CCGGGCCG
                                 CC _  CC
GAM958  LSP1    3' CATCAAGCATCCTGCATGGC  14237        G  CC
                                CATCAAGCATCT GC  GGC
                                |||||||||||| ||  |||
                                GTAGTTCGTAGG CG  CCG
                                      A  TA
GAM958  MSN     3' CATCAAGCTCTAGATGC    41241       A   CCCG
                                CATCAAGC TCTGG   GC
                                |||||||| |||||   ||
```

```
                                GTAGTTCG AGATC   CG
                                     _    TA__
GAM958  NRG1    5'  TCGAGCATCTGAAGCTGG   30348   A     __ CC
                                TC AGCATCTG  GC  GG
                                || ||||||||  ||  ||
                                AG TCGTAGAC  CG  CC
                                 C       TT  A_
GAM958  OPRD1   3'  CATCTAGCGGCCCGG      9507     A   ATCT
                                CATC AGC   GGCCCGG
                                |||| |||   |||||||
                                GTAG TCG   CCGGGCC
                                  A  ____
GAM958  PIK3R3  3'  CATCAAACATTGGTCTGGC   41437        ____
                                CATCAAGCA   TCTGGC
                                |||||||||   ||||||
                                GTAGTTTGT   AGACCG
                                     AACC
GAM958  PIM1    3'  ATCAAGCACTGTCCTGC    44963       T   GC  G
                                ATCAAGCA CTG  CC GC
                                |||||||| |||  || ||
                                TAGTTCGT GAC  GG CG
                                     _  A_  A
GAM958  PITX1   3'  CATCCAGTCCGCAGGCCCGGC  15315    AA____  TCT
                                CATC    GCA   GGCCCGGC
                                ||||    |||   ||||||||
                                GTAG    CGT   CCGGGCCG
                                  GTCAGG  ___
GAM958  PPP3CA  5'  CACGAGCACCCACCCCGGC   9609    CA      G
                                CAT  AGCATCTG CCCGGC
                                |||  |||||||| ||||||
                                GTG  TCGTGGGT GGGCCG
                                  C_       G
GAM958  PUNC    5'  TCAAGCACCGCGGTCTGG    44883        _  CCC
                                TCAAGCATC TGG   GG
                                ||||||||| |||   ||
                                AGTTCGTGG GCC   CC
                                     C   AGA
GAM958  RAD9    3'  CATCTAAGACACTGCCTGGC  21370    _  _ T  G  C
                                CATC AAG CA CTG CC GGC
                                |||| ||| || ||| || |||
                                GTAG TTC GT GAC GG CCG
                                  A  T  _  _ A
GAM958  ROM1    5'  TCAGCCCGGCCCGGC      7263     A  AT
                                TCA GC  CTGGCCCGGC
                                ||| ||  ||||||||||
                                AGT CG  GGCCGGGCCG
                                  _ __
GAM958  SH3BP2  3'  TCAAGCATCTTCACAGGG    16640        G_  CC
                                TCAAGCATCT  GC  GG
                                ||||||||||  ||  ||
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                                AGTTCGTAGA  TG  CC
                                      AG  TC
GAM958  SH3BP2   3'  TCAAGCACCCAGCTCGGC    16639        TG  C
                                TCAAGCATC  GC CGGC
                                |||||||||  || ||||
                                AGTTCGTGG  CG GCCG
                                      GT  A
GAM958  SLC1A3   5'  ATCAAGCAGTAACGAGG     20041        TC   CC
                                ATCAAGCA  TGGC  GG
                                ||||||||  ||||  ||
                                TAGTTCGT  ATTG  CC
                                     C_   CT
GAM958  SLC22A2  5'  GCAGGTCCTGGGCCCGGC    40525     ___    _
                                GCA   TCTGG CCCGGC
                                |||   ||||| ||||||
                                CGT   GGACC GGGCCG
                                  CCA    C
GAM958  SUFU     3'  CACCAAGCACCTTCTCTGG    32083          GGCCC
                                CATCAAGCATCT    GG
                                ||||||||||||    ||
                                GTGGTTCGTGGA    CC
                                       AGAGA
GAM958  TGFBR1   5'  CACCGCCTGTGGCCCGGC    21433     AA  ATC
                                CATC  GC   TGGCCCGGC
                                ||||  ||   |||||||||
                                GTGG  CG   ACCGGGCCG
                                  __  GAC
GAM958  TR2      5'  TCTCGCTCCTGGCCCGGC    43637    AA  AT
                                TC  GC  CTGGCCCGGC
                                ||  ||  ||||||||||
                                AG  CG  GACCGGGCCG
                                 AG  AG
GAM958  TRPV4    5'  TCAGGCAGAACCCGGC     41350     A   TCT
                                TCA GCA   GGCCCGGC
                                ||| |||   ||||||||
                                AGT CGT   TTGGGCCG
                                  C   C__
GAM959  SLC22A1LS 5'  GTGGGGGTTTCATGCTG    28256     CA     C   T
                                GTG  GGGGTT CAT CTG
                                |||  |||||| ||| |||
                                CAC  CCCCAA GTA GAC
                                  __     A   C
GAM959  SLC22A2  3'  GTGCAGGGATTTCTACT     40528          CCAT
                                GTGCAGGGGTT    TCTGTT
                                ||||||||||    ||||||
                                CACGTCCCTAA    AGATGA
                                       ____
GAM959  THBD     3'  ATGTAGGGGTTCTGTCTG    7421      C       CAT
                                GTG AGGGGTTC   TCTG
                                ||| ||||||||   ||||
```

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                                TAC TCCCCAAG   AGAC
                                  A       AC_
GAM959  TRIM39   3'  GTGCAGGGGTTTCTGTTTCCTC 34576          _ CA__   G
              CTCTG                   GTGCAGGGGTT C    TTCT TTCTG
                                |||||||||| |    |||| |||||
                                CACGTCCCCAA G    AGGA GAGAC
                                      A ACAA    G
GAM959  CLCA3    3'  AGTACAATTCTGCTGCTTGA   22259    G        C
                                GG ACAGTTCTGC GCTTGA
                                || |||||||||| ||||||
                                TC TGTTAAGACG CGAACT
                                 A         A
GAM959  CMRF35   5'  TGGGATGGTGCTAGTGGCTC   27437      CA  T   CC_
                                TGGGA  GT CTG   GCTT
                                |||||  || |||   ||||
                                ACCCT  CA GAT   CGAG
                                   AC  C   CAC
GAM959  CRP      3'  TGGGGCAATTCTAATGGCCT   43447      A       CC_
                                TGGG CAGTTCTG   GCTT
                                |||| ||||||||   ||||
                                ACCC GTTAAGAT   CGGA
                                  C       TAC
GAM959  EXTL1    3'  GGGACAGTTCTGTCTC      20870           CCG
                                GGGACAGTTCTG   CTT
                                ||||||||||||   |||
                                CCCTGTCAAGAC   GAG
                                      A__
GAM959  GPR48    3'  TGGGACAGTCCCTTTTTTGGCC 32993           GCCGC   A
              C                   TGGGACAGTTCT     TTG CCC
                                ||||||||||||     ||| |||
                                ACCCTGTCAGGG     AAC GGG
                                      AAAA_   C
GAM959  HSPG2    3'  GGGCAGTTCTGGGCCC      24367     A       CC
                                GGG CAGTTCTG  GCTT
                                ||| ||||||||  ||||
                                CCC GTCAAGAC  CGGG
                                  _       C_
GAM959  ITIH2    5'  GGACAGTTTTGCCAAGCTC    13633         C    __
                                GGACAGTT TGCC  GCTT
                                |||||||| ||||  ||||
                                CCTGTCAA ACGG  CGAG
                                     A    TT
GAM959  P2RX7    3'  TGGGACAGTTTGCTGTGCCT   15001          C   C__
                                TGGGACAGTT TGC   GCTT
                                |||||||||| |||   ||||
                                ACCCTGTCAA ACG   CGGA
                                      _   ACA
GAM960  ADD2     3'  GCCGCTGGTGACCGAC      32728         C    TTGAG
                                GCCGTTGG GACC     GAC
                                |||||||| ||||     |||
```

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                                CGGCGACC CTGG    CTG
                                    A  _____
GAM960  CACNA1A  3'  GCCGCTGGTGGCCGCCCGGCC  35734       CGA  TTGA  A
                                GCCGTTGG  CC   GG CC
                                ||||||||  ||   || ||
                                CGGCGACC  GG   CC GG
                                    ACC  CGGG  _
GAM960  EFNA4    3'  GCCCCCACGTGGCCTTGAGGA  23393    G  G   A__
                                GCC TT GCG  CCTTGAGGA
                                ||| || |||  |||||||||
                                CGG GG TGC  GGAACTCCT
                                  _  G  ACC
GAM960  EGFL4    3'  AGCCGTTGGCGCCGGGC    41556         A  TT A  A
                                AGCCGTTGGCG CC  G GG C
                                |||||||||| ||  | || |
                                TCGGCAACCGC GG  C CC G
                                      _  __ _  _
GAM960  FXYD2    3'  AGGCGTTGGCGATGCCACCTGG 34650    C       C____   A
            GG                    AG CGTTGGCGA    CTTG GG
                                || |||||||||    ||||  ||
                                TC GCAACCGCT    GGAC CC
                                 C       ACGGT   C
GAM960  MUC4     3'  AGCCGTTGCGGCTCAGGAGGAC 39659       G  AC  __
                                AGCCGTTG CG  CTT  GAGGAC
                                |||||||| ||  |||  ||||||
                                TCGGCAAC GC  GAG  CTCCTG
                                    _  C_  TC
GAM960  PGF      3'  GCCGTGGCGGCCCCAGCAGGA  15253      T   A_  TG_
                                GCCGT GGCG  CCT   AGGA
                                ||||| ||||  |||   ||||
                                CGGCA CCGC  GGG   TCCT
                                  _   CG  TCG
GAM960  SORCS2   5'  GTTGGGCGTGAGGACC      34064      _  ACCT
                                GTTGG CG   TGAGGACC
                                |||||  ||   ||||||||
                                CAACC GC   ACTCCTGG
                                  C  ____
GAM960  TRIM37   5'  GCCGCTGGCGACCCGCAGG   31625          TG
                                GCCGTTGGCGACCT  AGG
                                ||||||||||||||  |||
                                CGGCGACCGCTGGG  TCC
                                      CG
GAM960  ATP2B2   5'  AGGCGGCCGACTCCGGGTCCCG 11750        _ GGA  AAC
            GG                    AGGCGGTCG C   GG   CCCGGG
                                |||||||||  |   ||   ||||||
                                TCCGCCGGC G   CC   GGGCCC
                                    T AGG  CA_
GAM960  B3GAT1   5'  AGGGGTCAGGAACCCTGGG   38293    C   GCGG      C
                                AGG GGTC   AGGAACCC GGG
                                ||| ||||   |||||||| |||
```

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                                TCC CCAG   TCCTTGGG CCC
                                  _  ____      A
GAM960  C11orf13  3'  AGGCAGTCGTGGCCTTTGG   18483        C  AGGAA  CC_
                                AGGCGGTCG GG    CC   GG
                                ||||||||| ||    ||   ||
                                TCCGTCAGC CC    GG   CC
                                     A _____  AAA
GAM960  CAPN10   3'  AGGATCTGGGAGGGATCCTGGG 35760   C   GC    AAC  C
                                GG GGTC  GGAGG   CC GGG
                                || ||||  |||||   || |||
                                TC CTAG  CCTCC   GG CCC
                                 _   AC    CTA  A
GAM960  CDKN2B   5'  GGCCGGTCGTTAGCTCCGG   38548    _    CGG  GAACC
                                GGC GGTCG   AG    CCGG
                                ||| |||||   ||    ||||
                                CCG CCAGC   TC    GGCC
                                  G    AA_  GA___
GAM960  EGFL3    3'  GGCAGTACCAGGAGCTCTGGG  41708      C  GG   ACCCC
                                GGCGGT GC  AGGA    GGG
                                |||||| ||  ||||    |||
                                CCGTCA TG  TCCT    CCC
                                   _ G_   CGAGA
GAM960  HR       5'  AGGGGTCGGACTCCG      32908    C   GCGGA   A C
                                AGG GGTC    GGA C CCG
                                ||| ||||    ||| | |||
                                TCC CCAG    CCT G GGC
                                  _   _____  _ A
GAM960  MDM2     5'  AGGGGTCGCGGCCGCCCCTCGG 27811    C      AGGAA  _
           G                     AGG GGTCGCGG    CCC CGGG
                                ||| ||||||||    ||| ||||
                                TCC CCAGCGCC    GGG GCCC
                                  _      GGCG_  A
GAM960  PAX2     5'  GGCGGTCAGCAGAATGGCCCCG 19609       _    GAA
           GG                    GGCGGTC GCGGAG   CCCCGGG
                                ||||||| ||||||   |||||||
                                CCGCCAG CGTCTT   GGGGCCC
                                    T     ACC
GAM960  PDE4A    5'  AGGCTGGGCTTGGGGAGTCCCG 26245     __  CGC  A   AC
           GG                    AGGC  GGT   GG GGA  CCCGGG
                                ||||  |||   || |||  ||||||
                                TCCG  CCG   CC CCT  GGGCCC
                                  AC   AA_  _   CA
GAM960  PDE4D    5'  AGCTGGTGCGGGGCTCTGG   43889    _  C   A  AACCCC
                                GGC GGT GCGG GG     GG
                                ||| ||| |||| ||     ||
                                TCG CCA CGCC CC     CC
                                  A  _   _  GAGA__
GAM960  PPFIA3   3'  GGCGGTGAGGCCCCG      41424       CGCG   AA
                                GGCGGT   GAGG  CCCCG
                                ||||||   ||||  |||||
```

```
                                CCGCCA   CTCC  GGGGC
                                  ____   __
GAM960  RARG    3'  AGGGGTCACAGGGGCCCTGGG  9720     C      A  AA   C
                                AGG GGTCGCGG GG  CCC GGG
                                ||| |||||||| ||  ||| |||
                                TCC CCAGTGTC CC  GGG CCC
                                  _      _ C_   A
GAM960  SERPINE2  5'  GGCGGCCGCGGAGGGCGG    44005           AACCC
                                GGCGGTCGCGGAGG    CGG
                                ||||||||||||||    |||
                                CCGCCGGCGCCTCC    GCC
                                        C____
GAM960  SPI1    5'  GACGGTCGTGGGGCG      17076        C  A  AACCC
                                GGCGGTCG GG GG    CG
                                |||||||| || ||    ||
                                CTGCCAGC CC CC    GC
                                    A  _ _____
GAM960  TNFRSF9   3'  ACGTGTGTTGGGGGAATCCTGG 11449    _ CGC  A   C  C
            G                    GCG GT   GG GGAA CC GGG
                                ||| ||   || |||| || |||
                                TGC CA   CC CCTT GG CCC
                                  A  CAA  C    A  A
GAM960  XPNPEP2   5'  GGTGGGCAGAGGAGCTTTGGG  18155    C  TC      ACCCC
                                GG GG  GCGGAGGA    GGG
                                || ||  ||||||||    |||
                                CC CC  CGTCTCCT    CCC
                                  A  __       CGAAA
GAM960  ZNF264    5'  AGCTGGGACAGAGGAGCCCCGG 18266    _ TC      A
            G                    GGC GG  GCGGAGGA CCCCGGG
                                ||| ||  |||||||| |||||||
                                TCG CC  TGTCTCCT GGGGCCC
                                  A  C_       C
GAM961  ARIX    5'  GCCGGGCCAGGCCGGG     23181     CTC       A
                                GCC   GGGCCAGGCC GG
                                |||   |||||||||| ||
                                CGG   CCCGGTCCGG CC
                                  ___         C
GAM961  ARIX    5'  GCGGGGGCCGGGCCAGGC    23182    CCTC    A
                                GC    GGGCC GGCCAGGC
                                ||    ||||| ||||||||
                                CG    CCCGG CCGGTCCG
                                  CC__     C
GAM961  CST     5'  TGAGACCCTCGGGCTGTGGC   22174     AG       CA_
                                TGA  CCCTCGGGC   GGC
                                |||  |||||||||   |||
                                ACT  GGGAGCCCG   CCG
                                  CT        ACA
GAM961  DNM2    3'  TGGCAGCCGAGGCTGGGCCAGG 22389    A_   CTC    CA
            C                    TG  AGCC   GGGC  GGCCAGGC
                                ||  ||||   ||||  ||||||||
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                                AC  TCGG   TCCG  CCGGTCCG
                                 CG    C__    AC
GAM961  FBLN1    3'  GAGGCCAGATCAGGCCAGGC  27046    A   CTC  GC
                                GA GCC   GG  CAGGCCAGGC
                                || |||   ||  ||||||||||
                                CT CGG   TC  GTCCGGTCCG
                                 C   ___  TA
GAM961  FUT3     3'  TGAGGTTCCCGGCAGCCCAGGC 6642      AG__  TCG   C  G
                                TGA    CCC   GGC AG CCAGGC
                                |||    |||   ||| || ||||||
                                ACT    GGG   CCG TC GGTCCG
                                  CCAA   ___   _ G
GAM961  GYPC     5'  GCCAGGCCGGGCCAGGCCGGGC 32543     C__          A
                                GCC   TCGGGCCAGGCC GGC
                                |||   |||||||||||| |||
                                CGG   GGCCCGGTCCGG CCG
                                  TCC           C
GAM961  KCNJ5    3'  TGAGATTCTTGGGCCAAAAAGC 9443      AGCC  C       CC
                                TGA    CT GGGCCAGG  AGGC
                                |||    || ||||||||  ||||
                                ACT    GA CCCGGTTT  TTCG
                                  CTAA  A       __
GAM961  LU       3'  CGGAGCCTTGTCCCAGGCTGGG 24562    A    CTCGGG     CA
           C                     TG AGCC     CCAGGC  GGC
                                || ||||     ||||||  |||
                                GC TCGG     GGTCCG  CCG
                                 C    AACAG_     AC
GAM961  MARK3    5'  TGAGGCCCTCGGATCGGC    14364     A       CCA
                                TGA GCCCTCGGG   GGC
                                ||| |||||||||   |||
                                ACT CGGGAGCCT   CCG
                                  C        AG_
GAM961  MSF      3'  TGAGCCCTCGGGGAGCCAGGC  44742     A       CCA
                                TGA GCCCTCGGG   GGCCAGGC
                                ||| |||||||||   ||||||||
                                ACT CGGGAGCCC   TCGGTCCG
                                  _        C__
GAM961  MYO1D    3'  GCCGGGCTCCGGGCCAGGC    43497     ___   _
                                GCC   CTC GGGCCAGGC
                                |||   ||| |||||||||
                                CGG   GAG CCCGGTCCG
                                  CCC   G
GAM961  NUP62    3'  TGAGCCTGGGCCAGGC      29606     A   CTC
                                TGA GCC   GGGCCAGGC
                                ||| |||   |||||||||
                                ACT CGG   CCCGGTCCG
                                  _   A__
GAM961  PDE6D    5'  TGGAGACCTCGGGCTAGC    15162    A  C       CA
                                TG AG CCTCGGGC  GGC
                                || || ||||||||  |||
```

```
                                AC TC GGAGCCCG  TCG
                                 C  T      A_
GAM961  PDGFRB   3'  GAAGCCCGGTCAGGCCAGGC   42336       TC  GC
                                GAAGCCC  GG  CAGGCCAGGC
                                |||||||  ||  ||||||||||
                                CTTCGGG  CC  GTCCGGTCCG
                                   __  A_
GAM961  PIM2     3'  GCCAGGCCAGGCCAGGC     41025     CTC
                                GCC   GGGCCAGGCCAGGC
                                |||   ||||||||||||||
                                CGG   TCCGGTCCGGTCCG
                                  ____
GAM961  PPP3R1   5'  TGCGGCCCTCGGGTCGCCGGC  44085    AA       CCAG   A
                                TG  GCCCTCGGGG   GCC GGC
                                ||  |||||||||    ||| |||
                                AC  CGGGAGCCC    CGG CCG
                                 GC        AG__  _
GAM961  PSCD4    3'  ACTCCTCCTCCAGGCCAGGC   30117    _    GGG
                                GC CCTC   CCAGGCCAGGC
                                || ||||   ||||||||||
                                TG GGAG   GGTCCGGTCCG
                                 A   GA_
GAM961  RBM3     5'  GAGGTCCTCTCCGGGCCAGGC  43257    AG_ _  _
                                GA   CC CTC GGGCCAGGC
                                ||   || ||| |||||||||
                                CT   GG GAG CCCGGTCCG
                                 CCA  A   G
GAM961  REST     5'  TGGGGCCCCGGGCCTCGGC   24712    AA   T     A_
                                TG  GCCC CGGGCC  GGC
                                ||  |||| ||||||  |||
                                AC  CGGG GCCCGG  CCG
                                 CC   _     AG
GAM961  SH3BP2   3'  TGAGGCCCTCGGCCTAGAACAG 16642     A       G  _  GC
                                TGA GCCCTCGG CC AG  CAG
                                ||| |||||||| || ||  |||
                                ACT CGGGAGCC GG TC  GTC
                                  C       _  A  TT
GAM961  SIAT1    3'  TGACAGGACAGGGTCAGGCCAG 16723     AGCCCTC   C
           GC                     TGA      GGG CAGGCCAGGC
                                |||      ||| ||||||||||
                                ACT      CCC GTCCGGTCCG
                                  GTCCTGT   A
GAM961  SLC6A8   3'  GAAGCCTGAGCAGGCCAGG   24767       CTC   C
                                GAAGCC   GGGC AGGCCAGG
                                ||||||   |||| ||||||||
                                CTTCGG   CTCG TCCGGTCC
                                   A__   _
GAM961  SLC7A7   3'  TGAAGCTGCCTAGGCCAGGC   19580       __   C
                                TGAAGC  CCT GGGCCAGGC
                                ||||||  ||| |||||||||
```

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                                ACTTCG  GGA TCCGGTCCG
                                   AC  _
GAM961  SYNGR2   3'  TGAAGCCCTCTGGGCACAGGC  21746          _   _
                                TGAAGCCCTC GGGC CAGGC
                                |||||||||| |||| |||||
                                ACTTCGGGAG CCCG GTCCG
                                     A   T
GAM961  TP53BP1  5'  TGGAGACCTCGGGCAGGACCCA 24940    A  C      C  __
          GGC                     TG AG CCTCGGGC AGG  CCAGGC
                                || || |||||||| |||  ||||||
                                AC TC GGAGCCCG TCC  GGTCCG
                                 C  T       _  TG
GAM961  UNC119   3'  GAGGCCCAGCCAGGCCGGGC  38344    A   TCG       A
                                GA GCCC   GGCCAGGCC GGC
                                || ||||   ||||||||| |||
                                CT CGGG   TCGGTCCGG CCG
                                 C   ___       C
GAM961  ZAP70    5'  TGAGGCCCACGGTGGGCCAGGC 43341     A   T   GCCA
                                TGA GCCC CGG    GGCCAGGC
                                ||| |||| |||    ||||||||
                                ACT CGGG GCC    CCGGTCCG
                                  C   T  AC__
GAM961  KPNA3    3'  AGTTGTCAGCCTGTGG      13981     C       CTCGTGC
                                AGT GTCGGCCTG      GG
                                ||| |||||||||      ||
                                TCA CAGTCGGAC      CC
                                  A       A_______
GAM961  PIM1     5'  TCGTGGGGCTCGTGCGGCA   44971     C  CCT
                                TCGT GG   GCTCGTGCGGCA
                                |||| ||   ||||||||||||
                                AGCA CC   CGAGCACGCCGT
                                  C  ___
GAM962  NSF      5'  ACTGTTTGGCTTTGTCAA    41780     A   A
                                ACT TTTG CTTTGTCAA
                                ||| |||| |||||||||
                                TGA AAAC GAAACAGTT
                                  C   C
GAM963  MAP3K7IP1 3'  TGGAATGTTTACAACAGA    25934    A
                                TG AATGTTTACAATAGA
                                || ||||||||||||||
                                AC TTACAAATGTTGTCT
                                 C
GAM963  PPP1R3C  3'  TGAAATATTTACAGTAGAAA   23993          A
                                TGAAATGTTTACA TAGAAA
                                |||||||||||| ||||||
                                ACTTTATAAATGT ATCTTT
                                         C
GAM963  CACNB4   3'  GCCCCTTACTTAGCATAAA    8800          TTAT
                                GCCCCTTACTT    TAAA
                                ||||||||||    ||||
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                                CGGGGAATGAA   ATTT
                                      TCGT
GAM963  DCK     3'  ACTCTTCCCCTTATTTTA   8977      CG     C
                                ACTC  CCCCTTA TTTTA
                                ||||  ||||||| |||||
                                TGAG  GGGGAAT AAAAT
                                  AA     _
GAM963  DRIL1   3'  CCCCTGTTTTATTAAA     23365      TAC
                                CCCCT   TTTTATTAAA
                                |||||   ||||||||||
                                GGGGA   AAAATAATTT
                                  C__
GAM963  FKBP2   5'  ACGCCGCCCTCCCTTATT    20924    T    CTTA
                                AC CCGCCC   CTTTTATT
                                || ||||||   ||||||||
                                TG GGCGGG   GGGAATAA
                                 C    A___
GAM963  HOXB2   3'  ACTTTCCCCTTTTCCTATTATT 13430    CCG    A__  T
           AAA                    ACT   CCCCTT   CT TTATTAAA
                                |||   ||||||  || ||||||||
                                TGA   GGGGAA   GA AATAATTT
                                 AA_    AAG  T
GAM963  HOXB6   3'  CTCCTCTTCTTACTTCTA    40822     GCCC
                                CTCC    CTTACTTTTA
                                ||||    ||||||||||
                                GAGG    GAATGAAGAT
                                  AGAA
GAM963  IL16    3'  ACTCTGCCCTTATTTTA     21092     C   C   C
                                ACTC GCCC TTA TTTTA
                                |||| |||| ||| |||||
                                TGAG CGGG AAT AAAAT
                                  A   _  _
GAM964  GFPT2   3'  GACACAGAGAAACAGTATC   23041       AAT  TA
                                GACACAGA   AC  TATC
                                ||||||||   ||  ||||
                                CTGTGTCT   TG  ATAG
                                     CTT  TC
GAM964  HNRPH2  3'  AGACACAGCTCCTATAT     33330       AAATA
                                AGACACAG    CTATAT
                                ||||||||    ||||||
                                TCTGTGTC    GATATA
                                     GAG__
GAM964  IL17    3'  AAGAGGAGGAAATACTATATCC 13532     CACA
           G                     AAGA   GAAATACTATATCCG
                                ||||   ||||||||||||||
                                TTCT   CTTTATGATATAGGC
                                  CCTC
GAM964  LIPA    3'  TAAGACACAAAATGAATCC   6938          ATACTAT
                                TAAGACACAGAA     ATCC
                                ||||||||||||     ||||
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                                ATTCTGTGTTTT      TAGG
                                      ACT____
GAM964  MAP3K9   3'  GACACAGAAAAGCTCCTATCTC 41354         TA  A_   _
           G                    GACACAGAAA  CT  TATC CG
                                ||||||||||  ||  |||| ||
                                CTGTGTCTTT  GA  ATAG GC
                                      TC  GG    A
GAM964  OLFM1    3'  TAAGACACAGGCATAGCC    26779         AA  _
                                TAAGACACAG  ATA CT
                                ||||||||||  ||| ||
                                ATTCTGTGTC  TAT GG
                                      CG   C
GAM964  CSNK1G3  3'  TAATATGACTTATGAATA    20476          CTT
                                TAGTATGACTTA   GTA
                                ||||||||||||   |||
                                ATTATACTGAAT   TAT
                                      ACT
GAM964  NLGN1    3'  TAGTATACAATTTTTTGTATAA 31388        ACTTAC_
           TAA                    TAGTATG      TTGTATAATAA
                                ||||||||      ||||||||||||
                                ATCATAT      AACATATTATT
                                    GTTAAAA
GAM965  IGFBP7   3'  TTGATGTGTGATCTTTATTTTG 11413       GTAAG   TC
                                TTGATG    GAT  TTATTTTG
                                ||||||    |||  ||||||||
                                AACTAC    CTA  AATAAAAC
                                   ACA__   GA
GAM965  EED      3'  ACAACTCTAAATGCTCTACGTG 19140          ATGAATTA
           CC                     ATAACTCTAAAT       TGCC
                                ||||||||||||       ||||
                                TGTTGAGATTTA       ACGG
                                      CGAGATGC
GAM965  KLHL1    3'  TAACTCTAGTTATTGTATGC   34080        AA   GAAT
                                TAACTCTA  TAT    TATGC
                                ||||||||  |||    |||||
                                ATTGAGAT  ATA    ATACG
                                     CA   AC__
GAM966  CDH6     3'  TGGATGGATTTTACATTACTTT 22333      _   AC__
                                TGGA GGA    ACATTACTTT
                                ||||  |||    ||||||||||
                                ACCT CCT    TGTAATGAAA
                                   A   AAAA
GAM966  CNTNAP2  3'  TTACAGGAAGTGTATTACTTT  30498       T    AACAC
                                TTACA GGAGG     ATTACTTT
                                |||||  |||||    ||||||||
                                AATGT CCTTC     TAATGAAA
                                   _    ACA__
GAM966  SOX11    3'  TTACATGGAGACGGTTACTTT  17044          AACACA
                                TTACATGGAGG     TTACTTT
                                ||||||||||     |||||||
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                                AATGTACCTCT     AATGAAA
                                      GCC___
GAM966  SP100    3'  ATGGAGGAATAAAGTGACTTT  17053         CACATT_
                                ATGGAGGAA      ACTTT
                                |||||||||      |||||
                                TACCTCCTT      TGAAA
                                     ATTTCAC
GAM966  SP4      3'  ATGGAGGAAATACTT       17047          CACAT
                                ATGGAGGAA    TACTT
                                |||||||||    |||||
                                TACCTCCTT    ATGAA
                                     T____
GAM966  TEGT     3'  GGAAAGGGAACACATTACTTT  42098     ___
                                GGA   GGAACACATTACTTT
                                |||   ||||||||||||||
                                CCT   CCTTGTGTAATGAAA
                                  TTC
GAM966  ANKH     3'  GAGGCAGCTGTGTCTTTTGG   38316    A AA  A  C
                                GA G  AG TG GTCTTTTGG
                                || |  || || |||||||||
                                CT C  TC AC CAGAAAACC
                                 _ CG  G  A
GAM966  EGLN3    5'  TCGGAGGGCGCCTTTTGG    35210     A  AAAGAT
                                TCG AG     GCGTCTTTTGG
                                ||| ||     ||||||||||
                                AGC TC     CGCGGAAAACC
                                  C  C_____
GAM966  MKI67    3'  AGAAAGATGTCTGG        14513          CGTCT
                                AGAAAGATG    TTTGG
                                |||||||||    |||||
                                TCTTTCTAC    AGACC
                                     _____
GAM966  PSG5     3'  GAAGAAAAAGCAATTTTGGA   15802         T   TC
                                GAAGAAAGA GCG  TTTTGGA
                                ||||||||| |||  |||||||
                                CTTCTTTTT CGT  AAAACCT
                                     _  T_
GAM966  TDGF1    3'  GAAAAAAGAAGTAGTTTTTTGG 17362          TGC_  C
                                GAAGAAAGA    GT TTTTGG
                                |||||||||    || ||||||
                                CTTTTTTCT    CA AAAACC
                                     TCAT  A
GAM966  TGFB1    5'  TCGGAGAGAGATCCGTCTCCTG 8554      A   A    G
          GA                      TCG AGA AGAT CGTCTTTTGGA
                                ||| ||| |||| ||||||||||
                                AGC TCT TCTA GCAGAGGACCT
                                  C   C    G
GAM966  TOP1     3'  GAGGAAAGATGTGGGAAATGGA 17626     A       CGTCTTT
                                GA GAAAGATG      TGGA
                                || ||||||||      ||||
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                                CT CTTTCTAC      ACCT
                                 C       ACCCTTT
GAM967  COL1A2   3'  TGGGAAAGTGTTTTGAG    6387     CA       C
                                TGG  AAAGTGTTT GAG
                                |||  ||||||||| |||
                                ACC  TTTCACAAA CTC
                                  C_       A
GAM967  DNAJB9   3'  TGGTAAGAATGCAGTAGAAATT 29564    C  A    TTCG
           A                     TGG AA AGTGT    AGAAATTA
                                |||  || |||||    ||||||||
                                ACC TT TTACG    TCTTTAAT
                                  A  C    TCA_
GAM967  PAG      3'  TGGCACTTTTGAGAAATT    32959      AAAGTG   C
                                TGGCA     TTT GAGAAATT
                                |||||     ||| ||||||||
                                ACCGT     AAA CTCTTTAA
                                   GA____   _
GAM967  RFXAP    3'  TGTTAAAAGTGTTTTGAA    8058     GC       C
                                TG  AAAAGTGTTT GAG
                                ||  |||||||||| |||
                                AC  TTTTCACAAA CTT
                                 AA        A
GAM967  BCL11A   3'  CACATGCCAATTATTTGG    39705      A_ G
                                CACAT  C AATTATTTGG
                                |||||  | ||||||||||
                                GTGTA  G TTAATAAACC
                                   CG _
GAM967  LARS2    3'  TCCACATATTGGTTATTTG   31681        CGAA
                                TCCACATA    TTATTTG
                                ||||||||    |||||||
                                AGGTGTAT    AATAAAC
                                     AACC
GAM968  ACADM    5'  ACTCCTCTGGTCCCGCCCACT  6147     _  A  AA_
                                GC CC CT   CCCGCCCACT
                                || || ||   ||||||||||
                                TG GG GA   GGGCGGGTGA
                                 A  A  CCA
GAM968  ACTN4    5'  CGCCCACCAGCCTGTCCGCT   22274         A  CGC  A
                                CGCCCACTA CC   CC CT
                                |||||||| ||   || ||
                                GCGGGTGGT GG   GG GA
                                      C  ACA  C
GAM968  ASCL2    5'  CGCCTGCATCCACCCGCCCGCT 23185      __ _  A      A
                                CGCC  CA CTA CCCGCCC CT
                                ||||  || ||| ||||||| ||
                                GCGG  GT GGT GGGCGGG GA
                                  AC  A  _      C
GAM968  DDB2     3'  CCCTCTGCTACCACCCACT   6460      GCCCA   AC
                                CCC    CTA  CCGCCCACT
                                |||    |||  |||||||||
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                                GGG    GAT  GGTGGGTGA
                                  AGAC_  __
GAM968  EZH1    3'  CGCCTCTAACCCAGACCACT  12782     CA      C_
                                CGCC  CTAACCCG  CCACT
                                ||||  ||||||||  |||||
                                GCGG  GATTGGGT  GGTGA
                                  A_      CT
GAM968  GSTM4   5'  ACCCGCCCCCTCGGCCCCGC  9197        A  AA__
                                ACCCGCCC CT   CCCGC
                                |||||||| ||   |||||
                                TGGGCGGG GA   GGGCG
                                     G  GCCG
GAM968  PHLDA1  5'  CCGCCTCTCGCCGCCCACT  28873     CA  AAC
                                CCGCC  CT   CCGCCCACT
                                |||||  ||   |||||||||
                                GGCGG  GA   GGCGGGTGA
                                  A_  GC_
GAM968  RANBP2L1 5'  CCGCCCACGGAGGCCCACT  37022       TAACCC
                                CCGCCCAC     GCCCACT
                                ||||||||     |||||||
                                GGCGGGTG     CGGGTGA
                                     CCTC__
GAM968  RARG    5'  ACCCGCCCTGCCTGGCCTGCCC 9719        A__  AA  C
          ACT                     ACCCGCCC   CT  CC GCCCACT
                                |||||||   ||  || |||||||
                                TGGGCGGG   GA  GG CGGGTGA
                                     ACG  CC  A
GAM968  ABCD4   3'  AAGTGGAAAGGGAGATGTGGGG 33738     C        AGCA_
          A                      AAG GGAAGGGGAGG    GGA
                                ||| ||||||||||     |||
                                TTC CCTTTCCCTCT    CCT
                                  A         ACACC
GAM968  ABL1    3'  GGAGGAAGGTGCGGGA     23125     AG     A  A
                                GGA  GGGAGG GC GGA
                                |||  |||||| || |||
                                CCT  CCTTCC CG CCT
                                  __     A  C
GAM968  ACHE    3'  GCGGGAGGGGAGGACGG     8563      A       G A
                                GCGG AGGGGAGGA C GG
                                |||| ||||||||| | ||
                                CGCC TCCCCTCCT G CC
                                  C       _ _
GAM968  ACTB    3'  GGAAGGGGGGGGCACGAAG    9925        A  A   G
                                GGAAGGGG GG GCA GAAG
                                |||||||| || ||| ||||
                                CCTTCCCC CC CGT CTTC
                                     _ _   G
GAM968  ADD2    3'  AAGGGAAGGGGAGGAGAG    32720     C          C
                                AAG GGAAGGGGAGGAG AG
                                ||| ||||||||||||| ||
```

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                                TTC CCTTCCCCTCCTC TC
                                  _         _
GAM968  ADRBK1   3'  AGCTGGGAGGGGTAGGAG    11522     _ A    _
                                AGC GG AGGGG AGGAG
                                ||| || ||||| |||||
                                TCG CC TCCCC TCCTC
                                  A C    A
GAM968  AF3P21   3'  GGAGGGGAGGACATGA      32400     A       G G
                                GGA GGGGAGGA CA GA
                                ||| |||||||| || ||
                                CCT CCCCTCCT GT CT
                                  _       _ A
GAM968  ALMS1    5'  GGAGGGGGGGGAGGGA       31533     A   A   CA
                                GGA GGGG GGAG  GGA
                                ||| |||| ||||  |||
                                CCT CCCC CCTC  CCT
                                  C   _   __
GAM968  ALPI     3'  GGCACTGGGGGGGCAGGAAG   11579    AAG_   A  A
                                GG    GGG GG GCAGGAAG
                                ||    ||| || ||||||||
                                CC    CCC CC CGTCCTTC
                                 GTGA  _ _
GAM968  ALS2     3'  GGAAGGGACTCAGGAAG     34095         AGGAG
                                GGAAGGGG    CAGGAAG
                                ||||||||    |||||||
                                CCTTCCCT    GTCCTTC
                                     GA___
GAM968  AP2M1    3'  AAGGGAAGGCAGCAAAGCAGGA 19816     C     _ AG
                                AAG GGAAGG GG  GAGCAGGA
                                ||| |||||| ||  ||||||||
                                TTC CCTTCC TC  TTCGTCCT
                                  _     G  GT
GAM968  AQP6     5'  GCGAAGGGGAGGGGAA      38247     G       AGCA
                                GCG AAGGGGAGG    GGAA
                                ||| |||||||||    ||||
                                CGC TTCCCCTCC    CCTT
                                  _       _____
GAM968  ASB2     3'  AAGTGGAGGGGCACAGGGAAG  32048     C   A   AGGA    _
                                AAG GGA GGGG    GCAGG AAG
                                ||| ||| ||||    ||||| |||
                                TTC CCT CCCC    TGTCC TTC
                                  A   _    G___     C
GAM968  ASPH     3'  AAGCAGGAAGGGGAAGGAG   37132      _       _
                                AAGC GGAAGGGGA GGAG
                                |||| ||||||||| ||||
                                TTCG CCTTCCCCT CCTC
                                  T        T
GAM968  BAZ2A    3'  AGGGAAGCAAAAGGGCAGG   30300    C    G    A
                                AG GGAAG GGAGG GCAGG
                                || ||||| ||||| |||||
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                                TC CCTTC TTTTC CGTCC
                                 _    G    C
GAM968  BCL6    5'  AAGCTGAAGACACATGGGAGTG 39903     G  _______    GAGC
          GGAGG                  AAGC GAAG     GGGAG   AGG
                                ||||  ||||     |||||   |||
                                TTCG CTTC     CCCTC   TCC
                                  A   TGTGTA    ACCC
GAM968  BCL9    3'  AAGCAGAGGGTCACCAGCGGG  20232       A  GAGG_  A
                                AAGCGGA GGG    AGC GG
                                |||||||  |||    |||  ||
                                TTCGTCT CCC    TCG CC
                                   _  AGTGG   C
GAM968  BSN     3'  AGCAGGGGTGGGGTGGGGA   18389      AA__   A  AGCA
                                AGCGG   GGGG GG   GGA
                                |||||   ||||  ||   |||
                                TCGTC   CCCC CC   CCT
                                  CCCA   A  ____
GAM968  BTG2    3'  AAGGGGGAGGGGAGGGTTAGAG 27613    C  A      ___  C
          G                     AAG GG AGGGGAGG   AG AGG
                                |||  ||  ||||||||   ||  |||
                                TTC CC TCCCCTCC   TC TCC
                                  C  C       CAA  _
GAM968  BTG2    3'  AAGGGAAGGGGGGAGGGGA   27612    C      _  AGCA
                                AAG GGAAGGGG AGG   GGA
                                |||  |||||||  |||   |||
                                TTC CCTTCCCC TCC   CCT
                                  _       C  ____
GAM968  C1orf6  3'  GGGAGGGGAGAGGCAGGA   33533    A     GA
                                GG AGGGGAG  GCAGGA
                                ||  |||||||  ||||||
                                CC TCCCCTC  CGTCCT
                                 C      TC
GAM968  CACNA1F 3'  GGAGGGGAGGGCAGGA     23224    A     A
                                GGA GGGGAGG GCAGGA
                                |||  |||||||  ||||||
                                CCT CCCCTCC CGTCCT
                                  _     _
GAM968  CACNG3  5'  AAGGGGAAGGGGAGCGAA   27227    C       _
                                AAG GGAAGGGGAG GAG
                                |||  ||||||||||  |||
                                TTC CCTTCCCCTC CTT
                                  C        G
GAM968  CARP    5'  AAGAGGGAGGGGAGGGACAAG  30792    C  A      AG
                                AAG GG AGGGGAGG  CAGG
                                |||  ||  ||||||||  ||||
                                TTC CC TCCCCTCC  GTTC
                                  T  C       CT
GAM968  CD34    3'  AGAGGAGGGGGTAGGGGAAG  12109    C  A  _  AGCA
                                AG GGA GGGG AGG   GGAAG
                                ||  |||  ||||  |||   |||||
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                                TC CCT CCCC TCC    CCTTC
                                 T   C    A  ____
GAM968  CDS1     5'  GGTAGGAGGAGGAGAAGG    10401    A  _      C
                                GG AGG GGAGGAG AGG
                                || ||| ||||||| |||
                                CC TCC CCTCCTC TCC
                                 A   T      T
GAM968  CLC      3'  AAGTGGTAGGCAAGAAGCAGGA 12268     C  A   G
                                AAG GG AGG GAGGAGCAGGA
                                ||| || ||| ||||||||||
                                TTC CC TCC TTCTTCGTCCT
                                  A  A   G
GAM968  COL1A1   3'  AGTGGAGGGGAGGCCAAG    6363     C   A      AG
                                AG GGA GGGGAGG  CAGG
                                || ||| |||||||  ||||
                                TC CCT CCCCTCC  GTTC
                                 A   _      G_
GAM968  CRHR1    3'  AGAGGAAAAGGAGCAGGA    20433     A GG
                                GGA G  GAGGAGCAGGA
                                ||| |  ||||||||||
                                TCT C  TTCCTCGTCCT
                                  C TT
GAM968  CSF2RB   3'  GCGGGAGGGAAGGCAAG     7569       AA      A
                                GCGG  GGGGAGG GCAGG
                                ||||  ||||||| |||||
                                CGCC  TCCCTTC CGTTC
                                  C_      _
GAM968  CSK      5'  GCGGGGGAAGGGGGCGGGA   20463      AA      A_  A
                                GCGG  GGGGAGG  GC GGA
                                ||||  |||||||  || |||
                                CGCC  CCCTTCC  CG CCT
                                   __      CC  C
GAM968  CSK      5'  GGGAGGGGAGGGGCGCAGG   20467    A       A__
                                GG AGGGGAGG   GCAGG
                                || ||||||||   |||||
                                CC TCCCCTCC   CGTCC
                                 C       CCG
GAM968  CTSK     3'  GGGTGGAGAGAAGCAAAGTAGG 7577     AA          _____
            AAG                   GG  GGGGAGGAGCA    GGAAG
                                ||  ||||||||||    |||||
                                CC  CCTCTCTTCGT    CCTTC
                                 CA         TTCAT
GAM968  CYB561   3'  GGAGGGAGCCCCAGCAGGAAG  12545     AG    G___
                                GGA  GGGAG   AGCAGGAAG
                                |||  |||||   |||||||||
                                CCT  CCCTC   TCGTCCTTC
                                  __    GGGG
GAM968  DACH     5'  AGGGGAAGGGGAAAAAAGG   38869    C          C
                                AG GGAAGGGGAGGAG AGG
                                || ||||||||||||| |||
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                                TC CCTTCCCCTTTTT TCC
                                 C          _
GAM968  DBN1    3' GCGGGGAGGGGGTCCCAGG   38933     AA   A  AG_
                                GCGG  GGGG GG   CAGG
                                ||||  |||| ||   ||||
                                CGCC  TCCC CC   GTCC
                                  CC    _  AGG
GAM968  DCTN1   3' AAGCTGAACGGGGCAGGAA   35694     G   G   AGGA
                                AAGC GAA GGG    GCAGGAA
                                |||| ||| |||    |||||||
                                TTCG CTT CCC    CGTCCTT
                                  A   G  ____
GAM968  DDB1    3' AGAGGAGGGGGAGGGCAG    12558    C   A      A
                                AG GGA GGGGAGG GCAG
                                || ||| ||||||| ||||
                                TC CCT CCCCTCC CGTC
                                 T   C      _
GAM968  DDX3    5' AGGGAAGGGGAGGAGAGGGA  35810    C          CA
                                AG GGAAGGGGAGGAG  GGA
                                || ||||||||||||  |||
                                TC CCTTCCCCTCCTC  CCT
                                 _           TC
GAM968  DDX3    5' AGGGGAGGGGAAGAGGAGG   35811    C  A        C
                                AG GG AGGGGAGGAG AGG
                                || || |||||||||| |||
                                TC CC TCCCCTTCTC TCC
                                 _ C         C
GAM968  DUOX1   3' AAGAGGAGGAGGTATGGGA   32650          CA___
                                AAGGGGAGGAG    GGA
                                ||||||||||     |||
                                TTCTCCTCCTC    CCT
                                      CATAC
GAM968  DUOX2   3' AAGTGGAAGGGGGTACAAG   30442     C       AGGA
                                AAG GGAAGGGG    GCAGG
                                ||| ||||||||    |||||
                                TTC CCTTCCCC    TGTTC
                                  A       CA__
GAM968  EGR3    5' GGGAGGGGGGAGGGAA      40555    A    A   CA
                                GG AGGGG GGAG  GGAA
                                || ||||| ||||  ||||
                                CC TCCCC CCTC  CCTT
                                 C    _   ___
GAM968  EGR4    3' GGAAGAAGAGCGGGGA      12677     AGG      A_
                                GGA   GGAGGAGC  GGA
                                |||   ||||||||  |||
                                CCT   TCTTCTCG  CCT
                                  ____       CC
GAM968  EIF4EBP2 3' AGTGAGGGAGGTAGGGA    19890    AA     _ CA
                                GG  GGGGAGG AG  GGA
                                ||  ||||||| ||  |||
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                                TC  TCCCTCC TC  CCT
                                 AC      A  __
GAM968  EPHB1   3'  AAGGGAGGGGACTCTCAGG   20772    C  A    GGAG
                                AAG GGA GGGGA   CAGG
                                ||| ||| |||||   ||||
                                TTC CCT CCCCT   GTCC
                                  _  _    GAGA
GAM968  FGD1    5'  AGGGGAGGGGAGAGGAGG   20899    C A     G  C
                                AG GG AGGGGAG AG AGG
                                || || ||||||| || |||
                                TC CC TCCCCTC TC TCC
                                 _ C      _ C
GAM968  FOSL1   3'  GGAAGGGGAGGAGACATTGG  24138           _ __
                                GGAAGGGGAGGAG CA  GG
                                |||||||||||| ||  ||
                                CCTTCCCCTCCTC GT  CC
                                         T  AA
GAM968  FXR2    5'  AGCCGGAGGGGGAGCCGCGGG  22157    _  A    GA  A
                                AGC GGA GGGGAG  GC GG
                                ||| ||| ||||||  || ||
                                TCG CCT CCCCTC  CG CC
                                  G  C     GG  C
GAM968  FZD1    3'  GAGGGGGAGGGGGCAAAA   18613    A     A_
                                GA GGGGAGG  GCAGGA
                                || |||||||  ||||||
                                CT CCCCTCC  CGTTTT
                                 C      CC
GAM968  FZD7    3'  GCGGGAGGGGGCAGG      18632     A    AGGA
                                GCGG AGGGG   GCAGG
                                |||| |||||   |||||
                                CGCC TCCCC   CGTCC
                                  C   _____
GAM968  G6PT1   5'  GCGGGAGAGGAGGAGAGG   11163     A       C
                                GCGG AGGGGAGGAG AGG
                                |||| |||||||||| |||
                                CGCC TCTCCTCCTC TCC
                                  C       _
GAM968  GABRE   5'  AGGGGAAGGGGATGAAGGGAAG 35074   C       _   CA
                                AG GGAAGGGGA GGAG  GGAAG
                                || |||||||| ||||  |||||
                                TC CCTTCCCCT CTTC  CCTTC
                                 C       A  __
GAM968  GALNT2  3'  AGAGGAGGGGGAGGGCAG   20999    C  A     A
                                AG GGA GGGGAGG GCAG
                                || ||| ||||||| ||||
                                TC CCT CCCCTCC CGTC
                                 T  C     _
GAM968  GAS1    3'  GCGGGGGAGGAGGTCCAAG   13069     AA     AG
                                GCGG  GGGGAGG  CAGG
                                ||||  |||||||  ||||
```

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                                CGCC  CTCCTCC  GTTC
                                  CC      AG
GAM968  GFI1    3'  GGAGTGGAGGCAAGCAGG    23555    AGG    __
                                GGA   GGAGG  AGCAGG
                                |||   |||||  ||||||
                                CCT   CCTCC  TCGTCC
                                  CA_    GT
GAM968  GGA1    3'  GGGCGGGGCCGGAGCAGGA   30048    AA   A_
                                GG  GGGG  GGAGCAGGA
                                ||  ||||  |||||||||
                                CC  CCCC  CCTCGTCCT
                                 CG   GG
GAM968  GNA15   5'  GGACGGGAGGAGGTGGGGA   40902    AG      CA__
                                GGA  GGGAGGAG   GGA
                                |||  ||||||||   |||
                                CCT  CCCTCCTC   CCT
                                  G_      CACC
GAM968  GNAI2   3'  AAGCGGCGGGGGAACAGG    42644      AAG   A
                                AAGCGG   GGG GGAGCAGG
                                ||||||   ||| ||||||||
                                TTCGCC   CCC CCTTGTCC
                                   G__   _
GAM968  GNLY    5'  AGCAGGGTGCAGGGGGCAGGAA 29805      A____    AGGA
          G                      AGCGG    AGGGG   GCAGGAAG
                                |||||    |||||   ||||||||
                                TCGTC    TCCCC   CGTCCTTC
                                   CCACG    _____
GAM968  GPC1    3'  AGTGGGAGGAGGCGGGGA    13234    _      _ A_
                                AG GGGAGGAG C  GGA
                                || |||||||| |  |||
                                TC CCCTCCTC G  CCT
                                 A       C CC
GAM968  GRB14   5'  GCGGAGGAGGAGGGTGGGGA  21041      A     AGCA
                                GCGGA GGGGAGG   GGA
                                ||||| |||||||   |||
                                CGCCT CTCCTCC   CCT
                                   C      CACC
GAM968  GSR     5'  GGCAGAAGCAGCAGGAA    45408    AAG    G
                                GG   GGGAG AGCAGGAA
                                ||   ||||| ||||||||
                                CC   TCTTC TCGTCCTT
                                 G__    G
GAM968  HAP1    3'  AAGAGGAAGCCAGGGGCAGG  19495    C    GGG   A
                                AAG GGAAG   AGG GCAGG
                                |||  |||||   ||| |||||
                                TTC CCTTC   TCC CGTCC
                                  T    GG_   C
GAM968  HDAC2   5'  AGAGGAGGGGGCGCCGGGAAG  44948    C   A   AGGA  A_
                                AG GGA GGGG   GC  GGAAG
                                || ||| ||||   ||  |||||
```

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                                TC CCT CCCC   CG  CCTTC
                                 T  _   CG__  GC
GAM968  HDAC5   3'  GCAGCGTAGAGGAGCAGGA   40167     AAGG
                                GCGG   GGAGGAGCAGGA
                                ||||   ||||||||||||
                                CGTC   TCTCCTCGTCCT
                                  GCA_
GAM968  HHIP    5'  AAGTGGGAGGAGGAGAAGGA  35400    C  AA       C
                                AAG GG  GGGGAGGAG AGGA
                                ||| ||  ||||||||| ||||
                                TTC CC  CTCCTCCTC TCCT
                                  A __       T
GAM968  HIP12   3'  GCTGGGGTGGGGGGAGCAGGA  42402   _  AA_   A
                                GC GG   GGGG GGAGCAGGA
                                || ||   |||| |||||||||
                                CG CC   CCCC CCTCGTCCT
                                 A  CCA   _
GAM968  HLCS    3'  GGTGGGGGTGGGGACAGGAAG  7645    AA   A_  AG
                                GG  GGGG  GG  CAGGAAG
                                ||  ||||  ||  |||||||
                                CC  CCCC  CC  GTCCTTC
                                 AC    AC  CT
GAM968  HOXA3   3'  AGTGGCCTATCGAGGAGCAGGA 36191    C  AAGGG_
          AG                    AG GG     GAGGAGCAGGAAG
                                || ||     ||||||||||||
                                TC CC     CTCCTCGTCCTTC
                                 A  GGATAG
GAM968  HOXC10  3'  GGGAGGAGGGGCGGGGA    41491    AA     A  A_
                                GG  GGGGAGG GC  GGA
                                ||  ||||||| ||  |||
                                CC  CTCCTCC CG  CCT
                                 __      C  CC
GAM968  HOXC10  3'  GCGGGGAGAGGAAGGAGCGGGA 41490     A_  _       A
          AG                    GCGG  AG GGGAGGAGC GGAAG
                                ||||  || ||||||||| |||||
                                CGCC  TC CCTTCCTCG CCTTC
                                  CC  T       C
GAM968  HR      5'  GGAGCAAAGGGCGGGA     32925    A G    A  A
                                GGA G GGAGG GC GGA
                                ||| | ||||| || |||
                                CCT C TTTCC CG CCT
                                  _ G    _  C
GAM968  IGF2    5'  GCGAGGGGGAGAGAGG     8310     GA    AG   C
                                GCG  AGGGG  GAG AGG
                                |||  |||||  ||| |||
                                CGC  TCCCC  CTC TCC
                                  __    CT   _
GAM968  IL1R1   3'  AAGCTGGAGGACAGGGCAGG  9352      _  A   G   A
                                AAGC GGA GGG AGG GCAGG
                                |||| ||| ||| ||| |||||
```

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                                TTCG CCT CCT TCC CGTCC
                                  A  _  G  _
GAM968  ILF1    5'  GCGGGAGGAGGGGAGGAG   21111     A___
                                GCGG   AGGGGAGGAG
                                ||||   ||||||||||
                                CGCC   TCCCCTCCTC
                                  CTCC
GAM968  INPP1   5'  AAACGGAAGCGGCGGGGAGCAG 13569        G  A__
            GA                    AAGCGGAAG GG   GGAGCAGGA
                                |||||||||  ||   |||||||||
                                TTTGCCTTC CC   CCTCGTCCT
                                     G  GCC
GAM968  INPP5D  3'  GCAGGAGGAGCCAGCAGGA   44420     A    AGG
                                GCGG AGGGG   AGCAGGA
                                |||| |||||   |||||||
                                CGTC TCCTC   TCGTCCT
                                  C    GG_
GAM968  ITGA5   3'  AGTAGACCTAGGAGCAGGA   41495    CG  AGGGG
                                AG  GA    AGGAGCAGGA
                                ||  ||    ||||||||||
                                TC  CT    TCCTCGTCCT
                                 AT  GGA__
GAM968  ITGA7   3'  AAGGGGAAGTTGGGTGGGAGG  13607     C    _______
                                AAG GGAAG     GGGAGG
                                ||| |||||     ||||||
                                TTC CCTTC     CCCTCC
                                  C    AACCCA
GAM968  JPH2    3'  GCAGGAAGTCTATGGCAGGAAG 45378    _    GGGAGGA
                                GC GGAAG      GCAGGAAG
                                || |||||      ||||||||
                                CG CCTTC      CGTCCTTC
                                 T    AGATAC_
GAM968  JUND    3'  AAGGGGAGGGGGGGGACGG    23793     C  A    A  AG A
                                AAG GG AGGGG GG  C GG
                                ||| || ||||| ||  | ||
                                TTC CC TCCCC CC  G CC
                                  _  C    _  CT _
GAM968  JUP     3'  GCGCAGGGTGCAGCAGGAAG   13777     GA   GAGG
                                GCG  AGGG   AGCAGGAAG
                                |||  ||||   |||||||||
                                CGC  TCCC   TCGTCCTTC
                                  G_   ACG_
GAM968  KCNC4   5'  GGAGGGGGAGGAGACGAAG   22530     A       CAG
                                GGA GGGGAGGAG   GAAG
                                ||| |||||||||   ||||
                                CCT CCCCTCCTC   CTTC
                                  C        TG_
GAM968  KCNJ10  3'  AAGTGGAAAGGGGACAGTGGGA 13866     C       A  _  CA
                                AAG GGAAGGGG GG AG  GGA
                                ||| |||||||| || ||  |||
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                                TTC CCTTTCCC CT TC  CCT
                                  A       _ G  AC
GAM968  KCNJ3    5'  GCGGGGGGAGGAAAGG      13845      AA        C
                                GCGG  GGGGAGGAG AGG
                                ||||  ||||||||| |||
                                CGCC  CCCCTCCTT TCC
                                  __        _
GAM968  KCNN3    5'  AGCAGGAGGGGAGCTTGGA   13917       AA   A    A_
                                AGCGG  GGGG GGAGC  GGA
                                |||||  |||| |||||  |||
                                TCGTC  CTCC CCTCG  CCT
                                   __   _    AA
GAM968  KCNN3    5'  GCAGGGAGGGAGAGCAGGA   13920      AA     G
                                GCGG  GGGGAG AGCAGGA
                                ||||  |||||| |||||||
                                CGTC  TCCCTC TCGTCCT
                                  CC     _
GAM968  KIAA0857 3'  GGGAGGGGAAGACAGCAGGAAG 42474     A       __
                                GG AGGGGAGGA  GCAGGAAG
                                || |||||||||  ||||||||
                                CC TCCCCTTCT  CGTCCTTC
                                 C        GT
GAM968  KLF8     3'  AGCAGGGGGGGATGGGAA    28532       AA   A  GCA
                                AGCGG  GGGG GGA   GGAA
                                |||||  |||| |||   ||||
                                TCGTC  CCCC CCT   CCTT
                                   __   _  AC_
GAM968  KLHL3    3'  AGGGGAGGGGAGGATGGGGGA  44638    C  A       GCA_
                                AG GG AGGGGAGGA    GGA
                                || || |||||||||    |||
                                TC CC TCCCCTCCT    CCT
                                 _ C        ACCC
GAM968  KLK13    5'  CGGGAGGGGAGGGCAGG     31811     A       A
                                CGG AGGGGAGG GCAGG
                                ||| |||||||| |||||
                                GCC TCCCCTCC CGTCC
                                  C       _
GAM968  KRT3     3'  AGCGGAGGGGAGGCGCTGGA   38381       A      A  A
                                AGCGGA GGGGAGG GC GGA
                                |||||| ||||||| || |||
                                TCGCCT CCCCTCC CG CCT
                                   _      G  A
GAM968  KRTHB1   3'  GGAAGGGGAGAGGCAGGAAG   14028          GA
                                GGAAGGGGAG  GCAGGAAG
                                ||||||||||  ||||||||
                                CCTTCCCCTC  CGTCCTTC
                                      TC
GAM968  LANGERIN 3'  AGTGGAAGGAGAAGGGA     31843    C         AGCA
                                AG GGAAGGGGAGG    GGA
                                || ||||||||||    |||
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                                TC CCTTCCTCTTC    CCT
                                 A         ____
GAM968  LASS2    5'  ACGGGAGGGGAGGGCGGG    42666      A       A  A
                                GCGG AGGGGAGG GC GG
                                |||| |||||||| || ||
                                TGCC TCCCCTCC CG CC
                                  C       _  C
GAM968  LBX1     3'  GCGGGAGTGGCAGAGGAGG   27284      A  G  A    C
                                GCGG AG GG GGAG AGG
                                |||| || || |||| |||
                                CGCC TC CC TCTC TCC
                                  C  A  G    C
GAM968  LCN1     3'  AGAGGGGGCGCAGGGCAGG   42018      A   ___   A
                                GGA GGGG   AGG GCAGG
                                ||| ||||   ||| |||||
                                TCT CCCC   TCC CGTCC
                                  C    GCG   _
GAM968  LIF      3'  GGATGGGGGTGGAGCAGGA   14150      A    A_
                                GGA GGGG  GGAGCAGGA
                                ||| ||||  |||||||||
                                CCT CCCC  CCTCGTCCT
                                  A    CA
GAM968  LRP4     3'  GGGTGGGAGGAGGAGGA     42064     AAG       C
                                GG   GGGAGGAG AGGA
                                ||   |||||||| ||||
                                CC   CCCTCCTC TCCT
                                 CA_       C
GAM968  LU       3'  AAGGGAGGGCTGGGCAGG    24561     C   A   GA  A
                                AAG GGA GGG  GG GCAGG
                                ||| ||| |||  || |||||
                                TTC CCT CCC  CC CGTCC
                                  _  _   GA  _
GAM968  LYAAT1   3'  AGGGGAGGCAGGTAGGAA    38526         _  C_
                                AGGGGAGG AG  AGGAA
                                |||||||| ||  |||||
                                TCCCCTCC TC  TCCTT
                                     G  CA
GAM968  MAG      3'  GGCAGGAGACCAGGCAGGAAG 38747     A      __  A
                                GG AGGGGA  GG GCAGGAAG
                                || ||||||  || ||||||||
                                CC TCCTCT  TC CGTCCTTC
                                 G     GG  _
GAM968  MAP1B    5'  GCGGCGGAGAGGAGCGGGGA  25395      AA        A_
                                GCGG  GGGGAGGAGC  GGA
                                ||||  ||||||||||  |||
                                CGCC  CCTCTCCTCG  CCT
                                  G_         CC
GAM968  MAP3K12  3'  GAATGGGGTGGGGCAGGAA   26684     A    A  A
                                GGA GGGG GG GCAGGAA
                                ||| |||| || |||||||
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                                CTT CCCC CC CGTCCTT
                                  A   A  C
GAM968  MAPK3   3'  GCGGGTGGGGAGGAGAAG   43844     AA       C
                                GCGG  GGGGAGGAG AGG
                                |||| |||||||| |||
                                CGCC  CCCCTCCTC TTC
                                  CA       _
GAM968  MDFI    3'  GGCAGGCACCAGGAGCAGG   24619    A   GG__
                                GG AGG   AGGAGCAGG
                                || |||   |||||||||
                                CC TCC   TCCTCGTCC
                                 G   GTGG
GAM968  MECP2   3'  GCGGGAGGGGAGGTGCCTGG  22593     A      A  A_
                                GCGG AGGGGAGG GC  GG
                                |||| |||||||| ||  ||
                                CGCC TCCCCTCC CG  CC
                                  C       A  GA
GAM968  MEN1    3'  GCGGCAGGGGAGGCGGG     39185     A      AGCA
                                GCGG AGGGGAGG   GG
                                |||| ||||||||   ||
                                CGCC TCCCCTCC   CC
                                  G       GC__
GAM968  MKPX    5'  AGCGGCGGGGCGGGCGGGGA  33632      AA   A  A  A_
                                AGCGG  GGGG GG GC  GGA
                                ||||| |||| || ||  |||
                                TCGCC  CCCC CC CG  CCT
                                   G_   G  _  CC
GAM968  MMP2    3'  GCAGGGAGGGCTGAGCGGGAAG 21197     AA   AG   A
                                GCGG  GGGG  GAGC GGAAG
                                ||||  ||||  |||| |||||
                                CGTC  TCCC  CTCG CCTTC
                                  CC   GA   C
GAM968  MMP2    3'  GGTTGAAGGGAGGGGCAGG   21202    A__      A
                                GG   AGGGGAGG GCAGG
                                ||   |||||||| |||||
                                CC   TTCCCTCC CGTCC
                                 AAC       C
GAM968  MN1     5'  AGGGAAGGGGGTTGGGAG    14570    C      A___
                                AG GGAAGGGG   GGAG
                                || ||||||||   ||||
                                TC CCTTCCCC   CCTC
                                 _       CAAC
GAM968  MPP2    3'  GGCAGGGGAGGTAGGAGG    40798    A      _  C
                                GG AGGGGAGG AG AGG
                                || |||||||| || |||
                                CC TCCCCTCC TC TCC
                                 G       A  C
GAM968  MTA1L1  3'  GCAGAGGGGGAGGGGAGGGAAG 21889      A      AGCA
                                GCGGA GGGGAGG   GGAAG
                                ||||| |||||||   |||||
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                                CGTCT CCCCTCC   CCTTC
                                  C     CCTC
GAM968  MYO1D   3'  AAGTGGAAGGAGAGAGGAA   43483    C       GAGC
                                AAG GGAAGGGGAG   AGGAA
                                ||| ||||||||||   |||||
                                TTC CCTTCCTCTC   TCCTT
                                  A       _____
GAM968  NEUROD2  5' AGGGGAGGGGAGGGGGGGA   26054   C A     AGCA
                                AG GG AGGGGAGG   GGA
                                || || ||||||||   |||
                                TC CC TCCCCTCC   CCT
                                 _ C      CCC_
GAM968  NEUROD2  5' AGGGGAGGGGGGGGAGGGGG   26055   C  A  A  CA
                                AG GGA GGGG GGAG  GG
                                || ||| |||| ||||  ||
                                TC CCT CCCC CCTC  CC
                                 C  C   _   CC
GAM968  NF2     5'  AGCGGAAAGGGGAGTTGGGG   7064       _    GAGCA
                                AGCGGAA GGGGAG    GG
                                ||||||| ||||||    ||
                                TCGCCTT CCCCTC    CC
                                    T     AACC_
GAM968  NONO    3'  AGCTGGCACAGGAGCAGG    44354    _ AAGGGG
                                AGC GG     AGGAGCAGG
                                ||| ||     |||||||||
                                TCG CC     TCCTCGTCC
                                  A  GTG___
GAM968  NR1I2   3'  AAGAGGAGGGGAACGAGTGGGA 35096    C  A    _  CA
            AG                    AAG GGA GGGGAG GAG  GGAAG
                                ||| ||| |||||| |||  |||||
                                TTC CCT CCCCTT CTC  CCTTC
                                  T  _     G  AC
GAM968  NR4A1   3'  GGAAGGAGGGTAGGAAG    13416       A  AGC
                                GGAAGGGG GG   AGGAAG
                                |||||||| ||   ||||||
                                CCTTCCTC CC   TCCTTC
                                     _  A__
GAM968  NRBP    3'  GGGGGAAGGGACAGGA     30161    AA     AG
                                GG  GGGGAGG  CAGGA
                                ||  |||||||  |||||
                                CC  CCCTTCC  GTCCT
                                 __      CT
GAM968  NRGN    5'  GGGCGGGGAGAAGTGGA    26129    AA      CA
                                GG  GGGGAGGAG  GGA
                                ||  |||||||||  |||
                                CC  CCCCTCTTC  CCT
                                 CG       A_
GAM968  NT5M    3'  AAGGGAAGGGACATGCAGCAGG 33642    C      AGG__
            A                    AAG GGAAGGGG    AGCAGGA
                                ||| ||||||||    |||||||
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                                TTC CCTTCCCT    TCGTCCT
                                  _      GTACG
GAM968  NTRK3    3'  GGAAGGGAGATGTGAGGCAGG  14867       _ ___ GA
                                GGAAGGG GA   G  GCAGG
                                ||||||| ||   |  |||||
                                CCTTCCC CT   C  CGTCC
                                     T  ACA TC
GAM968  NTSR1    3'  AGAGGAGATGGGGGAGGGGTGG 14872    C   A___     AGCA_
           GGA                    AG GGA    GGGGAGG    GGA
                                || |||    |||||||    |||
                                TC CCT    CCCCTCC    CCT
                                 T   CTAC      CCACC
GAM968  NUDT2    5'  AAGCAGAAGGAGGTAGGAG   10112         _ _
                                AAGCGGAAGG GG AGGAG
                                |||||||||| || |||||
                                TTCGTCTTCC CC TCCTC
                                      T  A
GAM968  NYX      3'  AGGGGAAGGGGAGGGGAGGGGA 35442    C        AGCA_
           AG                     AG GGAAGGGGAGG    GGAAG
                                || ||||||||||    |||||
                                TC CCTTCCCCTCC    CCTTC
                                 C         CCTCC
GAM968  OCM      3'  GGAAGGGGGGCTTACAGAA   26190        A  A__
                                GGAAGGGG GG   GCAGGA
                                |||||||| ||   ||||||
                                CCTTCCCC CC   TGTCTT
                                     _  GAA
GAM968  PABPN1   3'  GCAATCTGGAGGGGCAGG    21607     AAGG    A
                                GCGG    GGAGG GCAGG
                                ||||    ||||| |||||
                                CGTT    CCTCC CGTCC
                                  AGA_    C
GAM968  PACSIN1  3'  AGGGGAAGGAGACGAGAGTGGG 45139    C       G   CA__
           A                     AG GGAAGGGGA GAG    GGA
                                || |||||||| |||    |||
                                TC CCTTCCTCT CTC    CCT
                                 C        G   TCAC
GAM968  PACSIN1  3'  AGTGGGAGGGGAGGGGCGGCAG 45143    C  A      A  A  A
                                AG GG AGGGGAGG GC GG AG
                                || || |||||||| || || ||
                                TC CC TCCCCTCC CG CC TC
                                 A  C       C  _  G
GAM968  PACSIN1  3'  AGTGGGAGGGGAGGGGCGG   45142    C  A      A  A
                                AG GG AGGGGAGG GC GG
                                || || |||||||| || ||
                                TC CC TCCCCTCC CG CC
                                 A  C       C  _
GAM968  PAFAH1B1 5'  AGGGGGAGGGGAGGGGA     7698     C  A      AGCA
                                AG GG AGGGGAGG    GGA
                                || || ||||||||    |||
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                                TC CC TCCCCTCC    CCT
                                 C  C       ____
GAM968  PAH      5'  CGGAGGGGAGGGGCTGAGG   7092       A      A __
                                CGGA GGGGAGG GC  AGG
                                |||| ||||||| ||  |||
                                GCCT CCCCTCC CG  TCC
                                  _      C  AC
GAM968  PAK4     3'  CGGGCTGGGAGGAGTGGGA   25249     AAG       CA
                                CGG   GGGAGGAG  GGA
                                |||   ||||||||  |||
                                GCC   CCCTCCTC  CCT
                                  CGA       AC
GAM968  PAX2     3'  GCTGGGAGGGGATGGGAG    19608    _ A     __
                                GC GG AGGGGA  GGAG
                                || || ||||||  ||||
                                CG CC TCCCCT  CCTC
                                 A  C     AC
GAM968  PAX5     3'  GGAGGGATGAGCAGGA      32513     AG    G
                                GGA  GGGA GAGCAGGA
                                |||  |||| ||||||||
                                CCT  CCCT CTCGTCCT
                                  __    A
GAM968  PAX9     3'  GCAGAAGGGTTGGAGGGCAGGA 26205          ___    A
                                GCGGAAGGG   GAGG GCAGGA
                                |||||||||   |||| ||||||
                                CGTCTTCCC   CTCC CGTCCT
                                     AAC    _
GAM968  PCDH7    5'  AGAGGGAGGGGAGGGAGGGGG  37108    C  A       _  CA
                                AG GG AGGGGAGG AG  GG
                                || || |||||||| ||  ||
                                TC CC TCCCCTCC TC  CC
                                 T  C       C  CC
GAM968  PCTK3    3'  AGTGGAGGGTGGGGGCCTGA   43774    C   A   GA  A  AG
                                AG GGA GGG  GG GC  GA
                                || ||| |||  || ||  ||
                                TC CCT CCC  CC CG  CT
                                 A  _   AC  C  GA
GAM968  PDGFB    3'  GGAAGGGGTGGCAGGA      15183         AGGA
                                GGAAGGGG    GCAGGA
                                ||||||||    ||||||
                                CCTTCCCC    CGTCCT
                                     AC__
GAM968  PFN2     3'  AAGGGAGGGGGGGGGCGGG    38160     C   A    A  A  A
                                AAG GGA GGGG GG GC GG
                                ||| ||| |||| || || ||
                                TTC CCT CCCC CC CG CC
                                  _   C    _ _  C
GAM968  PGF      3'  AAGTGTGAGGGGAGATCACGGG 15245     CG_  A      A_  A
                                AAG   GA GGGGAGG  GC GG
                                |||   || |||||||  || ||
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                                TTC   CT CCCCTCT  TG CC
                                  ACA  _      AG  C
GAM968  PKD2L1   5'  AGTGGAAGGAGAAACGGGA   32018    C   AG       A
                                AG GGA  GGGAGGAGC GGA
                                || |||  ||||||||| |||
                                TC CCT  TCCTCTTTG CCT
                                 A   __       C
GAM968  PLD2     3'  GGAGGGGGTTCAAGGGCAGGAA 15381     A   _____  A
          G                      GGA GGGG    AGG GCAGGAAG
                                ||| ||||    ||| ||||||||
                                CCT CCCC    TCC CGTCCTTC
                                  C    AAGT   _
GAM968  PML      5'  AAGCTGAAGGGGAGGCGTGA   37720      G        AGCAG
                                AAGC GAAGGGGAGG     GA
                                |||| ||||||||||     ||
                                TTCG CTTCCCCTCC     CT
                                  A         GCA__
GAM968  POMZP3   5'  CGGAGAAGAGGAGTGGGGA    29239      A       CA_
                                CGGA GGGGAGGAG   GGA
                                |||| |||||||||   |||
                                GCCT CTTCTCCTC   CCT
                                  _        ACC
GAM968  POU2AF1  3'  GGAGGGAGGGGAAGGAA     26370     AG     AGC
                                GGA  GGGAGG   AGGAA
                                |||  ||||||   |||||
                                CCT  CCCTCC   TCCTT
                                  __      CCT
GAM968  PRKACA   3'  AAGTGGGAGAGGGGGCAGGA   15571     C  A    A  A
                                AAG GG AGGGG GG GCAGGA
                                ||| || ||||| || ||||||
                                TTC CC TCTCC CC CGTCCT
                                  A  C    _ _
GAM968  PRKCM    5'  CGGGAGGGGAGGGCGAGGA   15640     A       A  _
                                CGG AGGGGAGG GC AGGA
                                ||| |||||||| || ||||
                                GCC TCCCCTCC CG TCCT
                                  C        _ C
GAM968  PSMB2    3'  GGAGGGCGGAGCAGGAAG    15821     A   GA
                                GGA GGG  GGAGCAGGAAG
                                ||| |||  ||||||||||||
                                CCT CCC  CCTCGTCCTTC
                                  _   G_
GAM968  PTEN     5'  GCGGGAGGCGAGCGAGAGG   7217      A   G   _   C
                                GCGG AGG GAG GAG AGG
                                |||| ||| ||| ||| |||
                                CGCC TCC CTC CTC TCC
                                  C   G   G   _
GAM968  PTGFRN   3'  AACCGGCTGTGGGGGAGCAGG  42578    G   AAG_   A
                                AA CGG    GGG GGAGCAGG
                                || |||    ||| ||||||||
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                                TT GCC    CCC CCTCGTCC
                                 G   GACA  _
GAM968  PTK2B    3'  AGAGAAAGAGGGGCAGGAAG   19915     AG     A
                                GGA  GGGAGG GCAGGAAG
                                |||  |||||| ||||||||
                                TCT  TTCTCC CGTCCTTC
                                  CT     C
GAM968  PTPRG    5'  AAGGGGAGGGGAGAGGCAGG   15930     C  A      GA
                                AAG GG AGGGGAG  GCAGG
                                ||| || |||||||  |||||
                                TTC CC TCCCCTC  CGTCC
                                  _ C      TC
GAM968  PTPRG    5'  AGGGGAAGGGGAGGGGA     15931    C          AGCA
                                AG GGAAGGGGAGG    GGA
                                || ||||||||||    |||
                                TC CCTTCCCCTCC    CCT
                                 C          _____
GAM968  PYCR1    3'  GGAGGTCAGGAGCAGGA     43124     A  GG
                                GGA GG  AGGAGCAGGA
                                |||  ||  ||||||||||
                                CCT CC  TCCTCGTCCT
                                  _ AG
GAM968  RAB3A    3'  GCGGGGGGGGGGGTTCAGGA   16066      AA    A  AG
                                GCGG  GGGG GG  CAGGA
                                ||||  |||| ||  |||||
                                CGCC  CCCC CC  GTCCT
                                   CC    _  AA
GAM968  RAB5C    3'  AAGGGGAGGAAGTGGGAA    40803           CA_
                                AAGGGGAGGAG   GGAA
                                ||||||||||   ||||
                                TTCCCCTCCTT   CCTT
                                       CAC
GAM968  RAB6A    5'  AGCGGAAGGGCGGGCA      16097          GA  A
                                AGCGGAAGGG  GG GCA
                                ||||||||||  || |||
                                TCGCCTTCCC  CC CGT
                                      G_  _
GAM968  RAD23B   3'  AGGGAAGGGGAAAAGACAGG   16133    C          _
                                AG GGAAGGGGAGGAG CAGG
                                || ||||||||||||| ||||
                                TC CCTTCCCCTTTTC GTCC
                                 _           T
GAM968  RGS9     3'  GGAGGGAGGGTCAGGAA     19263     AG     AG
                                GGA  GGGAGG  CAGGAA
                                |||  ||||||  ||||||
                                CCT  CCCTCC  GTCCTT
                                  __      CA
GAM968  RORB     5'  GGAAGGGCAGCAGCAGGA    27922        G  G
                                GGAAGGG AG AGCAGGA
                                ||||||| || |||||||
```

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                                CCTTCCC TC TCGTCCT
                                    G  G
GAM968  RXRB     3'  GGGGGGGGCGGCGGGAAG    35044    AA   A  A_  A
                                GG  GGGG GG  GC GGAAG
                                ||  |||| ||  || |||||
                                CC  CCCC CC  CG CCTTC
                                 __   _  GC  C
GAM968  SAA4     3'  GAGAGCAGAGGAGCAGGAA   27138   GA  G
                                G  AG GGAGGAGCAGGAA
                                |  || ||||||||||||
                                C  TC TCTCCTCGTCCTT
                                 TC  G
GAM968  SALL1    3'  GCGGGGTGGGGGGCAAGGA   16457     AAG   A  A  _
                                GCGG   GGG GG GCA GGA
                                ||||   ||| || ||| |||
                                CGCC   CCC CC CGT CCT
                                   CCA  _ _  T
GAM968  SCAMP2   3'  GGCTGAGGGGGGAGAGAA    25032    AA_   A   C
                                GG   GGGG GGAG AGGA
                                ||   |||| |||| ||||
                                CC   TCCC CCTC TCTT
                                 GAC   _   _
GAM968  SIGLEC6  5'  AGTGGAGGGGAAGGACTGCGGG 40929    C   A      __  A_
            GA                    AG GGA GGGGAGGA  GC  GGA
                                || ||| ||||||||  ||  |||
                                TC CCT CCCTTCCT  CG  CCT
                                 A  C       GA  CC
GAM968  SIX3     5'  GGAGGGGGGAGCAGGA     24025     A   A
                                GGA GGGG GGAGCAGGA
                                ||| |||| |||||||||
                                CCT CCCC CCTCGTCCT
                                  _   _
GAM968  SIX3     3'  GCGGAGGGGAAGGAGTGGG   24023      A       CA
                                GCGGA GGGGAGGAG  GG
                                ||||| |||||||||  ||
                                CGCCT CCCTTCCTC  CC
                                   C       AC
GAM968  SLC19A2  5'  GCGCGAGGGGAGGGGACCCGG  42889     GA      A_  A_
                                GCG  AGGGGAGG  GC  GG
                                |||  ||||||||  ||  ||
                                CGC  TCCCCTCC  TG  CC
                                  GC       CC  GG
GAM968  SLC20A1  5'  GCGGAGCGGGAGACGAGG    40451      AG     AGC
                                GCGGA  GGGAGG   AGG
                                |||||  ||||||   |||
                                CGCCT  CCCTCT   TCC
                                   CG     GC_
GAM968  SLC22A1L 5'  AAGCAGGAGGCTGGCGGAGCAG 14981       A   __  A
            G                     AAGCGG AGG  GG GGAGCAGG
                                ||||||  |||  ||  ||||||||
```

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                                TTCGTC TCC  CC CCTCGTCC
                                   C   GA  G
GAM968  SLC4A2   3' GGAGGGAGGGGCATGGGA    16774     AG     A  __
                                GGA  GGGAGG GCA  GGA
                                |||  |||||| |||  |||
                                CCT  CCCTCC CGT  CCT
                                  __     C   AC
GAM968  SLC6A3   3' AGCCGGGAGCAGGGAGCAGG   9806     _ A  G  A
                                AGC GG AG GG GGAGCAGG
                                ||| || || || ||||||||
                                TCG CC TC TC CCTCGTCC
                                  G  C  G  _
GAM968  SLC9A5   3' AAGTGGCAGGGGTTAGGAGCAG 21381     C  A    __
             G                   AAG GG AGGGG  AGGAGCAGG
                                ||| || |||||  |||||||||
                                TTC CC TCCCC  TCCTCGTCC
                                  A  G    AA
GAM968  SLC9A5   3' AAGGGAAGGGGCTAAAGCAGGA 40758     C       A_
             AG                  AAG GGAAGGGG  GGAGCAGGAAG
                                ||| ||||||||  ||||||||||
                                TTC CCTTCCCC  TTTCGTCCTTC
                                  _       GA
GAM968  SMARCD1  3' AAGGGAAGCTGGGGGTGGGAAG 40078     C    __  A  AGCA
                                AAG GGAAG  GGG GG    GGAAG
                                ||| |||||  ||| ||    |||||
                                TTC CCTTC  CCC CC    CCTTC
                                  _    GA   _  AC__
GAM968  SMARCD1  3' AAGGGAGGGAAAATGGCAGGAA 40079     C  A      A_
             G                   AAG GGA GGGGAGG  GCAGGAAG
                                ||| ||| |||||||  ||||||||
                                TTC CCT CCCTTTT  CGTCCTTC
                                  _  _      AC
GAM968  SMCX     3' GAGAGGGAGAAGGGGGTAGGAA 20070     AG       C____
             G                   GA  GGGAGGAG    AGGAAG
                                ||  ||||||||    ||||||
                                CT  CCCTCTTC    TCCTTC
                                  CT       CCCCA
GAM968  SNL      3' GCGGAGGGGAGAGTGGGGA    16942       A      AGCA
                                GCGGA GGGGAGG    GGA
                                |||||| |||||||   |||
                                CGCCT CCCCTCT    CCT
                                   _      CACC
GAM968  SORBS1   3' AAGTGGAGGGGAGGGGAA    31701     C   A      AGCA
                                AAG GGA GGGGAGG    GGAA
                                ||| ||| |||||||    ||||
                                TTC CCT CCCCTCC    CCTT
                                  A  _      _____
GAM968  SORCS2   3' AGAGGAGGGGGAGGAGGGA   34043    C   A       CA
                                AG GGA GGGGAGGAG  GGA
                                || ||| |||||||||  |||
```

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                                TC CCT CCCCTCCTC  CCT
                                 T  C       __
GAM968  SOX11    3'  GGGTGGGGAGAAGAGGCAGG  17030    AA      ___
                                GG  GGGGAGGA  GCAGG
                                ||  ||||||||  |||||
                                CC  CCCCTCTT  CGTCC
                                 CA       CTC
GAM968  SOX11    3'  AAGCGGGAGGGGAGGCGGGAAG 16999       A      AGCA
                                AAGCGG AGGGGAGG   GGAAG
                                ||||||| ||||||||   |||||
                                TTCGCC TCCCCTCC   CCTTC
                                   C       GC__
GAM968  SRGAP2   3'  AAGCAGAGGGCAGTGGGAA   43971       A  G  GAGCA
                                AAGCGGA GGG AG    GGAA
                                ||||||| ||| ||    ||||
                                TTCGTCT CCC TC    CCTT
                                   _  G  AC___
GAM968  STK11    3'  GCGGGCGGAACCGGCAGGAAG  7835      AA   AGGA
                                GCGG  GGGG   GCAGGAAG
                                ||||  ||||   ||||||||
                                CGCC  CCTT   CGTCCTTC
                                  CG   GGC_
GAM968  SYN2     5'  GCGGAAGGCGAGATTGAGG   39460       G   AGC
                                GCGGAAGG GAGG   AGG
                                |||||||| ||||   |||
                                CGCCTTCC CTCT   TCC
                                     G   AAC
GAM968  TAF12    3'  CGGAAGTTGGGGTAGGAG    24867      ___   _
                                CGGAA   GGGG AGGAG
                                |||||   |||| |||||
                                GCCTT   CCCC TCCTC
                                   CAA   A
GAM968  TAF4     3'  AGCGGGGTGGGAGGGGAAGGGA 17254      AAG     AGCA_
           AG                    AGCGG   GGGAGG    GGAAG
                                |||||   ||||||    |||||
                                TCGCC   CCCTCC    CCTTC
                                  CCA     CCTTC
GAM968  TAF4     3'  AGGGGAGGGGAGGGCAGG    17255    C  A      A
                                AG GG AGGGGAGG GCAGG
                                || || |||||||| |||||
                                TC CC TCCCCTCC CGTCC
                                 _  C       _
GAM968  TAF4     3'  AGTGGAGGGGAAGGGA     17257    C   A     AGCA
                                AG GGA GGGGAGG   GGA
                                || ||| |||||||   |||
                                TC CCT CCCCTTC   CCT
                                 A  _     _____
GAM968  TAP2     3'  AGGGGAAGGGGCTGGGGAAG  8078     C      A_  AGCA
                                AG GGAAGGGG  GG   GGAAG
                                || ||||||||  ||   |||||
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                                TC CCTTCCCC  CC    CCTTC
                                 C       GA  ____
GAM968  TBL1X    3'  AGCGCAAGGGGAGGAGAGG   24870      G         C
                                AGCG AAGGGGAGGAG AGG
                                |||| |||||||||| |||
                                TCGC TTCCCCTCCTC TCC
                                  G         _
GAM968  TBL1X    3'  GGTGGGAGAGGGCGGAA     24896     AA      A  A
                                GG  GGGGAGG GC GGAA
                                ||  ||||||| || ||||
                                CC  CCTCTCC CG CCTT
                                 AC      _ _
GAM968  TBR1     3'  AGGGGGAGGGGAATGTAGGA   27311    C  A      GAGC
                                AG GG AGGGGAG    AGGA
                                || || |||||||    ||||
                                TC CC TCCCCTT    TCCT
                                 C  C       ACA_
GAM968  TCF1     3'  AGCTGGAAGGAGTTGGGGCAGG 8086      _       A_  A
           AAG                    AGC GGAAGGGG  GG GCAGGAAG
                                ||| ||||||||  || ||||||||
                                TCG CCTTCCTC  CC CGTCCTTC
                                  A       AA  C
GAM968  TCF8     3'  AAACGGGAGGTGCAGCAGGAAG 36228     G     ___
                                GAA GGGAGG   AGCAGGAAG
                                ||| ||||||   |||||||||
                                TTT CCCTCC   TCGTCCTTC
                                  G      ACG
GAM968  TEGT     3'  GAGGGGAACCCCAGGAAG    42096    A     GAG
                                GA GGGGAG   CAGGAAG
                                || ||||||   |||||||
                                CT CCCCTT   GTCCTTC
                                 _     GGG
GAM968  TEM1     3'  GCTGGGCCTGGGGAGCAGGAAG 33794    _ AAGG  A
                                GC GG    GG GGAGCAGGAAG
                                || ||    || ||||||||||
                                CG CC    CC CCTCGTCCTTC
                                 A  CGGA  _
GAM968  TEM7     3'  AGCTGAGGGTGGAGTAGG    33798     G  A   GA   C
                                AGC GA GGG  GGAG AGG
                                ||| || |||  |||| |||
                                TCG CT CCC  CCTC TCC
                                  A  _   A_    A
GAM968  TFAP2A   3'  GCGGGGCGGGAGGAGAG     17397      AAG       C
                                GCGG   GGGAGGAG AG
                                ||||   |||||||| ||
                                CGCC   CCCTCCTC TC
                                  CCG       _
GAM968  TIAM1    3'  GCAGAGTTAGGGCAGGAAG    17526       AG GG   A
                                GCGGA  G  AGG GCAGGAAG
                                |||||  |  ||| ||||||||
```

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                                CGTCT  C  TCC CGTCCTTC
                                   __ AA  _
GAM968  TIMP3    3'  AAGGGAAGCTCAGCGGGAA   7438        G__  A
                                AAGGGGAG  AGC GGAA
                                ||||||||  ||| ||||
                                TTCCCTTC  TCG CCTT
                                    GAG  C
GAM968  TK1      3'  AGGCGGCAGTGGCAGGAA    17548    _ _ GA
                                AGG GG AG  GCAGGAA
                                ||| || ||  |||||||
                                TCC CC TC  CGTCCTT
                                  G  G  AC
GAM968  TLX1     5'  AAGTAGAAGGGGGAGGGGA   24329    CG     _  AGCA
                                AAG  GAAGGGG AGG   GGA
                                |||  ||||||| |||   |||
                                TTC  CTTCCCC TCC   CCT
                                  AT      C  _____
GAM968  TLX1     5'  GGGGAGGGGGAGAGGAA    24344    AA   A   C
                                GG  GGGG GGAG AGGAA
                                ||  |||| |||| |||||
                                CC  TCCC CCTC TCCTT
                                 CC   _   _
GAM968  TMPRSS4  3'  GGTGGGCAGGGCAGGAA    33393    AA  G  A
                                GG  GGG AGG GCAGGAA
                                ||  ||| ||| |||||||
                                CC  CCC TCC CGTCCTT
                                 A_  G  _
GAM968  TP63     3'  AAGAGGAAGGGGAGGAGCTAGG 18988    C          _
                                AAG GGAAGGGGAGGAGC AGG
                                ||| |||||||||||||| |||
                                TTC CCTTCCCCTCCTCG TCC
                                  T           A
GAM968  TPM2     5'  GCGAGGAGGACGGAGCGGGA  17644     AA   _   A
                                GCGG  GGGGA GGAGC GGA
                                ||||  ||||| ||||| |||
                                CGCT  CTCCT CCTCG CCT
                                  C_    G   C
GAM968  TRAF1    3'  GGTGGGGCCTCTAGGCAGGAAG 24944    AA   AGGA___
                                GG  GGGG     GCAGGAAG
                                ||  ||||     ||||||||
                                CC  CCCC     CGTCCTTC
                                 A_   GGAGATC
GAM968  TSLP     5'  AGTGAAAGGGGAGGGGAGGAAG 39693    C        AGC
                                AG GGAAGGGGAGG   AGGAAG
                                || ||||||||||   ||||||
                                TC CTTTCCCCTCC   TCCTTC
                                 A         CC_
GAM968  UBE2V1   3'  GCGGGAGTGGAGGAGCGTGG  35346     A  G      A_
                                GCGG AG GGAGGAGC  GG
                                |||| || ||||||||  ||
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                                CGCC TC CCTCCTCG  CC
                                  C  A       CA
GAM968  UBL5     3'  AGAGGAAAGCGGGGCAGGAAG  35872    C     GGA  A
                                AG GGAAGG   GG GCAGGAAG
                                || |||||||  || ||||||||
                                TC CCTTTC   CC CGTCCTTC
                                 T     GC_ _
GAM968  USP5     3'  AAGGGGGAGGGGAGGCACAGG  18500     C  A      A
                                AAG GG AGGGGAGG GCAGG
                                ||| || |||||||| |||||
                                TTC CC TCCCCTCC TGTCC
                                  C  C       G
GAM968  WNT5A    5'  GCGGGAGGGAAGGGCAGG    18120      A       A
                                GCGG AGGGGAGG GCAGG
                                |||| |||||||| |||||
                                CGCC TCCCTTCC CGTCC
                                  C       _
GAM968  WNT7A    5'  AGCGGGAGGAGGGAGGGA    21520      A    A   CA
                                AGCGG AGGGG GGAG  GGA
                                ||||| ||||| ||||  |||
                                TCGCC TCCTC CCTC  CCT
                                  C    _   __
GAM968  ZIC1     5'  AAGTGGGTGGGGGGGGTGAA   18222     C  AA   A  AGCAG
                                AAG GG  GGGG GG    GAA
                                ||| ||  |||| ||    |||
                                TTC CC  CCCC CC    CTT
                                  A  CA   _  CA___
GAM968  ZIC3     5'  AGCAGGGAGGGGGGTGTTGGCGG 18242      AA   A  A____  A
          G                      AGCGG  GGGG GG    GC GG
                                |||||  |||| ||    || ||
                                TCGTC  TCCC CC    CG CC
                                  CC   _  ACAAC  C
GAM968  ZNF148   5'  AGGGGAAGGGGGGGAGGGGG   35022    C       A   CA
                                AG GGAAGGGG GGAG  GG
                                || |||||||| ||||  ||
                                TC CCTTCCCC CCTC  CC
                                 C       _   CC
GAM968  ZNF216   5'  AAGTGGGAGGAGGGAAGCGAGG 25648    C  A    A   _
                                AAG GG AGGGG GGAGC AGG
                                ||| || ||||| ||||| |||
                                TTC CC TCCTC CTTCG TCC
                                  A  C    C    C
GAM968  ZNF216   5'  AAGCGAGGGGGGGGCCGAGG   25647     GA    A  A __
                                AAGCG  AGGGG GG GC  AGG
                                |||||  ||||| || ||  |||
                                TTCGC  TCCCC CC CG  TCC
                                   __    _ _ GC
GAM969  CNGB3    3'  CTGGGTGTTAGCAATGGGAT   33306     ___      C
                                CTGG   TTAGCAA GGGAT
                                ||||   ||||||| |||||
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                                GACC   AATCGTT CCCTA
                                  CAC      A
GAM969  DPYSL2   3'  GCAGGTGGTTAGCACCAG    10753     C       A
                                GCAG TGGTTAGCA CGG
                                |||| ||||||||| |||
                                CGTC ACCAATCGT GTC
                                  C       G
GAM969  EIF2C1   3'  GCCAGCTAACAGTGGGAT    29179    TG     AC
                                GC  GTTAGCA  GGGAT
                                ||  |||||||  |||||
                                CG  CGATTGT  CCCTA
                                 GT      CA
GAM969  TRPV1    3'  CAGCAGCCCCCCGTGGCAACGG 38793        GG  A__
          G                      CAGCAGCT  TT   GCAACGGG
                                ||||||||  ||   ||||||||
                                GTCGTCGG  GG   CGTTGCCC
                                    GG  CAC
GAM969  TSLP     5'  GCAGCCGGCGGTGGGAT     39697         TAGCAAC
                                GCAGCTGGT      GGGAT
                                |||||||||      |||||
                                CGTCGGCCG      CCCTA
                                    CCA____
GAM969  ASGR2    3'  TACAATGAATTACAGA      38956        GCTG
                                TACAATGA    TGCAGG
                                ||||||||    ||||||
                                ATGTTACT    ATGTCT
                                    TA__
GAM969  B4GALT4  3'  ACAATGAGCTGTAACAGG    19097           _
                                ACAATGAGCTGTG CAGG
                                |||||||||||| ||||
                                TGTTACTCGACAT GTCC
                                       T
GAM969  BCL11A   3'  TACAATAAAAAGCCAGG     39719         CT  G
                                TACAATGAG  GT CAGG
                                |||||||||  || ||||
                                ATGTTATTT  CG GTCC
                                    TT  _
GAM969  CAD      3'  TACAGGTTTAAGGTGCAGG   20294      A___   CT
                                TACA   TGAG  GTGCAGG
                                ||||   ||||  |||||||
                                ATGT   ATTC  CACGTCC
                                  CCAA   __
GAM969  COL19A1  3'  TACAGAGCTGAGGCAGG     12379      AT     T_
                                TACA  GAGCTG  GCAGG
                                ||||  ||||||  |||||
                                ATGT  CTCGAC  CGTCC
                                  __     TC
GAM969  CRHR2    3'  ACAGGGGAGCTGTGCAGG    12439     AT_
                                ACA   GAGCTGTGCAGG
                                |||   ||||||||||||
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                                TGT   CTCGACACGTCC
                                  CCC
GAM969  DCX     5'  TACAATGACTATGAAGG     8143         G    C
                                TACAATGA CTGTG AGG
                                |||||||| ||||| |||
                                ATGTTACT GATAC TCC
                                     _    T
GAM969  DDX10   3'  TACAGTAAGCAAGACAGG    20575      A    TGT
                                TACA TGAGC   GCAGG
                                |||| |||||   |||||
                                ATGT ATTCG   TGTCC
                                  C    TTC
GAM969  DLEC1   3'  CACACTTAGCTGTGCAGG    28816      ATG
                                TACA   AGCTGTGCAGG
                                ||||   ||||||||||
                                GTGT   TCGACACGTCC
                                  GAA
GAM969  DNAJB1  3'  TACAATGAGTCTAAAGG     26033         _  TGC
                                TACAATGAG CTG   AGG
                                ||||||||| |||   |||
                                ATGTTACTC GAT   TCC
                                     A   T__
GAM969  DTNB    3'  TACATGCAGGGCTGTGCAGGC  34868      A  A___        III
                                TACA TG    GCTGTGCAGG   C
                                |||| ||    ||||||||||   |
                                ATGT AC    CGACACGTCC   G
                                  _ GTCC         III
GAM969  F11     5'  TGAATGAGCTTGTGTAGG    6553    C      _  C
                                A AATGAGCT GTG AGG
                                | |||||||| ||| |||
                                A TTACTCGA CAC TCC
                                 C       A   A
GAM969  GSPT1   3'  CACAGTATTGTGCAGG      13305      A  AGC
                                TACA TG   TGTGCAGG
                                |||| ||   ||||||||
                                GTGT AT   ACACGTCC
                                  C  A__
GAM969  GYG     3'  TACAGGGTGCCACTGCAGG    19969      ATGA   _
                                TACA    GCTG TGCAGG
                                ||||    |||| ||||||
                                ATGT    CGGT ACGTCC
                                  CCCA    G
GAM969  GYPB    3'  TACAGGCAGCATGCAGG     13323      ATG   T
                                TACA   AGC GTGCAGG
                                ||||   ||| |||||||
                                ATGT   TCG TACGTCC
                                  CCG   _
GAM969  HRH1    3'  TACAATGAGTCTGAGG      9255          _  TGC
                                TACAATGAG CTG   AGG
                                ||||||||| |||   |||
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                                ATGTTACTC GAC   TCC
                                     A  ___
GAM969  IGBP1    3'  TACAGAGCTGAAGCAGG     11390     AT     T_
                                TACA  GAGCTG  GCAGG
                                ||||  ||||||  |||||
                                ATGT  CTCGAC  CGTCC
                                  __     TT
GAM969  KIAA0857 3'  ACAATGAGAGTGAGCAGG    42462        C_  T
                                ACAATGAG  TG GCAGG
                                ||||||||  || |||||
                                TGTTACTC  AC CGTCC
                                     TC  T
GAM969  KRT4     3'  CACAGTGAGCTGCAGG      14001      A     GT
                                TACA TGAGCT  GCAGG
                                |||| ||||||  |||||
                                GTGT ACTCGA  CGTCC
                                  C     __
GAM969  MATN1    3'  TACGGCGGACACGTGCAGG    14368     AA  AG _
                                TAC  TG  C TGTGCAGG
                                |||  ||  | ||||||||
                                ATG  GC  G GCACGTCC
                                  CC  CT T
GAM969  MNT      3'  ATGAGGTATCTGTGCAGG     33703      ____
                                ATGAG    CTGTGCAGG
                                |||||    |||||||||
                                TACTC    GACACGTCC
                                   CATA
GAM969  MXI1     3'  CACAGTGGGACTGTGAGG     39012      A  A_     C
                                TACA TG  GCTGTG AGG
                                |||| ||  |||||| |||
                                GTGT AC  TGACAC TCC
                                  C  CC     _
GAM969  NCOA6    5'  TACAATGAGCCGAGATGG     30440           TGCA
                                TACAATGAGCTG    GG
                                ||||||||||||    ||
                                ATGTTACTCGGC    CC
                                       TCTA
GAM969  NPAT     3'  TACAATGAAAGTGCAGG      42617         CT
                                TACAATGAG  GTGCAGG
                                |||||||||  |||||||
                                ATGTTACTT  CACGTCC
                                     T_
GAM969  P2RY1    3'  TACGATAATATATGCAGG     15009     A    GC
                                TAC ATGA  TGTGCAGG
                                ||| ||||  ||||||||
                                ATG TATT  ATACGTCC
                                  C    AT
GAM969  P4HB     3'  CACAATGAGCCCACGACAGG   9543          _ TG  _
                                TACAATGAG C  TG CAGG
                                |||||||||  |  || ||||
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                                GTGTTACTC G  GC GTCC
                                     G GT  T
GAM969  RAB5C    3'  TACAGAAAGGTGCAGG      40808      AT   CT
                                TACA  GAG  GTGCAGG
                                ||||  |||  |||||||
                                ATGT  TTC  CACGTCC
                                  CT  __
GAM969  RAP1B    3'  TACAATAAGCTACAAG      31823          GT
                                TACAATGAGCT  GCAGG
                                ||||||||||  |||||
                                ATGTTATTCGA  TGTTC
                                          __
GAM969  SERPINI1 3'  CACAATGACATAACAGG     22721        G TGT
                                TACAATGA C   GCAGG
                                ||||||||  |  |||||
                                GTGTTACT G   TGTCC
                                     _ TAT
GAM969  SLC24A1  3'  CACAATGAGCTGCAGG      21815          GT
                                TACAATGAGCT  GCAGG
                                ||||||||||  |||||
                                GTGTTACTCGA  CGTCC
                                          __
GAM969  STK10    3'  CACAGGAGCCTGTGCGGG     25614      AT   _    A
                                TACA  GAGC TGTGC GG
                                ||||  |||| ||||| ||
                                GTGT  CTCG ACACG CC
                                  C_   G    C
GAM969  SURF5    3'  ACAGCTGCTCTGTGCAGG     39498     A_  AG
                                ACA  TG  CTGTGCAGG
                                |||  ||  |||||||||
                                TGT  AC  GACACGTCC
                                  CG  GA
GAM969  TLR2     5'  CACAATGAGCCCCACAGG     17558          G
                                TACAATGAGCT TGCAGG
                                ||||||||||| ||||||
                                GTGTTACTCGG GTGTCC
                                       G
GAM969  TNFRSF11A 3'  TACAATGAACACACACTGG    19279          _  TG A
                                TACAATGAGC TG  C GG
                                |||||||||| ||  | ||
                                ATGTTACTTG GT  G CC
                                      T  GT A
GAM969  VLDLR    3'  TACAATGTATGTACAGG      43008        AGC
                                TACAATG   TGTGCAGG
                                |||||||   ||||||||
                                ATGTTAC   ACATGTCC
                                    AT_
GAM969  WHSC1    3'  TACAATGATGGCAGG        39377        GC  T
                                TACAATGA  TG GCAGG
                                ||||||||  || |||||
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                                ATGTTACT  AC CGTCC
                                   __  _
GAM969  ZNF216   3'  TACAATAAGCTTCAAAGG    25659          GTGC
                                TACAATGAGCT    AGG
                                ||||||||||    |||
                                ATGTTATTCGA    TCC
                                      AGTT
GAM970  PDK4     3'  TAGCATAAAGACAAAAACA   45545      C   AT
                                TAGCA AAA  CAAAAACA
                                ||||| |||  ||||||||
                                ATCGT TTT  GTTTTTGT
                                   A   CT
GAM970  SORBS1   3'  GCACAGGCATTGAAAACAAAT 31707       AA_  CA
                                GCACA   AT  AAAACAAAT
                                |||||   ||  |||||||||
                                CGTGT   TA  TTTTGTTTA
                                   CCG  AC
GAM970  ADAM11   3'  TGCGGAGCCAGGAGTTGAA   14390    TA   A  TTT
                                TG  GAG CT   GAGTTGAA
                                ||  ||| ||   ||||||||
                                AC  CTC GG   CTCAACTT
                                 GC   _  TC_
GAM970  ARF4L    3'  TGGGGAGACTCCCCAGTTG   43078    TA       G
                                TG  GAGACTTTT AGTTG
                                ||  ||||||||| |||||
                                AC  CTCTGAGGG TCAAC
                                 CC        G
GAM970  ASPH     3'  TGTAGAAATTTTTGATAAGAA  37146        C     GTT
                                TGTAGAGA TTTTGA   GAA
                                ||||||||| ||||||   |||
                                ACATCTTT AAAACT   CTT
                                     A     ATT
GAM970  CDKN2C   5'  GAGCGCTTTTTGAGTTGAAAAA 38562     AC__
                                GAG    TTTTGAGTTGAAAAA
                                |||    ||||||||||||||||
                                CTC    AAAACTCAACTTTTT
                                  GCGA
GAM970  EXTL2    3'  TGTAGAGACTTCTGGAGTAGA  11022            _   T
                                TGTAGAGACTTTTG AGT GA
                                |||||||||||||| ||| ||
                                ACATCTCTGAAGAC TCA CT
                                       C   T
GAM970  GPR84    3'  TGGAGAGACTTGATTTG     33780    T      TT   G
                                TG AGAGACT  TGA TTG
                                || |||||||  ||| |||
                                AC TCTCTGA  ACT AAC
                                 C      __  A
GAM970  IGF1     3'  GAACTCTTTTGAGTTGAA    8339      A_
                                GAG  CTTTTGAGTTGAA
                                |||  ||||||||||||
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                                CTT  GAAAACTCAACTT
                                  GA
GAM970  MYO1A    3'  TGCAGAGAGGCTGCGGGTTG  23923        CT  _  A
                                TGTAGAGA  TT TG GTTG
                                ||||||||  || || ||||
                                ACGTCTCT  GA GC CAAC
                                     CC  C  C
GAM970  PRDM16   3'  TAGGGACTTTTGGGATCTGA  35247     A       AG__
                                TAG GACTTTTG    TTGA
                                ||| ||||||||    ||||
                                ATC CTGAAAAC    GACT
                                  C       CCTA
GAM970  STCH     3'  TAGAGACTTTCTTTTGTGGAAA 28080          GA__  T
           A                     TAGAGACTTTT    GT GAAAA
                                ||||||||||    || |||||
                                ATCTCTGAAAG    CA CTTTT
                                       AAAA  C
GAM970  YWHAZ    3'  TGTAGAGAAAGTAGTTGAAAA  18205        CTTTTG
                                TGTAGAGA     AGTTGAAAA
                                ||||||||     |||||||||
                                ACATCTCT     TCAACTTTT
                                     TTCA__
GAM971  BLTR2    5'  TCAGGGCTCTCACCGGGCT   33372     ATAA       TTTTT
                                TCA   CTCTCACT    GCT
                                |||   ||||||||    |||
                                AGT   GAGAGTGG    CGA
                                  CCC_       CC___
GAM971  CYP2B6   3'  TCGATAATCTCACTCCT     8923     A   C
                                TC ATAA TCTCACTTTT
                                || |||| ||||||||||
                                AG TATT AGAGTGAGGA
                                 C   _
GAM971  HMGCR    3'  TCAATAACTCTGCTGACCCCCT 9237           CA  TT   G
                                TCAATAACTCT  CT  TTT CT
                                ||||||||||  ||  ||| ||
                                AGTTATTGAGA  GA  GGG GA
                                       C_  CT   G
GAM971  RIMS1    3'  TCAGTGACTCTCACCAGCATG  43737     ATA       TTTT
                                TCA   ACTCTCACT    TG
                                |||   |||||||||    ||
                                AGT   TGAGAGTGG    AC
                                  CAC        TCGT
GAM971  SORCS1   3'  TCAGTAACTCTCCTCCTTTA  38101     A       A
                                TCA TAACTCTC CTTTTTTG
                                ||| |||||||| ||||||||
                                AGT ATTGAGAG GAGGAAAT
                                  C       _
GAM971  TACC1    3'  TCAGAACTTTCACTCCCACTA  26600     AT    C     TT TG
                                TCA  AACT TCACTT  T  CTA
                                |||  |||| ||||||  |  |||
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                                AGT  TTGA AGTGAG  G  GAT
                                  C_    A      __ GT
GAM971  ABCB9    5'  AGCAGGCTCGGGTCTGG     33351         AACAAT
                                GGCAGGCTC     GTCTGG
                                |||||||||     ||||||
                                TCGTCCGAG     CAGACC
                                     CC_____
GAM971  ADORA2A  5'  AGGCAGGCTCAGCACGGA    8598           ACAAT  C
                                AGGCAGGCTCA    GT TGGA
                                ||||||||||    || ||||
                                TCCGTCCGAGT    CG GCCT
                                      ______ T
GAM971  ALDH3B1  3'  AGGCAGGCGCGATGGTGGGAG  45057         TCAACA   TCT
                                AGGCAGGC     ATG   GGAG
                                ||||||||     |||   ||||
                                TCCGTCCG     TAC   CCTC
                                     CGC___   CAC
GAM971  ANK1     3'  AGGCAGGATTGAAGCCTGGAG  33849        CTCAACAAT
                                AGGCAGG       GTCTGGAG
                                |||||||       ||||||||
                                TCCGTCC       CGGACCTC
                                    TAACTT___
GAM971  ARNT2    3'  GGCAAGCTCAAGCCTGCTGGAG 31361           CAA  T
                                GGCAGGCTCAA   TG CTGGAG
                                ||||||||||   || ||||||
                                CCGTTCGAGTT   AC GACCTC
                                      CGG  _
GAM971  BAK1     5'  GGTGGCTCAGCAGGGTGGAG   45109    CA     A  ATGTC
                                GG  GGCTCA CA     TGGAG
                                ||  |||||| ||     |||||
                                CC  CCGAGT GT     ACCTC
                                 A_     C  CCC__
GAM971  CLCN6    3'  GGCGGGCCAGCCTGG       34718     A   T  ACAAT
                                GGC GGC CA     GTCTGG
                                ||| ||| ||     ||||||
                                CCG CCG GT     CGGACC
                                  C   _ ______
GAM971  COX10    5'  AGGAGAGCGTGGTGTCTGGAG  10546     CA   TCAACAA
                                AGG  GGC      TGTCTGGAG
                                |||  |||      |||||||||
                                TCC  TCG      ACAGACCTC
                                  TC   CACC___
GAM971  DDX11    3'  GGCAGGATGTTGTCTGGA    36178       CTCAACAA
                                GGCAGG       TGTCTGGA
                                ||||||       ||||||||
                                CCGTCC       ACAGACCT
                                   TACA_____
GAM971  DLEC1    3'  AGCAGGCCATGTTTGG       28843         CAACA   C
                                GGCAGGCT     ATGT TGG
                                ||||||||     |||| |||
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                                TCGTCCGG    TACA ACC
                                      _____   A
GAM971  DYSF    3'  AGGCAGGCCAGTCCCATGCTGG 18579        CAACA_  T
          AG                    AGGCAGGCT    ATG CTGGAG
                                |||||||||    ||| ||||||
                                TCCGTCCGG    TAC GACCTC
                                     TCAGGG  _
GAM971  EGR3    3'  AGGCAGGCTCAGCGATGG   40538         ACAAT  C_
                                AGGCAGGCTCA   GT  TGG
                                ||||||||||    ||  |||
                                TCCGTCCGAGT   CG  ACC
                                      _____ CT
GAM971  ELF3    5'  AGGCAGGCCGGCAGGCGGGAG 20749        CAA  AT  CT
                                AGGCAGGCT   CA  GT  GGAG
                                |||||||||   ||  ||  ||||
                                TCCGTCCGG   GT  CG  CCTC
                                     CC_  C_  C_
GAM971  GALR1   5'  GGTGGGTTCGGGAGCCCGGAG 11206    CA  C  AACAAT
                                GG  GG TC    GTCTGGAG
                                ||  || ||    ||||||||
                                CC  CC AG    CGGGCCTC
                                 AC  A  CCCT__
GAM971  HPCA    3'  AGGCAGGCTGGCTTTCTGG   13420        CAACAATG
                                AGGCAGGCT      TCTGG
                                |||||||||      |||||
                                TCCGTCCGA      AGACC
                                     CCGAA___
GAM971  ITGA1   3'  GGCAGGCTGAGCACTGG    41850        CAA  ATGT
                                GGCAGGCT   CA   CTGG
                                ||||||||   ||   ||||
                                CCGTCCGA   GT   GACC
                                    CTC  ____
GAM971  LTA     3'  AGGCAGGCTTGAAATCCTCAG  8237         CAACAAT   GG
                                AGGCAGGCT     GTCT  AG
                                |||||||||     ||||  ||
                                TCCGTCCGA     TAGG  TC
                                     ACTT___   AG
GAM971  MGAT1   3'  AGGCAGGCCGATGCAGCCTGG  14422        CAACAAT
                                AGGCAGGCT     GTCTGG
                                |||||||||     ||||||
                                TCCGTCCGG     CGGACC
                                     CTACGT_
GAM971  NORE1   3'  GGCAGGCTGCAGCTTCTCTGGA 36430        _  ACAATG
          G                     GGCAGGCT CA     TCTGGAG
                                ||||||||  ||    |||||||
                                CCGTCCGA GT     AGACCTC
                                     C  CGAAG_
GAM971  ODF2    5'  GGCAGGCTTGTCAATGA    14931        CAACAA   TG_
                                GGCAGGCT     TGTC   GA
                                ||||||||     ||||   ||
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                                CCGTCCGA     ACAG   CT
                                       _______   TTA
GAM971   PAX5     3'  AGGCAGGCTGGGCTGG      32507         CAACAAT T
                                AGGCAGGCT      G CTGG
                                |||||||||      | ||||
                                TCCGTCCGA      C GACC
                                     CC_____ _
GAM971   PTGIS    3'  GGCAGGCTGGGCAGAG      9674          CAACAAT TC
                                GGCAGGCT      G  TGGAG
                                ||||||||      |  |||||
                                CCGTCCGA      C  GTCTC
                                       ________ CC
GAM971   PTMS     3'  GGAGGGCGCAGTGTCTGGAG   15891    CA   T  ACAA
                                GG  GGC CA    TGTCTGGAG
                                ||  ||| ||    |||||||||
                                CC  CCG GT    ACAGACCTC
                                  TC   C  C___
GAM971   PYCR1    5'  GGCCAGGTCCATGTCTGG     43126     _   CT  ACAA
                                GGC AGG  CA    TGTCTGG
                                ||| |||  ||    |||||||
                                CCG TCC  GT    ACAGACC
                                  G   AG  _____
GAM971   SNRPA    3'  CAGGTGCAATGTCTGG      21400      CTCAA
                                CAGG     CAATGTCTGG
                                ||||     ||||||||||
                                GTCC     GTTACAGACC
                                   AC___
GAM971   SURF4    3'  AGGCAGGCTCGGGGCTGG    37651          AACAAT T
                                AGGCAGGCTC      G CTGG
                                ||||||||||      | ||||
                                TCCGTCCGAG      C GACC
                                     CCC____ _
GAM971   TCL1A    3'  GGCCAGGCTCAGGCCCTGG    35027     _      ACAATG
                                GGC AGGCTCA      TCTGG
                                ||| |||||||      |||||
                                CCG TCCGAGT      GGACC
                                  G      CCG___
GAM971   USH3A    5'  GGCAGGCTGAGTAAATGGGG   38158         CAAC_   TCT
                                GGCAGGCT     AATG   GG
                                ||||||||     ||||   ||
                                CCGTCCGA     TTAC   CC
                                     CTCAT    C__
GAM972   MBNL     3'  TGTAAAGTTAAATTGGCCATT  34327           A   TT
                                TGTAAAGTTAAA TTG  CCGTT
                                |||||||||||| |||  |||||
                                ACATTTCAATTT AAC  GGTAA
                                       _   C_
GAM972   SNCA     3'  TGTAGGGTTAATGTTCCATT   28660      AA    AAT
                                TGTA  GTTAA   TGTTCCGTT
                                ||||  |||||   |||||||||
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                                ACAT  CAATT   ACAAGGTAA
                                  CC    ___
GAM973  ADAM19   3'  TCTCCACAGCAAGGATGAC   37779     T     T_
                                TCTC CACAGCA  GATGAC
                                |||| |||||||  ||||||
                                AGAG GTGTCGT  CTACTG
                                  _      TC
GAM973  DLG5     5'  TCTCCCACAGCAAGGGAC    44467          TGAT
                                TCTCTCACAGCA   GAC
                                ||||||||||||   |||
                                AGAGGGTGTCGT   CTG
                                       TCC_
GAM973  GJA1     3'  TCTCTCACATTAATGAC     6731         GCA
                                TCTCTCACA   TGATGAC
                                |||||||||   |||||||
                                AGAGAGTGT   ATTACTG
                                     A__
GAM973  NFE2     5'  TCTTTCCAAGATGATGAC    26083    C  A   C
                                TCT TC CAG ATGATGAC
                                ||| || ||| ||||||||
                                AGA AG GTT TACTACTG
                                  A  _   C
GAM973  P23      3'  CCTCTCACAGGCTGGGGTGA   27338        CA  A__
                                TCTCTCACAG  TG   TGA
                                ||||||||||  ||   |||
                                GGAGAGTGTC  AC   ACT
                                     CG  CCC
GAM973  PFC      5'  TCTCTAACATAATGAC      15227      CAC
                                TCTCT   AGCATGATGAC
                                |||||   ||||||||||
                                AGAGA   TTGTATTACTG
                                  ___
GAM973  PIGC     3'  TCTCTTACCACAATGAC     15283      C  AG  TG
                                TCTCT AC  CA  ATGAC
                                ||||| ||  ||  |||||
                                AGAGA TG  GT  TACTG
                                   A  __  GT
GAM973  PLGL     3'  TCCCTCACAGACACAGAC    15392          _  _
                                TCTCTCACAG CAT GAT
                                |||||||||| ||| |||
                                AGGGAGTGTC GTG CTG
                                     T   T
GAM973  RARB     5'  TCCCTCACAGGCGCTGAC    32062          _ A_
                                TCTCTCACAG C  TGAT
                                |||||||||| |  ||||
                                AGGGAGTGTC G  ACTG
                                     C CG
GAM973  RP42     3'  TCTCTCACAGACACAGAC    33995          _  _
                                TCTCTCACAG CAT GAT
                                |||||||||| ||| |||
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                                AGAGAGTGTC GTG CTG
                                      T  T
GAM973  STXBP1   3'  CTCTTACAAACACGATGA    17205     C  _
                                CTCT ACAG CATGATGA
                                |||| |||| ||||||||
                                GAGA TGTT GTGCTACT
                                  A   T
GAM973  TRIM34   5'  TCTCTCCATGATGA       38976       ACAG
                                TCTCTC   CATGATGA
                                ||||||   ||||||||
                                AGAGAG   GTACTACT
                                   ____
GAM973  CDKN1B   3'  TCATGCAAGTCAAATATT    19803       GAC     C
                                TCATGCG  AGTCAAA ATT
                                |||||||  ||||||| |||
                                AGTACGT  TCAGTTT TAA
                                   ___     A
GAM973  FGF2     3'  GCCATCACAAACAGTTAAACAT 12840    T  _      C
           T                     GC CAT GCGGACAGT AAACATT
                                || ||| ||||||||| |||||||
                                CG GTA TGTTTGTCA TTTGTAA
                                 _  G       A
GAM973  GPR56    3'  GCTTGTGCAGTAGACAAACATT 25001     CA    AC  T
                                GCT  TGCGG  AG CAAACATT
                                |||  |||||  || ||||||||
                                CGA  ACGTC  TC GTTTGTAA
                                  AC    A_  T
GAM973  PITX2    3'  TCATATCCAGTCAAACATT    7253       CGGA
                                TCATG   CAGTCAAACATT
                                |||||   ||||||||||||
                                AGTAT   GTCAGTTTGTAA
                                   AG__
GAM974  POU2AF1  3'  ATTAAAATTAAACCTAATG   26364       CTAC
                                ATTAGA   AAACCTAATG
                                ||||||   ||||||||||
                                TAATTT   TTTGGATTAC
                                   TAA_
GAM974  CD9      3'  TACAAATGTCAATATTGAA    12098       TTTAA
                                TACAAGT    CAATATTGAA
                                |||||||    ||||||||||
                                ATGTTTA    GTTATAACTT
                                    CA___
GAM974  DTR      3'  TACAAGTTGTAACAGTTCAGAA 12615        T    ATATT
                                TACAAGTT TAACA    GAA
                                |||||||| |||||    |||
                                ATGTTCAA ATTGT    CTT
                                     C    CAAGT
GAM974  KCNA4    3'  TACAAGTTTAGTAACAAT    13800         __
                                TACAAGTTT  TAACAAT
                                |||||||||  |||||||
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                                ATGTTCAAA  ATTGTTA
                                     TC
GAM975  NOX1    3'  TCAAACCTGACGAGACC    30337       T  AAA
                                TCAAACCT GAC   ACC
                                |||||||| |||   |||
                                AGTTTGGA CTG   TGG
                                     _  CTC
GAM975  DGKG    3'  GCCGCCTCTAAGCAAACATGT  10655    _    TCCA
                                GCC CCTTT    AAACATGT
                                ||| |||||    ||||||||
                                CGG GGAGA    TTTGTACA
                                  C    TTCG
GAM975  MYO10   3'  TCCCCTCCTTTTTTAAGGCATG 29576    G  _     CC  AA
          T                      TC CC CCTTTT  AA  CATGT
                                || || ||||||  ||  |||||
                                AG GG GGAAAA  TT  GTACA
                                 G  A     AA  CC
GAM976  CRP     5'  ATGTATTCGGCTGAAAGTTCAG 43442        AGATTCGTT
          G                     ATGTATTC       TTCAGG
                                ||||||||       ||||||
                                TACATAAG       AAGTCC
                                     CCGACTTTC
GAM976  IVD     3'  TGTTTCAGATTTCA       13698     A       CGTTT
                                TGT TTCAGATT    TCA
                                ||| ||||||||    |||
                                ACA AAGTCTAA    AGT
                                _      _____
GAM976  PMP2    3'  TGTATTCAGTTTTGTCAATGG  15425        A  C   TTCA
                                TGTATTCAG TT GTT    GG
                                ||||||||| || |||    ||
                                ACATAAGTC AA CAG    CC
                                     A  A   TTA_
GAM977  DPYSL2  3'  TCTGCGGTTCCACGTGTGA   10758      AA   __    C
                                TCTGC  TTCC  GTGT GA
                                |||||  ||||  |||| ||
                                AGACG  AAGG  CACA CT
                                   CC    TG   _
GAM977  DSC1    3'  CTGCAATTCTTTCATG     22390        CGTG  G
                                CTGCAATTC    TC ATG
                                |||||||||    || |||
                                GACGTTAAG    AG TAC
                                     AA__  _
GAM977  HNRPK   5'  TCTGCAATGCTGTCGCCTG   36317       TCCG    A_
                                TCTGCAAT    TGTCG  TG
                                ||||||||    |||||  ||
                                AGACGTTA    ACAGC  AC
                                     CG__     GG
GAM977  LENG4   3'  TCTGCAATATTGGTGCGATGA  35890        TCC_   T
                                TCTGCAAT    GTG CGATGA
                                ||||||||    ||| ||||||
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                                AGACGTTA   CAC GCTACT
                                    TAAC  _
GAM977  MMP1    3'  TGCAACTCTGGCCTATATGA  14543       CGT  G__
                                TGCAATTC  GTC  ATGA
                                ||||||||  |||  ||||
                                ACGTTGAG  CGG  TACT
                                    AC_  ATA
GAM977  SHOC2   3'  TCTGCAACTTTCAGGAATGA  28898       CCGTGTC
                                TCTGCAATT     GATGA
                                |||||||||     |||||
                                AGACGTTGA     TTACT
                                    AAGTCC_
GAM977  TBL2    3'  GCAATGCCAATGTCGATGA  37408     T  _
                                GCAAT CCG TGTCGATGA
                                ||||| ||| |||||||||
                                CGTTA GGT ACAGCTACT
                                  C  T
GAM977  ZNF236  3'  TCTGCAATTATGTAACCCTG  28867       CC  TCGA
                                TCTGCAATT  GTG  TG
                                |||||||||  |||  ||
                                AGACGTTAA  CAT  AC
                                    TA  TGGG
GAM978  AGL     3'  GTATGTATTGTTACTGAA   8489      ATCTC
                                GTGTG   GTTACTGAA
                                |||||   |||||||||
                                CATAC   CAATGACTT
                                  ATAA_
GAM978  CDY1    3'  AATTGTGTGTCTCTGA    21713       A  GTTAC
                                AATTGTGTG TCTC   TGA
                                ||||||||| ||||   |||
                                TTAACACAC AGAG   ACT
                                    _  _____
GAM978  DMXL1   3'  TGTGAAGAAATTACTGAAA  24293     TCTC
                                TGTGA  GTTACTGAAA
                                |||||  ||||||||||
                                ACACT  TAATGACTTT
                                  TCTT
GAM978  DNMT2   3'  TGTGATTGTTTACTGAAA   20633     CTCG
                                TGTGAT  TTACTGAAA
                                ||||||  |||||||||
                                ACACTA  AATGACTTT
                                   ACA_
GAM978  ZFHX1B  3'  AATTGTGTGGTTACT     31336       ATCTC
                                AATTGTGTG   GTTACT
                                |||||||||   ||||||
                                TTAACACAC   CAATGA
                                    _____
GAM978  NEU1    5'  TTTAAAGCGCAGATGTCA   7732         A  A
                                TTTAAAGCGCA AT TCA
                                |||||||||| || |||
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                                AAATTTCGCGT TA AGT
                                      C  C
GAM979  FGF7     3'  TCCATAGTTAGTGTGGCTTGAT 12863       AATCTACGAA
              T                   TCCATG        GCTTGATT
                                  ||||||        ||||||||
                                  AGGTAT        CGAACTAA
                                     CAATCACAC_
GAM979  PRKY     3'  CATGAATCTGCGGATCTT    15689         A  AAG
                                  CATGAATCT CG   CTT
                                  ||||||||| ||   |||
                                  GTACTTAGA GC   GAA
                                       C  CTA
GAM979  ARHG     5'  GCTTCCAAGTTCCCAGGCT   44115         A    _
                                  GCTTCCAA TTCCT GGCT
                                  |||||||| ||||| ||||
                                  CGAAGGTT AAGGG CCGA
                                       C    T
GAM979  ATP2A2   3'  GGCTTCCAAGTTCTTAGATAA  11745         A  C  C
                                  GGCTTCCAA TTC TGG TAA
                                  ||||||||| ||| ||| |||
                                  CCGAAGGTT AAG ATC ATT
                                       C  A  T
GAM979  B4GALT7  3'  TGGTTTCTGAAGTCCTAACC   28552     C  CA  T
                                  TGG TTC  AA TCCTGGCT
                                  ||| |||  || ||||||||
                                  ACC AAG  TT AGGATTGG
                                    A  AC  C
GAM979  CACNA1E  3'  TGGCTTCCCAATTCTGTCT   8772         A    C  G
                                  TGGCTTCC AATTC TG CT
                                  |||||||| ||||| || ||
                                  ACCGAAGG TTAAG AC GA
                                       G    _  A
GAM979  CAMK4    3'  TGGCTTCCAGATCTGAAGGAAG 11951         A  CCT____
              CT                    TGGCTTCCA ATT      GGCT
                                    ||||||||| |||      ||||
                                    ACCGAAGGT TAG      TCGA
                                         C  ACTTCCT
GAM979  CLASP2   3'  TGGTTCCAAATTATCTAA    42083     C       CCTGG
                                  TGG TTCCAAATT    CTAA
                                  ||| |||||||||    ||||
                                  ACC AAGGTTTAA    GATT
                                    _       TA___
GAM979  EZH1     3'  TGGCATTTCAAATAGACCTAAC 12789     _  C    T__
              T                    TGGC TT CAAAT   CCTGGCT
                                   |||| || |||||   |||||||
                                   ACCG AA GTTTA   GGATTGA
                                     T  A    TCT
GAM979  SDC1     3'  TGGCTTCCAGATTTGG      16513         A  CC
                                  TGGCTTCCA ATT  TGG
                                  ||||||||| |||  |||
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                                ACCGAAGGT TAA  ACC
                                     C  __
GAM979  SLC4A5   5'  TGGCTTCCAGATTGTTTGTGCC 39433        A  CC_ _
            AA                    TGGCTTCCA ATT  TG GCTAA
                                |||||||||  |||  || |||||
                                ACCGAAGGT TAA  AC CGGTT
                                     C  CAA  A
GAM979  SORBS1   3'  GGCATTTCTGGCTAA      31708     TTCCAA  C
                                GGC     ATT CTGGCTAA
                                |||     ||| ||||||||
                                CCG     TAA GACCGATT
                                 _______  A
GAM979  TAF1C    3'  TGGCTCCAAATTGCTTGGCT  24993      T     C  _
                                TGGCT CCAAATT CT GGCT
                                ||||| ||||||| || ||||
                                ACCGA GGTTTAA GA CCGA
                                  _     C  A
GAM979  TCF2     3'  TGGCTTCCAGGCTCCCTGACT  7847         AA_
                                TGGCTTCCA  TTCCTGGCT
                                |||||||||  |||||||||
                                ACCGAAGGT  AGGGACTGA
                                     CCG
GAM980  ABCC3    3'  AGGGAGCGAGGGAGGCGGC   33413       C  A  AGTCCT
                                AGGGAGCG GG AGG     GC
                                |||||||| || |||     ||
                                TCCCTCGC CC TCC     CG
                                     T  C  GC____
GAM980  ACP2     3'  AGGGAGCGTGGAGGAGGCAAAT 11503       C  A  _____
            CCTG                   AGGGAGCG GGA GGAG    TCCTG
                                |||||||| ||| ||||    |||||
                                TCCCTCGC CCT CCTC    AGGAC
                                     A  _   CGTTT
GAM980  ARIH1    5'  AGGGAGCGAGGGGGCCGCTTGC 25085       C  AA  A  _ _
            T                   AGGGAGCG GG  GG GTC CT GCT
                                |||||||| ||  || ||| || |||
                                TCCCTCGC CC  CC CGG GA CGA
                                     T  __  _  C  A
GAM980  BMP1     3'  AGGGATGGCGATGGGGTCCTGC 25969      GC   AA  A
            T                   AGGGA  GCGG  GG GTCCTGCT
                                |||||  ||||  || ||||||||
                                TCCCT  CGCT  CC CAGGACGA
                                  AC   AC  _
GAM980  ENG      3'  GGCGAGCGCGGGGGGGCCGGGGC 6502    _     AA  A  CT_
            T                   GG GAGCGCGG  GG GTC  GCT
                                || ||||||||  || |||  |||
                                CC CTCGCGCC  CC CGG  CGA
                                 G      C_  _  CCC
GAM980  EPB49    3'  AGGGAGGCGGAAGGCCCAGCT  12722      C      AG  T
                                AGGGAG GCGGAAGG  TCC GCT
                                |||||| ||||||||  ||| |||
```

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                                TCCCTC CGCCTTCC  GGG CGA
                                  _      __  T
GAM980  GAB2    3'  AGGGGGCTGGAAGGAAGCCT  38672     A  GC      T
                                AGGG GC  GGAAGGAG CCT
                                |||| ||  |||||||| |||
                                TCCC CG  CCTTCCTT GGA
                                  C  A_      C
GAM980  NCOA3   3'  GGGGGTGGGGAAGGAAAAGCT  27217     AGCGC      TCCT
                                GGG    GGAAGGAG   GCT
                                |||    ||||||||   |||
                                CCC    CCTTCCTT   CGA
                                  CCACC      TT__
GAM980  THBD    3'  GGGTGCGGGGAGGGTC     7428     A  C  A  A
                                GGG GCG GG AGG GTC
                                ||| ||| || ||| |||
                                CCC CGC CC TCC CAG
                                  A  _ C  _
GAM980  CACNA1A 3'  CGCTGCTGTGGCCCCCCG   35729     T  T__
                                CGCT CT   GCCCCCCG
                                |||| ||   ||||||||
                                GCGA GA   CGGGGGGC
                                  C  CAC
GAM980  CAPNS1  5'  CCGCTCCCGGGCCTCCCG   11976       T_  C
                                TCGCTTCT  GCC CCCG
                                ||||||||  ||| ||||
                                GGCGAGGG  CGG GGGC
                                     CC   A
GAM980  DSCAM   5'  CCGCTCCCCGGCCTCCCG   10795        _  C
                                TCGCTTCTTG CC CCCG
                                |||||||||| || ||||
                                GGCGAGGGGC GG GGGC
                                     C  A
GAM980  EPHB2   3'  CACCGCTTGGTTCTTCCC   32664       _____   G
                                CATCGCT   TCTT CCC
                                |||||||   |||| |||
                                GTGGCGA   AGAA GGG
                                    ACCA   _
GAM980  FOXF2   3'  CATCGCTTGGCCTCTTTCCG  11127       CTT   CC___
                                CATCGCTT   GCC    CCG
                                ||||||||   |||    |||
                                GTAGCGAA   CGG    GGC
                                     C__   AGAAA
GAM980  FPRL1   5'  CACCGCTTTTCAGTCCCC   11146       C   CC
                                CATCGCTT TTG  CCCC
                                |||||||| |||  ||||
                                GTGGCGAA AGT  GGGG
                                     A   CA
GAM980  GRM4    3'  CACCGCCCCGGCCCCTCG   9155        TT    C
                                CATCGCTTC  GCCCC CG
                                |||||||||  ||||| ||
```

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                                GTGGCGGGG  CGGGG GC
                                     C_    A
GAM980  HHIP    5'  CACCGCTTCTCGCGCGCCCCCG 35404          ___
                                CATCGCTTCTTGC   CCCCCG
                                ||||||||||||   ||||||
                                GTGGCGAAGAGCG   GGGGGC
                                    CGC
GAM980  HIVEP1  5'  CCGCTCCCCGGTCCCCCG    13376        C_
                                TCGCTTCTTG  CCCCCG
                                ||||||||||  ||||||
                                GGCGAGGGGC  GGGGGC
                                     CA
GAM980  JAG2    5'  CAGCGCCCGCCCGCCCTCCG   13702    T   _     C
                                CA CGCTT CTTGCCC CCG
                                || ||||| ||||||| |||
                                GT GCGGG GGGCGGG GGC
                                 C    C      A
GAM980  MAPRE2  5'  CGCTCGCTCGCCTCTCCG    30691      _    CC_
                                CGCTT CTTGCC   CCG
                                ||||| ||||||   |||
                                GCGAG GAGCGG   GGC
                                   C     AGA
GAM980  MLLT2   3'  CATCGCTCCCATCCCTCG    25496        TGC   C
                                CATCGCTTCT   CCC CG
                                ||||||||||   ||| ||
                                GTAGCGAGGG   GGG GC
                                     TA_   A
GAM980  NCOR2   3'  CACCGCCCGCCCCCCCCCG   26725       TC  G
                                CATCGCT  TT CCCCCCG
                                |||||||  || |||||||
                                GTGGCGG  GG GGGGGGC
                                    GC  G
GAM980  NRAP    3'  CACTGCTTCTGCCCCCCG    40189    C    T
                                CAT GCTTCT GCCCCCCG
                                ||| |||||| ||||||||
                                GTG CGAAGA CGGGGGGC
                                  A     _
GAM980  OPRD1   5'  CACCGGCCCAGCCCCCCG    9506      C   TT
                                CATCG TTC  GCCCCCCG
                                ||||| |||  ||||||||
                                GTGGC GGG  CGGGGGGC
                                   C   T_
GAM980  PTTG1IP 5'  CATCTGCCCCGCCCCTCG    20282     GCT      C
                                CATC   TCTTGCCCC CG
                                ||||   ||||||||| ||
                                GTAG   GGGGCGGGG GC
                                  AC_       A
GAM980  ROBO1   5'  CATCGCCCTCGGCCCCTCG   39481       T   _   C
                                CATCGCT CTTG CCCC CG
                                ||||||| |||| |||| ||
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                                GTAGCGG GAGC GGGG GC
                                   _   C   A
GAM980  RRP22   5'  CGCTTCTCGTCGCCCCTCG   27006       ___    C
                                CGCTTCTT  GCCCC CG
                                ||||||||  ||||| ||
                                GCGAAGAG  CGGGG GC
                                    CAG   A
GAM980  RUNX3   3'  ATCCCCCCTCCCCCG     20316    G   TGC
                                ATC CTTCT  CCCCCG
                                ||| |||||  ||||||
                                TAG GGGGA  GGGGGC
                                  G   ___
GAM980  RXRG    5'  CATCGCTTCCTAGCAGCCCG  27940         _ CC
                                CATCGCTTCTT GC  CCCG
                                |||||||||| ||  ||||
                                GTAGCGAAGGA CG  GGGC
                                       T  TC
GAM980  SET7    5'  TCGCCCACTTGCCCCTCG    36160      _     C
                                TCGCTT CTTGCCCC CG
                                ||||||| |||||||| ||
                                AGCGGG GAACGGGG GC
                                   T      A
GAM980  SLC12A4 5'  CGCTGTCCCCGCCCCTCG    22894     __      C
                                CGCT  TCTTGCCCC CG
                                ||||  ||||||||| ||
                                GCGA  GGGGCGGGG GC
                                  CA       A
GAM980  SLC30A4 5'  CACCGCCTCTCCCC       30010        TGCC
                                CATCGCTTCT   CCCC
                                ||||||||||   ||||
                                GTGGCGGAGA   GGGG
                                      ____
GAM980  SURF6   3'  CACCGTTCCTCCTCCC     27587     C   G  C
                                CATCG TTCTT CC CCC
                                ||||| ||||| || |||
                                GTGGC AAGGA GG GGG
                                   _   _ A
GAM980  TR2     5'  CATCGCCCGCCTTTCCCG    43633      TCT   C__
                                CATCGCT  TGCC  CCCG
                                |||||||  ||||  ||||
                                GTAGCGG  GCGG  GGGC
                                   ___   AAA
GAM980  WRN     5'  CACCGCCCGCCCCCCG     8131       TCT
                                CATCGCT  TGCCCCCCG
                                |||||||  |||||||||
                                GTGGCGG  GCGGGGGGC
                                   ___
GAM980  XPR1    5'  CGCTTCTCTCCTCCTCCG    21849      TG _ _
                                CGCTTCT  CC CC CCG
                                |||||||  || || |||
```

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                                GCGAAGA  GG GG GGC
                                   GA  A  A
GAM980  ZNF179   3'  CATCACCCTCCCCC       28374       T  TGC
                                CATCGCT CT   CCCCC
                                ||||||| ||   |||||
                                GTAGTGG GA   GGGGG
                                   _  ___
GAM981  DPYD     3'  CCATTAAAAGAGGATGAGTT  41292     A      TT  T
                                CCAT AAAAGAG  AT AGTT
                                |||| |||||||  || ||||
                                GGTA TTTTCTC  TA TCAA
                                  A      C_  C
GAM981  IDS      3'  TACCACAGAAAGGGTTATT   25962       A    A
                                TACCATA AAAG GTTATT
                                ||||||| |||| ||||||
                                ATGGTGT TTTC CAATAA
                                   C    C
GAM981  MTMR8    3'  TACCATAAGAAAGTTAT     31756        AA
                                TACCATAA  AGAGTTAT
                                ||||||||  ||||||||
                                ATGGTATT  TTTCAATA
                                   C_
GAM981  QDPR     3'  TACCACAAAAGGAGTTAAGGCA 7239          A     T__
           GTT                    TACCATAAAA GAGTTA   TAGTT
                                ||||||||||| ||||||   |||||
                                ATGGTGTTTT CTCAAT   GTCAA
                                     C     TCC
GAM981  NEUROD1  3'  CTCTTAATTTTTTCTCCTCTT  14758       C___
                                CTCTTAA    TTCTTCTTTT
                                |||||||    ||||||||||
                                GAGAATT    AAGAGGAGAA
                                   AAAA
GAM981  RPN2     3'  TCTTGACTCCTTTTCTTG    16395     A      C
                                TCTT ACTTCTT TTTTTG
                                |||| ||||||| ||||||
                                AGAA TGAGGAA AAGAAC
                                  C      _
GAM981  SELP     3'  CTCCTGGCTTCTGTGGCTTGTG 16550      AA    TCTT
                                CTCTT  CTTCT    TTTGTG
                                |||||  |||||   ||||||
                                GAGGA  GAAGA    GAACAC
                                   CC    CACC
GAM981  STAT1    3'  CTCTTAATCTACTTTTTGTG   40214       CT   T
                                CTCTTAA  TCT CTTTTTGTG
                                |||||||  ||| |||||||||
                                GAGAATT  AGA GAAAAACAC
                                   __  T
GAM982  C14orf1  3'  TCAGCTCAAATCCCACCTCTT  28419     C  _  CAC
                                TCA GC CAA   GTCCCACCTCTT
                                ||| || |||   ||||||||||||
```

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                                AGT CG GTT   TAGGGTGGAGAA
                                  _ A  ___
GAM982  CARD4    5'  CGCCGCCACAATCTCCACCTCT 25891      AA   _ _
             T                   CGCC  CACG TC CCACCTCTT
                                 ||||  |||| || |||||||||
                                 GCGG  GTGT AG GGTGGAGAA
                                   CG   T  A
GAM982  MAF      5'  TCACGCCAATGTGCTCCC    23839        CAC _
                                 TCACGCCAA   G TCCC
                                 |||||||||   | ||||
                                 AGTGCGGTT   C AGGG
                                       ACA G
GAM982  OSM      3'  GCCCAGCTCCCACCTCTT    33912     AA  CG
                                 GCC  CA  TCCCACCTCTT
                                 |||  ||  ||||||||||
                                 CGG  GT  AGGGTGGAGAA
                                  __  CG
GAM982  PCDH15   5'  TCATTCACATGTTCCACCTCTT 37509     CGCCA   C  C
                                 TCA    ACA GT CCACCTCTT
                                 |||    ||| || |||||||||
                                 AGT    TGT CA GGTGGAGAA
                                  AAG__   A  A
GAM982  RAG1     3'  ACTCCAACCTACCACCTCTT   7782     G    ACGTC
                                 AC CCAAC    CCACCTCTT
                                 || |||||    |||||||||
                                 TG GGTTG    GGTGGAGAA
                                  A    GAT__
GAM982  UCP3     3'  GCCCAGGAATCCACCTCTT    17853     AACAC   C
                                 GCC    GTCC ACCTCTT
                                 |||    |||| |||||||
                                 CGG    TAGG TGGAGAA
                                  GTCCT   _
GAM982  ATP2A2   3'  AGAGAAATGTGGCGACTTGG   11743        AC__   GGCC
                                 AGAGAAAT   CGAC   GG
                                 ||||||||   ||||   ||
                                 TCTCTTTA   GCTG   CC
                                      CACC   AA__
GAM982  BCL7A    3'  AGAGAAATACTAGTGACAG    34199        C___
                                 AGAGAAATAC   GACGG
                                 ||||||||||   |||||
                                 TCTCTTTATG   CTGTC
                                       ATCA
GAM982  BIG1     3'  AGAGAAATATGTGACAGGTAG  26954        CC_   CC
                                 AGAGAAATA  GACGG  GG
                                 |||||||||  |||||  ||
                                 TCTCTTTAT  CTGTC  TC
                                       ACA    CA
GAM982  DMRT2    3'  AGAGAAATTCCGTCGGGGTGG  27257        A  A  CC_
                                 AGAGAAAT CCG CGG   GG
                                 |||||||| ||| |||   ||
```

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                                TCTCTTTA GGC GCC   CC
                                    A   A  CCA
GAM982  FGR     3'  AGAGAGGGTTGATGCCCGGACA 23496      AATACC  CGG
              G                  AGAGA     GA   CCGGACAG
                                 |||||     ||  ||||||||
                                 TCTCT     CT   GGCCTGTC
                                   CCCAA_  ACG
GAM982  KCNC3   5'  GAGAGACCGACGGGATTGG   22503     AAT      CC__
                                 GAGA   ACCGACGG   GG
                                 ||||   ||||||||   ||
                                 CTCT   TGGCTGCC   CC
                                   C__      CTAA
GAM982  PPARGC1  3'  AAAGAAATACTGGCTTCAAA  29946         CGAC  __
                                 AGAGAAATAC   GGC  CGGA
                                 ||||||||||   |||  ||||
                                 TTTCTTTATG   CCG  GTTT
                                      A___   AA
GAM982  TCF3    3'  GAGAGGCAGCCGGACA     43321     AATACCGA
                                 GAGA      CGGCCGGACA
                                 ||||      ||||||||||
                                 CTCT      GTCGGCCTGT
                                   CC_______
GAM983  LHX2    5'  CTAATGATACATGCTACA    21982          CA
                                 TTAATGATACA  CTATA
                                 ||||||||||  |||||
                                 GATTACTATGT  GATGT
                                       AC
GAM983  MS4A1   3'  TTAATGATACAATACTGC    6605          CACT
                                 TTAATGATACA   ATACTGT
                                 ||||||||||   |||||||
                                 AATTACTATGT   TATGACG
                                       ____
GAM983  TRHDE   3'  TGGTACCACTATACTGT     30115    A  A
                                 TG TAC CACTATACTGT
                                 || ||| ||||||||||
                                 AC ATG GTGATATGACA
                                  C  _
GAM983  CAPNS1   3'  AGCAACTGGGGCATGTTTATTT 11973     GT  A__  C
              C                   AGTA  TG   CA GTTTATTTC
                                  ||||  ||   || |||||||||
                                  TCGT  AC   GT CAAATAAAG
                                    TG  CCC  A
GAM983  GCA     3'  AAAGAGTTGACATTACATTT   29161     T     ___
                                 AAAG AGTTGAC   ACGTTT
                                 |||| |||||||   ||||||
                                 TTTC TCAACTG   TGTAAA
                                   _      TAA
GAM983  HDLBP   3'  AGTCAAGGACGTTTATTTC   42744     TG C_
                                 AGT  A  ACGTTTATTTC
                                 |||  |  ||||||||||
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                                TCA  T  TGCAAATAAAG
                                  GT CC
GAM983  PITX3    3'  AGTCCGCGCACGTTTATTTC  22755     AGT  A
                                AGT   TG CACGTTTATTTC
                                |||   || ||||||||||||
                                TCA   GC GTGCAAATAAAG
                                  GGC  _
GAM983  SLC1A5   3'  AAATAGTTGACACTCAATTT  44211          GTTT
                                AAGTAGTTGACAC   ATTT
                                ||||||||||||   ||||
                                TTTATCAACTGTG   TAAA
                                       AGT_
GAM984  ACCN2    5'  CCCGGCCCCGCTCGGCTCC   33438    G       CCCCCAC  _
                                CC CGGCCCCGC      GC CC
                                || |||||||||      || ||
                                GG GCCGGGGCG      CG GG
                                 _       AGC_____  A
GAM984  ACK1     3'  CCTTGGCCTTGCTCCATCCCCG 25110   GC   CC  CCC   CG
                                CC  GGCC  GC   CCA  CCCG
                                ||  ||||  ||   |||  ||||
                                GG  CCGG  CG   GGT  GGGC
                                 AA    AA  A__   AG
GAM984  ADAMTS12 5'  CCGCGGCCTCGCAGCC     36287        C   CCCCCAC
                                CCGCGGCC CGC      GCC
                                |||||||| |||      |||
                                GGCGCCGG GCG      CGG
                                     A   T_______
GAM984  ALDH3A2  5'  CCGCGACCTCCACGCC     42914        CCGCCCC
                                CCGCGGCC      CCACGCC
                                ||||||||      |||||||
                                GGCGCTGG      GGTGCGG
                                     A_______
GAM984  ASK      5'  CCGCCTCGCGCTCGCCCCTCGT 27472     G__  CC_     CCAC
           GCC                    CCGC   GC   CGCCCC    GCC
                                ||||   ||   ||||||    |||
                                GGCG   CG   GCGGGG    CGG
                                  GAG  CGA     AGCA
GAM984  ASK      5'  CCGTGCCCCGCCTCGCGCTCG  27473    CG      CCCCA   C
                                CCG  GCCCCGCC    CGC CG
                                |||  ||||||||    ||| ||
                                GGC  CGGGGCGG    GCG GC
                                  A_       AGC__   A
GAM984  ASL      5'  CGGCGTCCTCCACGCCCG    43530     CCCG  CC
                                CGGC    CC  CCACGCCCG
                                ||||    ||  |||||||||
                                GCCG    GG  GGTGCGGGC
                                  CA__  A_
GAM984  ATF4     5'  CCGCGCCCCGCCCACCGCCCG  11721      G       CCCA
                                CCGCG CCCCGCCC    CGCCCG
                                ||||| ||||||||    ||||||
```

```
                                GGCGC GGGGCGGG   GCGGGC
                                  _      TG__
GAM984  ATP11A   3'  CCGCGGCCCTTCCCAGCTGGCT 44173        CG   CCCAC  C
            CG                   CCGCGGCCC  CCC    GC CG
                                 |||||||||  |||    || ||
                                 GGCGCCGGG  GGG    CG GC
                                      AA   TCGAC  A
GAM984  CAPNS1   5'  CCGCGGCCCTCGTGTCGCCCG  11975        _  CCCCCCA
                                 CCGCGGCCC CG      CGCCCG
                                 |||||||||  ||      ||||||
                                 GGCGCCGGG GC      GCGGGC
                                      A  ACA____
GAM984  CAV2     5'  CCCGGCCCCGCCCCCCCTCG   10287    G          A_
                                 CC CGGCCCCGCCCCCC  CG
                                 ||  ||||||||||||||  ||
                                 GG GCCGGGGCGGGGGG  GC
                                  _           GA
GAM984  CDR2     5'  CCGCCGTCCCGCCTCAGCC    44021     _ GC     CCC  C
                                 CCGC G  CCCGCC   CA GCC
                                 ||||  |  ||||||   ||  |||
                                 GGCG C  GGGCGG   GT CGG
                                   G A_     A__  _
GAM984  CHRNA4   5'  CGCGGCCCCGCCCGGCCC    8850           CCCAC
                                 CGCGGCCCCGCCC    GCCC
                                 ||||||||||||     ||||
                                 GCGCCGGGGCGGG    CGGG
                                       C_____
GAM984  CKAP1    5'  CGTGGCCCCGCCCTGCCC    43881    C       CCCAC
                                 CG GGCCCCGCCC    GCCC
                                 ||  ||||||||||     ||||
                                 GC CCGGGGCGGG    CGGG
                                  A        A_____
GAM984  CRHR1    5'  CCGCGGCCCGGCCCGGCCC   20438        C   CCCAC
                                 CCGCGGCCC GCCC    GCCC
                                 |||||||||  ||||    ||||
                                 GGCGCCGGG CGGG    CGGG
                                      C   C_____
GAM984  CRMP1    5'  CGGCCCCGCTCCCAGC      10596        CC   C
                                 CGGCCCCGC  CCCA GC
                                 |||||||||  ||||  ||
                                 GCCGGGGCG  GGGT CG
                                      A_   _
GAM984  CSNK1D   5'  CCCGGCTCCGCCCCCCTCAC  40064    G   C       A
                                 CC CGGC CCGCCCCCC CGC
                                 ||  ||||  |||||||||  |||
                                 GG GCCG GGCGGGGGG GTG
                                  _   A        A
GAM984  CSNK1D   5'  CACGGCCCCGCTTTCACC    40062          CCCCCA
                                 CGCGGCCCCGC     CGCC
                                 ||||||||||      ||||
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```
                                GTGCCGGGGCG     GTGG
                                      AAA___
GAM984  CYFIP2   5'  CGGCCCCGCCCCGGCCC     43907          CCAC
                                CGGCCCCGCCCC    GCCC
                                ||||||||||||   ||||
                                GCCGGGGCGGGG    CGGG
                                      C___
GAM984  DBN1     5'  CCGCGCCTCCGGGCCGCGTCCG 38928      G _  CCCC  A  C
                                CCGCG CC CCG    CC CG CCG
                                ||||| || |||    || || |||
                                GGCGC GG GGC    GG GC GGC
                                   _ A   CC__  C  A
GAM984  DDX38    3'  GCAGCCCCGCTCCCGCCATGCC 30413          _  _  C
                                GCGGCCCCGC CCC CCA GCC
                                |||||||||| ||| ||| |||
                                CGTCGGGGCG GGG GGT CGG
                                      A   C   A
GAM984  DPP6     3'  CCCGGCCCCGCCCCGCCC    39128    G         CCAC
                                CC CGGCCCCGCCCC    GCCC
                                || ||||||||||||    ||||
                                GG GCCGGGGCGGGG    CGGG
                                  _         _____
GAM984  DSCAM    5'  CCGCGCTCCGCCCGGCCC     10794      G C     CCCAC
                                CCGCG C CCGCCC     GCCC
                                ||||| | ||||||     ||||
                                GGCGC G GGCGGG     CGGG
                                   _ A     C_____
GAM984  DVL1     5'  GCGCCCCGCCCGGCCC      40411     G      CCCAC
                                GCG CCCCGCCC     GCCC
                                ||| ||||||||     ||||
                                CGC GGGGCGGG     CGGG
                                  _       C_____
GAM984  DVL3     5'  CCGCGCTTCCGCTCCCCACTCT 20677      GCC   C     G__
           CCCG                    CCGCG   CCGC CCCCAC   CCCG
                                |||||   |||| ||||||   ||||
                                GGCGC   GGCG GGGGTG   GGGC
                                   GAA    A     AGA
GAM984  FANCC    3'  CCGCGTCCCCGCCCAGCA    43273      G      CC
                                CCGCG CCCCGCCC  CA
                                |||||  ||||||||  ||
                                GGCGC GGGGCGGG  GT
                                   A       TC
GAM984  FANCG    5'  CCGTGGCTCGGCCCTTCCTCG  21554     C   CCC    C_  A
                                CCG GGC   GCCC  CC CG
                                |||  |||   ||||  || ||
                                GGC CCG   CGGG  GG GC
                                  A   AGC    AA  A
GAM984  FBXL3A   5'  CCGCGCTCCGCCCGCATCC    29125      G C     CCCA  C
                                CCGCG C CCGCCC    CG CC
                                ||||| | ||||||    || ||
```

```
                                GGCGC G GGCGGG   GT GG
                                  _ A    C___  A
GAM984  FBXL5   5'  CCGCGGCCGCCGCCTCTCCA  37945       _   CC_
                                CCGCGGCC CCGCC  CCA
                                |||||||| |||||  |||
                                GGCGCCGG GGCGG  GGT
                                    C    AGA
GAM984  FHL2    5'  CCGTGCCCCCGCCCCGGGC   11107    CG   _   CCAC
                                CCG  GCCCC GCCCC   GC
                                |||  ||||| |||||   ||
                                GGC  CGGGG CGGGG   CG
                                 A_   G   CC__
GAM984  FPGS    3'  CGCGGCCCTGCAGCGCC    22427       C  CCCCCA
                                CGCGGCCC GC    CGCC
                                |||||||| ||    ||||
                                GCGCCGGG CG    GCGG
                                    A  TC_____
GAM984  FZD10   5'  CGGGCCCCCGCCCATGCCCG  28451   C    _   CCCAC
                                CG GGCCCC GCCC   GCCCG
                                || |||||| ||||    |||||
                                GC CCGGGG CGGG    CGGGC
                                 _    G   TA___
GAM984  G6PD    5'  CCCGGCCCCGCCCCTACTGTCC 7597    G        CC  GC_
          G                      CC CGGCCCCGCCCC  AC  CCG
                                || ||||||||||||  ||  |||
                                GG GCCGGGGCGGGG  TG  GGC
                                 _         A_  ACA
GAM984  GAK     3'  CCGGGGCTCCAGAGGCCACGCC 23532    C  C  CCCC
          CG                     CCG GGC CCG   CCACGCCCG
                                ||| ||| |||   |||||||||
                                GGC CCG GGT   GGTGCGGGC
                                 C  A  CTCC
GAM984  GNB1    5'  CCCGGCCCCGCTCCCCAC    13199   G      C
                                CC CGGCCCCGC CCCCAC
                                || |||||||| ||||||
                                GG GCCGGGGCG GGGGTG
                                 _       A
GAM984  GPRC5B  5'  CCGCGGCCCCCGCTCCACGCAC 32173        _ _  CC_
          GCCCG                   CCGCGGCCCC GC CC  CACGCCCG
                                |||||||||| || ||  ||||||||
                                GGCGCCGGGG CG GG  GTGCGGGC
                                    G  A  TGC
GAM984  GPT     5'  GGCCCCGCCCCACCC      23635          CCAC
                                GGCCCCGCCCC   GCCC
                                ||||||||||   ||||
                                CCGGGGCGGGG   TGGG
                                              ____
GAM984  GRB10   5'  CCGCGGCCCCGCCGCGC     23652          CCCCA
                                CCGCGGCCCCGCC    CGC
                                ||||||||||||    |||
```

```
                                GGCGCCGGGGCGG    GCG
                                      C____
GAM984  GSTM4   5'  CCTCGGCCCCGCTGCGCCC   9200    G      CCCCCA
                                CC CGGCCCCGC    CGCCC
                                || |||||||||    |||||
                                GG GCCGGGGCG    GCGGG
                                 A       AC____
GAM984  HBQ1    5'  GCGACCCCGCTGCGCC     23729         CCCCCA
                                GCGGCCCCGC    CGCC
                                ||||||||||    ||||
                                CGCTGGGGCG    GCGG
                                      AC____
GAM984  HCN2    3'  CCGCCGGCCCTGCCCGTCC   10166    _   C   C_
                                CCGC GGCCC GCCC  CC
                                |||| ||||| ||||  ||
                                GGCG CCGGG CGGG  GG
                                  G    A   CA
GAM984  HRB     5'  CCGCGGCCGCCGCCCTCC    21085       _    C
                                CCGCGGCC CCGCCC CC
                                |||||||| |||||| ||
                                GGCGCCGG GGCGGG GG
                                     C     A
GAM984  IFNGR2  5'  CCGCGCCCCCGCCCCCGCCC  24383     G       CAC
                                CCGCG CCCCGCCCCC  GCCC
                                ||||| ||||||||||  ||||
                                GGCGC GGGGCGGGGG  CGGG
                                  G       ___
GAM984  IL6R    5'  CCTCGGCCCCGCGCCGCGCTCG 8173    G      CCC  A  C
                                CC CGGCCCCGC  CC CGC CG
                                || |||||||||  || ||| ||
                                GG GCCGGGGCG  GG GCG GC
                                 A       C__  C  A
GAM984  INHBB   3'  CCGTGCCCCTGCCTTGCAC   13551    CG   _  CCC
                                CCG  GCCCC GCC  CAC
                                |||  ||||| |||  |||
                                GGC  CGGGG CGG  GTG
                                  A_    A  AAC
GAM984  IQGAP2  5'  GCGCCCCGCCGGCGCGCTCG  27370    G    CCCCA  C
                                GCG CCCCGCC    CGC CG
                                ||| |||||||    ||| ||
                                CGC GGGGCGG    GCG GC
                                  _     CCGC_  A
GAM984  JAG2    5'  CCGCCGCCGCCCCGCGCCC    13709   _   C  A
                                CC CCGCC CCC CGCCC
                                || ||||| ||| |||||
                                GG GGCGG GGG GCGGG
                                 C    C  C
GAM984  JUND    5'  CCGCGGCCTCCCGGGGGGCCCG 23800       CCG  CCCAC
                                CCGCGGCC  CCC    GCCCG
                                ||||||||  |||    |||||
```

```
                                GGCGCCGG  GGG   CGGGC
                                    A__  CCCCC
GAM984  KCNA7   5'  GCGGCCCCGCCTCGGCC    36658         CCCCAC
                                GCGGCCCCGCC    GCC
                                ||||||||||     |||
                                CGCCGGGGCGG    CGG
                                     AGC___
GAM984  LAMC1   5'  CCGCGCCCCGCCTCCGCG   14082     G     CC  A
                                CCGCG CCCCGCC  CC CG
                                ||||| |||||||  || ||
                                GGCGC GGGGCGG  GG GC
                                  _     A_  C
GAM984  MAF     5'  CCCTGCCCGCGCCCCCCGCGCC 23822   GCG   _     A
           CG                    CC   GCCC CGCCCCCC CGCCCG
                                 ||   |||| |||||||| ||||||
                                 GG   CGGG GCGGGGGG GCGGGC
                                  GA_   C      C
GAM984  MAPK3   5'  GCGGCCCCGCCCGAGGCCC   43843         CCCAC
                                GCGGCCCCGCCC    GCCC
                                ||||||||||||    ||||
                                CGCCGGGGCGGG    CGGG
                                     CTC__
GAM984  MIF     5'  CCGCGGCCGCCGCTGAGCTACG 14510       _   CCCCC_  C_
           TGCC                  CCGCGGCC CCGC    ACG  CC
                                 |||||||| ||||     |||  ||
                                 GGCGCCGG GGCG     TGC  GG
                                    C    ACTCGA   AC
GAM984  MLLT1   5'  CCGGGCCCCGCGTCGCC    25484    C     CCCCCA  C
                                CCG GGCCCCGC     CGC C
                                ||| ||||||||     ||| |
                                GGC CCGGGGCG     GCG G
                                  _      CA_____   A
GAM984  MLLT2   5'  CCAGCGGGCCCCCACGCC    25497   _   CCCC    C   C
                                CC GCGG   GCCCCC ACGC C
                                || ||||   |||||| |||| |
                                GG CGCC   CGGGGG TGCG G
                                 T   _____    _   A
GAM984  MSF     5'  GCGCCCCCGCCCCGCCCCCG   44731    G      _ ACG
                                GCG CCCCGCCCC CC   CCCG
                                ||| |||||||| ||   ||||
                                CGC GGGGCGGGG GG   GGGC
                                  G       C ___
GAM984  MTL5    5'  CCGCGAGCTTCGCCTTGACCCC 22268      _ CC   _____
                                CCGCG GC  CGCC   CCCC
                                ||||| ||  ||||   ||||
                                GGCGC CG  GCGG   GGGG
                                   T  AA   AACT
GAM984  MUCDHL  3'  CCGCGCCCTCGCCCTCATCG   34934     G   _   CC  _
                                CCGCG CCC CGCCC  CA CG
                                ||||| ||| |||||  || ||
```

```
                                GGCGC GGG GCGGG  GT GC
                                  _  A    A_ A
GAM984  MUS81   5' CGGCGCTCCACGCCC      36062     CCC  CCC
                                CGGC   GC   CCACGCCC
                                ||||   ||   ||||||||
                                GCCG   CG   GGTGCGGG
                                  ___  A__
GAM984  NKX3A   5' GCGGCCCCGCCTTGGCC     26114          CCCCAC
                                GCGGCCCCGCC     GCC
                                ||||||||||      |||
                                CGCCGGGGCGG     CGG
                                      AAC___
GAM984  NOC4    5' CCCGGCCCCGTTTGGGCCTCG  25866    G      CCCCCCAC  _
                                CC CGGCCCCG       GCC CG
                                || ||||||||       ||| ||
                                GG GCCGGGGC       CGG GC
                                 _       AAACC___   A
GAM984  NORE1   3' CCTGGCCTTGTCTCCCACACC  36428    GC   CCGCCC
                                CC  GGCC     CCCACGCC
                                ||  ||||     ||||||||
                                GG  CCGG     GGGTGTGG
                                 A_   AACAGA
GAM984  NOX4    5' CCGCGCTGCGCTCTGTGCCCG  32594      G CC   CCCCCAC
                                CCGCG C  CGC      GCCCG
                                ||||| |  |||      |||||
                                GGCGC G  GCG      CGGGC
                                  _ AC   AGACA__
GAM984  NPAS2   5' CCGCGGCCGCCGCTCCTGGGCC 14817         _   C  CCAC
                                CCGCGGCC CCGC CC    GCC
                                |||||||| |||| ||    |||
                                GGCGCCGG GGCG GG    CGG
                                     C    A  ACC_
GAM984  NRXN2   5' CCCCGGCCCCGCCCGGCCC   31475    G        CCCAC
                                CC CGGCCCCGCCC    GCCC
                                || ||||||||||     ||||
                                GG GCCGGGGCGGG    CGGG
                                 G         C____
GAM984  NTRK2   5' CCGGGCTCCGGCGCCTCACGCC 26146    C   _  C  C  C
          CG                      CCG GGC CC GC CC CACGCCCG
                                ||| ||| || || || ||||||||
                                GGC CCG GG CG GG GTGCGGGC
                                  _   A  C  C  A
GAM984  OCLN    5' CGCGGTCCTGCTTCCCACACCC 14901      C  C  CC
                                CGCGG CC GC  CCCACGCCC
                                ||||| || ||  |||||||||
                                GCGCC GG CG  GGGTGTGGG
                                   A  A  AA
GAM984  OLFM1   5' CCTGGCTCGTGTCCCCACGCC  26768    GC   CC  CC_
                                CC  GGC  CG   CCCCACGCC
                                ||  |||  ||   |||||||||
```

```
                                GG  CCG  GC   GGGGTGCGG
                                 A_   A_  ACA
GAM984  OPHN1    5'  GCGCCCCGCCCCAGCGAAGCCC 14966     G        CCAC__
             G                   GCG CCCCGCCCC     GCCCG
                                 ||| |||||||||     |||||
                                 CGC GGGGCGGGG     CGGGC
                                  _       TCGCTT
GAM984  P3       5'  CCGCGGCCCCGCCAGGCCTCG  33376           CCCCAC  _
                                 CCGCGGCCCCGCC     GCC CG
                                 ||||||||||||      ||| ||
                                 GGCGCCGGGGCGG     CGG GC
                                         TC_____   A
GAM984  PAX2     3'  CCGCGGCTCCACCCGTCC    19620        C     C_
                                 CCGCGGC CCGCCC  CC
                                 |||||||  ||||||  ||
                                 GGCGCCG GGTGGG  GG
                                     A      CA
GAM984  PIAS1    5'  CCTGGCCCCGCCCCGGCCC   32076    GC        CCAC
                                 CC  GGCCCCGCCCC   GCCC
                                 ||  ||||||||||    ||||
                                 GG  CCGGGGCGGGG   CGGG
                                  A_         C___
GAM984  PPP2R5D  5'  GCGGCCCCGCTCCGGCTCCG   26460         C  CCAC  _
                                 GCGGCCCCGC CC    GC CCG
                                 ||||||||| ||    || |||
                                 CGCCGGGGCG GG    CG GGC
                                       A  C___  A
GAM984  PPP3CC   5'  CCGCGGCCGCCGCCTTCTCCTC 24675        _    CC__  A
             G                   CCGCGGCC CCGCC    CC CG
                                 ||||||||  |||||    || ||
                                 GGCGCCGG GGCGG    GG GC
                                     C     AAGA  A
GAM984  PRDM16   3'  CCGGGGCCCCGCCCGCCTCCG  35244     C        _  CA
                                 CCG GGCCCCGCCC CC  CG
                                 ||| ||||||||| ||  ||
                                 GGC CCGGGGCGGG GG  GC
                                   C         C  AG
GAM984  PTPN2    5'  CCGCGCCCCGCCCCCACG    15911      G        C
                                 CCGCG CCCCGCCCCC ACG
                                 |||||  |||||||||  |||
                                 GGCGC GGGGCGGGGG TGC
                                        _        _
GAM984  PTPRJ    5'  CGGGCCCCGCCGTGCGCCCG   15953    C       CCCCA
                                 CG GGCCCCGCC    CGCCCG
                                 || |||||||||    ||||||
                                 GC CCGGGGCGG    GCGGGC
                                  _       CAC__
GAM984  RASGRP1  5'  CCGCGGCCCGCGCTCCCGGTGC 25076         _  C   CAC
             C                   CCGCGGCCC CGC CCC   GCC
                                 |||||||| ||| |||   |||
```

```
                                GGCGCCGGG GCG GGG  CGG
                                     C  A  CCA
GAM984  RDBP    5'  CCACGGTCTCCGGCCGCGCCCG 16231      CC_  CCCC  A
                                CCGCGG  CCG   CC CGCCCG
                                ||||||  |||   || ||||||
                                GGTGCC  GGC   GG GCGGGC
                                   AGA  C___  C
GAM984  RRM2B   5'  CCCGGCCCCGCCTCCCCCG   42715   G       _   A
                                CC CGGCCCCGCC CCCC CG
                                || |||||||||| |||| ||
                                GG GCCGGGGCGG GGGG GC
                                 _       A   _
GAM984  SIX2    5'  GCGTCCCCGCCCGCCC     32609    G      CCCAC
                                GCG CCCCGCCC    GCCC
                                ||| ||||||||    ||||
                                CGC GGGGCGGG    CGGG
                                  A      _____
GAM984  SLC12A7  3'  GCTGCCCACGCCGTCCTCCGTG 27330   G  _  __ _ AC
           CC                    GC GCCC CGCC  CC CC  GCC
                                || |||| ||||  || ||  |||
                                CG CGGG GCGG  GG GG  CGG
                                 A   T   CA  A  CA
GAM984  SLC22A12 5'  CCGTGGCTCCTGCCTCCACTCA 40330    C  _ C  CC   __
           CC                    CCG GGC CC GCC  CCAC  GCC
                                ||| ||| || |||  ||||  |||
                                GGC CCG GG CGG  GGTG  TGG
                                  A  A A  A_   AG
GAM984  SMARCC2  5'  CGGGCCCCGCCGCCGCCC   40072   C      CCCCA
                                CG GGCCCCGCC    CGCCC
                                || |||||||||    |||||
                                GC CCGGGGCGG    GCGGG
                                 _       CG___
GAM984  SNCB    3'  CCTGGCCCTGTCCATGCCC   16929   GC   CGCCCC  C
                                CC  GGCCC     CCA GCCC
                                ||  |||||     ||| ||||
                                GG  CCGGG     GGT CGGG
                                 A_    ACA___  A
GAM984  SNX6    5'  CCGCGCCCGCCCCGCGCCC   34560     GC      CCA
                                CCGCG  CCCGCCCC  CGCCC
                                |||||  ||||||||  |||||
                                GGCGC  GGGCGGGG  GCGGG
                                   __      C__
GAM984  SOX12   5'  CCGCGGCTCGGCCCGGCCCCC  28033       ____   C
                                CCGCGGC   CCCG CCCCC
                                |||||||   |||| |||||
                                GGCGCCG   GGGC GGGGG
                                   AGCC   C
GAM984  SP3     5'  CCGCCGCCAGCCCACGCC    44373   _   C_
                                CC CCGCC  CCCACGCC
                                || |||||  ||||||||
```

```
                                GG GGCGG  GGGTGCGG
                                 C    TC
GAM984  SPTAN1   5'  CCGCGGCCTCCGCTCCACACC  17099       _   CCC
                                CCGCGGCC CCGC   CCACGCC
                                |||||||| ||||   |||||||
                                GGCGCCGG GGCG   GGTGTGG
                                    A   A__
GAM984  SWAP70   5'  CCGCGGCCCTGCTGCCCC    43422        C  C_
                                CCGCGGCCC GC  CCCC
                                ||||||||| ||  ||||
                                GGCGCCGGG CG  GGGG
                                    A  AC
GAM984  TFG      5'  CCGCGGCCGCCGCCTCTCC   25870        _    CC_
                                CCGCGGCC CCGCC   CC
                                |||||||| |||||   ||
                                GGCGCCGG GGCGG   GG
                                    C    AGA
GAM984  TFRC     5'  CGCGGCCCCGCTCCATCCCG   17430         C  CCACG
                                CGCGGCCCCGC CC    CCCG
                                |||||||||| ||    ||||
                                GCGCCGGGGCG GG    GGGC
                                    A  TA___
GAM984  TMOD     3'  CCTGGCCCCGCCTCCAGTTACC 17599    GC       _ CCAC
           C                     CC  GGCCCCGCC CC    GCCC
                                ||  |||||||| ||    ||||
                                GG  CCGGGGCGG GG    TGGG
                                 A_       A  TCAA
GAM984  UGCG     5'  CCGCGGCCCCGCGCTCCG    17866          CCCCCAC  _
                                CCGCGGCCCCCGC      GC CCG
                                ||||||||||||      || |||
                                GGCGCCGGGGCG      CG GGC
                                      ________  A
GAM984  WNT2     5'  CCGCGCCCCCGCCCCCCGCTCG 18103      G        AC  C
                                CCGCG CCCCGCCCCCC  GC CG
                                ||||| ||||||||||  || ||
                                GGCGC GGGGCGGGGGG  CG GC
                                   G         __  A
GAM984  ZNF26    5'  GGCCCCGTCCACGCCC      43803       CCCC
                                GGCCCCG   CCACGCCC
                                |||||||   ||||||||
                                CCGGGGC   GGTGCGGG
                                   A___
GAM984  ADAM12   5'  TGCGTCGCGCGCGCCGTTCT 18480     _        CGCGG
           GG                     TGCG CGCGCGCGCGCC    GG
                                |||| ||||||||||||    ||
                                ACGC GCGCGCGCGCGG    CC
                                  A          CAAGA
GAM984  CRHBP    3'  GCGCGCGTGCGCTCAAGG    40510       C   CCG
                                GCGCGCG GCGC   CGGGG
                                ||||||| ||||   |||||
```

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                                CGCGCGC CGCG   GTTCC
                                    A   A__
GAM984  EGR3    3'  GCGCGCGTGCGTGCGGCGGG  40549       C  C  CC
                                GCGCGCG GCG GC  GCGGG
                                ||||||| ||| ||  |||||
                                CGCGCGC CGC CG  CGCCC
                                    A  A  C_
GAM984  GAD2    5'  TGCGCGCGCGTGCGTGCCGTGT 9057         C  C_  CGG
          GG                    TGCGCGCGCG GCG  CCG   GG
                                |||||||||| |||  |||   ||
                                ACGCGCGCGC CGC  GGC   CC
                                      A  AC   ACA
GAM984  GAN     5'  TGCGCGCGCGCCCGCCCG    35153          G
                                TGCGCGCGCGC CGCCCG
                                |||||||||| ||||||
                                ACGCGCGCGCG GCGGGC
                                      G
GAM984  GRAF    5'  GCGCGCGGCGCCCAGCCGGGGG 31450       C    _ _
                                GCGCGCG GCGCCC GC GGGGG
                                ||||||| |||||| || |||||
                                CGCGCGC CGCGGG CG CCCCC
                                    _    T  G
GAM984  NEURL   5'  TGCGCGCGCGGGTGCCCG    20105         CGC
                                TGCGCGCGCG   GCCCG
                                |||||||||   |||||
                                ACGCGCGCGC   CGGGC
                                      CCA
GAM984  PARK2   3'  TGCGCGCGCGCGCCCCCGG   30377          CG_  GCGG
                                TGCGCGCGCGCG   CCC   G
                                ||||||||||||  |||   |
                                ACGCGCGCGCGC   GGG   C
                                      III  GGCG
GAM984  PARK2   3'  TGTGCGCGCGCGCGCGCC    30381    C        ____
                                TG GCGCGCGCGCGC   CC
                                || ||||||||||||   ||
                                AC CGCGCGCGCGCG   GG
                                 A          CIII
GAM984  RAB33A  5'  TGCGCGCGCGCGCGTGAAGGGG 22001           CCCGC
          G                     TGCGCGCGCGCGCG    GGGGG
                                ||||||||||||||    |||||
                                ACGCGCGCGCGCGC    CCCCC
                                      ACTT_
GAM984  RCV1    3'  TGTGCGCGCGCGTGCCCCCGG  16224    C      CG___  GCGG
                                TG GCGCGCGCG    CCC   G
                                || |||||||||    |||   |
                                AC CGCGCGCGC    GGG   C
                                 A       ACIII  GGCG
GAM984  RCV1    3'  TGTGCGCGCGCGTGTGCCCCCG 16225    C      CG_____  GCGG
          G                     TG GCGCGCGCG     CCC   G
                                || |||||||||      |||   |
```

```
                                AC CGCGCGCGC      GGG   C
                                 A        ACACIII  GGCG
GAM984  S100A11   5'  GCGCGCGGCGTGCGGG     24732        C   CCC
                                GCGCGCG GCG   GCGGG
                                ||||||| |||   |||||
                                CGCGCGC CGC   CGCCC
                                   _  A__
GAM984  SLC12A7   3'  TGCGCGCGTGTGCCCCTGGG  27334        CGC  G   GC
                                TGCGCGCG   GC CCC  GGG
                                ||||||||   || |||  |||
                                ACGCGCGC   CG GGG  CCC
                                     ACA  _   A_
GAM984  TACSTD1   5'  TGCGCGCGCGCCGAGAAGAGGG 14303          G  CCCGC
              G                  TGCGCGCGCGC CG    GGGGG
                                ||||||||||| ||    |||||
                                ACGCGCGCGCG GC    TCCCC
                                      _  TCTTC
GAM984  VGF      3'  GCGCGCGCGCGCGGCGGGGG   17992           CCC
                                GCGCGCGCGCGCG   GCGGGGG
                                ||||||||||||   |||||||
                                CGCGCGCGCGCGC   CGCCCCC
                                          ___
GAM984  ZIC1     5'  TGGCGCGCGCGCGCCGCGCGG  18240    C          _
                                TG GCGCGCGCGCGCC CGCGG
                                || |||||||||||| |||||
                                AC CGCGCGCGCGCGG GCGCC
                                 _          C
GAM984  ZNF278   5'  GCGCGCGCGCGCGCCGCGG   36797            C
                                GCGCGCGCGCGCGCC GCGG
                                |||||||||||||| ||||
                                CGCGCGCGCGCGCGG CGCC
                                          _
GAM985  ASCL1    3'  TCTCCCCCTCCCAACG      43748    G        CCCCT
                                TC CCCCCTCCCG    CG
                                || ||||||||||    ||
                                AG GGGGGAGGGT    GC
                                 A        T_____
GAM985  ASK      5'  CCTCGCGCTCGCCCCTCG    27474       CCC   CC
                                CCTCGC   CTC  GCCCCTCG
                                ||||||   |||  ||||||||
                                GGAGCG   GAG  CGGGGAGC
                                   C__   __
GAM985  ASK      5'  CCTCGTGCCTGCCTTCTCGC   27475      CCC   CCC   C_
                                CCTCG   CCT   GCC  CTCGC
                                |||||   |||   |||  |||||
                                GGAGC   GGA   CGG  GAGCG
                                  AC_   ____  AA
GAM985  ATP6V1G2 5'  TCTCCTCCTCCAGCTCG     39629    G  C    C  CCC
                                TC CC CCTCC GC   TCG
                                || || ||||| ||   |||
```

```
                                AG GG GGAGG CG   AGC
                                 A  A    T ___
GAM985  BAX     5'  CCCGCCGCCGCCTCTCG     39870       CCCTC    C
                                CTCGCC    CCGCC CTCG
                                ||||||    ||||| ||||
                                GGGCGG    GGCGG GAGC
                                   C____    A
GAM985  BCL9    3'  CTCCCCCCTCCCCCCACCCCTC 20237     G   __
            GC                    CTC CCCC  CTCCCGCCCCTCGC
                                ||| ||||  ||||||||||||||
                                GAG GGGG  GGGGGGTGGGGAGCG
                                  G   AG
GAM985  CACNG8   5'  CTCGCACCAGAGGCCCCGCTCT 43525      _  CC___     CCC
            TCG                   CTCGC CC    TCCCGC   TCG
                                ||||| ||    ||||||   |||
                                GAGCG GG    GGGGCG   AGC
                                   T  TCTCC     AGA
GAM985  CALM3    3'  CCTCGACCCCTCCTGGGC    23231      C      C__
                                CCTCG CCCCTCC   GC
                                ||||| |||||||   ||
                                GGAGC GGGGAGG   CG
                                   T      ACC
GAM985  CCND1    5'  CCTCGCGCTCTTCTGCCCCTCG 38203       CCC   CC__
            C                    CCTCGC   CTC    GCCCCTCGC
                                ||||||   |||   |||||||||
                                GGAGCG   GAG    CGGGGAGCG
                                   C__   AAGA
GAM985  CD63     5'  CTGCGCCCCCCGGCCCCTCG   12133    _      CCC
                                CT CGCCCCCT   GCCCCTCG
                                || ||||||||   ||||||||
                                GA GCGGGGGG   CGGGGAGC
                                 C       C__
GAM985  CDC2L2   5'  CCTGCGGGCCTCCCGCTCCTTG 37936     C  CC_      C   C
            C                    CCT GC   CCTCCCGC CCT GC
                                ||| ||   |||||||| ||| ||
                                GGA CG   GGAGGGCG GGA CG
                                  _  CCC       A   A
GAM985  CHES1    5'  CCTGCCCCCCCCGCTGCTTCTCG 23283     C       CC_  CC
            C                    CCT GCCCCCTC   GC  CTCGC
                                ||| ||||||||   ||  |||||
                                GGA CGGGGGGG   CG  GAGCG
                                  _       CGA  AA
GAM985  CHRNB2   3'  CCTGCCCTTCCACCCCT     8856      C    CCTC
                                CCT GCCC    CCGCCCCT
                                ||| ||||    ||||||||
                                GGA CGGG    GGTGGGGA
                                  _    AA__
GAM985  DDX26    5'  CCTCCGCCTCCTCCTGCC    29090      _  C    C
                                CCTC GCC CCTCC GCC
                                |||| ||| ||||| |||
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                                GGAG CGG GGAGG CGG
                                  G  A    A
GAM985  DLC1    5'  CTCGCCGCTCCCTGCCCCTCG  25904      CC   _
                                CTCGCC  CTCCC GCCCCTCG
                                ||||||  ||||| ||||||||
                                GAGCGG  GAGGG CGGGGAGC
                                   C_    A
GAM985  DMRT1   5'  CTGGCCCCCTCTCTCG     34981    C      CCGCCC
                                CT GCCCCCTC     CTCG
                                || ||||||||     ||||
                                GA CGGGGGAG     GAGC
                                 C      A_____
GAM985  DYRK2   5'  CCTCCCGGCCGCCCCTCG    27036    _  TC
                                CC CCC  CCGCCCCTCG
                                || |||  ||||||||||
                                GG GGG  GGCGGGGAGC
                                 A  CC
GAM985  G6PD    3'  CTCGCCCCTTTCCTCCCCCT  7603       C_  CG
                                CTCGCCCC  TCC  CCCCT
                                ||||||||  |||  |||||
                                GAGCGGGG  AGG  GGGGA
                                    AA  AG
GAM985  GCS1    5'  CCTCTCCGGCTCCCGCCTCTCG 26698     G  CC      C
           C                     CCTC CC  CTCCCGCC CTCGC
                                ||||  ||  |||||||| |||||
                                GGAG GG  GAGGGCGG GAGCG
                                  A  CC       A
GAM985  GPR2    3'  CCTGCCCCCTCCTCTAGATTCG 32481    C       CGCCCC_
           C                     CCT GCCCCCTCC      TCGC
                                ||| |||||||||      ||||
                                GGA CGGGGGAGG      AGCG
                                  _       AGATCTA
GAM985  HHEX    5'  CGCGCTCCGGCCCCTCG    15566    CCC   C
                                CGC  CTCC GCCCCTCG
                                |||  |||| ||||||||
                                GCG  GAGG CGGGGAGC
                                  C__   C
GAM985  HLF     5'  CCTGCCTCGAACCCCTCG    13389    C  CCC  CC
                                CCT GCC  TC  GCCCCTCG
                                ||| |||  ||  ||||||||
                                GGA CGG  AG  TGGGGAGC
                                  _  ___  CT
GAM985  HNRPD   5'  CCTTCGCCTCCCACTCTCGC  36390    _  CCC    CC
                                CCT CGCC  TCCCGC  CTCGC
                                ||| ||||  ||||||  |||||
                                GGA GCGG  AGGGTG  GAGCG
                                  A   ___    A_
GAM985  INHBB   5'  CCTCGCCCTCACTGCCTCGC  13553       CCTCC  C_
                                CCTCGCCC   CGC  CCTCGC
                                ||||||||   |||  ||||||
```

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                                GGAGCGGG    GTG  GGAGCG
                                    A____   AC
GAM985  JJAZ1    5'  CCTGCCTCCTCCCCCC     31687     C  C     G
                                CCT GCC CCTCCC CCC
                                ||| ||| |||||| |||
                                GGA CGG GGAGGG GGG
                                  _  A    _
GAM985  KCNK10   5'  CCTTACCCCCTCCCCACG    39681     CG     CCCG   T
                                CCT  CCCCCT   CCCC CG
                                |||  ||||||   |||| ||
                                GGA  GGGGGA   GGGG GC
                                  AT     ____   T
GAM985  KCNQ3    5'  CCTCGCCCCCGCCGGCCGCTTC 21127          T  C   C  _
              GC                  CCTCGCCCCC CC GCC CT CGC
                                ||||||||| || ||| || |||
                                GGAGCGGGGG GG CGG GA GCG
                                     C  C   C  A
GAM985  LYPLA1   5'  CCGCCCTGCCCTGCCCCTCGC  26758       CCT   _
                                TCGCCC   CCC GCCCCTCGC
                                ||||||   ||| |||||||||
                                GGCGGG   GGG CGGGGAGCG
                                   AC_   A
GAM985  MAF      5'  CCTTGCGCTCGCCTCCTTGC   23826     C  CCC   CC   _   C
                                CCT GC   CTC  GCC CCT GC
                                ||| ||   |||  ||| ||| ||
                                GGA CG   GAG  CGG GGA CG
                                  A  C__   __   A   A
GAM985  MAP1B    5'  CCTCCGCCCTCTCCCAGC    25392      _    C    _
                                CCTC GCCC CTCCC GC
                                |||| |||| ||||| ||
                                GGAG CGGG GAGGG CG
                                  G    A    T
GAM985  MAPRE3   3'  CCATGCCCCCAAGCCCCCCTCG 29529    TC     TC_  G
              C                   CC  GCCCCC   CC CCCCTCGC
                                ||  ||||||   || ||||||||
                                GG  CGGGGG   GG GGGGAGCG
                                 TA     TTC  _
GAM985  MGAT1    5'  CCCGCCTCCTTTCCCCGC    14427       C  ___
                                CTCGCC CCT   CCCGC
                                ||||||  |||   |||||
                                GGGCGG GGA   GGGCG
                                   A   AAG
GAM985  MGEA5    5'  CCTTCCCCCTCCTTCTCG    29215     CG      CGCCC
                                CCT  CCCCCTCC    CTCG
                                |||  ||||||||    ||||
                                GGA  GGGGGAGG    GAGC
                                  A_       AA___
GAM985  MMP25    3'  CCTTGTCCTCCCCGCCCCTC   35384     CGCC  CT
                                CCT    CC  CCCGCCCCTC
                                |||    ||  ||||||||||
```

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                                GGA   GG  GGGCGGGGAG
                                  ACA_  AG
GAM985  MNT     3'  CTCTGTCCCCTCCCCGGGCCCC 33712    GC_     ___    _
             CTCGC                  CTC   CCCCTCCC   GCCCC TCGC
                                ||| ||||||||  ||||| ||||
                                GAG  GGGGAGGG  CGGGG AGCG
                                  ACA      GCC    G
GAM985  NCKAP1   5'  CCTCCTCCCCTCCCGCCC    30254     GC
                                CCTC  CCCCTCCCGCCC
                                ||||  ||||||||||||
                                GGAG  GGGGAGGGCGGG
                                  GA
GAM985  NEUD4    3'  CCTCTCCCCCTCCCCCTG    21620     G       GCC   C
                                CCTC CCCCCTCCC   CCT G
                                |||| |||||||||  ||| |
                                GGAG GGGGGAGGG   GGA C
                                  A       ___   _
GAM985  OGDH     3'  CCTCTCCCTCTTCTGACCTGC  45010     GCC    CCGCC_  C
                                CCTC   CCCTC     CCT GC
                                ||||   |||||     ||| ||
                                GGAG   GGGAG     GGA CG
                                  A__     AAGACT  _
GAM985  PAPPA    5'  CCCCGCCCCCCCCTTCGC    15089           __
                                CCTCGCCCCCTCC  CGC
                                ||||||||||||  |||
                                GGGGCGGGGGGGG  GCG
                                       AA
GAM985  PGF      3'  CCTGTCCTTCCCTGCCCCTCG  15248    CGCC  C   _
                                CCT    CC TCCC GCCCCTCG
                                |||    || |||| ||||||||
                                GGA    GG AGGG CGGGGAGC
                                  CA__  A   A
GAM985  PK428    5'  CCTTCCCTCTCCTCTCG     18800    CG   C   CGCCC
                                CCT  CCC CTCC    CTCG
                                |||  ||| ||||    ||||
                                GGA  GGG GAGG    GAGC
                                  A_   A   A____
GAM985  PRDM16   3'  CCCCGCCCGCCTCCGTCCTTCG 35242        _    C C  C
                                CCTCGCCC CCTCC G CC TCG
                                |||||||| ||||| | || |||
                                GGGGCGGG GGAGG C GG AGC
                                     C    _ A  A
GAM985  PTPN11   5'  CCTCCTCCGCCCCCGCCCTTCG 38754     GC  C       C
             C                   CCTC  CC CTCCCGCCC TCGC
                                ||||  || |||||||| ||||
                                GGAG  GG GGGGGCGGG AGCG
                                  GA  C       A
GAM985  PTTG1IP  5'  CCTCGCCATCTGCCCCGCCCCT 20284       CC  __
             CGC                  CCTCGCC  CT  CCCGCCCCTCGC
                                |||||||  ||  ||||||||||||
```

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                                GGAGCGG  GA  GGGCGGGGAGCG
                                    TA  CG
GAM985  PTTG1IP  5'  CTCGCCCCGCTCCCTCG     20286        CTCCC  _
                                CTCGCCCC    GC CCCTCG
                                ||||||||    || ||||||
                                GAGCGGGG    CG GGGAGC
                                    _____  A
GAM985  PVR      3'  CCTCACCCTTGAGCCCTTTGC  27108        CCTCCC   CTC
                                CCTCGCCC    GCCC  GC
                                ||||||||    ||||  ||
                                GGAGTGGG    CGGG  CG
                                    AACT__   AAA
GAM985  RIMS1    5'  CCCGCCCCCTCTGCTCG     43728          CC  CCC
                                CTCGCCCCCTC  GC  TCG
                                ||||||||||  ||  |||
                                GGGCGGGGGAG  CG  AGC
                                     A_  ___
GAM985  ROBO1    5'  TCGCCCTCGGCCCCTCGC    39487       CC  CC
                                TCGCCC  TC  GCCCCTCGC
                                ||||||  ||  |||||||||
                                AGCGGG  AG  CGGGGAGCG
                                   __  C_
GAM985  RPS6KA1  5'  CCGCGCCCCCCCCGAGCCCCTCG 40379    T       CC
           C                    CC CGCCCCCTC  GCCCCTCGC
                                || |||||||||  |||||||||
                                GG GCGGGGGGGG  CGGGGAGCG
                                 C        CT
GAM985  S100B    5'  CTCACCCCTTCCTGGTCTCCTT 26567        C  CGCC__  C
           GC                    CTCGCCCC TCC     CCT GC
                                ||||||||| |||     ||| ||
                                GAGTGGGG AGG     GGA CG
                                    A   ACCAGA   A
GAM985  SET7     5'  CCTTCGCCCACTTGCCCCTCGC 36155     _    C  CCC
                                CCT CGCCC CT   GCCCCTCGC
                                ||| ||||| ||   |||||||||
                                GGA GCGGG GA   CGGGGAGCG
                                  A    T  A__
GAM985  SLC18A3  5'  CTGCGCTCCCCTCCCCTCGC   16829    _  _    CCCG
                                CT CGC CCCCT    CCCCTCGC
                                || ||| |||||    ||||||||
                                GA GCG GGGGA    GGGGAGCG
                                 C   A    _____
GAM985  SLC6A8   5'  CCTCGCCCTCTCCTTCCC    24757        C    CG
                                CCTCGCCC CTCC  CCC
                                |||||||| ||||  |||
                                GGAGCGGG GAGG  GGG
                                    A    AA
GAM985  SOX2     3'  CTCCCCCCTCCAGTTCG     45474     G      CGCCCC
                                CTC CCCCCTCC     TCG
                                ||| ||||||||     |||
```

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                                GAG GGGGGAGG     AGC
                                  _      TCA___
GAM985  SOX2    3'  GCACCCCTCCCATTTCCCTCG  45475    _      C__
                                GC CCCCTCCCG   CCCTCG
                                || |||||||||   ||||||
                                CG GGGGAGGGT   GGGAGC
                                 T       AAA
GAM985  TFCP2   5'  CTCGCTCTCTCCCTCG     24921      CCC   CCGC
                                CTCGC   CTC    CCCTCG
                                |||||   |||    ||||||
                                GAGCG   GAG    GGGAGC
                                  A__   A___
GAM985  TGIF    5'  CCTCCCCTCTCCGCTCCT    17499     CGC     _   C
                                CCT   CCCCTC CCGC CCT
                                |||   |||||| |||| |||
                                GGA   GGGGAG GGCG GGA
                                 ___     A    A
GAM985  TMPRSS3  5'  CCTTTCCCCCTCCCCTC     37061     CG     CCCG
                                CCT  CCCCCT    CCCCTC
                                |||  ||||||    ||||||
                                GGA  GGGGGA    GGGGAG
                                 AA     _____
GAM985  TNFRSF12 3'  TCACCCCCTCTCGACATTCG   19128          C  CCCC
                                TCGCCCCCTC CG    TCG
                                |||||||||| ||    |||
                                AGTGGGGGGAG GC    AGC
                                      A  TGTA
GAM985  WW45    5'  CCTCCTTCCCTCCCGAGCC   34817     GCC      CC
                                CCTC   CCCTCCCG  CC
                                ||||   ||||||||  ||
                                GGAG   GGGAGGGC  GG
                                  GAA       TC
GAM985  ZIC1    5'  CCTCCACTAGCCCCTCGC    18232      C___
                                CCTCC    GCCCCTCGC
                                |||||    |||||||||
                                GGAGG    CGGGGAGCG
                                   TGAT
GAM985  ZNF205   3'  CCTCGCCCTCCCCCATCG    18379        C     CCCC
                                CCTCGCCC CTCCCG    TCG
                                |||||||| ||||||    |||
                                GGAGCGGG GGGGGT    AGC
                                    A     _____
GAM985  AF1Q    5'  CCGCCCCCTCCTGCCTGACTC  27724          C   C__
                                TCGCCCCCTCC GCC   CTC
                                |||||||||||| |||   |||
                                GGCGGGGGAGG CGG   GAG
                                      A   ACT
GAM985  ALK     5'  CCGTCCTCTCCTGCCCCC    43833     C  C    C
                                TCG CC CTCC GCCCCT
                                ||| || |||| ||||||
```

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                                GGC GG GAGG CGGGGG
                                  A A   A
GAM985  ATF4    5'  GCCCCTCCCTGCTTGCAACTC  11725      C   _ CC____
                                GCCCC TCCC GC     CTC
                                ||||| |||| ||     |||
                                CGGGG AGGG CG     GAG
                                  _   A  AACGTT
GAM985  ATP1A1  5'  CCGCCTCCTCCCGCCGCTGC  8692       C       C  C
                                TCGCC CCTCCCGCC CT GC
                                ||||| ||||||||| || ||
                                GGCGG GGAGGGCGG GA CG
                                  A       C  _
GAM985  AXUD1   5'  TCGGTCCAGCCGCCCCTCGC  37493    CCC  TC
                                TCG   CC  CCGCCCCTCGC
                                |||   ||  ||||||||||
                                AGC   GG  GGCGGGGAGCG
                                  CA_  TC
GAM985  BDP1    5'  CCTCTCTCCCGCCGCCGCCGC  32948    CC_      _ _
                                CC   CTCCCGCC CC TCGC
                                ||   |||||||| || ||||
                                GG   GAGGGCGG GG GGCG
                                 AGA       C  C
GAM985  CACNA1C 3'  CCGCCTCCTCTCCCCGCCTC  8748       C   _ G  _
                                TCGCC CCTC CC CC CCTC
                                ||||| |||| || || ||||
                                GGCGG GGAG GG GG GGAG
                                  A   A  _  C
GAM985  CAPON   3'  CCGCCTCCATCTCCTCGCCC  41919    _    CGCC
                                CC CCTCC    CCTCGCCC
                                || |||||    ||||||||
                                GG GGAGG    GGAGCGGG
                                 C    TAGA
GAM985  CAPS    3'  GCCCCTGTGCCCCTCGCTCC  19762      CTCCC       _
                                GCCCC    GCCCCTCGC CC
                                |||||    ||||||||| ||
                                CGGGG    CGGGGAGCG GG
                                  ACA__        A
GAM985  CAPZA1  5'  CCGCCCCTTCCCTGCCCC    43712       C   _
                                TCGCCCC TCCC GCCCC
                                ||||||| |||| |||||
                                GGCGGGG AGGG CGGGG
                                   A   A
GAM985  CBLB    5'  TCTCCCCTCCCGCCCGACTC  20334    GC         __
                                TC  CCCCTCCCGCCC  CTC
                                ||  ||||||||||||  |||
                                AG  GGGGAGGGCGGG  GAG
                                 A_          CT
GAM985  CHRNA2  3'  TCCTCCCCTTCCGGAAGAGCCC 8831     GC    C   CCCCTC
                                TC  CCCCT CCG     GCCC
                                ||  ||||| |||     ||||
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                                AG  GGGGA GGC     CGGG
                                 GA    A   CTTCT_
GAM985  CHRNB2   3'  GCCCTTCCACCCCTTGTCC   8859      CCTC      CG_
                                GCCC   CCGCCCCT   CC
                                ||||   ||||||||   ||
                                CGGG   GGTGGGGA   GG
                                  AA__       ACA
GAM985  COL5A1   5'  TCGCCTCCTCCTCCTC     6420       C    CGCC
                                TCGCC CCTCC   CCTC
                                ||||| |||||   ||||
                                AGCGG GGAGG   GGAG
                                  A    A___
GAM985  COL7A1   5'  CCGCCTCTGTCCCTTGCTCC  6424    _   CCGC   C _
                                CC CCTC   CCCT GC CC
                                || ||||   |||| || ||
                                GG GGAG   GGGA CG GG
                                 C   ACA_   A  A
GAM985  DDX26    5'  TCGTCCCCCCCCGCCTCG    29098    C   T    CC
                                TCG CCCC CCCGCC  TCG
                                ||| |||| ||||||  |||
                                AGC GGGG GGGCGG  AGC
                                  A   _     __
GAM985  DDX26    5'  CCGCCTCCTCCTGCCTGCC   29089     C    C   CCTC
                                TCGCC CCTCC GCC   GCC
                                ||||| ||||| |||   |||
                                GGCGG GGAGG CGG   CGG
                                  A    A   A___
GAM985  DHFR     5'  CCGCCCCGCCCCCTCGTCCC  8991       CTCCCG     _
                                TCGCCCC     CCCCTCG CCC
                                |||||||     ||||||| |||
                                GGCGGGG     GGGGAGC GGG
                                   CG____      A
GAM985  DNM2     5'  GCTCCCGCCCGCCCGGGCC   22385   C  T     CTC
                                GC CCC CCCGCCC   GCC
                                || ||| |||||||   |||
                                CG GGG GGGCGGG   CGG
                                 A  C      CC_
GAM985  EGFL3    5'  CGCGCCCCGCCCCTCGCC    41706    CCCC
                                CGC   TCCCGCCCCTCGCC
                                |||   ||||||||||||||
                                GCG   GGGGCGGGGAGCGG
                                  C___
GAM985  EIF4A1   3'  TCCCCCCTCCTGCTGCTC    10869    G      C  CC
                                TC CCCCCTCC GC  CTC
                                || |||||||| ||  |||
                                AG GGGGGAGG CG  GAG
                                 _      A  AC
GAM985  F7       3'  CCCTCCCTCCCATGCCC     33336       GC   TC
                                CCCTCCC  CCC  GCCC
                                |||||||  |||  ||||
```

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                                GGGAGGG  GGG  CGGG
                                   A_   TA
GAM985  FUT7    3'  CCCCTCCCGTCTGCC      20992         CCC  C
                                CCCCTCCCG   CT GCC
                                |||||||||   || |||
                                GGGGAGGGC   GA CGG
                                    A__  _
GAM985  FZD5    5'  CGCCCCCTCCCTCCCCTCGCC  41046          G
                                CGCCCCCTCCC CCCCTCGCC
                                |||||||||||| |||||||||
                                GCGGGGGAGGG GGGGAGCGG
                                      A
GAM985  GABPA   5'  TCGCCCCCGCCCGCACTC    13038        T    CC
                                TCGCCCCC CCCGC  CTC
                                |||||||| |||||  |||
                                AGCGGGGG GGGCG  GAG
                                    C    T_
GAM985  GCS1    5'  TCTCCGGCTCCCGCCTCTCGCC 26700    G  CC      C
            C                    TC CC  CTCCCGCC CTCGCCC
                                || ||  |||||||| |||||||
                                AG GG  GAGGGCGG GAGCGGG
                                 A  CC       A
GAM985  GRM4    3'  CCGCCCCGGCCCCTCGTCC   9157        CTCCC      _
                                TCGCCCC    GCCCCTCG CC
                                |||||||    |||||||| ||
                                GGCGGGG    CGGGGAGC GG
                                    C____       A
GAM985  GTF2E2  5'  CCGCCCCCTTCCTGCGCCTC   13316        _  C  C
                                TCGCCCCCT CC GC CCTC
                                ||||||||| || || ||||
                                GGCGGGGGA GG CG GGAG
                                      A  A  C
GAM985  HERC2   3'  CCCTCCTCCCGCCTGGCTC   21691    _       C__
                                CCC CCTCCCGCC   CTC
                                ||| |||||||||   |||
                                GGG GGAGGGCGG   GAG
                                  A        ACC
GAM985  HIRA    3'  TCGCCCACCCCTTTGCCC    17743       CCTCCC     C_
                                TCGCCC     GCCCCT  GCCC
                                ||||||     ||||||  ||||
                                AGCGGG     TGGGGA  CGGG
                                   _______     AA
GAM985  HIVEP2  3'  CCTCCCACGAGTTCTTTGCCC  27550        CCC_ ___
                                CCTCCCGC   TC   GCCC
                                ||||||||   ||   ||||
                                GGAGGGTG   AG   CGGG
                                    CTCA  AAA
GAM985  IGFBP2  5'  CGCTTCTTCCTCCTCCCTCGCC 8255     CC___    CGC
            CC                    CGC    CCTCC   CCCTCGCCCC
                                |||    |||||   ||||||||||
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                                GCG    GGAGG   GGGAGCGGGG
                                  AAGAA    A__
GAM985  IRS1    5'  TCGCCTCCTCCCACCCCC    24429      C
                                TCGCC CCTCCCGCCCCT
                                ||||| ||||||||||||
                                AGCGG GGAGGGTGGGGG
                                   A
GAM985  JUNB    3'  TCGCCCCCTCTTCCCCTCCC  13767         CCG     G
                                TCGCCCCCTC   CCCCTC CC
                                ||||||||||   |||||| ||
                                AGCGGGGGAG   GGGGAG GG
                                     AA_     _
GAM985  KCNK10  5'  ACCCCCTCCCCACGCTCC    39679       CCCG   T  _
                                GCCCCCT    CCCC CGC CC
                                |||||||    |||| ||| ||
                                TGGGGGA    GGGG GCG GG
                                   ____    T   A
GAM985  KCNK3   3'  TCGCCCCTCCTGCTGCC     13914       C   C  CCCTC
                                TCGCCCC TCC GC    GCC
                                ||||||| ||| ||    |||
                                AGCGGGG AGG CG    CGG
                                   _   A  A____
GAM985  KCNMB4  5'  CCGCCCCCTCCCGCCCCC    30941
                                TCGCCCCCTCCCGCCCCT
                                ||||||||||||||||||
                                GGCGGGGGGAGGGCGGGGG

GAM985  KCNQ3   5'  TCGCCCCCGCCGGCCGCTTCGC 21131        T  C   C  _
          C                      TCGCCCCC CC GCC CT CGCC
                                ||||||||| || ||| || ||||
                                AGCGGGGG GG CGG GA GCGG
                                     C  C   C  A
GAM985  KCNQ3   5'  TCGCCTTCTCCGCTGCTGC   21132      CC    C  CC  C
                                TCGCC  CTCC GC  CT GC
                                |||||  |||| ||  || ||
                                AGCGG  GAGG CG  GA CG
                                   AA    _  AC  _
GAM985  LMO4    5'  TCGCTCGCTTGCTCGCTCC   27662     CCCCTCC   CC_    _
                                TCGC      CGC   CTCGC CC
                                ||||      |||   ||||| ||
                                AGCG      GCG   GAGCG GG
                                  A_______   AAC    A
GAM985  LNK     5'  CGTCCTCTCCCGCCCGCCGGCT 24199    C  C       _  C  _
          CC                     CG CC CTCCCGCCC CT GC CC
                                || || ||||||||| || || ||
                                GC GG GAGGGCGGG GG CG GG
                                 A  A       C  C  A
GAM985  LYL1    5'  CCGCCTTCTCCCCGCCCC    24577      CC    _
                                TCGCC  CTCCC GCCCC
                                |||||  ||||| |||||
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                                GGCGG  GAGGG CGGGG
                                  AA     G
GAM985  MAF     5'  GCTCCCTCGCTCGCCC     23834    C    CCGCCC
                                GC CCCTC     CTCGCCC
                                || |||||     |||||||
                                CG GGGAG     GAGCGGG
                                 A    C_____
GAM985  MAP3K9   5'  TCGTCCTCGCCCGCCGCCTC   41360     C  CCT    _
                                TCG CC   CCCGCC CCTC
                                ||| ||   |||||| ||||
                                AGC GG   GGGCGG GGAG
                                 A  AGC     C
GAM985  MAPK3    5'  TCCTCCCCTCCCACCGCCC   43848    GC        CCTC
                                TC  CCCCTCCCGCC   GCCC
                                ||  ||||||||||   ||||
                                AG  GGGGAGGGTGG   CGGG
                                 GA        _____
GAM985  MDFI     3'  CCCCCTCCCGCCCCACCCC   24613           TC
                                CCCCCTCCCGCCCC  GCCCC
                                ||||||||||||| |||||
                                GGGGGAGGGCGGGG  TGGGG
                                          __
GAM985  MGAT3    5'  TCGCCCCATCCCGGGCTC    14466       C    CCC
                                TCGCCCC TCCCG   CTC
                                ||||||| |||||   |||
                                AGCGGGG AGGGC   GAG
                                    T    CC_
GAM985  MMP25    3'  CCTCCCCGCCCCTCCCC    35383    CT       G
                                CC  CCCGCCCCTC CCC
                                ||  |||||||||| |||
                                GG  GGGCGGGGAG GGG
                                 AG        _
GAM985  MMP25    3'  CCGCGGGCCCGCCCCTTGTCC  35382     CCCCT       CG_
                                TCGC    CCCGCCCCT   CC
                                ||||    |||||||||   ||
                                GGCG    GGGCGGGGA   GG
                                  CCC__       ACA
GAM985  MOX2     3'  TCGCTCCCACCTCTTTTGC   42524     CCCC     C  C__
                                TCGC    TCCCGCC CT   GC
                                ||||    ||||||| ||   ||
                                AGCG    AGGGTGG GA   CG
                                  _____      A  AAA
GAM985  MPST     5'  TCCCCTCCTCCCGCCCCC    34441    G  _
                                TC CCC CCTCCCGCCCCT
                                || ||| ||||||||||||
                                AG GGG GGAGGGCGGGGG
                                 _  A
GAM985  MTL5     5'  TCGCCCCCCGCGAGCTTCGCC  22271         CCC_ CCC
                                TCGCCCCCT   GC   TCGCC
                                |||||||||   ||   |||||
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                                AGCGGGGGGG   CG  AGCGG
                                     CGCT  A__
GAM985  MUC12   3'  TCTCCTCTTGACCCGCCCC   45333   GC  C ___
                                TC  CC CT   CCCGCCCC
                                ||  || ||   ||||||||
                                AG  GG GA   GGGCGGGG
                                 A_  A  ACT
GAM985  MXI1    5'  CCGCCCCCTCCCGCCCCT    39015
                                TCGCCCCCTCCCGCCCCT
                                ||||||||||||||||||
                                GGCGGGGGAGGGCGGGGA

GAM985  NCKAP1  5'  TCCTCCCCTCCCGCCCGCGACC 30258   GC        CT  _
                                TC  CCCCTCCCGCCC  CG CC
                                ||  ||||||||||||  || ||
                                AG  GGGGAGGGCGGG  GC GG
                                 GA         C_  T
GAM985  NEO1    5'  CCTTCCCTCCCGCGCGCCTC   14752   __      C__
                                CC  CCCTCCCGC   CCTC
                                ||  |||||||||   ||||
                                GG  GGGAGGGCG   GGAG
                                 AA       CGC
GAM985  NMBR    5'  CCCTCCCTCTCGCCC      14802       GCCC
                                CCCTCCC   CTCGCCC
                                |||||||   |||||||
                                GGGAGGG   GAGCGGG
                                    A___
GAM985  OSBP    5'  TCACCCCCTCCCATCGC    14988          CCCC
                                TCGCCCCCTCCCG   TCGC
                                ||||||||||||   ||||
                                AGTGGGGGAGGGT   AGCG
                                          ____
GAM985  PAPPA   5'  CCGCCCCCCCCCTTCGCCCC   15090         __
                                TCGCCCCCTCC  CGCCCC
                                ||||||||||  ||||||
                                GGCGGGGGGGG  GCGGGG
                                      AA
GAM985  POU5F1  3'  CCTCCCCTCCCCCTGTCCC   15472      G_   CG_
                                CCTCCC  CCCCT   CCC
                                ||||||  |||||   |||
                                GGAGGG  GGGGG   GGG
                                   GA    ACA
GAM985  PRKCABP 3'  TCGCCCCCTTGCGCGGCGGCCC 29673        CC   CCCTC
          C                  TCGCCCCCT  CGC    GCCCC
                                |||||||||  |||    |||||
                                AGCGGGGGA  GCG    CGGGG
                                     AC   CCGC_
GAM985  PRX     3'  GCTCCTCAGCACCCTCGCCCC  34124    CC    CC  _
                                GC  CCTC  GC CCCTCGCCCC
                                ||  ||||  || ||||||||||
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                                CG  GGAG  CG GGGAGCGGGG
                                 A_   T_  T
GAM985  PTGFRN   3'  TCGCCCCTTCCTGCCAGCCC  42599       C   C   CCTC
                                TCGCCCC TCC GCC   GCCC
                                ||||||| ||| |||   ||||
                                AGCGGGG AGG CGG   CGGG
                                    A  A  T___
GAM985  PTPN11   5'  TCGCTCCTCCTCCGCCCC   38758     _ _    C
                                TCGC CC CCTCC GCCCC
                                |||| || ||||| |||||
                                AGCG GG GGAGG CGGGG
                                  A A    _
GAM985  PVR      3'  TCACCCTTGAGCCCTTTGCCCC 27113      CCTCCC   CTC
                                TCGCCC    GCCC  GCCCC
                                ||||||    ||||  |||||
                                AGTGGG    CGGG  CGGGG
                                   AACT__   AAA
GAM985  RAB1A    5'  TCGGCCCCTCCCTGCTCC   43189    C      _ C
                                TCG CCCCTCCC GC CC
                                ||| |||||||| || ||
                                AGC GGGGAGGG CG GG
                                  C      A A
GAM985  RIMS1    5'  CCGCCCCCTCTGCTCGC    43730         CC  CCC
                                TCGCCCCCTC  GC   TCGC
                                |||||||||  ||  ||||
                                GGCGGGGGAG  CG   AGCG
                                     A_ ___
GAM985  ROBO1    5'  TCGCCCTCGGCCCCTCGCCC  16362      CC  CC
                                TCGCCC  TC  GCCCCTCGCCC
                                ||||||  ||  ||||||||||
                                AGCGGG  AG  CGGGGAGCGGG
                                   __  C_
GAM985  ROR1     5'  TCGCCTCCGCCTGGCCGCCTC  22702      C  T  C_  _
                                TCGCC CC CC  GCC CCTC
                                ||||| || ||  ||| ||||
                                AGCGG GG GG  CGG GGAG
                                   A  C  AC   C
GAM985  SET7     5'  TCGCCCACTTGCCCCTCGCC   36161      C  CCC
                                TCGCCC CT   GCCCCTCGCC
                                |||||| ||  ||||||||||
                                AGCGGG GA   CGGGGAGCGG
                                   T  A__
GAM985  SHH      3'  CGCCCCCTCCCGCGCC      6794           CCCTC
                                CGCCCCCTCCCGC    GCC
                                ||||||||||||    |||
                                GCGGGGGAGGGCG    CGG
                                      _____
GAM985  SIRT1    5'  GCCCTCCTCCCTCGCCTC    29254     _     GCC
                                GCCC CCTCCC   CCTC
                                |||| ||||||   ||||
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                                CGGG GGAGGG   GGAG
                                  A     AGC
GAM985  SLC6A8   5'  TCGCCCTCTCCTTCCCGGC   24787      C   CG   CTC
                                TCGCCC CTCC  CCC   GC
                                |||||| ||||  |||   ||
                                AGCGGG GAGG  GGG   CG
                                   A   AA  C__
GAM985  SOX11    3'  GCTTTCTTCCTCTCACCCC   17024    CCCC  CCG  C
                                GC   TC   CC CTCGCCCC
                                ||   ||   || ||||||||
                                CG   AG   GG GAGTGGGG
                                 AA__  AA_  A
GAM985  SOX2     3'  GCACCCCTCCCATTTCCCTCG  45475   _      C__
                                GC CCCCTCCCG   CCCTCG
                                || |||||||||   ||||||
                                CG GGGGAGGGT   GGGAGC
                                 T       AAA
GAM985  TCAP     3'  CCCTCACCAGTACCTTTTGTCC 18948     _  CC_  CG___
              C                  CCCTC CCG   CCT    CCC
                                |||||  |||   |||    |||
                                GGGAG GGT   GGA    GGG
                                   T   CAT   AAACA
GAM985  TCF7L2   5'  TCACCCCCTCAAAGTTTTGCCC 36252         CCGCCCCTC
              C                  TCGCCCCCTC       GCCCC
                                ||||||||||       |||||
                                AGTGGGGGGAG       CGGGG
                                     TTTCAAAA_
GAM985  TCF8     3'  CCGCCCCTTCCTGCCGCCTC   36237      C   C   _
                                TCGCCCC TCC GCC CCTC
                                ||||||| ||| ||| ||||
                                GGCGGGG AGG CGG GGAG
                                   A   A   C
GAM985  TFCP2    5'  CCGCCCCTTTCTGCTGGAGGAC 24920       C_  CC  CCCTC_
              CCC                  TCGCCCC  TC  GC     GCCCC
                                |||||||  ||  ||     |||||
                                GGCGGGG  AG  CG     TGGGG
                                   AA  A_  ACCTCC
GAM985  TFCP2    5'  GCACCTTTTCCCCCGCCCC   24923    _  C___
                                GC CC   CTCCCGCCCC
                                || ||   ||||||||||
                                CG GG   GGGGGCGGGG
                                 T  AAAA
GAM985  TGIF     5'  CCCCTCTCCGCTCCTTTGTTCC 17498      _   C   CG___
                                CCCCTC CCGC CCT    CC
                                |||||| |||| |||    ||
                                GGGGAG GGCG GGA    GG
                                   A   A   AACAA
GAM985  TMPRSS2  5'  CGCTCCCCGCCCCTCGCCC   24934    CCCC
                                CGC   TCCCGCCCCTCGCCC
                                |||   ||||||||||||||
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                                GCG   GGGGCGGGGAGCGGG
                                  A___
GAM985  UBE3A   5'  TCGCCCTCGCCCGCCGCCTC  39283      CCT    _
                                TCGCCC  CCCGCC CCTC
                                ||||||  |||||| ||||
                                AGCGGG  GGGCGG GGAG
                                   AGC    C
GAM985  WEE1    5'  CCGCTTCTTGCCCCTCGTCCC  18085     CCCC  CC     _
                                TCGC   TC  GCCCCTCG CCC
                                ||||   ||  |||||||| |||
                                GGCG   AG  CGGGGAGC GGG
                                  A___  AA      A
GAM985  WNT6    3'  CGTTCCTCTCAAGCCCCTCGCC 27179   CC  _  CC
                                CG  CC CTC  GCCCCTCGCC
                                ||  || |||  ||||||||||
                                GC  GG GAG  CGGGGAGCGG
                                 AA  A   TT
GAM985  YY1     5'  CGCCTCCTCCCGCCCTC    18170     C       C
                                CGCC CCTCCCGCCC TC
                                |||| ||||||||||| ||
                                GCGG GGAGGGCGGG AG
                                  A       _
GAM985  YY1     5'  CCCCGCCTCCCTCGCC     18167     TC  GC
                                CCCC  CC  CCCTCGCC
                                ||||  ||  ||||||||
                                GGGG  GG  GGGAGCGG
                                  C_  A_
GAM985  ZIC1    5'  CCTCCACTAGCCCCTCGCCC  18233     C___
                                CCTCC   GCCCCTCGCCC
                                |||||   ||||||||||
                                GGAGG   CGGGGAGCGGG
                                   TGAT
GAM985  ZNF205  3'  GCCCTTTCTCGCCCTCGCCC  18381     CC  C    C
                                GCCC  TC CGCCC TCGCCC
                                ||||  || ||||| ||||||
                                CGGG  AG GCGGG AGCGGG
                                  AA  A    _
GAM986  AK3     3'  TATGGAGCGTGGATGTAGAA  30184      A  GTAC
                                TATGGA CG   TGGATGTAGAA
                                |||||| ||   ||||||||||
                                ATACCT GC   ACCTACATCTT
                                   C  _____
GAM986  CYP3A4  3'  ATGGAATGCAAGAGGTGTAG  32710      CG  CT_  A
                                ATGGAA  GTA   GG TGTAG
                                ||||||  |||   || |||||
                                TACCTT  CGT   CC ACATC
                                   A_   TCT  _
GAM986  EMX2    3'  TGGGATGGGGCTAGATATGGAA 44702    AAC  TA      A
                                TGG   GG  CTGGATGT GAA
                                |||   ||  |||||||| |||
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                                ACC   CC  GATCTATA CTT
                                  CTA  CC       C
GAM986  GCK      3'  TATGGGAGCTGAAGATGTAG  37931      AAC   ACT
                                TATGG   GGT   GGATGTAG
                                ||||||   |||   ||||||||
                                ATACC   TCG   TCTACATC
                                   C__   ACT
GAM986  TNFRSF6B 3'  TGGGGTGCCAAGGATGTAGAA 32365     AAC   A __
                                TGG   GGT CT  GGATGTAGAA
                                |||   ||| ||  ||||||||||
                                ACC   CCA GG  CCTACATCTT
                                  ___   C  TT
GAM986  APXL     3'  GATAACAGAGACAAATGC    11620          CTTCC
                                GATAACAGAG    AATGC
                                ||||||||||    |||||
                                CTATTGTCTC    TTACG
                                      TGT__
GAM986  CD58     3'  ATGACAGCCAAAACTAATGC  12131       A_      TCC
                                ATGATA  CAGAGCT   AATGC
                                ||||||  |||||||   |||||
                                TACTGT  GTTTTGA   TTACG
                                   CG      ___
GAM986  MAN1A1   3'  TGATAGCAGAGCTCTG      45101       A       CCAA
                                TGATA CAGAGCTT    TG
                                ||||| ||||||||    ||
                                ACTAT GTCTCGAG    AC
                                   C       _____
GAM986  PAFAH1B1 3'  CATGACAAAAATTCCAATG   7702        TAA    C
                                TATGA   CAGAG TTCCAATG
                                |||||   ||||| ||||||||
                                GTACT   GTTTT AAGGTTAC
                                   ___     T
GAM986  PRB1     3'  TATGATGACCTTTTTCCAATG  22773       A  AGAGC
                                TATGAT AC     TTCCAATG
                                |||||| ||    ||||||||
                                ATACTA TG     AAGGTTAC
                                   C  GAAA_
GAM986  TRPS1    3'  TGATATGTATTTTCCAATGC   30472       ACAGAGC
                                TGATA      TTCCAATGC
                                |||||      |||||||||
                                ACTAT      AAGGTTACG
                                   ACATAA_
GAM987  MCF2     5'  TGAAATACGAGCTGCTTCTTGG 23864           _  ACCGA__
            GTAG                   TGGAATACGAGC GT      GTAG
                                |||||||||||| ||      ||||
                                ACTTTATGCTCG CG      CATC
                                      A  AAGAACC
GAM988  BID      3'  TTCAAGTATATTAATGTA    10181          CAACA
                                TTCAGGTATAT    AATGTA
                                ||||||||||    ||||||
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                                AAGTTCATATA    TTACAT
                                      A____
GAM988  RDX     3'  AGTTACCAACAAATGTATA   16234    A
                                GGT TATCAACAAATGTATA
                                ||| ||||||||||||||||
                                TCA ATGGTTGTTTACATAT
                                 _
GAM988  ADRA2B  3'  TTTATATCACCATATAAT    8654       C
                                TTTATA CATCATATAAT
                                |||||| ||||||||||
                                AAATAT GTGGTATATTA
                                   A
GAM989  EP300   5'  TCCTTTTTCTCTTCGCCG    10999     GTTACTAG
                                TCCT       CTCTTCGCCG
                                ||||       ||||||||||
                                AGGA       GAGAAGCGGC
                                  AAAA_____
GAM989  PSMD9   3'  TCCTGTTACTGTTCCCCAG   15848         AGCTC   G
                                TCCTGTTACT    TTC CCGG
                                ||||||||||    ||| ||||
                                AGGACAATGA    AAG GGTC
                                      C_____   G
GAM990  RGL     3'  TATTTTACATTGCAGTATATAA 31544        _____
            ATCTA                 TATTTTAT   CGGTATATAAATCTA
                                ||||||||   ||||||||||||||||
                                ATAAAATG   GTCATATATTTAGAT
                                     TAAC
GAM990  CUL3    3'  GGAAAATCATGTCAATT     18737         ATA
                                GGAAAATCAT   TAATT
                                ||||||||||   |||||
                                CCTTTTAGTA   GTTAA
                                      CA_
GAM990  ITCH    3'  TAGGAAAATCTTGTATAT    36456         A__
                                TAGGAAAATC   TATAT
                                ||||||||||   |||||
                                ATCCTTTTAG   ATATA
                                      AAC
GAM991  GEM     3'  ATTCTGATTTTAAAAATATTTT 23544       GTT___
            TAT                   ATTCTGGT     AATATTTTTAT
                                ||||||||     ||||||||||||
                                TAAGACTA     TTATAAAAATA
                                     AAATTT
GAM991  PTGFRN  3'  TTCTGGGGCTATTTTTAT    42608       T  TAA
                                TTCTGG GT   TATTTTTAT
                                |||||| ||   |||||||||
                                AAGACC CG   ATAAAAATA
                                   C  ___
GAM991  SCML2   3'  ATTCTGATAAAATATTTTTAT  25885        TT
                                ATTCTGGTG  AATATTTTTAT
                                |||||||||  ||||||||||
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                                TAAGACTAT  TTATAAAAATA
                                     T_
GAM991  XYLB    3'  CTCTGGTGTTCTTTTATA    23022         AATA
                                TTCTGGTGTT   TTTTTATA
                                ||||||||||  ||||||||
                                GAGACCACAA   GAAAATAT
                                     _____
GAM991  MYO5A   3'  TAATATCTCTATATCATAGTGA 40757      _ AG       A
                                TAATA CT  TATATCATA TGA
                                ||||| ||  |||||||||| |||
                                ATTAT GA  ATATAGTAT ACT
                                   A  G_       C
GAM992  OGT     5'  CTACTAGGAATATGCTGGC   18783        C_____
                                CTACTAGG    GCTGGC
                                ||||||||    ||||||
                                GATGATCC    CGACCG
                                     TTATA
GAM992  XRCC3   3'  CACTACTAGAGACAAGGC    24100         C  T_
                                TACTACTAGG GC  GGC
                                |||||||||| ||  |||
                                GTGATGATCT TG  CCG
                                     C  TT
GAM992  MBL2    3'  GCCTGACTGGAGCACTTCATTA 6962         A     A_  C
           TA                    GCCTGACT GAGTAC  CA TATA
                                ||||||||  ||||||  || ||||
                                CGGACTGA CTCGTG  GT ATAT
                                     C     AA  A
GAM992  PUM1    3'  CTACACCAAGTATACACTATA  31233    _   G   C
                                CTG ACTA AGTA ACACTATA
                                ||| |||| |||| ||||||||
                                GAT TGGT TCAT TGTGATAT
                                  G   _   A
GAM992  TPM1    3'  CGCTGACTAAGCACAC      7483      C    A
                                CGC TGACT GAGTACAC
                                ||| ||||| ||||||||
                                GCG ACTGA TTCGTGTG
                                  _   _
GAM993  ADAM12  3'  TCTTTGTCCAATATCTACGAAT 18479      T      GTGT
           A                     TCTTT GTCCAATA   CGAATA
                                ||||| ||||||||   ||||||
                                AGAAA CAGGTTAT   GCTTAT
                                   _      AGAT
GAM993  EFG2    3'  TCTTTTATCTAGTTCTCTGAAT 37035        CAA   G_  _
                                TCTTTTGTC   TAGT  TC GAAT
                                |||||||||  ||||  || ||||
                                AGAAAATAG   ATCA  AG CTTA
                                     ____   AG  A
GAM993  LUZP1   3'  CTTTTGTCCAGTGTTAA    37960         ATA   CG
                                CTTTTGTCCA   GTGT  A
                                ||||||||||  ||||  |
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                                GAAAACAGGT   CACA  T
                                     ____    AT
GAM993   C5R1     3'  TGCCATTGGGGGAGGCTG    11927         AAAA  A
                                TGCTATTGG    AG CTG
                                |||||||||    || |||
                                ACGGTAACC    TC GAC
                                     CCC_  C
GAM993   CDH17    3'  TAATACTAAGGGAAAAGGCTG  19791         TT     A A
                                TAGTGCTA  GGAAAA G CTG
                                ||||||||  |||||| | |||
                                ATTATGAT  CCTTTT C GAC
                                     TC     _ C
GAM993   F13A1    3'  GTGCTATTATTCCCAAAAGGCT 44981         GA___     A
              G                  GTGCTATTG     AAAAG CTG
                                |||||||||     ||||| |||
                                CACGATAAT     TTTTC GAC
                                     AAGGG     C
GAM993   ITGAM    3'  TAGTATATCAAAAGAAGACTG  43517       C   TG   A
                                TAGTG TAT  GAA AAGACTG
                                ||||| |||  ||| |||||||
                                ATCAT ATA  TTT TTCTGAC
                                   _  GT   C
GAM993   LGMN     3'  TAGTTTTTCAGAAAAGACTG   24686      GCTA TG     A
                                TAGT    T  GAAAA GACTG
                                ||||    |  ||||| |||||
                                ATCA    A  CTTTT CTGAC
                                  AAA_ GT    _
GAM993   PAM      3'  AGTGCTATTGGGAAAATACTG  39883          A    G
                                AGTGCTATTGG AAAA ACTG
                                |||||||||||| |||| ||||
                                TCACGATAACC TTTT TGAC
                                     C    A
GAM993   PSEN1    3'  GCTGTAGAAAAAGACTG     28739     AT
                                GCT  TGGAAAAAGACTG
                                |||  ||||||||||||
                                CGA  ATCTTTTTCTGAC
                                  C_
GAM993   TNFSF4   3'  TAGTGCTATTTGACATCAGA   17751         G  AAA_
                                TAGTGCTATT GA    AGA
                                |||||||||| ||    |||
                                ATCACGATAA CT    TCT
                                     A  GTAG
GAM994   CIT      3'  ATAGTGTGTTTGGTGTTTT    43038      _    C
                                ATGG GTGTT GGTGTTTT
                                |||| ||||| ||||||||
                                TATC CACAA CCACAAAA
                                  A    A
GAM994   SOX9     3'  TTTTAAGGCTCAAGGTGTTTT  7378        T    GTTC
                                TTTTA GGGT    GGTGTTTT
                                ||||| ||||    ||||||||
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                                AAAAT TCCG    CCACAAAA
                                  _   AGTT
GAM994  SPF30    3'  TTTTAGCAGGTTGGTGTTTT  25241      _    GTTC
                                TTTTA TGGGT    GGTGTTTT
                                ||||| |||||    ||||||||
                                AAAAT GTCCA    CCACAAAA
                                   C    A___
GAM994  FBN1     5'  CCGCGCCCGGGGCTCG      42053    A      AGAT
                                CC CGCCCGGG    TTCG
                                || ||||||||    ||||
                                GG GCGGGCCC    GAGC
                                 C       C___
GAM995  BLAME    3'  AAACTGCAGGGTCTGGGG    33481         AGTTC   CC
                                AAGCTGCAG    GTCT  GG
                                |||||||||    ||||  ||
                                TTTGACGTC    CAGA  CC
                                      C____    CC
GAM995  CDKN2C   5'  GCTCGGCGCGCGTCTCCGGAG  38564     GCAGA  T
                                GCT    GT CGTCTCCGGAG
                                |||    || ||||||||||
                                CGA    CG GCAGAGGCCTC
                                  GCCG_  C
GAM995  DNMT3L   5'  GCTCAGGGTCCCCGG       30056     G   AGTTC
                                GCT CAG    GTCTCCGG
                                ||| |||    ||||||||
                                CGA GTC    CAGGGGCC
                                  _  C____
GAM995  EDARADD  5'  GCTGGCAGGCCTCCGG      38849     _   AGTTC
                                GCTG CAG    GTCTCCGG
                                |||| |||    ||||||||
                                CGAC GTC    CGGAGGCC
                                  C  _____
GAM995  GCN5L2   3'  AGCTGCAGGATCGGGTCCGGAG 40810        AGT   TC
                                AGCTGCAG   TCG  TCCGGAG
                                ||||||||   |||  |||||||
                                TCGACGTC   AGC  AGGCCTC
                                     CT_   CC
GAM995  GNAI2    3'  AAGCTGGGGGTCCAGGCTGGAG 42645      CAGA    TCTCC
                                AAGCTG    GTTCG    GGAG
                                ||||||    |||||    ||||
                                TTCGAC    CAGGT    CCTC
                                   CCC_    CCGA_
GAM995  HSF4     5'  AGCTGCAGAGTCCGCAGAG   40760           CTCC
                                AGCTGCAGAGTTCGT   GGAG
                                ||||||||||||||   ||||
                                TCGACGTCTCAGGCG   TCTC
                                                  ____
GAM995  MYCL2    3'  AGCTGCAGAGTCCAGCTGGGG  23895           T  CC
                                AGCTGCAGAGTTCG CT  GG
                                |||||||||||||| ||  ||
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                                TCGACGTCTCAGGT GA  CC
                                       C  CC
GAM995  NESH     3'  GCTGCAGAGGGGTGTCTGGGG  32339         TTC_   CC
                                GCTGCAGAG   GTCT  GG
                                |||||||||   ||||  ||
                                CGACGTCTC   CAGA  CC
                                     CCCA   CC
GAM995  PA2G4    3'  ACTTGCAGAACTCTGGA     43416    _     TTCGT   C
                                GCT GCAGAG    CTC GGA
                                ||| ||||||    ||| |||
                                TGA CGTCTT    GAG CCT
                                  A     _____  A
GAM995  PODXL    5'  GCCTGTGGGTGGCTCCGGAG   23976    GCAGA  TC T
                                GCT    GT  G CTCCGGAG
                                |||    ||  | ||||||||
                                CGG    CA  C GAGGCCTC
                                  ACACC  C_ _
GAM995  REQ      3'  GCCGCAGAGAGCCACTCTGGAG 26546         T_  T   C
                                GCTGCAGAG  TCG CTC GGAG
                                |||||||||  ||| ||| ||||
                                CGGCGTCTC  GGT GAG CCTC
                                     TC   _  A
GAM995  SLC21A2  3'  AGGTGCAGAGTCAGTCTGGGG  24795    C       C   CC
                                AG TGCAGAGTT GTCT  GG
                                || |||||||| ||||  ||
                                TC ACGTCTCAG CAGA  CC
                                 C       T   CC
GAM995  ZNF80    5'  AAGCTGCAGACGTTTGCGG    28328         GTT   CTC
                                AAGCTGCAGA   CGT   CGG
                                ||||||||||   |||   |||
                                TTCGACGTCT   GCA   GCC
                                     ___   AAC
GAM995  GAS7     3'  CACTTGACAGATGAGTGCACGG 25265      C       CTT__
           A                     CACT GGCAGATGA     CGGA
                                ||||| |||||||||     ||||
                                GTGA CTGTCTACT     GCCT
                                  A        CACGT
GAM995  GRM4     3'  CACACGGCAGATGGGCGG     9154      T       ACTT
                                CAC CGGCAGATG    CGG
                                ||| |||||||||    |||
                                GTG GCCGTCTAC    GCC
                                  T        CC__
GAM995  RANBP3   5'  TCGGCAGCTTCGGAAG      28766       ATGA
                                TCGGCAG   CTTCGGAAG
                                |||||||   |||||||||
                                AGCCGTC   GAAGCCTTC
                                     _____
GAM995  SREBF2   3'  CTCGGCAGGTGACAGCTAAGA 21402         A   TTCGG
                                CTCGGCAG TGAC    AAGA
                                |||||||| ||||    ||||
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                                GAGCCGTC ACTG    TTCT
                                    C   TCGA_
GAM995  TNFRSF6B  5'  CTCGGCAACACGGAAG     37282       ATGACTT
                                CTCGGCAG     CGGAAG
                                ||||||||     ||||||
                                GAGCCGTT     GCCTTC
                                    GT_____
GAM996  ACN     5'  CCATCCGCCCTGCAGCGCCCCT 31408        GATTAA_
                                CCATCCGCCC     CCCCT
                                ||||||||||     |||||
                                GGTAGGCGGG     GGGGA
                                     ACGTCGC
GAM996  ADRA2A   3'  CCCCCATCCATTAACC     8629         GCCCG
                                TCCCCATCC    ATTAACC
                                |||||||||    |||||||
                                GGGGGTAGG    TAATTGG
                                     _____
GAM996  AP2B1    3'  TCCCCATCTCTACTCAAATTCC 10494       C__  C   TTAA
                                TCCCCATC   GC CGA   CC
                                ||||||||   || |||   ||
                                AGGGGTAG   TG GTT   GG
                                    AGA  A   TAA_
GAM996  AQP6     3'  TCCTCACCCGCCCCCGCCT   38256    C      GATTAA  _
                                TCC CATCCGCCC     CC CCT
                                ||| |||||||||     || |||
                                AGG GTGGGCGGG     GG GGA
                                  A       _______  C
GAM996  ARHGEF5  3'  TCTCCATCCACAGAAGGCCTCT 24129    C      CC  TTAA  C
                                TC CCATCCGC  GA   CC CT
                                || ||||||||  ||    || ||
                                AG GGTAGGTG  CT    GG GA
                                 A       T_  TCC_  A
GAM996  ARHGEF5  3'  CCCATCTGATGTGTTAACCCCT 24127       CGCCCGA
                                CCCATC      TTAACCCCT
                                ||||||      |||||||||
                                GGGTAG      AATTGGGGA
                                   ACTACAC
GAM996  ARHGEF6  3'  TCCCCATCTGGCCAAATT    42803       C_  C
                                TCCCCATC  GCC GATT
                                ||||||||  ||| ||||
                                AGGGGTAG  CGG TTAA
                                    AC   T
GAM996  CCNT2    5'  TCCTCCTCCGCCCGCTCC    38495    _ A      ATTAA
                                TCC CC TCCGCCCG    CC
                                ||| || ||||||||    ||
                                AGG GG AGGCGGGC    GG
                                  A  _       GA___
GAM996  CRY2     3'  TCCCCATCCCTGAGTCCC    43587        GCCC  TTAAC
                                TCCCCATCC    GA    CCC
                                |||||||||    ||    |||
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                                AGGGGTAGG   CT    GGG
                                     GA__  CA___
GAM996  DAAM2    3'  TCCCCATCTCCCCAGTTTCCCT 45180       CG   A  AAC
                                TCCCCATC  CCCG TT   CCCT
                                ||||||||  |||| ||   |||||
                                AGGGGTAG  GGGT AA   GGGA
                                     AG   C  A__
GAM996  ERBB2IP  3'  TCCCCATTCTTTGCTTCCAGAT 33102       _ C__  __ _
           T                     TCCCCAT C   GC  CC GATT
                                ||||||| |   ||  || ||||
                                AGGGGTA G   CG  GG CTAA
                                     A AAA  AA  T
GAM996  GSTM5    3'  TCCCCATCAGCCTAGCCCC   9207        C   CGAT  A
                                TCCCCATC GCC    TA CCCC
                                |||||||| |||    || ||||
                                AGGGGTAG CGG    AT GGGG
                                     T  _____  C
GAM996  HRMT1L2  3'  TCCCCATCCCCCCCAGCCCAGGC 11362        G   A_  A_
           CCCT                    TCCCCATCC CCCG  TTA  CCCCT
                                |||||||||  ||||  |||  |||||
                                AGGGGTAGG GGGT  GGT  GGGGA
                                     G   CG   CC
GAM996  JUP      3'  TCCCCATCTCCCCTGGACGGTC 13781        CG   __   TAAC
           CCT                     TCCCCATC  CCC  GAT    CCCT
                                |||||||  |||  |||    ||||
                                AGGGGTAG  GGG  CTG    GGGA
                                     AG   AC   CCA_
GAM996  LARGE    3'  TCCCCATCGCTATAGCCCC   21868        C  CCGAT  A
                                TCCCCATC GC     TA CCCC
                                |||||||| ||     || ||||
                                AGGGGTAG CG     AT GGGG
                                     _  AT___  C
GAM996  MAB21L1  3'  TCTCCATCCGCTTCCCCT    24591    C      CCGATTAA
                                TC CCATCCGC       CCCCT
                                || ||||||||       |||||
                                AG GGTAGGCG       GGGGA
                                 A       AA_______
GAM996  NDRG1    3'  CCCATCCGTACTCAGCCTCT   40574        CCCGA   A  C
                                CCCATCCG     TTA CC CT
                                ||||||||     ||| || ||
                                GGGTAGGC     AGT GG GA
                                     ATG__   C  A
GAM996  NESH     3'  TCCCCATCTGCAGCAGGCCTCT 32343        C  CCGATTAA  C
                                TCCCCATC GC       CC CT
                                |||||||| ||       || ||
                                AGGGGTAG CG       GG GA
                                     A  TCGTCC__  A
GAM996  OPA3     3'  CCACCACGCCCGGTTAAC    36069      _     A
                                CCATC CGCCCG TTAAC
                                ||||| |||||| |||||
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                                GGTGG GCGGGC AATTG
                                  T     C
GAM996  P2RX3    5'  TCCCCATTCCTCCAACCCC   14996       _  G  CGATT
                                TCCCCAT CC CC    AACCCC
                                ||||||| || ||    ||||||
                                AGGGGTA GG GG    TTGGGG
                                   A  A  _____
GAM996  POLR2E   3'  TCTCCTGTCTGTCCCTCCCCT  40926    _  CA  CG_  GATTAA
                                TC CC  TC   CCC     CCCCT
                                || ||  ||   |||     |||||
                                AG GG  AG   GGG     GGGGA
                                 A  AC  ACA  A_____
GAM996  POLR2E   3'  TCCCCATCTCTCCTGTCTGTCC 40925        CGC  GATTAAC
           CT                     TCCCCATC   CC      CCCT
                                ||||||||   ||      ||||
                                AGGGGTAG   GG      GGGA
                                    AGA  ACAGACA
GAM996  S100A12  5'  CCCAGCCTAATGTTAACCCCT  24737     TCC   CG  __
                                CCCA   GCC  AT  TAACCCCT
                                ||||   |||  ||  ||||||||
                                GGGT   CGG  TA  ATTGGGGA
                                  ___   AT  CA
GAM996  ZNF278   5'  TCTCCGCCCGCCCGCCTCCCCT 36810    C  AT      ATTAA
                                TC CC  CCGCCCG    CCCCT
                                || ||  |||||||    |||||
                                AG GG  GGCGGGC    GGGGA
                                 A  CG      GGA__
GAM997  AGR2     3'  TGGTGTGGTGAGATGATAAC   26926     CA     C    G
                                TGG  TGGTGA ATGA TGAT
                                |||  |||||| |||| ||||
                                ACC  ACCACT TACT ATTG
                                  AC     C   _
GAM997  APM1     3'  TGGCATGGTGGTAGGCACCTGT 22022          A____   GA
           G                     TGGCATGGTG    CAT  GTG
                                ||||||||||    |||  |||
                                ACCGTACCAC    GTG  CAC
                                      CATCC   GA
GAM997  CLECSF12 3'  TGGCATGGTGGCATGCACCTG  44127          A    AGTGA
                                TGGCATGGTG CATG    TG
                                |||||||||| ||||    ||
                                ACCGTACCAC GTAC    AC
                                      C    GTGG_
GAM997  DNASE1L1 3'  TGGCAGGTGGCATGAGT     27504      T    A
                                TGGCA GGTG CATGAGT
                                ||||| |||| |||||||
                                ACCGT CCAC GTACTCA
                                   _    C
GAM997  EPB72    3'  GGCATGGTGGCATGAGCCTG   19900         A      GA
                                GGCATGGTG CATGAGT  TG
                                |||||||| |||||||  ||
```

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                                CCGTACCAC GTACTCG  AC
                                     C      G_
GAM997  GNA14    3'  TGGCATGGGACTGGCTCTG   20194       T  A  A  GA
                                TGGCATGG GAC TG GT  TG
                                |||||||| ||| || ||  ||
                                ACCGTACC CTG AC CG  AC
                                     _  _ _  AG
GAM997  HLA-DRA  3'  GCATGGTGATAATAAAATGAT  33314       CAT__
                                GCATGGTGA    GAGTGAT
                                |||||||||    |||||||
                                CGTACCACT    TTTACTA
                                     ATTAT
GAM997  SOX10    3'  TGGCATAGGTGGCATGGGCA  28016      _   A   A
                                TGGCAT GGTG CATG GTG
                                |||||| |||| |||| |||
                                ACCGTA CCAC GTAC CGT
                                   T   C   C
GAM997  MUCDHL   3'  GCGGCCATAGTGCTTG     34938       CGTTC  A
                                GCGGCCAT    AGT CTTG
                                ||||||||    ||| ||||
                                CGCCGGTA    TCA GAAC
                                     _____  C
GAM997  SNAPAP   3'  GCAGCTGGGGAACAGTACTTG  29697     CATCGTT
                                GCGGC      CAGTACTTG
                                |||||      |||||||||
                                CGTCG      GTCATGAAC
                                   ACCCCTT
GAM998  P2RY1    3'  TAGTGTTTTGTTATATACCA  15010      CTCA
                                TGGTGT   TTATATACTA
                                ||||||   ||||||||||
                                ATCACA   AATATATGGT
                                   AAAC
GAM999  FANCC    5'  TTAAATCGGGTGGTCCTCGC  43284       AAAT  AAA_
                                TTAAATCGGGT   GGT   GC
                                ||||||||||   |||   ||
                                AATTTAGCCCA   CCA   CG
                                     ____  GGAG
GAM999  GABRA2   3'  TTAAATCAGGTCCTAGGGTA  9044        AAAT_
                                TTAAATCGGGT    GGTA
                                ||||||||||    ||||
                                AATTTAGTCCA    CCAT
                                     GGATC
GAM999  ALS2     3'  AGTAGATAAATGGTATTTTTG  34090     TTTTCAC
                                AGTAG      GGTATTTTTG
                                |||||      ||||||||||
                                TCATC      CCATAAAAAC
                                   TATTTA_
GAM999  APM1     3'  AGTAGTTTGCATAATATTTT  22010       T  CG
                                AGTAGTTT CA  GTATTTT
                                |||||||| ||  |||||||
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                                TCATCAAA GT  TATAAAA
                                    C  AT
GAM999  FNTB    3'  GTTTTCACGGTACATGA    13007          TTT
                                GTTTTCACGGTAT   TGA
                                ||||||||||||   |||
                                CAAAAGTGCCATG   ACT
                                      T__
GAM999  PPT1    3'  AGTATTTTCCAAGCTTTTTGA  41548     G     C   A
                                AGTA TTTTCA GGT TTTTTGA
                                |||| |||||| ||| |||||||
                                TCAT AAAGGT TCG AAAAACT
                                  A     _  _
GAM1000 ABCD3   3'  ACTGCAGACTGAGAG      16016     A   GTA   A
                                ACT GTAG   ACT AGAG
                                ||| ||||   ||| ||||
                                TGA CGTC   TGA TCTC
                                  _   ___   C
GAM1000 CRABP1  3'  AGCACTAGGGATACAAGAGG   40750        TA  TA  T
                                AGCACTAG  GG  AC AAGAGG
                                ||||||||  ||  || ||||||
                                TCGTGATC  CC  TG TTCTCC
                                    __  TA  _
GAM1000 ELAC2   3'  GCACCAGTCCTAAGAG      32854         AGGTAA
                                GCACTAGT     CTAAGAG
                                ||||||||     |||||||
                                CGTGGTCA     GATTCTC
                                    G_____
GAM1000 HAP1    3'  AAGCAATAGGAGATTGAGAGG  19496      CTA    TAACTA
                                AAGCA   GTAGG     AGAGG
                                |||||   |||||     |||||
                                TTCGT   TATCC     TCTCC
                                  ___    TCTAAC
GAM1000 KRT5    5'  GCACTAGTGGGTTGGGAGG   7689         A   AACTAA
                                GCACTAGT GGT     GAGG
                                |||||||| |||     ||||
                                CGTGATCA CCA     CTCC
                                    C   ACC___
GAM1000 MMP25   3'  AAGCACTAGGGGGTCACTGAGG 35373         TA   A   AA
                                AAGCACTAG  GGT ACT  GAGG
                                |||||||||  ||| |||  ||||
                                TTCGTGATC  CCA TGA  CTCC
                                    CC   G   __
GAM1000 PACSIN1 3'  GCAGCTAGAGTGCTAAGAGG   45149    _   T  GTAA
                                GCA CTAG AG    CTAAGAGG
                                ||| |||| ||    ||||||||
                                CGT GATC TC    GATTCTCC
                                  C    _ AC__
GAM1000 PODXL   3'  GCACTAGTGGGTTATTTTACAA 23975        A   AAC_____
            GAGG                    GCACTAGT GGT      TAAGAGG
                                ||||||||| |||      |||||||
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                                CGTGATCA CCA      GTTCTCC
                                    C   ATAAAAT
GAM1000  TYRP1    3'  ACATTAGTAGGTGAAATGTAAG 43640     C       AACTAA_
             G                   GCA TAGTAGGT      GAGG
                                 ||| ||||||||      ||||
                                 TGT ATCATCCA      TTCC
                                   A       CTTTACA
GAM1000  CTSC     3'  TAAGCTTCTGAGATTGCT    12240        GAA    C
                                 TAAGCTTT   AGAT TGCT
                                 ||||||||   |||| ||||
                                 ATTCGAAG   TCTA ACGA
                                     AC_   _
GAM1000  LARS2    5'  AGGTCTGGATCTGCT      31672    C    AAA
                                 AG TTTG   GATCTGCT
                                 || ||||   ||||||||
                                 TC AGAC   CTAGACGA
                                  C   ___
GAM1000  LBR      5'  TCCTAAGCTTTTTTTTTTCTGC 40430     A       GAAAGA
             T                    TCC TAAGCTTT     TCTGCT
                                  ||| ||||||||     ||||||
                                  AGG ATTCGAAA     AGACGA
                                    _       AAAAAA
GAM1000  PP       3'  AAGCTTTGAAAAGC        34442            ATCT
                                 AAGCTTTGAAAG    GC
                                 ||||||||||||    ||
                                 TTCGAAACTTTT    CG
                                                 ____
GAM1000  RUNX1    3'  AGTTTGTCCGAGATCTGCT    12005    C    AA__
                                 AG TTTG    AGATCTGCT
                                 || ||||    |||||||||
                                 TC AAAC    TCTAGACGA
                                   _   AGGC
GAM1000  STC1     3'  TCCATAAGTTTGGGGACCT    17184        C    AAA
                                 TCCATAAG TTTG   GATCT
                                 |||||||| ||||   |||||
                                 AGGTATTC AAAC   CTGGA
                                      _    CC_
GAM1001  CD28     3'  TGCGTAGTGGGTTTAAATTT   26026       CTT    C_
                                 TGTGTA   GTGG  TTAAATTT
                                 ||||||   ||||  ||||||||
                                 ACGCAT   CACC  AATTTAAA
                                     ___    CA
GAM1001  CD80     3'  TGGGTAAAACAGCTTAAATTT  23280    T   CTT TG
                                 TG GTA   G  GCTTAAATTT
                                 || |||   |  ||||||||||
                                 AC CAT   T  CGAATTTAAA
                                  C   TT_ GT
GAM1001  SLC15A1  3'  TGTGTACGTGTGGCTTAAAT   22902        T
                                 TGTGTAC TGTGGCTTAAAT
                                 ||||||| ||||||||||||
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                                ACACATG ACACCGAATTTA
                                    C
GAM1001  FN1      3'  TATCACAGTAACAAGATCAT   38338        TT    _
                                TATCGCAGT  AATAA ATCAT
                                |||||||||  ||||| |||||
                                ATAGTGTCA  TTGTT TAGTA
                                     __    C
GAM1001  PPL      3'  CATCGCAGTTGTCCAGTCAT   15491         TAATAAA
                                TATCGCAGTT      TCAT
                                ||||||||||      ||||
                                GTAGCGTCAA      AGTA
                                      CAGGTC_
GAM1001  PTEN     3'  ACATATTTAATAAATCAT    7196     _
                                GCA GTTTAATAAATCAT
                                ||| ||||||||||||||
                                TGT TAAATTATTTAGTA
                                  A
GAM1002  ADRBK1   5'  GCGCTCGGCCGCGCCCGA    11531        _    GA
                                GCGCTCGGC GCGCC  GA
                                ||||||||| |||||  ||
                                CGCGAGCCG CGCGG  CT
                                     G    G_
GAM1002  C21orf2  3'  CGCTCGGCGGAGGATG      22301        CGCC  _
                                CGCTCGGCG   GAG ATG
                                |||||||||   ||| |||
                                GCGAGCCGC   CTC TAC
                                     ____   C
GAM1002  DAZL     5'  GCTTGGCGCACCACTTCTG   42777     C       AGA_
                                GCT GGCGCGCCG   TG
                                ||| |||||||||   ||
                                CGA CCGCGTGGT   AC
                                  A       GAAG
GAM1002  EBAG9    5'  GCGCCCGGCGTGACGTGA    20117         CGC  A
                                GCGCTCGGCG  CG GA
                                ||||||||||  || ||
                                CGCGGGCCGC  GC CT
                                      ACT  A
GAM1002  ETS2     5'  GCTGCTCGGTGCGCGCCG    23470    _   __
                                GC GCTCG  GCGCGCCG
                                || |||||  ||||||||
                                CG CGAGC  CGCGCGGC
                                 A    CA
GAM1002  HSF2BP   5'  GCGTCGGCGCGCCCTCTGA   28147     C       GAGA
                                GCG TCGGCGCGCC   TGA
                                ||| ||||||||||   |||
                                CGC AGCCGCGCGG   ACT
                                  _       GAG_
GAM1002  KCNQ4    5'  GCGCTCGGGGCGCTCAGA    21731       C   CG
                                GCGCTCGG GCGC  AGA
                                |||||||| ||||  |||
```

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                                CGCGAGCC CGCG  TCT
                                     C    AG
GAM1002  NAV2     5'  GCGCCTTTGGGGTGCCGGGATG 41143      C__  CGC    A
                                GCGCT   GG   GCCG GATG
                                |||||   ||   |||| ||||
                                CGCGG   CC   CGGC CTAC
                                   AAA  CCA    C
GAM1002  PTPRG    5'  GCGCTCGGCGGCCCGA      15937          C   GA
                                GCGCTCGGCG GCC  GA
                                |||||||||| |||  ||
                                CGCGAGCCGC CGG  CT
                                      _   G_
GAM1002  PYGB     5'  ACGCGAACGCCGGGATG     16041      TCGGC     A
                                GCGC    GCGCCG GATG
                                ||||    |||||| ||||
                                TGCG    TGCGGC CTAC
                                  CT___     C
GAM1002  TIMP3    5'  GCCCGGCGGGACGGGATG    7454         CGC  A
                                GCTCGGCG   CG GATG
                                ||||||||   || ||||
                                CGGGCCGC   GC CTAC
                                     CCT  C
GAM1002  EPHB3    3'  GCTGCTTGGCATCCCTGCACG  20787    GC  CCGA
                                GC  GC    CATCCCTGCGCG
                                ||  ||    ||||||||||||
                                CG  CG    GTAGGGACGTGC
                                 A_  AACC
GAM1003  EGR3     3'  TTAAATTCTATCTGTTGTGTTG 40565           AC_
                                TTGAATTCTATTT   GTGTTG
                                ||||||||||||   ||||||
                                AATTTAAGATAGA   CACAAC
                                       CAA
GAM1003  TLL2     3'  TGAATTCTGTTTGCAAGTTG   29758         A   A  T
                                TGAATTCT TTT CG GTTG
                                |||||||| ||| || ||||
                                ACTTAAGA AAA GT CAAC
                                     C   C  T
GAM1004  APM1     3'  GTGGATCACAAAGTCAGGAG   22016     A   C G
                                GTG ATC C AGAGTCAGGAG
                                ||| ||| | ||||||||||
                                CAC TAG G TTTCAGTCCTC
                                  C   T _
GAM1004  APPL     3'  GCGTGAACCTGGGAGGCGGAG  29009         CC_  A  CA
                                GCGTGAATC   GAG GT  GGAG
                                |||||||||   ||| ||  ||||
                                CGCACTTGG   CTC CG  CCTC
                                     ACC   _  __
GAM1004  BAZ2B    5'  AGGTGGATCACAAGGTCAGGAG 30321    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
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                                TC CAC TAG GTTC CAGTCCTC
                                 _  C  T   _
GAM1004  CASP2    3'  GTGGATCATGAGGTCAGGAG  37407    A  CC  A
                                GTG ATC  GAG GTCAGGAG
                                ||| |||  ||| ||||||||
                                CAC TAG  CTC CAGTCCTC
                                  C  TA  _
GAM1004  CASP2    3'  GCGTGAACCCGGGAGTTGGAG  37400       T   A   CA
                                GCGTGAA CCCG GAGT  GGAG
                                ||||||| |||| ||||  ||||
                                CGCACTT GGGC CTCA  CCTC
                                    _   C   A_
GAM1004  CASP8    3'  GTGGATCACGAGGTCAGGAG  37876    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1004  CASP8    3'  GCGTGAACCCGGGAGGCGGAG  37873       T   A  TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C  CG_
GAM1004  CDC6     3'  GCAGATCACTTGAGGGTCAGGA 10362    GA  CC__  A
           G                     GT  ATC    GAG GTCAGGAG
                                 ||  |||    ||| ||||||||
                                 CG  TAG    CTC CAGTCCTC
                                  TC   TGAA   C
GAM1004  CGB      5'  GTGGGGTCCTGGGAGCCAGGAG 8826     AA_  CGA
                                GTG   TCC   GAGTCAGGAG
                                |||   |||   ||||||||||
                                CAC   AGG   CTCGGTCCTC
                                  CCC   ACC
GAM1004  CR1      3'  GTGGATCACGAGGTCAGGAG  8200     A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1004  DSCR3    3'  GTGGGTCACGAGGTCAGGAG  25829    AA  C   A
                                GTG  TC CGAG GTCAGGAG
                                |||  || |||| ||||||||
                                CAC  AG GCTC CAGTCCTC
                                  CC  T   _
GAM1004  GHR      3'  GTGGATCACGAGGTCAGGAG  6716     A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1004  HCS      3'  GTGGATCACGAGGTCAGGAG  33232    A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
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```
                                CAC TAG GCTC CAGTCCTC
                                  C   T   _
GAM1004  HLCS     5'  AGGTGGATCACGAGGTCAGGAG 7636     C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _   C   T   _
GAM1004  HLX1     3'  AGCGTGAATGTCGGG       34985          CCCGAGA   A
                                AGCGTGAAT      GTC GG
                                |||||||||      ||| ||
                                TCGCACTTA      CAG CC
                                     ________  C
GAM1004  INMT     3'  GCGTGAACCCGGGAGGCGGAG  27677        T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CG_
GAM1004  INMT     3'  GTGGATCACCAGGTCAGGAG   27680     A   _   G   A
                                GTG ATC CC AG GTCAGGAG
                                ||| ||| || || ||||||||
                                CAC TAG GG TC CAGTCCTC
                                  C   T   _   _
GAM1004  KCNA6    3'  AGCTGGAGAGTCAGG       13806     G   AATCCC
                                AGC TG     GAGAGTCAGG
                                ||| ||     ||||||||||
                                TCG AC     CTCTCAGTCC
                                 _  _______
GAM1004  KCNJ4    3'  GCCTGGGTGCTGGAGTCAGGAG 22538    G   AATCCCGA
                                GC TG       GAGTCAGGAG
                                || ||       ||||||||||
                                CG AC       CTCAGTCCTC
                                 G  CCACGAC_
GAM1004  LY6E     3'  ACGTGAGGAGTCAGG       14274       ATCCCGA
                                GCGTGA      GAGTCAGG
                                ||||||      ||||||||
                                TGCACT      CTCAGTCC
                                   C_______
GAM1004  LYZ      3'  GTGGATCACAAGGTCAGGAG   6955      A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C   T   _
GAM1004  LYZ      3'  GCGTGAACCCGGGAGGTGGAG  6953        T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                    _   C   CA_
GAM1004  MTCP1    3'  GCCTGAAGAGTCAGG       30580     G   ATCCCG
                                GC TGA     AGAGTCAGG
                                || |||     |||||||||
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                                CG ACT     TCTCAGTCC
                                 G  _______
GAM1004  PACSIN1   3'  GCGGGGTGGAAGGGTCAGGAG  45151     TGAATCCC   A
                                GCG       GAG GTCAGGAG
                                |||       ||| ||||||||
                                CGC       TTC CAGTCCTC
                                  CCCACC__   C
GAM1004  PMCHL1    3'  AGGTGGATCACGAGGTCAGGAG 36665    C   A   C    A
                                AG GTG ATC CGAG GTCAGGAG
                                || ||| ||| |||| ||||||||
                                TC CAC TAG GCTC CAGTCCTC
                                 _  C   T   _
GAM1004  PODXL     3'  AGCGATGGAGAGTCAGGA    23954      _  AATCCC
                                AGCG TG     GAGAGTCAGGA
                                |||| ||     ||||||||||
                                TCGC AC     CTCTCAGTCCT
                                  T _______
GAM1004  PPFIA3    3'  GCCGACCGAGAGTCGGG     41421    G   ATC       A
                                GC TGA   CCGAGAGTC GG
                                || |||   ||||||||| ||
                                CG GCT   GGCTCTCAG CC
                                 _  ___       C
GAM1004  PPID      3'  GTGGATCACAAGGTCAGGAG   44616     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C   T   _
GAM1004  RP2       5'  GCGTGAACCCTGGGAACCCCGG 27933          CGA  GT A_
                                GCGTGAATCC   GA  C  GG
                                ||||||||||   ||  |  ||
                                CGCACTTGGG   CT  G  CC
                                      ACC  TG GG
GAM1004  SEDL      3'  GTGGATCACGAGGTCAGGAG   31010     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C   T   _
GAM1004  SEDL      3'  GTGGATCAACTGAGGTCAGGAG 31009     A   CC__   A
                                GTG ATC    GAG GTCAGGAG
                                ||| |||    ||| ||||||||
                                CAC TAG    CTC CAGTCCTC
                                  C   TTGA   _
GAM1004  SERPINB9  3'  GCGTGAACCCGGGAGGCGGAG  19996        T    A   TCA
                                GCGTGAA CCCG GAG   GGAG
                                ||||||| |||| |||   ||||
                                CGCACTT GGGC CTC   CCTC
                                     _   C   CG_
GAM1004  SERPINB9  3'  GTGGATCACGAGGTCAGGAG   19998     A   C    A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
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                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1004  TAPBP    3'  GCGTGAACCCGAGAGGCGGAG  17305       T      TCA
                                GCGTGAA CCCGAGAG  GGAG
                                ||||||| ||||||||  ||||
                                CGCACTT GGGCTCTC  CCTC
                                    _      CG_
GAM1004  TAZ      5'  GTGAGTCCCGAGATTGCGGAG  31772     A      GTCA
                                GTGA TCCCGAGA   GGAG
                                |||| ||||||||   ||||
                                CACT AGGGCTCT   CCTC
                                  C      AACG
GAM1004  TERF1    3'  GTGGATCATGAAGTCAGGAG  32743     A  CCGA
                                GTG ATC   GAGTCAGGAG
                                ||| |||   ||||||||||
                                CAC TAG   TTCAGTCCTC
                                  C  TAC_
GAM1004  TERF2    3'  GTGGATCACGAGGTCAGGAG  24913     A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1004  UGDH     3'  GCGTGAACCTGGGAAGCAGA  17884        CCGA  T
                                GCGTGAATC   GAG CAGG
                                |||||||||   ||| ||||
                                CGCACTTGG   TTC GTCT
                                     ACCC  _
GAM1004  VENTX2   3'  GCGGATCACAGGGTCAGGAG  30916     T  A  C G  A
                                GCG GA TC C AG GTCAGGAG
                                ||| || || | || ||||||||
                                CGC CT AG G TC CAGTCCTC
                                  _ _ T _ C
GAM1004  VHL      3'  GTGGATCACAAGGTCAGGAG  8116      A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GTTC CAGTCCTC
                                  C  T   _
GAM1004  VIPR2    3'  GCGTGAACCCGGGAGGCGGAG  18018       T   A  TCA
                                GCGTGAA CCCG GAG  GGAG
                                ||||||| |||| |||  ||||
                                CGCACTT GGGC CTC  CCTC
                                    _   C  CG_
GAM1004  WHSC1    3'  GTGGATCACGAGGTCAGGAG  39375     A  C   A
                                GTG ATC CGAG GTCAGGAG
                                ||| ||| |||| ||||||||
                                CAC TAG GCTC CAGTCCTC
                                  C  T   _
GAM1004  ZNF200   3'  AGTATGAATCCCCATGTGGGG  18371    CG      GAGA  CA
                                AG  TGAATCCC   GT  GG
                                ||  ||||||||   ||  ||
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                                TC  ACTTAGGG   CA  CC
                                 AT       GTA_  CC
GAM1004  AKT2     3'  TGGCAGCGAGCGTGC       11565         AGATCG  A
                                TGGTAGCGA     GC TGC
                                |||||||||     || |||
                                ACCGTCGCT     CG ACG
                                      _______  C
GAM1005  CASP8    3'  GAACTGAGATGTCAGCTCAT   37872     AACC   AC
                                GAA   GGA  GTCAGCTCAT
                                |||   |||  ||||||||||
                                CTT   TCT  CAGTCGAGTA
                                  GAC_   A_
GAM1005  CDH1     3'  TGGAGGCTGGGCACAGCAGCTC 20370      AAACC  A   T
              AT                   TGGA     GG ACG CAGCTCAT
                                |||||    || ||| ||||||||
                                ACCT     CC TGT GTCGAGTA
                                  CCGAC  G   C
GAM1005  NF1      3'  TGGCAAACCGGATGGGTTCA   7061      A       ACG__
                                TGG AAACCGGA     TCA
                                ||| ||||||||     |||
                                ACC TTTGGCCT     AGT
                                  G       ACCCA
GAM1005  PCLO     3'  TGGAAAACTGGCAGCCAC     45311         C  AACGT    T
                                TGGAAAAC GG     CAGC CAT
                                |||||||| ||     |||| |||
                                ACCTTTTG CC     GTCG GTG
                                     A ______   _
GAM1005  SLC4A5   5'  TGGAAACATCCATCAGCTCAT  39432       ACCGGAA
                                TGGAAA      CGTCAGCTCAT
                                ||||||      ||||||||||||
                                ACCTTT      GTAGTCGAGTA
                                   GTAG___
GAM1005  SLC9A6   3'  TGGAAAATCTGAACATCA     26833        CCG
                                TGGAAAA   GAACGTCA
                                |||||||   ||||||||
                                ACCTTTT   CTTGTAGT
                                     AGA
GAM1005  HSPA5    3'  TTCAACTCCACTCTGA      23792          AAGTT
                                TTCAACTTCA    TTCTGA
                                ||||||||||    ||||||
                                AAGTTGAGGT    GAGACT
                                      ______
GAM1005  KCNMB4   3'  CTTCTTATAGGGTTTTCTGAAA 30943      AAA____
              T                  CTTC      GTTTTCTGAAAT
                                ||||      ||||||||||||
                                GAAG      CAAAAGACTTTA
                                  AATATCC
GAM1005  LGMN     3'  TTCAGCTTCAAATTCTCAGAA  24689      A      G    T
                                TTCA CTTCAAA TTTTC GAA
                                |||| ||||||| ||||| |||
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                                AAGT GAAGTTT AAGAG CTT
                                  C      _    T
GAM1006  C4orf1   3'  TACTAAATGCCCATTTGTAACT 40490        A   TAA  G
              GA                  TACTAAAT CCC   TG AACTGA
                                  |||||||| |||   || ||||||
                                  ATGATTTA GGG   AC TTGACT
                                     C   TAA  A
GAM1006  LANCL1   3'  CCAAATAATTGGAACTG     25852        CCCTAA
                                  CTAAATA     TGGAACTG
                                  |||||||     ||||||||
                                  GGTTTAT     ACCTTGAC
                                     TA____
GAM1006  TCF12    3'  TACTGATAACTCTGGAACTG   17343      AAAT  CCTAA
                                  TACT    AC    TGGAACTG
                                  ||||    ||    ||||||||
                                  ATGA    TG    ACCTTGAC
                                    CTAT  AG___
GAM1006  TMOD     3'  TACTAAATACCATAGCCATG   17601          CTA    AAC
                                  TACTAAATACC   ATGG   TG
                                  ||||||||||   ||||   ||
                                  ATGATTTATGG   TATC   AC
                                        ___    GGT
GAM1007  ADAM19   3'  GGGCCACAGGAAAGGTGGGG   37772    ___       A  AA
                                  GG   ACAGGAAA GT  GG
                                  ||   |||||||| ||  ||
                                  CC   TGTCCTTT CA  CC
                                   CGG       C  CC
GAM1007  AQP6     5'  GAGATTGGGGAAAGTAAGG    38245      A  ACA    A
                                  GAGAT GG   GGAAA GTAAGG
                                  ||||| ||   ||||| ||||||
                                  CTCTA CC   CCTTT CATTCC
                                    A ___    _
GAM1007  B4GALT1  3'  TGAGGTGGAACAGGAGGCTTTA 11291      ATA       AAAGTA
              GG                  TGAG   GGACAGGA     AGG
                                  ||||   ||||||||     |||
                                  ACTC   CTTGTCCT     TCC
                                    CAC       CCGAAA
GAM1007  C18orf1  3'  TGAGGCAGGTAGAGAAGTAAGG 41234      A    ACA   A
                                  TGAG TAGG   GGA AAGTAAGG
                                  |||| ||||   ||| ||||||||
                                  ACTC GTCC   TCT TTCATTCC
                                    C    A__   C
GAM1007  CACNA1C  3'  GAAAACAGGAAAGGTGAGG   8752     TA        A  A
                                  GA  GGACAGGAAA GT AGG
                                  ||  |||||||||| || |||
                                  CT  TTTGTCCTTT CA TCC
                                   __         C  C
GAM1007  DDX11    3'  TGGGACAGGATAGGGAGCAGGG 36180    A      C   AAA    A
                                  TG GATAGGA AGG   AGTA GG
                                  || ||||||| |||   |||| ||
```

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                                AC CTGTCCT TCC   TCGT CC
                                 C      A  C__   C
GAM1007  DISC1    3'  AGATCACAGGAGAAGTAAGG  33025     AGG     A
                                AGAT   ACAGGA AAGTAAGG
                                ||||   |||||| ||||||||
                                TCTA   TGTCCT TTCATTCC
                                  G__     C
GAM1007  EIF2C1   3'  CAGGGAGGAGAAGTAAG    29175     AC    A
                                TAGG  AGGA AAGTAAG
                                ||||  |||| |||||||
                                GTCC  TCCT TTCATTC
                                  C_   C
GAM1007  FHL1     3'  TGGTATAGGGCAGAAAGTAAGG 11099    AG    A    AA
                                TG  ATAGG CAGGA  AGTAAGG
                                ||  ||||| |||||  |||||||
                                AC  TATCC GTCTT  TCATTCC
                                 CA    C    __
GAM1007  GUCY1B2  3'  TGAGAGGAAGGAAAAGTGAGG  19965      TA   C       A
                                TGAGA  GGA AGGAAAAGT AGG
                                |||||  ||| |||||||||| |||
                                ACTCT  CCT TCCTTTTCA TCC
                                   __  _       C
GAM1007  IKBKB    3'  TGAGAGAGGACAGGGAGCAGGG 41812       T      AAA    A
                                TGAGA AGGACAGG   AGTA GG
                                ||||| ||||||||   |||| ||
                                ACTCT TCCTGTCC   TCGT CC
                                   C       C__    C
GAM1007  KRT6B    3'  TGAGAAGAAAAGTA       24480       TAGGACA       A
                                TGAGA      GGAAAAGT A
                                |||||      |||||||| |
                                ACTCT      TCTTTTCA T
                                   ________       C
GAM1007  MAPT     3'  TGGGAAGGACAGGGGGCTCGG  32588    A  T       AAAA  AA
                                TG GA AGGACAGG    GT  GG
                                || || ||||||||    ||  ||
                                AC CT TCCTGTCC    CG  CC
                                 C  _       CC__  AG
GAM1007  MTMR8    3'  TGAGGGAGCACAAAAAAGTGAG 31759      AT  G    G     A
            G                    TGAG  AG ACAG AAAAGT AGG
                                ||||  || |||| |||||| |||
                                ACTC  TC TGTT TTTTCA TCC
                                  CC  G    _     C
GAM1007  NGFB     3'  TGAGGTAGGGAGGGGCCCAGG  14772      A    AC   AAAA  A_
                                TGAG TAGG  AGG    GT  AGG
                                |||| ||||  |||    ||  |||
                                ACTC ATCC  TCC    CG  TCC
                                  C   C_   C___  GG
GAM1007  PDGFRB   3'  GATCCCAGGGAAGTAAGG    42337     AGGA    AA
                                GAT    CAGG  AAGTAAGG
                                |||    ||||  ||||||||
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                                CTA   GTCC  TTCATTCC
                                  GG__   C_
GAM1007  PPP2R5A  3'  TGAGACAAAGAGAAGGGTAAGG 26443        ACA   AA
                                TGAGATAGG   GGAA  GTAAGG
                                |||||||||   ||||  ||||||
                                ACTCTGTTT   TCTT  CATTCC
                                     C__   CC
GAM1007  RORC     3'  GGAAAGGAAAAGGGTGAGG   22812     C      TA__
                                GGA AGGAAAAG   AGG
                                ||| ||||||||   |||
                                CCT TCCTTTTC   TCC
                                  T      CCAC
GAM1007  CBFA2T3  3'  GGATTTTGATTTCTTGTGTT  23265      CGCTTG
                                GGATT     TCTTGTGTT
                                |||||     |||||||||
                                CCTAA     AGAACACAA
                                   AACTAA
GAM1007  MADH3    3'  GGGTTTGCTCGTGTGT     25350    A  C     CTT
                                GG TT GCTTGT   GTGT
                                || || ||||||   ||||
                                CC AA CGAGCA   CACA
                                 C  A     ____
GAM1008  HAGH     5'  GCTGTGCCGCGAGCCTCCGCC  23713    _          ACGG
                                GC GTGCCGCGAGCCT    CGCT
                                || ||||||||||||    ||||
                                CG CACGGCGCTCGGA    GCGG
                                 A           G___
GAM1008  POLS     3'  GCGTGCCGCGAGCCCGGC    28121            TA
                                GCGTGCCGCGAGCC  CGGC
                                ||||||||||||||  ||||
                                CGCACGGCGCTCGG  GCCG
                                                __
GAM1008  SNX9     3'  AGTGTGCCGTGGCCACAGCAGC 32148    C     CGA  _ _
            GCT                    AG GTGCCG   GCC TA CGGCGCT
                                || ||||||   ||| || |||||||
                                TC CACGGC   CGG GT GTCGCGA
                                 A     AC_   T  C
GAM1009  EPHB6    5'  TCACAATGAAGACAAACAG   20801            TTT
                                TCATAATGAAGACA   TAG
                                ||||||||||||||   |||
                                AGTGTTACTTCTGT   GTC
                                         TT_
GAM1009  GAS7     3'  TATTATAATAAAGAATCCCAGA 18886     C        C
            G                   TAT ATAATGAAGA ATTTTAGAG
                                ||| |||||||||| |||||||||
                                ATA TATTATTTCT TAGGGTCTC
                                  A        _
GAM1009  PUM2     3'  CATTGCCAGAGACATTTTAG   31659     AA_ GA
                                CAT   T  AGACATTTTAG
                                |||   |  ||||||||||
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                                GTA   G  TCTGTAAAATC
                                  ACG TC
GAM1009  DGUOK    3'  TCTCATGAGGTCTTCTTGTT   38965        AAC   GAA
                                TCTCATGA   GTC   TTGTT
                                ||||||||   |||   |||||
                                AGAGTACT   CAG   AACAA
                                    C__   AAG
GAM1009  GRM1     3'  GTCTCATGCTGATGGATTGTT  9137         AAAC  C  A
                                GTCTCATG    GT GA TTGTT
                                ||||||||    || || |||||
                                CAGAGTAC    TA CT AACAA
                                    GAC_  C  _
GAM1009  ITSN1    3'  TGTTTCATGAAACAGGAAATTG 16662     C        TC
              TT                  TGT TCATGAAACG  GAATTGTT
                                ||| ||||||||||  ||||||||
                                ACA AGTACTTTGT  TTTAACAA
                                  A         CC
GAM1010  PFN2     3'  GTTGGGATACCTAATGTC    38162          CGTC
                                GTTGGGATGCT    GATGTC
                                ||||||||||    ||||||
                                CAACCCTATGG    TTACAG
                                      A___
GAM1010  PLS1     3'  TTGGGATGTTCTAGCCAATGT  15414        C  __
                                TTGGGATG TC  GTCGATGT
                                ||||||||  ||  ||||||||
                                AACCCTAC AG  CGGTTACA
                                    A  AT
GAM1010  SLC9A1   3'  TACGTGGTTGTCGATG      43240      T  GATGCTC
                                TACGT GG      GTCGATG
                                |||||  ||      |||||||
                                ATGCA CC      CAGCTAC
                                  _  AA_____
GAM1010  ZIC3     3'  ACAATTGCAATTAACAAGATGT 18241          A  ____
              AG                    ACAATTGCAGT AA    ATGTAG
                                ||||||||||  ||    ||||||
                                TGTTAACGTTA TT    TACATC
                                      A  GTTC
GAM1011  ATP2B3   3'  AATGGATTTGGGTCC       34971         CAGGGA   A
                                AATGGATTT     GGG CC
                                |||||||||     ||| ||
                                TTACCTAAA     CCC GG
                                      _____  A
GAM1011  IL8RA    3'  TGGAAAGCATTTGGGGAGGGAC 8444       TTT  ____
                                TGGA   CA    GGGAGGGAC
                                ||||   ||   |||||||||
                                ACCT   GT    CCCTCCCTG
                                  TTC  AAAC
GAM1011  PYCR1    3'  AATGGAGGGCAGGGAGGGGCCG 43122        TTT        A
                                AATGGA   CAGGGAGGG CCG
                                ||||||   ||||||||| |||
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                                TTACCT   GTCCCTCCC GGC
                                   CCC       C
GAM1011  EBI2     3'  TTCTCTTGGGCTTACTTCCGA  22394          ____   AA
                                TTCTCTTGG   ACT  CGA
                                |||||||||   |||  |||
                                AAGAGAACC   TGA  GCT
                                     CGAA   AG
GAM1011  ZNF261   3'  GTCATTCTCTGCCTCTGAGGA  22992          T GA  AAC
                                GTCATTCTCT G  CT   GAGGA
                                |||||||||| |  ||   |||||
                                CAGTAAGAGA C  GA   CTCCT
                                     _ G_  GA_
GAM1012  ARNT2    3'  TATGTCCCACGGCACAG     31364          ATCA   TCT
                                TATGTCCCAC    GGT   CAG
                                |||||||||    |||   |||
                                ATACAGGGTG    CCG   GTC
                                     ____   T__
GAM1012  DDEF2    3'  TATGCCTATTTATTCTCAG   19327       CCACATCAG
                                TATGTC       GTTCTCAG
                                ||||||       ||||||||
                                ATACGG       TAAGAGTC
                                   ATAAA____
GAM1012  DIAPH2   3'  TGTTTCACTGGTTCTCAGA   28690     CC   ATCA
                                TGT  CAC    GGTTCTCAGA
                                |||  |||    ||||||||||
                                ACA  GTG    CCAAGAGTCT
                                  AA   A___
GAM1012  FOXE1    3'  GTCTCAAGTTCTCAG       20946     CCACA
                                GTC    TCAGGTTCTCAG
                                |||    ||||||||||||
                                CAG    AGTTCAAGAGTC
                                  _____
GAM1012  HIP12    3'  TATGTCTCACCTCACTCCCCAG 42406       C   A   GG
            A                    TATGTC CAC TCA  TTCTCAGA
                                ||||||| ||| |||  ||||||||
                                ATACAG GTG AGT  AGGGGTCT
                                   A   G   G_
GAM1012  RAI3     3'  TGTCTTGTACAGTTTTCTCAGA 19570      CCACAT   G_
                                TGTC     CAG  TTCTCAGA
                                ||||     |||  ||||||||
                                ACAG     GTC  AAGAGTCT
                                  AACAT_   AA
GAM1012  ADAM17   3'  GTCCATTCTCTGGTGG      34832          AA
                                GTCCATTCTT  TGGTGG
                                ||||||||||  ||||||
                                CAGGTAAGAG  ACCACC
                                     __
GAM1012  ATP6V0D1 3'  GTCCATCCTTGGTGG       21727          TAA
                                GTCCATTCT   TGGTGG
                                |||||||||   ||||||
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                                CAGGTAGGA  ACCACC
                                           ___
GAM1012 ETV5    3' CATTCTTAATGTACTAAG   20846        GTG_
                                CATTCTTAATG   GAG
                                ||||||||||   |||
                                GTAAGAATTAC   TTC
                                      ATGA
GAM1012 GRM7    3' GTCCATTCTAAAGAGC     9190        TAATGGT
                                GTCCATTCT     GGAGAGC
                                |||||||||     |||||||
                                CAGGTAAGA     TTTCTCG
                                           _______
GAM1012 MARK3   5' CCGTTCTTAGTTGGTGGAG  14354   A    A_
                                CC TTCTTA  TGGTGGAG
                                || ||||||  ||||||||
                                GG AAGAAT  ACCACCTC
                                 C     CA
GAM1012 PLA2R1  3' GTCTTTCTTAATGGTACGAG  28889    CA        GA
                                GTC  TTCTTAATGGTG  GAG
                                |||  ||||||||||||  |||
                                CAG  AAGAATTACCAT  CTC
                                  A_         G_
GAM1012 SOX11   3' GTCAGGAAAAATGGTGGGGAGC 17033    CATTCTT      A
                                GTC      AATGGTGG GAGC
                                |||      |||||||| ||||
                                CAG      TTACCACC CTCG
                                  TCCTTT_      C
GAM1012 TPM4    3' GTCCTGCATGGTGGAGAG   17648    ATTCTTA
                                GTCC     ATGGTGGAGAG
                                ||||     ||||||||||
                                CAGG     TACCACCTCTC
                                  ACG____
GAM1013 ADM     5' TGGCAAGGCTTGAGCTGTTCTA 10030        GCCCATTG
                                TGGCAAGGC      GTTCTA
                                |||||||||      ||||||
                                ACCGTTCCG      CAAGAT
                                     AACTCGA_
GAM1013 FUT9    3' TGGTAGGTTTATTTGGTTCTA  42736    CA  CGCCCA
                                TGG  AGG    TTGGTTCTA
                                |||  |||    |||||||||
                                ACC  TCC    AACCAAGAT
                                  A_  AAATA_
GAM1013 LYL1    5' TGGTGAGTGCCCTGGCTCT   24582    CA  GC   AT
                                TGG  AG  GCCC  TGGTTCT
                                |||  ||  ||||  |||||||
                                ACC  TC  CGGG  ACCGAGA
                                  AC  A_   __
GAM1014 ABCA4   3' AGGCCAAAGCTGCTAGTGGG  42554      CT       A
                                GGGCTG  GGGCTGCTAGT GG
                                ||||||  |||||||||| ||
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                                TCCGGT  TTCGACGATCA CC
                                  __         C
GAM1014  CACNB1   3'  CAGGGTTGCTGGGCTACAG   8777      C        T
                                TAGGG TGCTGGGCTGC AG
                                ||||| |||||||||||  ||
                                GTCCC ACGACCCGATG TC
                                   A        _
GAM1014  CAPN10   3'  GGGCTGCTGGACAGTGGG    35777          TGCT   A
                                GGGCTGCTGGGC   AGT GG
                                ||||||||||||   ||| ||
                                CCCGACGACCTG   TCA CC
                                       ____  C
GAM1014  PCTK3    3'  TAGGGCTGATGGAAAGAGTGGG 43786        C   CTGCT   A
                                TAGGGCTG TGGG    AGT GG
                                |||||||| ||||    ||| ||
                                ATCCCGAC ACCT    TCA CC
                                     T   TTC__   C
GAM1014  TEM6     5'  GGGCTGTCGGGCTAGTCGG   35556      C    GCT   A
                                GGGCTG TGGGCT   AGT GG
                                |||||| ||||||   ||| ||
                                CCCGAC GCCCGA   TCA CC
                                   A     ___  G
GAM1014  COL4A2   3'  TGATGGGGGCCAGGGCTGC   12323     AGTA    GCT
                                TGAT   GGGCT   GGGCTGC
                                ||||   |||||  |||||||
                                ACTA   CCCGG   CCCGACG
                                  CC__    T__
GAM1014  IL1R1    3'  TGAAGTGCCCTGGGCTGC    9371    T  _  G
                                G AGG GCT CTGGGCTGC
                                | ||| ||| |||||||||
                                A TTC CGG GACCCGACG
                                 C  A  _
GAM1014  STK13    5'  GTGGGCTGCTGGGCTGC     17200    A
                                GT GGGCTGCTGGGCTGC
                                || ||||||||||||||
                                CA CCCGACGACCCGACG
                                 _
GAM1015  BIN3     3'  TGGCATGCTGGGCTGCC     33087     T   AGTA
                                TGGC TGCT   GGGCTGCT
                                |||| ||||   ||||||||
                                ACCG ACGA   CCCGACGG
                                  T   _____
GAM1015  BLAME    3'  TGGCTGCCCAGGCTGC     33499      T  AGTA
                                TGGCT GCT   GGGCTGC
                                ||||| |||   |||||||
                                ACCGA CGG   TCCGACG
                                   _  G___
GAM1015  CA7      3'  GCTCGGGGTGGGGCTGCT    41198      CTA  A
                                GCTTG  GT GGGCTGCT
                                |||||  || ||||||||
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                                CGAGC   CA CCCGACGA
                                  CC_ C
GAM1015 CDK10    3' GGTTGTTGTAGGGCTGCT    38151    C   CTA
                                GG TTG   GTAGGGCTGCT
                                || |||   ||||||||||
                                CC AAC   CATCCCGACGA
                                 _  AA_
GAM1015 CKMT2    5' TGGCCTGCTGGCTATGCT    12267        AGTAG   __
                                TGGCTTGCT    GGCT  GCT
                                |||||||||    ||||  |||
                                ACCGGACGA    CCGA  CGA
                                     _____   TA
GAM1015 COL18A1  3' GCTTCAGCCTGGGGTTGCT   39056     __  AGTA   C
                                GCTT  GCT    GGG TGCT
                                ||||  |||    ||| ||||
                                CGAA  CGG    CCC ACGA
                                  GT   AC__   A
GAM1015 COL4A2   5' CGGCTTCAGGGCTGC       12314      GCTAG
                                TGGCTT    TAGGGCTGC
                                ||||||    |||||||||
                                GCCGAA    GTCCCGACG
                                  _____
GAM1015 DUOX2    3' GGTAGAAGTAGGGCTGCT    30447    CTTGCT
                                GG     AGTAGGGCTGCT
                                ||     ||||||||||||
                                CC     TCATCCCGACGA
                                 ATCT__
GAM1015 KIR3DL2  3' TGGTTTTGAGACAGGGCTG   27557    C  GCT  _
                                TGG TT   AG TAGGGCTG
                                ||| ||   || ||||||||
                                ACC AA   TC GTCCCGAC
                                 A  AC_  T
GAM1015 LZTS1    3' TGGCTGTCCAGAGGCTGCT   34278     TG   TA
                                TGGCT  CTAG  GGGCTGCT
                                |||||  ||||  ||||||||
                                ACCGA  GGTC  TCCGACGA
                                   CA   __
GAM1015 MSN      3' TGGCATGACTCCAGGGCTGCT 41250     T  _  AG
                                TGGC TG CT  TAGGGCTGCT
                                |||| || ||  ||||||||||
                                ACCG AC GA  GTCCCGACGA
                                  T  T  G_
GAM1015 MTNR1B   3' TGGCGTTGATGGGCTGCT    25558     _  CTA  A
                                TGGC TTG   GT GGGCTGCT
                                |||| |||   || ||||||||
                                ACCG AAC   TA CCCGACGA
                                  C  ___  _
GAM1015 NSEP1    5' GGCGGCGGTGGGGCTGCT    43999    TT  TA  A
                                GGC  GC  GT GGGCTGCT
                                |||  ||  || ||||||||
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                                CCG  CG  CA CCCGACGA
                                  C_  C_  C
GAM1015  PCDH12   3'  GCTTACAAGGGGCTGCT     32451       T  TA
                                GCTTGC AG  GGGCTGCT
                                |||||| ||  ||||||||
                                CGAATG TC  CCCGACGA
                                   T  __
GAM1015  PGLS     3'  AGCCCCGGGTAGGGCTGCT   28980       GCTA
                                GGCTT   GTAGGGCTGCT
                                |||||   ||||||||||
                                TCGGG   CATCCCGACGA
                                  GCC_
GAM1015  PLXNA1   3'  GGCTTCAGGGCTGC       43624       GCTAG
                                GGCTT    TAGGGCTGC
                                |||||    |||||||||
                                CCGAA    GTCCCGACG

                                  _____
GAM1015  RENT1    3'  TGGGTTTGTCAAGGCTGCT   16262     C  GCTAG
                                TGG TT    TAGGGCTGCT
                                ||| ||    ||||||||||
                                ACC AA    GTTCCGACGA
                                  C  ACA__
GAM1015  SLC10A2  3'  GCTTGCTGCAGCTGC       7816        A  AG
                                GCTTGCT GT  GGCTGC
                                ||||||| ||  ||||||
                                CGAACGA CG  TCGACG

                                  _  __
GAM1015  STIM1    5'  TGGCTGCGGGGCTGC       41136       T  TAGTA
                                TGGCT GC    GGGCTGC
                                ||||| ||    |||||||
                                ACCGA CG    CCCGACG
                                  _  C____
GAM1015  SURF4    3'  TGGCTTGCAGGGTGCTGCT   37660        T  TA  _
                                TGGCTTGC AG  GG GCTGCT
                                |||||||| ||  || ||||||
                                ACCGAACG TC  CC CGACGA
                                   _  __  A
GAM1015  TLL2     5'  TGGTTACACAGGGCTGCT    29759     C    TAG
                                TGG TTGC   TAGGGCTGCT
                                ||| ||||   ||||||||||
                                ACC AATG   GTCCCGACGA
                                  _    T__
GAM1015  UC28     3'  TGGCTTACTAATTGC       34695           AGGGC
                                TGGCTTGCTAGT    TGC
                                ||||||||||||    |||
                                ACCGAATGATTA    ACG

                                   _____
GAM1015  VENTX2   3'  TGTTTTGTCCCGAGGCTGCT  30927    GC  _  AGTA
                                TG  TTG CT   GGGCTGCT
                                ||  ||| ||   ||||||||
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                                AC  AAC GG    TCCGACGA
                                 AA   A  GC__
GAM1015  WARS     3'  GGCTCCACTGTGGGGCTGCT   42624     _ TG  A  A
                                GGC T  CT GT GGGCTGCT
                                ||| |  || || ||||||||
                                CCG G  GA CA CCCGACGA
                                  A GT  _  C
GAM1015  CDK6     3'  CTGTAGGGCTTGCTGAGGGG   10384     GCCT
                                CTG    GCTTGCTGAGGGG
                                |||    ||||||||||||
                                GAC    CGAACGACTCCCC
                                  ATCC
GAM1015  CELSR2   3'  GCAGGAATTGCTGAGGGGA   10850     T  CCTGC
                                GC GG    TTGCTGAGGGGA
                                || ||    ||||||||||||
                                CG CC    AACGACTCCCCT
                                 T  TT___
GAM1015  GPRC5C   3'  GCTGGCCTGCCAGGGG      35132          TGCTG
                                GCTGGCCTGCT    AGGGG
                                ||||||||||    |||||
                                CGACCGGACGG    TCCCC
                                              _____
GAM1015  MAP1A    3'  TCACTGGCTTGCTTGGG      14349         C    GCTGA
                                TCGCTGGC TGCTT    GGG
                                |||||||| |||||    |||
                                AGTGACCG ACGAA    CCC
                                     A    _____
GAM1015  SOST     3'  GCTGGCGGGCTGAGGGG     36105       CTGCTT
                                GCTGGC     GCTGAGGGG
                                ||||||     |||||||||
                                CGACCG     CGACTCCCC
                                   CC____
GAM1016  BF       5'  TCCTGGCTTGCTTTGCTTG   11811    G    C    _
                                TC CTGGC TGCTT GCTTG
                                || ||||| ||||| |||||
                                AG GACCG ACGAA CGAAC
                                 _    A    A
GAM1016  GRIA1    5'  CCTTCCTTGCTTGCTTGC    9087     GG  _
                                CT  CCT GCTTGCTTGC
                                ||  ||| ||||||||||
                                GG  GGA CGAACGAACG
                                 AA   A
GAM1016  LRP1     3'  TCGCTTGCCGGCTTGCTCGC  14228      G  T
                                TCGCT GCC GCTTGCTTGC
                                ||||| ||| ||||||||||
                                AGCGA CGG CGAACGAGCG
                                   A   C
GAM1016  PSME3    5'  GCTGGCTTACTCACTGCTCGC  25125       C   TG  T
                                GCTGGC TGCT  CT GCTCGC
                                |||||| ||||  || ||||||
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                                CGACCG ATGA  GA CGAGCG
                                   A   GT  _
GAM1016  SLC16A1   5'  TCGCTCGCTGCCTCGTTTGCT  16817      G  C    _ C
                                TCGCT GC TGCTT G TTGCT
                                ||||| || ||||| | |||||
                                AGCGA CG ACGGA C AACGA
                                   G  _    G A
GAM1016  SLC25A15  3'  TAGCCTGCTTGCACTCA     30671           TT
                                TGGCCTGCTTGC  GCTCG
                                ||||||||||||  |||||
                                ATCGGACGAACG  TGAGT
                                      __
GAM1016  TRIM9     5'  GCTTGCTTTCTTGCTTGCTTGC 31570     G  CTG        C
                                GCT GC   CTTGCTTGCT GC
                                ||| ||   |||||||||| ||
                                CGA CG   GAACGAACGA CG
                                  A  AAA         A
GAM1016  TRIM9     5'  GCTTGCTTTCTTGCTTGCTTGC 31571     G  C____         C
              TTGC                 GCT GC     TGCTTGCTTGCT GC
                                ||| ||     |||||||||||| ||
                                CGA CG     ACGAACGAACGA CG
                                  A  AAAGA          A
GAM1016  TRIM9     5'  TCGCTTGCTTGCTTGCT     38139       GGCC
                                TCGCT    TGCTTGCTTGCT
                                |||||    ||||||||||||
                                AGCGA    ACGAACGAACGA
                                      ____
GAM1016  TRIM9     5'  TCGCTCGCTTGCTTGCTTGC   31580       G  C
                                TCGCT GC TGCTTGCTTGC
                                ||||| || ||||||||||
                                AGCGA CG ACGAACGAACG
                                   G  A
GAM1016  SLC16A1   5'  TCGCTCGCTGCCTCGTTTGCTT 16818          G   _ C
              G                   TTGCTCGCTG CCT G TTGCTTG
                                |||||||||| ||| | |||||||
                                AGCGAGCGAC GGA C AACGAAC
                                      _   G A
GAM1016  SOD3      5'  CCTGCTTGCTGGCCTGCCCG   16954       C
                                CTTGCT GCTGGCCTGCTTG
                                ||||||  ||||||||||||
                                GGACGA CGACCGGACGGGC
                                   A
GAM1016  TBL1X     3'  TTGCTTCTGTTTTTGCTTG   24902      CG   GCC_
                                TTGCT  CTG    TGCTTG
                                |||||  |||    ||||||
                                AACGA  GAC    ACGAAC
                                   A_   AAAA
GAM1016  TRIM9     5'  CTTGCTTGCTTGCTTGCTT   31563       C   GGCC
                                CTTGCT GCT    TGCTTGCTT
                                ||||||  |||    |||||||||
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                                GAACGA CGA    ACGAACGAA
                                   A  ____
GAM1016  TRIM9    5'  CTCGCTCGCTTGCTTGCTT   31561          GGCC
                                CTTGCTCGCT    TGCTTGCTT
                                ||||||||||    |||||||||
                                GAGCGAGCGA    ACGAACGAA
                                      ____
GAM1016  TRIM9    5'  CTTGCTTGCTTTCTTGCTTGCT 31564       C   GGCC
              TG                  CTTGCT GCT    TGCTTGCTTG
                                ||||||| |||    ||||||||||
                                GAACGA CGA    ACGAACGAAC
                                   A   AAGA
GAM1016  TRIM9    5'  TGCTTGCTTTCTTGCTTGCTTG 31581     C   GGCC
                                TGCT GCT    TGCTTGCTTG
                                |||| |||    ||||||||||
                                ACGA CGA    ACGAACGAAC
                                  A   AAGA
GAM1017  CYLN2    3'  CTGGTGTGGACTGGGCTGCT   18050    A  AG  CT
                                CT GT  GG  GCTGGGCTGCT
                                || ||  ||  ||||||||||||
                                GA CA  CC  TGACCCGACGA
                                 C  CA  __
GAM1017  CYP3A5   5'  TGCTGCTGTTTGCTGGGCTG   8931      A  AGGGC
                                TGCT GT     TGCTGGGCTG
                                |||| ||     ||||||||||
                                ACGA CG     ACGACCCGAC
                                  _  ACAA_
GAM1017  STK13    5'  GTGGGCTGCTGGGCTGC     17200    A
                                GT GGGCTGCTGGGCTGC
                                || ||||||||||||||
                                CA CCCGACGACCCGACG
                                 _
GAM1017  STK13    5'  GCTGCTGGGCTGCTGGGCTG   17199    A  A
                                GCT GT GGGCTGCTGGGCTG
                                ||| || ||||||||||||||
                                CGA CG CCCGACGACCCGAC
                                  _  A
GAM1017  CEACAM1  3'  TGGTTTTCTTCTCTTTGCTAGT 11837     CTTG  G  GC
                                TGG    CTT CTT  TTGCTAGT
                                |||    ||| |||  ||||||||
                                ACC    GAA GAG  AACGATCA
                                  AAAA   _   A_
GAM1017  DMRT2    3'  TGGATTTGTTTGCTTGCTTGCT 27271     C_  C
                                TGG  TTG TTGCTTGCTTGCT
                                |||  ||| ||||||||||||
                                ACC  AAC AACGAACGAACGA
                                  TA   A
GAM1018  DLG5     5'  TCTGGGAGGTTTTGGGGG    44468      C__
                                TTTGG   GTTTTGGGGG
                                |||||   ||||||||||
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                                AGACC   CAAAACCCCC
                                  CTC
GAM1018 JAM2     5' CTGTTCTGTTTTGGGGG     34541       GGC
                                CTGTTT   GTTTTGGGGG
                                ||||||   ||||||||||
                                GACAAG   CAAAACCCCC
                                  A__
GAM1018 YWHAZ    3' TGTTTGGTGTTTTCTGC     18206        C    GGGG
                                TGTTTGG GTTTT   GC
                                ||||||| |||||   ||
                                ACAAACC CAAAA   CG
                                   A    GA__
GAM1019 PLCB4    3' AGTAAATTTTTGTGGATTTG  9581     C  CC       C
                                GGT AGT  TTTGTGGAT TG
                                ||| |||  ||||||||| ||
                                TCA TTA  AAACACCTA AC
                                  T  A_       A
GAM1019 SHANK2   3' CGGGCAGTCCTGTCTG      29454     T      TTGTGGA
                                CGG CAGTCCT      TCTG
                                ||| |||||||      ||||
                                GCC GTCAGGA      AGAC
                                  C      C_______
GAM1019 SHOC2    3' GTTAGTTTTGTGGATCTGCA  28895    C  CC
                                GT AGT  TTTGTGGATCTGCA
                                || |||  ||||||||||||||
                                CA TCA  AAACACCTAGACGT
                                 A  __
GAM1019 ZNF268   5' CGGTCAGTTTTGTGTGCCT   41761        CC     GA
                                CGGTCAGT  TTTGTG  TCT
                                ||||||||  ||||||  |||
                                GCCAGTCA  AAACAC  GGA
                                    __     AC
GAM1020 PIGH     3' TGACATACTGTGTC        21303         C  AATC
                                TGACATACT GT    GTC
                                ||||||||| ||    |||
                                ACTGTATGA CA    CAG
                                    _ _____
GAM1020 CD1A     5' TCAATATTTTCCCATGTATT   43408          GGT
                                TCAGTATTTTC   TGTATT
                                ||||||||||   ||||||
                                AGTTATAAAAG   ACATAA
                                      GGT
GAM1020 CTNNA1   3' TCTAGTATCAGTGTTGTATT   42323    _     TTCG
                                TC AGTATT    GTTGTATT
                                || ||||||    ||||||||
                                AG TCATAG    CAACATAA
                                 A     TCA_
GAM1020 DOCK1    3' TCAGTATTCTTAATGCTGT    10719         CG__
                                TCAGTATTTT    GTTGT
                                ||||||||||    |||||
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                                AGTCATAAGA   CGACA
                                     ATTA
GAM1020 HIVEP3   5' TCAGTATTGCCATTGTATT   35991       T  G
                                TCAGTATT TCG TTGTATT
                                |||||||| ||| |||||||
                                AGTCATAA GGT AACATAA
                                     C  _
GAM1020 LPHH1    5' AGTATTTTCTTTGTATT    29386       GG
                                AGTATTTTC  TTGTATT
                                |||||||||  |||||||
                                TCATAAAAG  AACATAA
                                     A_
GAM1020 NRAS     3' TCAGTATTCATTTTTGTATT  14853       TCGG
                                TCAGTATTT   TTGTATT
                                |||||||||   |||||||
                                AGTCATAAG   AACATAA
                                     TAAA
GAM1020 PCDHGA8  5' AGTGTTTTCGGTTGCATT   30415    A
                                AGT TTTTCGGTTGTATT
                                ||| ||||||||||||||
                                TCA AAAAGCCAACGTAA
                                  C
GAM1020 PPP2R5E  3' TCAATTTCATGGTTGTATT   26477     A  TC
                                TCAGT TTT  GGTTGTATT
                                ||||| |||  |||||||||
                                AGTTA AAG  CCAACATAA
                                   _  TA
GAM1020 RBBP8    3' GTATTTTCAAAATTGTATT   16172       __
                                GTATTTTCG  GTTGTATT
                                |||||||||  ||||||||
                                CATAAAAGT  TAACATAA
                                     TT
GAM1020 SPOCK    3' TCAGTATTTTATGTGTACT   41743        CG  T
                                TCAGTATTTT  GT GTATT
                                ||||||||||  || |||||
                                AGTCATAAAA  CA CATGA
                                     TA  _
GAM1020 STAU     3' TCAGTATTTTCAGTATATAT  32698          _
                                TCAGTATTTTCGGT TGTAT
                                |||||||||||||| |||||
                                AGTCATAAAAGTCA ATATA
                                       T
GAM1020 ZNF146   3' TCAGTATCTTCTTATATT   28357        GG
                                TCAGTATTTTC  TTGTATT
                                ||||||||||  |||||||
                                AGTCATAGAAG  AATATAA
                                     __
GAM1021 ATP1A2   3' TGCCACCTCTAGCAAT     8713       GGGA
                                TGCCAC   TTTAGCAAT
                                ||||||   |||||||||
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                                ACGGTG   AGATCGTTA
                                   G___
GAM1021 BCL11B   3' TGCCACGCTTAGCAAT     39759       GGA
                                TGCCACG   TTTAGCAAT
                                |||||||   |||||||||
                                ACGGTGC   GAATCGTTA
                                    ___
GAM1021 CLCA3    3' TGTCACAGTTAGCAAT     22266    C    GAT
                                TG CACGG   TTAGCAAT
                                || |||||   ||||||||
                                AC GTGTC   AATCGTTA
                                 A    ___
GAM1021 COL19A1  3' TGACGAGATGTTTAGCAAT   12384   C     __
                                C ACGGGAT  TTAGCAAT
                                | |||||||  ||||||||
                                A TGCTCTA  AATCGTTA
                                 C      CA
GAM1021 DDOST    3' TGCCACTTTTAGCAAT     23349      GGGA
                                TGCCAC    TTTAGCAAT
                                ||||||    |||||||||
                                ACGGTG    AAATCGTTA
                                   A___
GAM1021 EFNA4    3' TGCCCTGGTCCAGCAAT    23394     ACG  A
                                TGCC   GG TTTAGCAAT
                                ||||   || |||||||||
                                ACGG   CC AGGTCGTTA
                                  GA_  _
GAM1021 IL17BR   3' TGCTACATTAGTTAGCAAT   33108    C   GGAT
                                TGC ACG    TTAGCAAT
                                ||| |||    ||||||||
                                ACG TGT    AATCGTTA
                                  A   AATC
GAM1021 MDFI     3' TGTCAGGTCCTCAGCAAT    24621    C  C  GA
                                TG CA GG  TTTAGCAAT
                                || || ||  |||||||||
                                AC GT CC  GAGTCGTTA
                                 A  _  AG
GAM1021 MEN1     5' TGCTGGGCAGTTTAGCAAT   39236    CAC   A__
                                TGC   GGG   TTTAGCAAT
                                |||   |||   |||||||||
                                ACG   CCC   AAATCGTTA
                                  A__   GTC
GAM1021 PIP5K1A  3' TGCCAAGTCCAGCAAT     18660      CG  A
                                TGCCA  GG TTTAGCAAT
                                |||||  || |||||||||
                                ACGGT  TC AGGTCGTTA
                                    __  _
GAM1021 PPARGC1  3' TACCACGGCATGAAGGCAAT  29957        G  TTA_
                                TGCCACGG AT   GCAAT
                                |||||||| ||   |||||
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                                ATGGTGCC TA   CGTTA
                                    G  CTTC
GAM1021  PPP1R2   3'  GCCATTTAATTAGCAAT    26418     CGG   T
                                GCCA   GATT AGCAAT
                                ||||   |||| ||||||
                                CGGT   TTAA TCGTTA
                                  AAA   _
GAM1021  TACC1    3'  GCAAAAAGATTTAGCAAT    26595    CAC
                                GC   GGGATTTAGCAAT
                                ||   ||||||||||||
                                CG   TTCTAAATCGTTA
                                 TTT
GAM1021  TP63     3'  TGCCACAGGAAAACCAAT    19003         TTTAG
                                TGCCACGGGA    CAAT
                                ||||||||||    ||||
                                ACGGTGTCCT    GTTA
                                      TTTG_
GAM1021  TRAF5    3'  TGCCACAGTTCACCAGCA    21476        GAT_
                                TGCCACGG    TTAGCA
                                ||||||||    ||||||
                                ACGGTGTC    GGTCGT
                                    AAGT
GAM1021  WNT15    3'  TGCCACAGGAGGTCCTGGCA   18149          ___   A
                                TGCCACGGGA   TTT GCA
                                ||||||||||   ||| |||
                                ACGGTGTCCT   GGA CGT
                                      CCA   C
GAM1021  CBFA2T2  3'  TCTAGAACTACCCAGAATGA   22978     A   C   ACGT
                                TCTA AAC TAC    GGAATGA
                                |||| ||| |||    |||||||
                                AGAT TTG ATG    TCTTACT
                                  C   _   GG__
GAM1021  FUT9     3'  TAAAACCGAATGGAATGA    42734        TACAC
                                TAAAACC    GTGGAATGA
                                |||||||    |||||||||
                                ATTTTGG    TACCTTACT
                                    CT___
GAM1021  GALNT2   3'  TCTGGGTAGACACGTGGGATGA 21011     AAAACCT       A
                                TCT      ACACGTGG ATGA
                                |||      |||||||| ||||
                                AGA      TGTGCACC TACT
                                  CCCATC_       C
GAM1021  KCNJ6    3'  TCTAAACCTACATTAATGA    13863       A     CGTGG
                                TCTAAA CCTACA    AATGA
                                |||||| ||||||    |||||
                                AGATTT GGATGT    TTACT
                                    _     AA___
GAM1021  MTMR6    3'  TCTAAAACCACAATCAGTGAC  45281         T   CG   AA
                                TCTAAAACC ACA  TGG  TGAC
                                ||||||||| |||  |||  ||||
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                                AGATTTTGG TGT  GTC  ACTG
                                      _  TA  __
GAM1021  SPAG6    3'  TAAAATCTACCTGTAGAAC   29703      C   AC
                                TAAAA CTAC  GTGGAAT
                                ||||| ||||  |||||||
                                ATTTT GATG  CATCTTG
                                   A   GA
GAM1021  TRPM2    5'  TCTAGAGACACATGGGGTG   17697     AAACCT      AA
                                TCTA     ACACGTGG  TG
                                ||||     ||||||||  ||
                                AGAT     TGTGTACC  AC
                                  CTC___       CC
GAM1022  ABCC2    3'  TGACATTTATTTTCTTAAC   7563      TG   C
                                TGG  TTTA TTTCTTAAC
                                |||  |||| |||||||||
                                ACT  AAAT AAAGAATTG
                                  GT   A
GAM1022  BGN      3'  TTGCACGGTGTTTCTTT     11824           A
                                TTGCATGGTGTTT CTTT
                                |||||||||||| ||||
                                AACGTGCCACAAA GAAA
                                      _
GAM1022  CSPG3    3'  GCATGGTGTCTACTTCTTA   20487             T
                                GCATGGTGTTTACTT CTTA
                                |||||||||||||| ||||
                                CGTACCACAGATGAA GAAT
                                      _
GAM1022  HIP1     3'  TGTTTAAGTGCTTTCTTAAC  23763      _____
                                TGTTTA   CTTTCTTAAC
                                ||||||   ||||||||||
                                ACAAAT   GAAAGAATTG
                                   TCAC
GAM1022  PTEN     3'  CATGGTGTTTTATCCCTCTT  7204          A__
                                CATGGTGTTT   CTTTCTT
                                ||||||||||   |||||||
                                GTACCACAAA   GGGAGAA
                                     ATA
GAM1022  TEM7R    3'  TTGCATGGGCTGTTTTTCTTA 37272        T   TAC
                                TTGCATGG GTT   TTTCTTA
                                |||||||| |||   |||||||
                                AACGTACC CGA   AAAGAAT
                                     _  CAA
GAM1022  CTNNA1   3'  AGCATTACTAACAAGCTAAT  42321        GTT G
                                GGCATTAT   C AAGCTAAT
                                ||||||||   | ||||||||
                                TCGTAATG   G TTCGATTA
                                     ATT _
GAM1022  PRDM2    3'  AGGCATCAAGAGCTGATA    29249        TGTTCGA   A
                                AGGCATTA      AGCT ATA
                                ||||||||      |||| |||
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                                TCCGTAGT      TCGA TAT
                                    TC_____   C
GAM1022  TRAM     3'  AGGCATTATGTTTTAAAAG   30698          C__
                                AGGCATTATGTT   GAAG
                                ||||||||||||  ||||
                                TCCGTAATACAA   TTTC
                                      AAT
GAM1023  CLN6     3'  TTGCTCAACAGCCACAGTAG   32831      G____
                                TTGT    AGCCACAGTAG
                                ||||    ||||||||||||
                                AACG    TCGGTGTCATC
                                  AGTTG
GAM1023  STAT6    3'  TTCAGATTGTGTACAGTAGA   17163      T     AGCC
                                TTCA ATTGTG    ACAGTAGA
                                |||| ||||||    ||||||||
                                AAGT TAACAC    TGTCATCT
                                  C     A___
GAM1023  CTH      3'  TGACCTGTAATTATAACAT    12514          TGTG  C
                                TGGCCTGTA    AT ATAACAT
                                |||||||||    || |||||||
                                ACTGGACAT    TA TATTGTA
                                     ____ A
GAM1023  GNB2     3'  TGGCCTGTAGTGTGGGCAT    23605          _    AT
                                TGGCCTGTA TGTG  CAT
                                ||||||||| ||||  |||
                                ACCGGACAT ACAC  GTA
                                     C    CC
GAM1023  MYOC     3'  TGGCTTGTGGTAACCATGTAAC 7032       C   AT      __
            ATG                    TGGC TGT  GTGATCA  TAACATG
                                |||| |||  |||||||  |||||||
                                ACCG ACA  CATTGGT  ATTGTAC
                                  A  C_      AC
GAM1023  PPAT     3'  TGGCCTGCTATAATATAATATG 15485         A     C    C
                                TGGCCTGT TGTGAT ATAA ATG
                                |||||||| |||||| |||| |||
                                ACCGGACG ATATTA TATT TAC
                                     _     _   A
GAM1023  RAD54B   3'  TGGCGTATATGGGTCAT     39587      CT      A_
                                TGGC  GTATGTG  TCAT
                                ||||  |||||||  ||||
                                ACCG  CATATAC  AGTA
                                  __       CC
GAM1024  CTSF     3'  CAGGGTGGGAATGGGGT     45365     A   TGTTTA
                                TAG GTG     AATGGGGT
                                ||| |||     ||||||||
                                GTC CAC     TTACCCCA
                                  C   CC____
GAM1024  DKK1     3'  TCTAGAATTAAATGGGGT     29273         GTGTT
                                TCTAGAGT    TAAATGGGGT
                                ||||||||    ||||||||||
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                                AGATCTTA    ATTTACCCCA
                                        _____
GAM1024  KLHL3    3'  TCTGAGTAAAATGGGG      44648     A    TGTTT
                                TCT GAGTG    AAATGGGG
                                ||| |||||    ||||||||
                                AGA CTCAT    TTTACCCC
                                  _    _____
GAM1025  C11orf13  3'  GAGGAGCCCTCTGTGACC    18484        GAGAA
                                GAGGAGCT    GTGACC
                                ||||||||    ||||||
                                CTCCTCGG    CACTGG
                                     GAGA_
GAM1025  CTPS     3'  TGAGAAACAAGGTGACC     44802        T   AA
                                TGAGGAGC GAG  GTGACC
                                |||||||| |||  ||||||
                                ACTCTTTG TTC  CACTGG
                                        _  __
GAM1025  DCC      3'  TAACTGAGTGGTCCTGATGGGT 23345        GAG__   GAA
              GACC                  TAACTGAG    CTGA   GTGACC
                                |||||||    ||||  ||||||
                                ATTGACTC    GACT   CACTGG
                                     ACCAG    ACC
GAM1025  FEN1     3'  AACTGCCTGAGAAGTG      19955       AGGAG
                                AACTG    CTGAGAAGTG
                                |||||    ||||||||||
                                TTGAC    GACTCTTCAC
                                   G____
GAM1025  GALE     5'  ACTGAGGACTGGAGAGT     41796        G  _  A
                                ACTGAGGA CTG AGA GT
                                |||||||| ||| ||| ||
                                TGACTCCT GAC TCT CA
                                     _  C  _
GAM1025  GPR65    5'  ACTGAGGAGCTTGATAAAT   40733          _ G
                                ACTGAGGAGCT GA AAGT
                                |||||||||| || ||||
                                TGACTCCTCGA CT TTTA
                                       A  A
GAM1025  GRB10    3'  ACTGAGGAGCAGAGAAATG   23645          T
                                ACTGAGGAGC GAGAAGTG
                                |||||||||| ||||||||
                                TGACTCCTCG CTCTTTAC
                                      T
GAM1025  KCNN4    3'  TAACTGAGAGCTGGAGGT    13928        G    A  A
                                TAACTGAG AGCTG GA GT
                                |||||||| ||||| || ||
                                ATTGACTC TCGAC CT CA
                                     _    _  C
GAM1025  NOS1     3'  AACTGAGGACAAGTGAC     8367         G TGAG
                                AACTGAGGA C    AAGTGAC
                                ||||||||| |    |||||||
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                                TTGACTCCT G   TTCACTG
                                    _ _____
GAM1025 PLAC1   5' AACTGAAGAGGGGTGC     34749        CTGAGAA  A
                                AACTGAGGAG     GTG C
                                ||||||||||     ||| |
                                TTGACTTCTC     CAC G
                                     CC_____   C
GAM1025 SELL    3' CAACTGAAAAAGAGAGGTG   8510         CT   A
                                TAACTGAGGAG  GAGA GTG
                                ||||||||||  |||| |||
                                GTTGACTTTTT  CTCT CAC
                                     __   C
GAM1025 SLC6A6  3' GACTGAGCTTGGAAGTGAC   16787   G_   GA
                                GA  GAGCT  GAAGTGAC
                                ||  |||||  ||||||||
                                CT  CTCGA  CTTCACTG
                                 GA    AC
GAM1025 SLC9A1  5' CTGAGGAAAGTGAC       43233       GCTGAG
                                CTGAGGA     AAGTGAC
                                |||||||     |||||||
                                GACTCCT     TTCACTG
                                    _______
GAM1025 SP100   3' TGATGGAGGAATAAAGTGAC  17056    _   CTGA
                                TGA GGAG   GAAGTGAC
                                ||| ||||   ||||||||
                                ACT CCTC   TTTCACTG
                                  A   CTTA
GAM1025 ST7     3' CTGAAGAGCAGTGAC       32938        TGAGA
                                CTGAGGAGC    AGTGAC
                                |||||||||    ||||||
                                GACTTCTCG    TCACTG
                                    _____
GAM1025 TRAF1   3' TGAGGAGCTGGGAGGAC     24949        A  A T
                                TGAGGAGCTG GA G GAC
                                |||||||||| || | |||
                                ACTCCTCGAC CT C CTG
                                     C  _ _
GAM1025 TRIM8   3' AAGCTGCTTGAGAAGTGC    36279    GA  _      A
                                GAG  GCT GAGAAGTG C
                                |||  ||| |||||||| |
                                TTC  CGA CTCTTCAC G
                                  GA  A       C
GAM1025 YES1    3' ACTTGGGGAAAAAAAAGTG   24115    GA_   CT
                                ACT   GGAG  GAGAAGTG
                                |||   ||||  ||||||||
                                TGA   CCTT  TTTTTCAC
                                  ACC   T_
GAM1025 ZNFN2A1 3' TGAGGAGCTGGGTGC      41366        AGAA  A
                                TGAGGAGCTG   GTG C
                                ||||||||||   ||| |
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                                ACTCCTCGAC    CAC G
                                      C___  _
GAM1025 CYP4B1   3' AGCCATCTGGGACCCCAT    8936        A_ ACTTCG
                                AGTCATCT  GA     TCCCAT
                                ||||||||  ||     ||||||
                                TCGGTAGA  CT     GGGGTA
                                    CC  _______
GAM1025 HUNK     3' GTCATCTAGATCCCACCCTCCC 31076         A __ G
           ATT                    GTCATCTAGA CT  TC TCCCATT
                                ||||||||||  ||  || |||||||
                                CAGTAGATCT GG  GG AGGGTAA
                                      A  GT  G
GAM1025 SYT1     3' AGTTTTCTAGAACTTGT     24851     CA        C
                                AGT  TCTAGAACTT GT
                                |||  ||||||||||  ||
                                TCA  AGATCTTGAA CA
                                  AA        _
GAM1025 TERF1    3' AATCATCTAGAAAATTCAT    32739          C_
                                AGTCATCTAGAA  TTCGT
                                ||||||||||||  |||||
                                TTAGTAGATCTT  AAGTA
                                      TT
GAM1026 CALM1    3' TTCTTCTAGAGGGGGGAAAAAG 27865         CGCGTTA
                                TTTTTCTAGA      GAAAAAG
                                ||||||||||      |||||||
                                AAGAAGATCT      CTTTTTC
                                      CCCCC__
GAM1026 PHKA2    3' TTTTTCTAGATTCCAGAA    7120          CGCG
                                TTTTTCTAGA    TTAGAA
                                ||||||||||    ||||||
                                AAAAAGATCT    GGTCTT
                                      AA__
GAM1027 PCDHGC3  5' TTTCAGCGGGTTAGCGCT    37053        T  CC   CATC
                                TTTCAGCG GG  AGC    GCT
                                ||||||||  ||  |||    |||
                                AAAGTCGC CC  TCG    CGA
                                    _  AA  _____
GAM1027 NOLA3    3' TGGCTGGCAAAAAGGCATCAGG 33006          TGCTGA
                                TGGCTGGTAAG     CATCAGG
                                ||||||||||      |||||||
                                ACCGACCGTTT     GTAGTCC
                                      TTCC__
GAM1027 PHKG1    5' TGGCTGGTTAAGTGCTTGCAGG 26312        _     GACAT
                                TGGCTGGT AAGTGCT     CAGG
                                ||||||||  |||||||    ||||
                                ACCGACCA TTCACGA     GTCC
                                    A      AC___
GAM1027 PODXL    3' TGGCTGGTGAAGTGTGACCCAG 23986        _    C    A
           G                     TGGCTGGT AAGTG TGAC TCAGG
                                ||||||||  |||||  ||||  |||||
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                                ACCGACCA TTCAC ACTG GGTCC
                                    C    _   _
GAM1027 RAB3A    3'  TGGCTGGTAGGGGCCGGGTCAG 16077        AGT   ACA
            G                    TGGCTGGTA  GCTG  TCAGG
                                 |||||||||  ||||  |||||
                                 ACCGACCAT  CGGC  AGTCC
                                     CCC   CC_
GAM1028 ABCD2    3'  TTGATACATTTTAGCCAT    23156       AAGG
                                 TTGATATA   TGGCCAT
                                 ||||||||   |||||||
                                 AACTATGT   ATCGGTA
                                     AAA_
GAM1028 CAT      3'  TTAATATAATAGGCCAT     11988       AGGT
                                 TTGATATAA  GGCCAT
                                 |||||||||  ||||||
                                 AATTATATT  CCGGTA
                                     AT__
GAM1028 CD83     3'  CTGAAAAGGTGGCCAT      20137     TAT
                                 TTGA  AAAGGTGGCCAT
                                 ||||  ||||||||||||
                                 GACT  TTTCCACCGGTA
                                   ___
GAM1028 ETV3     3'  CTTGATACTGAATAGCC      23477       AAA
                                 CTTGATAT  GGTGGCC
                                 ||||||||  |||||||
                                 GAACTATG  TTATCGG
                                     AC_
GAM1028 HMGN2    3'  TTGTGCCAAGGTGGCCAT    24324     ATATA
                                 TTG    AAGGTGGCCAT
                                 |||    ||||||||||
                                 AAC    TTCCACCGGTA
                                   ACGG_
GAM1028 KCNK2    3'  CTTGATGATAGATGACCAT    30565      ATAA
                                 CTTGAT   AGGTGGCCAT
                                 ||||||   ||||||||||
                                 GAACTA   TCTACTGGTA
                                    CTA_
GAM1028 KIF5C    3'  TTGATATAAACCACCAT     21173       GG G
                                 TTGATATAAA  T GCCAT
                                 ||||||||||  | |||||
                                 AACTATATTT  G TGGTA
                                      __ G
GAM1028 MTRF1    3'  CTTGATATAGGTCCA       20187       AA   GG
                                 CTTGATAT  AGGT  CCA
                                 ||||||||  ||||  |||
                                 GAACTATA  TCCA  GGT
                                      __   __
GAM1028 NFE2L2   3'  TTAATATAAAAAATGCCAT   26089         TG
                                 TTGATATAAAGG  GCCAT
                                 ||||||||||||  |||||
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                                AATTATATTTTT  CGGTA
                                      TA
GAM1028 PLAB     5' CTCGATATGAGGACACCAT   42317       AA   TG
                                CTTGATAT  AGG  GCCAT
                                ||||||||  |||  |||||
                                GAGCTATA  TCC  TGGTA
                                    C_   TG
GAM1028 RASGRP1  3' CTTGATACTGTTTAGCCAT   25077       AAAGG
                                CTTGATAT    TGGCCAT
                                ||||||||    |||||||
                                GAACTATG    ATCGGTA
                                    ACAA_
GAM1028 SEMG1    3' CTTGATATTGGTCCA      16555       AAAGG  _
                                CTTGATAT    TGG CCA
                                ||||||||    ||| |||
                                GAACTATA    ACC GGT
                                    _____  A
GAM1028 SLC7A6   3' CTGGATAGTAATGGCCAT    19592    T   TAAA
                                CT GATA    GGTGGCCAT
                                || ||||    |||||||||
                                GA CTAT    TTACCGGTA
                                 C   CA__
GAM1028 SRGAP1   5' AACATGAAAGGTGGTCAT    43591      _      C
                                GATAT AAAGGTGG CAT
                                ||||| |||||||| |||
                                TTGTA TTTCCACC GTA
                                   C       A
GAM1028 TMPRSS4  3' TTAATAATAGTGGCCAT     33396      TAAA
                                TTGATA    GGTGGCCAT
                                ||||||    |||||||||
                                AATTAT    TCACCGGTA
                                   TA__
GAM1028 ITGA11   3' GTCACCATCAAGCCCTTGC   29201        AAACA
                                GTCACCATCAA    TTGC
                                ||||||||||    ||||
                                CAGTGGTAGTT    AACG
                                      CGGG_
GAM1028 JAG1     3' CATCACCATTAGGACATC    6851        CAAAA
                                CGTCACCAT    ACATT
                                |||||||||    |||||
                                GTAGTGGTA    TGTAG
                                    ATCC_
GAM1028 NFIA     3' GTTACAGAAAAACATTGCC   43223    C  CATC
                                GT AC    AAAAACATTGCC
                                || ||    ||||||||||||
                                CA TG    TTTTTGTAACGG
                                 A  TC__
GAM1028 PLIN     3' GTGGCCATCAAAAAGAGC    15401    CA       CATT
                                GT  CCATCAAAAA    GC
                                ||  ||||||||||    ||
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                                CA  GGTAGTTTTT   CG
                                 CC        CT__
GAM1028  TMEPAI   3'  CACGTCACCAGCAGGTCCCGCC 33589          T  AAAACA
                                CACGTCACCA CA     TTGCC
                                |||||||||| ||     |||||
                                GTGCAGTGGT GT     GGCGG
                                      C  CCAG__
GAM1029  CAMLG    3'  TATGGCAGTTACTGAGTTAGTT 11954     C       CAA
              A                  TAT GCAGTTAT   GGTTAGTTA
                                ||| ||||||||   |||||||||
                                ATA CGTCAATG   TCAATCAAT
                                  C       AC_
GAM1029  IL17BR   3'  GCATTATCAAAATGGTTA    33107     G      ___
                                GCA TTATCAA   GGTTA
                                ||| |||||||   |||||
                                CGT AATAGTT   CCAAT
                                  _      TTA
GAM1029  ATRX     3'  TAACCCTCAGTTTCTAACTTTC 39609        AA___   TT
                                TAACCCT    TCT  GCTTTT
                                |||||||    |||  ||||||
                                ATTGGGA    AGA  TGAAAG
                                     GTCAA   T_
GAM1029  BDKRB2   3'  ACCCTTTGCTTTTC       8394       AATCT
                                ACCCT    TTGCTTTTC
                                |||||    |||||||||
                                TGGGA    AACGAAAAG
                                  _____
GAM1029  BUB3     3'  TAACCTTAACCTCGCTTT    21804      C      T
                                TAACC TAATCTT GCTTT
                                ||||| ||||||| |||||
                                ATTGG ATTGGAG CGAAA
                                   A      _
GAM1029  CSNK1G3  3'  AACCCATATTGCTTTTC     20473      TAATCT
                                AACCC     TTGCTTTTC
                                |||||     |||||||||
                                TTGGG     AACGAAAAG
                                   TAT___
GAM1029  DAP      3'  TAACCTTAATCTCATCTTC   43691      C      TG
                                TAACC TAATCTT  CTTT
                                ||||| |||||||  ||||
                                ATTGG ATTAGAG  GAAG
                                   A      TA
GAM1029  DUT      3'  ACCTTTAATCTCTCCTTTTC  12623     C_      G
                                ACC  TAATCTTT CTTTTC
                                |||  |||||||| ||||||
                                TGG  ATTAGAGA GAAAAG
                                  AA       G
GAM1029  EGR3     3'  ACCAAAATTTTTGCTTTT    40534     CT   C
                                ACC  AAT TTTGCTTTT
                                |||  ||| |||||||||
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                                TGG  TTA AAACGAAAA
                                  TT   A
GAM1029  GOLGA4   5'  AACTCCTCCTCTTTGCTTTTC  41053    _  AA
                                AAC CCT  TCTTTGCTTTTC
                                |||  |||  ||||||||||||
                                TTG GGA  AGAAACGAAAAG
                                  A   GG
GAM1029  IGFBP5   5'  AACCCTAACACCTCTTTTC   8266        C   G
                                AACCCTAAT TTT CTTTTC
                                |||||||||  |||  ||||||
                                TTGGGATTG GGA GAAAAG
                                      T   _
GAM1029  ITGB1    3'  CCCTACAGTTTTGCTTTTC   38046     ATC_
                                CCCTA   TTTGCTTTTC
                                |||||   ||||||||||
                                GGGAT   AAACGAAAAG
                                   GTCA
GAM1029  KIF5B    5'  TAACCCTAATGCTCACTTC   21140        C  TG
                                TAACCCTAAT TT  CTTT
                                ||||||||||  ||  ||||
                                ATTGGGATTA GA  GAAG
                                      C  GT
GAM1029  LANCL1   3'  TAACCCTAGATCCACTTTT   25855       ATC  TG
                                TAACCCTA   TT  CTTTT
                                ||||||||   ||  |||||
                                ATTGGGAT   AG  GAAAA
                                     CT_  GT
GAM1029  LARGE    3'  CCCTGATCTTGTGGCTTT    21861     A    T__
                                CCCT ATCTT   GCTTT
                                ||||  |||||   |||||
                                GGGA TAGAA   CGAAA
                                  C    CAC
GAM1029  LPIN1    5'  CCCCGGTCTTGCCCTTC     42635     AA   T
                                CCCT  TCTT GCTTTTC
                                ||||  ||||  |||||||
                                GGGG  AGAA CGGGAAG
                                  CC   _
GAM1029  PACSIN1  3'  CAACCCTGGTCTGCTTC     45144       AATC
                                TAACCCT    TTTGCTTT
                                |||||||    ||||||||
                                GTTGGGA    AGACGAAG
                                    CC__
GAM1029  TLL2     3'  CCTAATCTTTAACACTTT    29748         ___
                                CCTAATCTTT   GCTTT
                                ||||||||||   |||||
                                GGATTAGAAA   TGAAA
                                      TTG
GAM1029  TTID     5'  CAACCTTGGTCTGCTCTTC   27712      CTAATC
                                TAACC     TTTGCTTTTC
                                |||||     ||||||||||
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                                GTTGG     AGACGAGAAG
                                  AACC__
GAM1030  BCAT1    3'  TTTGATGATTGCAATTCATTT  42388      _     CCA
                                TTTG TGGTT   CAATTCATTT
                                |||| |||||   ||||||||||
                                AAAC ACTAA   GTTAAGTAAA
                                  T    C__
GAM1030  NLGN1    3'  TTTGTATATATACAATTCATTT 31393       GTTCC
                                TTTGTG    ACAATTCATTT
                                ||||||    ||||||||||
                                AAACAT    TGTTAAGTAAA
                                   ATATA
GAM1030  NPHP1    3'  TGGTTCCATCATTT       41684        CAAT
                                TGGTTCCA    TCATTT
                                ||||||||    ||||||
                                ACCAAGGT    AGTAAA
                                    _____
GAM1030  PPP2R2B  3'  ATTTCCCCACAGTTCATTT   21328    GG      A
                                GT  TTCCACA TTCATTT
                                ||  ||||||| |||||||
                                TA  GGGGTGT AAGTAAA
                                 AA      C
GAM1030  SHOC2    3'  TTTTGTGGATCTGCAACT    28901        T  CA
                                TTTTGTGG TC  CAATT
                                |||||||| ||  |||||
                                AAAACACC AG  GTTGA
                                     T  AC
GAM1030  SLC6A3   3'  TTTGTGGTTTCCTCCATTTC   9817         _  ACAA
                                TTTGTGGTT CC    TTCATTTC
                                |||||||||| ||    ||||||||
                                AAACACCAA GG    AGGTAAAG
                                     A  _____
GAM1031  ASTN     3'  TGGGAGCTGGGAGAGTGTTGGT 42956     A   T    C  _  CA
            G                    TGG AGCT GGGGG AG GT  GTG
                                ||| |||| ||||| || ||  |||
                                ACC TCGA CCCTC TC CA  CAC
                                  C   _    _  A  AC
GAM1031  ATP1B2   3'  TGGGTGGGTGGGTCAGTG    11741      _  CA_
                                TGGG GG   GGTCAGTG
                                |||| ||   ||||||||
                                ACCC CC   CCAGTCAC
                                  A  CAC
GAM1031  CALB2    3'  TGGAAGTTTGGGGTGGGTGGTG 11937       C     GCA   CA
                                TGGAAG TTGGGG   GGT  GTG
                                |||||| ||||||   |||  |||
                                ACCTTC AACCCC   CCA  CAC
                                   A     AC_   C_
GAM1031  CASP10   3'  GAAGTTTGGGGGGACAAGT   37385      C      __
                                GAAG TTGGGGG  CAGGT
                                |||| |||||||  |||||
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                                CTTC AACCCCC  GTTCA
                                  A      CT
GAM1031  CD7      3'  TGGGGGTTGGGGGGCCTGCTGGT 26007     AAGC       AG  CA
                G                  TGG    TTGGGGGC  GT  GTG
                                   |||    ||||||||  ||  |||
                                   ACC    AACCCCCG  CG  CAC
                                     CCC_       GA  AC
GAM1031  CRHR1    3'  TGGACATGGGCAGGTCAGT    20452      AGCTTGG
                                   TGGA      GGGCAGGTCAGT
                                   ||||      ||||||||||||
                                   ACCT      CCCGTCCAGTCA
                                     GTA____
GAM1031  CRHR1    3'  TGGAGGCCTGGGGGGGT      20453      A        CA
                                   TGGA GCTTGGGGG  GGT
                                   |||| |||||||||  |||
                                   ACCT CGGACCCCC  CCA
                                     C        __
GAM1031  CTGF     3'  TGGGGCTACAGGCAGGTCAGTG 12508      AA   T G
                                   TGG  GCT G GGGCAGGTCAGTG
                                   |||  ||| | ||||||||||||
                                   ACC  CGA T TCCGTCCAGTCAC
                                     C_   _ G
GAM1031  DNMT3L   5'  TGGGGTTTGGGGACCTCAGTG  30074     AAGC       AGG
                                   TGG    TTGGGGGC   TCAGTG
                                   |||    ||||||||   ||||||
                                   ACC    AACCCCTG   AGTCAC
                                     CCA_       G__
GAM1031  FACL4    3'  TGGGAGTTGGGGGGCAGAT    35689     A  C
                                   TGG AG TTGGGGGGCAGGT
                                   ||| || ||||||||||||
                                   ACC TC AACCCCCGTCTA
                                     C  _
GAM1031  GPC1     3'  TGGAGGCTGGGGGGGTGGG    13261      A   T    CA
                                   TGGA GCT GGGGG  GG
                                   |||| ||| |||||  ||
                                   ACCT CGA CCCCC  CC
                                     C   C    AC
GAM1031  JUP      3'  TGGGGGCTTAGGGCAGTTGGTC 13784      AA       G ___    A
                GGTG                  TGG  GCTTGGGG CA   GGTC GTG
                                      |||  |||||||| ||   |||| |||
                                      ACC  CGAATCCC GT   CCAG CAC
                                        CC       _ CAA    C
GAM1031  MMP19    5'  TGGGAGCCTTGGGGGAGCAGTG 35596      A  _      CA  T
                                      TGG AGC TTGGGGG  GG CAGTG
                                      ||| ||| |||||||  || |||||
                                      ACC TCG AACCCCC  TC GTCAC
                                        C  G      __ _
GAM1031  RANBP3   3'  TGGGGGCTGGGGGGCAGG     28773      AA   T
                                      TGG  GCT GGGGGGCAGG
                                      |||  ||| |||||||||
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                                ACC  CGA CCCCCGTCC
                                  CC  _
GAM1031  TSC      3'  GGAGGTGGCGGTGGGTCAGTG  32834     AGCT   G  CA
                                GGA    TGG GG  GGTCAGTG
                                |||    ||| ||  ||||||||
                                CCT    ACC CC  CCAGTCAC
                                  CC__   G  AC
GAM1031  WDR3     3'  GGGGCGTAGGGGTGGGTCAGTG 27690     AA  T     CA
                                GG  GC TGGGGG  GGTCAGTG
                                ||  || ||||||  ||||||||
                                CC  CG ATCCCC  CCAGTCAC
                                 C_  C     AC
GAM1032  BDP1     3'  GCCTGGGCAACAGAAC      32949     GAG   TAAA
                                GCT   TGG    CAACAGAAC
                                |||   |||    |||||||||
                                CGG   ACC    GTTGTCTTG
                                  ____  C___
GAM1032  CORO2B   5'  CCAGCTTGGGCAACAGAA    42075    _  GAG   TAAA
                                CC GCT   TGG    CAACAGAA
                                || |||   |||    ||||||||
                                GG CGA   ACC    GTTGTCTT
                                 T   ___   C___
GAM1032  EFNB2    3'  GCAGAGCCCTGGGTAACAGAAC 19881    T   ____    AACA
                                GC GAGT    GGTA    ACAGAAC
                                || ||||    ||||    |||||||
                                CG CTCG    CCAT    TGTCTTG
                                 T    GGAC   _____
GAM1032  GCGR     5'  GCTGAGTGGCAGAGCAGCAGA  6694          AA_  A
                                GCTGAGTGGTA   CA CAGA
                                ||||||||||   || ||||
                                CGACTCACCGT   GT GTCT
                                       CTC  C
GAM1032  HMOX1    3'  CCCTGCTATAAAAACAACAGAA 13411    G   AGTGGT
              C                  CC CTG     AAACAACAGAAC
                                || |||     ||||||||||||
                                GG GAC     TTTGTTGTCTTG
                                 _  GATATT
GAM1032  HRG      3'  TGTAGTGGTGAGTGACAGAA   7653     _     AAACA
                                TG AGTGGT     ACAGAA
                                || ||||||     ||||||
                                AC TCACCA     TGTCTT
                                 A     CTCAC
GAM1032  HS3ST2   3'  GCTGTGTTCATAGCAACAGAAC 25813      A  GGTAAA
                                GCTG GT     CAACAGAAC
                                ||||  ||     |||||||||
                                CGAC CA     GTTGTCTTG
                                  A  AGTATC
GAM1032  PIM2     3'  CCTTGGGGTAACAACAG     41021    GC  AGT    A
                                CC  TG   GGTAA CAACAG
                                ||  ||   ||||| ||||||
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                                GG  AC   CCATT GTTGTC
                                 A_  C__    _
GAM1032  PIP5K1B   5'  GCTTAGTAGCAACAGA      18666     G     TAAA
                                GCT AGTGG    CAACAGA
                                ||| |||||    |||||||
                                CGA TCATC    GTTGTCT
                                  A    _____
GAM1032  RBM3      3'  CTGTATGAGACACAACAGAA   43255     A    TAA
                                CTG GTGG   ACAACAGAA
                                ||| ||||   |||||||||
                                GAC TACT   TGTTGTCTT
                                  A    CTG
GAM1032  RET       3'  CGTGAGTGGTACAG        33933     C       AAACA
                                CG TGAGTGGT     ACAG
                                || ||||||||     ||||
                                GC ACTCACCA     TGTC
                                 _      ______
GAM1032  SMAC      3'  CCACTGAGTGGGGAGACAG   39894           TAAACA
                                CCGCTGAGTGG     ACAG
                                ||||||||||      ||||
                                GGTGACTCACC     TGTC
                                      CCTC__
GAM1032  SOST      3'  CCGTGAGTGGTGGGCAGAA    36102     C       AAACAA
                                CCG TGAGTGGT     CAGAA
                                ||| ||||||||     |||||
                                GGC ACTCACCA     GTCTT
                                  _       CCC___
GAM1032  WBSCR14   3'  GCTGAGTGAGCAGCAG      37287         TAAA  A
                                GCTGAGTGG    CA CAG
                                |||||||||    || |||
                                CGACTCACT    GT GTC
                                     C___  C
GAM1032  ZNF10     5'  CCTTGAGTGACAGCAGA     31733     GC     GTAA   A
                                CC  TGAGTG    ACA CAGA
                                ||  ||||||    ||| ||||
                                GG  ACTCAC    TGT GTCT
                                 A_     _____   C
GAM1032  ICA1      3'  TCATCTTTGTCAGCACCTTCA  35293         AC  A    C
                                TTATCTTT  CA CACC TCA
                                ||||||||  || |||| |||
                                AGTAGAAA  GT GTGG AGT
                                    CA  C    A
GAM1032  INPP5D    3'  TTATTATCTATATCTCCACCCT 44427          TTACCAA
              CA                  TTATTATCT      CACCCTCA
                                ||||||||||      ||||||||
                                AATAATAGA      GTGGGAGT
                                     TATAGAG
GAM1032  MS4A1     3'  TTATCTTTACCAGAACTCA    6606            ACACC
                                TTATCTTTACCA    CTCA
                                ||||||||||||    ||||
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                                AATAGAAATGGT    GAGT
                                      CTT__
GAM1032 PCDH11X  3' TTATTTTTACTGAACACCCT  37319     C    C_
                                TTAT TTTAC  AACACCCT
                                |||| |||||  ||||||||
                                AATA AAATG  TTGTGGGA
                                  A    AC
GAM1032 PCDH11Y  3' TTATTTTTACTGAACACCCT  37364     C    C_
                                TTAT TTTAC  AACACCCT
                                |||| |||||  ||||||||
                                AATA AAATG  TTGTGGGA
                                  A    AC
GAM1033 ATP6V1A1 3' ATAAAATGATTTTTTTTCATG 11777     TC   C
                                ATAA  TGAT TTTTTTCATG
                                ||||  |||| ||||||||||
                                TATT  ACTA AAAAAAGTAC
                                  TT   A
GAM1033 SMARCA3  3' ATAATCCCTAATTTTTTCATG 16898       GATC
                                ATAATCT   TTTTTTCATG
                                |||||||   ||||||||||
                                TATTAGG   AAAAAAGTAC
                                    GATT
GAM1033 TGFA     3' TAAATGACTGGTCCCCCTTTCA 17444      AAT  A_
          TG                    TAAAT  CTG  TCTTTTTTCATG
                                |||||  |||  ||||||||||||
                                ATTTA  GAC  GGGGGAAAGTAC
                                  CT_  CA
GAM1033 ITGAV    3' AGAAAAGTAATTTATAT    13629            III
                                AGAAAAGTAATTTATA  T
                                ||||||||||||||||  |
                                TCTTTTCATTAAATAT  A
                                         III
GAM1033 LRP4     3' TAAGAAAAGCTAAATTTATA  42065        __
                                TAAGAAAAGT  AATTTATA
                                ||||||||||  ||||||||
                                ATTCTTTTCG  TTAAATAT
                                      AT
GAM1034 EPHA2    3' GAGGTACCCTGTTTACTT   20737   CAA   ATA
                                GA  GCCCT  TTTACTT
                                ||  |||||  |||||||
                                CT  TGGGA  AAATGAA
                                 CCA   C__
GAM1034 FACL2    3' AGTGCAAGCCCTGTTGTGCTTG 34433   A_     ATATTTA
                                AG  CAAGCCCT     CTTG
                                ||  ||||||||     ||||
                                TC  GTTCGGGA     GAAC
                                 AC      CAACAC_
GAM1034 PXMP3    5' TACTTGCCAGAAGCTCAGA   7230      C      AAATCA
                                TACT GTCAGAAG     CAGA
                                |||| ||||||||     ||||
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                                ATGA CGGTCTTC     GTCT
                                  A       GA____
GAM1034  SULT1C1   3'  TACTGTTAATCATCACAGA   9843      C  CAGAAGAA
                                TACT GT       ATCACAGA
                                |||| ||       ||||||||
                                ATGA CA       TAGTGTCT
                                  _ ATTAG___
GAM1035  CEP1      3'  TATAAAAACATTGGCATTAATG 28139        TTA  ____
              GT                  TATAAAAAC  GGT   ATGGT
                                |||||||||  |||   |||||
                                ATATTTTTG  CCG   TACCA
                                     TAA  TAAT
GAM1035  FAT       3'  TATAAAAACTGTGTCATGGT  23490        TAGG
                                TATAAAAACT   TATGGT
                                ||||||||||   ||||||
                                ATATTTTTGA   GTACCA
                                     CACA
GAM1035  HDAC4     3'  TATAAAAACTCATTAGGT    25781         GGTAT
                                TATAAAAACTTA    GGT
                                ||||||||||||    |||
                                ATATTTTTGAGT    CCA
                                      AAT__
GAM1035  IFNAR2    3'  TACAAAAATTTGCTAGGCATGG 9321        C___
              T                  TATAAAAA   TTAGGTATGGT
                                |||||||||  ||||||||||
                                ATGTTTTT   GATCCGTACCA
                                     AAAC
GAM1035  NDRG3     3'  AACTTAGCTGGGTATGGT    36743       ____
                                AACTTA   GGTATGGT
                                ||||||   ||||||||
                                TTGAAT   CCATACCA
                                   CGAC
GAM1035  PTGES     3'  TACAAAAATTAGCTGGGTATGG 22184       C  ____
              T                  TATAAAAA TTA   GGTATGGT
                                |||||||| |||   ||||||||
                                ATGTTTTT AAT   CCATACCA
                                     _  CGAC
GAM1035  RAB23     3'  TATAAAAATTAGGTATGAT   32221       C
                                TATAAAAA TTAGGTATGGT
                                |||||||| ||||||||||
                                ATATTTTT AATCCATACTA
                                      _
GAM1035  SEDL      3'  TACAAAAATTAGCCAGGTGTGG 31011       C___     A
              T                  TATAAAAA   TTAGGT TGGT
                                |||||||||  |||||| ||||
                                ATGTTTTT   GGTCCA ACCA
                                     AATC     C
GAM1035  TRAF5     3'  TACAAAAATTACCTGGGTGTGG 21475       ___   A  A
              T                  TATAAAA  ACTT GGT TGGT
                                |||||||  |||| ||| ||||
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                                ATGTTTT  TGGA CCA ACCA
                                    TAA   C  C
GAM1035  WDR1     3'  TAAAAACTTGGACACGGT    32750        A  _
                                TAAAAACTT GG TATGGT
                                ||||||||| || ||||||
                                ATTTTTGAA CC GTGCCA
                                     _ T
GAM1035  HUNK     3'  TACAGCTGATCCCCTTTCATCA 31079     ATTAAC
                C                TACA     TTTTTTTCATCAC
                                ||||     |||||||||||||
                                ATGT     GGGGAAAGTAGTG
                                  CGACTA
GAM1035  NLGN1    3'  TACAATTCATTTTTTTCAAAAC 31386       AAC       TC
                C                TACAATT   TTTTTTTCA  ACC
                                |||||||   |||||||||  |||
                                ATGTTAA   AAAAAAAGT  TGG
                                    GT_       TT
GAM1035  OGT      5'  CAATTAACTTTTACTTATC   18782          T  C
                                CAATTAACTTTT TT ATC
                                |||||||||||| || |||
                                GTTAATTGAAAA GA TAG
                                      T  A
GAM1035  PCDHB15  3'  TTAACTTTCATATCACC     33192        TTTC
                                TTAACTTTT   ATCACC
                                |||||||||   ||||||
                                AATTGAAAG   TAGTGG
                                     TA__
GAM1035  POU4F1   3'  TACAATAACTTTTTTCC     26395       T
                                TACAAT AACTTTTTTTC
                                |||||| ||||||||||
                                ATGTTA TTGAAAAAAGG
                                  _
GAM1036  AGL      3'  TCAATATTATAATAAATGA   8491            TAAAT
                                TCAATATTATGATA    ATGA
                                ||||||||||||||    ||||
                                AGTTATAATATTAT    TACT
                                      T____
GAM1036  RAB27A   3'  TCAACATTATAAATATGA    21365          TATAA
                                TCAATATTATGA    ATATGA
                                ||||||||||||    ||||||
                                AGTTGTAATATT    TATACT
                                     _____
GAM1036  SEL1L    3'  TCAACATTATGAGTTTTATGA  22849          TATAAA
                                TCAATATTATGA     TATGA
                                ||||||||||||     |||||
                                AGTTGTAATACT     ATACT
                                      CAAA__
GAM1037  CD8A     3'  GAGGGATTCATTTTCCAGGG   12091     T  A
                                GAG GA TTCATTTTCCAGGG
                                ||| || ||||||||||||||
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                                CTC CT AAGTAAAAGGTCCC
                                  C _
GAM1037 LZTR1    3' TCAGTGAATTAATGAGTTTGGG 27641    G       CATTTTCCA_
             GC                   TC AGTGAATT        GGGC
                                || ||||||||        ||||
                                AG TCACTTAA        CCCG
                                 _       TTACTCAAAC
GAM1037 RGS16    3' TCAAGTGAGCCTCCTTTCAGGG 16326        A_  A    C
             C                    TCGAGTGA  TTC TTTTC AGGGC
                                ||||||||  ||| ||||| |||||
                                AGTTCACT  GAG GAAAG TCCCG
                                     CG  _   _
GAM1038 CHEK1    3' TTTCAAATTCAGATACTAA   10464            _
                                TTTCAAATTCAGAT TTAA
                                |||||||||||||| ||||
                                AAAGTTTAAGTCTA GATT
                                          T
GAM1038 TRHDE    3' TATCATTTCTGATAAAT     30111      TT
                                TATC  TTTCTGATAAAT
                                ||||  ||||||||||||
                                ATAG  AAAGACTATTTA
                                  T_
GAM1039 AP1M1    5' GCGGCAGCGACGGTGGG     37171    T        A  A
                                G CGGCGGCGACG TGG G
                                | ||||||||||| ||| |
                                C GCCGTCGCTGC ACC C
                                _         C  C
GAM1039 BAALC    5' AGGAGGCGGCGGCGGCGA    36033      T      A
                                AGGAG CGGCGGCG CGA
                                ||||| |||||||| |||
                                TCCTC GCCGCCGC GCT
                                   C       C
GAM1039 BMP3     5' AGGAGCCGGCGGCGGAGCCGAG 10187            A___   T
             G                    AGGAGTCGGCGGCG   CGA GG
                                ||||||||||||||   ||| ||
                                TCCTCGGCCGCCGC   GCT CC
                                         CTCG  _
GAM1039 CPNE3    5' GAAGTCGAGCGACGGTGGAGA  19383        GC      A
                                GGAGTCG  GGCGACG TGGAGA
                                |||||||  ||||||| ||||||
                                CTTCAGC  TCGCTGC ACCTCT
                                    __      C
GAM1039 EGR1     3' AGGGGTCAGGCATATGATGGAG 12654     A  _   GCGAC
             A                    AGG GTC GGCG     GATGGAGA
                                ||| ||| ||||     ||||||||
                                TCC CAG CCGT     CTACCTCT
                                  C  T   ATA__
GAM1039 ELAVL1   5' GGAGGCGGCGGCGGCGCGG   10880      T      A  A
                                GGAG CGGCGGCG CG TGG
                                |||| |||||||| || |||
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                                CCTC GCCGCCGC GC GCC
                                  C       C  _
GAM1039  FMNL     5'  GGGGCGGCGGCGGTGG      25309     A T       ACGA
                                GG G CGGCGGCG    TGG
                                || | ||||||||    |||
                                CC C GCCGCCGC    ACC
                                 C _       C___
GAM1039  GARS     5'  GGAGGCGGCGGCGGGCAAGGAG 13060      T       A_   T
              A                  GGAG CGGCGGCG  CGA GGAGA
                                |||| ||||||||  ||| |||||
                                CCTC GCCGCCGC  GTT CCTCT
                                  C       CC  _
GAM1039  IL12RB2  5'  GGAGCTGGCGGCGAGTGAG    11431       C       CGATG
                                GGAGT GGCGGCGA     GAG
                                ||||| ||||||||     |||
                                CCTCG CCGCCGCT     CTC
                                   A       CA___
GAM1039  KCNMB4   5'  GGAGTGGGCGGCGAGGGG     30948       C       CGAT
                                GGAGT GGCGGCGA    GG
                                ||||| ||||||||    ||
                                CCTCA CCGCCGCT    CC
                                   C       CC__
GAM1039  MADH7    5'  AGGAGCGGCGGCGGCCCGAGG  25359       T       A__   T
                                AGGAG CGGCGGCG   CGA GG
                                ||||| ||||||||   ||| ||
                                TCCTC GCCGCCGC   GCT CC
                                  _       CGG   _
GAM1039  MAGEA9   5'  AGGAGCTGGGCGATGGAG    23848       CGGC    CGA
                                AGGAGT    GGCGA   TGGAG
                                ||||||    |||||   |||||
                                TCCTCG    CCGCT   ACCTC
                                   AC__    ____
GAM1039  NFIC     3'  GGATTCCTGGGACGATGGAGA  24644     G  GGC  C
                                GGA TC   GG GACGATGGAGA
                                ||| ||   || ||||||||||
                                CCT AG   CC CTGCTACCTCT
                                  A  GA_  _
GAM1039  PABPC4   5'  GGAGTCGGCGGGCTTGGAGA   19227           CGACGA
                                GGAGTCGGCGG     TGGAGA
                                ||||||||||      ||||||
                                CCTCAGCCGCC     ACCTCT
                                      CGA___
GAM1039  PLCG1    5'  GGGGCGGCGGCGGCACAGG    15374     A T       A  AT
                                GG G CGGCGGCG CG  GG
                                || | |||||||| ||  ||
                                CC C GCCGCCGC GT  CC
                                 C _       C  GT
GAM1039  PLXNA1   3'  GGAGTCGGTGGCAACGGG     43623         C       AT
                                GGAGTCGG GGCGACG  GG
                                |||||||| |||||||  ||
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                                CCTCAGCC CCGTTGC  CC
                                   A     __
GAM1039  PRX     3'  AGGGTTGGCAGGTGGAG     34103     A  C    CGACGA
                                AGG GT GGCGG     TGGAG
                                ||| || |||||     |||||
                                TCC CA CCGTC     ACCTC
                                  _ A    C_____
GAM1039  PRX     3'  AGGAGCGGCGGCGGCCAGCCGG 34100      T      A_  A_
                                AGGAG CGGCGGCG  CG  TGG
                                ||||| ||||||||  ||  |||
                                TCCTC GCCGCCGC  GT  GCC
                                   _       CG  CG
GAM1039  SLC9A3R2  5'  GGGGCGGCGGCGGCGCTGG   41531    A T      A  A
                                GG G CGGCGGCG CG TGG
                                || | |||||||| || |||
                                CC C GCCGCCGC GC ACC
                                 C _       C  G
GAM1039  SMG1     5'  AGGAGGCGGCGGCGGA      31502      T      GACGAT
                                AGGAG CGGCGGC     GGA
                                ||||| |||||||     |||
                                TCCTC GCCGCCG     CCT
                                   C     _______
GAM1039  UMPK     3'  AGGGGCTGGGGTCCGATGGAGA 29775     A  C  C  CGA
                                AGG GT GG GG   CGATGGAGA
                                ||| || || ||   |||||||||
                                TCC CG CC CC   GCTACCTCT
                                  C  A  _  AG_
GAM1039  USP14    5'  GGAGGCGGCGGCGCAGGAGA   23116     T      ACGAT
                                GGAG CGGCGGCG    GGAGA
                                |||| ||||||||    |||||
                                CCTC GCCGCCGC    CCTCT
                                  C       GT___
GAM1039  YWHAH    3'  AAGAATCGGTGATGATGG    18190        CGGC  C
                                AGGAGTCGG    GA GATGG
                                |||||||||    || |||||
                                TTCTTAGCC    CT CTACC
                                     A___  A
GAM1039  OTP      3'  TCGCGTCGAAGGTGT       37004      A      CGGCGC
                                TCGCG TCGAAGGT     GT
                                ||||| ||||||||     ||
                                AGCGC AGCTTCCA     CA
                                   _      _______
GAM1040  ALPP     3'  TGGGGAGGCAGGGGAGTCTTCC 42874     A    _____    AAA
                                TGGG GAGGC    GAGTC   CC
                                |||| |||||    |||||   ||
                                ACCC CTCCG    CTCAG   GG
                                   _    TCCC    AA_
GAM1040  ANKRA2   5'  AGACAGCGAGTCGGGCCTTCC  35752     GA       AAA
                                GGA  GGCGAGTC   CCTTCC
                                |||  ||||||||   ||||||
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                                TCT  TCGCTCAG   GGAAGG
                                  G_       CCC
GAM1040  AXL      3'  TGGGAAGGTGGAGTTTTCC   34892       G   C_    CAAA
                                TGGGA AGG  GAGT    CC
                                ||||| |||  ||||    ||
                                ACCCT TCC  CTCA    GG
                                   _   AC    AAA_
GAM1040  BCL11A   5'  TGGGAGAGCCGTCATGGCTT   39722         G GA    AAC
                                TGGGAGAG C  GTCA   CTT
                                |||||||| |  ||||   |||
                                ACCCTCTC G  CAGT   GAA
                                     G __    ACC
GAM1040  CACNA1C  3'  TGGGAGAGGGCAGCGCCTTCC  8760          CG   CAAA
                                TGGGAGAGG  AGT    CCTTCC
                                |||||||||  |||    ||||||
                                ACCCTCTCC  TCG    GGAAGG
                                     CG   C___
GAM1040  CHAD     3'  GGGAGAGGCTCAGCCTTC    10418         GAG   AA
                                GGGAGAGGC   TCA  CCTTC
                                |||||||||   |||  |||||
                                CCCTCTCCG   AGT  GGAAG
                                     ___   C_
GAM1040  DSCR1    3'  TGGGAAAGGTGATACGTTTTCC 20640         C  GTCAAACC
                                TGGGAGAGG GA       TTCC
                                ||||||||| ||       ||||
                                ACCCTTTCC CT       AAGG
                                     A  ATGCAA__
GAM1040  FOXF1    3'  GGGAGAGGTGGAACCCT     11121         CGAGTCA
                                GGGAGAGG      AACCTT
                                ||||||||      ||||||
                                CCCTCTCC      TTGGGA
                                     ACC_____
GAM1040  IL17     3'  TGGTACTCAGTCAAACCTTCC  13534     GAGAGG G
                                TGG     C AGTCAAACCTTCC
                                |||     | ||||||||||||||
                                ACC     G TCAGTTTGGAAGG
                                  ATGA__ _
GAM1040  IPF1     3'  TGAGAGAGCGGGTTTTCC    6824         G  A  CAAA
                                TGGGAGAG CG GT    CC
                                |||||||| || ||    ||
                                ACTCTCTC GC CA    GG
                                     _  C  AAA_
GAM1040  ITGB7    5'  TGGGGCAAGTCAGACTTTC   9429      AGAG       A  C
                                TGGG    GCGAGTCA AC TTC
                                ||||    |||||||| || |||
                                ACCC    CGTTCAGT TG AAG
                                  _____       C  A
GAM1040  MARK3    5'  GGGAGGGCGGCTCCCTTCC   14361       A    A  CAAA
                                GGGAG GGCG GT    CCTTCC
                                ||||| |||| ||    ||||||
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                                CCCTC CCGC CG    GGAAGG
                                  _   _ AG__
GAM1040  MATP     5'  TGGGAGAGGAACCTT      32100          CGAGTCA
                                TGGGAGAGG      AACCTT
                                |||||||||      ||||||
                                ACCCTCTCC      TTGGAA
                                          ________
GAM1040  SIM2     3'  GGAGAGGCGGGCACATCCCTTC 22878          A  _  AA
              C                  GGAGAGGCG GT CA  CCTTCC
                                |||||||||  ||  ||  ||||||
                                CCTCTCCGC CG GT  GGAAGG
                                      C  T  AG
GAM1040  SLC21A9  5'  GGGAGAGGAGGCAAATCTTC   28568        CG  T    C
                                GGGAGAGG  AG CAAA CTTC
                                ||||||||  ||  ||||  ||||
                                CCCTCTCC  TC GTTT GAAG
                                     __  C    A
GAM1040  SPTBN2   3'  TGGGAGAGGGGGGTTACC     28077          CGA  CAA
                                TGGGAGAGG   GT   ACC
                                |||||||||   ||   |||
                                ACCCTCTCC   CA   TGG
                                     CC_  A__
GAM1040  WNT8B    3'  TGGGAGAGCGGGTTCCCCATTC 40591          G  A  CAAA  _
              C                  TGGGAGAG CG GT    CC TTCC
                                |||||||| ||  ||    ||  ||||
                                ACCCTCTC GC CA    GG AAGG
                                     _  C  AGG_  T
GAM1041  ACVR1B   3'  TAGCACTGGCAACACCTC    33764      G  A__
                                TAG AC   CAACACCTC
                                |||  ||   |||||||||
                                ATC TG   GTTGTGGAG
                                  G  ACC
GAM1041  DKK1     3'  AATAGGCAGTGCAGCACCT   29268        A  ___  A
                                AATAGG CA   CA CACCT
                                ||||||  ||   ||  |||||
                                TTATCC GT   GT GTGGA
                                    _  CAC  C
GAM1041  EGLN1    5'  AATAGAACACTTGCAACAC   35157           _____
                                AATAGGACAC    AACAC
                                ||||||||||    |||||
                                TTATCTTGTG    TTGTG
                                      AACG
GAM1041  KPNB2    3'  CAGTGACGGCAACACCTC    13999     _   A_
                                TAG GAC  CAACACCTC
                                |||  |||  |||||||||
                                GTC CTG  GTTGTGGAG
                                  A   CC
GAM1041  MCM6     3'  CAATAGGACAGCACATACCT  25406          _  AC_
                                TAATAGGACA CA   ACCT
                                ||||||||||  ||   ||||
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                                GTTATCCTGT GT   TGGA
                                      C  GTA
GAM1041  PCDHB2   3'  TAAAAGGAGACACCTC      33194     T    CACA
                                TAA AGGA    ACACCTC
                                ||| ||||    |||||||
                                ATT TCCT    TGTGGAG
                                  T   C___
GAM1041  SMN1     3'  TAAGACACTCTAACACTTC    35643        ___    C
                                TAGGACAC   AACAC TC
                                ||||||||   ||||| ||
                                ATTCTGTG   TTGTG AG
                                     AGA    A
GAM1041  SMN1     3'  TAAGACACTCTAACACTTC    35643        ___    C
                                TAGGACAC   AACAC TC
                                ||||||||   ||||| ||
                                ATTCTGTG   TTGTG AG
                                     AGA    A
GAM1041  SP4      5'  TAACAGGACAAACCCTC      17052         C   A
                                TAATAGGACA AAC CCTC
                                |||||||||| ||| ||||
                                ATTGTCCTGT TTG GGAG
                                      _  _
GAM1041  ADD1     3'  TGAGGCTCAGGAGGGTGAC    30529    T     ACACGT
                                TG GGCTCA     AGGGTGAC
                                || ||||||     ||||||||
                                AC CCGAGT     TCCCACTG
                                 T     CC____
GAM1041  ADD1     3'  TGAGGCTCAGGAGGGTGAC    30529    T     ACACGT
                                TG GGCTCA     AGGGTGAC
                                || ||||||     ||||||||
                                AC CCGAGT     TCCCACTG
                                 T     CC____
GAM1041  CBFA2T2  3'  TGTGGCTCAGCAGGTGC      22983         ACAC    _
                                TGTGGCTCA    GTAGG GT
                                |||||||||    ||||| ||
                                ACACCGAGT    CGTCC CG
                                     ____     A
GAM1041  CDC25A   3'  TGTGGCTCAGAGCAGCTTGACA 12153         ACAC    GG
                                TGTGGCTCA    GTAG  TGACA
                                |||||||||    ||||  |||||
                                ACACCGAGT    CGTC  ACTGT
                                     CT__    GA
GAM1041  CRLF1    5'  TGCGGCTCGGCGGCGGTGGCG  21902        AACA_  TAG
                                TGTGGCTC    CG   GGTG
                                ||||||||    ||   ||||
                                ACGCCGAG    GC   CCGC
                                     CCGCC  CA_
GAM1041  ENTPD6   3'  TGTGGCTCAGCTGACCCGTGG  10345         ____  A   A
                                TGTGGCTCA    AC CGT GG
                                |||||||||    || ||| ||
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                                ACACCGAGT   TG GCA CC
                                     CGAC  G  _
GAM1041  FSTL3    3'  TGTGGTTTACACGCAGG    25224      CTCA
                                TGTGG   ACACGTAGG
                                |||||   |||||||||
                                ACACC   TGTGCGTCC
                                  AAA_
GAM1041  GAPD     5'  TGTGGCTCGGCTGGCGAC    13053       AACAC  AG
                                TGTGGCTC    GT  GGTGAC
                                ||||||||    ||  ||||||
                                ACACCGAG    CG  CCGCTG
                                     C____  A_
GAM1041  HNRPH2   5'  TGGCTCAATGCAATTTTGGTG  33332       CA  TAG__
                                TGGCTCAA  CG    GGTG
                                ||||||||  ||    ||||
                                ACCGAGTT  GT    CCAC
                                     AC  TAAAA
GAM1041  MOCS1    3'  TGTGGCTCAGGGCCACGTGGTG 45128        A___    AG
                                TGTGGCTCA   CACGT  GGTG
                                |||||||||   |||||  ||||
                                ACACCGAGT   GTGCA  CCAC
                                     CCCG    __
GAM1041  SLC16A2  3'  TGTGGCTCAGCCTGAGATG   27163        ACACGTA
                                TGTGGCTCA     GGGTG
                                |||||||||     |||||
                                ACACCGAGT     TCTAC
                                     CGGAC__
GAM1041  TLX1     3'  TGTGGCTCTGGGGTGAC     24350       AACACGTA
                                TGTGGCTC      GGGTGAC
                                ||||||||      |||||||
                                ACACCGAG      CCCACTG
                                     AC_______
GAM1042  BLK      3'  CCAGTCTGGCTTCTGTAGC   11842     CACCA      C
                                CCAG    GCTTCTGT GGT
                                ||||    |||||||| |||
                                GGTC    CGAAGACA TCG
                                  AGAC_      _
GAM1042  COL17A1  3'  CCAGCATCAGGTTTTCTGT   39077      C   C__
                                CCAGCA CAG   TTCTGT
                                |||||| |||   ||||||
                                GGTCGT GTC   AAGACA
                                   A   CAA
GAM1042  CYP4A11  3'  CAGCACAGAGCTTGGTGT    8934       C_    CTGTC
                                CAGCAC  AGCTT    GGTGT
                                ||||||  |||||    |||||
                                GTCGTG  TCGAA    CCACA
                                   TC    ______
GAM1042  DAPP1    3'  CAGCATCTGCTTCTGATTTGT  30813      CCA      TCGG
                                CAGCA   GCTTCTG    TGT
                                |||||   |||||||    |||
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                                GTCGT  CGAAGAC   ACA
                                  AGA     TAA_
GAM1042  DTNA    3'  CATCACCAGTTTTCATGT   37370   G    C_  _
                                CA CACCAG  TTC TGT
                                || ||||||  ||| |||
                                GT GTGGTC  AAG ACA
                                 A     AA  T
GAM1042  DTNB    3'  CCAGCTTGCTCCTCGTC    37600     ACCA    _
                                CCAGC   GCTTCT GTC
                                |||||   |||||| |||
                                GGTCG   CGAGGA CAG
                                  AA__    G
GAM1042  FSTL3   3'  CCAGCACCTGGCTGGTGT   25216       A_  TCTGTC
                                CCAGCACC  GCT    GGTGT
                                ||||||||  |||    |||||
                                GGTCGTGG  CGA    CCACA
                                    AC  _______
GAM1042  FUS1    3'  GCACCAGCCTTAGGGTGT   28586        CTGTC
                                GCACCAGCTT   GGTGT
                                ||||||||||   |||||
                                CGTGGTCGGA   CCACA
                                     ATC__
GAM1042  HOXD4   5'  CCAGCGCCGGCTGCTTCTAGTC 31169      A  A___    _
                                CCAGC CC   GCTTCT GTC
                                ||||| ||   |||||| |||
                                GGTCG GG   CGAAGA CAG
                                  C  CCGA    T
GAM1042  IHPK1   3'  GCAATGGCTGAAATCGGTGTC  45488    CCA   TCT
                                GCA   GCT   GTCGGTGTC
                                |||   |||   |||||||||
                                CGT   CGA   TAGCCACAG
                                  TAC   CTT
GAM1042  KCNA7   5'  CCAGCCCGGTGTCCGGTGT   36643       C_   _
                                CCAGCTT  TGTC GGTGT
                                |||||||  |||| |||||
                                GGTCGGG  ACAG CCACA
                                    CC   G
GAM1042  LARGE   5'  CCAGCGCCGTTTCTCTGTC   21859      A  AGC_
                                CCAGC CC   TTCTGTC
                                ||||| ||   |||||||
                                GGTCG GG   GAGACAG
                                  C  CAAA
GAM1042  RBM3    5'  CCAGTGCCTGCTCGTCGGTGT  43254     CA  A   CT
                                CCAG  CC GCTT  GTCGGTGT
                                ||||  || ||||  ||||||||
                                GGTC  GG CGAG  CAGCCACA
                                  AC  A   __
GAM1042  RGS2    3'  ACCAGCTTCTCCTAGTC     16313         G  GGT
                                ACCAGCTTCT TC   GTC
                                |||||||||| ||   |||
```

```
                                TGGTCGAAGA GG   CAG
                                      _ AT_
GAM1042 VANGL2   5' CAGCACCGGCTTCTTTAGGC  43454       A     GTC
                                CAGCACC GCTTCT   GGT
                                ||||||| ||||||   |||
                                GTCGTGG CGAAGA   CCG
                                    C     AAT
GAM1042 VEGF     3' CCAGGGCTGGGTTTGTCGGTGT 17946     CACCA   TC___
                                CCAG    GCT    TGTCGGTGT
                                ||||    |||    |||||||||
                                GGTC    CGA    ACAGCCACA
                                  C____   CCCAA
GAM1042 XT3      3' CCGGCGCTGGCCTCTGAGT   33662    A  ACCA     TC
                                CC GC   GCTTCTG  GGT
                                || ||   |||||||  |||
                                GG CG   CGGAGAC  TCA
                                 C  CGAC      __
GAM1042 ZNF195   3' CAGTGTCATTTCTGAACGTGTC 28379    CAC  GC    TCG
                                CAG   CA  TTCTG   GTGTC
                                |||   ||  |||||   |||||
                                GTC   GT  AAGAC   CACAG
                                  ACA  A_    TTG
GAM1042 AXIN1    5' CGGCGGGCGGGACCCGGCG   41377     A  A   __ G
                                CGG CG GTGG  C CGGCG
                                ||| || ||||  | |||||
                                GCC GC CGCC  G GCCGC
                                  _ C    CT G
GAM1042 CD81     3' GGGCGAGTGGCTCCCAGGA   20346    A      G__   C
                                GG CGAGTGGC   CGG GA
                                || ||||||||   ||| ||
                                CC GCTCACCG   GTC CT
                                 C       AGG  _
GAM1042 CHST2    5' CCGGGCCGGCGGCGCGGCG   41712      A_  A
                                CCGG  CG GTGGCGCGGCG
                                ||||  || ||||||||||||
                                GGCC  GC CGCCGCGCCGC
                                  CG  _
GAM1042 CSNK2A2  5' CGGCGGCGGCGCGGCG      12484     A  A
                                CGG CG GTGGCGCGGCG
                                ||| || ||||||||||||
                                GCC GC CGCCGCGCCGC
                                  _ _
GAM1042 EP300    5' CGCGCGGCGGCCGGCG      10978    GA  A    G
                                CG  CG GTGGC CGGCG
                                ||  || ||||| |||||
                                GC  GC CGCCG GCCGC
                                 GC  _    _
GAM1042 F8A      3' CGGACGAGTGGAAGGA      29107          CGC  C
                                CGGACGAGTGG   GG GA
                                ||||||||||   || ||
```

```
                                GCCTGCTCACC   TC CT
                                      T__  _
GAM1042  FXYD7    5'  GGATGCTTTGGCGGCGAAG   35129    CGAG_   GC
                                GGA    TGGC  GGCGAAG
                                |||    ||||  |||||||
                                CCT    ACCG  CCGCTTC
                                  ACGAA   __
GAM1042  MAP1B    5'  CCGCGAGAGTGCGCGGCG    25391    _ C    G
                                CCG GA GAGTG CGCGGCG
                                ||| || ||||| |||||||
                                GGC CT CTCAC GCGCCGC
                                  G _    _
GAM1042  NEDD4L   3'  GGACGAGTGCGTGGTGAAG   31620       G  C  C
                                GGACGAGTG CG GG GAAG
                                ||||||||| || || ||||
                                CCTGCTCAC GC CC CTTC
                                      _ A  A
GAM1042  PABPC4   5'  CCGGGCGGGCGGCGAA     19220     ACGA   C
                                CCGG   GTGG GCGGCGAA
                                ||||   |||| ||||||||
                                GGCC   CGCC CGCCGCTT
                                  _____   _
GAM1042  PAFAH1B2 5'  CGGCGGGTGGCGCGTCG    15072    A  A     G
                                CGG CG GTGGCGCG CG
                                ||| || |||||||| ||
                                GCC GC CACCGCGC GC
                                  _ C       A
GAM1042  PITX1    3'  CCGGATCCAGCGCGGCG    15318     CGAG
                                CCGGA   TGGCGCGGCG
                                |||||   ||||||||||
                                GGCCT   GTCGCGCCGC
                                   AG__
GAM1042  TIMP3    5'  CGGCGGGCGGCCTCCCGGCGAA 7449     A  A    G___
              G                  CGG CG GTGGC   CGGCGAAG
                                ||| || |||||   ||||||||
                                GCC GC CGCCG   GCCGCTTC
                                  _ C    GAGG
GAM1042  TMEPAI   5'  CAGGAGGCGCGCGGCG     33591    AC   TG
                                CGG  GAG  GCGCGGCG
                                |||  |||  ||||||||
                                GTC  CTC  CGCGCCGC
                                  __  CG
GAM1042  UBE3A    5'  GGCGGATGGCTACGCGGCG   39282    A  AG   ___
                                GG CG  TGGC   GCGGCG
                                || ||  ||||   ||||||
                                CC GC  ACCG   CGCCGC
                                 _ CT   ATG
GAM1042  VGF      3'  CCGGCGCGCGCGCGCGGCG   17987     A  A  _
                                CCGG CG GTG GCGCGGCG
                                |||| || ||| ||||||||
```

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                                GGCC GC CGC CGCGCCGC
                                  _ G  G
GAM1042 ZNF219   5' CGGGGGGCGGCGCGGCG    32327    ACGA
                                CGG   GTGGCGCGGCG
                                |||   ||||||||||
                                GCC   CGCCGCGCCGC
                                 CCC_
GAM1043 BMPR1B   3' CCACTGGGAAGCAGGACG   10202      CATTCTAAA
                                TCACTGG       CAGGACG
                                |||||||       |||||||
                                GGTGACC       GTCCTGC
                                    CTTC_____
GAM1043 HMGA2    3' TCTTTGGTGTTCTAAACAGA  18529   AC  CA
                                TC  TGG  TTCTAAACAGG
                                ||  |||  ||||||||||
                                AG  ACC  AAGATTTGTCT
                                 AA  AC
GAM1043 MAP1A    3' TCACTGGCTTGCTTGGGGCGA 14350       ATT  AAACA  A
                                TCACTGGC  CT    GG CGA
                                ||||||||  ||    || |||
                                AGTGACCG  GA    CC GCT
                                    AAC  ACC__ _
GAM1043 MEIS1    3' CATTGGCATTCCAGGGTGGGGC 14414   C       AACA_  A
          G                      CA TGGCATTCTA    GG CG
                                || ||||||||||    || ||
                                GT ACCGTAAGGT    CC GC
                                 A        CCCAC  C
GAM1043 RANBP2L1 5' TCTTTGGTGTGTTGAACAGGAC 37027   AC  CATTCTA
          GA                     TC  TGG     AACAGGACGA
                                ||  |||     ||||||||||
                                AG  ACC     TTGTCCTGCT
                                 AA  ACACAAC
GAM1043 RARG     3' TCACTGGCGGTCTGGGA    9727       AT  AAACA
                                TCACTGGC  TCT    GGA
                                ||||||||  |||    |||
                                AGTGACCG  AGA    CCT
                                    CC  C____
GAM1043 ZNF278   3' TCGCTGGCATCTGAGAGG   36809   A     T  AAAC
                                TC CTGGCAT CT    AGG
                                || ||||||| ||    |||
                                AG GACCGTA GA    TCC
                                 C      _  CTC_
GAM1044 ADH4     5' CCTGCCGGCCTCTTACC    8574         AAAA
                                TCTGCCGGCC   TACC
                                ||||||||||   ||||
                                GGACGGCCGG   ATGG
                                     AGA_
GAM1044 ATSV     3' CCGACCGACCAGGATACC   20224    _     AA
                                CTG CCGGCCA  ATACC
                                ||| |||||||  |||||
```

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                                GGC GGCTGGT  TATGG
                                  T      CC
GAM1044  EPHB2    3'  CCTGTGACCAAAATACC     32667      CC
                                TCTG  GGCCAAAATACC
                                ||||  ||||||||||||
                                GGAC  CTGGTTTTATGG
                                  A_
GAM1044  FZD3     3'  TCTATTAGCTAAAATACC    32631      CC   C
                                TCTG  GGC AAAATACC
                                ||||  ||| ||||||||
                                AGAT  TCG TTTTATGG
                                  AA   A
GAM1044  GLI3     5'  TCTTCGACCAAAAATGCC    6736       GC       TA_
                                TCT  CGGCCAAAA   CC
                                |||  |||||||||   ||
                                AGA  GCTGGTTTT   GG
                                  A_        TAC
GAM1044  HOXA3    3'  TCTTCGGCCAAAGAACC     36200      GC       AT
                                TCT  CGGCCAAA  ACC
                                |||  ||||||||  |||
                                AGA  GCCGGTTT  TGG
                                  A_       CT
GAM1044  JRK      3'  GCCAAAATGCCAAAATACC   44500      _____
                                GCCG    GCCAAAATACC
                                ||||    ||||||||||
                                CGGT    CGGTTTTATGG
                                  TTTA
GAM1044  JRK      3'  TCTGAGCCAAAATGCC      44502      CC       A
                                TCTG  GGCCAAAAT CC
                                ||||  ||||||||| ||
                                AGAC  TCGGTTTTA GG
                                  __        C
GAM1044  KCND3    3'  TCTGCCGACCCCACC       22535          AAAA
                                TCTGCCGGCC    TACC
                                ||||||||||    ||||
                                AGACGGCTGG    GTGG
                                      G___
GAM1044  NR2C2    3'  TGCACATACCAAAATACC     17676      _ _
                                TGC CG GCCAAAATACC
                                ||| || ||||||||||
                                ACG GT TGGTTTTATGG
                                  T  A
GAM1045  DNMT3B   3'  TGCCGGGTAAAAGACATATACA 27882          T  _    G
                                TGCCGGGT AAA ACATA ACA
                                |||||||| ||| ||||| |||
                                ACGGCCCA TTT TGTAT TGT
                                     T  C    A
GAM1045  LANCL1   3'  AGCTAAAAGCATAGGCACA    25846          _    A
                                GGTTAAAA CATAG CACA
                                |||||||| ||||| ||||
```

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                                TCGATTTT GTATC GTGT
                                    C    C
GAM1045 NMI     3' CCGGGTTAAAAAGCTATAG   21718          C___
                                CCGGGTTAAAA   ATAG
                                ||||||||||   ||||
                                GGCCCAATTTT   TATC
                                     TCGA
GAM1045 UTY     3' TGCAGGGTTAAAATACAA    28319    C       C
                                TGC GGGTTAAAA ATAG
                                ||| ||||||||| ||||
                                ACG CCCAATTTT TGTT
                                  T       A
GAM1045 AQP6    3' TTTGTCTTTTTCTTTATCCAAG 38262          _____    T
             T                   TTTGTCTTTTT    TCCAA GT
                                 ||||||||||    ||||| ||
                                 AAACAGAAAAA    AGGTT CA
                                      GAAAT   _
GAM1045 EGR3    3' TTTGTCTTTTTTCTAAGTA   40566          C  T
                                TTTGTCTTTTTTC AA GTG
                                ||||||||||||| || |||
                                AAACAGAAAAAAG TT CAT
                                       A  _
GAM1045 MTCP1   3' TTTGTCTTTTAATGTGTTTA  30589         TTCC
                                TTTGTCTTTT   AATGTGTTTA
                                |||||||||   ||||||||||
                                AAACAGAAAA   TTACACAAAT
                                      ____
GAM1045 PITPNB  3' TCTTCATCAATGTGTTT    29627      TTTC
                                TCTTT   CAATGTGTTT
                                |||||   ||||||||||
                                AGAAG   GTTACACAAA
                                  TA__
GAM1045 SRR     3' GTCTTTAATGTGTTT      34967      TTTCC
                                GTCTTT    AATGTGTTT
                                ||||||    |||||||||
                                CAGAAA    TTACACAAA
                                     _____
GAM1045 TNFRSF13C 3' TTTGTCTTTTTTCAGATTCATT 38122          CAATG
             T                   TTTGTCTTTTTTC    TGTTT
                                 ||||||||||||    |||||
                                 AAACAGAAAAAAG    GTAAA
                                       TCTAA
GAM1046 F8      3' TACTGTAGTAGTTATTGTA   6567      T      __
                                TACT GTAGTAGTT  TGTG
                                |||| |||||||||  ||||
                                ATGA CATCATCAA  ACAT
                                  _       TA
GAM1046 HIF1A   3' ACTAACCAAGTTTGTGCAGTAT 11345    TGTAGT
                                ACT     AGTTTGTGCAGTAT
                                |||     ||||||||||||||
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                                TGA     TCAAACACGTCATA
                                  TTGGT_
GAM1046  PLAG1    3'  CTTGTAATATGTGTAGTA    15350        GTT    C
                                CTTGTAGTA   TGTG AGTA
                                |||||||||   |||| ||||
                                GAACATTAT   ACAC TCAT
                                     ___    A
GAM1047  CENTD1   5'  AAGTTTCTTAAAATGTTATTTT 40133           ACAA
                                AAGTTTCTTAAAA    TATTTT
                                ||||||||||||    ||||||
                                TTCAAAGAATTTT    ATAAAA
                                      ACA_
GAM1047  DSC3     3'  CAAGTTTCTTTAAAAGCAA   12595         A   _
                                CAAGTTTCTT AAAA CAA
                                |||||||||| |||| |||
                                GTTCAAAGAA TTTT GTT
                                      A   C
GAM1047  PTPRB    3'  CAAGTTTTTAAAAACAA     15924        C
                                CAAGTTT TTAAAAACAA
                                ||||||| ||||||||||
                                GTTCAAA AATTTTTGTT
                                     _
GAM1047  ZNF217   3'  AGTTTCTTAATAAAATATTTT  27190         A  C
                                AGTTTCTTAA AA AATATTTT
                                |||||||||| || ||||||||
                                TCAAAGAATT TT TTATAAAA
                                      A  _
GAM1047  PSMB2    3'  TAAGAAATTAGTAGCTGAAGTT 15822       CTT     __
           T                     TAAGAAA   GTAGCT  AGTTT
                                |||||||   ||||||  |||||
                                ATTCTTT   CATCGA  TCAAA
                                    AAT     CT
GAM1048  EGFL5    3'  GAGTATTGCTTTAATGGTCAAT 44528     C       TAAA_
           TT                     GAG ATTGCTTTA     CAATTT
                                ||| |||||||||     ||||||
                                CTC TAACGAAAT     GTTAAA
                                  A        TACCA
GAM1048  IL12B    3'  TTACTTAAATATTTAAATAGC  13523          TTT
                                TTACTTAAAT   GTTTAAATAGC
                                |||||||||   ||||||||||
                                AATGAATTTA   TAAATTTATCG
                                     ___
GAM1049  HMGB3    3'  TATGTACAACTTTGATACAGTT 23779       T       A  T
           T                     TATGT CAACTTTGA AT GTTT
                                |||||  |||||||| || ||||
                                ATACA GTTGAAACT TG CAAA
                                   T       A  T
GAM1050  TERF2    3'  TACAGATTACCAGGGATTTAAA 24914      TTG     AA
           T                     TATA   TACCA  GATTTAAAT
                                ||||   |||||  |||||||||
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                                ATGT  ATGGT  CTAAATTTA
                                  CTA    CC
GAM1051  ACCN1    3'  TGATTGTGCAGTTCTGATTCCA 9916      T      AC___
             G                   TGATT TGCAGTTC    CCAG
                                 ||||| ||||||||    ||||
                                 ACTAA ACGTCAAG    GGTC
                                   C       ACTAA
GAM1051  CARD4    5'  CCTGACTTACAATCAC     25890       T    T
                                 CCTGATTT GCAGT CAC
                                 |||||||| ||||| |||
                                 GGACTGAA TGTTA GTG
                                      _    _
GAM1051  CLCN4    3'  CCCCTGATGTTGGTTCA    12279       T  CA
                                 CCCCTGAT TTG  GTTCA
                                 |||||||| |||  |||||
                                 GGGGACTA AAC  CAAGT
                                     C  __
GAM1051  CPD      3'  CCCCTGATTTAGTATAAGTTCA 10558         TGC___
                                 CCCCTGATTT     AGTTCA
                                 ||||||||||     ||||||
                                 GGGGACTAAA     TCAAGT
                                      TCATAT
GAM1051  CYP3A43  3'  CTAATTATTCACCCA      38397      TTGCA
                                 CTGATT    GTTCACCCA
                                 ||||||    |||||||||
                                 GATTAA    TAAGTGGGT
                                     ______
GAM1051  DAPK1    3'  CCCTTGGTTCTGCAGTCCAAAC 22356    C  A        CC
             AG                    CCC TG TTTTGCAGTTCA  CAG
                                 ||| || ||||||||||||  |||
                                 GGG AC AAGACGTCAGGT  GTC
                                   A  C          TT
GAM1051  DLX4     3'  CTGATTTTGCACCCA      39615         AGTTC
                                 CTGATTTTGC    ACCCA
                                 ||||||||||    |||||
                                 GACTAAAACG    TGGGT
                                     ______
GAM1051  F13A1    3'  CTGATTTTGCCCCCA      44980         AGTT A
                                 CTGATTTTGC    C CCCA
                                 ||||||||||    | ||||
                                 GACTAAAACG    G GGGT
                                     _____ _
GAM1051  FZD6     5'  CCTGATTTTACCAC       18626         AGTT
                                 CCTGATTTTGC    CAC
                                 ||||||||||||   |||
                                 GGACTAAAATG    GTG
                                     _____
GAM1051  MKI67    3'  CCGCTGATTTCTGCATTCATTC 14516    _    _    G    CC
             AG                    CC CTGATT TTGCA TTCA  CAG
                                 || |||||| ||||| ||||  |||
```

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                                GG GACTAA GACGT AAGT  GTC
                                 C     A    _   AA
GAM1051  POP4     3'  CCTCTGACTTCTTCAC      27366   _      GCAG
                                CC CTGATTTT   TTCAC
                                || ||||||||   |||||
                                GG GACTGAAG   AAGTG
                                 A      ____
GAM1051  RNMT     3'  CCTCTATTTTGCAGACCC    19150    G_       TTC
                                CCT  ATTTTGCAG   ACCC
                                |||  |||||||||  ||||
                                GGA  TAAAACGTC   TGGG
                                  GA       ___
GAM1051  SLC35A1  3'  CTGTATTAGCAGTTCACTCAG  26949    _  TT       C
                                CTG ATT  GCAGTTCAC CAG
                                ||| |||  ||||||||| |||
                                GAC TAA  CGTCAAGTG GTC
                                  A  T_       A
GAM1051  SORBS1   3'  CCTGACTTCATCACTCA     31705         CAGT   C
                                CCTGATTTTG   TCAC CA
                                ||||||||||   |||| ||
                                GGACTGAAGT   AGTG GT
                                      ____   A
GAM1051  SPAG9    3'  ATTTGTGCACTTCACCCAG   19561     _   G
                                ATTT TGCA TTCACCCAG
                                |||| |||| |||||||||
                                TAAA ACGT AAGTGGGTC
                                  C   G
GAM1051  S100A10  5'  ACGGGTCTAGGAATTAC    40385     AC  AAGATAT
                                ACGG  CT     GGGGATTGC
                                ||||  ||     |||||||||
                                TGCC  GA     TCCTTAATG
                                  CA  ________
GAM1051  SHC1     3'  ACAGATGGTATGTGGGGATTG  16692      CCTAAG  A
                                ACGGA     AT TGGGGATTG
                                |||||     || |||||||||
                                TGTCT     TA ACCCCTAAC
                                   ACCA__  C
GAM1052  NOS1     3'  TGGGAGACAGCCCCTTTAA   8381     A   A   ATAAA
                                TGG AGA CAG    CCTTTAA
                                ||| ||| |||    |||||||
                                ACC TCT GTC    GGAAATT
                                  C   _   GG___
GAM1052  RNF7     3'  GGAAGGACCACCTTTAA     30646      AACA   AA
                                GGAAG   GAT  ACCTTTAA
                                |||||   |||  ||||||||
                                CCTTC   CTG  TGGAAATT
                                   _____  G_
GAM1053  ADAM19   3'  TAGAGTAAGGAGGAAGA     37775      ACAAA
                                TAGA    AAGGAGGAAGA
                                ||||    ||||||||||
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```
                                ATCT    TTCCTCCTTCT
                                  CA___
GAM1053  ANGPT1   3'  TCTAGACAAAAAAAAAAGAA  40246       AC
                                TCTAGA  AAAAAGGAGGAA
                                ||||||  ||||||||||||
                                AGATCT  TTTTTTTTTCTT
                                   GT
GAM1053  ARHGDIB  5'  TAGAACAGGAAGGAAG     10127       AAAA
                                TAGAACA   GGAGGAAG
                                |||||||   ||||||||
                                ATCTTGT   CTTCCTTC
                                   C___
GAM1053  ASB2     3'  TCCAGAACAAGTGGAGG     32054         AAA
                                TCTAGAACAA  GGAGG
                                ||||||||||  |||||
                                AGGTCTTGTT  CCTCC
                                      CA_
GAM1053  BBS4     3'  TCAAGAACAAAATACAGGGAGG 37498    T       A____
                                TC AGAACAAAA    GGAGG
                                || |||||||||    |||||
                                AG TCTTGTTTT    CCTCC
                                 T       ATGTC
GAM1053  CACNA1B  3'  TCTAGAGTAAAAGAGGGGAGGA 8744       AC   A___
                                TCTAGA  AAAA   GGAGGA
                                ||||||  ||||   ||||||
                                AGATCT  TTTT   CCTCCT
                                   CA   CTCC
GAM1053  CALM1    3'  TCTAGAGGGGGGAAAAAGGAG  27863      AC____
                                TCTAGA     AAAAAGGAG
                                ||||||     |||||||||
                                AGATCT     TTTTTCCTC
                                   CCCCCC
GAM1053  CASP2    3'  TCTAGGACAAAAAGGGCGGAGG 37401      A       A_  A
            A                    TCTAG ACAAAAAGG  GGA GA
                                |||||  |||||||||  ||| ||
                                AGATC TGTTTTTCC  CCT CT
                                   C        CG   C
GAM1053  CCND1    3'  TAGAATATGAAGAAGAA     38221      CAAAAAG
                                TAGAA      GAGGAAGAA
                                |||||      |||||||||
                                ATCTT      CTTCTTCTT
                                   ATA____
GAM1053  CHRNE    3'  TCCAGGGTGGGGAAGAA     6346       AACAAAAA  A
                                TCTAG      GG GGAAGAA
                                |||||      || |||||||
                                AGGTC      CC CCTTCTT
                                   CCA_____  _
GAM1053  CST1     3'  TAGAAGCAAGAAGGAAG     12496      CAAA
                                TAGAA   AAGGAGGAAG
                                |||||   ||||||||||
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                                ATCTT   TTCTTCCTTC
                                  CG__
GAM1053  CST4     3'  TAGAAGCAAGAAGGAAG     12498      CAAA
                                TAGAA   AAGGAGGAAG
                                |||||   ||||||||||
                                ATCTT   TTCTTCCTTC
                                  CG__
GAM1053  DDB1     3'  TCTAAATAAAAAGAGGA     12560      ACA
                                TCTAGA  AAAAGGAGGA
                                ||||||  ||||||||||
                                AGATTT  TTTTTCTCCT
                                   A__
GAM1053  EPB42    3'  TAGAACAAGGGTTGGCAGGAGA 6516         AAA__ _   A
                                TAGAACAA    GG AGGA GA
                                ||||||||    || |||| ||
                                ATCTTGTT    CC TCCT CT
                                     CCCAA  G   _
GAM1053  ESRRG    3'  TAGAAAAAAGGGGAAG     42448      CA    A
                                TAGAA  AAAAGG GGAAG
                                |||||  |||||| |||||
                                ATCTT  TTTTCC CCTTC
                                  __    _
GAM1053  FBN2     3'  TCTAAGACAGGGAGGAAAGAA  12806     GA   AAAA     _
                                TCTA  ACA   GGAGGAA GAA
                                ||||  |||   ||||||| |||
                                AGAT  TGT   CCTCCTT CTT
                                  TC  C___     T
GAM1053  FBXL11   3'  AGAGGAAAGGAGGGAGA    29423    ACAA      A
                                AGA   AAAGGAGG AGA
                                |||   |||||||| |||
                                TCT   TTTCCTCC TCT
                                 CC__       C
GAM1053  GABRA3   5'  TCTGAGCGGAAAGGAGAGAAG  9045     A  ACAA     _
                                TCT GA   AAAGGAG GAAG
                                ||| ||   ||||||| ||||
                                AGA CT   TTTCCTC CTTC
                                 _ CGCC      T
GAM1053  GNAS     5'  TCTGAGCAAGAAGAAGG     38665    A  A   A
                                TCT GA CAA AAGGAGG
                                ||| || ||| |||||||
                                AGA CT GTT TTCTTCC
                                 _ C   C
GAM1053  IL13RA1  3'  CAGAGAAAAGAGGAA      11442     ACAA
                                TAGA   AAAGGAGGAA
                                ||||   ||||||||||
                                GTCT   TTTTCTCCTT
                                  C___
GAM1053  IL1R1    3'  CCTAGGCAAAGGAGGAGGAAG  9356      AA   A_
                                TCTAG  CAAA  AGGAGGAAG
                                |||||  ||||  |||||||||
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                                GGATC  GTTT  TCCTCCTTC
                                  C_   CC
GAM1053  KLHL1    3'  AGAACAAAATTCTAAAGGAG  34075        _______
                                AGAACAAAA     AGGAG
                                |||||||||     |||||
                                TCTTGTTTT     TCCTC
                                    AAGATT
GAM1053  KMO      3'  TCTAGAATGAAAAAGAAA    18961        CA
                                TCTAGAA  AAAAGGAGG
                                |||||||  |||||||||
                                AGATCTT  TTTTTCTTT
                                   AC
GAM1053  LAIR1    3'  TCTAGATGAAGAGGAA      34698        ACAAAA
                                TCTAGA     AGGAGGAA
                                ||||||     ||||||||
                                AGATCT     TTCTCCTT
                                   AC____
GAM1053  LILRB4   3'  TCTTGAGCAAAGGGAAGAAG  27781     A  A    AA
                                TCT GA CAAA  GGAGGAAG
                                ||| || ||||  ||||||||
                                AGA CT GTTT  CCTTCTTC
                                  A  C    C_
GAM1053  LRP4     3'  TCTAGGAGGAGGAAGAA     42068      AACAAAA
                                TCTAG      AGGAGGAAGAA
                                |||||      ||||||||||
                                AGATC      TCCTCCTTCTT
                                  C_______
GAM1053  MAOB     3'  TCTAAAACAGAAGGTGAGGA  41032         A  AG_
                                TCTAGAACA AA   GAGGA
                                ||||||||| ||   |||||
                                AGATTTTGT TT   CTCCT
                                     C  CCA
GAM1053  MN1      3'  TCTAGAGGAAAAAGGCTTAAG  14595       AC      AGG
                                TCTAGA  AAAAAGG   AAG
                                ||||||  |||||||   |||
                                AGATCT  TTTTTCC   TTC
                                   CC      GAA
GAM1053  MTMR2    3'  CCTAGAATGGAGAAAG      32065        CAAAAA
                                TCTAGAA     GGAGGAAG
                                |||||||     ||||||||
                                GGATCTT     CCTCTTTC
                                   A_____
GAM1053  NDUFV3   5'  TCTAGAGGAAAGGATGAA    34343       ACAA     G
                                TCTAGA    AAAGGA GAA
                                ||||||    |||||| |||
                                AGATCT    TTTCCT CTT
                                   CC__     A
GAM1053  NPAT     3'  TAAAACAAAGAGAACAGA    42615        AAA     _
                                TAGAACAA   GGAGGA AGA
                                ||||||||   |||||| |||
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                                ATTTTGTT  TCTCTT TCT
                                    ___     G
GAM1053  NR3C2    3'  TCTAGAGGAAAAGGGAAA    9472       ACA     A
                                TCTAGA  AAAAGG GGAA
                                ||||||  |||||| ||||
                                AGATCT  TTTTCC CTTT
                                   CC_    _
GAM1053  OAS2     3'  CTGGAAGGAAAAAGGAGGA   32550    A  C_
                                CT GAA  AAAAAGGAGGA
                                || |||  ||||||||||
                                GA CTT  TTTTTCCTCCT
                                 C  CC
GAM1053  PAFAH1B1 3'  TCCAGAGGAAAAGAGGGAGGA  7722       AC   A__
                                TCTAGA  AAAA  GGAGGA
                                ||||||  ||||  ||||||
                                AGGTCT  TTTT  CCTCCT
                                   CC   CTC
GAM1053  PCDH11Y  5'  TCTGGATAAAAGGAGGCAAG  37329    A  ACA      _
                                TCT GA  AAAAGGAGG AAG
                                ||| ||  |||||||| |||
                                AGA CT  TTTTCCTCC TTC
                                 C  A__       G
GAM1053  PCDHB13  3'  TAAAACAAAGGGAGAAAGAAC  33186        AA
                                TAGAACAAA  GGAGGAAGAAC
                                |||||||||  ||||||||||
                                ATTTTGTTT  CCTCTTTCTTG
                                     C_
GAM1053  PLCB4    5'  CTAGGGTAAAAGGAAGAGGA  9583     AACA       A
                                CTAG   AAAAGGAGGA GA
                                ||||   |||||||||| ||
                                GATC   TTTTCCTTCT CT
                                  CCA_       C
GAM1053  PLD2     3'  TCAAGGGCAGGAAGAGGAAG  15385    T  AA  AAA
                                TC AG  CA  AGGAGGAAG
                                || ||  ||  |||||||||
                                AG TC  GT  TTCTCCTTC
                                 T  CC  CC_
GAM1053  PML      3'  TCTGGGATGAAAGGAGAAGGGA 37738    A_  ACAA       A_
            AC                   TCT  GA   AAAGGAGGA  GAAC
                                ||| ||   |||||||||  ||||
                                AGA  CT   TTTCCTCTT  CTTG
                                  CC  AC__       CC
GAM1053  PMX1     3'  CCCAGAGGGAGGAGGAA     35506       ACAAAA
                                TCTAGA     AGGAGGAA
                                ||||||     ||||||||
                                GGGTCT     TCCTCCTT
                                   CCC___
GAM1053  POMZP3   5'  TCTGAACGAAGGAGGA      29248     A    AAA
                                TCT GAAC   AAGGAGGA
                                ||| ||||   ||||||||
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                                AGA CTTG   TTCCTCCT
                                  _   C__
GAM1053  POU3F4   3'  CTAGAATGAAAGGAAAGAGA  7169       CAA      GA
                                CTAGAA   AAAGGAG  AGA
                                ||||||   |||||||  |||
                                GATCTT   TTTCCTT  TCT
                                   AC_      TC
GAM1053  PPARGC1  3'  TCCAGGGCAAAAAGGAGAA   29966      AA
                                TCTAG  CAAAAAGGAGGA
                                |||||  ||||||||||||
                                AGGTC  GTTTTTCCTCTT
                                   CC
GAM1053  PPT1     3'  TCGAGAATGGAATAGGAAGAAC 41554    T    CAAAAAGG
                                TC AGAA       AGGAAGAAC
                                || ||||       |||||||||
                                AG TCTT       TCCTTCTTG
                                 C   ACCTTA__
GAM1053  PRKR     3'  TAGAACAAAGAGATGAGG     15679        A  __
                                TAGAACAAA AG  GAGG
                                ||||||||| ||  ||||
                                ATCTTGTTT TC  CTCC
                                      C  TA
GAM1053  PSMB9    3'  CCTGGGACAAAAGAAGAAAGA  15828     AGA     A
                                TCT   ACAAAA GGAGGAAGA
                                |||   |||||| |||||||||
                                GGA   TGTTTT CTTCTTTCT
                                  CCC     _
GAM1053  PSMD9    3'  AAAATAAAAGGGAGGAAGAA   15841     C    A
                                AGAA AAAA GGAGGAAGAA
                                |||| |||| ||||||||||
                                TTTT TTTT CCTCCTTCTT
                                  A   C
GAM1053  PTPN7    3'  TCTCAGATTCAAGGAGGAGGAA 38717     _  ACAAA       A
                                TCT AGA     AAGGAGGA GAA
                                ||| |||     |||||||| |||
                                AGA TCT     TTCCTCCT CTT
                                  G   AAG__       C
GAM1053  PTPN7    5'  TCTAGGACGGAAGGGAGAAAG  38716      A  AA  A
                                TCTAG AC  AA GGAGGAAG
                                ||||| ||  || ||||||||
                                AGATC TG  TT CCTCTTTC
                                   C  CC  C
GAM1053  PTPRO    3'  TCTGGAAGCAAGGGAGGA    36226     A  _  AAA
                                TCT GAA CAA   GGAGGA
                                ||| ||| |||   ||||||
                                AGA CTT GTT   CCTCCT
                                  C   C   C__
GAM1053  PYCS     3'  TCTCAAAAAAGGGGGAAGAA   16039     AGAAC      A
                                TCT     AAAAAGG GGAAGAA
                                |||     ||||||| |||||||
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                                AGA    TTTTTCC CCTTCTT
                                  GT___      C
GAM1053  RABIF    3'  TCTAGAGCAAGAAAAAGCGGGA 16128       A  __    A  A
                G                  TCTAGA CAA  AAAGG GG AG
                                   |||||| |||  ||||| || ||
                                   AGATCT GTT  TTTTC CC TC
                                      C   CT    G  C
GAM1053  RASGRP1  3'  GAATGGAGAGGAGGAAGAA   25078     CAAAA
                                   GAA    AGGAGGAAGAA
                                   |||    ||||||||||
                                   CTT    TCCTCCTTCTT
                                     ACCTC
GAM1053  SALL2    3'  TCTGGAGCAGGGGGAGGAAGAA 41904     A  A  AAAA
                                   TCT GA CA   GGAGGAAGAA
                                   ||| || ||   ||||||||||
                                   AGA CT GT   CCTCCTTCTT
                                     C  C  CCC_
GAM1053  SDC4     3'  TCTAGAACCAAGGAAGAA    16531        AAA
                                   TCTAGAAC   AAGGAGGAA
                                   ||||||||   |||||||||
                                   AGATCTTG   TTCCTTCTT
                                        G__
GAM1053  SDHC     3'  TCTAAACAAATAAGGAGAA   42980       A   _
                                   TCTAGA CAAA AAGGAGGA
                                   |||||| |||| ||||||||
                                   AGATTT GTTT TTCCTCTT
                                      _   A
GAM1053  SMARCC1  3'  TCCAGAACAAAAACAAAAGGA  16905           __
                                   TCTAGAACAAAAA  GGAGGA
                                   ||||||||||||  ||||||
                                   AGGTCTTGTTTTT  TTTCCT
                                           GT
GAM1053  SRRM1    3'  ACAAAAGAAGGAGGGGGAAC  25187       __     AA
                                   ACAAAA  AGGAGG  GAAC
                                   ||||||  ||||||  ||||
                                   TGTTTT  TCCTCC  CTTG
                                      CT     CC
GAM1053  STAC     3'  CCTAGAACAGCAGGAAGGA   17133        AAA   _
                                   TCTAGAACA   AGGA GGA
                                   |||||||||   |||| |||
                                   GGATCTTGT   TCCT CCT
                                        CG_    T
GAM1053  TH1L     3'  TCCAGGATGGGGAGGAAAA   32311      AACAAAAA
                                   TCTAG       GGAGGAAGA
                                   |||||       |||||||||
                                   AGGTC       CCTCCTTTT
                                     CTACC___
GAM1053  THRA     3'  CAGAGAAAGGGGGAAG      17518      ACAA    A
                                   TAGA    AAAGG GGAAG
                                   ||||    ||||| |||||
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                                GTCT    TTTCC CCTTC
                                  C___     C
GAM1053  TNFRSF11A 3'  TCTAGAATAAGAAGAA      19280        CAAA
                                TCTAGAA    AAGGAGGA
                                |||||||    ||||||||
                                AGATCTT    TTCTTCTT
                                   A___
GAM1053  TOP2A    3'  TAGAAAAGGAGGAAGA      9882        CAAA
                                TAGAA    AAGGAGGAAGA
                                |||||    ||||||||||
                                ATCTT    TTCCTCCTTCT
                                  ____
GAM1053  UBE2L3   3'  TAAAACAAAGAGAGCAGAAC   17831         AA    GA
                                TAGAACAAA  GGAG  AGAAC
                                |||||||||  ||||  |||||
                                ATTTTGTTT  TCTC  TCTTG
                                     C_    G_
GAM1053  WNT8B    3'  CTAGGAGAGGGGAGGAGGAAC  40586      AACAAAAA     A
                                CTAG       GGAGGA GAAC
                                ||||       |||||| ||||
                                GATC       CCTCCT CTTG
                                  CTCTCC__     C
GAM1053  ZNF189   3'  CCTAGAACAAGAAATAAGGA   18366          _   G
                                TCTAGAACAA AAA GAGGA
                                |||||||||| ||| |||||
                                GGATCTTGTT TTT TTCCT
                                     C   A
GAM1053  ZNF83    5'  TAGAAAAAATACCTGAGGAAGA 32892       C   AAG__
            AC                    TAGAA AAA     GAGGAAGAAC
                                |||||| |||     ||||||||||
                                ATCTT TTT     CTCCTTCTTG
                                   T   ATGGA
GAM1053  ACP1     3'  CAACTGATTTCCATCTACAA   28233              G
                                CAACTGATTTTCATCTG GG
                                |||||||||||||||| ||
                                GTTGACTAAAGGTAGAT TT
                                          G
GAM1053  CACNA1C  5'  CAACTGATTTTTTCTCAA    8746           CA   G
                                CAACTGATTTT  TCT GG
                                ||||||||||  ||| ||
                                GTTGACTAAAA  AGA TT
                                     A_   G
GAM1053  IL1RAP   3'  TGATTTTTAAAAGGGTC     13509        CATCT
                                TGATTTT    GGGGGGTC
                                |||||||    ||||||||
                                ACTAAAA    TTTCCCAG
                                   AT___
GAM1053  MADH6    3'  TGATATCTGGGGGGT       24608      TTTC
                                TGAT    ATCTGGGGGGT
                                ||||    ||||||||||
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                                ACTA    TAGACCCCCCA
                                  ____
GAM1053  PCDH11X   3'  ACTGATTTTTGTCACTATTGGT 37291        ___   T   GGG
                                ACTGATTT   TCA CTG   GGT
                                ||||||||   ||| |||   |||
                                TGACTAAA   AGT GAT   CCA
                                    AAC   _   AA_
GAM1053  PCDH11Y   3'  ACTGATTTTTGTCACTATTGGT 37331        ___   T   GGG
                                ACTGATTT   TCA CTG   GGT
                                ||||||||   ||| |||   |||
                                TGACTAAA   AGT GAT   CCA
                                    AAC   _   AA_
GAM1053  RAB18    3'  CAAATAACTTATTTGGGGGGT  34570     C     TCATC
                                CAA TGATTT     TGGGGGGT
                                ||| ||||||     ||||||||
                                GTT ATTGAA     ACCCCCCA
                                  T     TAA__
GAM1053  RET      3'  CAACTGATTTTCTTAG      34154           ATCTGGGG
                                CAACTGATTTTC       GG
                                ||||||||||||       ||
                                GTTGACTAAAAG       TC
                                      AA_______
GAM1053  STAU2    3'  CTGATTTTTGTGGGGT      30802         CATC  G
                                CTGATTTT    TG GGGGT
                                ||||||||    || |||||
                                GACTAAAA    AC CCCCA
                                    _____  A
GAM1054  GPC1     3'  GGTGGACTTGCCTGTGT     13256     A   GTG
                                GGT GACT   TGTCTGTGT
                                ||| ||||   |||||||||
                                CCA CTGA   ACGGACACA
                                  C   ___
GAM1054  MTMR2    3'  TGGTAGACATGTGAATTGT    32070        T    TCTG
                                TGGTAGAC GTGTG    TGT
                                |||||||| |||||    |||
                                ACCATCTG TACAC    ACA
                                    _     TTA_
GAM1054  SLC10A1  3'  GGTAGACACCCTGTCTGTGT   16808        TGTG
                                GGTAGAC    TGTCTGTGT
                                |||||||    |||||||||
                                CCATCTG    ACAGACACA
                                   TGGG
GAM1054  TMOD     5'  TGGAAGAACTTGTCTGTGTC   17603     T   CTGTG
                                TGG AGA     TGTCTGTGTC
                                ||| |||     ||||||||||
                                ACC TCT     ACAGACACAG
                                  T   TGA__
GAM1055  KLHL3    3'  TTTGATGCTGCAAATGCC     44656         _   TC
                                TTTGATGTT TAA  GCC
                                ||||||||| |||  |||
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                                AAACTACGA GTT  CGG
                                     C   TA
GAM1056  CNTNAP2   3'  GTTACTTAATACTTTATCCAC  30490       _   TT
                                GTTACT AAT  CTTTATCCAC
                                |||||| |||  ||||||||||
                                CAATGA TTA  GAAATAGGTG
                                   A   T_
GAM1056  DSC3      3'  TTTATTACTAAAATATCC    35954          TTTCTT
                                TTTGTTACTAA     TATCC
                                ||||||||||     |||||
                                AAATAATGATT     ATAGG
                                      TT____
GAM1056  FSTL1     3'  TCACTTTAATTTCTTTATTCA  28222       __         C
                                TTACT  AATTTCTTTAT CA
                                |||||  |||||||||| ||
                                AGTGA  TTAAAGAAATA GT
                                   AA         A
GAM1056  VRK1      3'  TTTGTCAAACATTTTTATCCAC 18033        CTA    CT
                                TTTGTTA   ATTT  TTATCCAC
                                |||||||   ||||  ||||||||
                                AAACAGT   TAAA  AATAGGTG
                                    TTG   __
GAM1056  CAMLG     3'  TGTAAGGAAATGTAACA     11955          TTGC
                                TGTAAGGAGG   TGTAACA
                                ||||||||||   |||||||
                                ACATTCCTTT   ACATTGT
                                     _____
GAM1056  CHC1      3'  TGTGAGGGAGGTTGTGC     10430      TAA       C
                                TGTG   GGAGGTTG TGT
                                ||||   |||||||| |||
                                ACAC   CCTCCAAC ACG
                                  TC_       _
GAM1056  PYGM      5'  TGTGAGGGAGGTTGTGT     24702      TAA       C
                                TGTG   GGAGGTTG TGT
                                ||||   |||||||| |||
                                ACAC   CCTCCAAC ACA
                                  TC_       _
GAM1057  ADCY8     5'  GGAGGCCCGAGGCCGCG     10010        ACAG   A
                                GGAGGCC    CGA GGCCGCG
                                |||||||    ||| |||||||
                                CCTCCGG    GCT CCGGCGC
                                     _____  _
GAM1057  F8A       3'  GGAGGCAGGAGGCTGCG     29110       CAC  C  A   C
                                GGAGGC   AG GA GGC GCG
                                ||||||   || || ||| |||
                                CCTCCG   TC CT CCG CGC
                                   ___  _  _   A
GAM1057  FMNL      3'  GGCGGGCCACAGCGGAGG    25301    A_         A
                                GG  GGCCACAGCG AGG
                                ||  |||||||||| |||
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                                CC  CCGGTGTCGC TCC
                                 GC        C
GAM1057  FUT3     5'  AGGAGGCCATGGCAGG      6638          CA  GA
                                AGGAGGCCA  GC  AGG
                                |||||||||  ||  |||
                                TCCTCCGGT  CG  TCC
                                     AC  __
GAM1057  GNPI     3'  AGGAGCCACAGTGAGGCC    24183       G     C  A
                                AGGAG CCACAG GA GGCC
                                ||||| ||||||  || ||||
                                TCCTC GGTGTC CT CCGG
                                   _     A  _
GAM1057  HUNK     3'  GGAGGCCAAGGTGGGCAGATCG 31073         C  CGAA   CG__
              T                  GGAGGCCA AG    GGC    CGT
                                 ||||||||  ||    |||    |||
                                 CCTCCGGT TC    CCG    GCA
                                      _  CAC_   TCTA
GAM1057  LGALS3BP 3'  GGGAGCCTGCAGTGAGGGCGT  42936    AG   A_   C  A  CC
                                GG  GCC  CAG GA GG  GCGT
                                ||  |||  ||| || ||  ||||
                                CC  CGG  GTC CT CC  CGCA
                                 CT   AC   A  _  __
GAM1057  RERE     5'  GGAGGCCGCGCGGAGGCTGCG  29029        ACA   A    C
                                GGAGGCC   GCG AGGC GCG
                                |||||||   ||| |||| |||
                                CCTCCGG   CGC TCCG CGC
                                     CG_   C    A
GAM1057  SMS      5'  GGGGCCGCGCGGCGG       21398     A    ACA   AA   C C
                                GG GGCC   GCG  GGC G G
                                || ||||   |||  ||| | |
                                CC CCGG   CGC  CCG C C
                                 _   ____   G_   _ A
GAM1057  SPG4     5'  GGGGGCCACAGACCCCCGT    31399     A       CGAAGG  G
                                GG GGCCACAG     CC CGT
                                || ||||||||     || |||
                                CC CCGGTGTC     GG GCA
                                 C       TG____  G
GAM1057  ART3     5'  CTTCAGGATGGGATGTTGT    10138          TAA
                                CTTCAGGAT   ATGTTGT
                                |||||||||   |||||||
                                GAAGTCCTA   TACAACA
                                     CCC
GAM1057  BBOX1    5'  CTTCAGGAGTAGATGCTGT    19601         T  A
                                CTTCAGGA TA ATGTTGT
                                |||||||| || |||||||
                                GAAGTCCT AT TACGACA
                                     C  C
GAM1057  CCND3    3'  CCTTCAGGCTTAGATGTGG    12059         A   A    TGTT
                                CCTTCAGG TTA ATGT    GG
                                |||||||| ||| ||||    ||
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                                GGAAGTCC AAT TACA    CC
                                    G   C    ____
GAM1058  CAV2     3'  CATCTTAATAGTTTTCTT    10286      A
                                TATT TAATAGTTTTCTT
                                |||| ||||||||||||
                                GTAG ATTATCAAAAGAA
                                  A
GAM1058  DSCAM    3'  TTAATATATTTTGGCAATTTTC 10810          ATAA
              TT                 TTAATATATT    TAGTTTTCTT
                                |||||||||    ||||||||||
                                AATTATATAA    GTTAAAAGAA
                                     AACC
GAM1059  CDC7L1   3'  CTGTCATTGATATATACCA    18602       CCAC_
                                CTGTC     TATATACCA
                                |||||     |||||||||
                                GACAG     ATATATGGT
                                   TAACT
GAM1059  CPA3     3'  TGCCCCACTGTATATCAC     12418         A    C
                                TGTCCCACT TATA CAC
                                ||||||||| |||| |||
                                ACGGGGTGA ATAT GTG
                                     C    A
GAM1059  GAS1     3'  CTATCTGTCCCAAGCCA      13065     _       CTATATA
                                CTA CTGTCCCA       CCA
                                ||| ||||||||       |||
                                GAT GACAGGGT       GGT
                                  A       TC_____
GAM1059  GRM1     3'  CTGCTGTCCCATCATCCCA    9133     A       C   ATA
                                CT CTGTCCCA TAT   CCA
                                || |||||||| |||   |||
                                GA GACAGGGT GTA   GGT
                                 C       A   G__
GAM1059  HCS      3'  CACTGTCCCTGAATACCAC    33223         ACTAT
                                TACTGTCCC     ATACCAC
                                |||||||||     |||||||
                                GTGACAGGG     TATGGTG
                                     ACT__
GAM1059  NAPB     3'  CACTGTCCTACATCCA       43169         CAC     A
                                TACTGTCC   TATAT CCA
                                ||||||||   ||||| |||
                                GTGACAGG   ATGTA GGT
                                     ___    _
GAM1059  NFIA     3'  TGACTGTCCCGTTATATA     43224    T       AC
                                C ACTGTCCC  TATATA
                                | ||||||||  ||||||
                                A TGACAGGG  ATATAT
                                 C       CA
GAM1059  NR3C2    3'  CTGCTGCCCCACGCCA       9470     A       TATATA
                                CT CTGTCCCAC      CCA
                                || |||||||||      |||
```

```
                                GA GACGGGGTG     GGT
                                 C       C_____
GAM1059 PCDH11X  3' CTGTGTCAACCTATACCAC   37302     CC  CTA
                                CTGT  CA   TATACCAC
                                ||||  ||   ||||||||
                                GACA  GT   ATATGGTG
                                  CA  TGG
GAM1059 PCDH11Y  3' CTGTGTCAACCTATACCAC   37341     CC  CTA
                                CTGT  CA   TATACCAC
                                ||||  ||   ||||||||
                                GACA  GT   ATATGGTG
                                  CA  TGG
GAM1059 SLC7A6   3' CTGCTGTGCCATACCA      19591    A   C   CTATA
                                CT CTGT CCA    TACCA
                                || |||| |||    |||||
                                GA GACA GGT    ATGGT
                                 C   C  _____
GAM1059 SYCP1    5' CTGTCCCATTAAATTCCA    17231       C  T  A
                                CTGTCCCA TA AT CCA
                                |||||||| || || |||
                                GACAGGGT AT TA GGT
                                     A  T  A
GAM1059 SYT4     3' CACTGTCTCACACACCA     41657       C   TAT
                                TACTGTC CAC   ATACCA
                                ||||||| |||   ||||||
                                GTGACAG GTG   TGTGGT
                                    A  ___
GAM1059 TSLP     3' CTACTTGTATATACCA      39695      GTCCCAC
                                CTACT      TATATACCA
                                |||||      |||||||||
                                GATGA      ATATATGGT
                                  AC_____
GAM1059 YES1     3' CACTGTCCTTCATTACCA    24116       CAC   A
                                TACTGTCC   TAT TACCA
                                ||||||||   ||| |||||
                                GTGACAGG   GTA ATGGT
                                     AA_  _
GAM1059 ZNF180   3' CACTTTTCACTATATATCA   29934     GTCC       C
                                TACT    CACTATATA CA
                                ||||    ||||||||| ||
                                GTGA    GTGATATAT GT
                                  AAA_        A
GAM1059 ABL1     3' ACACAGAGGCAGGGCTTT    28699       ATCTTTC
                                GCACAGA      CAGGGCTTT
                                |||||||      |||||||||
                                TGTGTCT      GTCCCGAAA
                                    CC_____
GAM1059 ADCY2    3' GCAGAGAATCTTTTTACT    42144     C       CCAGG
                                GCA AGAATCTTT     GCT
                                ||| |||||||||     |||
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                                CGT TCTTAGAAA    TGA
                                  C       AA___
GAM1059 C5R1    3' GCGAGAATCTTTCTACTT   11919   AC       CAGG
                                GC  AGAATCTTTC   GCTT
                                ||  ||||||||||   ||||
                                CG  TCTTAGAAAG   TGAA
                                 C_       A___
GAM1059 CDH16   3' GCCCAGTTCTCTGGGGCTTTA 19786   A  AA   CCA
                                GC CAG  TCTTT   GGGCTTTA
                                || |||  |||||  ||||||||
                                CG GTC  AGAGA   CCCGAAAT
                                 G  A_    C__
GAM1059 FMR2    3' GCACGGGCCCCAGGGTTTTA  12967    AGAATCT     C
                                GCAC     TTCCAGGG TTTA
                                ||||     |||||||| ||||
                                CGTG     GGGGTCCC AAAT
                                  CCC_____      A
GAM1059 HADHA   3' GCACAGGGCTTTCTTCCAGA  6765      AATC__
                                GCACAG    TTTCCAGG
                                ||||||    ||||||||
                                CGTGTC    GAAGGTCT
                                   CCGAAA
GAM1059 LGALS3BP 3' GCAGAGCATCAGGGCTTT   42933    C  AATCTTTC
                                GCA AG      CAGGGCTTT
                                ||| ||      |||||||||
                                CGT TC      GTCCCGAAA
                                  C  GTA_____
GAM1059 MCF2    3' GCGCAGTATTTTTCCAAA    23863    A  A  C
                                GC CAG AT TTTCCAGG
                                || ||| || ||||||||
                                CG GTC TA AAAGGTTT
                                 C  A  A
GAM1059 NBS1    3' ACAGGTCTTTCCATTCT     42985     AA      GGG
                                ACAG  TCTTTCCA   CT
                                ||||  ||||||||   ||
                                TGTC  AGAAAGGT   GA
                                  C_       AA_
GAM1059 NFKB1   3' GCAGTGGAATTTTAGGGCTTT 19653    CA_   C   CC
                                GCA   GAAT TTT  AGGGCTTT
                                |||   |||| |||  ||||||||
                                CGT   CTTA AAA  TCCCGAAA
                                  CAC   _  __
GAM1059 UMOD    3' GCACAGGGCTTTCCGCT     17888      AAT     AGG
                                GCACAG   CTTTCC   GCT
                                ||||||   ||||||   |||
                                CGTGTC   GAAAGG   CGA
                                   CC_     ___
GAM1060 CASP10  3' TGTAGTTCTATTTCTAAATAA 37394    _     GCAAGC
                                TG AGTTCTA     TCTAAATAA
                                || |||||||     |||||||||
```

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                                AC TCAAGAT     AGATTTATT
                                 A      AA____
GAM1060  CHN2     3'  TGAGTTCTATTGCTAAAATAA  19813         GCAA   CT
                                TGAGTTCTA   GCT  AAATAA
                                |||||||||   |||  ||||||
                                ACTCAAGAT   CGA  TTTATT
                                     AA__   T_
GAM1060  KITLG    3'  AGCTGCAAGTTCTAAAT     9462      CTA    C
                                AGTT   GCAAG TCTAAAT
                                ||||   ||||| |||||||
                                TCGA   CGTTC AGATTTA
                                  ___    A
GAM1060  SOX11    3'  TGAGTTCTAACAGGTTTTAAAT 17041           AGCTC
                                TGAGTTCTAGCA    TAAAT
                                ||||||||||||    |||||
                                ACTCAAGATTGT    ATTTA
                                       CCAAA
GAM1060  SYK      3'  TGAGTCCTGGGACAGGCT    17240        A__   A
                                TGAGTTCT   GCA GCT
                                ||||||||   ||| |||
                                ACTCAGGA   TGT CGA
                                     CCC   C
GAM1060  ALK      3'  GACATTTGGTCTCTGGTTTGT  43834     __    GGAA
                                GAC  TTGGT   CTGGTTTGT
                                |||  |||||   |||||||||
                                CTG  AACCA   GACCAAACA
                                  TA    GA__
GAM1060  CALCB    3'  TAAGGTTTGGTGGAGCTG    44712      AC       A
                                TGAG  TTGGTGGA CTG
                                ||||  |||||||| |||
                                ATTC  AACCACCT GAC
                                  CA       C
GAM1060  GAS7     3'  TGAGACGAGCTGGTTTG     25283       TTGGTG  A
                                TGAGAC     GA CTGGTTTG
                                ||||||     || ||||||||
                                ACTCTG     CT GACCAAAC
                                   _______  C
GAM1060  HUNK     3'  TGAGTTTGGTGGAATTG     31086      AC       C
                                TGAG  TTGGTGGAA TG
                                ||||  ||||||||| ||
                                ACTC  AACCACCTT AC
                                  A_       A
GAM1060  OGDH     3'  TGAGACTGGTGGGGAGGATTGT 45018        T    AACT  T
                                TGAGACT GGTGG    GG TTGT
                                ||||||| |||||    || ||||
                                ACTCTGA CCACC    CC AACA
                                    _    CCT_  T
GAM1061  ARHGEF7  3'  TGTCTGGATTCATCAGTCA   19372      CA  C      GGT
                                TGTC  GGA TCATCGG   TCA
                                ||||  ||| |||||||   |||
```

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                                ACAG  CCT AGTAGTC   AGT
                                  A_  A      ___
GAM1061  ENTPD6   3'  GTCCAGGACAGGAGGGTT    10339        TCATC
                                GTCCAGGAC    GGGGTT
                                |||||||||    ||||||
                                CAGGTCCTG    TCCCAA
                                     TCC__
GAM1061  KCNJ3    3'  TGTTCAGAGCTCATCTTTGT   13854    C   GA     GGG
                                TGT CAG  CTCATC   GT
                                ||| |||  ||||||   ||
                                ACA GTC  GAGTAG   CA
                                  A  TC     AAA
GAM1061  APOE     3'  CAGGAGGACGGCTGGGGCGGG  6216         A  GCCTCA   A
                                CAGGAGGAC GC     GCG GG
                                ||||||||| ||     ||| ||
                                GTCCTCCTG CG     CGC CC
                                     C  ACCC__   _
GAM1061  CYP11B1  3'  AGAGGACAGTGCTTGCTG    41626        C  CTCA  GA
                                GGAGGACAG GC    GC  G
                                ||||||||| ||    ||  |
                                TCTCCTGTC CG    CG  C
                                     A  AA__  A_
GAM1061  CYP24    5'  CAGAAGGACTCGGCGA      8941          AGCGCC  A
                                CAGGAGGAC     TC GCGA
                                |||||||||     || ||||
                                GTCTTCCTG     AG CGCT
                                     _______  C
GAM1061  GUK1     3'  CAGGGGACAGCCCAGCGAG   9230      A     GCC
                                CAGG GGACAGC   TCAGCGAG
                                |||| |||||||   ||||||||
                                GTCC CCTGTCG   GGTCGCTC
                                  _      ___
GAM1061  HSD17B1  3'  GGGAGACAGCGGCTGAG     7659     AG      CCTCA  _
                                GG  GACAGCG    GC GAG
                                ||  |||||||    || |||
                                CC  CTGTCGC    CG CTC
                                 CT      ______  A
GAM1061  IL10RA   3'  GGGGCAGCAAAGTGAGG     40623    A  A    CCTC  C
                                GG GG CAGCG    AG GAGG
                                || || |||||    || ||||
                                CC CC GTCGT    TC CTCC
                                 _  _    T___  A
GAM1061  ILF1     3'  GGAGGACAGAGTTTCACTCG   21112        CGCC   G_
                                GGAGGACAG    TCA  CG
                                |||||||||    |||  ||
                                CCTCCTGTC    AGT  GC
                                     TCAA   GA
GAM1061  INMT     3'  CAGGAGAATGGCGTCAACCCAG 27673        CA   CC    G_
            G                    CAGGAGGA  GCG  TCAGC  AGG
                                ||||||||  |||  |||||  |||
```

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                                GTCCTCTT  CGC  AGTTG  TCC
                                    AC  __    GG
GAM1061  LAPTM5   3'  CAGGAGGAGCAGGCCAGCGAGG 27602        _  C  TC
                                CAGGAGGA CAG GCC  AGCGAGG
                                |||||||| ||| |||  |||||||
                                GTCCTCCT GTC CGG  TCGCTCC
                                    C  _  __
GAM1061  LEF1     5'  CAGCAGGACAGCGGGCGGAAGC 32201     G       CCTC__   A
            GGG                   CAG AGGACAGCG     AGCG GG
                                ||| |||||||||     |||| ||
                                GTC TCCTGTCGC     TCGC CC
                                  G       CCGCCT   _
GAM1061  LETM1    3'  CAGGAGGACAGGTGCCCAG   29496          C_  T
                                CAGGAGGACAG  GCC CAG
                                ||||||||||  ||| |||
                                GTCCTCCTGTC  CGG GTC
                                      CA  _
GAM1061  MDM2     3'  CAGGAGAATGGTGCGAACCC  27805        CA__  __
                                CAGGAGGA   GCG  CCT
                                ||||||||   |||  |||
                                GTCCTCTT   CGC  GGG
                                    ACCA  TT
GAM1061  MEL      3'  GGAGGACACGAAGGAG     23869        G  CCTC  C
                                GGAGGACA CG   AG GAG
                                |||||||| ||   || |||
                                CCTCCTGT GC   TC CTC
                                    _  T___  _
GAM1061  MN1      5'  GGAGGGCAGCGAGACGAGG   14585      A    CCTCA
                                GGAGG CAGCG    GCGAGG
                                ||||| |||||    ||||||
                                CCTCC GTCGC    TGCTCC
                                  C    TC___
GAM1061  NOS1     3'  CAGGAGGCAGAGCGA       8371         A  CGCCTC
                                CAGGAGG CAG     AGCGA
                                ||||||| |||     |||||
                                GTCCTCC GTC     TCGCT
                                    _  _______
GAM1061  OSM      3'  CAGGGGGAGCAGCCAGCAGCGA 33911      A  CA  _  T_
            GG                    CAGG GGA  GC GCC  CAGCGAGG
                                |||| |||  || |||  ||||||||
                                GTCC CCT  CG CGG  GTCGCTCC
                                  C  __  T  TC
GAM1061  PIGR     3'  CAGGAGAATGGTGTCAACCTGG 43698        CAGCGCC    GA
                                CAGGAGGA      TCAGC  GG
                                ||||||||      |||||  ||
                                GTCCTCTT      AGTTG  CC
                                    ACCAC__    GA
GAM1061  PPIF     3'  CAGGAGGAAAGATCTCAGCGGG 25059        C  CGC      A
                                CAGGAGGA AG   CTCAGCG GG
                                |||||||| ||   ||||||| ||
```

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                                GTCCTCCT TC   GAGTCGC CC
                                    T  TA_     _
GAM1061  PTGER4    5'  GGAGGACAGCGTTCAGGTGTGA 9655          CC    C___
              GG                  GGAGGACAGCG  TCAG    GAGG
                                  ||||||||||  ||||    ||||
                                  CCTCCTGTCGC  AGTC    CTCC
                                       A_    CACA
GAM1061  SFRP2     5'  GGAGGACAGCGCGGGCGAGG   43544          CTCA
                                  GGAGGACAGCGC    GCGAGG
                                  ||||||||||||    ||||||
                                  CCTCCTGTCGCG    CGCTCC
                                         CC__
GAM1061  SHOX2     5'  GGAGGGGGCACCCCAGCGGG   27840      ACA         A
                                  GGAGG   GCGCCTCAGCG GG
                                  |||||   ||||||||||| ||
                                  CCTCC   CGTGGGGTCGC CC
                                     CC_         _
GAM1061  SIRPB2    5'  CAGGAGGATGGGGCCAGGAGG  32995        CAGC   TC  C
                                  CAGGAGGA    GCC  AG GAGG
                                  ||||||||    |||  || ||||
                                  GTCCTCCT    CGG  TC CTCC
                                       ACCC   __  _
GAM1061  STAT6     3'  CAGGAGAAGCTTAGTGAG    17149        AC   GCCTC  C
                                  CAGGAGG  AGC    AG GAG
                                  |||||||  |||    || |||
                                  GTCCTCT  TCG    TC CTC
                                      __   AA___  A
GAM1061  TACSTD1   5'  GGAGGACAGCGACGAG     14301          CCTCA
                                  GGAGGACAGCG    GCGAG
                                  ||||||||||     |||||
                                  CCTCCTGTCGC    TGCTC
                                         _____
GAM1061  WNT1      3'  CAGGGGGCAGTGCAACAAGG   24077      A  A   C  CTC
                                  CAGG GG CAG GC   AGCGAGG
                                  |||| || ||| ||   |||||||
                                  GTCC CC GTC CG   TTGTTCC
                                    C  _   A  ___
GAM1062  DGKB      3'  GCTTATTGTCTGTCTGTG    45211        A
                                  GCTTATT TCTGTTTGTG
                                  |||||||  ||||||||||
                                  CGAATAA AGACAGACAC
                                      C
GAM1062  ECH1      3'  GCTTTATTGTTTGTG       40867      AT   C
                                  GCTT  TAT TGTTTGTG
                                  ||||  ||| ||||||||
                                  CGAA  ATA ACAAACAC
                                     __   _
GAM1062  MOG       3'  TAGCTTGTTTGTTTGTGTCT   14615        A  ATC       _
                                  TAGCTT TT   TGTTTGTG CT
                                  ||||||  ||   |||||||| ||
```

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                                ATCGAA AA   ACAAACAC GA
                                   C ___       A
GAM1062  RREB1    3'  GCTTTTGTCTGTGCT       16399      ATTATC
                                GCTT     TGTTTGTGCT
                                ||||     ||||||||||
                                CGAA     ACAGACACGA
                                  A_____
GAM1062  SACM1L   3'  TAGCTTATTACTGAACT     30428          T   TTTGT
                                TAGCTTATTA CTG    GCT
                                |||||||||| |||    |||
                                ATCGAATAAT GAC    TGA
                                      _  T____
GAM1062  VCAM1    3'  GCTTATTATTTGTCTATA    38781          C
                                GCTTATTAT TGTTTGTG
                                ||||||||| ||||||||
                                CGAATAATA ACAGATAT
                                     A
GAM1063  ABCB4    5'  TGACAGTTTCTTCAGTCTCTGC 7773     T       C     ACC
                                TG ACAGTTTC TTAGT   CTGC
                                || |||||||| |||||   ||||
                                AC TGTCAAAG AGTCA   GACG
                                 _       A     GA_
GAM1063  CDK3     3'  TGCTGAATTCCTTAGTGCTTTG 10381     ACAGT        ACCC
              C                  TGT     TTCCTTAGT    TGC
                                |||    |||||||||   |||
                                ACG    AAGGAATCA    ACG
                                  ACTT_       CGAA
GAM1063  EVC      5'  TGTGCAGTCTCCCGACTCCTGC 30978     A        TAGT _
                                TGT CAGTTTCCT    AC CCTGC
                                ||| |||||||||    || |||||
                                ACA GTCAGAGGG    TG GGACG
                                  C       C___  A
GAM1063  MLLT2    3'  TGTAGGGTTTCCCTCCTG    25515      CA       AGTAC
                                TGTA  GTTTCCTT    CCTG
                                ||||  ||||||||    ||||
                                ACAT  CAAAGGGA    GGAC
                                  CC       _____
GAM1063  PIGH     3'  TGTCAGTTTCCCATTGTTTTGC 21305     A        TAGTACCC
                                TGT CAGTTTCCT       TGC
                                ||| |||||||||       |||
                                ACA GTCAAAGGG       ACG
                                 _        TAACAAA_
GAM1063  RNTRE    3'  TACAGTTTTTTCAGTACTTTG  31258         CC      CC
                                TACAGTTT  TTAGTAC  TG
                                ||||||||  |||||||  ||
                                ATGTCAAA  AGTCATG  AC
                                     AA      AA
GAM1063  WNT11    3'  TGTCGGTTTCCTTTGATGTCCT 21545     ACA       AGTAC_
              GC                   TGT   GTTTCCTT     CCTGC
                                |||   ||||||||     |||||
```

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                                ACA  CAAAGGAA    GGACG
                                  GC_      ACTACA
GAM1063  PRH1    3'  ATGCCATGTTTCACG      26498        ACTCAT
                                ATGCCATGT    TTTACG
                                |||||||||    ||||||
                                TACGGTACA    AAGTGC
                                         _______
GAM1064  BRIP1   3'  TAATAACATTTACATTTCT   36782        C
                                TAATAACA TTACGTTTTT
                                |||||||| ||||||||||
                                ATTATTGT AATGTAAAGA
                                     A
GAM1065  ATSV    3'  TCTCTGCCCTGGGAACAAAGAG 20229     A_  CA  CTA
           AG                     TCTC  CCC  GGA   AAAGAGAG
                                ||||  |||  |||   ||||||||
                                AGAG  GGG  CCT   TTTCTCTC
                                  AC   AC   TG_
GAM1065  BRAF    3'  TCCACCTTAAAAAAAAAGAGAG 20265    T   CC   CT
                                TC CACC  AGGA  AAAAGAGAG
                                || ||||  ||||  |||||||||
                                AG GTGG  TTTT  TTTTCTCTC
                                 _   AA   T_
GAM1065  CDK5    3'  TCTCACCCCTCTCAAGAG    41778        AGGACTAA
                                TCTCACCCC      AAGAG
                                |||||||||      |||||
                                AGAGTGGGG      TTCTC
                                     AGAG____
GAM1065  CDKN1A  3'  CCTCACCCCCACAGCTAGAGGA 38506        A__  A   AAA
           G                     TCTCACCCC   GG CTA   GAG
                                |||||||||   || |||   |||
                                GGAGTGGGG   TC GAT   CTC
                                     GTG  _   CTC
GAM1065  CELSR3  3'  CCACCCCAGGAAGGAGAGAG   10828        CTAAA
                                TCACCCCAGGA    AGAGAG
                                ||||||||||    ||||||
                                GGTGGGGTCCT    TCTCTC
                                      TCC__
GAM1065  COL4A2  3'  TCCCACCCCGAGAAGGGA    12322        AG  CTAAA  A
                                TCTCACCCC  GA    AG GA
                                |||||||||  ||    || ||
                                AGGGTGGGG  CT    TC CT
                                     CT  _____  C
GAM1065  EGLN2   5'  CCTTGCCCTGGAAAGAGA    38822    CA   CA   CTAA
                                TCT  CCC  GGA   AAGAGA
                                |||  |||  |||   ||||||
                                GGA  GGG  CCT   TTCTCT
                                  AC   A_   ____
GAM1065  FTSJ2   3'  TCTCTTTTTGGTTAAAAAGAGA 30171     ACCCCA  ACT
           G                     TCTC     GG   AAAAGAGAG
                                ||||     ||   |||||||||
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                                AGAG     CC   TTTTCTCTC
                                  AAAAA_  AAT
GAM1065 IKBKG    3'  TCTACCCCAAAAGAG      45419     C     GGACTA
                                TCT ACCCCA     AAAGAG
                                ||| ||||||     ||||||
                                AGA TGGGGT     TTTCTC
                                  _     _______
GAM1065 MAPRE2   3'  TCACACCAGGATAAAAAGAG  30693      C     CT
                                TCAC CCAGGA  AAAAGAG
                                |||| ||||||  |||||||
                                AGTG GGTCCT  TTTTCTC
                                  T     AT
GAM1065 NPR1     5'  CTCACCCCGGGGCTCGAG    44579        A  A  AAAA
                                CTCACCCC GG CT    GAG
                                |||||||| || ||    |||
                                GAGTGGGG CC GA    CTC
                                    C  C  G___
GAM1065 PML      3'  TCTCGTCCAGGACCCTGAG   37737      ACC       AAAA
                                TCTC   CCAGGACT    GAG
                                ||||   ||||||||    |||
                                AGAG   GGTCCTGG    CTC
                                  CA_       GA__
GAM1065 SNL      3'  CTCACCCCAGGGCTCCCGGAG  16939          A  AAAA
                                CTCACCCCAGG CT    GAG
                                ||||||||||| ||    |||
                                GAGTGGGGTCC GA    CTC
                                      C  GGGC
GAM1065 SOD3     5'  TCTCTCCTGAAAAGAGA     16960      A  CCAG  CTA
                                TCTC CC    GA   AAAGAGA
                                |||| ||    ||   |||||||
                                AGAG GG    CT   TTTCTCT
                                  A  A___  ___
GAM1065 TCF8     3'  CCACCCCAGTGCTGAGGGAG  36234         GA  AAAA
                                TCACCCCAG  CT    GAG
                                |||||||||  ||    |||
                                GGTGGGGTC  GA    CTC
                                     AC  CTCC
GAM1065 TEM8     3'  TCTCAACTTTGGTAAAAGAGAG 38193       CCCCA  AC
                                TCTCA    GG  TAAAAGAGAG
                                |||||    ||  ||||||||||
                                AGAGT    CC  ATTTTCTCTC
                                   TGAAA  __
GAM1065 TK1      3'  CCTCACCCCAAGGAGA      17551           ACTAAAA
                                TCTCACCCCAGG      GAGA
                                ||||||||||||      ||||
                                GGAGTGGGGTTC      CTCT
                                                  _______
GAM1065 TRAF1    3'  TCTGACCCTGGAGAAAAAGAGA 24948     C    CA   CT
              G                   TCT ACCC  GGA  AAAAGAGAG
                                ||| ||||  |||  |||||||||
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                                AGA TGGG  CCT  TTTTCTCTC
                                  C    A_   CT
GAM1065  TRPV1    5'  TCTCACCCCAGAGGCCTCAGAG 38801          _ A  AAA
                                TCTCACCCCAG G CT   AGAG
                                |||||||||||  | ||   ||||
                                AGAGTGGGGTC C GG   TCTC
                                      T C  AG_
GAM1065  TTC1     3'  TCACCCTGATCATAAAAGAG   17709       CAGGAC
                                TCACCC     TAAAAGAG
                                ||||||     ||||||||
                                AGTGGG     ATTTTCTC
                                   ACTAGT
GAM1065  COL1A1   3'  CTGTTTCCGGGTTGGG      6374         ACTG
                                CTGTTTT    GGGTTGGG
                                |||||||    ||||||||
                                GACAAAG    CCCAACCC
                                    G___
GAM1065  FMR2     3'  CTGGCTGTTTTGCAACTGGG   12963    A      ___
                                CT GCTGTTTT   ACTGGG
                                || ||||||||   ||||||
                                GA CGACAAAA   TGACCC
                                 C       CGT
GAM1065  GNAI2    3'  CCGAGCGGCTGGGGTTGG    42647    T   T TTTTA
                                CC AGC G    CTGGGGTTGG
                                || ||| |    ||||||||||
                                GG TCG C    GACCCCAACC
                                 C   C _____
GAM1065  GORASP1  3'  CCTAATTCCCCCTTGGGGTTGG 36704      CTG    AC
            G                    CCTAG   TTTT  TGGGGTTGGG
                                |||||   ||||  ||||||||||
                                GGATT   GGGG  ACCCCAACCC
                                   AA_   GA
GAM1065  MMP14    3'  CTGGCTGTTCTGCCTTTGGG   22637    A     TTA   GGG
                                CT GCTGTT   CTG   TTGGG
                                || ||||||   |||   |||||
                                GA CGACAA   GAC   AACCC
                                 C     ___   GGA
GAM1065  MRPL49   3'  CTAGTGAGCTGGGGTTGG    43024      C  TTTTA
                                CTAG TG    CTGGGGTTGG
                                |||| ||    ||||||||||
                                GATC AC    GACCCCAACC
                                  _  TC___
GAM1065  NUP88    3'  CTACCTGTTTTACAATATGGG  41476     G       ____
                                CTA CTGTTTTAC    TGGG
                                ||| |||||||||    ||||
                                GAT GACAAAATG    ACCC
                                  G        TTAT
GAM1065  SIRT2    3'  TAGAGATTTGCTGGGGTTGGG  36147     CT    TA
                                TAG  GTTT  CTGGGGTTGGG
                                |||  ||||  ||||||||||
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                                ATC  TAAA  GACCCCAACCC
                                  TC    C_
GAM1066 B3GALT3  3'  ACTACCACCATCTGTCTTAA  37666      ATAG     A
                                ACTAC    TTATCT TCTTAA
                                |||||    |||||| ||||||
                                TGATG    GGTAGA AGAATT
                                   GT__     C
GAM1066 ACAA1    3'  CATGTGGTTTTGCTTTTGTGG  11491     _  ACTATATAA
                                CATG GG        TTTTGTGG
                                |||| ||        ||||||||
                                GTAC CC        AAAACACC
                                  A  AAAACG___
GAM1066 PPP2R5D  3'  TGGGCTGTGGCCCTGTGG    26462      A  ATATAA
                                TGGG CT     TTTTGTGG
                                |||| ||     ||||||||
                                ACCC GA     GGGACACC
                                  _  CACC__
GAM1066 RAB5A    3'  TGGGATTATTTTCTTGTGG    20015      C   ATAA
                                TGGGA TAT    TTTTGTGG
                                ||||| |||    ||||||||
                                ACCCT ATA    AGAACACC
                                   A   AA__
GAM1066 TNFSF4   3'  TGAGACTATATATG        17757          AATTTT
                                TGGGACTATAT     GTG
                                ||||||||||     |||
                                ACTCTGATATA     TAC
                                          _______
GAM1067 ABCD1    3'  GGGTGGTGCCCGGCCCGAGG   6204       T  _  A__    AA
                                GGGT GG GC   GCCC  AGG
                                |||| || ||   ||||  |||
                                CCCA CC CG   CGGG  TCC
                                  _  A  GGC    C_
GAM1067 ADAM11   3'  ACGGTGGGTGCCAGG       34652      GT    CA   CAA
                                ACGG  TGGG  GCC   AGG
                                ||||  ||||  |||   |||
                                TGCC  ACCC  CGG   TCC
                                  __    A_   ____
GAM1067 CACNG1   3'  GAGCCTGCGGCAGCCCAGAGG  8803       _  _       A
                                GGGT TG GGCAGCCCA AGG
                                |||| || ||||||||| |||
                                CTCG AC CCGTCGGGT TCC
                                  G  G        C
GAM1067 CD79A    3'  GGAGGTGGGGCAGTTTAGAGG  34647   C    T     CCCAA
                                A GGGT GGGCAG     AGG
                                | |||| ||||||     |||
                                C TCCA CCCGTC     TCC
                                 C    C     AAATC
GAM1067 EVPL     3'  ACAGTGGTTGGACAGA      12764     ACG        CCCAA
                                ACA   GGTTGGGCAG    A
                                |||   ||||||||||    |
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                                TGT   CCAACCTGTC    T
                                  CA_       _____
GAM1067  FBXO7    5'  CGGGCAGGCGGCCTAAAGG   29139      T   A   C
                                CGGGT GGGC GCC AAAGG
                                ||||| |||| ||| |||||
                                GCCCG TCCG CGG TTTCC
                                   _   C   A
GAM1067  GAS7     3'  GGGCCAGGGCAGCCCAAAGG  25276      _
                                GGGTT GGGCAGCCCAAAGG
                                ||||| ||||||||||||||
                                CCCGG CCCGTCGGGTTTCC
                                   T
GAM1067  GRB7     3'  GGGCGGCGGGCAGCCTGAAGG 23641      __       CA
                                GGGT  TGGGCAGCC  AAGG
                                ||||  |||||||||  ||||
                                CCCG  GCCCGTCGG  TTCC
                                   CC        AC
GAM1067  LASS2    5'  CGCGAGCAGCCCAAG      42671    GGT         A
                                CG   TGGGCAGCCCAA G
                                ||   |||||||||||| |
                                GC   GCTCGTCGGGTT C
                                  ___          C
GAM1067  LYN      5'  CAGCGCGTCTGGCCCGGAGG   14283    A  G   GGGCA    AA
                                CA CG GTT     GCCC  AGG
                                || || |||     ||||  |||
                                GT GC CAG     CGGG  TCC
                                 C  G   AC___    CC
GAM1067  LZTFL1   5'  CAGCGGCGGCAGCCTAAAGG   33769    A   GTTG      C
                                CA CGG    GGCAGCC AAAGG
                                || |||    ||||||| |||||
                                GT GCC    CCGTCGG TTTCC
                                 C   G___      A
GAM1067  NCOA6    5'  GGGTAATCCAGCCCAAAGG   30438      TGGG
                                GGGT    CAGCCCAAAGG
                                ||||    ||||||||||
                                CCCA    GTCGGGTTTCC
                                   TTAG
GAM1067  NFKBIL2  5'  ACGGCACAGCCCAGAG      30238      GTTGG       A
                                ACGG     GCAGCCCA AG
                                ||||     |||||||| ||
                                TGCC     TGTCGGGT TC
                                   G____       C
GAM1067  PIK3CD   3'  ACAGCAGGTTCCCAAA      22722     A     GGGCAG
                                ACA CGGGTT     CCCAAA
                                ||| ||||||     ||||||
                                TGT GTCCAA     GGGTTT
                                   C     _______
GAM1067  PLTP     5'  GGGATGGCGGGCAGCTCAGGGG 26347     T___       C  AA
                                GGG    TGGGCAGC CA  GG
                                |||    |||||||| ||  ||
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                                CCC   GCCCGTCG GT  CC
                                  TACC      A  CC
GAM1067  PTPN11   5'  ACATCGGGCTGGCCCGAG   38751    A     GGCA   AA
                                ACA CGGGTTG   GCCC  AG
                                ||| |||||||   ||||  ||
                                TGT GCCCGAC   CGGG  TC
                                  A     _____   C_
GAM1067  PVT1     3'  ACGTGCCAAGCAGCTCAAAGG  42305    G  TG     C
                                ACG GT  GGCAGC CAAAGG
                                ||| ||  |||||| ||||||
                                TGC CG  TCGTCG GTTTCC
                                  A  GT     A
GAM1067  RAB36    3'  ACGGGCCTACAGCTTGAGG   22231       GG    CCAA
                                ACGGGTT  GCAGC   AGG
                                |||||||  |||||   |||
                                TGCCCGG  TGTCG   TCC
                                    A_    AAC_
GAM1067  SLC6A1   5'  ACAGCAGTTTTGCGGCTCAAGG 40483    A   G  GG  A  C   A
             G                   ACA CGG TT  GC GC CAA GG
                                ||| ||| ||  || || ||| ||
                                TGT GTC AA  CG CG GTT CC
                                  C   _ AA  C  A   C
GAM1067  SLC9A5   3'  GGTGACATGGCAGCCCAGAGG  21391    TG___       A
                                GGT    GGCAGCCCA AGG
                                |||    ||||||||| |||
                                CCA    CCGTCGGGT TCC
                                  CTGTA       C
GAM1067  SORCS3   3'  CGGGTTGGTCAGCTCTGAGG   31418       G   CCAA
                                CGGGTTGG CAGC    AGG
                                |||||||| ||||   |||
                                GCCCAACC GTCG    TCC
                                    A   AGAC
GAM1067  SOX9     3'  ACAATATAAGGCAGCCCAAAGG 7370      GTT_
                                ACGG   GGGCAGCCCAAAGG
                                ||||   ||||||||||||||
                                TGTT   TCCGTCGGGTTTCC
                                  ATAT
GAM1067  SREBF2   3'  GCTGGGCACAGGCCTGAGG   21404       ___  CAA
                                GTTGGGCA   GCC   AGG
                                ||||||||   |||   |||
                                CGACCCGT   CGG   TCC
                                    GTC   AC_
GAM1067  ST7      3'  CAACGGGGTGGATGGCGGAGG  30265       T   CA  CCAA
                                CAACGGG TGGG  GC    AGG
                                |||||||  ||||  ||    |||
                                GTTGCCC ACCT  CG    TCC
                                    C   AC  CC__
GAM1067  SYNGR2   3'  ACCACGGGAGGCAGCCCAGAGG 21741    A    TT       A
                                AC ACGGG  GGGCAGCCCA AGG
                                || |||||  |||||||||| |||
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                                TG TGCCC  TCCGTCGGGT TCC
                                 G    __        C
GAM1067  TCF19    5'  AACTGGTTGAACCTCCGAGG   45553     G      AG  CAA
                                AAC GGTTGGGC  CC   AGG
                                ||| ||||||||  ||   |||
                                TTG CCAACTTG  GG   TCC
                                  A       GA  C__
GAM1067  TEGT     3'  ACCAGCATGGGCAGCTCAGAGG 42093    G  _      C  A
                                AC GGT TGGGCAGC CA AGG
                                || ||| |||||||| || |||
                                TG TCG ACCCGTCG GT TCC
                                 G  T       A  C
GAM1067  TK1      3'  GGGCCAAGGCTCAAAGG     17555      TG  CA  C
                                GGGT  GG  GC CAAAGG
                                ||||  ||  || ||||||
                                CCCG  TC  CG GTTTCC
                                  GT  __  A
GAM1067  WISP1    5'  GACCGAGCAGCCCAGAGG    38900    GT         A
                                G  TGGGCAGCCCA AGG
                                |  ||||||||||| |||
                                C  GCTCGTCGGGT TCC
                                 TG         C
GAM1067  WNT15    3'  GGCTGGGCAGCTTGAAGG    18148           CCA
                                GGTTGGGCAGC   AAGG
                                ||||||||||   ||||
                                CCGACCCGTCG   TTCC
                                       AAC
GAM1067  WNT3A    3'  CAGCAGCTCTGGGCAGCC    37537    A  G_
                                CA CGG  TTGGGCAGCC
                                || |||  ||||||||||
                                GT GTC  GACCCGTCGG
                                 C  GA
GAM1067  ZNF257   3'  GGGTTGAGAACTTTTAAAGG   37910        C  CC__
                                GGGTTGGG AGC    AAAGG
                                |||||||| |||   |||||
                                CCCAACTC TTG    TTTCC
                                     _  AAAA
GAM1067  ACK1     5'  CCCTCTCCCTCCTGGGGCTC   25108         AC    AAA
                                CCCTCTCCC  TCTTG   CTC
                                |||||||||  |||||   |||
                                GGGAGAGGG  AGGAC   GAG
                                     __    CCC
GAM1067  ADAMTS8  3'  TCTCCTCTTCCCCCTTA     28167    C    C  A
                                TC CCTCT CC CTCTTG
                                || ||||| || ||||||
                                AG GGAGA GG GGGAAT
                                 A    A  _
GAM1067  ADCY7    3'  CTCTCTACCTGTTTGAAACC   9985       CC   C__
                                CTCTC  ACT   TTGAAACT
                                |||||  |||   ||||||||
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                                GAGAG  TGG   AACTTTGG
                                  A_   ACA
GAM1067  ARHGEF12  3'  TCCCACTCTGGGCACCTTGGGA 31650     _   CC_  T   AA
            CT                    TCCC CTCT   CAC CTTG  ACT
                                  |||| ||||   ||| ||||  |||
                                  AGGG GAGA   GTG GAAC  TGA
                                    T   CCC   _   CC
GAM1067  ASH1     3'  CCTCTCCCTCTCCACTAGCTC  32974        A   TGAAA
                                  CCTCTCCC CTCT    CTC
                                  |||||||| ||||    |||
                                  GGAGAGGG GAGG    GAG
                                      A   TGATC
GAM1067  ATRN     3'  TCCCTACTCCCACCCCCA    40283     CT
                                  TCCC  CTCCCACTCTTG
                                  ||||  ||||||||||||
                                  AGGG  GAGGGTGGGGGT
                                    AT
GAM1067  ATSV     3'  TCTCCCTCCCACCAGAGGAACT 20228    C  T      CTTGA
            C                     TC CC CTCCCACT    AACTC
                                  || || ||||||||    |||||
                                  AG GG GAGGGTGG    TTGAG
                                   A  _      TCTCC
GAM1067  BACE     3'  CCTCTCCCCTCAACT      29044        A   TTGA
                                  CCTCTCCC CTC    AACT
                                  |||||||| |||    ||||
                                  GGAGAGGG GAG    TTGA
                                          _  ____
GAM1067  BMP1     3'  TCCCCTCCCCATCGGCTC    25992        T   ____
                                  TCCCCTC CCCA    CTC
                                  ||||||| ||||    |||
                                  AGGGGAG GGGT    GAG
                                      _    AGCC
GAM1067  CBLB     5'  TCCCCTCCCGCCCGACTC    20333        __  _
                                  TCCCCTCT  CCC ACTC
                                  ||||||||  ||| ||||
                                  AGGGGAGG  GGG TGAG
                                       GC   C
GAM1067  CD4      3'  CCCCCTCTCCCAGCAAAGCTC  8326          _____
                                  TCCCCTCTCCCA     CTC
                                  ||||||||||||     |||
                                  GGGGGAGAGGGT     GAG
                                         CGTTTC
GAM1067  CELSR3   3'  CCCTCTCCCACTTTCCCTACC  10832          C  GAA
                                  CCCTCTCCCACT TT   ACT
                                  |||||||||||| ||   |||
                                  GGGAGAGGGTGA AG   TGG
                                         A  GGA
GAM1067  CISH     3'  TCCCCTCTCCCATGCCTTG   30027          C_
                                  TCCCCTCTCCCA  TCTTG
                                  ||||||||||||  |||||
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                                AGGGGAGAGGGT GGAAC
                                      AC
GAM1067 CKTSF1B1 3' CTCTCCCACCCTCAAAATTC 30086          TG  C
                                CTCTCCCACTCT AAA TC
                                |||||||||||| ||| ||
                                GAGAGGGTGGGA TTT AG
                                      GT  A
GAM1067 CSF3R   3' TCCCCTCTTCTCCAGCTAGCTC 8909        _ _ _____
                                TCCCCTCT C CCA   CTC
                                |||||||| | |||   |||
                                AGGGGAGA G GGT   GAG
                                     A A  CGATC
GAM1067 DCTN1   5' TCCCCTCTGCTGCCTGA   35703       CCCA _
                                TCCCCTCT   CT CTTGA
                                ||||||||   || |||||
                                AGGGGAGA   GA GGACT
                                     C___  C
GAM1067 DDAH2   3' TCCCCTCCCCCAATATTGAGGC 30357          CTC   AA
            TC                    TCCCCTCTCCCA  TTGA CTC
                                ||||||||||||  ||||  |||
                                AGGGGAGGGGGT  AACT GAG
                                      TAT   CC
GAM1067 ECE1    3' TCCCCTCCTCCGTCTTGGCTC 10818       TC AC   AAA
                                TCCCCTC CC TCTTG  CTC
                                ||||||| || |||||  |||
                                AGGGGAG GG AGAAC  GAG
                                    GA C_   C__
GAM1067 EIF4A1  3' TCCCCCCTCCTGCTGCTC   10869        CA _
                                TCCCCTCTCC CT CTT
                                |||||||||| || |||
                                AGGGGGGAGG GA GAG
                                      AC C
GAM1067 FN1     5' TCCCCTCTTCCCGCTCGCG  38339       _ A  T
                                TCCCCTCT CCC CTC TG
                                |||||||| ||| ||| ||
                                AGGGGAGA GGG GAG GC
                                     A  C  C
GAM1067 GAP43   5' TCCACCTCTTTTCTGGAA   13049    _   CCCAC  T
                                TCC CCTCT    TCT GAA
                                ||| |||||    ||| |||
                                AGG GGAGA    AGA CTT
                                  T   AA___  C
GAM1067 GDF5    3' TCCTCTTCTCTCCCACTC   8147     C___
                                TCC   CTCTCCCACTC
                                |||   ||||||||||
                                AGG   GAGAGGGTGAG
                                  AGAA
GAM1067 GDF5    3' TCTTCTCTCCCACTCTTG   8148    CC
                                TC CTCTCCCACTCTTG
                                ||  ||||||||||||||
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                                AG  GAGAGGGTGAGAAC
                                 AA
GAM1067  GFI1     3'  TCCCCTCTCATTACCAACT   23557        ____  _
                                TCCCCTCTC    CCA CT
                                |||||||||    ||| ||
                                AGGGGAGAG    GGT GA
                                     TAAT   T
GAM1067  GRAF     3'  TCCCCTCTCTCCCTCTTAAA  31455        _  A
                                TCCCCTCTC CC CTCTTGAA
                                |||||||||  ||  ||||||||
                                AGGGGAGAG GG GAGAATTT
                                     A  _
GAM1067  GRIK3    3'  CTCTCCCATACCCCAAACTC  9096         CT   G
                                CTCTCCCA  CTT AAACTC
                                ||||||||  |||  ||||||
                                GAGAGGGT  GGG TTTGAG
                                     AT   G
GAM1067  GRIN2A   3'  TCCCCTCTCTGTTTCTAACT  9115         CCAC   TGA
                                TCCCCTCTC    TCT   AACT
                                |||||||||    |||   ||||
                                AGGGGAGAG    AGA   TTGA
                                     ACAA   ___
GAM1067  HDAC8    3'  CCCTCTCTCCCAGGGCTC    32970    _      ___
                                CCC CTCTCCCA   CTC
                                |||  ||||||||   |||
                                GGG GAGAGGGT   GAG
                                  A       CCC
GAM1067  HERC2    3'  TCCCTCCTCCCGCCTGGCT   21695     CT    ACT    AAA
                                TCCC  CTCCC   CTTG   CT
                                ||||  |||||   ||||   ||
                                AGGG  GAGGG   GGAC   GA
                                  AG    C__    C__
GAM1067  HIS1     5'  TCCCCCTTCCCACAGCTC    26995      TC     T_
                                TCCCC  TCCCAC  CTT
                                |||||  ||||||  |||
                                AGGGG  AGGGTG  GAG
                                   GA     TC
GAM1067  ICAM1    3'  TCCCCTCTCATCAGGCTAGA  43435         C_  CT  T
                                TCCCCTCTC  CA  CT GA
                                |||||||||  ||  || ||
                                AGGGGAGAG  GT  GA CT
                                     TA  CC  T
GAM1067  IGFBP5   5'  TCTCCCACTTTGCCACC     8276         C   AA
                                TCTCCCACT TTG  ACT
                                |||||||||  |||  |||
                                AGAGGGTGA AAC  TGG
                                     _  GG
GAM1067  IL20RA   3'  CTTTCTCACTCTTGAACTACT  30876    C  C        __
                                CT TC CACTCTTGAA  ACT
                                || || ||||||||||  |||
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                                GA AG GTGAGAACTT  TGA
                                 A  A         GA
GAM1067  ITPR2    5'  CCCTCTCCGCTCCCACCTC    13673         CA     GAAA
                                CCCTCTCC  CTCTT    CTC
                                ||||||||  |||||    |||
                                GGGAGAGG  GAGGG    GAG
                                    C_     TG__
GAM1067  KCNJ5    3'  TCCCCTCCCCTGCTCCCAGGCT 9441           CA     AAA
              C                  TCCCCTCTCC  CTCTTG   CTC
                                ||||||||||  ||||||   |||
                                AGGGGAGGGG  GAGGGT   GAG
                                     AC     CC_
GAM1067  LDB3     3'  TCCTCTTCCCCACCCAGA    44112     C  CT      TT
                                TCC CT  CCCACTC  GA
                                ||| ||  |||||||  ||
                                AGG GA  GGGTGGG  CT
                                  A  AG      T_
GAM1067  LHX4     3'  TCTGCTCTCCCACTGCTT    37853    CC         _
                                TC  CTCTCCCACT CTT
                                ||  ||||||||||| |||
                                AG  GAGAGGGTGA GAA
                                 AC         C
GAM1067  LIF      3'  TCTTCCACTCATCAAACT    14153     C     TTG
                                TCT CCACTC   AAACT
                                ||| ||||||   |||||
                                AGA GGTGAG   TTTGA
                                  A     TAG
GAM1067  LMNB1    3'  TCCCCTCCTCATAAGAACT    24533       TCCCA   T   _
                                TCCCCTC    CTC TGA AACT
                                |||||||    ||| ||| ||||
                                AGGGGAG    GAG ATT TTGA
                                    ______  T   C
GAM1067  LRP1     5'  TCCCCCTCCCCGGGCGAAGCTC 14226      T    ACTCT    A
                                TCCCC CTCCC    TGAA CTC
                                ||||| |||||    |||| |||
                                AGGGG GAGGG    GCTT GAG
                                   _    GCCC_   C
GAM1067  MAP3K5   3'  TCTCCTCTCCCTTCGA     25446    C      ACTC
                                TC CCTCTCCC    TTGA
                                || ||||||||    ||||
                                AG GGAGAGGG    AGCT
                                 A       A___
GAM1067  MAPT     3'  CCTCTCCCACTCCCACT     32578           GAA
                                CCTCTCCCACTCTT   ACT
                                ||||||||||||||   |||
                                GGAGAGGGTGAGGG   TGA
                                         ___
GAM1067  MBP      3'  TCCCCCCTTCCACTTCTC    44893        C    _
                                TCCCCTCT CCACT CTT
                                |||||||| ||||| |||
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                                AGGGGGGA GGTGA GAG
                                    A    A
GAM1067 MLLT7    3' TCCCCTTTCCCCTCCCATCTC 25533      C   A    AAA
                                TCCCCT TCCC CTCTTG  CTC
                                |||||| |||| ||||||  |||
                                AGGGGA AGGG GAGGGT  GAG
                                   A  _    A__
GAM1067 MMP15    3' CCCCCTCTCCCTGGGGCTC   14559         A____
                                TCCCCTCTCCC    CTC
                                ||||||||||    |||
                                GGGGGAGAGGG    GAG
                                      ACCCC
GAM1067 MYEOV    5' TCCTGCTCCTGAATGGACTC  39879    CA      ___
                                TCC  CTCTTGAA  ACTC
                                |||  ||||||||  ||||
                                AGG  GAGGACTT  TGAG
                                  AC       ACC
GAM1067 MYO7A    5' TCCCCTCTTCCTCTGTCTGGCT 7029       C  A  C  GAAA
            C                    TCCCCTCT CC CT TT   CTC
                                |||||||| || || ||   |||
                                AGGGGAGA GG GA AG   GAG
                                    A  A  C  ACC_
GAM1067 NOL3     3' TCCCCTCTTCTAGTCTCACT  19493       CCCAC   GAA
                                TCCCCTCT    TCTT  ACT
                                ||||||||    ||||  |||
                                AGGGGAGA    AGAG  TGA
                                    AGATC   ___
GAM1067 NR2F2    3' TCCCCTCTCTTCTTTTAGCAAA 34241       CCA  C  __
            CT                   TCCCCTCTC  CT TTG  AAACT
                                |||||||||  || |||  |||||
                                AGGGGAGAG  GA AAT  TTTGA
                                    AA_  A  CG
GAM1067 P53AIP1  3' TCCTCCCTCCCATCACCACAGC 35240    C      C  TTGAAA_
            TC                   TCC CTCTCCCA TC     CTC
                                ||| |||||||| ||     |||
                                AGG GGGAGGGT AG     GAG
                                  A      _  TGGTGTC
GAM1067 PAFAH1B1 5' TCTCCTTCTCGCTCCCTAGACT 7724    _ C   CCA    GAA
            C                    TC CC TCTC  CTCTT  ACTC
                                || || ||||  |||||  ||||
                                AG GG AGAG  GAGGG  TGAG
                                 A  A   C__    ATC
GAM1067 PCDHB9   3' TCCCCTCTTAATTGAAA    33323       CCCACTC
                                TCCCCTCT     TTGAAA
                                ||||||||     ||||||
                                AGGGGAGA     AACTTT
                                    ATT____
GAM1067 PCSK1    5' TCCCCCTTCCCACCCTCGGGCT 7754      TC        AAA
            C                    TCCCC  TCCCACTCTTG  CTC
                                |||||  ||||||||||  |||
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                                AGGGG  AGGGTGGGAGC   GAG
                                  GA         CC_
GAM1067  PDE1B    3'  TCCCCTCCCCACACATAGGGCT 9566        T    TCTTGAAA
             C                    TCCCCTC CCCAC       CTC
                                  ||||||| |||||       |||
                                  AGGGGAG GGGTG       GAG
                                     _    TGTATCCC
GAM1067  PIP5K1A  3'  TCCCCTCTTTACCTTAGCT   18658        CCC  T   AAA
                                  TCCCCTCT   AC CTTG   CT
                                  ||||||||   || ||||   ||
                                  AGGGGAGA   TG GAAT   GA
                                       AA_ _    C__
GAM1067  POU5F1   3'  TCCCCTCCCCTGTTCCCC    15474         CA__
                                  TCCCCTCTCC    CTCT
                                  ||||||||||    ||||
                                  AGGGGAGGGG    GGGG
                                        ACAA
GAM1067  PTGS2    3'  CCCTCTTCCCAAAAGAAA    9685        _   CTCTT
                                  CCCTCT CCCA    GAAA
                                  |||||| ||||    ||||
                                  GGGAGA GGGT    CTTT
                                     A   TTT__
GAM1067  PTN      5'  TCCCCTCTCTCCACTTTG    44391         _    C
                                  TCCCCTCTC CCACT TTG
                                  ||||||||| ||||| |||
                                  AGGGGAGAG GGTGA AAC
                                        A    _
GAM1067  RAB2L    3'  TCCCCTCTGCCCTGGGGCTC   21920        _  A____
                                  TCCCCTCT CCC    CTC
                                  |||||||| |||    |||
                                  AGGGGAGA GGG    GAG
                                       C   ACCCC
GAM1067  SET7     5'  TCCCTTCGCCCACTTGCCCCTC 36159     C  T     CT  AAA
                                  TCCC TC CCCACT  TG   CTC
                                  |||| || ||||||  ||   |||
                                  AGGG AG GGGTGA  AC   GAG
                                    A  C      __ GGG
GAM1067  SLC16A2  3'  TCCCCTTCCCAAAAGAAA    27156       C    CTCTT
                                  TCCCCT TCCCA    GAAA
                                  |||||| |||||    ||||
                                  AGGGGA AGGGT    CTTT
                                     _    TTT__
GAM1067  SLC1A4   3'  TCCCCTCTATCCAAACACAAAC 16757        C_  CTCTTG
             T                    TCCCCTCT  CCA     AAACT
                                  ||||||||  |||     |||||
                                  AGGGGAGA  GGT     TTTGA
                                       TA   TTGTG_
GAM1067  SLC24A1  3'  CCCTTCCCACTCCACT     21818      C       TGAA
                                  CCCT TCCCACTCT    ACT
                                  |||| |||||||||    |||
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                                GGGA AGGGTGAGG   TGA
                                  _      ____
GAM1067  SLC6A3   3'  CTCCTTTCTCTCGAAACT    9810      CA_
                                CTCC   CTCTTGAAACT
                                ||||   ||||||||||
                                GAGG   GAGAGCTTTGA
                                  AAA
GAM1067  SLC6A8   3'  TCCTCTCTCTCCTCCCTC    24786     C    _ A
                                TCC CTCTC CC CTCTT
                                ||| ||||| || |||||
                                AGG GAGAG GG GGGAG
                                  A    A A
GAM1067  STAT4    5'  CTCCTCCCACTTGAGGCT    17145     _     CT   AA
                                CTC TCCCACT  TGA  CT
                                ||| |||||||  |||  ||
                                GAG AGGGTGA  ACT  GA
                                  G      __   CC
GAM1067  SVIL     5'  CCTTCTGAAAGCTTGAAACT   34726    C   CCCACT
                                CC TCT     CTTGAAACT
                                || |||     |||||||||
                                GG AGA     GAACTTTGA
                                 A   CTTTC_
GAM1067  SVIL     5'  TCTTCCGCTAGTCAAAACTC   34737     C  A  C_ TG
                                TCT CC CT  T  AAACTC
                                ||| || ||  |  ||||||
                                AGA GG GA  A  TTTGAG
                                  A  C  TC GT
GAM1067  SYN2     3'  TCCCCTCCCCGCTTTCCT    17241          CAC_
                                TCCCCTCTCC    TCTT
                                ||||||||||    ||||
                                AGGGGAGGGG    AGGA
                                      CGAA
GAM1067  TJP1     5'  CCCTCCCCTGCACATGGACTC  17537         __   TCTTGAA
                                CCCTCTCC  CAC      ACTC
                                ||||||||  |||      ||||
                                GGGAGGGG  GTG      TGAG
                                     AC   TACC___
GAM1067  TLL1     5'  CTCCCCACCCGGAGGCTC    29735     T     TT  AA
                                CTC CCCACTC  GA  CTC
                                ||| |||||||  ||  |||
                                GAG GGGTGGG  CT  GAG
                                  _      C_  CC
GAM1067  TRIM9    3'  CCTTCTCCCACTCCTGCCAACT 31560    C          A_
              C                  CC TCTCCCACTCTTG  AACTC
                                 || ||||||||||||  |||||
                                 GG AGAGGGTGAGGAC  TTGAG
                                  A           GG
GAM1067  VEGF     5'  TCTCCTCTTCCTTCTCTT    17972    C    _ CA
                                TC CCTCT CC  CTCTT
                                || ||||| ||  |||||
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                                AG GGAGA GG  GAGAA
                                 A    A  AA
GAM1067  WNT15    3'  CCCTCTCTCCCGTCCAAAA   18146    _     AC   T
                                CCC CTCTCCC  TCT GAA
                                ||| |||||||  ||| |||
                                GGG GAGAGGG  AGG TTT
                                  A      C_   T
GAM1067  YWHAG    3'  CCCTCTCCGTTTTCAGCCCTC  29792        _____ _
                                CCCTCTCC     CA CTCTT
                                ||||||||     || |||||
                                GGGAGAGG     GT GGGAG
                                     CAAAA  C
GAM1067  ZNF146   3'  TCCTCACTCCCATTCCTA    28360     CCT     C
                                TCC   CTCCCA TCTTG
                                |||   |||||| |||||
                                AGG   GAGGGT AGGAT
                                  AGT     A
GAM1068  BAALC    3'  AGTAAGGATTAGTTTCTG    36034        ATC   CTG
                                AGTAAGGA   AGT   TTCTG
                                ||||||||   |||   |||||
                                TCATTCCT   TCA   AAGAC
                                     AA_   ___
GAM1068  CKM      3'  AGTGAGGGAGCAGGACTCTGGT 12259     A   AAT   TCTG
                                AGT AGG   CAG    TTCTGGT
                                ||| |||   |||    |||||||
                                TCA TCC   GTC    GAGACCA
                                  C   CTC   CT__
GAM1068  DUSP4    5'  GTAAGGAAATCGGCTCTCTGGT 38423        _ A T  G
                                GTAAGGAA TC G CT TTCTGGT
                                |||||||| || | || |||||||
                                CATTCCTT AG C GA GAGACCA
                                     T  C _  _
GAM1068  EDNRA    3'  AGTGAAGAATCGTAAGTTCTGG 41991     A      A  CT
              T                  AGT AGGAATC GT  GTTCTGGT
                                ||| ||||||| ||  ||||||||
                                TCA TTCTTAG CA  CAAGACCA
                                  C      _  TT
GAM1068  ENO2     3'  AGTGAGAGGTTGCTCTGG    12708     A  GAATC  TC
                                AGT AG    AG  TGTTCTGG
                                ||| ||    ||  ||||||||
                                TCA TC    TC  ACGAGACC
                                  C  _____  CA
GAM1068  LEP      3'  GGAACCTTGTTCTGG       6915        AGTC
                                GGAATC    TGTTCTGG
                                ||||||    ||||||||
                                CCTTGG    ACAAGACC
                                   A___
GAM1068  LFG      3'  GGAGAGAAATGTTCTGGT    44140     ATC  TC_
                                GGA   AG   TGTTCTGGT
                                |||   ||   |||||||||
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                                CCT   TC   ACAAGACCA
                                  C__  TTT
GAM1068  C21orf33  3'  GTCAAGAACCAACCTTTCATGG 21624      _  GT TTGT    C  C
                                GTCA GA  C    CCTT CA GG
                                |||| ||  |    |||| || ||
                                CAGT CT  G    GGAA GT CC
                                  T  TG TT__    A  A
GAM1068  EFNB1    3'  GTGAGGGCCAGCTCCTTCCATG 20727    C  A   TTG      C
            GC                    GT AG GTC   TCCTTCCA GGC
                                || || |||   |||||||| |||
                                CA TC CGG   AGGAAGGT CCG
                                 C  C   TCG       A
GAM1068  EMP3     5'  GTCGGAGTCTTGTCCCTC    10905     A
                                GTC GAGTCTTGTCCTTC
                                ||| ||||||||||||||
                                CAG CTCAGAACAGGGAG
                                  C
GAM1068  LPO      5'  GCCTTGTCTTTTCACGGC    42740         C  C
                                GTCTTGTC TT CACGGC
                                |||||||| || ||||||
                                CGGAACAG AA GTGCCG
                                     A  A
GAM1068  RFX1     3'  GTCAGAGTTTGCAGCTGCGGC  16297        C    CCTTCCA
                                GTCAGAGT TTGT      CGGC
                                |||||||| ||||      ||||
                                CAGTCTCA AACG      GCCG
                                     _    TCGAC__
GAM1068  SLC16A2  3'  TCAGAGTCTACCTTTCATGGC  27155         TGT    C  C
                                TCAGAGTCT   CCTT CA GGC
                                |||||||||   |||| || |||
                                AGTCTCAGA   GGAA GT CCG
                                     T__    A  A
GAM1069  CRMP1    3'  GTTGTTAAGTAAAAATGGGAG  10600          C  __
                                GTTGTTAAGTA GA  GGGAG
                                |||||||||| ||  |||||
                                CAACAATTCAT TT  CCCTC
                                       T  TA
GAM1069  PCDHB16  5'  TGATGTTGTACAGGGAGGAG   34146    T    AA    G
                                TG TGTT  GTAC AGGGAGGAG
                                || ||||  |||| |||||||||
                                AC ACAA  CATG TCCCTCCTC
                                 T   __   _
GAM1069  PLP2     3'  TGTTGTTGGGGTGGGGAGGAG  15410       AAGTACGA
                                TGTTGTT       GGGAGGAG
                                |||||||       ||||||||
                                ACAACAA       CCCTCCTC
                                    CCCCAC__
GAM1069  PPP5C    3'  TGCTTGAGTGGGGGAGGAG   26496     GTTA   ACGA
                                TGTT    AGT    GGGAGGAG
                                ||||    |||    ||||||||
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                                ACGA   TCA   CCCTCCTC
                                  AC__  CC__
GAM1069 PPP2CA   3' TGTGCAGTCACATCGTCT   15517       A   CGTCA
                                TGTGCAG CACA    TCGTCT
                                ||||||| ||||    ||||||
                                ACACGTC GTGT    AGCAGA
                                   A  _____
GAM1070 ADAMTS13 3' CGTGGGCTGCACGTC     40032    A  TTCA       A
                                CG TG   GCTGCACGT C
                                || ||   ||||||||| |
                                GC AC   CGACGTGCA G
                                 _ C___       C
GAM1070 KRT3     3' TGCGATGCTGATGCGTGC    38383        CA_ _
                                TGCGATGTT   GC TGC
                                |||||||||   || |||
                                ACGCTACGA   CG ACG
                                      CTA  C
GAM1070 MX1      3' TGTGATGTTCAGCATGTGTCAG 14691    C        ___ _ C
              T                  TG GATGTTCAGC   TG CA GT
                                || ||||||||||   || || ||
                                AC CTACAAGTCG   AC GT CA
                                 A        TAC  A _
GAM1070 MNT      3' TGGCAGTGGCTGGGTTTGG   33727      A  CTTC  AT
                                TGGCA TG   GC  GGTTTGG
                                ||||| ||   ||  |||||||
                                ACCGT AC   CG  CCAAACC
                                   C  _____  AC
GAM1070 ZFH4     5' TGGGGTGTTTTTCGGGTTTGGT 36025     CAATGC_   CAT
                                TGG      TTCG   GGTTTGGT
                                |||      ||||   ||||||||
                                ACC      AAGC   CCAAACCA
                                  CCACAAA   ___
GAM1071 AQP6     3' TTTCACACACTCTCCATCT   38261          G  _
                                TTTCACACACTC TCC TCT
                                |||||||||||| ||| |||
                                AAAGTGTGTGAG AGG AGA
                                       _  T
GAM1071 BCAT1    3' TTTCCATTGTATCCTCTA    42387      A  CACTC
                                TTTC CA    GTCCTCTA
                                |||| ||    ||||||||
                                AAAG GT    TAGGAGAT
                                  _ AACA_
GAM1071 COL4A6   3' ACGCACCCACCCCTCTACTTC  37971    A    GT _    C
                                AC CACTC  CC TCTAC TC
                                || |||||  || ||||| ||
                                TG GTGGG  GG AGATG AG
                                 C    TG  G    A
GAM1071 COL9A2   3' CACCCATCAGTGCTCTACCTC  12337        ____
                                CACTCGTC   CTCTACCTC
                                ||||||||   |||||||||
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                                GTGGGTAG   GAGATGGAG
                                     TCAC
GAM1071  SRGAP1   5'  TTTCAACAGCACTCTACCT   43614      C   CTC TC
                                TTTCA ACA   G  CTCTACCT
                                ||||| |||   |  ||||||||
                                AAAGT TGT   C  GAGATGGA
                                   _  ___ GT
GAM1071  ANKH     3'  TGGGAGGGAAGTACCGTAGTAC 38328      CATCC       A
             A                   TGGGA    GTACCGTA TACA
                                |||||    |||||||| ||||
                                ACCCT    CATGGCAT ATGT
                                   CCCTT       C
GAM1071  HTR1D    5'  TTGAGACATTCGTGTGTTTAAT 9269          C   ACCG_
                                TTGGGACAT CGT     TAAT
                                ||||||||| |||     ||||
                                AACTCTGTA GCA     ATTA
                                      A   CACAA
GAM1072  STK38    3'  CCTGGGCTCTCCTCGTTA    28578    GT_  A   TAC
                                CC   GC TTT   CCTCGTTA
                                ||   || |||   ||||||||
                                GG   CG AGA   GGAGCAAT
                                 ACC  _   ___
GAM1072  B29      3'  TGTTTTAAAGAAAGTGTGTAC  36712     CCA      TC
                                TGTT   TAGAGGA  GTGTGTAC
                                ||||   |||||||  ||||||||
                                ACAA   ATTTCTT  CACACATG
                                  A__      T_
GAM1072  DBH      3'  TGTTCCATGGGGATCGT     8975         AGA
                                TGTTCCAT   GGATCGT
                                ||||||||   |||||||
                                ACAAGGTA   CCTAGCA
                                     CC_
GAM1072  MTMR8    3'  TGTTCAATAGAGGATTGT    31761       C        C
                                TGTTC ATAGAGGAT GT
                                ||||| ||||||||| ||
                                ACAAG TATCTCCTA CA
                                   T        A
GAM1072  PRKCN    3'  TATTCCATTTTGTGTGTGT   25168         AGAGGATC
                                TGTTCCAT       GTGTGT
                                ||||||||       ||||||
                                ATAAGGTA       CACACA
                                     AAACA___
GAM1073  ABCD1    3'  TGCCCTGGACAGGGCC      6209        T AG GT
                                TGCCCT G  C  GGGGCC
                                ||||||  |  |  ||||||
                                ACGGGA C  G  TCCCGG
                                   _ CT __
GAM1073  ACE      3'  GCCCTTGGGCAGGGCC      8982         A  GT
                                GCCCTTG GC  GGGGCC
                                ||||||| ||  ||||||
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                                CGGGAAC CG  TCCCGG
                                    C  __
GAM1073  BCL2L11   3'  TGCCCTTAAGTGGAC      39790         CGTG
                                TGCCCTTGAG   GGGC
                                ||||||||||   ||||
                                ACGGGAATTC   CCTG
                                     A___
GAM1073  BIG1      3'  TGCCAAAAACGTGGGGC     26958      CTT
                                TGCC  GAGCGTGGGGC
                                ||||  ||||||||||
                                ACGG  TTTGCACCCCG
                                  TT_
GAM1073  BSN       3'  TGCCCTTGCGTGGTGCC     18419       GA     G
                                TGCCCTT  GCGTGG GCC
                                |||||||  |||||| |||
                                ACGGGAA  CGCACC CGG
                                   __     A
GAM1073  C5R1      3'  TGCTTTTGAGACAGAGCC    11928     CC     C TG
                                TGC  TTGAG G  GGGCC
                                |||  ||||| |  |||||
                                ACG  AACTC T  CTCGG
                                  AA    _ GT
GAM1073  CAPN10    3'  GCCCTTGACCCAGGCC      35774        G GTG
                                GCCCTTGA C   GGGCC
                                ||||||||  |   |||||
                                CGGGAACT G   TCCGG
                                     _ GG_
GAM1073  CDKN2C    5'  TGCCCTGGAGCAGAGCC     38570       T    GT
                                TGCCCT GAGC  GGGGCC
                                ||||||  ||||  ||||||
                                ACGGGA CTCG  TCTCGG
                                   C   __
GAM1073  CENPB     5'  TGCCCTTGACCGGCAGGCC   43018         G  TG
                                TGCCCTTGA CG  GGGCC
                                |||||||||  ||  |||||
                                ACGGGAACT GC  TCCGG
                                     G  CG
GAM1073  CHGA      5'  GCTGGCGGTGTGGGGCC     10467    CCT  A  ___
                                GC   TG GC   GTGGGGCC
                                ||   || ||   ||||||||
                                CG   AC CG   CACCCCGG
                                 ___  _  CCA
GAM1073  CHST6     3'  GCCCTTGAGTAGGAGCC     34679         CGT
                                GCCCTTGAG   GGGGCC
                                |||||||||   ||||||
                                CGGGAACTC   CCTCGG
                                     AT_
GAM1073  CLCN6     3'  TGCCTTTGCATGGGGCC     34722      C  GA
                                TGCC TT  GCGTGGGGCC
                                ||||  ||  ||||||||||
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                                ACGG AA  CGTACCCCGG
                                  _ A_
GAM1073 CLN6    3' CCCTTGAAACCCTGGGCC    32825       _ GTG
                                CCCTTGAG C   GGGCC
                                |||||||| |   |||||
                                GGGAACTT G   CCCGG
                                     T GGA
GAM1073 CLTCL1  3' TGTCCTTGAACTGACC     41890    C      GTGG
                                TG CCTTGAGC   GGCC
                                || ||||||||   ||||
                                AC GGAACTTG   CTGG
                                 A      A___
GAM1073 COPS3   5' TGCCCTTGAGCTGAGAGC    18900         GT
                                TGCCCTTGAGC  GGGGC
                                ||||||||||  |||||
                                ACGGGAACTCG  TCTCG
                                       AC
GAM1073 DAPP1   3' TGCTCTTTAATAAGGCC     30817    C  GAGC
                                TGC CTT   GTGGGGCC
                                ||| |||   ||||||||
                                ACG GAA   TATTCCGG
                                  A  AT__
GAM1073 DRD2    3' TGCCCCTGAGCTGGGGGGCC  9021          GT_
                                TGCCCTTGAGC  GGGGCC
                                ||||||||||  ||||||
                                ACGGGGACTCG  CCCCGG
                                       ACC
GAM1073 DSPG3   5' TGCCCCTGACCAATGGC     41176        G  TGG
                                TGCCCTTGA CG  GGC
                                |||||||| ||  |||
                                ACGGGGACT GT  CCG
                                     G  TA_
GAM1073 DXYS155E 3' TGCTTCTTGTGGGGCC     22962    C_  GAGC
                                TGC  CTT   GTGGGGCC
                                |||  |||   ||||||||
                                ACG  GAA   CACCCCGG
                                  AA  _____
GAM1073 EGLN2   5' TGTCCTTGACGCAGATGCC   38842   C    G  TG  _
                                TG CCTTGA CG  GG GCC
                                || |||||| ||  || |||
                                AC GGAACT GC  CT CGG
                                 A     _ GT  A
GAM1073 EPOR    3' TGCTCCTGAGAGAGGCC     6521     C    CGT
                                TGC CTTGAG   GGGGCC
                                ||| ||||||   ||||||
                                ACG GGACTC   CTCCGG
                                  A     T__
GAM1073 EYA1    5' TGCCCATGGAGCCTCGGGGC  7992      TT_   G_
                                TGCCC   GAGC  TGGGGC
                                |||||   ||||  ||||||
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                                ACGGG  CTCG  GCCCCG
                                  TAC   GA
GAM1073  FBLN1   3'  GCCTCCCCGTGGGGCC     27049    _  GAG
                                GCC CTT  CGTGGGGCC
                                ||| |||  |||||||||
                                CGG GGG  GCACCCCGG
                                 A  ___
GAM1073  FCRH3   3'  TGCCCTTGTAACCCTGGC    38115       _  GTGG
                                TGCCCTTG AGC   GGC
                                |||||||| |||   |||
                                ACGGGAAC TTG   CCG
                                    A  GGA_
GAM1073  FER     5'  TGCTCTTCAGTGATGGCC    23494    C  G GC  _
                                TGC CTT A  GTGG GGCC
                                ||| ||| |  |||| ||||
                                ACG GAA T  CACT CCGG
                                 A  G __   A
GAM1073  FKRP    3'  TGCCCTAGAGCGCAGGGC    35900      T    TG
                                TGCCCT GAGCG  GGGC
                                |||||| |||||  ||||
                                ACGGGA CTCGC  CCCG
                                   T    GT
GAM1073  GARP    3'  CTCGGGCTATGTGGGGCC    24309     A  ___
                                CTTG GC  GTGGGGCC
                                |||| ||  ||||||||
                                GAGC CG  CACCCCGG
                                  C  ATA
GAM1073  GNA15   3'  TGCCCCAGGTGGGGCC     40909      TG  C
                                TGCCCT  AG GTGGGGCC
                                ||||||  || ||||||||
                                ACGGGG  TC CACCCCGG
                                  __  _
GAM1073  GPR44   3'  TGCCCTCGAGGAGC       21961       GCGT
                                TGCCCTTGA   GGGGC
                                |||||||||   |||||
                                ACGGGAGCT   CCTCG
                                   ____
GAM1073  HDAC1   3'  TGCCCTGAGCTCGGGGCC   22444      T   G
                                TGCCCT GAGC TGGGGCC
                                |||||| |||| |||||||
                                ACGGGA CTCG GCCCCGG
                                   _   A
GAM1073  HOXD4   3'  TGCCCTCGGGCAGGATGC   31182       A  T  _
                                TGCCCTTG GCG GGG GC
                                |||||||| ||| ||| ||
                                ACGGGAGC CGT CCT CG
                                    C  _  A
GAM1073  HPN     5'  GCGGTGGCGTGGGGCC     13459    CCT  A
                                GC  TG GCGTGGGGCC
                                ||  || ||||||||||
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                                CG   AC CGCACCCCGG
                                 CC_  _
GAM1073  HR       5'  TGCCCTCATGGGGC       32935       TGAG
                                TGCCCT   CGTGGGGC
                                ||||||   ||||||||
                                ACGGGA   GTACCCCG
                                   ____
GAM1073  HTR2C    3'  TGCCCTTGTGGCAGAC      9294        A_  GTG
                                TGCCCTTG  GC   GGGC
                                ||||||||  ||   ||||
                                ACGGGAAC  CG   TCTG
                                    AC  ___
GAM1073  IHPK1    3'  TGCCTTGAACTTGGCC      45497     C     GTGG
                                TGCC TTGAGC   GGCC
                                |||| ||||||   ||||
                                ACGG AACTTG   CCGG
                                  _     AA__
GAM1073  IHPK3    3'  TGCCCTTGGAGCGAGC      38377       _   TGG
                                TGCCCTTG AGCG   GGC
                                |||||||| ||||   |||
                                ACGGGAAC TCGC   TCG
                                    C   ___
GAM1073  IL1RL1LG 3'  TGCCTGTGTGGGGCC      27798     CT  AGC
                                TGCC  TG   GTGGGGCC
                                ||||  ||   ||||||||
                                ACGG  AC   CACCCCGG
                                  __ A__
GAM1073  IMPDH1   3'  TGCCCCTGGGGTGGGGGCC   9415        AGC    _
                                TGCCCTTG   GTGGGG CC
                                ||||||||   |||||| ||
                                ACGGGGAC   CACCCC GG
                                    CC_     C
GAM1073  ITGA7    3'  TGCCCCTGAGGAAGCC      13610        CGT
                                TGCCCTTGAG   GGGGCC
                                ||||||||||   ||||||
                                ACGGGGACTC   CTTCGG
                                   ____
GAM1073  IVD      5'  TGCCCTTGGACCGCACC     13696       _ G   GGG
                                TGCCCTTG A CGT   GCC
                                |||||||| | |||   |||
                                ACGGGAAC T GCG   TGG
                                    C G   ___
GAM1073  KCNH2    3'  TGCCCCTCTCACTGGGGCC   6950        GA_  G
                                TGCCCTT   GC TGGGGCC
                                |||||||   || |||||||
                                ACGGGGA   TG ACCCCGG
                                    GAG  _
GAM1073  KCNH3    3'  TGCCCTGAGCCAGCGGGCC   42091       T   __    G
                                TGCCCT GAGC  GTGGG CC
                                |||||| ||||  ||||| ||
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                                ACGGGA CTCG  CGCCC GG
                                   _   GT    _
GAM1073  KCNK5    3'  GCCCTTGACATCATGGCC    19035       G   GG_
                                GCCCTTGA CGT   GGCC
                                |||||||| |||   ||||
                                CGGGAACT GTA   CCGG
                                   _  GTA
GAM1073  LCP1     3'  TGCCCTTGACAGCTGGC     14110       GC  GG
                                TGCCCTTGA  GT  GGC
                                |||||||||  ||  |||
                                ACGGGAACT  CG  CCG
                                     GT  A_
GAM1073  LRP1     3'  TGCCCCTGGAGTTGGGGC    14229       _ CG
                                TGCCCTTG AG  TGGGGC
                                |||||||| ||  ||||||
                                ACGGGGAC TC  ACCCCG
                                   C  A_
GAM1073  LRRC2    3'  TGTCCTTAAGCACAAGCC    36002    C      TG  G
                                TG CCTTGAGCG  GG CC
                                || |||||||||  || ||
                                AC GGAATTCGT  TC GG
                                 A       GT  _
GAM1073  M17S2    5'  GCCCGAGACTCGTGGGGC    36589     TT  G_
                                GCCC  GA  CGTGGGGC
                                ||||  ||  ||||||||
                                CGGG  CT  GCACCCCG
                                  CT  GA
GAM1073  MADH3    3'  TGCCCTTCAAAGTGGGGCC   25352       G  C
                                TGCCCTT AG GTGGGGCC
                                ||||||| || ||||||||
                                ACGGGAA TT CACCCCGG
                                   G  T
GAM1073  MAN2A2   3'  GCCCTTGGCCTAGGCC     25949       A  G   G
                                GCCCTTG GC TGGG CC
                                ||||||| || |||| ||
                                CGGGAAC CG ATCC GG
                                   _  G   _
GAM1073  MAN2A2   3'  TGTCCTTGAGCCCTTGGCC  25955    C      GTGG
                                TG CCTTGAGC   GGCC
                                || ||||||||   ||||
                                AC GGAACTCG   CCGG
                                 A      GGAA
GAM1073  MAP3K12  3'  TGCCCTTAGCCACAGC     26695       G  G  G
                                TGCCCTT AGC TG GGC
                                ||||||| ||| || |||
                                ACGGGAA TCG GT TCG
                                   _  _  G
GAM1073  MMP15    3'  TGCCCCTGGGTGGAAGGC    14564       AGC  __
                                TGCCCTTG  GTGG  GGC
                                ||||||||  ||||  |||
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                                ACGGGGAC  CACC  CCG
                                    C__   TT
GAM1073  MMP8    5'  TGTCCTCTGGGTAGGGCC   14549   C   GAGC
                                TG CCTT   GTGGGGCC
                                || ||||   ||||||||
                                AC GGAG   CATCCCGG
                                 A   ACC_
GAM1073  NDST1   5'  GCTCACTCCGTGGGGCC    11370   C__  GAG
                                GC  CTT  CGTGGGGCC
                                ||  |||  |||||||||
                                CG  GAG  GCACCCCGG
                                 AGT  ___
GAM1073  NRIP1   5'  GCGGGCGGGCGTGGGGCC   40964   CCT  A
                                GC  TG GCGTGGGGCC
                                ||  || ||||||||||
                                CG  GC CGCACCCCGG
                                 CCC  C
GAM1073  P4HB    3'  TGCCTTGAACAGGC      9551     C    GTG
                                TGCC TTGAGC  GGGC
                                |||| ||||||  ||||
                                ACGG AACTTG  TCCG
                                  _    ___
GAM1073  PABPN1  3'  TACCCTTGAGCAGGCC    21609        GTG
                                TGCCCTTGAGC  GGGCC
                                ||||||||||  |||||
                                ATGGGAACTCG  TCCGG
                                      ___
GAM1073  PAX2    5'  TGCCTTCCCCGTGGGGC    19640    C  GAG
                                TGCC TT  CGTGGGGC
                                |||| ||  ||||||||
                                ACGG AG  GCACCCCG
                                  A  GG_
GAM1073  PCLO    3'  TGCTTTGAACAGGGCC     45310    CC    GT
                                TGC  TTGAGC  GGGGCC
                                |||  ||||||  ||||||
                                ACG  AACTTG  TCCCGG
                                  A_    __
GAM1073  PLXNB2  3'  TGACCTTTGACGTGGGGCC  29650   C   GA
                                TG CCTT  GCGTGGGGCC
                                || ||||  ||||||||||
                                AC GGAA  TGCACCCCGG
                                 T   AC
GAM1073  PML     3'  TGCTGTGATGGGTGGGGCC  37741   CCT  GC_
                                TGC  TGA  GTGGGGCC
                                |||  |||  ||||||||
                                ACG  ACT  CACCCCGG
                                  AC_  ACC
GAM1073  PPP1R8  5'  TGCCCTTGTGGATGCGCC   39734      GAGC   ___
                                TGCCCTT  GTGGG  GCC
                                |||||||  |||||  |||
```

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                                ACGGGAA   CACCT  CGG
                                   ____   ACG
GAM1073  PPP2R5B  3'  TGCCCTTGCCCAAGGCC    26451      GA  G
                                TGCCCTT  GC TGGGGCC
                                |||||||  || |||||||
                                ACGGGAA  CG GTTCCGG
                                   __  G
GAM1073  PPP5C    3'  TGCCCTGGGGCGGGGCC    26494      T AGC
                                TGCCCT G   GTGGGGCC
                                ||||||| |   ||||||||
                                ACGGGA C   CGCCCCGG
                                   _ CC_
GAM1073  PRKACA   3'  TGCCCTTAGCAAGTGGGGCC  15588       G  __
                                TGCCCTT AGC  GTGGGGCC
                                ||||||| |||  ||||||||
                                ACGGGAA TCG  CACCCCGG
                                   _  TT
GAM1073  PYGO2    5'  GCCCTTGGGCTGCACC     41950      A  G  GG
                                GCCCTTG GC TG  GCC
                                ||||||| || ||  |||
                                CGGGAAC CG AC  TGG
                                   C  _  G_
GAM1073  RNF6     5'  TGCCCTCGAATTGGCC     25581       CGTGG
                                TGCCCTTGAG    GGCC
                                ||||||||||    ||||
                                ACGGGAGCTT    CCGG
                                     AA___
GAM1073  SCA1     3'  TACCCCATGTGGGGCC     7285       TGAGC
                                TGCCCT    GTGGGGCC
                                ||||||    ||||||||
                                ATGGGG    CACCCCGG
                                   TA___
GAM1073  SDC1     3'  GCCCAGGGTGGGGCC      16504     TTG  C
                                GCCC   AG GTGGGGCC
                                ||||   || ||||||||
                                CGGG   TC CACCCCGG
                                  ___  C
GAM1073  SIT      3'  TGCCCCTGCTACGGGGGGC  30901       A_  T
                                TGCCCTTG  GCG GGGGC
                                ||||||||  ||| |||||
                                ACGGGGAC  TGC CCCCG
                                    GA   C
GAM1073  SMARCA5  5'  TGCTCTTCCGCGGGGC    18781    C  GAG
                                TGC CTT   CGTGGGGC
                                ||| |||   ||||||||
                                ACG GAA   GCGCCCCG
                                  A  G__
GAM1073  SMN1     5'  TGCGCAGCGTGGGGCC     35645    CCTTG
                                TGC    AGCGTGGGGCC
                                |||    ||||||||||
```

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                                ACG    TCGCACCCCGG
                                  CG___
GAM1073  SMOH    3'  TGTCCCTGGGGTGAGGCC    24819    C    AGC
                                TG CCTTG   GTGGGGCC
                                || |||||   ||||||||
                                AC GGGAC   CACTCCGG
                                 A    CC_
GAM1073  SOX9    3'  TGCCTTCCACATGGGGCC    7375      C  GA
                                TGCC TT  GCGTGGGGCC
                                |||| ||  ||||||||||
                                ACGG AA  TGTACCCCGG
                                  _ GG
GAM1073  TBX1    3'  TGCCCTTGGGGCAGGGTGGCC  38771        A_   T  _
                                TGCCCTTG  GCG GG GGCC
                                ||||||||  ||| || ||||
                                ACGGGAAC  CGT CC CCGG
                                     CC   C  A
GAM1073  TCF3    3'  TGCATCTACCATGGGGCC    43330    CC   AG
                                TGC  TTG  CGTGGGGCC
                                |||  |||  |||||||||
                                ACG  GAT  GTACCCCGG
                                  TA   G_
GAM1073  TFE3    3'  TACCCTCCATGGGGCC      27170       GAG
                                TGCCCTT   CGTGGGGCC
                                |||||||   |||||||||
                                ATGGGAG   GTACCCCGG
                                    ___
GAM1073  TGFA    3'  TGCCCTCGAAAACCTGGC    17448          CG GG
                                TGCCCTTGAG  T  GGC
                                ||||||||||  |  |||
                                ACGGGAGCTT  G  CCG
                                      TT GA
GAM1073  TRH     3'  TGCCCTCCCAGGGGC       28292        GAG  T
                                TGCCCTT   CG GGGGC
                                |||||||   || |||||
                                ACGGGAG   GT CCCCG
                                    G__  _
GAM1073  XPNPEP2  3'  TGTCCTTAGGCAAAGCC     18158    C    G  C TG
                                TG CCTT AG G  GGGCC
                                || |||| || |  |||||
                                AC GGAA TC C  TTCGG
                                 A    _ _ GT
GAM1073  XRCC3    3'  TGCCGAGGTGGGGCC       24110      CTT   C
                                TGCC   GAG GTGGGGCC
                                ||||   ||| ||||||||
                                ACGG   CTC CACCCCGG
                                  ___   _
GAM1073  ZNF8    3'  CCTTTACAAAATGGGGCC    41965      GA ___
                                CCTT  GC   GTGGGGCC
                                ||||  ||   ||||||||
```

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                                GGAA  TG   TACCCCGG
                                  A_  TTT
GAM1073  ASCL2    5'  GGGGCTTCTGGCACGGC     23187      G   CA  ATG
                                GGGGC TTC  GC   ACGGC
                                ||||| |||  ||   |||||
                                CCCCG AAG  CG   TGCCG
                                  _   AC  ___
GAM1073  DGCR2    3'  GGGGCATTCTGGATGGTGG   23099        CAGC   AC
                                GGGGCGTTC    ATG  GG
                                |||||||||    |||  ||
                                CCCCGTAAG    TAC  CC
                                     ACC_   CA
GAM1073  PRV1     3'  AAGGGACGGTTGAGTGTGGTGG 43872        TTCC  CA  AC
                                AAGGGGCG    AG  TG  GG
                                ||||||||    ||  ||  ||
                                TTCCCTGC    TC  AC  CC
                                     CAAC  AC  CA
GAM1074  BACH1    5'  GCTGAGGCGCGGCGCGGCCC   10147    _ A       CTA
                                GC GA GCGCGGCGT   GCCC
                                || || |||||||||   ||||
                                CG CT CGCGCCGCG   CGGG
                                 A  C       C__
GAM1074  BCR      5'  GCGAGGCGCGGGCGCTGC    34635      A     _ T  A
                                GCGA GCGCGG CG CT GC
                                |||| |||||| || || ||
                                CGCT CGCGCC GC GA CG
                                  C     C  _  _
GAM1074  BMP6     5'  CGGAGCGCGGCCGCTGTGGCCC 11863    A      _  CTA_
                                CG AGCGCGGC GT    GCCC
                                || ||||||||  ||    ||||
                                GC TCGCGCCG CG    CGGG
                                 C       G  ACAC
GAM1074  DDOST    3'  GCGGAGAGGGCTCTAGCCCC   23347     A  CGC   G
                                GCG AG   GGC TCTAGCCCC
                                ||| ||   ||| |||||||||
                                CGC TC   CCG AGATCGGGG
                                  C  TC_   _
GAM1074  EFNB1    5'  CACGAGGCGCGACGGGGGC    20710      A       TCTA
                                CGCGA GCGCGGCG    GC
                                ||||| ||||||||    ||
                                GTGCT CGCGCTGC    CG
                                   C       CCC_
GAM1074  KCNK1    5'  CGGAGCGCGGCCCGCCGCC    13888    A      GTCTA  _
                                CG AGCGCGGC     GCC CC
                                || ||||||||     ||| ||
                                GC TCGCGCCG     CGG GG
                                 C       GG____   C
GAM1074  KRT16    5'  ACGCCAGGTGCGGCATCC     45446      GA  C_
                                ACGC  AG  GCGGCGTCT
                                ||||  ||  |||||||||
```

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                                TGCG  TC  CGCCGTAGG
                                  G_  CA
GAM1074  MATK     5'  CGCGAGGCGCCGCGGCC     40307      A   G   TCTA
                                CGCGA GCGC GCG    GCC
                                ||||| |||| |||    |||
                                GCGCT CGCG CGC    CGG
                                  C    G  ____
GAM1074  NRXN1    5'  CGCGGAGCGGGTGGCTGCTCC  39839     A   C  CGT  A  _
                                CGCG AGCG GG   CT GC CC
                                |||| |||| ||   || || ||
                                GCGC TCGC CC   GA CG GG
                                  C   _  ACC  _  A
GAM1074  RRAS     3'  GCGAAGGCAGCTAGTCCC    26557       C    GTC  _
                                GCGAAG GCGGC   TAG CCC
                                |||||| |||||   ||| |||
                                CGCTTC CGTCG   ATC GGG
                                  _    ___   A
GAM1074  S100A11  5'  CGCGGCGTGCGGGTCTGGAGCC 24730     AA  __   C   __
                                CGCG  GC  GCGG GTCT  AGCC
                                ||||  ||  |||| ||||  ||||
                                GCGC  CG  CGCC CAGA  TCGG
                                  __ CA   _   CC
GAM1074  SMARCD3  5'  CGGAGCGCGGCCGCCCGCTCC  16926    A      _   A  _
                                CG AGCGCGGC GTCT GC CC
                                || |||||||| |||| || ||
                                GC TCGCGCCG CGGG CG GG
                                 C      G   _  A
GAM1074  STAT1    5'  GCGGGGGCGCGGCGGTGCAGCC 40216     AA_      TC_
                                GCG   GCGCGGCG   TAGCC
                                |||   ||||||||   |||||
                                CGC   CGCGCCGC   GTCGG
                                  CCC       CAC
GAM1075  ACRC     3'  TGTGAAAAATATGGAACTCAAG 38129         C__   A   T_
            TAAGA                  TGTGAAAAAT   GAA TCG  TAAGA
                                |||||||||   ||| |||  |||||
                                ACACTTTTTA   CTT AGT  ATTCT
                                      TAC   G   TC
GAM1076  APOBEC2  3'  TAAAAAAATACCCAACTTAACA 27707         ___
            T                   TAAAAAAATA   AACTTAACAT
                                |||||||||   ||||||||||
                                ATTTTTTTAT   TTGAATTGTA
                                      GGG
GAM1076  PLAG1    3'  CTTGTAAAAAAATAAACC    15349
                                TTTGTAAAAAAATAAACT
                                ||||||||||||||||||
                                GAACATTTTTTTATTTGG

GAM1076  RAG1     3'  TTTGTAAGAAAATAAACT    7790         A
                                TTTGTAA AAAATAAACT
                                ||||||| ||||||||||
```

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                                AAACATT TTTTATTTGA
                                   C
GAM1076 ST7     3'  TTTGTAAAAACAAACCATTTAA 30275        AA     ___
             CAT                  TTTGTAAAA  ATAAACT   TAACAT
                                  |||||||||  |||||||   ||||||
                                  AAACATTTT  TGTTTGG   ATTGTA
                                     __      TAA
GAM1077 RRM2B   3'  TTCCTCTATGTATAAAT     42732        C
                                  TTCCTCTAT GTATAAAT
                                  |||||||||  ||||||||
                                  AAGGAGATA CATATTTA
                                     _
GAM1077 COL3A1  3'  TCTTTCTGATGGGAGACAT   6390      G  A    _
                                  TCTT CT ATGGGA ATAT
                                  ||||  ||  ||||||  ||||
                                  AGAA GA TACCCT TGTA
                                    A  C     C
GAM1077 GRINL1A 3'  TTGCTAATGGGAATGTAA    43006           A
                                  TTGCTAATGGGAAT TAA
                                  ||||||||||||||  |||
                                  AACGATTACCCTTA ATT
                                        C
GAM1078 ABCC3   3'  GTGAAGGTGGTTGTGG      33426          CA  A
                                  GTGGAGGTGGT  TG GG
                                  ||||||||||  ||  ||
                                  CACTTCCACCA  AC CC
                                     __  A
GAM1078 ADARB1  3'  GTGGAGGTGGTCCACACAGGG  31882          ATG__
                                  GTGGAGGTGGTC    AGGG
                                  ||||||||||||    ||||
                                  CACCTCCACCAG    TCCC
                                        GTGTG
GAM1078 AK2     3'  GTGGAGATGGTTTTTTGA    30190          CA__
                                  GTGGAGGTGGT   TGA
                                  ||||||||||   |||
                                  CACCTCTACCA   ACT
                                        AAAA
GAM1078 ALDOC   3'  TGCCCTCAGTCATGAGGG    23159    GAGG
                                  TG   TGGTCATGAGGG
                                  ||   ||||||||||||
                                  AC   GTCAGTACTCCC
                                   GGGA
GAM1078 ANPEP   3'  GCGGGGTTGGCATGAGGG    10098     A  _  T
                                  GTGG GGT GG CATGAGGG
                                  ||||  |||  ||  ||||||||
                                  CGCC CCA CC GTACTCCC
                                    _  A  _
GAM1078 AP1S1   3'  GTGGAGGTAGGTTATGGGAC  10501         TCA  A
                                  GTGGAGGTGG   TG GGGAC
                                  ||||||||||   ||  |||||
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                                CACCTCCATC   AT CCCTG
                                     CA_  A
GAM1078 APLP2    3' GTGGAGGTGAGGGGA      44923         TCATGA
                                GTGGAGGTGG     GGGA
                                ||||||||||     ||||
                                CACCTCCACT     CCCT
                                     C_____
GAM1078 AQP6     5' GGACTCAAGCATGAGGGAC   11641    GG   T
                                GGA  TGG CATGAGGGAC
                                |||  ||| ||||||||||
                                CCT  GTT GTACTCCCTG
                                  GA   C
GAM1078 ARD1     3' GTGGGGTGAGGAGGG      18575     A    TCAT
                                GTGG GGTGG    GAGGG
                                |||| |||||    |||||
                                CACC CCACT    CTCCC
                                  _    C___
GAM1078 ARF1     3' GTGGGGTGCTCCCGAGGG    43310     A   G  A
                                GTGG GGTG TC TGAGGG
                                |||| |||| || ||||||
                                CACC CCAC AG GCTCCC
                                  _   G  G
GAM1078 ARL2     3' GTGAAGGTTGAGGGA      11693        GGTCA
                                GTGGAGGT    TGAGGGA
                                ||||||||    |||||||
                                CACTTCCA    ACTCCCT
                                     _____
GAM1078 ATP6V0B  3' GTGGAGGTGGGGGA       19727         TCATGA
                                GTGGAGGTGG     GGGA
                                ||||||||||     ||||
                                CACCTCCACC     CCCT
                                     _______
GAM1078 ATSV     3' GTGGAGGTGGTTGGGG     20227          CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACCTCCACCA  AC CCC
                                     __ _
GAM1078 B3GALT5  3' GTGGGAGTGGTTCAAGTCAGGG 37685      AG    _  TG__
                                GTGG  GTGGT CA    AGGG
                                ||||  ||||| ||    ||||
                                CACC  CACCA GT    TCCC
                                  CT    A  TCAG
GAM1078 B4GALT6  5' GTGGAGGGGGGAGAGGG    40852        T  TCAT
                                GTGGAGG GG    GAGGG
                                ||||||| ||    |||||
                                CACCTCC CC    CTCCC
                                   _ CCT_
GAM1078 BAK1     5' ATGGAGGTCCCGAGGG      45106        GG  A
                                GTGGAGGT  TC TGAGGG
                                ||||||||  || ||||||
```

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                                TACCTCCA  GG GCTCCC
                                   __  _
GAM1078 BAT1    3' GTGGGGGCTGTCAGGG      21590      A  G   TGA
                                GTGG GGT GTCA  GGG
                                |||| ||| ||||  |||
                                CACC CCG CAGT  CCC
                                  C  A  ___
GAM1078 BLAME   3' GTGGGTGTGGGAAAGGGA    33494      AG   TCAT
                                GTGG  GTGG   GAGGGA
                                ||||  ||||   ||||||
                                CACC  CACC   TTCCCT
                                  CA   CT__
GAM1078 BRF1    3' GTGGGGGTGTCTGCCTCGGAC 11339      A   G  A  AG__
                                GTGG GGTG TC TG   GGAC
                                |||| |||| || ||   ||||
                                CACC CCAC AG AC   CCTG
                                  C   _ _ GGAG
GAM1078 BRPF1   3' GTAGAGGTGGTGGGA       43815          CATGA
                                GTGGAGGTGGT    GGGA
                                ||||||||||    ||||
                                CATCTCCACCA    CCCT
                                      _____
GAM1078 CA3     5' GCGGAGGTGGGCGAAGGG    23213          TCAT
                                GTGGAGGTGG   GAGGG
                                |||||||||   |||||
                                CGCCTCCACC   TTCCC
                                     CGC_
GAM1078 CA3     5' GTCGAGGTGACGGGG       23215    G     GTC   A
                                GT GAGGTG  ATG GGG
                                || ||||||  ||| |||
                                CA CTCCAC  TGC CCC
                                 G    ___  _
GAM1078 CACNA2D2 3' GTGGAGGTGGGGTGGGG    25722          TCA  A
                                GTGGAGGTGG  TG GGG
                                |||||||||  || |||
                                CACCTCCACC  AC CCC
                                     CC_ _
GAM1078 CDK9    3' GTGGGTGGGTGAGGGA      10390      AG   TCA
                                GTGG  GTGG  TGAGGGA
                                ||||  ||||  |||||||
                                CACC  CACC  ACTCCCT
                                  __   C__
GAM1078 COL4A6  3' GAGGTGACTGTTGTGAGGG   37974       ___ CA
                                GAGGTG  GT  TGAGGG
                                ||||||  ||  ||||||
                                CTCCAC  CA  ACTCCC
                                   TGA  AC
GAM1078 DNCI1   3' GTGGGGGCTGCAGTGGGG    44992      A  G  CA  A
                                GTGG GGT GT  TG GGG
                                |||| ||| ||  || |||
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                                CACC CCG CG  AC CCC
                                  C   A  TC  _
GAM1078  DRD2     3'  TGGAGGTGGGAGGG       9022          TCAT
                                TGGAGGTGG   GAGGG
                                |||||||||   |||||
                                ACCTCCACC   CTCCC
                                     ____
GAM1078  EGFL4    3'  GTGGAGGTGGTGGGG      41583          CAT A
                                GTGGAGGTGGT  G GGG
                                ||||||||||  | |||
                                CACCTCCACCA  C CCC
                                     ___ _
GAM1078  EGFL4    5'  GTGAGGGTGAGTGGGGGAC   41581    GA    TCA  A
                                GTG  GGTGG  TG GGGAC
                                |||  |||||  || |||||
                                CAC  CCACT  AC CCCTG
                                  TC    C__  C
GAM1078  ENIGMA   3'  TGGAGGTGAAAGGG       41637         TCAT
                                TGGAGGTGG   GAGGG
                                |||||||||   |||||
                                ACCTCCACT   TTCCC
                                     ____
GAM1078  FGD1     3'  GTGGTAGGGTATTGAGGGA   20911     A  T   CA
                                GTGG GG GGT  TGAGGGA
                                |||| || |||  |||||||
                                CACC TC CCA  ACTCCCT
                                  A  _   TA
GAM1078  FMNL     5'  GTGGCGGTGGCGGGG      25313     A     CAT A
                                GTGG GGTGGT  G GGG
                                |||| ||||||  | |||
                                CACC CCACCG  C CCC
                                  G    ___ _
GAM1078  G6PD     3'  GTGGAGGTGGGTGCCCAGGG  7610          TCATG_
                                GTGGAGGTGG    AGGG
                                ||||||||||    ||||
                                CACCTCCACC    TCCC
                                      CACGGG
GAM1078  GARP     3'  GTGGGGCTGGGCAGGGAC    24316     A  __  CATG
                                GTGG GGT  GGT   AGGGAC
                                |||| |||  |||   ||||||
                                CACC CCG  CCG   TCCCTG
                                  _   AC  ____
GAM1078  HDAC1    3'  GGGGAAGAAACGTGAGGGAC  22443   T    TGGTCA
                                G GGAGG     TGAGGGAC
                                | |||||     ||||||||
                                C CCTTC     ACTCCCTG
                                 C    TTTGC_
GAM1078  HHIP     5'  GGAGGTGGCGGGGA       35412         CAT A
                                GGAGGTGGT   G GGGA
                                |||||||||   | ||||
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                                CCTCCACCG   C CCCT
                                    ___ _
GAM1078  HOXC13   3'  GTGGAGGCTGGGGATGGGA   40670       _   TCAT  _
                                GTGGAGG TGG    GA GGGA
                                ||||||| |||    || ||||
                                CACCTCC ACC    CT CCCT
                                    G   C___  A
GAM1078  HSPB2    3'  GGAGGTAGAGAGGGA      11364        TCAT
                                GGAGGTGG    GAGGGA
                                ||||||||    ||||||
                                CCTCCATC    CTCCCT
                                    T___
GAM1078  HSPG2    3'  GTGGAGGTGGGTGGGG      24368         TCA  A
                                GTGGAGGTGG   TG GGG
                                ||||||||||   || |||
                                CACCTCCACC   AC CCC
                                     C__  _
GAM1078  HTR6     5'  GGAGGTGAGTGGGGGGAC    9310         TCA  A_
                                GGAGGTGG   TG  GGGAC
                                ||||||||   ||  |||||
                                CCTCCACT   AC  CCCTG
                                    C__  CC
GAM1078  HYOU1    3'  GTGGGGGTGGGGTGAGGG    40641     A    TCA
                                GTGG GGTGG   TGAGGG
                                |||| |||||   ||||||
                                CACC CCACC   ACTCCC
                                  C    CC_
GAM1078  IGFBP5   5'  GTGGAGATGGCGTTGGGG    8274          CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACCTCTACCG  AC CCC
                                     CA  _
GAM1078  ITGB3    3'  GTGGAGGTGCTATGGATGAGGG 6840          GTC___
              AC                  GTGGAGGTG     ATGAGGGAC
                                |||||||||     |||||||||
                                CACCTCCAC     TACTCCCTG
                                    GATACC
GAM1078  KCNK3    3'  GGAGAGTGGTGAGGGA      13907      _    CAT
                                GGAG GTGGT   GAGGGA
                                |||| |||||   ||||||
                                CCTC CACCA   CTCCCT
                                  T    ___
GAM1078  KLK2     3'  GTAGGGGTGGGACAGGGG    24468      A    TC  GA
                                GTGG GGTGG  AT  GGG
                                |||| |||||  ||  |||
                                CATC CCACC  TG  CCC
                                  C    C_  TC
GAM1078  KRT15    3'  GTGGGGAGTGGCAAGGGAC   14014      A_     CAT
                                GTGG  GGTGGT   GAGGGAC
                                ||||  ||||||   |||||||
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                                CACC  TCACCG   TTCCCTG
                                  CC     ___
GAM1078  LASS1    3'  GGAGGTGGTGGCCGCAGGGAC  34610         CA_  _
                                GGAGGTGGT   TG AGGGAC
                                |||||||||   || ||||||
                                CCTCCACCA   GC TCCCTG
                                    CCG  G
GAM1078  MAP3K9   3'  GTGGAGGGTGGGGGA      41359        _   TCATGA
                                GTGGAGG TGG     GGGA
                                |||||||  |||     ||||
                                CACCTCC ACC     CCCT
                                   C  _______
GAM1078  MEOX1    3'  GTGAAGGTGGGATTGGGG    30401          TCA  A
                                GTGGAGGTGG   TG GGG
                                ||||||||||   || |||
                                CACTTCCACC   AC CCC
                                     CTA  _
GAM1078  MLC1     3'  GTGGGGGTGGCCTGCAGAC   40152      A      A  AG
                                GTGG GGTGGTC TG  GGAC
                                ||||  |||||||  ||  ||||
                                CACC CCACCGG AC  TCTG
                                  C       _  G_
GAM1078  MPHOSPH1 3'  GTGGGGATGGTTAATGGG    32115      A     CA   _
                                GTGG GGTGGT  TGA GGG
                                ||||  ||||||  ||| |||
                                CACC CTACCA  ATT CCC
                                  C      __   A
GAM1078  MSX2     3'  GTGGGGCGGTGGGGG       42299      A     CAT A
                                GTGG GGTGGT   G GGG
                                ||||  ||||||   | |||
                                CACC CCGCCA   C CCC
                                  _     ____ C
GAM1078  NDUFB3   5'  GTAGAGACTACATGAGGGAC   14744        TG T
                                GTGGAGG  G CATGAGGGAC
                                |||||||  | ||||||||||
                                CATCTCT  T GTACTCCCTG
                                    GA _
GAM1078  NHLH1    5'  GTGGAAGTGGTGGG        24657          CATGA
                                GTGGAGGTGGT    GGG
                                ||||||||||     |||
                                CACCTTCACCA    CCC
                                               _____
GAM1078  OPHN1    3'  ATGGAGGTGCTGTGGGG     14962         G CA  A
                                GTGGAGGTG T  TG GGG
                                |||||||||  |  || |||
                                TACCTCCAC G  AC CCC
                                     _ AC  _
GAM1078  PACE4    3'  GTCGAGGTGGTCGTTCAGG   15055    G       ATGA
                                GT GAGGTGGTC    GGG
                                ||  |||||||||   |||
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                                CA CTCCACCAG    TCC
                                 G        CAAG
GAM1078 PDE4A    5'  GTGGAGGCGGTGGGGG      26278          CAT A
                                GTGGAGGTGGT   G GGG
                                ||||||||||   | |||
                                CACCTCCGCCA   C CCC
                                      ___ C
GAM1078 PLCB2    3'  GTGGAGGTGAGTGGG       21322         _ CATGA
                                GTGGAGGTG GT    GGG
                                |||||||| ||    |||
                                CACCTCCAC CA    CCC
                                     T _____
GAM1078 POU2AF1  5'  GTGAAGGTGGTGTGGGG     26374          CA  A
                                GTGGAGGTGGT  TG GGG
                                ||||||||||  || |||
                                CACTTCCACCA  AC CCC
                                      C_ _
GAM1078 PRG2     3'  GGAGGTGGAGGGAGGGA     15563        TCAT
                                GGAGGTGG   GAGGGA
                                ||||||||   ||||||
                                CCTCCACC   CTCCCT
                                     TCC_
GAM1078 RASGRP2  5'  GTGGAGGTCGGGGGGCGTGGGGA 25175        ____  CA  A
          C                      GTGGAGGT   GGT  TG GGGAC
                                ||||||||   |||  || |||||
                                CACCTCCA   CCG  AC CCCTG
                                     GCCC   C_ _
GAM1078 RET      3'  GTGGGGGTGCGTCCTCCCAGGG 33939     A   _  ATG__
                                GTGG GGTG GTC    AGGG
                                |||| |||| |||    ||||
                                CACC CCAC CAG    TCCC
                                  C   G   GAGGG
GAM1078 RFX1     3'  GTGGGGTTGCTGGGG      16298     A   G  CA  A
                                GTGG GGT GT  TG GGG
                                |||| ||| ||  || |||
                                CACC CCA CG  AC CCC
                                  _   A  __  _
GAM1078 SCA2     5'  GCGGAGGTGCGGATAGGGAC  16476        GTCATG
                                GTGGAGGTG    AGGGAC
                                |||||||||    ||||||
                                CGCCTCCAC    TCCCTG
                                     GCCTA_
GAM1078 SETDB1   3'  TGGAGGTGGAGAAGGGA    29684        TCAT
                                TGGAGGTGG   GAGGGA
                                |||||||||   ||||||
                                ACCTCCACC   TTCCCT
                                     TC__
GAM1078 SLC22A3  3'  GGAGGTGGACGGGAGGGAC  35052        TCAT
                                GGAGGTGG   GAGGGAC
                                ||||||||   |||||||
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                                CCTCCACC   CTCCCTG
                                    TGCC
GAM1078 SLC35A2  3' GTGGAGCTGGCAGGG     24953      G   CATG
                                GTGGAG TGGT   AGGG
                                |||||| ||||   ||||
                                CACCTC ACCG   TCCC
                                   G   ____
GAM1078 SOX10    3' GTGGAGGAGGACTGGGG    28012      T  TCA  A
                                GTGGAGG GG  TG GGG
                                ||||||| ||  || |||
                                CACCTCC CC  AC CCC
                                    T  TG_ _
GAM1078 SPTB     3' GGAGGTGGCTGCAGGGA    7380        CA  _
                                GGAGGTGGT  TG AGGGA
                                |||||||||  || |||||
                                CCTCCACCG  AC TCCCT
                                    __  G
GAM1078 TAGLN    3' GTAGAGGTGATGGGG      40619       GTC   A
                                GTGGAGGTG  ATG GGG
                                |||||||||  ||| |||
                                CATCTCCAC  TAC CCC
                                    ___  _
GAM1078 TGFBR2   5' GTGGAGGTGGACATTTGA   17474        T  GAGG
                                GTGGAGGTGG CAT   GA
                                |||||||||| |||   ||
                                CACCTCCACC GTA   CT
                                     T  AA__
GAM1078 TRIM34   3' ATGGGGGTGGTTCCTATGGAC 38970     A    _ ATGAG
                                GTGG GGTGGT C    GGAC
                                |||| |||||| |    ||||
                                TACC CCACCA G    CCTG
                                  C    A GATA_
GAM1078 TYK2     3' GTGGAGATGGTGGG       40860         CATGA
                                GTGGAGGTGGT    GGG
                                ||||||||||    |||
                                CACCTCTACCA    CCC
                                    _____
GAM1078 UBTF     3' GTGGGGGAGGCCAGGGGGG  30617     A  T   TGA
                                GTGG GG GGTCA  GGG
                                |||| || |||||  |||
                                CACC CC CCGGT  CCC
                                  C  T   CCC
GAM1078 VDR      3' GGAGGTGGCAGAGGAGGG   7521        CAT_
                                GGAGGTGGT   GAGGG
                                |||||||||   |||||
                                CCTCCACCG   CTCCC
                                     TCTC
GAM1078 VIPR2    3' GTGGAGTTGGGTGGGG     18025      G  TCA  A
                                GTGGAG TGG  TG GGG
                                |||||| |||  || |||
```

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                                CACCTC ACC   AC CCC
                                   A   C__  _
GAM1078 XPNPEP2  3'  GGAGGTGGGCTCAGGGAC    18154        TCATG
                                GGAGGTGG    AGGGAC
                                ||||||||    ||||||
                                CCTCCACC    TCCCTG
                                     CGAG_
GAM1078 XRCC3    3'  GTGGAGGCACTGAGTGG     24107        GGTCA   _
                                GTGGAGGT    TGAG GG
                                ||||||||    |||| ||
                                CACCTCCG    ACTC CC
                                     TG___    A
GAM1078 XRCC3    3'  GTGGGGGGTGGAGGG       24108      A  T   CAT
                                GTGG GG GGT   GAGGG
                                |||| || |||   |||||
                                CACC CC CCA   CTCCC
                                  _ _   C__
GAM1078 ZNF175   3'  GTGGAGATGGAAAGGG      28366         TCAT
                                GTGGAGGTGG    GAGGG
                                ||||||||||    |||||
                                CACCTCTACC    TTCCC
                                      T___
GAM1078 ZNF274   5'  GGAGGCCTCTGGTGAGGGAC   32250       ____   CAT
                                GGAGGT    GGT   GAGGGAC
                                ||||||    |||   |||||||
                                CCTCCG    CCA   CTCCCTG
                                   GAGA   ___
GAM1078 EN2      5'  CGTCCGGCCGCCTCGGGC     10947     C T       G
                                CG C CGGCCGCCT CGGGT
                                || | ||||||||| |||||
                                GC G GCCGGCGGA GCCCG
                                 A _       _
GAM1078 G6PT1    5'  CGCCTCGGTGGCCCCTCGTGC  11162        CC    G_  G
                                CGCCTCGG  GCCT  CG GT
                                ||||||||  ||||  || ||
                                GCGGAGCC  CGGG  GC CG
                                     AC    GA  A
GAM1078 GPD2     5'  GCCTCGGCCCGGGTC       7627         GCCTG    A
                                GCCTCGGCC     CGGGT C
                                |||||||||     ||||| |
                                CGGAGCCGG     GCCCA G
                                      _____    C
GAM1078 KCNA7    5'  CGCCTCGGCCGCCTCGG     36650           G
                                CGCCTCGGCCGCCT CGG
                                |||||||||||||| |||
                                GCGGAGCCGGCGGA GCC
                                                _
GAM1078 NEUROD2  3'  GCCTCGGCAGCTGGGT      26060        C  CTGC
                                GCCTCGGC GC    GGGT
                                ||||||||  ||    ||||
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                                CGGAGCCG CG    CCCA
                                     T  A___
GAM1078  NUP50    5'  GCGCTCGGCCGCTTCCGGTGC  28408    _       CTG   _
                                GC CTCGGCCGC   CGG GT
                                || |||||||||   ||| ||
                                CG GAGCCGGCG   GCC CG
                                 C        AAG   A
GAM1078  OPRD1    5'  CGCCCCGGCCGCCCCGCTGT   9514            _  GG
                                CGCCTCGGCCGCCT GC  GT
                                |||||||||||||| ||  ||
                                GCGGGGCCGGCGGG CG  CA
                                         G  A_
GAM1078  PIG3     5'  CCTCGGCCGCCTCCAGACC    22193          G   GT
                                CCTCGGCCGCCT CGG  ACC
                                |||||||||||| |||  |||
                                GGAGCCGGCGGA GTC  TGG
                                       G   __
GAM1078  PROS1    5'  CGCCTCGGTCTGAGCCGTGC   44612        CC___   _
                                CGCCTCGG     GCC TGC
                                ||||||||     ||| |||
                                GCGGAGCC     CGG ACG
                                     AGACT   C
GAM1078  PTP4A2   5'  GCCCGGCCGCCGCTGC      38632     T      T  GG
                                GCC CGGCCGCC GC  GT
                                ||| |||||||| ||  ||
                                CGG GCCGGCGG CG  CG
                                  _       _  A_
GAM1078  SLC17A5  3'  GCCCGGCCGCTTCGCAT     29688     T     CTG  G
                                GCC CGGCCGC   CG GT
                                ||| |||||||   || ||
                                CGG GCCGGCG   GC TA
                                  _      AA_  G
GAM1078  SUV39H2  5'  CGCCTCGGCCCCGCCTCGTGC  36012          __    G  G
                                CGCCTCGGCC  GCCT CG GT
                                ||||||||||  |||| || ||
                                GCGGAGCCGG  CGGA GC CG
                                      GG   _  A
GAM1078  ZNF205   5'  GCCTCCGCCGTCTGCAGACA   18382      G    C     GT
                                GCCTC GCCG CTGCGG  A
                                ||||| |||| ||||||  |
                                CGGAG CGGC GACGTC  T
                                   G    A     TG
GAM1079  ADAMTS5  3'  AGAGAGAAAGTAGTTGTGAAAA 28174          _  AATA_
            TA                   AGAGAGAAAG AG     AAAATA
                                ||||||||||  ||     ||||||
                                TCTCTCTTTC TC     TTTTAT
                                      A  AACAC
GAM1079  ADAT1    3'  GAAGAAAGAAAGGCTGGGAATA 28995          A____
                                GAAGAGAGAAAG     GAATA
                                ||||||||||||     |||||
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                                CTTCTTTCTTTC    CTTAT
                                      CGACC
GAM1079  ADCY2    3'  GAAGACAGGAAAATAAAA    42142      G  AAA
                                GAAGA AG   GAGAATAAAA
                                ||||| ||   ||||||||||
                                CTTCT TC   CTTTTATTTT
                                   G  ___
GAM1079  AHR      3'  GAAGAGAGTAACAAAAAT    11548        _  A
                                GAAGAGAG AA GAGAAT
                                |||||||| || ||||||
                                CTTCTCTC TT TTTTTA
                                     A  G
GAM1079  BSN      3'  AGAGAGAAACAAAAGAAAAAT  18387         G    T
                                AGAGAGAAA AGAA AAAAAT
                                ||||||||| |||| ||||||
                                TCTCTCTTT TTTT TTTTTA
                                     G    C
GAM1079  BSN      3'  GAAGAGAGAAAGGGGGAGA    18400          ____
                                GAAGAGAGAAA    GAGA
                                ||||||||||    ||||
                                CTTCTCTCTTT    CTCT
                                      CCCC
GAM1079  C7       3'  AAAGAGAAATAAGGAATA     8227          _   A
                                GAAGAGAGA AAG GAATA
                                ||||||||| ||| |||||
                                TTTCTCTTT TTC CTTAT
                                     A  _
GAM1079  CFTR     3'  GAGGAGAGAAAAAGGAATA    7952     A        _
                                GA GAGAGAAAGAG AATA
                                || ||||||||||| ||||
                                CT CTCTCTTTTTC TTAT
                                  C          C
GAM1079  CKN1     3'  GAAGAAAGAATAAAATA      6350           AG
                                GAAGAGAGAA  AGAATA
                                ||||||||||  ||||||
                                CTTCTTTCTT  TTTTAT
                                     A_
GAM1079  CTH      5'  GAAGAGAGGAAAAGAACA     12512         A
                                GAAGAGAG AAGAGAATA
                                |||||||| |||||||||
                                CTTCTCTC TTTTCTTGT
                                     C
GAM1079  DSPG3    3'  GAAGAGAGCAGTAAGAAT     41175         AAA_
                                GAAGAGAG    GAGAAT
                                ||||||||    ||||||
                                CTTCTCTC    TTCTTA
                                     GTCA
GAM1079  EVA1     3'  GAGAGACATAAAAATAAAAAT  40345       AA_
                                GAGAGA   GAGAATAAAAAT
                                ||||||   ||||||||||||
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                                CTCTCT   TTTTTATTTTTA
                                   GTA
GAM1079  FBXL11   3'  AAAGAGAGAGGGGGAACAA   29420        AAGA
                                GAAGAGAGA   GAATAA
                                |||||||||   ||||||
                                TTTCTCTCT   CTTGTT
                                     CCCC
GAM1079  FGF23    3'  AAAGAGAGGGAGGAAAAT    33946       AAA_
                                GAAGAGAG   GAGAAT
                                ||||||||   ||||||
                                TTTCTCTC   CTTTTA
                                     CCTC
GAM1079  GATA3    3'  GAGAGAGAAGGAAAATA     13095    A     A
                                GA GAGAGAA GAGAATA
                                || ||||||| |||||||
                                CT CTCTCTT CTTTTAT
                                 _     C
GAM1079  GDI2     5'  AAGAGAAAGAGAGGAAAA    11255         AT
                                GAGAGAAAGAGA  AAAA
                                ||||||||||||  ||||
                                TTCTCTTTCTCT  TTTT
                                      CC
GAM1079  GSBS     3'  GAAGAGAGAGACAAAGAG    44999        _____
                                GAAGAGAGA   AAGAG
                                |||||||||   |||||
                                CTTCTCTCT   TTCTC
                                     CTGT
GAM1079  HD       3'  AAAGAGAGAAGGGAGAAT    13338         A_
                                GAAGAGAGAA  GAGAAT
                                ||||||||||  ||||||
                                TTTCTCTCTT  CTCTTA
                                      CC
GAM1079  HTR2C    3'  GAAGGGAGGGAGAGCAAAAATA 9284      A   AAA   A
                                GAAG GAG   GAGA TAAAAATA
                                |||| |||   |||| ||||||||
                                CTTC CTC   CTCT GTTTTTAT
                                  C   C__   C
GAM1079  LGR6     3'  GAAGAGAGGGGAAGAGAA    44478        A__
                                GAAGAGAG   AAGAGAA
                                ||||||||   |||||||
                                CTTCTCTC   TTCTCTT
                                     CCC
GAM1079  LRP8     3'  GAAAAGAGAAATAAGAGA    37793        ___
                                GAAGAGAGAA   AGAGA
                                ||||||||||   |||||
                                CTTTTCTCTT   TCTCT
                                      TAT
GAM1079  MEF2C    5'  GAGAGAGAGAGAGAGAAAAAAA 14409   _     A     T
             A                   GA AGAGAGA AGAGAA AAAAA
                                || ||||||| |||||| |||||
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                                CT TCTCTCT TCTCTT TTTTT
                                 C      C     T
GAM1079  MPP2     3'  AAAGAGGAGCAGGAGAAT    40786       _ AAA
                                GAAGAG AG   GAGAAT
                                |||||| ||   ||||||
                                TTTCTC TC   CTCTTA
                                   C  GTC
GAM1079  MSR1     3'  AGAGAGAAACCAAAAATA    14653        __
                                AGAGAGAAA  GAGAATA
                                |||||||||  |||||||
                                TCTCTCTTT  TTTTTAT
                                     GG
GAM1079  NRAP     5'  GAAGAGAGAGGACAAAGA    26122        A___
                                GAAGAGAGA    AGAGA
                                |||||||||    |||||
                                CTTCTCTCT    TTTCT
                                     CCTG
GAM1079  PCDH11X  3'  AGAGAGAAAATGTGAAAATA  37292         ____
                                AGAGAGAAA    GAGAATA
                                |||||||||    |||||||
                                TCTCTCTTT    CTTTTAT
                                     TACA
GAM1079  PCDH11Y  3'  AGAGAGAAAATGTGAAAATA  37332         ____
                                AGAGAGAAA    GAGAATA
                                |||||||||    |||||||
                                TCTCTCTTT    CTTTTAT
                                     TACA
GAM1079  PCMT1    3'  GAAGAAAGAGCAGAAGATA   23941        A_  GA
                                GAAGAGAGA  AGA  ATA
                                |||||||||  |||  |||
                                CTTCTTTCT  TCT  TAT
                                     CG   TC
GAM1079  PCNA     3'  GAATAGAGAAAAAAAATA    15119     G
                                GAA AGAGAAAGAGAATA
                                ||| ||||||||||||||
                                CTT TCTCTTTTTTTTAT
                                  A
GAM1079  PRELP    3'  GAGAGAGAGAAAACGAAT    15550    _       A
                                GA AGAGAGAAAG GAAT
                                || |||||||||| ||||
                                CT TCTCTCTTTT CTTA
                                 C        G
GAM1079  PTMS     3'  AGGGAGAAAGAGAGCAAA    15880    A       A
                                AG GAGAAAGAGA TAAA
                                || |||||||||| ||||
                                TC CTCTTTCTCT GTTT
                                 C        C
GAM1079  SLC4A4   3'  AAAGACTTAAGAGAATAAAAAT 19056      GAGA
            A                    GAAGA   AAGAGAATAAAAATA
                                |||||   ||||||||||||||
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                                TTTCT   TTCTCTTATTTTTAT
                                  GAA_
GAM1079  STC1     3'  AAAGAGAGAAATTTGCTAGGAA 17167          _______  A
                TA                  GAAGAGAGAA      AG GAATA
                                    ||||||||||      || |||||
                                    TTTCTCTCTT      TC CTTAT
                                       TAAACGA  _
GAM1079  TRPS1    5'  AGAGAGAAAGAGAAAGGAAATA 30456            TAA
                                    AGAGAGAAAGAGAA   AAATA
                                    ||||||||||||||   |||||
                                    TCTCTCTTTCTCTT   TTTAT
                                            TCC
GAM1079  CYP3A4   3'  AATACTTTTGTAAAGTGGTCTT 32709            ACT_
                TAT                   AATATTTTTGTAAA   TTTTTAT
                                    ||||||||||||||   |||||||
                                    TTATGAAAACATTT   AGAAATA
                                            CACC
GAM1080  GATM     3'  TAAGTCTTTCTCTCCTTTA   11231          CTCA   C
                                    TAAGTTTTTT   TCTCC TTA
                                    ||||||||||   ||||| |||
                                    ATTCAGAAAG   AGAGG AAT
                                         ____    A
GAM1080  IL1RAP   3'  ATGTTTCCCCATTTCCCTT   13499    T       C
                                    GT TTTTCTCAT TCCCTT
                                    || |||||||| ||||||
                                    TA AAAGGGGTA AGGGAA
                                     C       A
GAM1080  LCT      3'  GTTTTTGCTCCCTTA      14111       TCTCAT
                                    GTTTTT     CTCCCTTA
                                    ||||||     ||||||||
                                    CAAAAA     GAGGGAAT
                                       C_____
GAM1080  LPIN2    3'  TAAGTTTTTTCTTTTTCC    31218          CATC
                                    TAAGTTTTTTCT   TCC
                                    ||||||||||||   |||
                                    ATTCAAAAAAGA   AGG
                                           AAA_
GAM1080  MAGP2    3'  AAGTTTAGTCTCCCTT      18497       TTTCTCA
                                    AAGTTT      TCTCCCTT
                                    ||||||      ||||||||
                                    TTCAAA      AGAGGGAA
                                       TC_____
GAM1080  MTAP     3'  GTTTTTTTTTTCCCCCTTAA  14678       CTCA
                                    GTTTTTT   TCTCCCTTAA
                                    |||||||   ||||||||||
                                    CAAAAAA   AGGGGGAATT
                                       AAA_
GAM1080  NR5A2    3'  AAGTTTGTAGTCATTTCCCTTA 19234       TTTC   C
                A                    AAGTTT   TCAT TCCCTTAA
                                    ||||||   |||| ||||||||
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                                TTCAAA   AGTA AGGGAATT
                                   CATC   A
GAM1080 UCP3     3' AGTTTTTTCTCTTGTTCCTT  17851         ATCTC
                                AGTTTTTTCTC    CCTT
                                ||||||||||    ||||
                                TCAAAAAAGAG    GGAA
                                     AACAA
GAM1080 YWHAG    3' TAAGTTTTCTTTTCATCT    29798        C_
                                TAAGTTTTTT  TCATCT
                                ||||||||||  ||||||
                                ATTCAAAAGA  AGTAGA
                                     AA
GAM1080 B3GALT2  3' CATAAAAGTGCATTGTATAC  19109       ATTTAG
                                TATAAAA     GTATTGTATAC
                                |||||||     ||||||||||
                                GTATTTT     CGTAACATATG
                                   CA____
GAM1080 BTG1     3' TAAAAATTTAGGTATGT     11912           T
                                TAAAAATTTAGGTAT GT
                                |||||||||||||| ||
                                ATTTTTAAATCCATA CA
                                                _
GAM1080 CYP39A1  3' ATAAAAATTTAAGTATGC    32463            T
                                ATAAAAATTTAGGTAT GT
                                |||||||||||||| ||
                                TATTTTTAAATTCATA CG
                                                _
GAM1080 MPP6     3' TATAAAAATTCAGAAGTGTAC 32395           TAT
                                TATAAAAATTTAGG   TGTAT
                                ||||||||||||   |||||
                                ATATTTTTAAGTCT   ACATG
                                      TC_
GAM1080 RAB23    3' TATAAAAATTAGGTATGATAT 32222        T     T
                                TATAAAAATT AGGTAT GTAT
                                |||||||||| |||||| ||||
                                ATATTTTTAA TCCATA TATA
                                      _     C
GAM1081 CCR9     3' CACTGGCAAGACCTGCAG    36295    CG   C_
                                CAC  GGC  GACCTGCAG
                                |||  |||  |||||||||
                                GTG  CCG  CTGGACGTC
                                  A_   TT
GAM1081 CELSR3   3' CACCGACCCTCTGCAG      10824       G  GAC
                                CACCGG CC   CTGCAG
                                ||||||  ||   ||||||
                                GTGGCT GG   GACGTC
                                   G  A__
GAM1081 CIT      3' CACCGGGCGCTGACAG      43042        CGAC  _
                                CACCGGGC    CTG CAG
                                ||||||||    ||| |||
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                                GTGGCCCG   GAC GTC
                                    C___   T
GAM1081  EFNB2    3'  CACCGGGCGCTGCAG      19876       CGAC
                                CACCGGGC   CTGCAG
                                ||||||||   ||||||
                                GTGGCCCG   GACGTC
                                    C___
GAM1081  EMS1     3'  CACAGGGCCGACCTGAG     23423     C       C
                                CAC GGGCCGACCTG AG
                                ||| |||||||||| ||
                                GTG CCCGGCTGGAC TC
                                  T       _
GAM1081  FOXD2    5'  CACCGGGCCGAAGCGCAG    20953         CC
                                CACCGGGCCGA  TGCAG
                                ||||||||||  |||||
                                GTGGCCCGGCT  GCGTC
                                      TC
GAM1081  HPCAL1   3'  CACCGGGCCGGGCAG      39541         ACCT
                                CACCGGGCCG   GCAG
                                |||||||||   ||||
                                GTGGCCCGGC   CGTC
                                    C___
GAM1081  KLHL2    3'  CATCAAAAACCTGCAG     28525    C   CC
                                CA CGGG  GACCTGCAG
                                || ||||  |||||||||
                                GT GTTT  TTGGACGTC
                                 A   __
GAM1081  LNK      5'  CGCCGGGGAAACTTTGCAG   24198   A    CC   C_
                                C CCGGG  GAC  TGCAG
                                | |||||  |||  |||||
                                G GGCCC  TTG  ACGTC
                                 C    CT   AA
GAM1081  LYPLA1   5'  CACCGGGCGCACGCTCAG    26755       _ G  _  G
                                CACCGGGC C AC CT CAG
                                |||||||| | || || |||
                                GTGGCCCG G TG GA GTC
                                    C _  C  _
GAM1081  MECP2    3'  CACCGGGCAGGTCCTCCAG   22577       CGA_   G
                                CACCGGGC   CCT CAG
                                ||||||||   ||| |||
                                GTGGCCCG   GGA GTC
                                    TCCA   G
GAM1081  MSL3L1   5'  CACCAGGCAACCTGCAG     38579       C
                                CACCGGGC GACCTGCAG
                                |||||||| |||||||||
                                GTGGTCCG TTGGACGTC
                                    _
GAM1081  MYO1F    3'  CACCAGGCCGGCAGGCAG    44370         ACCT
                                CACCGGGCCG   GCAG
                                |||||||||   ||||
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                                GTGGTCCGGC   CGTC
                                     CGTC
GAM1081  OVOL1    3'  CACTGGGGACCTGCAG     21272    C  CC
                                CAC GGG  GACCTGCAG
                                ||| |||  |||||||||
                                GTG CCC  CTGGACGTC
                                  A  __
GAM1081  PHKA1    5'  CACCAGGCCCCGCAG      15274       GAC
                                CACCGGGCC  CTGCAG
                                |||||||||  ||||||
                                GTGGTCCGG  GGCGTC
                                     ___
GAM1081  PIK3CD   3'  CACCGGGCAGGTCCTGAG   22725       CGA_   C
                                CACCGGGC   CCTG AG
                                ||||||||   |||| ||
                                GTGGCCCG   GGAC TC
                                    TCCA   _
GAM1081  PPP2R2C  5'  CACTGGCACCTGCAG      41542    CG  CG
                                CAC  GGC  ACCTGCAG
                                |||  |||  ||||||||
                                GTG  CCG  TGGACGTC
                                  A_  __
GAM1081  TARBP2   3'  CACCAGGCACTGGCAG     39540       CG  CT
                                CACCGGGC  AC  GCAG
                                ||||||||  ||  ||||
                                GTGGTCCG  TG  CGTC
                                    __ AC
GAM1081  TCEB3    3'  CACCTGCAGACTGCAG     17315     GG  C  C
                                CACC  GC GAC TGCAG
                                ||||  || ||| |||||
                                GTGG  CG CTG ACGTC
                                  A_  T  _
GAM1081  TNFRSF8  3'  CACCAGACCCCTGCAG     10312       GA
                                CACCGGGCC  CCTGCAG
                                |||||||||  |||||||
                                GTGGTCTGG  GGACGTC
                                     __
GAM1081  TSSC4    3'  CACCGGTGCCACCTGCAG   25038      _  G
                                CACCGG GCC ACCTGCAG
                                |||||| ||| ||||||||
                                GTGGCC CGG TGGACGTC
                                   A  _
GAM1081  DGKG     3'  CGTGCGCCTGCTGAGCCC    10653     TAC       A
                                CGTG   CGCCTGCTGA CCC
                                ||||   |||||||||| |||
                                GCAC   GCGGACGACT GGG
                                  ___        C
GAM1081  RAD50    3'  TCGGCTGTACTGCTGAACCC  39440    T  ACCGC
                                TCG GT    CTGCTGAACCC
                                ||| ||    ||||||||||
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                                AGC CG    GACGACTTGGG
                                  _ ACAT_
GAM1081  SELE    3'  CGTCCTTGCCTGCTGGAC    7804     A __      A
                                TGT CC  GCCTGCTG AC
                                ||| ||  |||||||| ||
                                GCA GG  CGGACGAC TG
                                  _ AA       C
GAM1081  SUFU    3'  GTGTGATGTGCTGAACCTCA  32096     ACCGCC       C
                                GTGT     TGCTGAACC CA
                                ||||     ||||||||| ||
                                CACA     ACGACTTGG GT
                                  CTAC__       A
GAM1081  UNG     3'  GTGCTGCCTTAAAAACCCCA  38945     ACC   GCT
                                GTGT   GCCT   GAACCCCA
                                ||||   ||||   ||||||||
                                CACG   CGGA   TTTGGGGT
                                  A__    ATT
GAM1082  MME     3'  TATTTCTGTAACTTTTTTT   28614        AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                           __
GAM1082  MME     3'  TATTTCTGTAACTTTTTTT   28603        AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                           __
GAM1082  MME     3'  TATTTCTGTAACTTTTTTT   28603        AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                           __
GAM1082  MME     3'  TATTTCTGTAACTTTTTTT   28603        AA
                                TATTTTTGTA  ACTTTTTTT
                                ||||||||||  |||||||||
                                ATAAAGACAT  TGAAAAAAA
                                           __
GAM1082  BACE2   3'  TTGAAGAGAGAAGAGAA     39998          A
                                TTGAAGAGAGAA GAGAA
                                ||||||||||| |||||
                                AACTTCTCTCTT CTCTT
                                           _
GAM1082  BACE2   3'  TTGAAGAGAGAAGAGAA     39998          A
                                TTGAAGAGAGAA GAGAA
                                ||||||||||| |||||
                                AACTTCTCTCTT CTCTT
                                           _
GAM1082  BACE2   3'  TTGAAGAGAGAAGAGAA     39998          A
                                TTGAAGAGAGAA GAGAA
                                ||||||||||| |||||
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                                AACTTCTCTCTT CTCTT
                                        _
GAM1082  CDX1     3'  TTGAAAAGAGAAGAAAA     12218           A
                                TTGAAGAGAGAA GAGAA
                                |||||||||||| |||||
                                AACTTTTCTCTT CTTTT
                                        _
GAM1082  CLN2     3'  TTGAAAAGAGAAAGATGA    7561            _
                                TTGAAGAGAGAAAGA GA
                                |||||||||||||| ||
                                AACTTTTCTCTTTCT CT
                                          A
GAM1082  COCH     3'  TTAAGGAGAGAAATAGAA    19863     A      G
                                TTGA GAGAGAAA AGAA
                                |||| |||||||| ||||
                                AATT CTCTCTTT TCTT
                                  C       A
GAM1082  D8S2298E 3'  TTGAAGAGGCAGAAAGGA    24976       __    A
                                TTGAAGAG  AGAAAG GA
                                ||||||||  |||||| ||
                                AACTTCTC  TCTTTC CT
                                     CG    _
GAM1082  DEFA5    3'  TTGGAGAGAGAAATTTAGAA   34245    A      G__
                                TTG AGAGAGAAA   AGAA
                                ||| |||||||||   ||||
                                AAC TCTCTCTTT   TCTT
                                  C       AAA
GAM1082  EMX2     5'  CTGAAGAGAGGGGGGAAA    44686         AAA_
                                TTGAAGAGAG    GAGA
                                ||||||||||    ||||
                                GACTTCTCTC    CTTT
                                      CCCC
GAM1082  FGF23    3'  TTAAAGAGAGGGAGGAA     33959         AA  A
                                TTGAAGAGAG  AG GAA
                                ||||||||||  || |||
                                AATTTCTCTC  TC CTT
                                      CC  _
GAM1082  GATA3    3'  TTGAGAGAGAAGGAAAA     13102     A     A
                                TTGA GAGAGAA GAGAA
                                |||| ||||||| |||||
                                AACT CTCTCTT CTTTT
                                  _     C
GAM1082  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922          A_____
                                TTGAAGAGAGAA     GAGA
                                ||||||||||||     ||||
                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1082  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922          A_____
                                TTGAAGAGAGAA     GAGA
                                ||||||||||||     ||||
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                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1082  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922          A_____
                                TTGAAGAGAGAA     GAGA
                                ||||||||||||     ||||
                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1082  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922          A_____
                                TTGAAGAGAGAA     GAGA
                                ||||||||||||     ||||
                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1082  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922          A_____
                                TTGAAGAGAGAA     GAGA
                                ||||||||||||     ||||
                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1082  KCNA3    3'  AAGAGAGAGAGGGTAAA     13788        AA   AA
                                AAGAGAGA  GAG  TAAA
                                ||||||||  |||  ||||
                                TTCTCTCT  CTC  ATTT
                                     __   CC
GAM1082  MOG      3'  CTGGAGAGAGAAATGGAA    14610     A       GA
                                TTG AGAGAGAAA  GAA
                                ||| |||||||||  |||
                                GAC TCTCTCTTT  CTT
                                  C        AC
GAM1082  MTCP1    3'  CTGAAGAGTCAGGAGGATAAAA 30576        AGAAA   A
              A                  TTGAAGAG    GAG ATAAAAA
                                 ||||||||    ||| |||||||
                                 GACTTCTC    CTC TATTTTT
                                     AGTC_   C
GAM1082  NHLH1    3'  TTGAAGAAGGAGCAAGAA    24662        A  AA
                                TTGAAGAG GA  GAGAA
                                ||||||||  ||  |||||
                                AACTTCTT CT  TTCTT
                                     C  CG
GAM1082  OPCML    3'  TGAGTAGTAGGGAGAGAATA   14954     AG  _  AA
                                TGA  AG AG  AGAGAATA
                                |||  ||  ||  ||||||||
                                ACT  TC TC  TCTCTTAT
                                  CA  A  CC
GAM1082  PARK2    3'  TTGAAAAGAGAATTAGAA    30383          AG
                                TTGAAGAGAGAA  AGAA
                                ||||||||||||  ||||
                                AACTTTTCTCTT  TCTT
                                      AA
GAM1082  PARK2    3'  TTGAAAAGAGAATTAGAA    30383          AG
                                TTGAAGAGAGAA  AGAA
                                ||||||||||||  ||||
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                                AACTTTTCTCTT  TCTT
                                      AA
GAM1082  PARK2    3'  TTGAAAAGAGAATTAGAA    30383          AG
                                TTGAAGAGAGAA  AGAA
                                ||||||||||||  ||||
                                AACTTTTCTCTT  TCTT
                                      AA
GAM1082  PCDH11X  3'  TTGCAGAGAGAAAATGTGAA  37321    A       A__
                                TTG AGAGAGAAAG   GAA
                                ||| ||||||||||   |||
                                AAC TCTCTCTTTT   CTT
                                  G        ACA
GAM1082  PCDH11X  3'  TTGCAGAGAGAAAATGTGAA  37321    A       A__
                                TTG AGAGAGAAAG   GAA
                                ||| ||||||||||   |||
                                AAC TCTCTCTTTT   CTT
                                  G        ACA
GAM1082  PCDH11Y  3'  TTGCAGAGAGAAAATGTGAA  37366    A       A__
                                TTG AGAGAGAAAG   GAA
                                ||| ||||||||||   |||
                                AAC TCTCTCTTTT   CTT
                                  G        ACA
GAM1082  PFKFB2   3'  TTGAAGAGACAAAAGTGAA   26310        _    A
                                TTGAAGAGA GAAAG GAA
                                |||||||||| ||||| |||
                                AACTTCTCT TTTTC CTT
                                     G    A
GAM1082  PKD2L1   5'  TTGAAGAGGGGAGAGGGGAGAA 32024       ___   AA_
           TA                    TTGAAGA   GAGA   GAGAATA
                                |||||||   ||||   |||||||
                                AACTTCT   CTCT   CTCTTAT
                                   CCC    CCC
GAM1082  PPP1R12B 3'  CTGAAGAGGGTGATAGAAA   36971       A__  A
                                TTGAAGAG   GA AGAGA
                                ||||||||   || |||||
                                GACTTCTC   CT TCTTT
                                     CCA  A
GAM1082  PPP1R12B 3'  CTGAAGAGGGTGATAGAAA   36971       A__  A
                                TTGAAGAG   GA AGAGA
                                ||||||||   || |||||
                                GACTTCTC   CT TCTTT
                                     CCA  A
GAM1082  PPP1R12B 3'  CTGAAGAGGGTGATAGAAA   36971       A__  A
                                TTGAAGAG   GA AGAGA
                                ||||||||   || |||||
                                GACTTCTC   CT TCTTT
                                     CCA  A
GAM1082  PTPN13   3'  TTAAGGAGAGAAATGGAA    38784     A      GA
                                TTGA GAGAGAAA  GAA
                                ||||  ||||||||  |||
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                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1082  PTPN13   3'  TTAAGGAGAGAAATGGAA    38782      A       GA
                                TTGA GAGAGAAA  GAA
                                |||| ||||||||  |||
                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1082  PTPN13   3'  TTAAGGAGAGAAATGGAA    38782      A       GA
                                TTGA GAGAGAAA  GAA
                                |||| ||||||||  |||
                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1082  RRAS2    3'  CTGAGGAGAGAAAGAGAA    29307      A
                                TTGA GAGAGAAAGAGAA
                                |||| ||||||||||||
                                GACT CTCTCTTTCTCTT
                                  C
GAM1082  S100A12  3'  TTGGTGAGGGAAAGAAAA    24738     AA   A
                                TTG  GAG GAAAGAGAA
                                |||  ||| |||||||||
                                AAC  CTC CTTTCTTTT
                                  CA   C
GAM1082  SCD      3'  GAAGAGAGAGAGGATAA     22828          AA   A
                                GAAGAGAGA  GAG ATAA
                                |||||||||  ||| ||||
                                CTTCTCTCT  CTC TATT
                                       __   C
GAM1082  SIM2     3'  TTGAAGAAAGGGTTAAATAAAA 22886           AAAGA
            A                    TTGAAGAGAG     GAATAAAAA
                                ||||||||||     |||||||||
                                AACTTCTTTC     TTTATTTTT
                                     CCAA_
GAM1082  SMARCD2  3'  TTGAGGAAAGAAAAGAA     16923      A       A
                                TTGA GAGAGAA GAGAA
                                |||| ||||||| |||||
                                AACT CTTTCTT TTCTT
                                  C      _
GAM1082  SPOCK    3'  TTCAAGAGAGAAAAAAAA    41745    G
                                TT AAGAGAGAAAGAGAA
                                || ||||||||||||||
                                AA TTCTCTCTTTTTTTT
                                  G
GAM1082  VANGL2   3'  TTGAAGAGAAGAAAAGAGA   43467          __
                                TTGAAGAGA  GAAAGAGA
                                |||||||||  ||||||||
                                AACTTCTCT  TTTTCTCT
                                     TC
GAM1082  WHSC1L1  3'  TTGAAGGGAAAGAGAA      35721        AGA
                                TTGAAG   GAAAGAGAA
                                ||||||   |||||||||
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                                AACTTC  CTTTCTCTT
                                   C__
GAM1082 YWHAH   3' TTGAAGAAAGAGGTGGGAG  18196        AA___
                                TTGAAGAGAGA   GAG
                                ||||||||||   |||
                                AACTTCTTTCT   CTC
                                     CCACC
GAM1083 MME     3' TATTTCTGTAACTTTTTTT  28603        AA
                                TATTTTTGTA ACTTTTTTT
                                |||||||||| |||||||||
                                ATAAAGACAT TGAAAAAAA
                                  __
GAM1083 MME     3' TATTTCTGTAACTTTTTTT  28603        AA
                                TATTTTTGTA ACTTTTTTT
                                |||||||||| |||||||||
                                ATAAAGACAT TGAAAAAAA
                                  __
GAM1083 MME     3' TATTTCTGTAACTTTTTTT  28614        AA
                                TATTTTTGTA ACTTTTTTT
                                |||||||||| |||||||||
                                ATAAAGACAT TGAAAAAAA
                                  __
GAM1083 MME     3' TATTTCTGTAACTTTTTTT  28603        AA
                                TATTTTTGTA ACTTTTTTT
                                |||||||||| |||||||||
                                ATAAAGACAT TGAAAAAAA
                                  __
GAM1083 BACE2   3' TTGAAGAGAGAAGAGAA    39998         A
                                TTGAAGAGAGAA GAGAA
                                |||||||||||| |||||
                                AACTTCTCTCTT CTCTT
                                  _
GAM1083 BACE2   3' TTGAAGAGAGAAGAGAA    39998         A
                                TTGAAGAGAGAA GAGAA
                                |||||||||||| |||||
                                AACTTCTCTCTT CTCTT
                                  _
GAM1083 BACE2   3' TTGAAGAGAGAAGAGAA    39998         A
                                TTGAAGAGAGAA GAGAA
                                |||||||||||| |||||
                                AACTTCTCTCTT CTCTT
                                  _
GAM1083 CDX1    3' TTGAAAAGAGAAGAAAA    12218         A
                                TTGAAGAGAGAA GAGAA
                                |||||||||||| |||||
                                AACTTTTCTCTT CTTTT
                                  _
GAM1083 CLN2    3' TTGAAAAGAGAAAGATGA   7561           _
                                TTGAAGAGAGAAAGA GA
                                |||||||||||||| ||
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                                AACTTTTCTCTTTCT CT
                                        A
GAM1083  COCH     3'  TTAAGGAGAGAAATAGAA    19863      A       G
                                TTGA GAGAGAAA AGAA
                                |||| |||||||| ||||
                                AATT CTCTCTTT TCTT
                                  C       A
GAM1083  D8S2298E  3'  TTGAAGAGGCAGAAAGGA    24976         __     A
                                TTGAAGAG  AGAAAG GA
                                ||||||||  |||||| ||
                                AACTTCTC  TCTTTC CT
                                     CG     _
GAM1083  DEFA5    3'  TTGGAGAGAGAAATTTAGAA   34245     A       G__
                                TTG AGAGAGAAA   AGAA
                                ||| |||||||||   ||||
                                AAC TCTCTCTTT   TCTT
                                  C        AAA
GAM1083  EMX2     5'  CTGAAGAGAGGGGGGAAA    44686          AAA_
                                TTGAAGAGAG    GAGA
                                ||||||||||    ||||
                                GACTTCTCTC    CTTT
                                      CCCC
GAM1083  FGF23    3'  TTAAAGAGAGGGAGGAA     33959          AA  A
                                TTGAAGAGAG  AG GAA
                                ||||||||||  || |||
                                AATTTCTCTC  TC CTT
                                      CC  _
GAM1083  GATA3    3'  TTGAGAGAGAAGGAAAA     13102      A      A
                                TTGA GAGAGAA GAGAA
                                |||| ||||||| |||||
                                AACT CTCTCTT CTTTT
                                  _      C
GAM1083  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37923           A_____
                                TTGAAGAGAGAA      GAGA
                                ||||||||||||      ||||
                                AACTTCTCTCTT      CTCT
                                      CACGAC
GAM1083  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922           A_____
                                TTGAAGAGAGAA      GAGA
                                ||||||||||||      ||||
                                AACTTCTCTCTT      CTCT
                                      CACGAC
GAM1083  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922           A_____
                                TTGAAGAGAGAA      GAGA
                                ||||||||||||      ||||
                                AACTTCTCTCTT      CTCT
                                      CACGAC
GAM1083  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922           A_____
                                TTGAAGAGAGAA      GAGA
                                ||||||||||||      ||||
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                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1083  HK1      3'  TTGAAGAGAGAAGTGCTGGAGA 37922           A_____
                                TTGAAGAGAGAA     GAGA
                                ||||||||||||     ||||
                                AACTTCTCTCTT     CTCT
                                      CACGAC
GAM1083  KCNA3    3'  AAGAGAGAGAGGGTAAA     13788        AA   AA
                                AAGAGAGA  GAG  TAAA
                                ||||||||  |||  ||||
                                TTCTCTCT  CTC  ATTT
                                    __   CC
GAM1083  MOG      3'  CTGGAGAGAGAAATGGAA    14610     A       GA
                                TTG AGAGAGAAA  GAA
                                ||| |||||||||  |||
                                GAC TCTCTCTTT  CTT
                                  C        AC
GAM1083  MTCP1    3'  CTGAAGAGTCAGGAGGATAAAA 30576        AGAAA   A
               A                 TTGAAGAG    GAG ATAAAAA
                                ||||||||    ||| |||||||
                                GACTTCTC    CTC TATTTTT
                                     AGTC_   C
GAM1083  NHLH1    3'  TTGAAGAAGGAGCAAGAA    24662        A  AA
                                TTGAAGAG GA  GAGAA
                                ||||||||  ||  |||||
                                AACTTCTT CT  TTCTT
                                     C  CG
GAM1083  OPCML    3'  TGAGTAGTAGGGAGAGAATA   14954     AG  _  AA
                                TGA  AG AG  AGAGAATA
                                |||  ||  ||  ||||||||
                                ACT  TC TC  TCTCTTAT
                                  CA  A  CC
GAM1083  PARK2    3'  TTGAAAAGAGAATTAGAA    30383          AG
                                TTGAAGAGAGAA  AGAA
                                ||||||||||||  ||||
                                AACTTTTCTCTT  TCTT
                                      AA
GAM1083  PARK2    3'  TTGAAAAGAGAATTAGAA    21280          AG
                                TTGAAGAGAGAA  AGAA
                                ||||||||||||  ||||
                                AACTTTTCTCTT  TCTT
                                      AA
GAM1083  PARK2    3'  TTGAAAAGAGAATTAGAA    21280          AG
                                TTGAAGAGAGAA  AGAA
                                ||||||||||||  ||||
                                AACTTTTCTCTT  TCTT
                                      AA
GAM1083  PCDH11X  3'  TTGCAGAGAGAAAATGTGAA  37321     A       A__
                                TTG AGAGAGAAAG   GAA
                                ||| ||||||||||   |||
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                                AAC TCTCTCTTTT  CTT
                                  G        ACA
GAM1083  PCDH11X  3'  TTGCAGAGAGAAAATGTGAA  37321    A       A__
                                TTG AGAGAGAAAG  GAA
                                ||| ||||||||||  |||
                                AAC TCTCTCTTTT  CTT
                                  G        ACA
GAM1083  PCDH11Y  3'  TTGCAGAGAGAAAATGTGAA  37366    A       A__
                                TTG AGAGAGAAAG  GAA
                                ||| ||||||||||  |||
                                AAC TCTCTCTTTT  CTT
                                  G        ACA
GAM1083  PFKFB2   3'  TTGAAGAGACAAAAGTGAA   26310        _    A
                                TTGAAGAGA GAAAG GAA
                                ||||||||| ||||| |||
                                AACTTCTCT TTTTC CTT
                                     G    A
GAM1083  PKD2L1   5'  TTGAAGAGGGGAGAGGGGAGAA 32024       ___   AA_
           TA                    TTGAAGA  GAGA  GAGAATA
                                |||||||  ||||  |||||||
                                AACTTCT  CTCT  CTCTTAT
                                   CCC   CCC
GAM1083  PPP1R12B 3'  CTGAAGAGGGTGATAGAAA   36971       A__  A
                                TTGAAGAG  GA AGAGA
                                ||||||||  || |||||
                                GACTTCTC  CT TCTTT
                                     CCA  A
GAM1083  PPP1R12B 3'  CTGAAGAGGGTGATAGAAA   36971       A__  A
                                TTGAAGAG  GA AGAGA
                                ||||||||  || |||||
                                GACTTCTC  CT TCTTT
                                     CCA  A
GAM1083  PPP1R12B 3'  CTGAAGAGGGTGATAGAAA   36971       A__  A
                                TTGAAGAG  GA AGAGA
                                ||||||||  || |||||
                                GACTTCTC  CT TCTTT
                                     CCA  A
GAM1083  PTPN13   3'  TTAAGGAGAGAAATGGAA    38782     A      GA
                                TTGA GAGAGAAA  GAA
                                |||| ||||||||  |||
                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1083  PTPN13   3'  TTAAGGAGAGAAATGGAA    38782     A      GA
                                TTGA GAGAGAAA  GAA
                                |||| ||||||||  |||
                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1083  PTPN13   3'  TTAAGGAGAGAAATGGAA    38784     A      GA
                                TTGA GAGAGAAA  GAA
                                |||| ||||||||  |||
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                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1083  RRAS2    3'  CTGAGGAGAGAAAGAGAA    29307      A
                                TTGA GAGAGAAAGAGAA
                                |||| ||||||||||||
                                GACT CTCTCTTTCTCTT
                                  C
GAM1083  S100A12  3'  TTGGTGAGGGAAAGAAAA    24738     AA  A
                                TTG  GAG GAAAGAGAA
                                |||  ||| |||||||||
                                AAC  CTC CTTTCTTTT
                                  CA   C
GAM1083  SCD      3'  GAAGAGAGAGAGGATAA     22828         AA  A
                                GAAGAGAGA  GAG ATAA
                                |||||||||  ||| ||||
                                CTTCTCTCT  CTC TATT
                                     __   C
GAM1083  SIM2     3'  TTGAAGAAAGGGTTAAATAAAA 22886          AAAGA
             A                   TTGAAGAGAG    GAATAAAAA
                                ||||||||||    |||||||||
                                AACTTCTTTC    TTTATTTTT
                                     CCAA_
GAM1083  SMARCD2  3'  TTGAGGAAAGAAAAGAA     16923      A      A
                                TTGA GAGAGAA GAGAA
                                |||| ||||||| |||||
                                AACT CTTTCTT TTCTT
                                  C      _
GAM1083  SPOCK    3'  TTCAAGAGAGAAAAAAAA    41745    G
                                TT AAGAGAGAAAGAGAA
                                || ||||||||||||||
                                AA TTCTCTCTTTTTTTT
                                  G
GAM1083  VANGL2   3'  TTGAAGAGAAGAAAAGAGA   43467         __
                                TTGAAGAGA  GAAAGAGA
                                |||||||||  ||||||||
                                AACTTCTCT  TTTTCTCT
                                     TC
GAM1083  WHSC1L1  3'  TTGAAGGGAAAGAGAA      35721       AGA
                                TTGAAG   GAAAGAGAA
                                ||||||   |||||||||
                                AACTTC   CTTTCTCTT
                                   C__
GAM1083  YWHAH    3'  TTGAAGAAAGAGGTGGGAG    18196          AA___
                                TTGAAGAGAGA    GAG
                                ||||||||||    |||
                                AACTTCTTTCT    CTC
                                     CCACC
GAM1084  AGPAT2   3'  TGAGACCAGTGACAGAA     26929        T   AG
                                TGAGACCA TGA  AGAG
                                |||||||| |||  ||||
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                                ACTCTGGT ACT  TCTT
                                    C  G_
GAM1084 APM1    3' GAGAGAGAGAGAGAG      22013     CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 ARHGEF6 3' GAGAGAGGGAGAGAGAGAGAG 42801     CCATT A    A
                                GAGA    GA GAGAGA AGAG
                                ||||    || |||||| ||||
                                CTCT    CT CTCTCT TCTC
                                  CTCC_ _    C
GAM1084 ARHGEF6 3' GAGAAAGAGAAGAGAGAGGGAG 42800     CCATT      AA
                                GAGA    GAAGAGAGA  GAG
                                ||||    |||||||||  |||
                                CTCT    CTTCTCTCT  CTC
                                  TTCT_       CC
GAM1084 ATP8A2  3' TGAGGCCTGGGAGAAAGA   45268     A AT  AAGA
                                TGAG CC  TG   GAGAAAGA
                                |||| ||  ||   ||||||||
                                ACTC GG  AC   CTCTTTCT
                                  C __  C___
GAM1084 BAI2    5' TGAGAGGGAGAGAAAG     11798     CCATTGAA
                                TGAGA      GAGAGAAAG
                                |||||      |||||||||
                                ACTCT      CTCTCTTTC
                                   CC_______
GAM1084 BSN     3' TGAGCCAAGAGAAGAGAGAAAG 18417     A  TT_
                                TGAG CCA   GAAGAGAGAAAG
                                |||| |||   ||||||||||||
                                ACTC GGT   CTTCTCTCTTTC
                                  _  TCT
GAM1084 CARKL   3' GAGAGAGAGAGAGAG      29993     CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 CDK5R2  3' GAGAGGAACAGGAGAGAGAG  19470     CCATTGA A   A
                                GAGA      AG GAGA AGAG
                                ||||      || |||| ||||
                                CTCT      TC CTCT TCTC
                                  CCTTG__ _   C
GAM1084 CDK5R2  3' GAGGAACAGGAGAGAGAGGGAG 19472     ACCATT A    AA
                                GAG     GA GAGAGA  GAG
                                |||     || ||||||  |||
                                CTC     CT CTCTCT  CTC
                                 CTTGTC _    CC
GAM1084 CENTD2  5' GAGAGAGAGAGAGAG      31594     CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
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                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 CHD2    5' GAGAGAGAGAGAGAG      10445    CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 CLCN3   3' GAGAGAGAGAGAGAG      12272    CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 DPYSL2  5' GAGAGAGAGAGAGAG      10750    CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 DPYSL2  5' GAGAGAGAGAGAGAGAAGGAG 10751    CCATT _    A
                                GAGA    GA AGAGAGAA GAG
                                ||||    || |||||||| |||
                                CTCT    CT TCTCTCTT CTC
                                  CT___ C      C
GAM1084 DXS1283E 3' GAGAGAGAGAGAGAG     43354    CCATT A    A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _    C
GAM1084 ENO2    3' TGAGGGAAGAGAGAAAGA   12717    ACCATT
                                TGAG    GAAGAGAGAAAGA
                                ||||    ||||||||||||
                                ACTC    CTTCTCTCTTTCT
                                  C_____
GAM1084 EYA3    3' GAGAGAGAAAGAGAGAAAGAG 12774    CCATT
                                GAGA    GAAGAGAGAAAGAG
                                ||||    ||||||||||||||
                                CTCT    TTTCTCTCTTTCTC
                                  CTC__
GAM1084 EYA3    3' GAGAGGGAGAGAGAGAAAGAG 12775    CCATT A
                                GAGA    GA GAGAGAAAGAG
                                ||||    || ||||||||||
                                CTCT    CT CTCTCTTTCTC
                                  CCCT_ _
GAM1084 FBXL11  3' GAGGCAAAAGAGAGA      29428    AC TT
                                GAG CA GAAGAGAGA
                                ||| || |||||||||
                                CTC GT TTTCTCTCT
                                  C_ __
GAM1084 FTSJ2   3' GAGAGAGAGAGAAAG      30168    CCATT A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
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                                CTCT    CT CTCTCTTTC
                                  _____ _
GAM1084  FTSJ2    3'  GAGAGAGAAAGAGAGAGAGAG  30167     CCATT       A
                                GAGA    GAAGAGAGA AGAG
                                ||||    ||||||||| ||||
                                CTCT    TTTCTCTCT TCTC
                                  CTC__       C
GAM1084  FVT1     3'  GAGAGAGAGAGAGAG      13030     CCATT  A     A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _     C
GAM1084  GAC1     3'  TGAGACTGTACAGAGAAAGAG  26796      CAT  AAG
                                TGAGAC   TG   AGAGAAAGAG
                                ||||||   ||   ||||||||||
                                ACTCTG   AC   TCTCTTTCTC
                                   ___ ATG
GAM1084  GLUD1    3'  TGAGTCAGGAGAGAAAG     23591      AC  TTGAA
                                TGAG  CA    GAGAGAAAG
                                ||||  ||    |||||||||
                                ACTC  GT    CTCTCTTTC
                                  A_  C____
GAM1084  HCN4     3'  TGAGACCAGAGATGGGGAGAGA 24232        TT  A___
                                TGAGACCA  GA    GAGAGA
                                ||||||||  ||    ||||||
                                ACTCTGGT  CT    CTCTCT
                                     CT  ACCC
GAM1084  HMGA2    3'  GAGAGAGGGAGAGGGAGAG   18515     CCATT  A_    AA
                                GAGA    GA  GAGAG  AGAG
                                ||||    ||  |||||  ||||
                                CTCT    CT  CTCTC  TCTC
                                  _____  CC    CC
GAM1084  HMGA2    5'  GAGAGAGAGAGAGAG       18514     CCATT  A     A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _     C
GAM1084  HMGA2    3'  GAGAGGGAGAGAGAGAGAG   18516     CCATT  A     A
                                GAGA    GA GAGAGA AGAG
                                ||||    || |||||| ||||
                                CTCT    CT CTCTCT TCTC
                                  CC___ _     C
GAM1084  IGF1R    3'  GAGAGGAGAGAGAAAG      9328      CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
                                CTCT    CT CTCTCTTTC
                                  C____ _
GAM1084  KIF3B    3'  GAGAGAGGAGAGAAAG      22036     CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
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                                CTCT    CT CTCTCTTTC
                                  _____ C
GAM1084 LPL     3' TGAGACAAAAAAGAAGGGGGAG 6944       CATT__ ____
            AGA                   TGAGAC    GAA   GAGAGA
                                  ||||||    |||   ||||||
                                  ACTCTG    CTT   CTCTCT
                                    TTTTTT  CCCC
GAM1084 LPXN    3' GAAGAGAGGGAGAAAGAG   22068       ____
                                  GAAGAGA   GAAAGAG
                                  |||||||   |||||||
                                  CTTCTCT   CTTTCTC
                                     CCCT
GAM1084 MEIS1   3' GAGGAAAAGAGAGAGAAAGAG 14416    ACCATT A
                                  GAG     GA GAGAGAAAGAG
                                  |||     || ||||||||||
                                  CTC     CT CTCTCTTTCTC
                                    CTTTT_ _
GAM1084 NFIA    5' GAGAGAGGAAGAGAGAGAGAG 43211     CCATT       A
                                  GAGA    GAAGAGAGA AGAG
                                  ||||    ||||||||| ||||
                                  CTCT    CTTCTCTCT TCTC
                                    CTC__       C
GAM1084 NFIA    5' GAGAGGAGAAAGAGGGAGAGAG 43212     CCATT    A A
                                  GAGA    GAAGAG GA AGAG
                                  ||||    |||||| || ||||
                                  CTCT    TTTCTC CT TCTC
                                    CCTC_     C C
GAM1084 NFIA    5' GAGAGAGAGAGAGAG      43209     CCATT A    A
                                  GAGA    GA GAGAGA AG
                                  ||||    || |||||| ||
                                  CTCT    CT CTCTCT TC
                                    _____ _     C
GAM1084 NFIA    5' GAGAGAGAGAGAGAGAA    43210     CCATT _
                                  GAGA    GA AGAGAGAA
                                  ||||    || ||||||||
                                  CTCT    CT TCTCTCTT
                                    CT___ C
GAM1084 NPR1    5' GAGAGAGAGAGAGAGAAAG  44581     CCATT _
                                  GAGA    GA AGAGAGAAAG
                                  ||||    || ||||||||||
                                  CTCT    CT TCTCTCTTTC
                                    CT___ C
GAM1084 NPR1    5' GAGAGAGAGAGAGAG      44580     CCATT A    A
                                  GAGA    GA GAGAGA AG
                                  ||||    || |||||| ||
                                  CTCT    CT CTCTCT TC
                                    _____ _     C
GAM1084 NTRK2   3' GAGATGGAAAGAGAGAAAGAG 26147     CCATT
                                  GAGA    GAAGAGAGAAAGAG
                                  ||||    ||||||||||||||
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                                CTCT    TTTCTCTCTTTCTC
                                  ACC__
GAM1084  PAX5     3'  GAGGAAGAGAGGAAGA      32508     ACCATT       A
                                GAG     GAAGAGAG AAGA
                                |||     |||||||| ||||
                                CTC     CTTCTCTC TTCT
                                  _______       C
GAM1084  PCDHA1   3'  GAGAGAGAGAGAGAGAAAGAG  36397      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA1   3'  AGAAAAGAGAGAGAGA      36394     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  ______       C
GAM1084  PCDHA10  3'  GAGAGAGAGAGAGAGAAAGAG  36564      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA10  3'  AGAAAAGAGAGAGAGA      36562     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  ______       C
GAM1084  PCDHA11  3'  AGAAAAGAGAGAGAGA      36572     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  ______       C
GAM1084  PCDHA11  3'  GAGAGAGAGAGAGAGAAAGAG  36576      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA12  3'  AGAAAAGAGAGAGAGA      36593     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                  ______       C
GAM1084  PCDHA12  3'  GAGAGAGAGAGAGAGAAAGAG  36596      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA13  3'  GAGAGAGAGAGAGAGAAAGAG  36604      CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA13  3'  AGAAAAGAGAGAGAGA     36601    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA2   3'  AGAAAAGAGAGAGAGA     36464    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA2   3'  GAGAGAGAGAGAGAGAAAGAG  36468     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA3   3'  AGAAAAGAGAGAGAGA     36473    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA3   3'  GAGAGAGAGAGAGAGAAAGAG  36475     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA4   3'  AGAAAAGAGAGAGAGA     36486    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA4   3'  GAGAGAGAGAGAGAGAAAGAG  33144     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA5   3'  GAGAGAGAGAGAGAGAAAGAG  36497     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA5   3'  AGAAAAGAGAGAGAGA     36495    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA6   3'  GAGAGAGAGAGAGAGAAAGAG  36511     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA6   3'  AGAAAAGAGAGAGAGA     36508    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA7   3'  GAGAGAGAGAGAGAGAAAGAG  36519     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA7   3'  AGAAAAGAGAGAGAGA     36516    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA8   3'  GAGAGAGAGAGAGAGAAAGAG  33148     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHA8   3'  AGAAAAGAGAGAGAGA     36526    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA9   3'  AGAAAAGAGAGAGAGA     36536    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHA9   3'  GAGAGAGAGAGAGAGAAAGAG  36546     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHAC1  3'  AGAAAAGAGAGAGAGA     36616    CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCDHAC1  3'  GAGAGAGAGAGAGAGAAAGAG  36619     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHAC2  3'  GAGAGAGAGAGAGAGAAAGAG  36630     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  PCDHAC2  3'  AGAAAAGAGAGAGAGA     36627     CCATT       A
                                AGA    GAAGAGAGA AGA
                                |||    ||||||||| |||
                                TCT    TTTCTCTCT TCT
                                 _____       C
GAM1084  PCTK1    3'  CGGGACTGCAGGAGAGAAAGAG 37470    A   CAT  AA_
                                TG GAC   TG   GAGAGAAAGAG
                                || |||   ||   ||||||||||
                                GC CTG   AC   CTCTCTTTCTC
                                 C   ___  GTC
GAM1084  PPARGC1  3'  GAGAGAGAGAGAGAG      29954     CCATT  A     A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _     C
GAM1084  PPOX     5'  TGAGAGAAAATGAGGGAGAAGG 7183       CCAT_   A A    A
             AG                   TGAGA    TGA G GAGAA GAG
                                |||||    ||| | ||||| |||
                                ACTCT    ACT C CTCTT CTC
                                   CTTTT   _ C    C
GAM1084  PPT2     3'  TGAAAATAAAGAGAGAGAGAG  39928      CCAT        A
                                TGAGA    TGAAGAGAGA AGAG
                                |||||    |||||||||| ||||
                                ACTTT    ATTTCTCTCT TCTC
                                   T___         C
GAM1084  PRELP    3'  GAGAAAGAAGGGGAGAGAGAG  15549     CCATT    A_    A
                                GAGA    GAAG  GAGA AGAG
                                ||||    ||||  |||| ||||
                                CTCT    CTTC  CTCT TCTC
                                  TT___    CC    C
GAM1084  PTK2B    3'  TGAGGGCCGAAGAGGAA     19926     A_  ATT     A
                                TGAG  CC   GAAGAG GAA
                                ||||  ||   |||||| |||
                                ACTC  GG   CTTCTC CTT
                                  CC  ___     _
GAM1084  RUNX3    3'  TGAGACCACCTAGGGGAAAG   20327          GA  AGA
                                TGAGACCATT  AG   GAAAG
                                ||||||||||  ||   |||||
                                ACTCTGGTGG  TC   CTTTC
                                      A_  CC_
GAM1084  SH3BP5   3'  TGAGGGTGAGAAGAGAAAGAG  22127     ACCAT   AG
                                TGAG    TGA  AGAGAAAGAG
                                ||||    |||  ||||||||||
                                ACTC    ACT  TCTCTTTCTC
                                  CC___   CT
GAM1084  SIX2     3'  GAGAAGGAGAGAGAAAG     32605      CCATT  A
                                GAGA    GA GAGAGAAAG
                                ||||    || |||||||||
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                                CTCT    CT CTCTCTTTC
                                  TC___ _
GAM1084 SLC18A3  3' TGGACAAGAGAGAAAG     16837    A  CATTG
                                TG GAC    AAGAGAGAAAG
                                || |||    ||||||||||
                                AC CTG    TTCTCTCTTTC
                                 _  _____
GAM1084 SLC7A6   3' TGAAACCACAAGGGAGGGGGAG 19597         TG  A  AAA
                                TGAGACCAT  AAG GAG  GAG
                                |||||||||  ||| |||  |||
                                ACTTTGGTG  TTC CTC  CTC
                                     __  C  CCC
GAM1084 SPTA1    5' GAGAGAGAGAGAGAG       17097     CCATT  A     A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____ _     C
GAM1084 TBL1X    3' GAGAGAGAGAGAGAAAGAG   24882     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
                                CTCT    CT TCTCTCTTTCTC
                                  _____ C
GAM1084 TCN1     3' GAACATGTAGAGAGAGAAG   9863    C  T A     _
                                GA CAT G AGAGAGA AAG
                                || ||| | ||||||| |||
                                CT GTA C TCTCTCT TTC
                                 T  _ A     C
GAM1084 TGFBR2   3' TGAGACTTTTGATATAAAAAGA 17486       CA   AGAG
            G                    TGAGAC  TTGA   AGAAAGAG
                                ||||||  ||||   ||||||||
                                ACTCTG  AACT   TTTTTCTC
                                   AA   ATA_
GAM1084 TNFRSF14 5' CCAGAAGAGAAAGAG      19232    TTGAA
                                CCA    GAGAGAAAGAG
                                |||    ||||||||||
                                GGT    TTCTCTTTCTC
                                  C____
GAM1084 TNFSF5   3' GAGGTTGAGAGAGAGA     6326     ACCA   _
                                GAG   TTGA AGAGAGA
                                |||   |||| |||||||
                                CTC   AACT TCTCTCT
                                  C___   C
GAM1084 TNFSF5   3' GAGATGGAGAGAGAGAG    6324     CCAT  A     A
                                GAGA   TG AGAGAGA AG
                                ||||   || ||||||| ||
                                CTCT   AC TCTCTCT TC
                                  ____ C     C
GAM1084 TRPS1    5' GAGAGAGAGAGAGAGAAAGAG 30464     CCATT  _
                                GAGA    GA AGAGAGAAAGAG
                                ||||    || ||||||||||||
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                                CTCT    CT TCTCTCTTTCTC
                                  CT___  C
GAM1084  TRPS1    5'  GAGAGAGAGAGAGAG      30463     CCATT  A     A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____  _     C
GAM1084  TRPV1    5'  GAGAGAGAGAGAGAG      38795     CCATT  A     A
                                GAGA    GA GAGAGA AG
                                ||||    || |||||| ||
                                CTCT    CT CTCTCT TC
                                  _____  _     C
GAM1084  DUOX2    3'  TAAAATATTTTACAGCTC    30448            A
                                TAAAATATTTTACG CTC
                                |||||||||||||| |||
                                ATTTTATAAAATGT GAG
                                        C
GAM1085  CA3      3'  TGTGAAATTTTAGATAACAGAA 23222           TACCAA
            AA                    TGTGAAATTTTG     AGAAAA
                                ||||||||||||     ||||||
                                ACACTTTAAAAT     TCTTTT
                                      CTATTG
GAM1085  FZD1     3'  TGTGGAGTTCTGTACCTTAAGA 18620      AAA       A_
                                TGTG   TTTTGTACC  AAGA
                                ||||   |||||||||  ||||
                                ACAC   AAGACATGG  TTCT
                                  CTC        AA
GAM1085  IGFBP4   3'  TGTGTAACACCAAAGA      11411     A   TTTGT
                                TGTG AAT    ACCAAAGA
                                |||| |||    ||||||||
                                ACAC TTG    TGGTTTCT
                                  A  _____
GAM1085  MTMR7    3'  TGTGAAATATTTGTATTGCACT 42906        _     C__  AA
            GAA                    TGTGAAAT TTTGTA   CA  GAA
                                |||||||| ||||||   ||  |||
                                ACACTTTA AAACAT   GT  CTT
                                     T     AAC  GA
GAM1085  NPPB     3'  TGGAAATTTTGTGCTCAAAG   14827    T       AC_
                                TG GAAATTTTGT   CAAAG
                                || ||||||||||   |||||
                                AC CTTTAAAACA   GTTTC
                                  _        CGA
GAM1085  PODXL    3'  TGGAAATGGAAGCCCAAAGAA  23985    T    TTTGTA
                                TG GAAAT     CCAAAGAA
                                || |||||     ||||||||
                                AC CTTTA     GGTTTCTT
                                  _    CCTTCG
GAM1085  PRKAR1A  3'  TGTGAAATTTTGTTTAAAAAA  15616           ACC
                                TGTGAAATTTTGT   AAAGAA
                                ||||||||||||   ||||||
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                                ACACTTTAAAACA  TTTTTT
                                      AA_
GAM1085  RPL30    3'  GTGAAATTTTGTAGGTGAAAA  9741          CCAAA
                                GTGAAATTTTGTA    GAAAA
                                |||||||||||||    |||||
                                CACTTTAAAACAT    CTTTT
                                      CCA__
GAM1085  TAPBP    3'  TGTGAGATTTTATAACAAAA  17309      A       C
                                TGTGA ATTTTGTA CAAAG
                                ||||| |||||||| |||||
                                ACACT TAAAATAT GTTTT
                                   C       T
GAM1085  TGM4     3'  GTGGATGGAATACCAAAGAAA  17465    AAATTTT
                                GTG      GTACCAAAGAAA
                                |||      ||||||||||||
                                CAC      TATGGTTTCTTT
                                  CTACCT_
GAM1085  TNFSF15  3'  TGTGAAATTTTGGCCCCAAA  23054         TA_
                                TGTGAAATTTTG  CCAAA
                                ||||||||||||  |||||
                                ACACTTTAAAAC  GGTTT
                                      CGG
GAM1085  TP53BP2  3'  TGTGAAATTTTTGCCAAAA  24065         GTA
                                TGTGAAATTTT  CCAAAG
                                ||||||||||  ||||||
                                ACACTTTAAAA  GGTTTT
                                      AC_
GAM1085  TRPM8    3'  TGTAAAATTTTGAAAGA    35864          TACC
                                TGTGAAATTTTG   AAAGA
                                ||||||||||||   |||||
                                ACATTTTAAAAC   TTTCT
                                      _____
GAM1085  WNT11    3'  TGAGAAGTGCCACCCCAAAGAA 21543    T  ATT TG A
            AA                    TG GAA  T  T CCAAAGAAAA
                                || |||  |  | ||||||||||
                                AC CTT  G  G GGTTTCTTTT
                                 T  CAC GT G
GAM1085  FANCF    3'  TCAATGCTTTAAAGGGAC    35536          ATATAT
                                TCAATGTTTTAAA    GGAC
                                ||||||||||||     ||||
                                AGTTACGAAATTT    CCTG
                                      C_____
GAM1085  GPR65    5'  TCAATGCTTTTAAAGGGTGGA  40736        A  TATA
                                TCAATGTTTT AAA   TGGA
                                |||||||||| |||   ||||
                                AGTTACGAAA TTT   ACCT
                                      A  CCC_
GAM1085  LMNB1    3'  TGCAACAAAGTGTATGGACA  24534    TT   ATA
                                TGT  TAAA  TATGGACA
                                |||  ||||  ||||||||
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                                ACG  GTTT   ATACCTGT
                                  TT    CAC
GAM1085  MEN1     5'  AATGTTTTAAAATATTATG   39141              _
                                AATGTTTTAAAATAT ATG
                                ||||||||||||||| |||
                                TTACAAAATTTTATA TAC
                                        A
GAM1085  PLAG1    3'  AATATTTTAAATCTGGTATATG 15342           A____
              GACA                  AATGTTTTAAA    TATATGGACA
                                ||||||||||    ||||||||||
                                TTATAAAATTT    ATATACCTGT
                                      AGACC
GAM1085  S100A11  3'  TCATGTTTTAAAAAAGTGACA  24734     A        TATATG
                                TCA TGTTTTAAAA     GACA
                                ||| ||||||||||     ||||
                                AGT ACAAAATTTT     CTGT
                                  _        TTCA__
GAM1085  SLC9A6   3'  TCAATGTTCTAACTGGA     26832           AATATA
                                TCAATGTTTTAA     TGGA
                                ||||||||||||     ||||
                                AGTTACAAGATT     ACCT
                                       G_____
GAM1085  SOD2     3'  CAAGTCCCCAAAGTATATGGA  8465      T   TA  _
                                CAA GTTT  AAA TATATGGA
                                ||| ||||  ||| ||||||||
                                GTT CAGG  TTT ATATACCT
                                  _   GG   C
GAM1086  ACVRL1   5'  ACGGCGGGCTGGGGTCCGGCGC 6161      A   AC  GC____
              GG                    ACG GCG  GC     CCGGCGCGG
                                ||| |||  ||     |||||||||
                                TGC CGC  CG     GGCCGCGCC
                                  _  C_  ACCCCA
GAM1086  ARNTL    5'  CGGCGGCGGTGAGTCCGGCGCG 10136    A  A   ACGCGC
              G                     CG CG GCG     CCGGCGCGG
                                || || |||     |||||||||
                                GC GC CGC     GGCCGCGCC
                                 C  _   CACTCA
GAM1086  ATP11A   3'  CGGCGGGCGGAGCTGCAGTGCG 44174    A  A   AC  GCC   C
              G                     CG CG GCG  GC   CGG GCGG
                                || || |||  ||   ||| ||||
                                GC GC CGC  CG   GTC CGCC
                                 C  C   CT  AC_   A
GAM1086  BACE     5'  CGGCGGGCGGCGGCGCG     39958    A   AC   CC
                                CG GCG  GCG  CGGCGCG
                                || |||  |||  |||||||
                                GC CGC  CGC  GCCGCGC
                                  _  C_   C_
GAM1086  BSG      3'  CGGCGGCGGCGCAGACGG    42693    A  A   AC    CC    C
                                CG CG GCG  GCGC  GGCG G
                                || || |||  ||||  |||| |
```

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                                GC GC CGC  CGCG  CTGC C
                                 C  _  __   T_   A
GAM1086 BSG     3' CGGCGGCGGCGCAGACGCG   42692   A A  AC   CC
                                CG CG GCG  GCGC  GGCGCG
                                || || |||  ||||  ||||||
                                GC GC CGC  CGCG  CTGCGC
                                 C  _  __   T_
GAM1086 DSCAM   5' CGCGAGCGACGCGCCGG    10799   A         C
                                CG CGAGCGACGCGCC GG
                                || ||||||||||||| ||
                                GC GCTCGCTGCGCGG CC
                                 _         _
GAM1086 DVL3    5' CGGCGGCGGCGCGCGGCGCGG 20678   A A  A    CC
                                CG CG GCG CGCGC  GGCGCGG
                                || || ||| |||||  |||||||
                                GC GC CGC GCGCG  CCGCGCC
                                 C  _  C    __
GAM1086 E2F1    5' GACAGGCGGCGGCGGCGGCGCG 44487     A  A C  C_
             G                   GACG GCG CG GC  CGGCGCGG
                                |||| ||| || ||  ||||||||
                                CTGT CGC GC CG  GCCGCGCC
                                  C  C  _ CC
GAM1086 ELK4    5' GAGCGACGCCGCGCGCGG    12703         _ CCG
                                GAGCGACGC GC   GCGCGG
                                |||||||| ||   ||||||
                                CTCGCTGCG CG   CGCGCC
                                     G ___
GAM1086 EN2     5' CGCCGGCCGCGCTCGGCGCGG  10943   A A GA   C
                                CG CG GC  CGCGC CGGCGCGG
                                || || ||  ||||| ||||||||
                                GC GC CG  GCGCG GCCGCGCC
                                 G  _ __    A
GAM1086 FKBP1A  5' CGGGCGGCGCGACGGGCGG   38277   A  A   CC  C
                                CG GCG CGCG  CGG GCGG
                                || ||| ||||  ||| ||||
                                GC CGC GCGC  GCC CGCC
                                 C  C   T_  _
GAM1086 FOXG1B  5' CGGCGGCGGCGCGGGAGCG   23502   A A  A   CCC  C
                                CG CG GCG CGCG   GG GCG
                                || || ||| ||||   || |||
                                GC GC CGC GCGC   CC CGC
                                 C  _  C   ___  T
GAM1086 FOXG1B  5' CGGCGCGCGGGCGGCGCG    23501   A  A   CC
                                CG GCG CGCG  CGGCGCG
                                || ||| ||||  |||||||
                                GC CGC GCGC  GCCGCGC
                                 _  _   CC
GAM1086 FOXG1B  5' CGGCGGCGGCGGCGC      23503   A  AC  CC
                                CG GCG  GCG  CGGCGC
                                || |||  |||  ||||||
```

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                                GC CGC  CGC  GCCGCG
                                 _  __   C_
GAM1086  GNB2     5'  CGGCGGCGGCGGCGGCGGCGCG 23598    A  A   A  C  C_
                G                 CG CG GCG CG GC  CGGCGCGG
                                  || || ||| || ||  ||||||||
                                  GC GC CGC GC CG  GCCGCGCC
                                   C  _   C  _  CC
GAM1086  GPC1     5'  CGGCGGCGGCGCGGGGCGCG   13240    A  A   A   CCC
                                  CG CG GCG CGCG   GGCGCG
                                  || || ||| ||||   ||||||
                                  GC GC CGC GCGC   CCGCGC
                                   C  _   C   C__
GAM1086  GPC1     5'  CGGCGGCGGCGGCGGCGCG   13242    A   A  C  C_
                                  CG GCG CG GC  CGGCGCG
                                  || ||| || ||  |||||||
                                  GC CGC GC CG  GCCGCGC
                                   _  C  _  CC
GAM1086  HDAC4    5'  CGGCGGCGGCGGCGGCGCG   25758    A   A  C  C_
                                  CG GCG CG GC  CGGCGCG
                                  || ||| || ||  |||||||
                                  GC CGC GC CG  GCCGCGC
                                   _  C  _  CC
GAM1086  HDAC4    5'  CGGCGGCGGCGCGGGC     25757    A   A  C  C   C
                                  CG GCG CG GC CGG GC
                                  || ||| || || ||| ||
                                  GC CGC GC CG GCC CG
                                   _  C  _  C  _
GAM1086  HK2      5'  CGGCGAGGGTGCGCCCGGCTGG 6787     A   C___       GC
                                  CG GCGA   GCGCCCGGC  GG
                                  || ||||   |||||||||  ||
                                  GC CGCT   CGCGGGCCG  CC
                                   _   CCCA       A_
GAM1086  IGFBP2   5'  CGGCAGCGCGGCGCGG     8256     A  AC   CC
                                  CG GCG  GCGC  GGCGCGG
                                  || |||  ||||  |||||||
                                  GC CGT  CGCG  CCGCGCC
                                   _  __   __
GAM1086  IRS2     5'  GAGGATGCCCGGCGC      40704     C  CGC
                                  GAG GA   GCCCGGCGC
                                  ||| ||   |||||||||
                                  CTC CT   CGGGCCGCG
                                    _ A__
GAM1086  ISL1     5'  CGGCGGCGGCAGACTCGGCGCG 13594    A  A   A  C  C
                G                 CG CG GCG CG GC CGGCGCGG
                                  || || ||| || || ||||||||
                                  GC GC CGC GT TG GCCGCGCC
                                   C  _   C  C  A
GAM1086  JAG2     5'  CGGCGGCGGCGCGGGC     13715    A   A  C  C   C
                                  CG GCG CG GC CGG GC
                                  || ||| || || ||| ||
```

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                                GC CGC GC CG GCC CG
                                 _  C  _  C  _
GAM1086 JAG2    5' CGGCGGCGGCGGCGGCGCG  13716   A  A  C  C_
                                CG GCG CG GC  CGGCGCG
                                || ||| || ||  |||||||
                                GC CGC GC CG  GCCGCGC
                                 _  C  _  CC
GAM1086 KCNN2   5' CGACAGCGGCGAGGAGGTGCGG 34666     G   AC   CCC_ C
                                CGAC AGCG  GCG   GG GCGG
                                |||| ||||  |||   || ||||
                                GCTG TCGC  CGC   CC CGCC
                                  _   __  TCCT  A
GAM1086 KLF4    5' CGGCGGCGCAGGGCGCGG   20153   A  AC   CC
                                CG GCG  GCGC  GGCGCGG
                                || |||  ||||  |||||||
                                GC CGC  CGCG  CCGCGCC
                                 _  __   TC
GAM1086 MSI1    5' CGCGGGCGGCGCGGGCAGCGG  14639   A  A   A   CCC  _
                                CG CG GCG CGCG   GGC GCGG
                                || || ||| ||||   ||| ||||
                                GC GC CGC GCGC   CCG CGCC
                                 _ C  C   ___  T
GAM1086 NR2C2   5' CGGCGGGCGGCCCCCGGCGCGG 17669   A  A   AC  G
                                CG CG GCG  GC CCCGGCGCGG
                                || || |||  || ||||||||||
                                GC GC CGC  CG GGGCCGCGCC
                                 C  C  __  G
GAM1086 PK428   5' CGGCGGCGGCGCGGGC     18801   A  A  C  C  C
                                CG GCG CG GC CGG GC
                                || ||| || || ||| ||
                                GC CGC GC CG GCC CG
                                 _  C  _  C  _
GAM1086 PRKY    5' GCGGCGCGGCAGCCGCGG   15699    A   CC   _
                                GCG CGCG  CGGC GCGG
                                ||| ||||  |||| ||||
                                CGC GCGC  GTCG CGCC
                                  C   C_   G
GAM1086 PSD     3' CGGACACCGCGTCCGGCGCGG  15784   AG  A   C
                                CG  CG CGCG CCGGCGCGG
                                ||  || |||| |||||||||
                                GC  GT GCGC GGCCGCGCC
                                 CT  G   A
GAM1086 PTGS2   5' CGGCGGGCAGGGCGCGGCGCGG 9686    A  A  AC   CC
                                CG CG GCG  GCGC  GGCGCGG
                                || || |||  ||||  |||||||
                                GC GC CGT  CGCG  CCGCGCC
                                 C  C  CC   __
GAM1086 RNTRE   5' CGGCCGAGCAGATCCGGCGCGG 31253   A_    ACGCGC
                                CG  CGAGCG    CCGGCGCGG
                                ||  ||||||    |||||||||
```

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                                GC  GCTCGT    GGCCGCGCC
                                 CG    CTA___
GAM1086  RPL36A   5'  GCGTGAGCGCTATCGGCGCGG 34292    AC_   C__
                                GCG   GCGC   CGGCGCGG
                                |||   ||||   ||||||||
                                CGC   CGCG   GCCGCGCC
                                  ACT   ATA
GAM1086  SNX9     5'  CGGCTGGGCCCCGGCGCG    32151    A  GAC  G
                                CG GC   GC CCCGGCGCG
                                || ||   || |||||||||
                                GC CG   CG GGGCCGCGC
                                 _ ACC  _
GAM1086  SRM      5'  CGGGCGGGCGGGCGGCGCGG   17114    A   AC   CC
                                CG GCG  GCG  CGGCGCGG
                                || |||  |||  ||||||||
                                GC CGC  CGC  GCCGCGCC
                                 C   C_   CC
GAM1086  SRM      5'  CGGGCGGCGCGGGGCGCGG   17113    A   A    CCC
                                CG GCG CGCG   GGCGCGG
                                || ||| ||||   |||||||
                                GC CGC GCGC   CCGCGCC
                                 C   C    C__
GAM1086  TMEPAI   5'  CGGCGCGGCGGCGCGGCGCGG  33604    A_   A  C  C
                                CG  GCG CG GC CGGCGCGG
                                ||  ||| || || ||||||||
                                GC  CGC GC CG GCCGCGCC
                                 CG   C  _  C
GAM1086  TMEPAI   5'  CGGCGGCGCGGCGCGGGGCGCG 33605    A  A   AC    CC
            G                    CG CG GCG  GCGC  GGCGCGG
                                || || |||  ||||  |||||||
                                GC GC CGC  CGCG  CCGCGCC
                                 C  _   GC    CC
GAM1086  TOP1     5'  CGGCAGGCGAGGCGGCGG    17625    A   AC   CC_    C
                                CG GCG  GCG   CGGCG G
                                || |||  |||   ||||| |
                                GC CGT  CGC   GCCGC C
                                 _   C_   TCC    A
GAM1086  TSLP     5'  CGAGCGACGCGCAGCCGGCG  39694          __
                                CGAGCGACGCGC  CCGGCG
                                ||||||||||||  ||||||
                                GCTCGCTGCGCG  GGCCGC
                                       TC
GAM1086  USP13    5'  CGGCGGCGGCGGCGC      19481    A   AC   CC
                                CG GCG  GCG  CGGCGC
                                || |||  |||  ||||||
                                GC CGC  CGC  GCCGCG
                                 _   __   C_
GAM1086  WEE1     5'  GCGGCAGCGGCGGCGCGG    18098    A _   CC
                                GCG C GCG  CGGCGCGG
                                ||| | |||  ||||||||
```

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                                CGC G CGC  GCCGCGCC
                                  C T   C_
GAM1086  ZNF219   5'  CGGCGGGCCGGCGGCGCG    32323    A   ACGC   __
                                CG GCG    GCC  CGGCGCG
                                || |||    |||  |||||||
                                GC CGC    CGG  GCCGCGC
                                 _   C___   CC
GAM1086  BMP1     3'  TGCTGCTCTCACTGTGCCCGTC 25999      C      C__
            G                    TGCT TTCTCGC   GCCCGTCG
                                |||| |||||||   ||||||||
                                ACGA GAGAGTG   CGGGCAGC
                                  C      ACA
GAM1086  CDC2L2   5'  CCTGTTCTTCTCGATGTC    37937      C       CCGCCC
                                CCTG TCTTCTCG      GTC
                                |||| ||||||||      |||
                                GGAC AGAAGAGC      CAG
                                  A       TA____
GAM1086  POLK     5'  CCTGCTTTTCTACCCGTC    32136       C    CGCC
                                CCTGCT TTCT    GCCCGTC
                                |||||| ||||    |||||||
                                GGACGA AAGA    TGGGCAG
                                   A   _____
GAM1086  SIRT7    5'  ACCTGCTCTTCCGCTTCCG    32415          T   CGC
                                ACCTGCTCTTC CGC   CCG
                                |||||||||||| |||   |||
                                TGGACGAGAAG GCG   GGC
                                      _   AA_
GAM1087  BACE2    3'  TTGAAGAGAGAAGAGAAC    39999           A
                                TTGAAGAGAGAA GAGAAT
                                |||||||||||| ||||||
                                AACTTCTCTCTT CTCTTG
                                      _
GAM1087  BNC      3'  TTGAAGAAGGAACTGAAAAT   11858         A   A_
                                TTGAAGAG GAA  GAGAAT
                                |||||||| |||  ||||||
                                AACTTCTT CTT  CTTTTA
                                     C   GA
GAM1087  CASP2    3'  TTGAAGAGGGTGACTAGAG   37405         A__  A_
                                TTGAAGAG   GA  AGAG
                                |||||||   ||  ||||
                                AACTTCTC   CT  TCTC
                                     CCA  GA
GAM1087  CDX1     3'  TTGAAAAGAGAAGAAAA     12218           A
                                TTGAAGAGAGAA GAGAA
                                |||||||||||| |||||
                                AACTTTTCTCTT CTTTT
                                      _
GAM1087  CLN2     3'  TTGAAAAGAGAAAGATGA    7561             _
                                TTGAAGAGAGAAAGA GA
                                |||||||||||||| ||
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                                AACTTTTCTCTTTCT CT
                                        A
GAM1087  EMX2     5'  CTGAAGAGAGGGGGGAAAAT   44687          AAA_
                                TTGAAGAGAG    GAGAAT
                                ||||||||||    ||||||
                                GACTTCTCTC    CTTTTA
                                      CCCC
GAM1087  ENAM     3'  TTGAAGGGAAGAAAGGAAT    36680       A_      A
                                TTGAAG  GAGAAAG GAAT
                                ||||||  ||||||| ||||
                                AACTTC  TTCTTTC CTTA
                                   CC      _
GAM1087  FGF23    3'  TTAAAGAGAGGGAGGAA      33959          AA  A
                                TTGAAGAGAG  AG GAA
                                ||||||||||  || |||
                                AATTTCTCTC  TC CTT
                                      CC  _
GAM1087  GATA3    3'  TTGAGAGAGAAGGAAAAT     13103      A      A
                                TTGA GAGAGAA GAGAAT
                                ||||| ||||||| ||||||
                                AACT CTCTCTT CTTTTA
                                  _      C
GAM1087  GPRC5B   3'  TTGAAATGAATAAGGGAATAAA 32181        A   A   A
            AT                    TTGAAG GAG AAG GAATAAAAT
                                ||||||| ||| ||| |||||||||
                                AACTTT CTT TTC CTTATTTTA
                                   A   A   C
GAM1087  GRIN2A   3'  TTGAGGAGAATAAGAAT     9116       A A    A
                                TTGA G GAGAA GAGAAT
                                ||||| | ||||| ||||||
                                AACT C CTCTT TTCTTA
                                  _ _    A
GAM1087  NR2F6    3'  CTGAGGAGAGAAGCCAGAG    23449      A     ___
                                TTGA GAGAGAA   AGAG
                                |||| |||||||   ||||
                                GACT CTCTCTT   TCTC
                                  C      CGG
GAM1087  PKD2L1   5'  TTGAAGAGGGGAGAGGGGAGAA 32023        ___   AA_
            T                    TTGAAGA   GAGA   GAGAAT
                                |||||||   ||||   ||||||
                                AACTTCT   CTCT   CTCTTA
                                    CCC    CCC
GAM1087  PRPSAP2  3'  TTCAAAAGAGGAGAATAAA   15740    G      AAA
                                TT AAGAGAG   GAGAATAAA
                                || |||||||   |||||||||
                                AA TTTTCTC   CTCTTATTT
                                 G      ___
GAM1087  PTPN13   3'  TTAAGGAGAGAAATGGAA    38782      A      GA
                                TTGA GAGAGAAA  GAA
                                |||| ||||||||  |||
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                                AATT CTCTCTTT  CTT
                                  C       AC
GAM1087  RRAS2    3'  CTGAGGAGAGAAAGAGAA    29307      A
                                TTGA GAGAGAAAGAGAA
                                |||| ||||||||||||
                                GACT CTCTCTTTCTCTT
                                  C
GAM1087  SMARCC1  3'  TTAAAGAGGGAGAAAAAAA   16907        __
                                TTGAAGA  GAGAAAGAGA
                                |||||||  ||||||||||
                                AATTTCT  CTCTTTTTTT
                                    CC
GAM1087  SPOCK    3'  TTCAAGAGAGAAAAAAAAT   41746    G
                                TT AAGAGAGAAAGAGAAT
                                || ||||||||||||||||
                                AA TTCTCTCTTTTTTTTA
                                 G
GAM1087  SRGAP2   3'  CTGAAGAGAGACCTTGTAAAAT 43979          AAGAGAA
                                TTGAAGAGAGA      TAAAAT
                                ||||||||||      ||||||
                                GACTTCTCTCT      ATTTTA
                                      GGAAC__
GAM1087  WHSC1L1  3'  TTGAAGGGAAAGAGAA     35721       AGA
                                TTGAAG   GAAAGAGAA
                                ||||||   |||||||||
                                AACTTC   CTTTCTCTT
                                   C__
GAM1088  ADAR     3'  AGCAGATGCGTGGAATTCA   31901         CC  CG__
                                AGCAGATGCG  GG   CA
                                ||||||||||  ||   ||
                                TCGTCTACGC  CC   GT
                                      A_  TTAA
GAM1088  ADCY2    3'  GAGCAGATGCGGTTGGCG    42143          CC_
                                GAGCAGATGCG   GGCG
                                ||||||||||   ||||
                                CTCGTCTACGC   CCGC
                                      CAA
GAM1088  ADRBK1   3'  GAGGGTGCGCCAACCCA     11529     CAGA     GCGC
                                GAG   TGCGCCG   ACCCA
                                |||   |||||||   |||||
                                CTC   ACGCGGT   TGGGT
                                  CC__     _____
GAM1088  ADRBK1   3'  GGGCAGATGGGGTCGCACCCAG 11536   A      CGCC  _
                                G GCAGATG   GG CGCACCCAG
                                | |||||||   || |||||||||
                                C CGTCTAC   CC GCGTGGGTC
                                 C      C___  A
GAM1088  ADRBK2   3'  GCAGATGCTGCTGGGACCAG   23130        _  C  CGCAC
                                GCAGATGC GC GG    CCAG
                                |||||||| || ||    ||||
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                                CGTCTACG CG CC    GGTC
                                    A  A  CT___
GAM1088  CDK5R2   5'  GAGCGGGGCCGGCGCCCA   19471     AGATGC      AC
                                GAGC    GCCGGCGC  CCA
                                ||||    ||||||||  |||
                                CTCG    CGGCCGCG  GGT
                                  CCC___      __
GAM1088  CHST1    5'  GAGCAGCTGCAGCGCCCA   18905      A  GCC    AC
                                GAGCAG TGC   GGCGC  CCA
                                ||||||| |||   |||||  |||
                                CTCGTC ACG   TCGCG  GGT
                                   G  ___    __
GAM1088  CYP19    3'  GAGCAGATGACCAATAGCACC  36304       C    C_
                                GAGCAGATG GCCGG  GCACC
                                ||||||||| |||||  |||||
                                CTCGTCTAC TGGTT  CGTGG
                                     _    AT
GAM1088  CYP21A2  3'  GAGCAGATGGGACATCCGG   7983        ___  _
                                GAGCAGATG   CG CCGG
                                |||||||||   || ||||
                                CTCGTCTAC   GT GGCC
                                     CCT  A
GAM1088  DVL3     3'  GAGCAGTTAGCGCACC     20680       ATGCGCC
                                GAGCAG      GGCGCACC
                                ||||||      ||||||||
                                CTCGTC      TCGCGTGG
                                   AA_____
GAM1088  EN1      3'  GAGCAGATGCTTTCTCCCCCAG 10910         GCCGGCGCA
                                GAGCAGATGC       CCCAG
                                ||||||||||       |||||
                                CTCGTCTACG       GGGTC
                                     AAAGAGG__
GAM1088  FXYD6    3'  GAGCAGATGGCCATGTGGCTCA 35115        C  _____  G
                                GAGCAGATG GCC   GGC CA
                                ||||||||| |||   ||| ||
                                CTCGTCTAC CGG   CCG GT
                                     _  TACA  A
GAM1088  HMG20A   3'  AGCAGATGTCAGCATCC    32863       CGC    CA
                                AGCAGATG  CGGCG  CC
                                ||||||||  |||||  ||
                                TCGTCTAC  GTCGT  GG
                                     A__    A_
GAM1088  LAPTM5   3'  GAACAGATGTGCCTGATTTCA  27603       C  GGCG__
                                GAGCAGATG GCC     CA
                                ||||||||| |||     ||
                                CTTGTCTAC CGG     GT
                                     A  ACTAAA
GAM1088  LMO4     5'  GGCAGGCAGGCGCACCCA   27657   A   ATGC  C
                                G GCAG   GC GGCGCACCCA
                                | ||||   || ||||||||||
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                                C CGTC    CG CCGCGTGGGT
                                _   ____  T
GAM1088 SIX1     5' AACGGCCGGCGCACTCA     25593      C        C
                                GATG GCCGGCGCAC CA
                                |||| |||||||||| ||
                                TTGC CGGCCGCGTG GT
                                  _        A
GAM1088 ZNF219   5' AGATGCGCCGGGCCCC      32314          C  A
                                AGATGCGCCGG GC CCC
                                |||||||||| || |||
                                TCTACGCGGCC CG GGG
                                     _ _
GAM1088 ZNF38    5' GCAATGCTCCTGCACCCAG   45363      A   G  GGC
                                GCAG TGC CC   GCACCCAG
                                |||| ||| ||   ||||||||
                                CGTT ACG GG   CGTGGGTC
                                  _   A  A__
GAM1088 ACK1     5' CCGGTTCGGGCTGCTGCAGCA 25109      C   A       CG
                                CCGG TCG GCTGCTGCA  GCA
                                |||| ||| |||||||||  |||
                                GGCC AGC CGACGACGT  CGT
                                  A   C       __
GAM1088 ACVR1B   3' ACCAGTTCGAGGTGTGGCA   33755      C    C  CT
                                ACCGG TCGAG TG  GCA
                                ||||| ||||| ||  |||
                                TGGTC AGCTC AC  CGT
                                   A    C  AC
GAM1088 ADAM23   5' CCGGCTCGGCGCGCATGG    19201        A  T  T   C
                                CCGGCTCG GC GC GCA GG
                                |||||||| || || ||| ||
                                GGCCGAGC CG CG CGT CC
                                     _ _ _  A
GAM1088 AES      5' CCGGCTCGGGCTGCTGGGGGC 10052        A      CAC
                                CCGGCTCG GCTGCTG   GGC
                                |||||||| |||||||   |||
                                GGCCGAGC CGACGAC   CCG
                                    C      CC_
GAM1088 EYA1     5' GGCTCGGGCTGCCGAGC     7990        A      CAC
                                GGCTCG GCTGCTG   GGC
                                |||||| |||||||   |||
                                CCGAGC CGACGGC   TCG
                                   C      ___
GAM1088 GNB2     5' GGCCCGAGGCCTGTGGC     23600        CT   GCAC
                                GGCTCGAG  GCT    GGC
                                ||||||||  |||    |||
                                CCGGGCTC  CGG    CCG
                                    __   ACA_
GAM1088 GRIN2C   5' GGCTCGAGTGTACGTGGCA   9126         C  C   AC
                                GGCTCGAG TG TGC  GGCA
                                |||||||| || |||  ||||
```

```
                                CCGAGCTC AC ATG  CCGT
                                    _ _  CA
GAM1088  MAF     5'  CCGGCCCGGGCTGCAGGC    23823        AGCT     C
                                CCGGCTCG   GCTGCA GGC
                                ||||||||   |||||| |||
                                GGCCGGGC   CGACGT CCG
                                    C___    _
GAM1088  NPTX1   5'  ACCGGCTCGGGCTGTGGCTCG  14829         A   CT  A
                                ACCGGCTCG GCTG  GC CG
                                ||||||||| ||||  || ||
                                TGGCCGAGC CGAC  CG GC
                                     C   AC  A
GAM1088  NTSR1   5'  CCGGCTCGGGCTGCGCGGGGC  14880         A    T  AC
                                CCGGCTCG GCTGC GC  GGC
                                |||||||| ||||| ||  |||
                                GGCCGAGC CGACG CG  CCG
                                    C    _ CC
GAM1088  PITX1   3'  CCGGCTCGACTCTTGCACGGC  15319         G  GC
                                CCGGCTCGA CT  TGCACGGC
                                ||||||||| ||  ||||||||
                                GGCCGAGCT GA  ACGTGCCG
                                     _ GA
GAM1088  PLIN    3'  CCGGCCCGGGGCGCGGC     15398        AGCTGCT  A
                                CCGGCTCG      GC CGGC
                                ||||||||      || ||||
                                GGCCGGGC      CG GCCG
                                    CC_____  C
GAM1088  PSCD4   5'  TCGGGCTGGCCCGGCA     30133     A   CT  A
                                TCG GCTG  GC CGGCA
                                ||| ||||  || |||||
                                AGC CGAC  CG GCCGT
                                  C   __  G
GAM1088  VEGF    5'  CCGGCTCGGGCTGTGGGGC   17948         A   C  CAC
                                CCGGCTCG GCTG TG   GGC
                                |||||||| |||| ||   |||
                                GGCCGAGC CGAC AC   CCG
                                    C   _ C__
GAM1089  AMPD3   5'  CGCCCGGGCCGCGGCGCCAAC  7895          _  A
                                CGCCCGGGCC CG CGCCGAT
                                |||||||||| || |||||||
                                GCGGGCCCGG GC GCGGTTG
                                     C  C
GAM1089  BNC     3'  GGCCCACTGGTGTCGATCTGC  11854       ACGC___
                                GGCCCG      CGATCTGC
                                ||||||      ||||||||
                                CCGGGT      GCTAGACG
                                   GACCACA
GAM1089  EBAG9   5'  CGCCTGGCGCCCGGCGTGAC   20116     C  _    A  CC
                                CGCC GG GCCCG CG  GAT
                                |||| || ||||| ||  |||
```

```
                                GCGG CC CGGGC GC  CTG
                                  A G    C A_
GAM1089  EGLN2    5'  CGCCCGGGCCCATGGTGC    38824          AC__
                                CGCCCGGGCCCG   GC
                                ||||||||||||  ||
                                GCGGGCCCGGGT   CG
                                      ACCA
GAM1089  FBN1     5'  CGCCCGGGGCTCGGTCTG    42054        CCCGAC _ A
                                CGCCCGGG    GC CG TCTG
                                ||||||||    || || ||||
                                GCGGGCCC    CG GC AGAC
                                    _______ A  C
GAM1089  GAMT     5'  CGCCCGGGCCCGCTCCCTG   6681           ACG  GAT
                                CGCCCGGGCCCG  CC  CTG
                                ||||||||||||  ||  |||
                                GCGGGCCCGGGC  GG  GAC
                                      GA_ ___
GAM1089  HSF4     5'  CGCTCGGGCCCGGCCGCTG   40765    C      AC   AT
                                CGC CGGGCCCG  GCCG  CTG
                                ||| ||||||||  ||||  |||
                                GCG GCCCGGGC  CGGC  GAC
                                  A      __   __
GAM1089  INSM1    5'  GCCCGGGCGCGGCGGCTG    13578        C  A  CCGAT
                                GCCCGGGC CG CG    CTG
                                |||||||| || ||    |||
                                CGGGCCCG GC GC    GAC
                                     C  C  C____
GAM1089  ITGB1    5'  CGTTCGGGCCCGGTCCCCCGC  38047    CC       ACG  GA
                                CG  CGGGCCCG   CC  TCTGC
                                ||  ||||||||   ||  |||||
                                GC  GCCCGGGC   GG  GGGCG
                                 AA       CA_ __
GAM1089  KCNK1    5'  CGCCCGGGCCTGGCTCCCG   13887         CGAC  CGA
                                CGCCCGGGCC   GC   TCTG
                                ||||||||||   ||   ||||
                                GCGGGCCCGG   CG   GGGC
                                      AC__  A__
GAM1089  KRTHA5   3'  CCCTGGGCCTGGGCTCTG    14022    _    CGAC  CGA
                                CCC GGGCC    GC   TCTG
                                ||| |||||    ||   ||||
                                GGG CCCGG    CG   AGAC
                                  A    ACC_ ___
GAM1089  SLC6A3   5'  CGCCCGGGCCTGGGCTTTG   9809          CGAC  CGATC
                                CGCCCGGGCC   GC    TG
                                ||||||||||   ||    ||
                                GCGGGCCCGG   CG    AC
                                      ACC_  AA___
GAM1089  ADAMTS8  5'  AAGAGGCTCGTGCACTGGTC  28158     A        GC
                                AAGA GTTCGTGCAC  GTC
                                ||||  ||||||||||  |||
```

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                                TTCT CGAGCACGTG  CAG
                                  C         AC
GAM1089  CD4      3'  GAGGTTCTGCACAGGGT     8328     A    G     CGTC
                                GA GTTC TGCACG    GGT
                                || |||| ||||||    |||
                                CT CAAG ACGTGT    CCA
                                 C    _     C___
GAM1089  GTF2I    5'  AGGGGCCCGTGCGTGTCGGTC  37433    AA       AC C
                                AG  GTTCGTGC  G GTCGGTC
                                ||  ||||||||  | |||||||
                                TC  CGGGCACG  C CAGCCAG
                                 CC        __ A
GAM1089  PAFAH1B2 5'  GCGGGTGGCGCGTCGGT     15073    TC   CA
                                GT  GTG  CGCGTCGGT
                                ||  |||  |||||||||
                                CG  CAC  GCGCAGCCA
                                 CC   C_
GAM1090  NQO1     3'  GTATAGATCAGAAATAAAGTAT 9478          _    TC_
                                GTATAGAT AGGG   GAGTAT
                                |||||||| ||||   ||||||
                                CATATCTA TCTT   TTCATA
                                     G    TAT
GAM1090  EFG2     3'  TTCGTCCAATAAATAAAG    37036         AC   C
                                TTCGTCTA  GTA GTAAAG
                                ||||||||  ||| ||||||
                                AAGCAGGT  TAT TATTTC
                                     __   T
GAM1091  DGKE     3'  TTACGTGTCTGAATAA      18892          T  C
                                TTACGTGTCT GA GTAG
                                |||||||||| || ||||
                                AATGCACAGA CT TATT
                                     _  _
GAM1091  HRG      3'  TGTCTCAAGTGATGTAGTG   7654        _____  C
                                TGTCT    TGA GTAGTG
                                |||||    ||| ||||||
                                ACAGA    ACT CATCAC
                                   GTTC   A
GAM1091  HYAL4    5'  TTACGTATCTTCTGCTTTAGTG 29344          __ ACG
                                TTACGTGTCT  TG   TAGTG
                                |||||||||  ||   |||||
                                AATGCATAGA  AC   ATCAC
                                     AG  GAA
GAM1091  PKIG     3'  TTACAGTGTCTTGAAAGTG   28195     _       CGT
                                TTAC GTGTCTTGA   AGTG
                                |||| |||||||||   ||||
                                AATG CACAGAACT   TCAC
                                  T        T__
GAM1091  SYT4     3'  TTACATGTTTAATACAGTG   41663         C    CG
                                TTACGTGT TTGA  TAGTG
                                |||||||| ||||  |||||
```

```
                                AATGTACA AATT  GTCAC
                                    _   AT
GAM1091  DTNB    3'  CTCGTCCTCTGTGCCTGAGC  37601        CAC   CGT
                                TTCGTCCTC  GTCT  AGC
                                |||||||||  ||||  |||
                                GAGCAGGAG  CGGA  TCG
                                    ACA   C__
GAM1091  FMR2    3'  TTCATCCTCCATGTTTAATTAG 12990         C  CTCG_
                                TTCGTCCTCCA GT   TAG
                                |||||||||||  ||   |||
                                AAGTAGGAGGT CA   ATC
                                     A  AATTA
GAM1091  LOH11CR2A 5'  TTCTCCTCATTCTCGTAG   31195    G   CACG
                                TTC TCCTC   TCTCGTAG
                                |||  |||||   ||||||||
                                AAG AGGAG   AGAGCATC
                                  _    TA__
GAM1091  PCDH9   5'  GTCCTCCATCAGTGGC     44406        CG  TC  A
                                GTCCTCCA  TC  GT GC
                                ||||||||  ||  || ||
                                CAGGAGGT  AG  CA CG
                                    __  T_  C
GAM1091  STS     5'  TTCATCCTCTGTTCAT     7395          CAC  C
                                TTCGTCCTC  GT TCGT
                                |||||||||  || ||||
                                AAGTAGGAG  CA AGTA
                                    A__  _
GAM1092  CD34    3'  GCTTTCCCCCGTCACACGTTT  12118    CC   A   C
                                GC  TCCC CCG CGCGCGTTT
                                ||  |||| ||| |||||||||
                                CG  AGGG GGC GTGTGCAAA
                                 AA   _   A
GAM1092  FOLH1   5'  CAGTTTCTCCACCACAGCAGT  20989    CCC  _     C  C
                                CAG  TC CCACCGC GCG GT
                                |||  || ||||||| ||| ||
                                GTC  AG GGTGGTG CGT CA
                                  AA_  A      T  _
GAM1092  KLF7    3'  CAGCCCCCTGCCTCATGGCGTT 18980        CCACC  GC___
           T                     CAGCCCTC    GCC    GCGTTT
                                |||||||     |||    ||||||
                                GTCGGGGG    CGG    CGCAAA
                                    A____   AGTAC
GAM1092  LRRC2   5'  GCCTGCCCGCCGCGGCTGTTT  36030    CT   A   C  GC
                                GCC  CCC CCGC GC  GTTT
                                |||  ||| |||| ||  ||||
                                CGG  GGG GGCG CG  CAAA
                                  AC   C   C  A_
GAM1092  PRKY    3'  GCTTCTCACTGCACACATTT   15702    CC  C   C  C
                                GC  TC CAC GC GCGCGTTT
                                ||  || ||| || ||||||||
```

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                                CG  AG GTG CG TGTGTAAA
                                 A_  A   A  _
GAM1092  RLF      3'  AGCCCTCCCACCCTGGGACC  29677          _____
                                AGCCCTCCCACC    GCC
                                ||||||||||||    |||
                                TCGGGAGGGTGG    TGG
                                      GACCC
GAM1092  SLC2A4   3'  GCTCTCCCACCCCTGC     9798     C      G  GC
                                GC CTCCCACC CC  GC
                                || ||||||||  ||  ||
                                CG GAGGGTGG GG  CG
                                 A       _  A_
GAM1092  SOX4     5'  GCTCTCTCACCGCGCTGCAGTT 16988    C   C     C  _  _
              T                  GC CTC CACCGC GC GC GTTT
                                || ||| |||||| || || ||||
                                CG GAG GTGGCG CG CG CAAA
                                 A  A     _  A  T
GAM1092  ACTN1    5'  GCCCGGTTCCGCCGCGGCGC   9933     G   A  G  AC
                                GC CGG TC GC  CGCGGCGC
                                || ||| || ||  ||||||||
                                CG GCC AG CG  GCGCCGCG
                                 G   A  G  __
GAM1092  BYSL     5'  GCGTGGTGCGTTCCCGCGGCGC 19756     C  AT  GCA
              CG                   GCG GG  CG   CCGCGGCGCCG
                                ||| ||  ||   ||||||||||
                                CGC CC  GC   GGCGCCGCGGC
                                  A  AC  AAG
GAM1092  GEM      5'  GCCGGATCGGCGTCGGGGCG   23546    G       AC  C
                                GC CGGATCGGC  CG GGCG
                                || |||||||||  || ||||
                                CG GCCTAGCCG  GC CCGC
                                 _       CA  C
GAM1092  INHBB    5'  GCGCGGCTTGGCGCGGCGC    13559       ATC   ACC
                                GCGCGG   GGC   GCGGCGC
                                ||||||   |||   |||||||
                                CGCGCC   CCG   CGCCGCG
                                   GAA   ___
GAM1092  JPH3     5'  GCGCGGGCGGCCGCGGCGCCG  34019       AT    AC
                                GCGCGG  CGGC  CGCGGCGCCG
                                ||||||  ||||  ||||||||||
                                CGCGCC  GCCG  GCGCCGCGGC
                                   C_   __
GAM1092  OXTR     5'  GCGCGGACGGCGTCTGGATGCG 9525         T    ACC_____
              GCGC                  GCGCGGA CGGC       GCGGCGC
                                ||||||| ||||       |||||||
                                CGCGCCT GCCG       CGCCGCG
                                   _   CAGACCTA
GAM1092  PKD2     5'  GCGCGGGTGCGCGGCGCC    41074       ATCG  ACC
                                GCGCGG   GC   GCGGCGCC
                                ||||||   ||   ||||||||
```

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                              CGCGCC   CG  CGCCGCGG
                                 CA__ ___
GAM1092 PTTG1IP  5' GCCCGGAACAGCCGCGGCGCCG 20287   G   T   AC
                              GC CGGA CGGC  CGCGGCGCCG
                              || |||| ||||  ||||||||||
                              CG GCCT GTCG  GCGCCGCGGC
                               G   T   __
GAM1092 RRAS2    5' GCGCGGTAGCGCGGCGC    29308      ATC   ACC
                              GCGCGG  GGC  GCGGCGC
                              ||||||  |||  |||||||
                              CGCGCC  TCG  CGCCGCG
                                 A__  ___
GAM1092 SGT      5' GCGCTTGCGCACCGCGGTGCCG 16617     GGATCG       C
                              GCGC    GCACCGCGG GCCG
                              ||||    ||||||||| ||||
                              CGCG    CGTGGCGCC CGGC
                                AACG__       A
GAM1092 SLC16A1  5' GCGCGGATCGCAGCGC     16813       GGCACC
                              GCGCGGATC    GCGGCGC
                              |||||||||    |||||||
                              CGCGCCTAG    CGTCGCG
                                           _______
GAM1092 TES      5' GCGGAACTCCCGCGGCGCCG  43539      TCGGCA
                              GCGGA    CCGCGGCGCCG
                              |||||    ||||||||||
                              CGCCT    GGCGCCGCGGC
                                 TGAG__
GAM1093 ADAR     3' TAGCAAACACAAAGGGAAAGGA 31909       T   A_   A
                   AA                  TGGCAAAT TAGA  GAAA GAAA
                              |||||||| ||||  |||| ||||
                              ATCGTTTG GTTT  CTTT CTTT
                                   T   CC   C
GAM1093 AKAP2    5' GGCAGGGGAAAGAGGAAAGAAA 28497     AATTT_  A   A
                   A                   GGCA    AGA GAAA GAAAA
                              ||||    ||| |||| |||||
                              CCGT    TCT CTTT CTTTT
                                CCCCTT  C   _
GAM1093 AP1S1    3' TGGCAAGGTTAGAAAAAA    10503      AT
                              TGGCAA  TTAGAAGAAA
                              ||||||  ||||||||||
                              ACCGTT  AATCTTTTTT
                                 CC
GAM1093 BACE     3' GCAAATTTAGAAATTGAAAA  39962          AAAA
                              GCAAATTTAGAAG   GAAAA
                              ||||||||||||   |||||
                              CGTTTAAATCTTT   CTTTT
                                     AA__
GAM1093 BAZ2A    3' TAGCAAATAAAACAGAAAAGAA 30313       TTAGA
                   AA                  TGGCAAAT    AGAAAAGAAAA
                              ||||||||    ||||||||||
```

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                                ATCGTTTA    TCTTTTCTTTT
                                    TTTTG
GAM1093  BCL7B    3'  GCAGATTTCAAAGAAAAG    11805     A   A
                                GCA ATTT GAAGAAAAG
                                ||| |||| |||||||||
                                CGT TAAA TTTCTTTTC
                                  C   G
GAM1093  C18orf2  3'  TGGCAGAGAGAAGAAAA     36411      AATTT
                                TGGCA    AGAAGAAAA
                                |||||    |||||||||
                                ACCGT    TCTTCTTTT
                                   CTC__
GAM1093  CD69     3'  TGGCAAATTTCTCTAAAAAGA  12140         AGAA
                                TGGCAAATTT   GAAAAGA
                                ||||||||||   |||||||
                                ACCGTTTAAA   TTTTTCT
                                     GAGA
GAM1093  COL3A1   5'  TGTGCAAAAAGGAGAAAAGAAA 6391    _    TTT  A
            A                    TG GCAAA   AG AGAAAAGAAAA
                                || |||||   || ||||||||||
                                AC CGTTT   TC TCTTTTCTTTT
                                 A    T__  C
GAM1093  CORO1C   3'  TGGCAACATTAAAAAAGAAA   30726       ATTTAGA
                                TGGCAA      AGAAAAGAAA
                                ||||||      ||||||||||
                                ACCGTT      TTTTTTCTTT
                                    GTAA___
GAM1093  CTNNA2   3'  TGGCACAACTAGAAGAGGAAA  20498      AAT      AAA
                                TGGCA   TTAGAAGA   GAAA
                                |||||   ||||||||   ||||
                                ACCGT   GATCTTCT   CTTT
                                   GTT      C__
GAM1093  GRIK3    3'  TGGCAGCTTTAGAAACCCACAG 9101       AA      AAA__
            AA                    TGGCA  TTTAGAAG    AGAA
                                |||||  ||||||||    ||||
                                ACCGT  AAATCTTT    TCTT
                                   CG      GGGTG
GAM1093  HELLS    3'  GCATTACTAGAAGAAAGGA   32848    AAT       A
                                GCA   TTAGAAGAAA GA
                                |||   |||||||||| ||
                                CGT   GATCTTCTTT CT
                                  AAT       C
GAM1093  HPSE     3'  TGGAGACTCAGAAGGGAAGA  27420    CAA       AA
                                TGG   ATTTAGAAG  AAGA
                                |||   |||||||||  ||||
                                ACC   TGAGTCTTC  TTCT
                                  TC_       CC
GAM1093  HYAL3    3'  TGGCAGCAGGGAAAAGAA    18649      AATT   AA
                                TGGCA   TAG  GAAAAGAA
                                |||||   |||  ||||||||
```

```
                              ACCGT   GTC  CTTTTCTT
                                C___  C_
GAM1093  IL13RA1  3'  TGGCAGAGAAAAGA       11448      AATTTA  A
                              TGGCA     GA GAAAAGA
                              |||||     || |||||||
                              ACCGT     CT CTTTTCT
                                _______ _
GAM1093  KCNJ6    5'  GCAAAAAAGAAAAG       13857      TTTA
                              GCAAA   GAAGAAAAG
                              |||||   |||||||||
                              CGTTT   TTTCTTTTC
                                _____
GAM1093  KIT      3'  GCAAGTTGAAAGAAAAGAAAA  6897      AT  AG
                              GCAA  TT  AAGAAAAGAAAA
                              ||||  ||  ||||||||||||
                              CGTT  AA  TTCTTTTCTTTT
                                C_  CT
GAM1093  KPNA1    3'  TGGCGCCAATAGAGGAAAGAAA 44320     AAATT   A   A
            A                  TGGC    TAGA GAAA GAAAA
                              ||||    |||| |||| |||||
                              ACCG    ATCT CTTT CTTTT
                                CGGTT   C   _
GAM1093  KRT1     3'  TGGGAAACAGCAGAAAAGAAA  25940    C   TT  A
                              TGG AAAT  AG AGAAAAGAAA
                              ||| ||||  || ||||||||||
                              ACC TTTG  TC TCTTTTCTTT
                                C   __  G
GAM1093  LUZP1    3'  TGGCAAACCAAGGGAAGA    37966       TA__
                              TGGCAAATT   GAAGA
                              |||||||||   |||||
                              ACCGTTTGG   CTTCT
                                    TTCC
GAM1093  MAPK10   5'  GGCAAAGGAGAAGAAAA     39981      TTT
                              GGCAAA  AGAAGAAAA
                              ||||||  |||||||||
                              CCGTTT  TCTTCTTTT
                                 CC_
GAM1093  MPDZ     3'  GCAAGAAGAAAAGAA      19256     AATTT
                              GCA    AGAAGAAAAGAA
                              |||    ||||||||||||
                              CGT    TCTTCTTTTCTT
                                _____
GAM1093  MTAP     3'  GCAAATTTAATAGGGGGAGAA  14674        A  AAA_
                              GCAAATTTAG AG   AGAA
                              |||||||||| ||   ||||
                              CGTTTAAATT TC   TCTT
                                    A  CCCC
GAM1093  MUC3B    3'  GGCTCAGAAGGGGAGAA     45341     AAAT     AAA
                              GGC   TTAGAAG  AGAA
                              |||   |||||||  ||||
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```
                                CCG   AGTCTTC  TCTT
                                  ____     CCC
GAM1093  MXI1    3'  AGCAAACTAGAAAAGA     39011       TAGA
                                GGCAAATT   AGAAAAGA
                                ||||||||   ||||||||
                                TCGTTTGA   TCTTTTCT
                                   ____
GAM1093  NFRKB   5'  TGACTTCAGAAGAAGAG    26103     AAA       A
                                TGGC  TTTAGAAGAA AG
                                ||||  |||||||||| ||
                                ACTG  AAGTCTTCTT TC
                                  ___       C
GAM1093  PACE    3'  TGGCTAGGGTAGAAAAGAAAA  15040     AAATT  A__
                                TGGC    TAG  AGAAAAGAAAA
                                ||||    |||  ||||||||||
                                ACCG    ATC  TCTTTTCTTTT
                                  _____  CCA
GAM1093  PCSK2   3'  GCCAATATGGGAGAAAAGAAA  15127   A  TTAGA
                                GC AAT    AGAAAAGAAA
                                || |||    ||||||||||
                                CG TTA    TCTTTTCTTT
                                 G  TACCC
GAM1093  PLCG2   3'  TGGCAGGCTTGAAGAAAA    43676      AA  A
                                TGGCA  TTT GAAGAAAA
                                |||||  ||| ||||||||
                                ACCGT  GAA CTTCTTTT
                                   CC  _
GAM1093  PMX1    5'  GGCAAACAGAAGAAGAGA    35513       TT     A
                                GGCAAAT  AGAAGAA AGA
                                |||||||  ||||||| |||
                                CCGTTTG  TCTTCTT TCT
                                   __     C
GAM1093  PPP3R1  5'  GGCAGAGAAGAAGAAAGGA   44082     AATTT      A
                                GGCA    AGAAGAAA GA
                                ||||    |||||||| ||
                                CCGT    TCTTCTTT CT
                                  CTCT_      C
GAM1093  PTGS2   3'  TGGCTAAAAGAAGAAAAGAAAA 9696      AAATTT
                                TGGC    AGAAGAAAAGAAAA
                                ||||    ||||||||||||||
                                ACCG    TCTTCTTTTCTTTT
                                  ATTT__
GAM1093  PTK2B   3'  GCAAACACATGAGAAAAGAA   19918      T  GA
                                GCAAAT TA  AGAAAAGAA
                                ||||||  ||  |||||||||
                                CGTTTG GT  TCTTTTCTT
                                   T  AC
GAM1093  RAI14   3'  GGCAGATGGGAAGAAAA    31804     A  TTA
                                GGCA AT   GAAGAAAA
                                |||| ||   ||||||||
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                                CCGT TA   CTTCTTTT
                                  C  CC_
GAM1093  REGL     3'  GCAAATTTAGCAGAGGAGA   27122          A   AA
                                GCAAATTTAG AGA  AGA
                                |||||||||| |||  |||
                                CGTTTAAATC TCT  TCT
                                     G   CC
GAM1093  RFX5     3'  GCAAGACTGAGGAGAAAAGAAA 7795       _  T  A
                                GCAA ATT AG AGAAAAGAAA
                                |||| ||| || ||||||||||
                                CGTT TGA TC TCTTTTCTTT
                                  C   C  C
GAM1093  SHANK2   3'  TGACATTAAGAAGAAAGGAA  29472       AATTT       A
                                TGGCA     AGAAGAAA GAA
                                |||||     |||||||| |||
                                ACTGT     TCTTCTTT CTT
                                   AAT__       C
GAM1093  SSR4     5'  GCCTAGAGGAAAAGAAA     26582     AAAT     A
                                GC    TTAGA GAAAAGAAA
                                ||    ||||| |||||||||
                                CG    GATCT CTTTTCTTT
                                 ____     C
GAM1093  TCF3     3'  TGGCTTTAGAAGAATAAG    43333       AAA         _
                                TGGC   TTTAGAAGAA AAG
                                ||||   |||||||||| |||
                                ACCG   AAATCTTCTT TTC
                                  ___          A
GAM1093  TCIRG1   5'  GGCAGGACCAGAAGAGGAGA  25842      AAT       AA
                                GGCA   TTAGAAGA  AGA
                                ||||   ||||||||  |||
                                CCGT   GGTCTTCT  TCT
                                  CCT       CC
GAM1093  TDGF1    5'  TGGCAATTTAAGAAGAAAA   17367        A  T
                                TGGCAA TT AGAAGAAAA
                                |||||| || |||||||||
                                ACCGTT AA TCTTCTTTT
                                   A  T
GAM1093  TNC      5'  TGGGGATTTAGAAGCACAGA  13474     CAA        AAA
                                TGG   ATTTAGAAG   AGA
                                |||   |||||||||   |||
                                ACC   TAAATCTTC   TCT
                                  CC_       GTG
GAM1093  TRIM9    5'  TGGGGAAAAAGAAGAAAAGAAA 31582     CA  TTT
            A                    TGG  AA   AGAAGAAAAGAAAA
                                ||| ||   ||||||||||||||
                                ACC  TT   TCTTCTTTTCTTTT
                                  CC  TT_
GAM1093  UNRIP    5'  GGCAACAGGAAAAGAA      28421       ATT   AA
                                GGCAA   TAG  GAAAAGAA
                                |||||   |||  ||||||||
```

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                              CCGTT  GTC  CTTTTCTT
                                ___  __
GAM1093  WNT5A    3'  TGGCATATTTGAGAAAAAGAAA 18140      A   A  AG
             A                 TGGCA ATTT GA  AAAAGAAAA
                               ||||| |||| ||  |||||||||
                               ACCGT TAAA CT  TTTTCTTTT
                                  A   _  CT
GAM1093  ZNF277   5'  GGCAGAAAAGAAAAG      35084      AATTT
                               GGCA    AGAAGAAAAG
                               ||||    ||||||||||
                               CCGT    TTTTCTTTTC
                                 C____
GAM1093  ADRA2A   3'  GAGAGAGTTGGGAATGG     8636       A      A
                               GAGAGA TTGGGAAT GG
                               |||||| |||||||| ||
                               CTCTCT AACCCTTA CC
                                  C      _
GAM1093  ESRRA    3'  GAAGAGGGGGTAGGATTA    20829     TT   AA
                               GAA  GGG  TAGGATTA
                               |||  |||  ||||||||
                               CTT  CCC  ATCCTAAT
                                 CT   CC
GAM1093  LIPE     5'  TGGGAGGATTAGGAATAGGA   23815    A   A
                               TG GAG ATTGGGAATAGGA
                               || ||| ||||||||||||
                               AC CTC TAATCCTTATCCT
                                C   C
GAM1093  LY95     5'  GAGGGAATTGGGAGCTGG    22098     A       ATA
                               GAG GAATTGGGA   GG
                               ||| |||||||||   ||
                               CTC CTTAACCCT   CC
                                 C       CGA
GAM1093  PYGO2    3'  TGAGAGAAGTGGGGGTAG    41954        T    AA
                               TGAGAGAA TGGG  TAG
                               |||||||| ||||  |||
                               ACTCTCTT ACCC  ATC
                                    C    CC
GAM1093  RP2      3'  TGAAAGAACATTTAAATAGGAT 27936         TGG_
             TAA                 TGAGAGAAT    GAATAGGATTAA
                               |||||||||    ||||||||||||
                               ACTTTCTTG    TTTATCCTAATT
                                    TAAA
GAM1094  CENPF    5'  TCTCGGGGACGGGAAAACGAC  32283    G    A   C C
                               TC CGGG GAC G GGAAAACGAC
                               || |||| ||| | ||||||||||
                               AG GCCC CTG C CCTTTTGCTG
                                A   _   _ _
GAM1094  COL4A6   5'  TCCCGGGAGACTGCTAAGCGG  37976    G       C_____
                               TC CGGGAGAC     GCGG
                               || ||||||||     ||||
```

```
                                AG GCCCTCTG     CGCC
                                 G       ACGATT
GAM1094  DFFA     5'  TCGCGGGAGGCCGGAGCGG   20582        A ___
                                TCGCGGGAG CC   GCGG
                                ||||||||| ||   ||||
                                AGCGCCCTC GG   CGCC
                                      C  CCT
GAM1094  IRS2     3'  TCGAGGGAGCAGAAAACG    40715     C   GACC
                                TCG GGGA   GCGGAAAACG
                                ||| ||||   ||||||||||
                                AGC CCCT   CGTCTTTTGC
                                  T  ____
GAM1094  LDLR     3'  TCGATATTCACGATCACGGC   8029           T  C
                                TCGATATTCGCGATC GC GC
                                |||||||||||||| || ||
                                AGCTATAAGTGCTAG TG CG
                                         _  C
GAM1095  EGLN2    5'  TTACCTAGTACTGCC       38843         GGTA
                                TTACCTAGTAC   TGCT
                                ||||||||||   ||||
                                AATGGATCATG   ACGG
                                      ____
GAM1095  MAT2A    3'  GCCTACCTGGGAATGCT     25404        AGTAC  T
                                GCTTACCT    GG ATGCT
                                ||||||||    || |||||
                                CGGATGGA    CC TACGA
                                     C____  T
GAM1095  PTP4A2   3'  TAGCTTAGCAGGTATGCT    38640      TACC    C
                                TAGCT   TAGTA GGTATGCT
                                |||||   ||||| ||||||||
                                ATCGA   ATCGT CCATACGA
                                  ____   _
GAM1095  SYNGR1   3'  AGCTTACCTGGTACCCT     21751        AGTAC    G
                                AGCTTACCT    GGTAT CT
                                |||||||||    ||||| ||
                                TCGAATGGA    CCATG GA
                                     _____   G
GAM1095  RUNX1    3'  ATTCCATACTTCTGATCCT   12006          CG   ATA
                                ATTCCGTACTTC  GGT   CCT
                                ||||||||||||  |||   |||
                                TAAGGTATGAAG  CTA   GGA
                                       A_  ___
GAM1096  ADRB3    3'  AGCAGTAATAAGGGAACCAGA 6174          AA    CA
                                GGCAGTAATA  AGGGG  TAGA
                                ||||||||||  |||||  ||||
                                TCGTCATTAT  TCCCT  GTCT
                                      __    TG
GAM1096  AFP      5'  GGCAGTGGTGGAAGCACAA   10066       AATAAAA
                                GGCAGT      GGGGCATAG
                                ||||||      |||||||||
```

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                                CCGTCA      CTTCGTGTT
                                   CCAC___
GAM1096 BTG2     3'  AGGCAGTAATAAAGGACCTGGA 27615          AA     ATA
                                AGGCAGTAATAA  GGGGC   GA
                                ||||||||||||  ||||||   ||
                                TCCGTCATTATT  TCCTG   CT
                                      __     GAC
GAM1096 CYP4A11  3'  AGCAGTAATAGGAAACTAATAT 8932          AAA GG  ____
             AG                   GGCAGTAATA   G  GC    ATAG
                                ||||||||||   |  ||    ||||
                                TCGTCATTAT   C  TG    TATC
                                     C__ TT  ATTA
GAM1096 DRD2     3'  GGCAGTGAGGAGCATG      9017        AATAAA       A
                                GGCAGT     AGGGGCAT G
                                ||||||     |||||||| |
                                CCGTCA     TCCTCGTA C
                                   C_____       C
GAM1096 FBXL11   3'  GGCAGTCAGTGGGAGGCAAAAG 29433       AATAAAA     T_
             A                    GGCAGT      GGGGCA  AGA
                                ||||||      ||||||  |||
                                CCGTCA      CTCCGT  TCT
                                   GTCACC_     TT
GAM1096 FBXL11   3'  AGGCAGAATGAAGACACATGGA 29424       T   AA    G    A
                                AGGCAG AAT  AAGG GCAT GA
                                |||||| |||  |||| |||| ||
                                TCCGTC TTA  TTCT TGTA CT
                                   _  C_   G    C
GAM1096 IL1RN    3'  AGGCAGTGGCAAGAGGAG    8211         AA   A
                                AGGCAGT  TAA AGGGG
                                |||||||  ||| |||||
                                TCCGTCA  GTT TCCTC
                                    CC   C
GAM1096 KCNJ5    3'  AGGAAGTGACCCAGGGCATGGA 9430      C   A  AAAA      A
                                AGG AGT AT    GGGGCAT GA
                                ||| ||| ||    ||||||| ||
                                TCC TCA TG    TCCCGTA CT
                                  T   C  GG__      C
GAM1096 LANCL1   3'  AGGCAGTAATAGAAAGAGTAGA 25848          A     CA
                                AGGCAGTAATA AAGGGG  TAGA
                                |||||||||| ||||||  ||||
                                TCCGTCATTAT TTTCTC  ATCT
                                      C     __
GAM1096 LOH11CR2A 3'  AGGCAGTGGAAGAAAAGACAT  31187        AATAA
                                AGGCAGT     AAGGGGCAT
                                |||||||     |||||||||
                                TCCGTCA     TTTTCTGTA
                                    CCTTC
GAM1096 MECP2    3'  AGGCAGAAATGGAAGGGG    22573       T   AA
                                AGGCAG AAT  AAGGGG
                                |||||| |||  ||||||
```

```
                                TCCGTC TTA  TTCCCC
                                   T   CC
GAM1096  PLIN     3'  AGGCAGTAATGATGCA      15394          AAAA GG
                                AGGCAGTAAT    G  GCA
                                ||||||||||    |  |||
                                TCCGTCATTA    C  CGT
                                      _____ TA
GAM1096  PTBP1    3'  GGCGGTAGAAAGAGCACAGA   36722     A   ATAA
                                GGC GTA    AAGGGGCATAGA
                                ||| |||    ||||||||||||
                                CCG CAT    TTTCTCGTGTCT
                                  C   C___
GAM1096  PTEN     5'  AGGCAGTAGAAGGGGA      7201          ATAA     CAT
                                AGGCAGTA    AAGGGG   A
                                ||||||||    ||||||   |
                                TCCGTCAT    TTCCCC   T
                                     C___     ___
GAM1096  SLC7A8   3'  AGGTAGGATAAAAGGGG     29279     C  TA
                                AGG AG  ATAAAAGGGG
                                ||| ||  ||||||||||
                                TCC TC  TATTTTCCCC
                                  A  C_
GAM1096  SOX10    3'  AGACAGTAATGAGTTACAT    27992          AAA  GG
                                AGGCAGTAAT   AG  GCAT
                                ||||||||||   ||  ||||
                                TCTGTCATTA   TC  TGTA
                                      C__  AA
GAM1096  STK24    3'  AGGTGTACCAAAAGGGGCGTAG 18703     CA   A        A
                                AGG  GTA TAAAAGGGGC TAG
                                |||  ||| ||||||||||| |||
                                TCC  CAT GTTTTCCCCG ATC
                                  A_   G         C
GAM1096  TNF      3'  AGGGGGTAATAAAGGGA     44977     CA       A
                                AGG  GTAATAAA GGGG
                                |||  |||||||| ||||
                                TCC  CATTATTT CCCT
                                  CC       _
GAM1096  UCP2     3'  AGGTGGTAGGTAAAGGAGC   17844     CA   ATA
                                AGG  GTA   AAAGGGGC
                                |||  |||   ||||||||
                                TCC  CAT   TTTCCTCG
                                  AC   CCA
GAM1096  VAT1     3'  AGGCAGAGGTGAAAGCACATGG 26845       TAATAA   G    A
            A                    AGGCAG     AAGG GCAT GA
                                ||||||     |||| |||| ||
                                TCCGTC     TTTC TGTA CT
                                   TCCAC_    G    C
GAM1096  ABCA1    3'  CAATGGATGTGTCACCGGGAAA 24268       T     _ GT AA
                                CAATG GATGTG T  C  GAAA
                                ||||| ||||||  |  |  ||||
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                                GTTAC CTACAC G  G  CTTT
                                  _     A TG CC
GAM1096  ACATN    3'  TACAATGTGGTCATAAGAAA  21840    TG    T   __
                                TG  ATGTG GTCA  AGAAA
                                ||  ||||| ||||  |||||
                                AT  TACAC CAGT  TCTTT
                                 GT    _   AT
GAM1096  ANK1     3'  ATGTGGGAGAGTCAAGAAA   33881      ATGTGT
                                ATGTG     GTCAAGAAA
                                |||||     |||||||||
                                TACAC     CAGTTCTTT
                                   CCTCT_
GAM1096  APP      3'  ATGTGATAAATAATCAGGA   7912        TGT_   A
                                ATGTGATG    GTCA GA
                                ||||||||    |||| ||
                                TACACTAT    TAGT CT
                                     TTAT    C
GAM1096  CAPN9    5'  TGTGTGTGCCGGTCAAGAA   27358     A    __
                                TGTG TGTGT  GTCAAGAA
                                |||| |||||  ||||||||
                                ACAC ACACG  CAGTTCTT
                                  _    GC
GAM1096  CBFA2T2  3'  ATGTGTGTGGTCTGAGA     22967      A   T  A_
                                ATGTG TGTG GTC  AGA
                                ||||| |||| |||  |||
                                TACAC ACAC CAG  TCT
                                  _   _  AC
GAM1096  CD164    3'  ACATGAATGTGTGTCAGGGAA  25677       _       A_
                                ATGTGA TGTGTGTCA  GAA
                                |||||| |||||||||  |||
                                TGTACT ACACACAGT  CTT
                                   T        CC
GAM1096  COL15A1  3'  ATGGATGTACGTGAAAGAAA   12351     T       C_
                                ATG GATGTGTGT  AAGAAA
                                ||| |||||||||  ||||||
                                TAC CTACATGCA  TTCTTT
                                  _        CT
GAM1096  CREBBP   3'  AACAATATGATATAAGAA    20426           TGTCA
                                AACAATGTGATGTG    AGAA
                                ||||||||||||||    ||||
                                TTGTTATACTATAT    TCTT
                                                  _____
GAM1096  CYP1A1   3'  AATGTGATGTTCCCAGGAA   7969          GTG   A
                                AATGTGATGT   TCA GAA
                                ||||||||||   ||| |||
                                TTACACTACA   GGT CTT
                                      AG_   C
GAM1096  DGCR2    3'  ACAGTGTGAGAATGTGTCAAGA 23083     A    T_
            A                    ACA TGTGA  GTGTGTCAAGAA
                                ||| |||||  ||||||||||||
```

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                                TGT ACACT  TACACAGTTCTT
                                  C    CT
GAM1096  DVL3    3'  AATGTGGGGTAAAGTCAAGA  20667      AT  T_
                                AATGTG  GTG  GTCAAGA
                                ||||||  |||  |||||||
                                TTACAC  CAT  CAGTTCT
                                   CC   TT
GAM1096  FABP3   3'  CAATGTGGTGCTGAGTCGAG  43429      A  GT_  A
                                CAATGTG TGT   GTC AG
                                ||||||| |||   ||| ||
                                GTTACAC ACG   CAG TC
                                    C  ACT   C
GAM1096  FGF23   3'  ATGTGATGGCAGTGAGAAA   33948       T  TCA
                                ATGTGATG GTG   AGAAA
                                |||||||| |||   |||||
                                TACACTAC CGT   TCTTT
                                     _  CAC
GAM1096  FLRT2   5'  ACAATGTGGTGGGAAAAAGAAA 29833       AT  TGTC_
                                ACAATGTG  GTG    AAGAAA
                                ||||||||  |||    ||||||
                                TGTTACAC  CAC    TTCTTT
                                     __  CCTTT
GAM1096  FNTA    3'  AATGTGAGTGTGCAGA     12992       T    CA
                                AATGTGA GTGTGT  AGA
                                ||||||| ||||||  |||
                                TTACACT CACACG  TCT
                                     _    __
GAM1096  GABRR1  3'  AACAATGTAATGACACTTGAGG 13039         TG___  TCAA
           AA                    AACAATGTGATG    TG   GAA
                                ||||||||||||    ||   |||
                                TTGTTACATTAC    AC   CTT
                                      TGTGA  TC__
GAM1096  GARP    3'  TGTGATGTGATAGCTGAGA   24322       T__  CA
                                TGTGATGTG   GT  AGA
                                |||||||||   ||  |||
                                ACACTACAC   CG  TCT
                                     TAT  AC
GAM1096  GRINL1A 3'  AACAGTGAGTGTCAAGA    42992     AT   TGT
                                AACA  GTGA   GTGTCAAGA
                                ||||  ||||   |||||||||
                                TTGT  CACT   CACAGTTCT
                                   __   ____
GAM1096  HNRPDL  3'  AATGTGATAGCCCAGGAA    24169       T  G   A
                                AATGTGATG GT TCA GAA
                                ||||||||| || ||| |||
                                TTACACTAT CG GGT CTT
                                     _ _  C
GAM1096  INSM1   3'  ATAATGTATGTAGAAA      13574         CA
                                GTGATGTGTGT  AGAAA
                                ||||||||||  |||||
```

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                                TATTACATACA  TCTTT
                                          __
GAM1096  MEN1     5'  CAATGTGATAGGGGTCGAGAAA 39247          TGT   A
                                CAATGTGATG   GTC AGAAA
                                ||||||||||   ||| |||||
                                GTTACACTAT   CAG TCTTT
                                     CCC   C
GAM1096  MFGE8    3'  AATGTGATGTGTGAGAGA    25458           TCA
                                AATGTGATGTGTG   AGA
                                ||||||||||||   |||
                                TTACACTACACAC   TCT
                                       TC_
GAM1096  MGAT2    3'  TAATAAGTGTGTCAAGA     14453   T   T
                                A GTGA GTGTGTCAAGA
                                | |||| ||||||||||
                                A TATT CACACAGTTCT
                                 T   _
GAM1096  MUT      3'  ACAATGTAATGCTAAACTGAGA 7022           GTGTCA_
              AA                  ACAATGTGATGT      AGAAA
                                ||||||||||||      |||||
                                TGTTACATTACG      TCTTT
                                      ATTTGAC
GAM1096  PCDHB4   3'  ATGTGGTGGTCACAAGA     33196      A  T  GT
                                ATGTG TG GT  CAAGA
                                ||||| || ||  |||||
                                TACAC AC CA  GTTCT
                                   C  _  GT
GAM1096  PDGFRB   3'  TGTGATGTGTGATCTGGAA   42346          _  AA
                                TGTGATGTGTG TC  GAA
                                |||||||||| ||  |||
                                ACACTACACAC AG  CTT
                                       T  AC
GAM1096  RAB11A   3'  AACAATGTAGTGGAAGAA    21673         ATGT   TC
                                AACAATGTG    GTG  AAGAA
                                |||||||||    |||  |||||
                                TTGTTACAT    CAC  TTCTT
                                     _____   C_
GAM1096  RP42     3'  AACATATGTGATTTGCCAGGAA 33974      _      GTG    A
              A                   AACA ATGTGAT   TGTCA GAAA
                                |||| |||||||   ||||| ||||
                                TTGT TACACTA   ACGGT CTTT
                                  A      A__     C
GAM1096  SLC7A5   3'  CAAGTGCGTGCCGTCGAGA   18538     T   A    _   A
                                CAA GTG TGTGT GTC AGA
                                ||| ||| ||||| ||| |||
                                GTT CAC GCACG CAG TCT
                                  _  _    G   C
GAM1096  STATH    3'  TGTGATATGGTATGAAA     17165          T  CAA
                                TGTGATGTG GT   GAAA
                                |||||||| ||   ||||
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                                ACACTATAC CA   CTTT
                                     _ TA_
GAM1096  TPP2     3'  CAATGTGAGGCATTAAGAAA  17652        TGT    C
                                CAATGTGA   GTGT AAGAAA
                                ||||||||   |||| ||||||
                                GTTACACT   CGTA TTCTTT
                                     C__    A
GAM1096  VHL      3'  AATGTGATTGTATTTAAGAA  8103         _    GTC
                                AATGTGAT GTGT   AAGAA
                                |||||||| ||||   |||||
                                TTACACTA CATA   TTCTT
                                     A    AA_
GAM1097  CIT      3'  ATGAGACACACAATATACA   43041       CCAT   G
                                ATGAG    ATA ACAATATACA
                                |||||    ||| ||||||||||
                                TACTC    TGT TGTTATATGT
                                   _____  G
GAM1097  GAS1     3'  GAGCAGAGGCAATATACAT   13066      CATAT  A
                                GAGC     AG CAATATACAT
                                ||||     || ||||||||||
                                CTCG     TC GTTATATGTA
                                  TC___  C
GAM1097  HRB      3'  AGCCAATTTTAATATACAT   21080       TATAGAC
                                AGCCA      AATATACAT
                                |||||      |||||||||
                                TCGGT      TTATATGTA
                                   TAAAA__
GAM1097  SIRT1    3'  ATGAGCCAATATAGACATTACT 29252         _       ATA_
              ACAT                  ATGAGCCA TATAGACA    TACAT
                                |||||||| ||||||||    |||||
                                TACTCGGT ATATCTGT    ATGTA
                                     T       AATG
GAM1097  BASP1    3'  TGAAACAAGTTAGTATAGGAGA 44015    T     TA    A
                                TG AACAA  TTAG TATAGGAGA
                                || |||||  |||| |||||||||
                                AC TTGTT  AATC ATATCCTCT
                                 T    C_   _
GAM1097  BCL10    3'  AATAATAGAAATATATAGGAGA 19400      T    _____
                                AATA TAGA    TATAGGAGA
                                |||| ||||    |||||||||
                                TTAT ATCT    ATATCCTCT
                                  T    TTAT
GAM1097  FGF12    3'  ACAGTAGAGATATAGGAGA   34296     A  TT
                                ACA TA  AGATATAGGAGA
                                ||| ||  ||||||||||||
                                TGT AT  TCTATATCCTCT
                                  C  C_
GAM1098  CAPN7    5'  GCCGGGCTGGGGTCCACCG   30710         AAC    A
                                GCCGGGCT   GGGG TCACCG
                                ||||||||   |||| ||||||
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                                CGGCCCGA  CCCC GGTGGC
                                    ___   A
GAM1098 COX6B   3' CCTGGGGTGGGGATCAC    12404   _  CTAAC
                                CC GGG    GGGGATCAC
                                || |||    |||||||||
                                GG CCC    CCCCTAGTG
                                 A  CA___
GAM1098 SIM2    3' GCCGGGCTCGGTGGCGCCG   22876       AA  _ ATCA
                                GCCGGGCT  CGG GG   CCG
                                ||||||||  ||| ||   |||
                                CGGCCCGA  GCC CC   GGC
                                    __  A  GC__
GAM1098 TMEPAI  5' TCGCCGGGCTCGGGTCGCC   33623        AA   GA  A
                                TCGCCGGGCT  CGGG  TC CC
                                ||||||||||  ||||  || ||
                                AGCGGCCCGA  GCCC  AG GG
                                    __   __ C
GAM1098 FBXO7   5' CCTGGACCCGGAAGCGGCG   29137   _       AT_
                                CC GGACCCGGAAG   CG
                                || ||||||||||   ||
                                GG CCTGGGCCTTC   GC
                                 A         GCC
GAM1098 XPR1    3' CCGATCCGGAAGAGCTCG    21847     AC      __
                                CCGG  CCGGAAGA  TCG
                                ||||  ||||||||  |||
                                GGCT  GGCCTTCT  AGC
                                  A_      CG
GAM1099 CA14    3' TGATCAAAAATATACAACTTC  29063   T       _   A
                                TG ATCAAAAATAT CAAT TC
                                || ||||||||||| |||| ||
                                AC TAGTTTTTATA GTTG AG
                                 _        T   A
GAM1099 IRTA1   3' TGTATCATGAAATATCCATAC  36360       A_     A
                                TGTATCA  AAATATC ATAT
                                |||||||  ||||||| ||||
                                ACATAGT  TTTATAG TATG
                                    AC     G
GAM1099 SOX11   3' TGTATCAAAAATGTTTCAA   17043         A__
                                TGTATCAAAAAT   TCAA
                                ||||||||||||   ||||
                                ACATAGTTTTTA   AGTT
                                       CAA
GAM1099 VAPB    3' TGTACCAAGGCCTACCAAT   21877       AAA_
                                TGTATCAA   TATCAAT
                                ||||||||   |||||||
                                ACATGGTT   ATGGTTA
                                    CCGG
GAM1099 XRCC4   3' TGTATCAAAAATTTTATTATC  35427         ATCAA
                                TGTATCAAAAAT    TATC
                                ||||||||||||    ||||
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                                ACATAGTTTTTA    ATAG
                                      AAATA
GAM1099 COL4A4   3' TAATGTTTTATATTCATCTGTG 6405        TA___    AT
            ATGT                TAATGTTTT   TATCTG  ATGT
                                |||||||||   ||||||  ||||
                                ATTACAAAA   GTAGAC  TACA
                                     TATAA    AC
GAM1100 ADK     3' AATAAACATCATTTTTTAGATT 27479      G  AT
                                AGTAAA AT  TTTTTTAGATT
                                ||||||  ||  ||||||||||
                                TTATTT TA  AAAAAATCTAA
                                   G  GT
GAM1100 ATRN    3' AGAGGATCTTCCTTGTAGG   40263    A      AACAAA
                                AGA GATCTTCT    TAGG
                                |||  ||||||||    ||||
                                TCT CTAGAAGG    ATCC
                                  C       AAC___
GAM1100 HNRPA2B1 3' GAAGCCCATGGCAAATAGG   36310    A   TCTAA
                                GAAG TCT    CAAATAGG
                                ||||  |||   ||||||||
                                CTTC GGG    GTTTATCC
                                  _   TACC_
GAM1100 SELE    3' ACAGAAGAAAACAAATAG    7801        TCTTCT
                                ATAGAAGA    AACAAATAG
                                ||||||||    |||||||||
                                TGTCTTCT    TTGTTTATC
                                     T_____
GAM1100 UBE4A   3' GAAGATAAATGCAAATAGG   21971      CTTCTAA
                                GAAGAT      CAAATAGG
                                ||||||      ||||||||
                                CTTCTA      GTTTATCC
                                   TTTAC__
GAM1101 CD3E    3' TTAGGGGGTTGGTAGGGA    8816     A  A   A  C
                                TTA GGG TTGG TAG GA
                                ||| ||| |||| ||| ||
                                AAT CCC AACC ATC CT
                                  C  C   _  C
GAM1101 NCOA3   3' TTAAGAGATTGAAAAGAGCGAG 27221          T__    AA
            GCAT                TTAAGGGATTGGA   AGCGA  CAT
                                ||||||||||||   |||||  |||
                                AATTCTCTAACTT   TCGCT  GTA
                                      TTC    CC
GAM1101 OPA1    3' AGGGATCACAACGAAGCAT   39268       GG      A
                                AGGGATT  ATAGCGAA CAT
                                |||||||  |||||||| |||
                                TCCCTAG  TGTTGCTT GTA
                                   __       C
GAM1102 ATP7B   3' TCTAATATTGCATGAAATGTTT 6280        C_  ATT
            TT                  TCTAATGT  CA   AATGTTTTT
                                ||||||||  ||   |||||||||
```

```
                              AGATTATA GT  TTACAAAAA
                                  AC ACT
GAM1102 BCL11B   3' AATGTCCAATTTATTTTTA  39742        AA
                              AATGTCCAATT TGTTTTTA
                              |||||||||||  ||||||||
                              TTACAGGTTAA ATAAAAAT
                                          __
GAM1102 CYP24    3' TCTAGTTTCCCAATAATGTTTT 8951     ATG  AAT
           TA                  TCTA  TCC  TAATGTTTTTA
                              ||||  |||  ||||||||||||
                              AGAT  AGG  ATTACAAAAAT
                                CAA  GTT
GAM1102 EGFL5    5' CTAATGTCTAATTAGATTAATG 44521      CA_____
           TTTTT                CTAATGTC     ATTAATGTTTTT
                              ||||||||     ||||||||||||
                              GATTACAG     TAATTACAAAAA
                                  ATTAATC
GAM1102 ZNF137   3' TCTAATGTCAATTAAAGCTTT  18337       C    T
                              TCTAATGTC AATTAA GTTTT
                              |||||||||| |||||| |||||
                              AGATTACAG TTAATT CGAAA
                                   _    T
GAM1102 ATP7B    3' TCTAATATTGCATGAAATGTTT 6280       C_ ATT
           TT                  TCTAATGT  CA  AATGTTTTT
                              ||||||||  ||  |||||||||
                              AGATTATA  GT  TTACAAAAA
                                  AC  ACT
GAM1102 BCL11B   3' AATGTCCAATTTATTTTTA  35646        AA
                              AATGTCCAATT  TGTTTTTA
                              |||||||||||  ||||||||
                              TTACAGGTTAA  ATAAAAAT
                                          __
GAM1102 CYP24    3' TCTAGTTTCCCAATAATGTTTT 8951     ATG  AAT
           TA                  TCTA  TCC  TAATGTTTTTA
                              ||||  |||  ||||||||||||
                              AGAT  AGG  ATTACAAAAAT
                                CAA  GTT
GAM1102 EGFL5    5' CTAATGTCTAATTAGATTAATG 44521      CA_____
           TTTTT                CTAATGTC     ATTAATGTTTTT
                              ||||||||     ||||||||||||
                              GATTACAG     TAATTACAAAAA
                                  ATTAATC
GAM1102 ZNF137   3' TCTAATGTCAATTAAAGCTTT  18337       C    T
                              TCTAATGTC AATTAA GTTTT
                              |||||||||| |||||| |||||
                              AGATTACAG TTAATT CGAAA
                                   _    T
GAM1103 RPL15    3' CTAGTCTCCTGGAAGACATGGT 16391    CATG  A     A
                              TTAG   TTCT GAAGACAT GT
                              ||||   |||| |||||||| ||
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                                GATC    AGGA CTTCTGTA CA
                                  AG__    C       C
GAM1103  TPX1     3'  TTAGCATGTTTCAGGAAATAC  17667          _ TA    _
                                TTAGCATGTT C  GAAG AC
                                |||||||||| |  |||| ||
                                AATCGTACAA G  CTTT TG
                                     A TC    A
GAM1103  ZNF268   3'  TGTACTAAGAAGACATAGT    41766     T  _
                                TGT CTA GAAGACATAGT
                                ||| ||| ||||||||||
                                ACA GAT CTTCTGTATCA
                                  T   T
GAM1103  BECN1    3'  TTTCTATTTCATATTGTTA    19072          TATA   A
                                TTTCTATTTC    GTA TGTTA
                                ||||||||||    ||| |||||
                                AAAGATAAAG    TAT ACAAT
                                     _____  A
GAM1104  PDK4     3'  TATATCAAAAATATATCT     15206           TCAA
                                TGTATCAAAAATA    TATCT
                                ||||||||||||    |||||
                                ATATAGTTTTTAT    ATAGA
                                          _____
GAM1104  SDC1     3'  TGTGCAAAAACAAGTCGATATC 16514     AT       __  A
            TA                    TGT  CAAAAATA  TC ATATCTA
                                |||  ||||||||  || |||||||
                                ACA  GTTTTTGT  AG TATAGAT
                                  C_       TC  C
GAM1104  VAPB     3'  TGTACCAAGGCCTACCAAT    21877         AAA_
                                TGTATCAA    TATCAAT
                                ||||||||    |||||||
                                ACATGGTT    ATGGTTA
                                     CCGG
GAM1104  COL4A4   3'  TAATGTTTTATATTCATCTGTG 6405          TA___     AT
            ATGT                    TAATGTTTT    TATCTG  ATGT
                                |||||||||    ||||||  ||||
                                ATTACAAAA    GTAGAC  TACA
                                     TATAA     AC
GAM1105  TBR1     3'  TCAACATCCTATGGTTAAT    27315         A   TCCAA
                                TCAATATCC ATG     TTAAT
                                ||||||||| |||     |||||
                                AGTTGTAGG TAC     AATTA
                                     A   C_____
GAM1105  ADRA2A   5'  ATATATATACATATCAATATCT 8626        CAAAA
                                ATGTAT    ATATCAATATCT
                                ||||||    ||||||||||||
                                TATATA    TATAGTTATAGA
                                   TATG_
GAM1105  MMP10    3'  TATTAAAAACACCCATATCT   14551     C        A
                                TAT AAAAATATC ATATCT
                                ||| ||||||||| ||||||
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                                ATA TTTTTGTGG TATAGA
                                  A       G
GAM1105  NCOR2    3'  GTATCAAAAATATACCC    26741          TCAA
                                GTATCAAAAATA   TATCT
                                ||||||||||||  |||||
                                CATAGTTTTTAT   ATGGG
                                      ____
GAM1105  PDK4     3'  ATATATCAAAAATATATCT   15202          TCAA
                                ATGTATCAAAAATA   TATCT
                                ||||||||||||||  |||||
                                TATATAGTTTTTAT   ATAGA
                                      ____
GAM1105  SDC1     3'  ATGTGCAAAAACAAGTCGATAT 16499     AT      __ A
             CTA                   ATGT  CAAAAATA  TC ATATCTA
                                ||||  ||||||||  || |||||||
                                TACA  GTTTTTGT  AG TATAGAT
                                  C_       TC  C
GAM1105  SOX11    3'  ATGTATCAAAAATGTTTCAATA 17004          A__
                                ATGTATCAAAAAT   TCAATA
                                ||||||||||||||  ||||||
                                TACATAGTTTTTA   AGTTAT
                                      CAA
GAM1105  VAPB     3'  ATGTACCAAGGCCTACCAAT   21872        AAA_
                                ATGTATCAA    TATCAAT
                                |||||||||    |||||||
                                TACATGGTT    ATGGTTA
                                     CCGG
GAM1106  CYP1A1   3'  CAATGCAGGCTAGAATAGAA   7970      A        TAT
                                CAAT CAGGCTAGAAT   GAA
                                ||||  ||||||||||||  |||
                                GTTA GTCCGATCTTA   CTT
                                  C         T__
GAM1106  GNRH1    3'  CAACACAGCACTTTATTATG   9074        _  AGA
                                CAATACAG GCT   ATTATG
                                ||||||||  |||   ||||||
                                GTTGTGTC TGA   TAATAC
                                     G   AA_
GAM1106  KCNMB3   5'  CAGTCCACTCAGAATTATGAA  30836    ___  _
                                CAG   GCT AGAATTATGAA
                                |||   |||  ||||||||||||
                                GTC   TGA TCTTAATACTT
                                  AGG   G
GAM1106  PARK2    3'  CAATACAGGTAGAACAAAAGA  30370        C     TAT_
                                CAATACAGG TAGAAT    GA
                                |||||||||  ||||||   ||
                                GTTATGTCC ATCTTG    CT
                                     _     TTTT
GAM1106  PIK3CG   5'  CAATACAGGTTGGACTAGA   15302        _____
                                CAATACAGG    CTAGA
                                |||||||||    |||||
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                                GTTATGTCC    GATCT
                                     AACCT
GAM1106 ARF3    3' TTTATGAGAAGTGAGTGA    11680         AAAT   A
                                TTTATGAGAAG   TGGG TGA
                                ||||||||||   |||| |||
                                AAATACTCTTC   ACTC ACT
                                     ____   _
GAM1106 BCL9    5' TTTATGAGGAGAAATTCTGGA 20246        A     G_
                                TTTATGAG AGAAATT  GGA
                                |||||||| |||||||  |||
                                AAATACTC TCTTTAA  CCT
                                     C      GA
GAM1106 CLCN1   3' TTTATGAGGAGGTCGTGGG   6354         A  AAAT
                                TTTATGAG AG   TGGG
                                |||||||| ||   ||||
                                AAATACTC TC   ACCC
                                     C  CAGC
GAM1106 CXCL6   3' TTTATGAGAAGAGTGAG     16491          AAT
                                TTTATGAGAAGA   TGGG
                                ||||||||||||  ||||
                                AAATACTCTTCT   ACTC
                                       C__
GAM1106 DNMT3B  3' TTTAGGAGAAGAAAAAATGA  27885     T       TTG
                                TTTA GAGAAGAAA   GGATGA
                                |||| |||||||||  ||||||
                                AAAT CTCTTCTTT   TTTACT
                                  C       ___
GAM1106 DTR     3' CTTATGAGGGGAAGTGGG    12612        AA   AT
                                TTTATGAG  GAA  TGGG
                                ||||||||  |||  ||||
                                GAATACTC  CTT  ACCC
                                     CC   C_
GAM1106 FBXL7   3' TGAGAAGAAAATAAATGA    29415         TTG
                                TGAGAAGAAA   GGATGA
                                ||||||||||   ||||||
                                ACTCTTCTTT   TTTACT
                                       TA_
GAM1106 NFE2    3' TTTATCAGAAGGGAATGA    26085      G    AAATT
                                TTTAT AGAAG    GGGATGA
                                |||||| |||||    |||||||
                                AAATA TCTTC    CCTTACT
                                  G    _____
GAM1106 PIK3CG  5' TTTATGAGAAGATGTTGGA   15309          AA
                                TTTATGAGAAGA  TTGGG
                                ||||||||||||  |||||
                                AAATACTCTTCT  AACCT
                                       AC
GAM1106 PRG3    3' TTTATGAGCAGGAGAGGTTGGG 25898        A___   AA
                                TTTATGAG   AGA  TTGGG
                                ||||||||   |||  |||||
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                              AAATACTC   TCT  AACCC
                                  GTCC   CC
GAM1106  SPRR2C   3'  ATGAGAAGATGCAGGTG    27164        AAT   A
                              ATGAGAAGA   TGGG TG
                              |||||||||   |||| ||
                              TACTCTTCT   GTCC AC
                                  AC_   _
GAM1106  TCF12    3'  TTTATGAAGGAAAGCTTCTGGG 17348       ___   AAA
                              TTTATGA   GAAG   TTGGG
                              |||||||   ||||   |||||
                              AAATACT   TTTC   GACCC
                                  TCC   GAA
GAM1107  APTX     3'  TGTTAGCTGAACTTCAA    32811    C   GACC
                              TG TGGC   AACTTCAA
                              || ||||   ||||||||
                              AC ATCG   TTGAAGTT
                               A   AC__
GAM1107  PKNOX1   3'  TCGCTGCTGGGACTCCA    21312        C   CAAC
                              TCGCTGCTGG GAC   TTCA
                              |||||||||| |||   ||||
                              AGCGACGACC CTG   AGGT
                                  _  ____
GAM1107  RERE     3'  TCGCTGCTGTGACCAGGCCTC 29038        GC    A_
                              TCGCTGCTG  GACCA  CTTC
                              |||||||||  |||||  ||||
                              AGCGACGAC  CTGGT  GGAG
                                  A_    CC
GAM1107  KCNA3    5'  GTGGTTCACCAGCGTGT    13796    AA  AC
                              GTG  GT  TCACCAGCGTGT
                              |||  ||  ||||||||||||
                              CAC  CA  AGTGGTCGCACA
                                __  __
GAM1108  RNGTT    3'  AGTTGTTTAATATAGTACA   19163        _  C
                              AGTTGTTTA TA AGTACA
                              ||||||||| || ||||||
                              TCAACAAAT AT TCATGT
                                  T  A
GAM1108  CRADD    3'  TGCTGAGTAATCTGGCCTTTCA 19182        C____  AAC
           AG                   TGCTGAGTGA    CC   CAAG
                              ||||||||||    ||   ||||
                              ACGACTCATT    GG   GTTC
                                   AGACC  AAA
GAM1108  EIF4E    3'  CTGAGTAACATTAAGAG     12693        CCAACC   C
                              CTGAGTGAC     AAGA G
                              |||||||||     |||| |
                              GACTCATTG     TTCT C
                                  TAA___    A
GAM1108  LIMD1    3'  TGGTGAGATGAACCAAGACGG  30638    C   _   CCCA
                              TG TGAG TGA    ACCAAGACGG
                              || |||| |||    ||||||||||
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                                AC ACTC ACT    TGGTTCTGCC
                                 C    T  _____
GAM1108 POU2AF1  3' TGTGAGTGACCCTAAGAG    26380    C        AACC    C
                                TG TGAGTGACCC    AAGA G
                                || ||||||||||    |||| |
                                AC ACTCACTGGG    TTCT C
                                 _        A___    A
GAM1108 SIAT7D   3' GCTGCCCCAACCAGGGCG    30831     AGTGA      AGA
                                GCTG    CCCAACCA   CG
                                ||||    ||||||||  ||
                                CGAC    GGGTTGGT   GC
                                  G____       CCC
GAM1108 SLC6A12  5' TGCTGAGTGACCTCAGCCTAG  16804           _  A  A
                                TGCTGAGTGACC CA CC AG
                                |||||||||||| || || ||
                                ACGACTCACTGG GT GG TC
                                       A  C  A
GAM1108 VPREB1   3' TGCTGAGTGGCTCAGCCTCCTC 28324         ACC  A  AAGA
            GG                    TGCTGAGTG   CA CC    CGG
                                |||||||||   || ||    |||
                                ACGACTCAC   GT GG    GCC
                                     CGA  C  AGGA
GAM1108 VPS41    3' TGCTGAGTGTCCGCCA      30820         A  CAA
                                TGCTGAGTG CC   CCA
                                |||||||| ||   |||
                                ACGACTCAC GG   GGT
                                     A  C__
GAM1109 GAS11    3' TGAGTGCGGGGCACTCTGAGAA 11222    T         GGTT_
            GG                    A AGTGCGGGGCAC     GAAGG
                                | ||||||||||||     |||||
                                A TCACGCCCCGTG     CTTCC
                                 C          AGACT
GAM1109 CERD4    3' TCACCAAAGCCACTGG      28954         C    ACTTAT
                                TCACCAAA CCAC      TGG
                                |||||||| ||||      |||
                                AGTGGTTT GGTG      ACC
                                     C   _______
GAM1109 DSG1     3' TCACTAAACACACACTAGA    12602      C   C     TATT
                                TCAC AAAC CACACT    GGA
                                |||| |||| ||||||    |||
                                AGTG TTTG GTGTGA    TCT
                                  A    T     _____
GAM1109 DTR      3' TCATCAAATCCAGCACTGGA   12617     C   C  _   TATT
                                TCA CAAA CCA CACT    GGA
                                ||| |||| ||| ||||    |||
                                AGT GTTT GGT GTGA    CCT
                                  A   A  C    _____
GAM1109 FMR2     3' TCACCAAGCCTCCATCAAGA   12982        A  CA  C   TT
                                TCACCAA CC  CA TTA  GGA
                                ||||||| ||  || |||  |||
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                                AGTGGTT GG  GT AGT  TCT
                                    C  AG  _  __
GAM1109  GALNT2   3'  TCACCAGACTCCACCCAATGG  21010       A  _   A  TAT
                                TCACCA AC CCAC CT   TGG
                                |||||| || |||| ||   |||
                                AGTGGT TG GGTG GG   ACC
                                   C  A    _  TT_
GAM1109  LLGL1    3'  TCCCAGGCCCACACCCTGG   42510    A   AA       TA
                                TC CCA  CCCACACT  TTGG
                                || |||  ||||||||  ||||
                                AG GGT  GGGTGTGG  GACC
                                  _  CC       __
GAM1109  METTL1   5'  TCTACCAAATCCACGTGGA   35707    _     C    ACTTAT
                                TC ACCAAA CCAC     TGGA
                                || |||||| ||||      ||||
                                AG TGGTTT GGTG     ACCT
                                 A      A   C_____
GAM1109  MGA      3'  TCACCAAACTTCTGTTCTTAGA 41727         CCACACTTA
                                TCACCAAAC        TTGGA
                                |||||||||        |||||
                                AGTGGTTTG        AATCT
                                     AAGACAAG_
GAM1109  MS4A1    3'  ACCAGAACTCATGTATTGGA   6595      _  C  CACT
                                ACCA AAC CA    TATTGGA
                                |||| ||| ||    |||||||
                                TGGT TTG GT    ATAACCT
                                  C   A  AC__
GAM1109  NCOA3    3'  TCACCAATTCCACTGG      27219        AC    ACTTAT
                                TCACCAA  CCAC     TGG
                                |||||||  ||||     |||
                                AGTGGTT  GGTG     ACC
                                    AA   _______
GAM1109  POLS     3'  TCACCAGACCCATCATCACAGG 28124       A    _ C    T
                                TCACCA ACCCA CA TTAT GG
                                |||||| ||||| || |||| ||
                                AGTGGT TGGGT GT AGTG CC
                                    C    A  _   T
GAM1109  PTPRF    3'  ACCAGGCCCACTGGCCTGGAC  39026     AA    ACTTA
                                ACCA  CCCAC    TTGGAC
                                ||||  |||||    ||||||
                                TGGT  GGGTG    GACCTG
                                  CC    ACCG_
GAM1109  SULT1A3  3'  TCACTGTATCCACAACCTCCTG 17214     CAAAC    _  A
            G                    TCAC    CCACA CTT TTGG
                                ||||    ||||| ||| ||||
                                AGTG    GGTGT GGA GACC
                                  ACATA    T  G
GAM1109  TARDBP   3'  TCACCAAAGCCACAGG      28907        C    CTTATT
                                TCACCAAA CCACA     GG
                                |||||||| |||||     ||
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                                AGTGGTTT GGTGT     CC
                                    C    _______
GAM1109  TCF3     3'  CCAGGCCCACACCTGG      43319     AA       TAT
                                CCA  CCCACACT   TGG
                                |||  ||||||||   |||
                                GGT  GGGTGTGG   ACC
                                  CC       ___
GAM1109  TEM7     3'  CCAAATAAGCGTTTATTGGAC  33804       CCCACAC
                                CCAAA      TTATTGGAC
                                |||||      |||||||||
                                GGTTT      AATAACCTG
                                   ATTCGCA
GAM1110  ACTN2    3'  CAAAAAGCATGGGAACCTGGAA 9940            A  A
                                TAAAAAGCATGG AA TTGGAA
                                ||||||||||||| || ||||||
                                GTTTTTCGTACC TT GACCTT
                                        C  G
GAM1110  ADAMTS5  3'  AAAAGCATGGAATAGTGG    28170           AAT
                                AAAAGCATGGAA   TGG
                                ||||||||||||   |||
                                TTTTCGTACCTT   ACC
                                        ATC
GAM1110  ATP7A    3'  TGAAAGCATGGAGGATGG    6266    A        AAAT
                                A AAAGCATGGA    TGG
                                | ||||||||||    |||
                                A TTTCGTACCT    ACC
                                 C         CCT_
GAM1110  DSS1     5'  AAGCAGAAAAGTTGGAAC    26702       T    A
                                AAGCA GGAAA TTGGAAC
                                ||||| ||||| |||||||
                                TTCGT CTTTT AACCTTG
                                   _    C
GAM1110  DYRK1A   3'  TAAAAAGCAGGAAGGGA     38997         T   AATT
                                TAAAAAGCA GGAA    GGA
                                ||||||||| ||||    |||
                                ATTTTTCGT CCTT    CCT
                                      _   C___
GAM1110  GPR85    3'  AAAAAGTAAACTCTAATTGGAA 33252       CATGGAA_
              CC                  AAAAAG       AATTGGAACC
                                |||||||      ||||||||||
                                TTTTTC       TTAACCTTGG
                                   ATTTGAGA
GAM1110  HRMT1L1  3'  AACATGGAGCTCCGACC     42176        AAA  G  A
                                AGCATGGA   TT GA CC
                                ||||||||   || || ||
                                TTGTACCT   AG CT GG
                                     CG_  G  _
GAM1110  LANGERIN 3'  AGCAGGGCAATTGGAAC     31841      T  AA
                                AGCA GG  AATTGGAAC
                                ||||  ||  |||||||||
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                                TCGT CC  TTAACCTTG
                                  _ CG
GAM1110 LNK     3'  AAAGCATGAAGGAA       24193          AAATT
                                AAAGCATGGA    GGAA
                                ||||||||||    ||||
                                TTTCGTACTT    CCTT
                                      _____
GAM1110 MIR16   3'  TAAAAAGCCTGGAAAAGTGCAA 32497        A     T  G
            C                    TAAAAAGC TGGAAAA TG AAC
                                ||||||||| ||||||| || |||
                                ATTTTTCG ACCTTTT AC TTG
                                     G      C  G
GAM1110 PHTF1   3'  AAAAGCATGAAAATACAGG   27354           _  T
                                AAAAGCATGGAAA AT GG
                                |||||||||||||| || ||
                                TTTTCGTACTTTT TG CC
                                       A  T
GAM1110 PKHD1   3'  CAAAAAGCATGGAGAAATGG  39802           A  T
                                TAAAAAGCATGGA AA TGG
                                |||||||||||||| || |||
                                GTTTTTCGTACCT TT ACC
                                       C  T
GAM1110 RAB1A   3'  TGAAAGCATGGAAGAAAAAC  43191   A        AATT
                                A AAAGCATGGAA   GGAAC
                                | ||||||||||    |||||
                                A TTTCGTACCTT   TTTTG
                                 C         CT__
GAM1110 RAG1    3'  TAAAAAGCAAGGAAAACT    7787          T
                                TAAAAAGCA GGAAAATT
                                |||||||||| ||||||||
                                ATTTTTCGT CCTTTTGA
                                      T
GAM1110 RBMX    3'  TAAAAATTATGGAGGGGAAC  42811      GC    AAATT
                                TAAAAA  ATGGA    GGAAC
                                ||||||  |||||    |||||
                                ATTTTT  TACCT    CCTTG
                                    AA    CC___
GAM1110 RPS15A  5'  GCAGACGGATGAAATTGGA   9747     __   __
                                GCA  TGGA  AAATTGGA
                                |||  ||||  ||||||||
                                CGT  GCCT  TTTAACCT
                                  CT    AC
GAM1110 SLC21A9 3'  TAAAAAGGGAATTGGAAC    28569       CAT   AA
                                TAAAAAG   GGA  ATTGGAAC
                                |||||||   |||  ||||||||
                                ATTTTTC   CCT  TAACCTTG
                                      ___  __
GAM1110 SLC4A7  3'  AAAAGCCATAAAAATTGGAAC 18815       ATG
                                AAAAGC   GAAAATTGGAAC
                                ||||||   ||||||||||||
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                                TTTTCG   TTTTTAACCTTG
                                   GTA
GAM1110 TIE      3' AAAGCATGGGAACC       24051         AAAATTG
                                AAAGCATGG      GAACC
                                |||||||||      |||||
                                TTTCGTACC      CTTGG
                                        _______
GAM1110 TNFSF11  3' AAGAGCATGGATACTGA    37451    A       AA
                                AA AGCATGGA  ATTGG
                                || ||||||||  |||||
                                TT TCGTACCT  TGACT
                                 C       A_
GAM1110 APBA1    3' CCTCAAGGGAGTGCA      43087    C       AAAATT
                                CC CAAGGGAG     TGCA
                                || ||||||||     ||||
                                GG GTTCCCTC     ACGT
                                 A      _______
GAM1110 APG5L    3' CAAGGGGGAAAATCCCCA    22130       A       G
                                CAAGGG GAAAATTT CA
                                |||||| |||||||| ||
                                GTTCCC CTTTTAGG GT
                                   C       G
GAM1110 ARHGEF12 3' CCAAGGAGAAATTGAACTGCA 31636       G     AT___
                                CCAAGG AGAAA    TTGCA
                                |||||| |||||    |||||
                                GGTTCC TCTTT    GACGT
                                   _    AACTT
GAM1110 BCL7A    3' CCAAGGGCTTTGCAC      34202        AGAAAA
                                CCAAGGG     TTTGCAC
                                |||||||     |||||||
                                GGTTCCC     AAACGTG
                                   G_____
GAM1110 CD68     3' ACCCCGTCAAAGATTTGCA   40781      AAG    AAA
                                ACCCC   GGAGA   TTTGCA
                                |||||   |||||   ||||||
                                TGGGG   TTTCT   AAACGT
                                  CAG    ___
GAM1110 CEBPA    3' CCCCAAGGGAAAGCCAGC    20388          AAATTT
                                CCCCAAGGGAGA     GC
                                ||||||||||||     ||
                                GGGGTTCCCTTT     CG
                                       CGGT__
GAM1110 CPLX2    5' CCCACGGCAGAATTTGCA    27395     A  G   AA
                                CCCA GG AGA  ATTTGCA
                                |||| || |||  |||||||
                                GGGT CC TCT  TAAACGT
                                  G  G   __
GAM1110 CSNK1G2  3' CCCCAAGGGGCTGCA      10607        AGAAAAT
                                CCCCAAGGG      TTGCA
                                |||||||||      |||||
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                                GGGGTTCCC      GACGT
                                    C_______
GAM1110  DHCR7    3'  CCTCAGGGAAGAAAGCAC    10684    C  A       ATTT
                                CC CA GGGAGAAA    GCAC
                                || || ||||||||    ||||
                                GG GT CCTTCTTT    CGTG
                                 A  C       _____
GAM1110  DIAPH2   3'  CAAGGGAGAAAGAAGCA     28667           ATTT
                                CAAGGGAGAAA    GCA
                                ||||||||||    |||
                                GTTCCCTCTTT    CGT
                                      CTT_
GAM1110  EML1     3'  CCCCAAGGGAGAATGCA     40721            AATT
                                CCCCAAGGGAGAA    TGCA
                                ||||||||||||    ||||
                                GGGGTTCCCTCTT    ACGT
                                      _____
GAM1110  ERCC1    5'  CCTCAAGGGAAAGACTGCA    12760    C        AAAT
                                CC CAAGGGAGA    TTGCA
                                || |||||||||    |||||
                                GG GTTCCCTTT    GACGT
                                 A        CT__
GAM1110  FMR2     3'  ACCTCCGGGATGCAAATTTGCA 12947     _  AA    GA_
                                ACC CC  GGGA   AAATTTGCA
                                ||| ||  ||||   |||||||||
                                TGG GG  CCCT   TTTAAACGT
                                  A  __    ACG
GAM1110  FMR2     3'  ACCCCAGGTGAGGATTTACA   12946       A  _   AAA
                                ACCCCA GG GAG   ATTTGCA
                                |||||| || |||   |||||||
                                TGGGGT CC CTC   TAAATGT
                                   _  A   C__
GAM1110  GADD45B  5'  CCCCAGGGAGAAATTGCA    31828       A       AT
                                CCCCA GGGAGAAA  TTGCA
                                ||||| ||||||||  |||||
                                GGGGT CCCTCTTT  AACGT
                                   _      __
GAM1110  GARS     5'  GAGCGAACAGATTTGCACA    13057     A   A__
                                GGG GAA   ATTTGCACA
                                ||| |||   |||||||||
                                CTC CTT   TAAACGTGT
                                  G   GTC
GAM1110  GLO1     3'  CAAAGGAGAATTCTCACA    27467         AA   TG
                                CAAGGGAGA  ATT  CACA
                                |||||||||  |||  ||||
                                GTTTCCTCT  TAA  GTGT
                                      __  GA
GAM1110  JMJ      3'  CCCAAGGGAGGGGTGCA     22483          AAAATT
                                CCCAAGGGAG     TGCA
                                ||||||||||     ||||
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                                GGGTTCCCTC     ACGT
                                     CCC___
GAM1110 LIMK1    3' CCCAAAGGAGAACA       32528          AAATTT
                                CCCAAGGGAGA     GCA
                                ||||||||||     |||
                                GGGTTTCCTCT     TGT
                                      _______
GAM1110 MBNL     3' ACCCTCAAGAGTTTGCAC    34306     _     AGAAAA
                                ACCC CAAGGG     TTTGCAC
                                |||| ||||||     |||||||
                                TGGG GTTCTC     AAACGTG
                                  A     _______
GAM1110 MECP2    3' ACTCCGAGGGAAAAGGGGGAGC 22569    C  A      AATTT_
             A                   AC CC AGGGAGAA     GCA
                                || || ||||||||     |||
                                TG GG TCCCTTTT     CGT
                                 A  C       CCCCCT
GAM1110 MECP2    3' ACCCCAAGGCAGGGGCAGCA   22566         G  AAAATTT
                                ACCCCAAGG AG      GCA
                                |||||||||  ||      |||
                                TGGGGTTCC TC      CGT
                                     G  CCCGT__
GAM1110 MLLT2    3' CCCCAAGGGAGGAAATTCA   25498          A
                                CCCCAAGGGAG AAATTTG
                                |||||||||| |||||||
                                GGGGTTCCCTC TTTAAGT
                                      C
GAM1110 NAPB     3' AAGGAAGTAAGTTTGCACA   43163        A  A
                                AAGGGAG AA TTTGCACA
                                ||||||| || ||||||||
                                TTCCTTC TT AAACGTGT
                                    A  C
GAM1110 OCA2     3' CCTTGGGGAGAAAGGACACA  41190    CAA       ATTT
                                CC   GGGAGAAA    GCACA
                                ||   ||||||||    |||||
                                GG   CCCTCTTT    TGTGT
                                 AAC       CC__
GAM1110 OXTR     3' ACCCCAAGGAGGGGAGGGATAC 9517         _____    AAAATT
             A                   ACCCCAA    GGGAG     TGCA
                                |||||||    |||||     ||||
                                TGGGGTT    CCCTC     ATGT
                                    CCTC    CCT___
GAM1110 PCDHA9   3' CCCTTCTGAGAATTTGCA    36541     AAGG    AA
                                CCC    GAGA  ATTTGCA
                                |||    ||||  |||||||
                                GGG    CTCT  TAAACGT
                                  AAGA   __
GAM1110 PCOLN3   3' CCCAAGGGGAGGAGCTGCA   15749         A  AAAT
                                CCCAAGGG GA    TTGCA
                                |||||||| ||    |||||
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                                GGGTTCCC CT   GACGT
                                    _ CCTC
GAM1110 RUNX1   3' CAAGGCAGAAATCTGCA    12009     G   A
                                CAAGG AGAAA TTTGCA
                                ||||| ||||| ||||||
                                GTTCC TCTTT AGACGT
                                   G   _
GAM1110 SCML1   3' CCCAATCTAAATTTGCACA   27558     GGGAGA
                                CCCAA    AAATTTGCACA
                                |||||    ||||||||||
                                GGGTT    TTTAAACGTGT
                                   AGA___
GAM1110 SH2D2A  3' ACTCCAGGAGGAGAAACCAGGA 19563   C  A_     ATTT_
            CA                   AC CCA  GGGAGAAA    GCA
                                || |||  ||||||||    |||
                                TG GGT  TCCTCTTT    TGT
                                 A  CC      GGTCC
GAM1110 SLC2A3  3' CCCAAGGGAGGAAAAGCTGGCA 27974        _   T  _
                                CCCAAGGGAG AAAA TTG CA
                                |||||||||| |||| ||| ||
                                GGGTTCCCTC TTTT GAC GT
                                      C   C  C
GAM1110 TNFRSF1B 3' CCCAGGGGGAGAAACAAACA  9872     A_     ATTT
                                CCCA  GGGAGAAA   GCA
                                ||||  ||||||||   |||
                                GGGT  CCCTCTTT   TGT
                                  CC      GTT_
GAM1110 WEE1    3' CCAAAGGAGGGAAAGGGTGCA 18083       AA  TT__
                                CCAAGGGAG  AA   TGCA
                                |||||||||  ||   ||||
                                GGTTTCCTC  TT   ACGT
                                     CC  TCCC
GAM1110 WNT3A   3' CCCCAGGGAGAAGCCAACGCA  37539     A     AATT_
                                CCCCA GGGAGAA    TGCA
                                ||||| |||||||    ||||
                                GGGGT CCCTCTT    GCGT
                                   _     CGGTT
GAM1111 ATP2B4  5' GTCCAGGGTAGGTAGGTTCC   43200      TCCGCA
                                GTTCAGG     TAGGTTCC
                                |||||||     ||||||||
                                CAGGTCC     ATCCAAGG
                                    CATCC_
GAM1111 C4B     3' GTTCAGGTTCCTCCC      8236        _ GCATAGGT
                                GTTCAGGT CC      TCCC
                                |||||||| ||      ||||
                                CAAGTCCA GG      AGGG
                                    A _________
GAM1111 CDH5    3' GTTTGGGTCCCCAGGCCCA   12193    CA   G  TA  TT
                                GTT  GGTCC CA  GG  CCCA
                                |||  ||||| ||  ||  ||||
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                                CAA  CCAGG GT  CC  GGGT
                                  AC    G __ __
GAM1111  DFFB    3'  GTTCAGATCCGCGTGTTTCCTT 44602          ATAGG  __
             CCAG                  GTTCAGGTCCGC    TTC  CCAG
                                |||||||||||    |||  ||||
                                CAAGTCTAGGCG    AGG  GGTC
                                      CACAA   AA
GAM1111  GFRA1   5'  GTTCAGGTCCGACCCAA    23568          CATAGGTT
                                GTTCAGGTCCG      CCCAG
                                ||||||||||       |||||
                                CAAGTCCAGGC      GGGTT
                                      T_______
GAM1111  KLHL1   5'  TCGGGTCCGCAGGACC     34084    A      TA  TT
                                TC GGTCCGCA  GG  CC
                                || ||||||||  ||  ||
                                AG CCAGGCGT  CC  GG
                                 C       __  T_
GAM1111  GAD1    3'  ACTTGTCATTTGGTGG     30287          ATACCG
                                ACTTGTTATTTG     GG
                                ||||||||||||     ||
                                TGAACAGTAAAC     CC
                                      CA____
GAM1112  CDH12   3'  AATTTAGTAACTTACTAGA   19770          AGA  G
                                AATTTAGTAAC   TA TAGA
                                ||||||||||   || ||||
                                TTAAATCATTG   AT ATCT
                                      A__  G
GAM1112  DSC3    3'  ATGAATTTGGTAGTGCAGTAG  35942        A   ACAGA
                                ATGAATTT GTA    TAGTAG
                                ||||||||  |||    ||||||
                                TACTTAAA CAT    GTCATC
                                    C   CAC__
GAM1112  TRHDE   3'  ATGAATTCAGTGGTGATAG   30101          AACA
                                ATGAATTTAGT    GATAG
                                ||||||||||    |||||
                                TACTTAAGTCA    CTATC
                                      CCA_
GAM1112  CASP8   3'  CATTTGAATTTTTAAAAG    37870          TT
                                CATTTGAATTTTTA  AAG
                                ||||||||||||||  |||
                                GTAAACTTAAAAAT  TTC
                                       T_
GAM1112  CASP8   3'  CATTTGAATTTTTAAAAGA   37871           TT
                                CATTTGAATTTTTA  AAGA
                                ||||||||||||||  ||||
                                GTAAACTTAAAAAT  TTCT
                                       T_
GAM1112  ZNF264  3'  CACTTGAATTTTTATTTAAAA  18267             A
                                CATTTGAATTTTTATT AGAA
                                ||||||||||||||| ||||
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                                GTGAACTTAAAAATAA TTTT
                                       A
GAM1113 ABCC11   3' AAGTAGCCTATTCCAGGGT   37613    C    CC   AA
                                AAG AGCCTA  CCG  GGT
                                ||| ||||||  |||  |||
                                TTC TCGGAT  GGT  CCA
                                  A     AA   C_
GAM1113 ATP1A2   3' ACAGCCTTTGGGAGGTGGTT  8703       ACCCC  A
                                GCAGCCT    GA GGTGGTT
                                |||||||    || |||||||
                                TGTCGGA    CT CCACCAA
                                    AACC_  _
GAM1113 BTG1     5' AGCAGCCACCCCGGGC      11905       T     AA
                                AGCAGCC ACCCCG  GGT
                                ||||||| ||||||  |||
                                TCGTCGG TGGGGC  CCG

                                    _     __
GAM1113 FXYD6    3' AAGCAGCCGCCTCAGGT     35112       TACC  GA
                                AAGCAGCC   CC  AGGT
                                ||||||||   ||  ||||
                                TTCGTCGG   GG  TCCA
                                    C___  AG
GAM1113 LIMD1    3' AAGCAGTGTACCTTATCCTGGT 30625      CC   CCGAAGG
              T                  AAGCAG  TACC      TGGTT
                                 ||||||  ||||      |||||
                                 TTCGTC  ATGG      ACCAA
                                    AC   AATAGG_
GAM1113 LPO      3' GCAGCCACCCTGGGGC      42739       T   CGAA  T
                                GCAGCC ACCC   GG GGT
                                |||||| ||||   || |||
                                CGTCGG TGGG   CC CCG
                                   _   A___  _
GAM1113 MFAP2    3' AGCCTACCTCGGGGG       32704       C  AA  T
                                AGCCTACC CG  GG GG
                                |||||||| ||  || ||
                                TCGGATGG GC  CC CC
                                    A  __  _
GAM1113 MYO1D    3' AAGCGGCCGACCCTGAGGGC  43482     A  T   C  A
                                AAGC GCC ACCC GA GGT
                                |||| ||| |||| || |||
                                TTCG CGG TGGG CT CCG
                                  C   C    A  C
GAM1113 PDX1     3' AAGCGGTTTACCTAGAAAGGT  18486     AGCC   CC_
                                AAGC   TACC   GAAGGT
                                ||||   ||||   ||||||
                                TTCG   ATGG   TTTCCA
                                  CCAA   ATC
GAM1113 RFNG     3' GCAGCCCTGGGTCGGGGTGGTT 44770       ACCC_  AA
                                GCAGCCT    CG  GGTGGTT
                                |||||||    ||  |||||||
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                                CGTCGGG    GC  CCACCAA
                                   ACCCA  C_
GAM1113  SFN      3'  AAGTAGCCTGGTCCTGGGGT  43963    C    ACC  GAA  T
                                AAG AGCCT   CC   GG GGT
                                ||| |||||   ||   || |||
                                TTC TCGGA   GG   CC CCA
                                  A    CCA  A__  _
GAM1113  WNT3A    3'  AGCAGCCTACCCCAGAGCCG  37534           A  G
                                AGCAGCCTACCCCG AG TG
                                |||||||||||||| || ||
                                TCGTCGGATGGGGT TC GC
                                        C  G
GAM1113  ZNF76    3'  AGCTGGCCTCCAGGGAGGTGGT 18303    A_   A  CCGA
              T                  AGC  GCCT CC   AGGTGGTT
                                |||  |||| ||   ||||||||
                                TCG  CGGA GG   TCCACCAA
                                  AC   _ TCCC
GAM1113  BARHL1   3'  GGTCACGGGCTCATGGGTCAC  33473       GA   CACGA
                                GGTCACGG  GCTC    GTCAC
                                ||||||||  ||||    |||||
                                CCAGTGCC  CGAG    CAGTG
                                   __   TACC_
GAM1113  BSN      3'  GGTCATGTGGAGGACTCGGGTC 18412      CG_   CTCCA  A
              A                  GGTCA   GGAG    CG GTCA
                                |||||   ||||    || ||||
                                CCAGT   CCTC    GC CAGT
                                   ACA    CTGA_  C
GAM1113  TH1L     3'  GGTCGTGGGAGCCCAGCG    32309     AC     T  _
                                GGTC  GGGAGC CCA CG
                                ||||  |||||| ||| ||
                                CCAG  CCCTCG GGT GC
                                  CA     _  C
GAM1114  GALK1    5'  CCCCGTCGGCGCGGGATGCTC  6678           ACGC
                                CCCCGTTGGCGCG   GCTT
                                ||||||||||||   ||||
                                GGGGCAGCCGCGC   CGAG
                                        CCTA
GAM1114  NMB      5'  CGTTCGGGCGCGCTTC      43949      _  C  GAC
                                CGTT GG GC   GCGCTTC
                                |||| || ||   |||||||
                                GCAA CC CG   CGCGAAG
                                  G  _  ___
GAM1114  GRIN2A   3'  GTCGGGGGCACTTGTTTTT   9113     CA      C  C
                                GTC  GGGGCGTT GT TTT
                                |||  |||||||| || |||
                                CAG  CCCCGTGA CA AAA
                                  C_       A  A
GAM1115  ADARB1   5'  GCCGCTTGGCCGCCGCTG    31878      C    AC   _
                                GCCGC TGGCC  GTC CTG
                                ||||| |||||  ||| |||
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                                CGGCG ACCGG  CGG GAC
                                  A    __  C
GAM1115 ALPL    3' GCTTCCTGGGACCCTGGTG  7891    CG   CCACG
                                GC  CCTGG    TCCTGGTG
                                ||  |||||    ||||||||
                                CG  GGACC    GGGACCAC
                                 AA    CT___
GAM1115 AMN     3' CAGCCTCTGGCCGCCCAGGTG 36285     GC    AC   T
                                CAGCC  CTGGCC  GTCC GGTG
                                |||||  ||||||  |||| ||||
                                GTCGG  GACCGG  CGGG CCAC
                                  A_     __   T
GAM1115 MMP2    3' GCCACCTGGCCATGCCCTG   21198          C
                                GCCGCCTGGCCA GTCCTG
                                |||||||||||| ||||||
                                CGGTGGACCGGT CGGGAC
                                       A
GAM1115 NCOR2   3' GCCGCCCTGGCCGCCTG    26737      _    AC T
                                GCCGCC TGGCC  G CCTG
                                |||||| |||||  | ||||
                                CGGCGG ACCGG  C GGAC
                                   G    __ _
GAM1115 NFKB2   5' CAGCCGCCTGTCCGGG     14762        GGCCAC   T
                                CAGCCGCCT     GTCC GG
                                |||||||||     |||| ||
                                GTCGGCGGA     CAGG CC
                                      _______   C
GAM1115 PAX5    3' GCTCTCTGCCATCCTGGTG   32512   _ G_   CG
                                GC CT  GCCA  TCCTGGTG
                                || ||  ||||  ||||||||
                                CG GA  CGGT  AGGACCAC
                                 A  GA   __
GAM1115 PAX5    3' GCCCTTGGCCGTGGCCCTG   32511    GCC    AC_
                                GCC   TGGCC   GTCCTG
                                |||   |||||   ||||||
                                CGG   ACCGG   CGGGAC
                                  GA_    CAC
GAM1115 PITX1   5' GCCGCCTGGCTGCGACCTG   15325        CA  T
                                GCCGCCTGGC  CG CCTG
                                ||||||||||  || ||||
                                CGGCGGACCG  GC GGAC
                                      AC  T
GAM1115 RPS6KA2 3' AGCTGTGTGGCCACGGGAGCTG 34455    CGCC      TC__
                                AGC   TGGCCACG   CTG
                                |||   ||||||||   |||
                                TCG   ACCGGTGC   GAC
                                  ACAC      CCTC
GAM1115 SORCS2  3' CAGCCGCCGGCTTTGCTGGTG  34048       T  CACGTC
                                CAGCCGCC GGC     CTGGTG
                                |||||||| |||     ||||||
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                                GTCGGCGG CCG     GACCAC
                                     _  AAAC__
GAM1115 TNFRSF6B 3' CAGCTCCTGGTACCCTGGT  32348     CG    CCACG
                                CAGC  CCTGG    TCCTGGT
                                ||||  |||||    |||||||
                                GTCG  GGACC    GGGACCA
                                  A_    AT___
GAM1115 AGR2    5' GCCTTGTGTGAGTCGGCGGCTA 26923    C   GGCCGA
                                GCC TGTG     GGCGGCTA
                                ||| ||||     ||||||||
                                CGG ACAC     CCGCCGAT
                                  A   ACTCAG
GAM1115 B3GAT1  3' GCCCGTGGGCTGCTCT     38298     T     CGAG  GG
                                GCCC GTGGGC   GC  CT
                                |||| ||||||   ||  ||
                                CGGG CACCCG   CG  GA
                                  _     A___  A_
GAM1115 FAAH    3' CCTGTGGGCTGAGCTCTA    11050        C   G GG
                                CCTGTGGGC GAG C  CTA
                                ||||||||| ||| |  |||
                                GGACACCCG CTC G  GAT
                                     A   _ A_
GAM1115 FGF1    3' GCTCTGTGGGCTGGGGGTTA  37570    C      CGA  C  C
                                GC CTGTGGGC   GG GG TA
                                || ||||||||   || || ||
                                CG GACACCCG   CC CC AT
                                 A       AC_  _  A
GAM1115 IL2RB   3' GCCCTGTGGAGCTGCC      9384         GCCGA   G
                                GCCCTGTGG    GGC GCT
                                |||||||||    ||| |||
                                CGGGACACC    TCG CGG
                                     _____  A
GAM1115 LOXL1   3' GCCTGTGGGTTGGGGGCT    41184     C     CCGA  C
                                GCC TGTGGG    GG GGCT
                                ||| ||||||    || ||||
                                CGG ACACCC    CC CCGA
                                  _     AAC_  _
GAM1115 MAP3K7IP2 3' GCTCTGTGGGCTGACATTTAA 31522    C      CGA    GC
                                GC CTGTGGGC   GGCG  TAA
                                || ||||||||   ||||  |||
                                CG GACACCCG   CTGT  ATT
                                 A       A__    AA
GAM1115 MYOD1   3' GCCCTGTGGGGCGGGGG     42131         C  A  C
                                GCCCTGTGGG CG GG GG
                                |||||||||| || || ||
                                CGGGACACCC GC CC CC
                                     C  _  _
GAM1115 RFNG    3' GCCCTGGGTCGGGGTGG     44771       T  GC  A  C
                                GCCCTG GG  CG GG GG
                                ||||||  ||  || || ||
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                                CGGGAC CC  GC CC CC
                                   _ A_  C  A
GAM1115  RXRA     3'  CCCTCTCATCCCCGAGGCGGCT 16418     GTGGG__
                                CCCT      CCGAGGCGGCT
                                ||||      ||||||||||
                                GGGA      GGCTCCGCCGA
                                  GAGTAGG
GAM1115  SLC2A3   3'  CGCCCTGTGGCCCAGGC     27976         G  G
                                CGCCCTGTGG CC AGGC
                                |||||||||| || ||||
                                GCGGGACACC GG TCCG
                                      _  G
GAM1115  VGF      5'  CGTCCCGTGGGCTGGGCTCAGC 17990    C       CGA  __
             T                   CG CCTGTGGGC   GGC  GGCT
                                || |||||||||   |||  ||||
                                GC GGGCACCCG   CCG  TCGA
                                 A        AC_   AG
GAM1116  B4GALT1  3'  GTGCCCTGGCTGTGCCTTGGG  11287        A  ACGG   C_
                                GTGCCCTG GT    GCT  GGG
                                |||||||| ||    |||  |||
                                CACGGGAC CG    CGG  CCC
                                     _  ACA_   AA
GAM1116  EPHB3    3'  GCCCTGAGGGGCTTGGG     20786        TAC    C
                                GCCCTGAG   GGGCT GGG
                                ||||||||   ||||| |||
                                CGGGACTC   CCCGA CCC
                                     ___     A
GAM1116  FAAH     3'  GTGCCCTGACTAGGCTGGG   45466         G AC    C
                                GTGCCCTGA T  GGGCT GGG
                                ||||||||| |  ||||| |||
                                CACGGGACT A  TCCGA CCC
                                     G __    _
GAM1116  HM13     3'  GCCCTGAGAGGCTCGG      43109         TAC
                                GCCCTGAG   GGGCTCGG
                                ||||||||   ||||||||
                                CGGGACTC   TCCGAGCC
                                     ___
GAM1116  LAD1     3'  CCGTGCCCTGACTGTGGA    24487          GTAC
                                CCGTGCCCTGA    GGG
                                ||||||||||    |||
                                GGCACGGGACT    CCT
                                      GACA
GAM1116  LAMA4    5'  GTGCTCTTCCAGGGCTCGGG   14062     C  GAGTAC
                                GTGC CT     GGGCTCGGG
                                |||| ||     |||||||||
                                CACG GA     CCCGAGCCC
                                  A  AGGT__
GAM1116  LRP3     5'  GCTCTGGCTGCGGCTCGGG   42169    C   A  ACG
                                GC CTG GT   GGCTCGGG
                                || ||| ||   ||||||||
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                                CG GAC CG   CCGAGCCC
                                 A   _  ACG
GAM1116  MASP1    3'  GTCCCTGAGTATTCAGCCTGGG 40104    G       CG_  TC
                                GT CCCTGAGTA   GGC  GGG
                                || |||||||||   |||  |||
                                CA GGGACTCAT   TCG  CCC
                                 _       AAG   GA
GAM1116  MYLK2    3'  GCCCTGAGGCAAGCTCGGG   37524        TA
                                GCCCTGAG  CGGGCTCGGG
                                ||||||||  ||||||||||
                                CGGGACTC  GTTCGAGCCC
                                     C_
GAM1116  PPOX     5'  CGGCCCTCGCAGGGCTCGGG  7180     T    GA   C
                                CG GCCCT  GTA GGGCTCGGG
                                || |||||  ||| |||||||||
                                GC CGGGA  CGT CCCGAGCCC
                                 _    G_  _
GAM1116  SLC4A2   5'  CGTGCCCCGGGGGTCTCGGG  16773         AGTAC  _
                                CGTGCCCTG    GGG CTCGGG
                                |||||||||    ||| ||||||
                                GCACGGGGC    CCC GAGCCC
                                     C____   A
GAM1116  TRAF1    3'  GTGCCCTGAGGTCTTGG    24945         TACGGG  C
                                GTGCCCTGAG     CT GG
                                ||||||||||     || ||
                                CACGGGACTC     GA CC
                                      CA____  A
GAM1116  CCND1    3'  GTGGGATCGCGCCCGC     38219      TCC  C
                                GTGG   GG TCGCGCCCGC
                                ||||   || ||||||||||
                                CACC   CT AGCGCGGGCG
                                  ___  _
GAM1116  CLDN5    5'  GGTGCCTTTGCGCCCGC     17610      GT  GGCTC
                                GGTG  CC    GCGCCCGC
                                ||||  ||    ||||||||
                                CCAC  GG    CGCGGGCG
                                  __  AAA__
GAM1116  DXYS155E 3'  GTGGTCCGGGCTCGTGCG    22961         _  G_____
                                GTGGTCCGG CTC     CG
                                ||||||||| |||     ||
                                CACCAGGCC GAG     GC
                                     C   CACIII
GAM1116  ETS2     5'  ACGGTGGCTGCTCGGCGCCCGC 23464        CCG    _
            G                    ACGGTGGT   GCTCG CGCCCGCG
                                ||||||||   ||||| ||||||||
                                TGCCACCG   CGAGC GCGGGCGC
                                     A__     C
GAM1116  GPR81    3'  ACGGTGGCTCACGCC       37186       GGTCC
                                ACGGT    GGCTCGCGCC
                                |||||    ||||||||||
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                                TGCCA    CCGAGTGCGG
                                  _____
GAM1116 IFNAR2   5' GGTGGTCCGCGGGCTGCG    9320        ___   C
                                GGTGGTCC   GGCT GCG
                                ||||||||   |||| |||
                                CCACCAGG   CCGA CGC
                                    CGC   _
GAM1116 MBD1     3' GTGGGTTCCAGCTCGTGCTCG 31923     __      C  C
                                GTGG  TCCGGCTCG GC CG
                                ||||  ||||||||| || ||
                                CACC  AGGTCGAGC CG GC
                                  CA       A  A
GAM1116 TIAM1    5' ACGGTCGTCCGGGATCTCCGCG 17525     G     C_  GCGC
                                ACGGT GTCCGG  TC    CCGCG
                                ||||| ||||||  ||    |||||
                                TGCCA CAGGCC  AG    GGCGC
                                   G     CT  A___
GAM1117 ARF1     3' TCGATGGCAAATCGG      43311      C       CTT
                                TCGA GGCAAGTT   GG
                                |||| ||||||||   ||
                                AGCT CCGTTTAG   CC
                                  A      ___
GAM1117 ELMO1    3' TCTGGTGGGCAAGTTTTTGGG 39050     CGAC      C
                                TCT    GGCAAGTT TTGGG
                                |||    |||||||| |||||
                                AGA    CCGTTCAA AACCC
                                  CCAC       A
GAM1117 ITGAM    3' CTCTCTCGGTGGTGCAGTGG  43512       AC  CAA  TCT
                                CTCTCTCG  GG   GT   TGG
                                ||||||||  ||   ||   |||
                                GAGAGAGC  CC   CG   ACC
                                    CA  A__  TC_
GAM1117 NCALD    3' TCTCTTAGTGGCAAGTTC    36773      CGAC
                                TCTCT    GGCAAGTTC
                                |||||    |||||||||
                                AGAGA    CCGTTCAAG
                                   ATCA
GAM1117 PRM2     3' CTCACTCGGTGTTTCTTGG    15717     T    ACGGCAAG
                                CTC CTCG       TTCTTGG
                                ||| ||||       |||||||
                                GAG GAGC       AAGAACC
                                  T    CACA____
GAM1117 SLC2A6   5' CTCTCTCGGGGCGAGCGGAGGG 32768        AC   A   TCTT
                                CTCTCTCG  GGC AGT    GGG
                                ||||||||  ||| |||    |||
                                GAGAGAGC  CCG TCG    CCC
                                    C_   C   CCT_
GAM1117 CISH     3' CAGGGAAGAACCAGAGAAGCCA 40357      TTCCGC
                                TAGG     CCAGAGAAGCCA
                                ||||     ||||||||||||
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                                GTCC     GGTCTCTTCGGT
                                  CTTCTT
GAM1117 DVL1    3' GGGGGCCAGAGAAGCCA    40414    TTCC  C
                                GG   GCC AGAGAAGCCA
                                ||   ||| ||||||||||
                                CC   CGG TCTCTTCGGT
                                 CC__  _
GAM1117 GGT2    5' CAGGTTCCTTGGAGGCC    43923       GCCCA  AA
                                TAGGTTCC    GAG  GCC
                                ||||||||    |||  |||
                                GTCCAAGG    CTC  CGG
                                    AAC__  __
GAM1117 MAPK14  3' GGTCACAGGAGAAGCCAAA  40014    TC  CCA
                                GGT  CGC   GAGAAGCCAAA
                                |||  |||   ||||||||||
                                CCA  GTG   CTCTTCGGTTT
                                  __   TC_
GAM1117 MTA1L1  3' TAGGTTCCCACATGGGCCAA  21894       GCC  GAGAA
                                TAGGTTCC   CA    GCCAA
                                ||||||||   ||    |||||
                                ATCCAAGG   GT    CGGTT
                                    GT_  ACC__
GAM1117 PHKG2   3' AGGCCAGAGCCCAGAGGAGC  7127      CC_      A
                                AGGTT   GCCCAGAG AGC
                                |||||   |||||||| |||
                                TCCGG   CGGGTCTC TCG
                                   TCT      C
GAM1117 RANBP3  3' GGTGGCGGAGAAGCCA     28764    TCC  CCA
                                GGT   GC   GAGAAGCCA
                                |||   ||   |||||||||
                                CCA   CG   CTCTTCGGT
                                  C__  C__
GAM1117 RECQL   3' GCTGGCTCAGGGAAGCCAAA  16240    CC  C   A
                                GTT  GC CAG GAAGCCAAA
                                |||  || ||| |||||||||
                                CGA  CG GTC CTTCGGTTT
                                  C_  A   C
GAM1117 SEPN1   3' GGTTCTGCCCAGAGGCTCCA  42435     C      AAG
                                GGTTC GCCCAGAG   CCA
                                ||||| ||||||||   |||
                                CCAAG CGGGTCTC   GGT
                                   A      CGA
GAM1117 SNK     3' GGTTCCACCCAGTCCAGC    27364          AGA
                                GGTTCCGCCCAG   AGC
                                ||||||||||||   |||
                                CCAAGGTGGGTC   TCG
                                       AGG
GAM1117 SORCS2  3' CAGCCTCAGCCCAGAGAAGTCA 34049     G   C        C
                                TAG TTC GCCCAGAGAAG CA
                                ||| ||| |||||||||| ||
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                                GTC GAG CGGGTCTCTTC GT
                                  G   T         A
GAM1117 ZNF10    3' TAAGTTTGGCACAGAGAAGC   31740       CC  C
                                TAGGTT  GC CAGAGAAGC
                                ||||||  || |||||||||
                                ATTCAA  CG GTCTCTTCG
                                   AC  T
GAM1118 CABC1    5' GGGCCCTCGCTGTGGGCATG   33687    A  GCG   CC
                                GG CC   TGC  GTGGGCATG
                                || ||   |||  |||||||||
                                CC GG   GCG  CACCCGTAC
                                 C  GA_   A_
GAM1118 PLAB     5' ACGGGTCCTGGCCTGGGCATG  42316     A_  GCGT   CG
                                ACGG  CC    GCC  TGGGCATG
                                ||||  ||    |||  ||||||||
                                TGCC  GG    CGG  ACCCGTAC
                                  CA  AC__   __
GAM1118 ZNF144   5' GGGCTGCAGTGGGCAT     28341    ACC  G   CC
                                GG   GC TGC  GTGGGCAT
                                ||   || |||  ||||||||
                                CC   CG ACG  CACCCGTA
                                 ___  _   T_
GAM1118 GORASP1  3' GCATGTACACCAGCATTACAAA 36706     C     _  C
                                GCA GTACGC GGC ATTACAAA
                                ||| |||||| ||| ||||||||
                                CGT CATGTG TCG TAATGTTT
                                  A     G  _
GAM1118 MAPK14   3' AACACGTATGTGGTCACA    10602        CGC  CCA
                                AGCACGTA   GG   TTACA
                                ||||||||   ||   |||||
                                TTGTGCAT   CC   AGTGT
                                    ACA  ___
GAM1118 SLC19A1  3' AGCACGTCCGCGGTGACC    16843        A    ___
                                AGCACGT CGCGG   CC
                                ||||||| |||||   ||
                                TCGTGCA GCGCC   GG
                                   G    ACT
GAM1118 SRP19    3' GCATATACGCGAGATGCAAAC  17117    CG     CCATTA
                                GCA  TACGCGG     CAAAC
                                |||  |||||||     |||||
                                CGT  ATGCGCT     GTTTG
                                  AT      CTAC__
GAM1119 ARHGEF7  5' GAGCGCCGTGGCCGGCA     19363        CC  AGTA  A
                                GAGCGCCG  GG    CC GCA
                                ||||||||  ||    || |||
                                CTCGCGGC  CC    GG CGT
                                    A_  _____  C
GAM1119 CARKL    3' GAGCCTGCTGACCAGCA     29994     GCC  C GAGT
                                GAGC   GC G    ACCAGCA
                                ||||   || |    |||||||
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                                CTCG  CG C   TGGTCGT
                                  GA_ A ____
GAM1119 CD1D    5' GCGCCGCCGCTCACTTCAG  44300       GAG  CAG
                                GCGCCGCCG  TAC  CAG
                                |||||||||  |||  |||
                                CGCGGCGGC  GTG  GTC
                                     GA_  AA_
GAM1119 HDAC4   5' CGGCGCCGCCGGGGGCCCAG  25756   A      AGTA
                                CG GCGCCGCCGG   CCAG
                                || ||||||||||   ||||
                                GC CGCGGCGGCC   GGTC
                                 _       CCCG
GAM1119 LY6E    5' CGGACGCAGGTACCAGCA   14277   AG  CGCC  A
                                CG  CGC   GG GTACCAGCA
                                ||  |||   || |||||||||
                                GC  GCG   TC CATGGTCGT
                                 CT  _____ _
GAM1119 MARK1   5' CGGCGCCGCCGGGGTATGC  33008   A      A  CCA
                                CG GCGCCGCCGG GTA  GC
                                || |||||||||| |||  ||
                                GC CGCGGCGGCC CAT  CG
                                 _       C  A__
GAM1119 PHF1    5' GCCGCCGGGAGCCGGGCAG  15271       _  ACCA
                                GCCGCCGG AGT   GCAG
                                |||||||| |||   ||||
                                CGGCGGCC TCG   CGTC
                                     C  GCC_
GAM1119 PPP3CB  5' CGGCGCCGCCGGGGAACATGGC 34445   A      AGT  CA_
                                CG GCGCCGCCGG  AC  GC
                                || ||||||||||  ||  ||
                                GC CGCGGCGGCC  TG  CG
                                 _       CCT  TAC
GAM1119 PTK7    5' CGGGCGCCGCAGCAGC     15860   A    C  AGTAC
                                CG GCGCCGC GG    CAGC
                                || ||||||| ||    ||||
                                GC CGCGGCG TC    GTCG
                                 C     _ ______
GAM1119 ROBO1   5' CGAGCGCCGCTGCGAGGGCAG 39482       CG_  TACCA
                                CGAGCGCCGC  GAG   GCAG
                                |||||||||  |||   ||||
                                GCTCGCGGCG  CTC   CGTC
                                     ACG  C____
GAM1119 SECTM1  3' CGGGCGCCGCCGCGTCCTGC  16541   A      GA  A  A
                                CG GCGCCGCCG  GT CC GC
                                || |||||||||  || || ||
                                GC CGCGGCGGC  CA GG CG
                                 C       G_  _  A
GAM1119 TLL1    5' GATGCCGCCGGGACAGTA   29738   GC     ___
                                GA  GCCGCCGG  AGTA
                                ||  ||||||||  ||||
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                                CT  CGGCGGCC   TCAT
                                 A_       CTG
GAM1119  UBE3A    5'  CGAGCGCGCCGGGTCGGCA   7861        C    A  ACCA
                                CGAGCGC GCCGG GT    GCA
                                ||||||| ||||| ||    |||
                                GCTCGCG CGGCC CA    CGT
                                   _    _ GC__
GAM1119  ZNF148   5'  CGGGCGCGGCCGAAGTCGTCAG 35024    A   C       AC_
            C                    CG GCGC GCCGGAGT   CAGC
                                || |||| ||||||||   ||||
                                GC CGCG CGGCTTCA   GTCG
                                 C   C       GCA
GAM1119  CAV2     5'  CCCGGCTGGCGCGGTGCGGCT  10288        A   AGCT  C
                                CCCGGCTG CGC    CG GCT
                                |||||||| |||    || |||
                                GGGCCGAC GCG    GC CGA
                                     C   CCAC  _
GAM1119  HIP1     3'  CCCGGCTGGGCAGAGAATCTT  23752        AC    CTCGCG
                                CCCGGCTG  GCAG     CTT
                                ||||||||  ||||     |||
                                GGGCCGAC  CGTC     GAA
                                     C_    TCTTA_
GAM1119  TP53BP2  3'  CCTGCTGACGTAGATGCT    24059    G      C  CTCGC
                                CC GCTGACG AG     GCT
                                || ||||||| ||     |||
                                GG CGACTGC TC     CGA
                                 A      A  TA___
GAM1120  CD164    3'  AGCTTACCTTTCACTGTCTT   25678         ___   __
                                AGCTTACC   CGC  TCTT
                                ||||||||   |||  ||||
                                TCGAATGG   GTG  AGAA
                                     AAA   AC
GAM1120  EIF2C1   3'  AAGCTTGCTGCCAACACC    29164       ACCC   C TG
                                AAGCTT    GCT T  GCACT
                                ||||||    ||| |  |||||
                                TTCGAA    CGA G  TGTGG
                                   _____   C GT
GAM1120  GAB2     3'  GCCTACCTCAGGCACTC     38681       CGC  TT
                                GCTTACC   TC  GGCACTC
                                |||||||   ||  |||||||
                                CGGATGG   AG  CCGTGAG
                                   ___  T_
GAM1120  IL15RA   3'  AGCTTGCTCCTGGAGCCC    13529      ACCC       CA
                                AGCTT    GCTCTTGG  CTC
                                |||||    ||||||||  |||
                                TCGAA    CGAGGACC  GGG
                                   _____       TC
GAM1120  MYO10    3'  GCTGCCCGCAGCACTC      29572     TA    TCTT
                                GCT  CCCGC    GGCACTC
                                |||  |||||    |||||||
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                                CGA  GGGCG   TCGTGAG
                                  C_   ____
GAM1120  PSMD5    3'  AAGCTTGTCTGCTCTTAATGCA 22775       ACCC     __  C
              TTCC                  AAGCTT   GCTCTTG  GCA TCC
                                |||||||   |||||||  ||| |||
                                TTCGAA   CGAGAAT  CGT AGG
                                   CAGA     TA  A
GAM1120  REQ      3'  AGCTTGCTCGCTCCCAGCTCC  26540      ACC     TG  AC
                                AGCTT   CGCTCT  GC  TCC
                                |||||   ||||||  ||  |||
                                TCGAA   GCGAGG  CG  AGG
                                   CGA     GT  __
GAM1121  WHSC1L1   3'  TGCCAATAATGATGATTGGCGA 35716          AAATT   C
              A                   TGCCAATAAT    TTG GCGAA
                                ||||||||||    |||  |||||
                                ACGGTTATTA    AAC CGCTT
                                      CTACT  _
GAM1122  APM1     3'  CATGTATATATCTAATAAT   22011     _          III
                                TATG ATATATCTAATAA   T
                                ||||  ||||||||||||   |
                                GTAC TATATAGATTATT   A
                                  A          III
GAM1122  ACAD8    3'  TATCATGATTTACATTCAG   30790      GCA
                                TATTG   ATTTACATTCAG
                                |||||   ||||||||||||
                                ATAGT   TAAATGTAAGTC
                                  AC_
GAM1122  DDX3     3'  TTGAGGTTCAATCTTTACATTC 35828     TATTGG    __
              AG                  TTGA     CAATT  TACATTCAG
                                ||||     |||||  |||||||||
                                AACT     GTTAG  ATGTAAGTC
                                  CCAA__     AA
GAM1122  SIRT4    3'  TTGAGAAGGCATTTACATT   29263     TATT    A
                                TTGA    GGCA TTTACATT
                                ||||    ||||  ||||||||
                                AACT    CCGT AAATGTAA
                                  CTT_   _
GAM1123  TRPM6    3'  TAGTACCCCTGAGCTTTA    32795          AAA
                                TAGTACCCCT   CTTTA
                                ||||||||||   |||||
                                ATCATGGGGA   GAAAT
                                      CTC
GAM1123  ADD1     3'  GGAGAGTTGGCTTAAAGGT   30523    A      AC    C
                                A AGAGTTGG  TAAAG GT
                                |  ||||||||  |||||  ||
                                C TCTCAACC  ATTTC CA
                                 C       GA    _
GAM1123  ALEX1    5'  AAGGGTTGGACTGGCCTCCG   32484     A      AAA  GTA
                                AAG GTTGGACT   GC   CG
                                |||  ||||||||   ||   ||
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                                TTC CAACCTGA  CG  GC
                                  C      C__  GAG
GAM1123 CDC25C   3' AAAGAGTTGGCTGGC      35613         A  AAA
                                AAAGAGTTGG CT  GC
                                |||||||||| ||  ||
                                TTTCTCAACC GA  CG
                                      _  C__
GAM1123 PDE4B    3' GAGTTGGACTGGACAACA    15148         AAA  T
                                GAGTTGGACT  GCG ACG
                                ||||||||||  ||| |||
                                CTCAACCTGA  TGT TGT
                                     CC_  _
GAM1123 SERPINE1 3' GGAGAGTTGGGCCACAT     8291    A      A  AAA
                                A AGAGTTGG CT  GCGT
                                | ||||||||| ||  ||||
                                C TCTCAACC GG  TGTA
                                 C      C  ___
GAM1123 TRPV1    5' GGAGAGCTGGGCTCGT      38797   A      A  AAAG
                                A AGAGTTGG CT   CGT
                                | ||||||||| ||   |||
                                C TCTCGACC GA   GCA
                                 C      C  ____
GAM1124 AIM1     5' CACGACCGGCTCGTCCACTTG  45079        C   GCAG
                                CACGACCG CTCG   ACTTG
                                |||||||| ||||   |||||
                                GTGCTGGC GAGC   TGAAC
                                     C   AGG_
GAM1124 CMKLR1   5' CGAGGCTGTTGGGGAGACTTGC 19825     CC  CTC__  C
                                CGA  GC    GG AGACTTGC
                                |||  ||    || ||||||||
                                GCT  CG    CC TCTGAACG
                                  C_  ACAAC  C
GAM1124 FANCC    5' CCGCGGTCGCCCGGCAG     43272    A  AC   T
                                CC CG  CGCC CGGCAG
                                || ||  |||| ||||||
                                GG GC  GCGG GCCGTC
                                 C  CA   _
GAM1124 LEF1     5' CCGCGTCGCCGGGATTTG    32204    A  AC   TC  CA  C
                                CC CG  CGCC  GG  GA TTG
                                || ||  ||||  ||  || |||
                                GG GC  GCGG  CC  CT AAC
                                 C  A_   __  __  A
GAM1124 PTPRE    5' CCGCCGCCGCCTCGGCTCCAGC 38982    A_  A       AGA  T
                                CC  CG CCGCCTCGGC   CT GC
                                ||  || ||||||||||   || ||
                                GG  GC GGCGGAGCCG   GG CG
                                 CG  _         A__  T
GAM1124 TCF1     3' CCACGGTTGCTCGGCAGGCTC  8087       ACC  C      A
                                CCACG   GC TCGGCAG CTT
                                |||||   || ||||||| |||
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                                GGTGC   CG AGCCGTC GAG
                                  CAA _     C
GAM1124 TRPC1    5' CCACTGCTGCCTCGGCTCGA  17681     GACC      A_
                                CCAC   GCCTCGGC  GA
                                ||||   ||||||||  ||
                                GGTG   CGGAGCCG  CT
                                  ACGA      AG
GAM1125 C1QG     3' GGAGGAGAAGTCCATCTGGTGG 41687       _   GCG   AC
           GG                   GGAGGAGA GTCT   TTG  GGGG
                                |||||||| ||||  |||  ||||
                                CCTCCTCT CAGG   GAC  CCCC
                                    T   TA_   CA
GAM1125 FOXF1    3' GGAGGAGACTTCGGAGGTGGGG 11120       GT  G  TTGAC
                                GGAGGAGA  CT CG    GGGG
                                ||||||||  || ||    ||||
                                CCTCCTCT  GA GC    CCCC
                                    __  A  CTCCA
GAM1125 KCNC3    5' GGAGGAGGGGCGGGGCGGG   22507      AGTCT   TTGA
                                GGAGGAG    GCG    CGGG
                                |||||||    |||    ||||
                                CCTCCTC    CGC    GCCC
                                   CC___   CCC_
GAM1125 KCNC3    3' GGTGGGGTCTGCAAGGGG    22525    A  AGA     TTGAC
                                GG GG   GTCTGCG    GGGG
                                || ||   |||||||    ||||
                                CC CC   CAGACGT    CCCC
                                 A  C__      T_____
GAM1125 SCAP1    3' GAGAGGAGTCCAAGGCGTTGGT 19005     GA     ___     AC
           GGGG                   GAG  GAGTCT   GCGTTG  GGGG
                                ||| ||||||  ||||||  ||||
                                CTC  CTCAGG   CGCAAC  CCCC
                                  TC     TTC     CA
GAM1125 SYNGR3   3' GGGGCCTGCGTTGGTGGG    20098    AGA       AC
                                GG   GTCTGCGTTG  GGG
                                ||   ||||||||||  |||
                                CC   CGGACGCAAC  CCC
                                 C__         CA
GAM1125 ZIC3     5' GGAGGGGGTGTTGGCGGG    18250      AGA  CTGC   A
                                GGAGG   GT    GTTG CGGG
                                |||||   ||    |||| ||||
                                CCTCC   CA    CAAC GCCC
                                   CC_  _____    C
GAM1125 ARHGAP6  5' GGGGACTGGAACTTCCTCTGCT 30225    CA   CTTT  _
           G                    GG  GACT    CT CCTCTGCTG
                                ||  ||||    || |||||||||
                                CC  CTGA    GA GGAGACGAC
                                 C_   CCTT  A
GAM1125 ASTN     3' CAGGCTCTTTCTGAAAGGCTG  42942     A      CCTCT
                                CAG CTCTTTCT     GCTG
                                ||| ||||||||     ||||
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                                GTC GAGAAAGA    CGAC
                                  C       CTTTC
GAM1125 COG6    3' GGCAGTTTTTTTCTCCAATG  43764      ACTC      TC
                                GGCAG   TTTCTCC  TG
                                |||||   |||||||  ||
                                CCGTC   AAAGAGG  AC
                                   AAAA      TT
GAM1125 FLG     5' GCGGACTCTTGGTGGCTCTGCT 43362    A      TCTC_
             G                   GC GACTCTT    CTCTGCTG
                                 || |||||||    ||||||||
                                 CG CTGAGAA    GAGACGAC
                                  C      CCACC
GAM1125 HUNK    3' CAGTCTTTCTCTTCTG     31057     AC       C
                                CAG  TCTTTCTC TCTG
                                |||  |||||||| ||||
                                GTC  AGAAAGAG AGAC
                                  __       A
GAM1125 MADH6   5' CGGCGGCTCTTTCTCTC    24597      AGA       C
                                CGGC   CTCTTTCTC TC
                                ||||   ||||||||| ||
                                GCCG   GAGAAAGAG AG
                                  CC_       _
GAM1125 RNASE1   5' GACTTTGTTTTTCCTCTGCTG  16341     C__   C
                                GACT   TTT TCCTCTGCTG
                                ||||   ||| ||||||||||
                                CTGA   AAA AGGAGACGAC
                                  AAC   A
GAM1125 TEX13B  3' GGAGGTCTTCTCTGC      42291    C  AC    TCTC
                                GG AG  TCTT    CTCTGC
                                || ||  ||||    ||||||
                                CC TC  AGAA    GAGACG
                                 _  C_   ____
GAM1125 TNNC2   5' GGTGACCGGGACTCCTCTG   17614    CA    CTTT
                                GG  GACT    CTCCTCTG
                                ||  ||||    ||||||||
                                CC  CTGG    GAGGAGAC
                                 A_    CCCT
GAM1126 LIMD1   3' GAGGGAACATTTGGGTATAG   30631     TAT  C
                                GAG   AT TTTGGGTATAG
                                |||   || ||||||||||
                                CTC   TG AAACCCATATC
                                  CCT  T
GAM1126 MAGEL2  3' AAAGTATATTTATATATATAGA 33298         CTTTGG
             T                   AGAGTATAT     GTATAGAT
                                 |||||||||     ||||||||
                                 TTTCATATA     TATATCTA
                                      AATATA
GAM1126 ZFP36L1  3' AAGAATATATTCTATGGAT   22278          _  T
                                AAGAGTATAT CT TGGGT
                                |||||||||| || |||||
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                                TTCTTATATA GA ACCTA
                                      A  T
GAM1126  ZNF10    3'  AAGAGGGTATCTTTGGAC    31730      TA
                                AAGAG  TATCTTTGGGT
                                |||||  ||||||||||
                                TTCTC  ATAGAAACCTG
                                   CC
GAM1126  DGKI     3'  AATAGTCTTGATATATTTAGT  21781        _  AAG
                                AATAGTCT GA   ATTTAGT
                                |||||||| ||   |||||||
                                TTATCAGA CT   TAAATCA
                                     A  ATA
GAM1126  GABRP    3'  AGCACTGCAGAGATTTAGT   30554     _   AA_
                                AGT CTG   AGATTTAGT
                                ||| |||   |||||||||
                                TCG GAC   TCTAAATCA
                                  T   GTC
GAM1126  MMP25    3'  ATAGTCTAGAAGAATAGT    35375        A    TT
                                ATAGTCTG AAGA  TAGT
                                |||||||| ||||  ||||
                                TATCAGAT TTCT  ATCA
                                     C    T_
GAM1126  TAF4     3'  AATAGTCTAAAAAATCAGT   17253             T
                                AATAGTCTGAAAGATT AGT
                                |||||||||||||||| |||
                                TTATCAGATTTTTTAG TCA
                                                 _
GAM1126  VIL2     3'  GGAGTCTGAAAGCTCATAGT  18000    T        ATT_
                                A AGTCTGAAAG    TAGT
                                | ||||||||||    ||||
                                C TCAGACTTTC    ATCA
                                 C         GAGT
GAM1127  CSTB     3'  AGGAAGAGAAATGCAAAAGCAG 6435       AA_      TTCC_
              C                  AGGAA   AAATGCAA    GC
                                |||||   ||||||||    ||
                                TCCTT   TTTACGTT    CG
                                   CTC       TTCGT
GAM1127  D1S155E  3'  AAGGAAAAGAATGCAACT    28386        A
                                AAGGAAAA AATGCAATT
                                |||||||| |||||||||
                                TTCCTTTT TTACGTTGA
                                     C
GAM1127  EIF4EBP2 3'  AAGGAAAAAAATGCAGTTC   19889             A
                                AAGGAAAAAAATGCA TTC
                                |||||||||||||| |||
                                TTCCTTTTTTTACGT AAG
                                          C
GAM1127  FGA      3'  AAGAAGGAAATGCAAGGGGCC  34837      AA       TTCC
                                AGGAA  AAATGCAA   GCC
                                |||||  ||||||||   |||
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                                TTCTT  TTTACGTT    CGG
                                  CC       CCC_
GAM1127  FZD7     3'  CAAGGGGAAAAATGCATTCC   18629       AA        A
                                TAAGG  AAAAATGCA TTCC
                                |||||  ||||||||| ||||
                                GTTCC  TTTTTACGT AAGG
                                  CC        _
GAM1127  GALNT1   3'  AGGAAAAGAAATGCAAGC    33836        _       TTCC
                                AGGAAAA AAATGCAA    GC
                                |||||||  ||||||||    ||
                                TCCTTTT TTTACGTT    CG
                                   C       _____
GAM1127  GRB10    3'  AAGGAAGAAAATGCAATT     23643        A
                                AAGGAA AAAATGCAATT
                                ||||||  ||||||||||
                                TTCCTT TTTTACGTTAA
                                   C
GAM1127  HLA-F    3'  AGGCACAAGTGCAATTCTGC   33241     AAAA  A       C
                                AGG    AA TGCAATTC GC
                                |||    ||  ||||||||  ||
                                TCC    TT ACGTTAAG CG
                                  GTG_  C       A
GAM1127  IL5      3'  TAAGAAAAAAGTATATCAATTT 9398           A_  _    CC
            TGCC                    TAAGGAAAAA  ATG CAATT  GCC
                                ||||||||||  |||  |||||  |||
                                ATTCTTTTTT  TAT GTTAA  CGG
                                     CA   A     AA
GAM1127  SIM1     3'  TAAGGAAAATAAACATTTTGCC 22870          AAAT   A  CC
                                TAAGGAAAA    GCA TT  GCC
                                |||||||||    |||  ||  |||
                                ATTCCTTTT    TGT AA  CGG
                                     ATT_   A  A_
GAM1127  ZNF32    3'  AAGGAAAAAAAATCAGTTTGCC  45041           G  A  CC
                                AAGGAAAAAAAT CA TT  GCC
                                ||||||||||||  ||  ||  |||
                                TTCCTTTTTTTA GT AA  CGG
                                      _  C  A_
GAM1127  PIM1     3'  TGTCACTGGTACTCGG      44975       ATTTTG
                                TGTCAC     GGTACTCGG
                                ||||||     |||||||||
                                ACAGTG     CCATGAGCC
                                   A_____
GAM1128  FMN2     3'  AAATGCTGTGATGTGG      44283            ATT
                                AAATGCTGTGGTG   TGG
                                ||||||||||||   |||
                                TTTACGACACTAC   ACC
                                              ___
GAM1128  GPR30    5'  GCACCTGTGGTGGTTTG     11311      AAATG       A
                                GCAC    CTGTGGTG TTTG
                                ||||    |||||||| ||||
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                                CGTG    GACACCAC AAAC
                                  _____      C
GAM1128 LAF4    3' AAATGCTGTGGCTG       14039          GATT
                                AAATGCTGTGGT   TG
                                ||||||||||||  ||
                                TTTACGACACCG   AC
                                     ____
GAM1128 LDB3    3' TGCAGCGAGTGCTGTTTG   44113     CAAAT T_  G A
                                TGCA   GC  GTG TG TTTG
                                ||||    ||  ||| || ||||
                                ACGT   CG  CAC AC AAAC
                                  _____ CT  G  _
GAM1128 WFS1    3' TACACAGATGCTTATTTG   25641      A    GTGGTG
                                TGCACA ATGCT    ATTTG
                                |||||| |||||    |||||
                                ATGTGT TACGA    TAAAC
                                   C    A_____
GAM1128 CACNA2D2 3' CCCATAGTGTGTGTGT    25708     AACAG  TT
                                TCCAT   AGT  TGTGTGT
                                |||||    |||  |||||||
                                GGGTA   TCA  ACACACA
                                  _____  C_
GAM1128 CBFA2T2  3' ACAGAGTTTTGCTCTGTT   22964         G_
                                ACAGAGTTTTGT  TGTT
                                ||||||||||||  ||||
                                TGTCTCAAAACG  ACAA
                                      AG
GAM1128 EGLN2   5' TAACAGAGTTTGATTTGTTT  38833         T  G
                                TAACAGAGTTT GT TGTTT
                                |||||||||||  || |||||
                                ATTGTCTCAAA TA ACAAA
                                      C  A
GAM1128 HOXB3   5' TCCATACTGTCATGTGTGTTT 13442      ACAGA  T
                                TCCATA   GTT TGTGTGTTT
                                ||||||    ||| |||||||||
                                AGGTAT   CAG ACACACAAA
                                   GA___  T
GAM1128 PBX3    3' TAACATTGTGTGTT      26215      GAGTT
                                TAACA   TTGTGTGTT
                                |||||    |||||||||
                                ATTGT   AACACACAA
                                  _____
GAM1128 TYRP1   3' TCCATGAATGGAAATGTGTTT 43643     AACA   TTT_
                                TCCAT   GAGT   GTGTGTTT
                                |||||   ||||   ||||||||
                                AGGTA   CTTA   TACACAAA
                                   _____  CCTT
GAM1129 APBA1   3' GGCCTTCCAGAGAGGTGG   43089       ___  C
                                GGTCTTCC   GA GTGG
                                ||||||||   || ||||
```

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                                CCGGAAGG  CT CACC
                                     TCT  C
GAM1129  CD48    3'  AAGATCTTCTGGCCTTGAAGT  12130        CGACG  ____
                                AAGGTCTTC   TGGC   AAGT
                                |||||||||   ||||   ||||
                                TTCTAGAAG   ACCG   TTCA
                                     _____  GAAC
GAM1129  EFNB1   5'  GGTCTTCCCGCAGAGGTCT   20726        GA  TG CAA
                                GGTCTTCC  CG  G  GTCT
                                ||||||||  ||  |  ||||
                                CCAGAAGG  GC  C  CAGA
                                     __  GT TC_
GAM1129  GLO1    3'  AAGGTCTTCCACTAGAGTC   27466        G  G  CA
                                AAGGTCTTCC AC TGG  AGTC
                                |||||||||| || |||  ||||
                                TTCCAGAAGG TG ATC  TCAG
                                     _  _  __
GAM1129  HNRPH2   5'  GGCTCTTGGTGGCAAGT    33331   _   CCGAC
                                GG TCTT    GTGGCAAGT
                                || ||||    |||||||||
                                CC AGAA    CACCGTTCA
                                 G   C____
GAM1129  HRH1    3'  AGGTCTTCTGAACAATGG    9250        C_   _
                                AGGTCTTC  GACG TGG
                                ||||||||  |||| |||
                                TCCAGAAG  TTGT ACC
                                     AC   T
GAM1129  MLPH    3'  AAGGTCTTCGGTGTGTC    35866        CGAC  GCAA
                                AAGGTCTTC   GTG   GTC
                                |||||||||   |||   |||
                                TTCCAGAAG   CAC   CAG
                                     C___   A___
GAM1129  NFYC    3'  GGCAGAACAACGTGGCAAGTCT 30596    CTTC
                                GGT   CGACGTGGCAAGTCT
                                |||   ||||||||||||||
                                CCG   GTTGCACCGTTCAGA
                                  TCTT
GAM1129  PCK1    5'  GGCTCTTCCCGCCAGCAAGT  40944   _    GA  _
                                GG TCTTCC  CGT GGCAAGT
                                || ||||||  ||| |||||||
                                CC AGAAGG  GCG TCGTTCA
                                 G    __  G
GAM1129  PDE4C   3'  AGCTCTTTTAGGCAAGTC   9556    G   CCGACGT
                                AG TCTT      GGCAAGTC
                                || ||||      ||||||||
                                TC AGAA      CCGTTCAG
                                 G   AAT____
GAM1129  SPAP1   3'  AAGGTTTTATAGCAAGTC   39861      C  CCGAC
                                AAGGT TT    GTGGCAAGTC
                                ||||| ||    ||||||||||
```

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                                TTCCA AA    TATCGTTCAG
                                  A _____
GAM1129  TCF7L2   5'  AGATCTTCTGCACGCGTGAGT  36248       CG_   GCA
                                AGGTCTTC  ACGTG  AGT
                                ||||||||  |||||  |||
                                TCTAGAAG  TGCGC  TCA
                                    ACG   AC_
GAM1130  PBX3     3'  ATGCACTTATCAAGGCATGTA  26213     T     TT  CCC
                                ATGCA CTTATCAA  GC  GTA
                                ||||| ||||||||  ||  |||
                                TACGT GAATAGTT  CG  CAT
                                  _     C_  TA_
GAM1130  TRPM8    3'  GCATTTCAATTGCCTTGT    35859     CTTA      CC
                                GCAT   TCAATTGCC  GT
                                ||||   |||||||||  ||
                                CGTA   AGTTAACGG  CA
                                  A___      AA
GAM1130  ACCN2    3'  CCCGGGTTGGGGGAGAGGG   33439    CC    CAG
                                CCC  GTTGGG  GGAGAGGG
                                |||  ||||||  ||||||||
                                GGG  CAACCC  CCTCTCCC
                                 CC    ___
GAM1130  ALPPL2   3'  CCTCCTTGGCTGGGAGGG    42876   _ GTTG  A   A
                                CC CC   GGC GGGAG GG
                                || ||   ||| ||||| ||
                                GG GG   CCG CCCTC CC
                                 A  AA__  A   _
GAM1130  ARF3     3'  CCATGTAAAACAGGGAGAGGG  11670   CC  TG
                                CC  GT  GGCAGGGAGAGGG
                                ||  ||  ||||||||||||||
                                GG  CA  TTGTCCCTCTCCC
                                 TA  TT
GAM1130  ARIH1    5'  CCGAGGCGGGGAGAGGGCG   25087    TT   A
                                CCG  GGGC GGGAGAGGGCG
                                |||  |||| ||||||||||
                                GGC  TCCG CCCTCTCCCGC
                                  __   C
GAM1130  CCK      3'  CCGTTGGGCTGATGGC      8806         AGGGA  G
                                CCGTTGGGC    GA GGC
                                |||||||||    || |||
                                GGCAACCCG    CT CCG
                                    A____  A
GAM1130  ECH1     5'  CCCGTTAGCGGAGGGGGCG   40863       G AG   A
                                CCCGTTGG C  GGAG GGGCG
                                |||||||| |  |||| |||||
                                GGGCAATC G  CCTC CCCGC
                                   _ __   C
GAM1130  IL1RAP   5'  TTGGGAAGCTGAGAGGGCG   13511     C  G_
                                TTGGG AG  GAGAGGGCG
                                ||||| ||  |||||||||
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                                AACCC TC  CTCTCCCGC
                                  T  GA
GAM1130  KLHL3    3'  TTGGGGGTTGGGGAGAGGG   44655      CA___
                                TTGGG    GGGAGAGGG
                                |||||    |||||||||
                                AACCC    CCCTCTCCC
                                   CCAAC
GAM1130  MRC1     5'  CCTGATGGACAGGAGGGCG   14627    GT_      GAG
                                CC   TGGGCAGG   AGGGCG
                                ||   ||||||||   ||||||
                                GG   ACCTGTCC   TCCCGC
                                 ACT       ___
GAM1130  NRXN2    3'  CCCCTGGCAGGGAGAGGG    31476     GTTG
                                CCCC    GGCAGGGAGAGGG
                                ||||    ||||||||||||
                                GGGG    CCGTCCCTCTCCC
                                  A___
GAM1131  ATP8A2   3'  CATTCATGCCTGAAGACATC   45254         CGCCT_
                                CGTTCATGCC     CGTT
                                ||||||||||     ||||
                                GTAAGTACGG     GTAG
                                     ACTTCT
GAM1131  CASP10   3'  TTCATGCCTGTAGTCCCAGA   37369        CGCCTC
                                TTCATGCC     GTTCCAGA
                                ||||||||     ||||||||
                                AAGTACGG     CAGGGTCT
                                     ACAT__
GAM1131  FBXL7    5'  CGTCATGCCCGCCGTCTCCC   29401     T        _  G
                                CGT CATGCCCGCC TC TTCC
                                ||| |||||||||| || ||||
                                GCA GTACGGGCGG AG AGGG
                                  _        C  _
GAM1131  MLC1     3'  CGTTCATGTCTTCTCA      40150         CCCGCC  G  _
                                CGTTCATG     TC TTC CA
                                ||||||||     || ||| ||
                                GCAAGTAC     AG AAG GT
                                     _______  _   A
GAM1131  PIGN     3'  TTCATGCCTGCAAAACCTAGA  29554        C  CTCGTT  _
                                TTCATGCC GC     CC AGA
                                ||||||||  ||     ||  |||
                                AAGTACGG CG     GG TCT
                                     A  TTTT__  A
GAM1131  SHANK2   3'  GTTCATTCTAGAGCTGTTCCAG 29466       GCCC__  CTC
            A                    GTTCAT     GC   GTTCCAGA
                                ||||||     ||   ||||||||
                                CAAGTA     CG   CAAGGTCT
                                   AGATCT  A__
GAM1131  TNFSF4   3'  GTTCATGCTGGTGCCTGGTTTT 17750         CC__    C   CC
            AGA                    GTTCATGC    GCCT GTT  AGA
                                ||||||||    |||| |||  |||
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                                CAAGTACG   CGGA CAA  TCT
                                    ACCA   C   AA
GAM1131 PVR     3' GTCTTGGAGACCTAT      27112    G    ATGCG  C
                                GTC TTGGAG    GCC AT
                                ||| ||||||    ||| ||
                                CAG AACCTC    TGG TA
                                  _    _____  A
GAM1132 DXYS155E 3' CGGGCTCGTGCTGCGCCGGCG 22953    T  __ C
                                TGG CTC  GC GCGCCGGCG
                                ||| |||  || |||||||||
                                GCC GAG  CG CGCGGCCGC
                                  C   CA  A
GAM1132 LGMN    5' CGGTGGTGGCGCCGGC     24683    A   CTCGCC
                                CG TGGT     GCGCCGGC
                                || ||||     ||||||||
                                GC ACCA     CGCGGCCG
                                 C   C_____
GAM1132 TST     5' CGGACGCCGCGCTGGC     17705    TCT      C
                                TGG   CGCCGCGC GGC
                                |||   |||||||| |||
                                GCC   GCGGCGCG CCG
                                  T__       A
GAM1132 FGD1    5' TCTCGGCGGCGGCGGGC    20913    GC      CA
                                TC  CGGCGGCG  CGGGC
                                ||  ||||||||  |||||
                                AG  GCCGCCGC  GCCCG
                                 A_       C_
GAM1132 JAG2    5' TCGCTGGCGGCCGCGC     13734     C    GCA  G
                                TCGC GGCGGC   CG GC
                                |||| ||||||   || ||
                                AGCG CCGCCG   GC CG
                                  A     ___  G
GAM1132 SKI     3' TCGACGGCGGCGTGGCGGGC  16736    C      CA_
                                TCG CGGCGGCG   CGGGC
                                ||| ||||||||   |||||
                                AGC GCCGCCGC   GCCCG
                                  T       ACC
GAM1133 FGFR2   5' CAGGCTTGCGTTGCCTCC    35659     G       GGTGTG
                                CAGG TTGCGTTGC     CC
                                |||| |||||||||     ||
                                GTCC AACGCAACG     GG
                                  G       GA____
GAM1133 HR      5' CAGGGTTGCTGGTGC      32911         GTTGC
                                CAGGGTTGC    GGTGT
                                |||||||||    |||||
                                GTCCCAACG    CCACG
                                     A____
GAM1133 MUCDHL  3' GGGTCTGTGCTGTGCCC    34942      GC  T  GG
                                GGGTT  GT GC  TGTGCCC
                                |||||  || ||  |||||||
```

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                                CCCAG  CA CG  ACACGGG
                                  A_  _ __
GAM1133  POP4     3'  CAGTGTTAACCCCGGTGTGC  27365     G   CGT G
                                CAG GTTG   T CGGTGTGC
                                ||| ||||   | ||||||||
                                GTC CAAT   G GCCACACG
                                  A   TG_ G
GAM1133  ZNF265   3'  CAGGGTTGTTTAGTGT     24148       GC   GC
                                CAGGGTT  GTT  GGTGT
                                |||||||  |||  |||||
                                GTCCCAA  CAA  TCACA
                                   __  A_
GAM1133  ZNF42    5'  GGGTTTGGATGTGCC      18292      GCGT  C
                                GGGTT   TG GGTGTGCC
                                |||||   || ||||||||
                                CCCAA   AC CTACACGG
                                  _____ _
GAM1133  GK       5'  TTCAGGTCGGCCGGCGATTGCG 6735     G   C     ATTCC
            G                    TTC AGG CGGCCGG    GCGG
                                ||| ||| |||||||    ||||
                                AAG TCC GCCGGCC    CGCC
                                  _  A      GCTAA
GAM1133  SLC39A4  5'  TTCTGGGCTGGCTGAGGGCGG  39298    GA   C   CG  TTCC
                                TTC  GGC GGC  GA   GCGG
                                |||  ||| |||  ||   ||||
                                AAG  CCG CCG  CT   CGCC
                                  AC   A   A_  CC__
GAM1134  AMFR     3'  TTATTGAAATAAATTATCT   10081        ACA
                                TTATTGGAA   AAGTTGTCT
                                |||||||||   |||||||||
                                AATAACTTT   TTTAATAGA
                                     A__
GAM1134  GLO1     3'  TTGTGAAAAAAGTTGTTTCTG  27470    _   C      C
                                TTG GAAA AAAGTTGT TCTG
                                ||| |||| |||||||| ||||
                                AAC CTTT TTTCAACA AGAC
                                  A   _      A
GAM1134  MAPRE1   3'  TTATTGGAAAAGGAGTGAAACG 29526         CAA  _____
            TCT                   TTATTGGAAA   AGT   TGTCT
                                ||||||||||   |||   |||||
                                AATAACCTTT   TCA   GCAGA
                                     TCC   CTTT
GAM1134  MYL2     3'  TTATTGGAACATGGCCTCT   41336        A  AAGTT
                                TTATTGGAA CA    GTCTCT
                                ||||||||| ||    ||||||
                                AATAACCTT GT    CGGAGA
                                     _ AC___
GAM1134  RIMS1    3'  TTATTGGAATGACTC      43738         ACAAAGT  T
                                TTATTGGAA     TG CTC
                                |||||||||     || |||
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                                AATAACCTT      AC GAG
                                       _______ T
GAM1134  TIMM17A   3'  TATTGGAAGCAAGTTGTTTCTG 26790        ACA      C
                                TATTGGAA   AAGTTGT TCTG
                                |||||||| ||||||| ||||
                                ATAACCTT   TTCAACA AGAC
                                    CG_      A
GAM1134  TNKS      3'  TTATTAGAAACAATCCTCT    19055           AGTTG
                                TTATTGGAAACAA     TCTCT
                                ||||||||||||     |||||
                                AATAATCTTTGTT     GGAGA
                                       A____
GAM1135  DMD       3'  ACTTACTTACAAACCTG      19674         AAAC
                                ACTTACTTA    ACTTG
                                |||||||||    |||||
                                TGAATGAAT    TGGAC
                                     GTT_
GAM1135  IFNA2     3'  TTACTTATATCTTGAATATA   8295         AAACA
                                TTACTTA     CTTGAATATA
                                |||||||     ||||||||||
                                AATGAAT     GAACTTATAT
                                    ATA__
GAM1136  FMR1      3'  ACTAATGTTTGACAGGGTTTG  12936         CTCGT  G    C
                                ACTGATGT     GC AGGG TTG
                                ||||||||     || |||| |||
                                TGATTACA     TG TCCC AAC
                                    AAC__  _    A
GAM1136  PLAG1     3'  ACTGATGCTTTGTGTTTAGGGT 15343         CTC   CG_    C
           TTG                    ACTGATGT   GTG   AGGG TTG
                                ||||||||   |||   |||| |||
                                TGACTACG   CAC   TCCC AAC
                                    AAA   AAA    A
GAM1136  SOX11     5'  CTGGGTCTCGTGCGGAG     17019     AT        A
                                CTG  GTCTCGTGCG GGG
                                |||  |||||||||| |||
                                GAC  CAGAGCACGC CTC
                                  C_         _
GAM1137  CLASP2    3'  AAAGCTTTAAGCATTCC      42076           CGGA
                                AAAGTTTTAAGTA    CC
                                ||||||||||||    ||
                                TTTCGAAATTCGT    GG
                                       AA__
GAM1137  PER2      3'  TCCACAGTTTTAAGTCG      35619      A        A
                                TCCA AGTTTTAAGT CG
                                |||| |||||||||| ||
                                AGGT TCAAAATTCA GC
                                  G         _
GAM1137  SRGAP2    3'  CCTAAGAACGGTACGGACTGC  43977    A   TTTTAA       C
                                CC AAG      GTACGGAC GC
                                || |||      |||||||| ||
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                                GG TTC     CATGCCTG CG
                                 A  TTGC__       A
GAM1138 DPYSL3   3' TTGGGGGGCAGGCCAAGGG   10784       A  CTG
                                TTGGGG GCA   GGCCAAGGG
                                |||||| |||   |||||||||
                                AACCCC CGT   CCGGTTCCC
                                   C  ___
GAM1138 DYSF     3' AAAAAGCGTTGGGTTGGGGG   18578       AC   CCAA
                                GGGGAGC  TGGG   GGG
                                |||||||  ||||   |||
                                TTTTTCG  ACCC   CCC
                                    CA   AACC
GAM1138 ELAVL3   3' CACCAGGGGGCACTGGGCCGGG 10881     TG  A       AA
             GG                   TAT  GGG GCACTGGGCC  GGG
                                |||  ||| ||||||||||  |||
                                GTG  CCC CGTGACCCGG  CCC
                                  GT   C        CC
GAM1138 F2RL3    3' TTGGGGAGCAGAGTTGGGGG   19536        C___   CCAA
                                TTGGGGAGCA   TGGG   GG
                                ||||||||||   ||||   ||
                                AACCCCTCGT   ACCC   CC
                                     CTCA   ____
GAM1138 GAS11    3' TGGGGAGGCTGGGCCAAGGG   11223       CA
                                TGGGGAG  CTGGGCCAAGGG
                                |||||||  ||||||||||||
                                ACCCCTC  GACCCGGTTCCC
                                   C_
GAM1138 IL10     3' TTGGGGAATGAGGTTAGGG   8197        CAC   CCA
                                TTGGGGAG   TGGG   AGGG
                                ||||||||   ||||   ||||
                                AACCCCTT   ACTC   TCCC
                                     ___   CAA
GAM1138 MAFG     5' TATTGGGGGTCGTCATAACCCG 43132       AGCACTG_   AA
             GGG                  TATTGGGG      GGCC  GGG
                                |||||||       ||||  |||
                                ATAACCCC      TTGG  CCC
                                    CAGCAGTA   GC
GAM1138 PML      3' TGGGGAGGCCAAGCTGGGG   37745       CA TG   CAA
                                TGGGGAG  C  GGC   GGG
                                |||||||  |  |||   |||
                                ACCCCTC  G  TCG   CCC
                                   C_ GT   AC_
GAM1138 SLC35A2  3' TTGGTCCCAGCTGGGCCAAGGG 24954     GGAG  _
                                TTGG   CA CTGGGCCAAGGG
                                ||||   || ||||||||||||
                                AACC   GT GACCCGGTTCCC
                                  AGG_  C
GAM1138 TEM8     3' TTGGGGAGAGGCTGGGGG    38197       CA_    CCAA
                                TTGGGGAG   CTGGG   GG
                                ||||||||   |||||   ||
```

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                                AACCCCTC  GACCC   CC
                                    TCC   ____
GAM1138 VDR     3' TTGGTGGGCACTGAAGG    7534     _ A     GCCA
                                TTGG GG GCACTGG   AGG
                                |||| || |||||||   |||
                                AACC CC CGTGACT   TCC
                                  A _     _____
GAM1139 EHHADH  3' TTTGTTGGTTTTTTGTTT   12687        AATGAG
                                TTTGTTGGTTT    TTGTTT
                                ||||||||||     ||||||
                                AAACAACCAAA    AACAAA
                                      A_____
GAM1139 MEN1    5' TTTGTTAGTTTGTCTGTTT  39245        AATGAG
                                TTTGTTGGTTT    TTGTTT
                                ||||||||||     ||||||
                                AAACAATCAAA    GACAAA
                                      CA____
GAM1139 NOTCH2  3' TTTGTTGGTTCAATAAATT  35918
                                TTTGTTGGTTTAATGAGTT
                                |||||||||||||||||||
                                AAACAACCAAGTTATTTAA

GAM1139 RABIF   3' TTTGTTGTTACTGTTGTTGTTT 16130      GTTTAA  A_
          G                      TTTGTTG    TG  GTTGTTTG
                                 |||||||    ||  ||||||||
                                 AAACAAC    AC  CAACAAAC
                                     AATG__  AA
GAM1139 RPP30   3' TTTGTTGTTTTAATGGATTG  26943      G     AG
                                TTTGTTG TTTAATG  TTG
                                ||||||| |||||||  |||
                                AAACAAC AAATTAC  AAC
                                    A     CT
GAM1140 EPB41   5' GTCTGTTTTGAGTTCC     20767    CA      CAGCGA
                                GTC  TTTTGAGTT    CC
                                |||  |||||||||    ||
                                CAG  AAAACTCAA    GG
                                  AC      _______
GAM1141 ARHGEF12 3' TTCATTTTAGTTGGCAAAA  31654      C    A
                                TTCATTTT AGTTG CGGAG
                                |||||||| ||||| |||||
                                AAGTAAAA TCAAC GTTTT
                                     _   C
GAM1141 SNAI2   3' TTCTTTTCAGTTGAAATGA  16890    A       CG_
                                TTC TTTTCAGTTGA  GA
                                ||| ||||||||||  ||
                                AAG AAAAGTCAACT  CT
                                  _       TTA
GAM1141 SS18    3' TTCATTTTCAGTTATTGC   24843          ACGGA
                                TTCATTTTCAGTTG   GC
                                ||||||||||||||   ||
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                                AAGTAAAAGTCAAT    CG
                                      AA___
GAM1142  BASP1    3'  GGCACAGGCCCTGTG      44014     TAT       C
                                GGC   GCGGGCCC GTG
                                |||   |||||||| |||
                                CCG   TGTCCGGG CAC
                                  ___       A
GAM1142  CKAP1    5'  TACGAGCCGGGCTTCGTGG   43884     _ TATG    CC
                                TACG GC    CGGGC  CGTGG
                                |||| ||    |||||  |||||
                                ATGC CG    GCCCG  GCACC
                                  T _____     AA
GAM1142  FUS1     5'  GGCGCATGGCGGGCCCCGTGG  28589     _   _
                                GGC TATG CGGGCCCCGTGG
                                ||| |||| ||||||||||||
                                CCG GTAC GCCCGGGGCACC
                                  C    C
GAM1142  LAIR1    3'  CGGCCATGGGCTTTGTGG    14053       GC    CCC
                                CGGCTAT  GGGC   GTGG
                                |||||||  ||||   ||||
                                GCCGGTA  CCCG   CACC
                                   __    AAA
GAM1142  MAPK3    3'  GGTCCCGAGGCCCCGTGG    43845    _ ATGC
                                GG CT    GGGCCCCGTGG
                                || ||    ||||||||||
                                CC GG    TCCGGGGCACC
                                 A  GC__
GAM1142  WHSC1    3'  GGCTGTGACACCCCGTGG    39372     A  CGG
                                GGCT TG   GCCCCGTGG
                                ||||  ||   |||||||||
                                CCGA AC   TGGGGCACC
                                  C  TG_
GAM1143  ABCB1    5'  CTGGTTGCTTCCTGAAGT    9572     A       CATATT
                                CT GTTGTTTCC     TGGAGT
                                || |||||||||     ||||||
                                GA CAACGAAGG     ACTTCA
                                 C       _______
GAM1143  COL15A1  3'  CTAGTTTCAGATTATTTGGAGT 12352       GTTTCCCA
                                CTAGTT       TATTTGGAGT
                                ||||||       ||||||||||
                                GATCAA       ATAAACCTCA
                                   AGTCTA__
GAM1143  OTX1     3'  TAGTGGTTTTGATTTGGAGT   30989     T   CCCAT
                                TAGT GTTT    ATTTGGAGT
                                ||||  ||||    |||||||||
                                ATCA CAAA    TAAACCTCA
                                  C   AC___
GAM1144  DPP6     3'  GTAAGGACGGATGTAAA     39133       GTG    C
                                GTGAGG   ACGGA GTAAA
                                ||||||   ||||| |||||
```

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                              CATTCC   TGCCT CATTT
                                 ___     A
GAM1144 MAPK4    3' GTGAGGGTGAACGCA      15664         CGG
                              GTGAGGGTGA   ACGTA
                              ||||||||||   |||||
                              CACTCCCACT   TGCGT
                                    ___
GAM1144 THY1     3' GAGGTGGCCGCGTGGACGT   26624    C   AGG   AC
                              GA GTG   GTG  GGACGT
                              || |||   |||  ||||||
                              CT CAC   CGC  CCTGCA
                               C   CGG   A_
GAM1145 PCDHB13  5' TGGGAGGACGGTTCTGTGG   33187     T   T  TTT
                              TGGG AGG TG   GTTCTGTGG
                              |||| ||| ||   |||||||||
                              ACCC TCC GC   CAAGACACC
                                _   T  ___
GAM1145 PCDHB8   5' TGGGAGGACGGTTCTGTGG   33325     T   T  TTT
                              TGGG AGG TG   GTTCTGTGG
                              |||| ||| ||   |||||||||
                              ACCC TCC GC   CAAGACACC
                                _   T  ___
GAM1146 ALDH3A2  5' TGTAGGGGGTGGAGTGAGC   42923     CA   AT    CT  CA
                              TGT  AGG  GTGG  TG  AGC
                              |||  |||  ||||  ||  |||
                              ACA  TCC  CACC  AC  TCG
                                __   CC    TC  __
GAM1146 ARG2     3' TGTTAGGGATGTGGATAGAATA 10125     CAA      CTTGC__
            AGCA                  TGT   GGATGTGG      AAGCA
                              |||   ||||||||      |||||
                              ACA   CCTACACC      TTCGT
                                ATC       TATCTTA
GAM1146 BACE     3' GGTTTATGGCTTGTGGGCA   39966    A_       CAA
                              GG  TGTGGCTTG   GCA
                              ||  |||||||||   |||
                              CC  ATACCGAAC   CGT
                               AA        ACC
GAM1146 GPR48    3' TGTCAAGGATGGCAAG      32994          TGGCTT
                              TGTCAAGGATG     GCAAG
                              ||||||||||      |||||
                              ACAGTTCCTAC     CGTTC
                                    _______
GAM1146 SFTPA2   3' TGTCAAGGTGTGTGGCACA   27967        A_     TT
                              TGTCAAGG  TGTGGC  GCA
                              ||||||||  ||||||  |||
                              ACAGTTCC  ACACCG  TGT
                                   AC     __
GAM1147 IL12RB2  5' ATAGGCGCGATAAAATCGTG   11423     AA       TAGATA
                              GTA  CGCGATAA     GTG
                              |||  ||||||||     |||
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                                TAT  GCGCTATT     CAC
                                  CC       TTAG__
GAM1147  MAK      3'  AGTAAGCCAAGATAGT      25379       AC  GATAAT
                                AGTAA  GC     AGATAGT
                                |||||  ||     |||||||
                                TCATT  CG     TCTATCA
                                  __  GT____
GAM1147  SLC2A2   3'  GTAAAGGCAGATAGATAGTG   7349       C   ATA
                                GTAAA GCG   ATAGATAGTG
                                |||||  |||  ||||||||||
                                CATTT CGT   TATCTATCAC
                                  C  C__
GAM1148  ADCY2    3'  AAACATTAGCTTATACACGA   42136         CCTG
                                AAACATTAGC    ATGCACGA
                                ||||||||||    ||||||||
                                TTTGTAATCG    TATGTGCT
                                     AA__
GAM1148  ODF2     5'  TCGCTGATGGTTTCGG      14933     AA      CCATCT
                                TC  TGATGGTT     TCGG
                                ||  ||||||||     ||||
                                AG  ACTACCAA     AGCC
                                 CG       _______
GAM1149  CDH8     5'  TGCGCTGGCGAATGTCAA     12197        A   CGGAA
                                TGCGTTG CGA    GTGTCAA
                                |||||||  |||    |||||||
                                ACGCGAC GCT    TACAGTT
                                   C  ______
GAM1150  ADCY2    3'  ATCAGCTTCGATAAGTGCCTTT 42138       TC   GC   CA
                                ATCAGCT  TCG  GAG  CCTTT
                                |||||||  |||  |||  |||||
                                TAGTCGA  AGC  TTC  GGAAA
                                   __  TA   AC
GAM1150  AHSG     3'  AGCTTAGCAAGAGCACCTTT   11556      CT   C
                                AGCTT  CGG GAGCACCTTT
                                |||||  ||| ||||||||||
                                TCGAA  GTT CTCGTGGAAA
                                  TC  _
GAM1150  EPHB1    5'  GCTTCTCGGTATCCTTT     20774         CGAGCA
                                GCTTCTCGG     CCTTT
                                |||||||||     |||||
                                CGAAGAGCC     GGAAA
                                     ATA___
GAM1150  EXTL3    5'  CCAGCTTCTTATGATGCCTTT  11028         CGGC  GCA
                                TCAGCTTCT   GA   CCTTT
                                |||||||||   ||   |||||
                                GGTCGAAGA   CT   GGAAA
                                     ATA_  AC_
GAM1150  NFKB1    3'  CCGGCTCTCTGAGCACCTTT   19649    A   T   GGC
                                TC GCT CTC   GAGCACCTTT
                                || ||| |||   ||||||||||
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                                GG CGA GAG   CTCGTGGAAA
                                 C   _   A__
GAM1150  NUFIP1   3'  ATCAGCTTTCTTACCT      29592         C  GGCGAGC
                                ATCAGCTT TC      ACCT
                                ||||||||  ||      ||||
                                TAGTCGAA AG      TGGA
                                    _  AA_____
GAM1151  ABCD3    3'  TCACTGAAGCAGGTATAG    16021           GAT
                                TCACTGAAGCGGG   TGG
                                ||||||||||||   |||
                                AGTGACTTCGTCC   ATC
                                       AT_
GAM1151  AGRN     5'  CGTCTTCTCCTCGCGCCGC   44249    TC  _  GTA   A
                                CGT  TC CC   GTG CCGC
                                |||  ||  ||   ||| ||||
                                GCA  AG GG   CGC GGCG
                                  GA  A  AG_   _
GAM1151  APP      5'  TCCGCGTGCTCTCGCCTACCGC 7920     A   T   C   AGTG
                                TCC CGT CTC CGT    ACCGC
                                |||  |||  |||  |||    |||||
                                AGG GCA GAG GCG    TGGCG
                                  C   C   A   GA__
GAM1151  BCL2     3'  TCCACGTTCTTCATTGT     8524          CC   A
                                TCCACGTTCT  CGT GT
                                ||||||||||  |||  ||
                                AGGTGCAAGA  GTA CA
                                      A_   A
GAM1151  CSF1R    3'  GTTCTCCCCGTGTCGC      23312         GTA   AC
                                GTTCTCCC   GTG  CGC
                                ||||||||   |||  |||
                                CAAGAGGG   CAC  GCG
                                    G__   A_
GAM1151  DLG5     5'  CATGTCCTCCCATGACTGC   44449    C      GTA    C
                                CA GTTCTCCC   GTGAC GC
                                ||  ||||||||   |||||  ||
                                GT CAGGAGGG   TACTG CG
                                 A       ___     A
GAM1151  REGL     3'  TCCACATTTTCTCTAAGC    27123         __   CCGT
                                TCCACGT  TCTC    AGT
                                |||||||  ||||    |||
                                AGGTGTA  AGAG    TCG
                                   AA    AT__
GAM1151  SEC22L1  3'  GTTCTCCCTTACCAGTGAC   22200         G___
                                GTTCTCCC    TAGTGAC
                                ||||||||    |||||||
                                CAAGAGGG    GTCACTG
                                    AATG
GAM1151  SLC12A6  3'  TTCTGTAATGACTGC      23081      CCC       C
                                TTCT   GTAGTGAC GC
                                ||||   ||||||||  ||
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                                AAGA   CATTACTG CG
                                  ___       A
GAM1152  BAALC    5'  GGCTCTGGCGGCGGCT      36041         G A TCAA
                                GGCTCTGG C G    CGGCT
                                |||||||| | |    |||||
                                CCGAGACC G C    GCCGA
                                    _ C ____
GAM1152  CYLN2    3'  TGGCCTGGAAGTGGC       18070      T    C   CAAC
                                TGGC CTGGG AGT    GGC
                                |||| ||||| |||    |||
                                ACCG GACCT TCA    CCG
                                  _    _  _____
GAM1152  DAZ      5'  GGCTCTGGGAGGTGGCT     19854         C  TCAAC
                                GGCTCTGGG AG    GGCT
                                ||||||||| ||    ||||
                                CCGAGACCC TC    CCGA
                                    _ CA___
GAM1152  DDB1     3'  TGGCTCTGGGGGCAGCTGGCT  12561         __      CAAC
                                TGGCTCT  GGGCAGT   GGCT
                                |||||||  |||||||   ||||
                                ACCGAGA  CCCGTCG   CCGA
                                   CC      A___
GAM1152  DRPLA    3'  TGGCTCTGGGTGGCAGGC    12594         CA  CAAC
                                TGGCTCTGGG  GT   GGC
                                |||||||||  ||   |||
                                ACCGAGACCC  CG   CCG
                                    AC  T___
GAM1152  EGLN2    5'  TGGCTCTGGGGGTCCCACTC  38841         CA   AACG
                                TGGCTCTGGG  GTC   GCTC
                                |||||||||  |||   ||||
                                ACCGAGACCC  CAG   TGAG
                                    C_  GG__
GAM1152  ESRRA    3'  GGCTCTGGGCCCTGGCT     20834         AGTCAAC
                                GGCTCTGGGC      GGCT
                                ||||||||||      ||||
                                CCGAGACCCG      CCGA
                                    GGA____
GAM1152  GLUL     3'  GCTTTGGGCAGTTACACAG   13155     C      CA_
                                GCT TGGGCAGT   ACGG
                                ||| |||||||   ||||
                                CGA ACCCGTCA   TGTC
                                  A       ATG
GAM1152  GNPI     3'  GGCTCTGGGGGAAAAACGGCT 24186         CAGTC
                                GGCTCTGGG    AACGGCT
                                |||||||||    |||||||
                                CCGAGACCC    TTGCCGA
                                    CCTTT
GAM1152  GRM6     5'  TGGCTCTGGGGAGTTAGCTC  9178          C   CAAC
                                TGGCTCTGGG AGT    GGCTC
                                |||||||||| |||    |||||
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                                ACCGAGACCC TCA   TCGAG
                                      C  A___
GAM1152 LOH11CR2A 5' TGGCCCTGGGAGATGGCT   31194        C TCAAC
                                TGGCTCTGGG AG    GGCT
                                |||||||||| ||    ||||
                                ACCGGGACCC TC    CCGA
                                     _ TA___
GAM1152 LRP3    5' TGGCTCTGGCTGCGGCT    42170        G AGTCAA
                                TGGCTCTGG C    CGGCT
                                ||||||||| |    |||||
                                ACCGAGACC G    GCCGA
                                     _ AC____
GAM1152 MEN1    3' TGGCTCTAGGTGAGCGGTTC 39257        CAGTCAA  C
                                TGGCTCTGGG     CGG TC
                                ||||||||||     ||| ||
                                ACCGAGATCC     GCC AG
                                     ACTC___  A
GAM1152 MSN     3' GCTCTAGTTAGTGGCTC    41243      GC  CAAC
                                GCTCTGG AGT   GGCTC
                                ||||||| |||   |||||
                                CGAGATC TCA   CCGAG
                                    AA  ____
GAM1152 NFKB2   5' GGCTCTGTCTAGTGGCT    14764      GGC  CAAC
                                GGCTCTG  AGT   GGCT
                                |||||||  |||   ||||
                                CCGAGAC  TCA   CCGA
                                    AGA  ____
GAM1152 OLFM1   3' TGGCCTGGGCATGGAGGCT  26783    T    GTCAAC
                                TGGC CTGGGCA    GGCT
                                |||| |||||||    ||||
                                ACCG GACCCGT    CCGA
                                  _     ACCT__
GAM1152 PRNP    3' TGGCCTGGCATTAGCAACGGCT 7187     T  G GT__
            C                    TGGC CTGG CA   CAACGGCTC
                                |||| |||| ||   |||||||||
                                ACCG GACC GT   GTTGCCGAG
                                  _   _ AATC
GAM1152 SBF1    5' TGACTCTGCAGTGGC      42281      GG   CAAC
                                TGGCTCT  GCAGT   GGC
                                |||||||  |||||   |||
                                ACTGAGA  CGTCA   CCG
                                     __   ____
GAM1152 STK24   3' TGGCGCTGGGGTGGC      18708    T   CA CAAC
                                TGGC CTGGG  GT   GGC
                                |||| |||||  ||   |||
                                ACCG GACCC  CA   CCG
                                  C   __ ____
GAM1152 SURF5   3' TGGCTCTGGATATCTGTGGCTC 39512        CA  AAC
                                TGGCTCTGGG  GTC  GGCTC
                                ||||||||||  |||  |||||
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                                ACCGAGACCT  TAG   CCGAG
                                     A_   ACA
GAM1152  TEM5    3'  TGCCTCTGGGCTTGGCT    37247    G      AGTCAAC
                                TG CTCTGGGC      GGCT
                                || ||||||||      ||||
                                AC GAGACCCG      CCGA
                                 G       AA_____
GAM1152  TGM2    3'  TGGTGGGTGGTCAATGGCT   21443    CTC    CA    C
                                TGG   TGGG  GTCAA GGCT
                                |||   ||||  ||||| ||||
                                ACC   ACCC  CAGTT CCGA
                                  ___    AC    A
GAM1152  VASP    5'  TGGCTCCGGGCTCGGCT     17919          AGTCAA
                                TGGCTCTGGGC     CGGCT
                                ||||||||||      |||||
                                ACCGAGGCCCG     GCCGA
                                     A_____
GAM1152  WHSC1   3'  TGGCTCTGGGGGGGGGCT     39392         CAGTCAAC
                                TGGCTCTGGG      GGCT
                                ||||||||||      ||||
                                ACCGAGACCC      CCGA
                                     CCC_____
GAM1152  XBP1    3'  TGGCTTTGGGCAGTGGC     22926      C      CAAC
                                TGGCT TGGGCAGT    GGC
                                ||||| ||||||||    |||
                                ACCGA ACCCGTCA    CCG
                                   A       ____
GAM1153  AP1G1   3'  TTCTTGGTAACAAACATAC   10051         AT
                                TTCTTGGTGA  AACATAC
                                ||||||||||  |||||||
                                AAGAACCATT  TTGTATG
                                     GT
GAM1153  B4GALT6 3'  TTTCTTGGTAATACTCAT    40856          ATAA
                                TTTCTTGGTGA    CAT
                                ||||||||||    |||
                                AAAGAACCATT    GTA
                                      ATGA
GAM1153  CRY2    3'  TTTCTAGTGAAGGTGACATAC  43590      T     TA__
                                TTTCT GGTGAA    ACATAC
                                ||||| ||||||    ||||||
                                AAAGA TCACTT    TGTATG
                                   _     CCAC
GAM1153  CSNK1G3 3'  TTTCTTGCTGTCTAACATAC   20478       G  AA
                                TTTCTTG TG  TAACATAC
                                ||||||| ||  ||||||||
                                AAAGAAC AC  ATTGTATG
                                    G  AG
GAM1153  CYB561  3'  TTTCTTGGAGAACCATA     12549        T   AA
                                TTTCTTGG GAAT  CATA
                                |||||||| ||||  ||||
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                                AAAGAACC CTTG  GTAT
                                     T   __
GAM1153  EIF5A2   3'  TTTCTTGGACTGACATAC    33788        TGAATA
                                TTTCTTGG     ACATAC
                                ||||||||     ||||||
                                AAAGAACC     TGTATG
                                     TGAC__
GAM1153  FBXL3A   3'  CTTCTTGGATATTATAACATA  29127        TGA__
                                TTTCTTGG    ATAACATA
                                ||||||||    ||||||||
                                GAAGAACC    TATTGTAT
                                     TATAA
GAM1153  HGF      3'  TTTCTTGATGCCAGCACATA   45328        AATA_
                                TTTCTTGGTG    ACATA
                                ||||||||||    |||||
                                AAAGAACTAC    TGTAT
                                      GGTCG
GAM1153  NEBL     3'  TTCCTTGAATATAACATA    26915        TGA
                                TTTCTTGG   ATAACATA
                                ||||||||   ||||||||
                                AAGGAACT   TATTGTAT
                                     TA_
GAM1153  SCD      3'  TTTCTTGGAGAACCATA     22840        T   AA
                                TTTCTTGG GAAT  CATA
                                |||||||| ||||  ||||
                                AAAGAACC CTTG  GTAT
                                     T   __
GAM1153  SLC6A3   3'  TTTCCTGGTGAGACATAC    9816          ATA
                                TTTCTTGGTGA   ACATAC
                                ||||||||||   ||||||
                                AAAGGACCACT   TGTATG
                                      C__
GAM1153  TSN      3'  TTTCCTGGCACATA        21501         GAATA
                                TTTCTTGGT    ACATA
                                |||||||||    |||||
                                AAAGGACCG    TGTAT
                                     _____
GAM1153  APPL     3'  AAATGTGTGACTATGTA     29003         ATATT
                                AAATGTGTGG    TGTA
                                ||||||||||    ||||
                                TTTACACACT    ACAT
                                      GAT__
GAM1153  DIAPH2   3'  ATATAAAGTATTTGTATAAA   28665        _
                                GTGTGGA TATTTGTATAAA
                                ||||||| ||||||||||||
                                TATATTT ATAAACATATTT
                                     C
GAM1153  HAS3     3'  ATGCGTCCAATTGTATAAA   39768       GA  T
                                GTGTG  TA TTGTATAAA
                                |||||  || |||||||||
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                                TACGC  GT AACATATTT
                                   AG  T
GAM1153  NRG1     3'  GGATGTGGTCATTGTATAAA  30343    T     ATAT
                                A GTGTGG    TTGTATAAA
                                | ||||||    |||||||||
                                C TACACC    AACATATTT
                                 C      AGT_
GAM1153  PPARA    3'  TGGTGGATATTTGTGCAAAA  22772    T          A
                                TG GTGGATATTTGT TAAAA
                                || ||||||||||| |||||
                                AC CACCTATAAACA GTTTT
                                 _          C
GAM1153  RANBP3   3'  AAATGTATGGGTACCCAT    28745          A    TG
                                AAATGTGTGG TATT  T
                                |||||||||| ||||  |
                                TTTACATACC ATGG  A
                                      C    GT
GAM1153  SPG4     3'  AAATGTATGCCATGTATAAAA 31394         GATATT
                                AAATGTGTG     TGTATAAAA
                                |||||||||     |||||||||
                                TTTACATAC     ACATATTTT
                                      GGT___
GAM1154  EGLN3    3'  CAGCCCTTTCTAGAGGTATTAA 37855      ACAAATCAA
            T                    CAGC        AGGTATTAAT
                                ||||        ||||||||||
                                GTCG        TCCATAATTA
                                  GGAAAGATC
GAM1154  FAAH     3'  CAGTACAAATCACAAGGT    11049     C       _
                                CAG ACAAATCA AAGGT
                                ||| |||||||| |||||
                                GTC TGTTTAGT TTCCA
                                  A       G
GAM1154  GOCAP1   3'  AACACAAATTAAAGCTAT    35545         C    G
                                AGCACAAAT AAAG TAT
                                ||||||||| |||| |||
                                TTGTGTTTA TTTC ATA
                                      A    G
GAM1154  IL13RA1  3'  AGCACAAACCAAAGACAC    11438            GT
                                AGCACAAATCAAAG  AT
                                ||||||||||||||  ||
                                TCGTGTTTGGTTTC  TG
                                        TG
GAM1154  IMPA1    3'  CAGCACAATCAAATCAGTA    24390         A    __
                                CAGCACAA TCAAA  GGTA
                                |||||||| |||||  ||||
                                GTCGTGTT AGTTT  TCAT
                                      _    AG
GAM1154  KLHL3    3'  CAGCACAAACTAGAAAATA    44640         CA_
                                CAGCACAAAT   AAGGTA
                                ||||||||||   ||||||
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                                GTCGTGTTTG  TTTTAT
                                     ATC
GAM1154 MMP10   3' CAGTGCAATTCAAAAGCA   14550    CA  A
                                CAG  CAA TCAAAGGTA
                                |||  ||| |||||||||
                                GTC  GTT AGTTTTCGT
                                  AC  A
GAM1154 MPL     3' CAGCGAGATCAAAGGAACT  23879    ACAA     T
                                CAGC   ATCAAAGG ATT
                                ||||   |||||||| |||
                                GTCG   TAGTTTCC TGA
                                  CTC_     T
GAM1154 NOTCH2  3' CAGACAAATCAGGTA     35906    C      AA
                                CAG ACAAATCA  GGTA
                                ||| ||||||||  ||||
                                GTC TGTTTAGT  CCAT
                                  _     __
GAM1154 PRKG1   3' CAGCATCGATCAAAGGCATCA 26514     CAA
                                CAGCA  ATCAAAGGTATTA
                                |||||  ||||||||||||
                                GTCGT  TAGTTTCCGTAGT
                                   AGC
GAM1154 SCAP2   3' ACACAAATCAAATGGGTA   19441         __
                                GCACAAATCAAA  GGTA
                                ||||||||||||  ||||
                                TGTGTTTAGTTT  CCAT
                                      AC
GAM1154 SLC14A2 5' CAGTAAAATCAAAAGCA    28395    CAC
                                CAG   AAATCAAAGGTA
                                |||   ||||||||||||
                                GTC   TTTAGTTTTCGT
                                  AT_
GAM1154 USP6    3' AACACAAATCACACAACATTA 45022        AA_
                                AGCACAAATCA   GGTATTA
                                ||||||||||   |||||||
                                TTGTGTTTAGT   TTGTAAT
                                      GTG
GAM1155 EHD4    3' TTTTTGCCACTCTAAATAT   40211     _    C
                                TTTTT CCACTC AAATAT
                                ||||| |||||| ||||||
                                AAAAA GGTGAG TTTATA
                                   C     A
GAM1155 LOX     3' TTTTCCCACTTCAGAACACC  14190       C  _
                                TTTTTCCACT CA AATATT
                                |||||||||| || ||||||
                                AAAAGGGTGA GT TTGTGG
                                      A  C
GAM1156 CIT     3' TGAGCTGCGGCTGCTTTCTCAA 43058    A  ACAT    A
            A                    TGA CT    GTTGT TTCTCAAA
                                ||| ||    ||||| ||||||||
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                                ACT GA    CGACG AAGAGTTT
                                  C  CGC_    A
GAM1156  CYB561    3'  TGTTTATGTATTCTCAAA    12548    ___
                                TGT   TGTATTCTCAAA
                                |||   ||||||||||||
                                ACA   ACATAAGAGTTT
                                  AAT
GAM1156  MBNL      3'  TGACACTACATGTAATTC    34325    _       TGT
                                TGA ACTACATGT   ATTC
                                ||| |||||||||   ||||
                                ACT TGATGTACA   TAAG
                                  G        T__
GAM1156  MDM2      3'  TGAGCTACATATTCAAGTCAAA 27808    A       G  TTC
                                TGA CTACATGTT TA   TCAAA
                                ||| ||||||||| ||   |||||
                                ACT GATGTATAA GT   AGTTT
                                  C        _  TC_
GAM1156  MEN1      5'  TGAACTACCATGTCAACATATT 39234        _    ___
                                TGAACTAC ATGTT   GTATT
                                |||||||| |||||   |||||
                                ACTTGATG TACAG   TATAA
                                     G     TTG
GAM1156  PLA2G4C   3'  TGAGCACTTGTTGTATTCTCA  43862     AC   A
                                TGA  TAC TGTTGTATTCTCA
                                |||  ||| ||||||||||||
                                ACT  GTG ACAACATAAGAGT
                                  C_   A
GAM1156  PON1      3'  TGATTTGATAGTGTATTCTCAA 7779      ACTAC   T
              A                  TGA     ATG TGTATTCTCAAA
                                |||     ||| ||||||||||||
                                ACT     TAT ACATAAGAGTTT
                                  AAAC_   C
GAM1156  PWP2H     3'  TGGGCTACATGTGTGCAC    22785    AA      _
                                TG  CTACATGT TGTAT
                                ||  |||||||| |||||
                                AC  GATGTACA ACGTG
                                 CC       C
GAM1156  SCA1      3'  TGAACAGTATTCTCA       7295       TACATGTT
                                TGAAC       GTATTCTCA
                                |||||       |||||||||
                                ACTTG       CATAAGAGT
                                   T________
GAM1156  SCD       3'  TGTTTATGTATTCTCAAA    22838    ___
                                TGT   TGTATTCTCAAA
                                |||   ||||||||||||
                                ACA   ACATAAGAGTTT
                                  AAT
GAM1156  ACTN4     3'  TTGCATAGATACAGAGTG    22277          C  TT
                                TTGTATAGAT TA  GTG
                                |||||||||| ||  |||
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                                AACGTATCTA GT  CAC
                                      T  CT
GAM1156 CASP10   3' TGTATATGCACTGTGAA    37395      GATC
                                TGTATA   TATTGTGAA
                                ||||||   |||||||||
                                ACATAT   GTGACACTT
                                   AC__
GAM1156 CYP2B6   3' TTGTACAGCTTTGTGAA    8927       ATCTA
                                TTGTATAG   TTGTGAA
                                ||||||||   |||||||
                                AACATGTC   AACACTT
                                    GA___
GAM1156 DACH     3' TTGTACAGATTTTGTA     38884        CTA
                                TTGTATAGAT  TTGTG
                                ||||||||||  |||||
                                AACATGTCTA  AACAT
                                      A__
GAM1156 DSG1     3' TTGTATAAATCTGTGGTTGAA 12605          ATTG_
                                TTGTATAGATCT   TGAA
                                ||||||||||||   ||||
                                AACATATTTAGA   ACTT
                                       CACCA
GAM1156 GIF      3' TTGCATAGATTTAAAATGAA  23107        C  TT
                                TTGTATAGAT TA  GTGAA
                                |||||||||| ||  |||||
                                AACGTATCTA AT  TACTT
                                      A  TT
GAM1156 HDC      3' TTGTATCCTATTGTG      13373      AGA
                                TTGTAT  TCTATTGTG
                                ||||||  |||||||||
                                AACATA  GGATAACAC
                                     ___
GAM1156 LMO2     3' TTGTATAGAAACAATCTGTG  24555       TC __
                                TTGTATAGA  TA  TTGTG
                                |||||||||  ||  |||||
                                AACATATCT  GT  GACAC
                                      TT  TA
GAM1156 NCAM2    3' TTGTATAATCCATTGTGAA   21228      A
                                TTGTAT GATCTATTGTGAA
                                |||||| ||||||||||||
                                AACATA TTAGGTAACACTT
                                     _
GAM1156 PIK3R1   3' TTGCATAGCGCTGTGAA    42864       ATCTA
                                TTGTATAG   TTGTGAA
                                ||||||||   |||||||
                                AACGTATC   GACACTT
                                    GC___
GAM1156 PLAG1    3' TTATGTAGATCTATGTGA   15363     A       T
                                TTGT TAGATCTAT GTGA
                                |||| ||||||||| ||||
```

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                                AATA ATCTAGATA CACT
                                  C       _
GAM1156 PTPRZ1   5' TGTATAGATCGAAGTGA    15988         TATT
                                TGTATAGATC   GTGA
                                ||||||||||   ||||
                                ACATATCTAG   CACT
                                     CTT_
GAM1157 GABRR1   3' TGGAAATGTGAAATTTGTAGAA 13041        AT   ATT
           T                    TGGAAATGT  AATT  TGGAAT
                                |||||||||  ||||  ||||||
                                ACCTTTACA  TTAA  ATCTTA
                                     CT   AC_
GAM1157 HMG20A   3' TGGAGATGTATAAATTGG    32872     A      TTAT
                                TGGA ATGTATAA   TTGG
                                |||| ||||||||   ||||
                                ACCT TACATATT   AACC
                                  C      T___
GAM1157 TMPRSS3  3' GGAAACATATTATTTGGAAT  37063        AAT
                                GGAAATGTAT  TATTTGGAAT
                                ||||||||||  ||||||||||
                                CCTTTGTATA  ATAAACCTTA
                                     ___
GAM1158 ADAMTS5  3' TAAATTTCCAACACAAGGA   28182         G  TA
                                TAAATTTCCAA ATG  GA
                                |||||||||||| |||  ||
                                ATTTAAAGGTT TGT  CT
                                     G  TC
GAM1158 CCR2     3' TGATTTCCAAAGCAGA     8504    A      AT
                                A ATTTCCAAG  GTAGA
                                | |||||||||  |||||
                                A TAAAGGTTT  CGTCT
                                 C       __
GAM1158 CHD2     3' AAATTTCCAAGCACAAGAA   10435         ATGT
                                AAATTTCCAAG   AGAA
                                ||||||||||   ||||
                                TTTAAAGGTTC   TCTT
                                     GTGT
GAM1158 GABRA1   3' TAAATTCCCAGTGCAGA     9039         A A
                                TAAATTTCCA G TGTAGA
                                |||||||||| | ||||||
                                ATTTAAGGGT C ACGTCT
                                     _ _
GAM1158 GALNT1   3' TAAATTTCCATTTTTTAGAA  33841        AGATG
                                TAAATTTCCA    TAGAA
                                ||||||||||    |||||
                                ATTTAAAGGT    ATCTT
                                     AAAAA
GAM1158 HTR2C    3' CAAATTTCCAGGATGCTGA   9280         A    A
                                TAAATTTCCA GATGT GA
                                |||||||||| ||||| ||
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                                GTTTAAAGGT CTACG CT
                                      C     A
GAM1158 IL1RAP   3' AATTTCCATTTATTGTAGAA  13495        AGA__
                                AATTTCCA    TGTAGAA
                                ||||||||    |||||||
                                TTAAAGGT    ACATCTT
                                     AAATA
GAM1158 MADH7    3' TAAATTTCCAATGAGAA     25374         AG   T
                                TAAATTTCCA  ATG AGAA
                                ||||||||||  ||| ||||
                                ATTTAAAGGT  TAC TCTT
                                      __  _
GAM1158 MYBL1    3' TAAACTTCTAAGTGCAG     41980        C   A
                                TAAATTTC AAG TGTAG
                                |||||||| ||| |||||
                                ATTTGAAG TTC ACGTC
                                     A  _
GAM1158 NKTR     3' AACTTCAAAATGTAGAA     23925       C
                                AATTTC AAGATGTAGAA
                                |||||| ||||||||||
                                TTGAAG TTTTACATCTT
                                      _
GAM1158 NPC2     3' TAAATTTCCAGGTGTAGAA   26966         A A
                                TAAATTTCCA G TGTAGAA
                                |||||||||| | |||||||
                                ATTTAAAGGT C ACATCTT
                                      _ C
GAM1158 NR4A2    5' TTTCCAAGATTTTTAGAA    26175         G__
                                TTTCCAAGAT   TAGAA
                                ||||||||||   |||||
                                AAAGGTTCTA   ATCTT
                                     AAA
GAM1158 PRDM4    3' TAAACTTCCAAGTGGCCAG   29665          A __
                                TAAATTTCCAAG TG  TAG
                                |||||||||||| ||  |||
                                ATTTGAAGGTTC AC  GTC
                                      _  CG
GAM1158 THBS1    3' TAAATTTCCAGGCAGAA     17512         AGAT
                                TAAATTTCCA   GTAGAA
                                ||||||||||   ||||||
                                ATTTAAAGGT   CGTCTT
                                     C___
GAM1159 ATP6V1G2 3' TGAGCAGGATATTTATAAG   39060       TTT
                                TGAGTAG   TGTTTATAAG
                                |||||||   ||||||||||
                                ACTCGTC   ATAAATATTC
                                    CT_
GAM1159 DBT      3' TGAGTAGCTGGGACTATA    12555        TTGT
                                TGAGTAGTT    TTATA
                                |||||||||    |||||
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                                ACTCATCGA   GATAT
                                     CCCT
GAM1159 PSMD5   3' TGAGTAGCTGAGATTATA   22781       TTGT
                                TGAGTAGTT   TTATA
                                |||||||||   |||||
                                ACTCATCGA   AATAT
                                     CTCT
GAM1159 TNFRSF1B 3' TGAGTAGCTGGGACTATA   9878        TTGT
                                TGAGTAGTT   TTATA
                                |||||||||   |||||
                                ACTCATCGA   GATAT
                                     CCCT
GAM1159 TRHDE   3' TGAATTGTTTGTTTATAAG   30112     A   T
                                TGAGT GTTT GTTTATAAG
                                ||||| |||| |||||||||
                                ACTTA CAAA CAAATATTC
                                   A   _
GAM1159 ABCE1   3' ACAAAAAAAGTTCAGAGT   40497      C  C
                                ACAAAAA AG TCAGAGT
                                ||||||| || |||||||
                                TGTTTTT TC AGTCTCA
                                    T  A
GAM1159 ADCY7   3' CAAGAACGGCTCAGCATTTG  9981     A  A    AG__
                                CAA AAC GCTCAG   TG
                                ||| ||| ||||||   ||
                                GTT TTG CGAGTC   AC
                                  C  C     GTAA
GAM1159 ALS2    3' AAACAGCTTAGAAAAAGT   34087      C   T_
                                AAACAGCT AGAG  GGT
                                |||||||| ||||  |||
                                TTTGTCGA TCTT  TCA
                                     A   TT
GAM1159 CCRL1   3' ACAAAGATGGTACAGAGTGGTC 32425     AACAGCT
                                ACAAA      CAGAGTGGTT
                                |||||      ||||||||||
                                TGTTT      GTCTCACCAG
                                   CTACCAT
GAM1159 CD69    3' AAAAACAGCTTATAATT    12136        CAGA
                                AAAAACAGCT   GTGGTT
                                ||||||||||   ||||||
                                TTTTTGTCGA   TATTAA
                                     A___
GAM1159 CDR2    3' CAAGAGCAGCTTGTGGCT   44017    AAA   CAGA
                                CAA  CAGCT   GTGGTT
                                |||  |||||   ||||||
                                GTT  GTCGA   CACCGA
                                  CTC   A___
GAM1159 CR1     3' CAAAATATTAGGAGTGGTTAT 8198      ACAGCTCA
                                CAAAA      GAGTGGTTAT
                                |||||      ||||||||||
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                                GTTTT      CTCACCAATA
                                   ATAATC__
GAM1159 CSTB    3' CAAAAGCAGCTGCAGAAT    6436       A    _
                                CAAAA CAGCT CAGAGT
                                ||||| ||||| ||||||
                                GTTTT GTCGA GTCTTA
                                   C    C
GAM1159 CUGBP1  3' ACAAAATCAAGTGGTT      27276      ACAGC   G
                                ACAAAA    TCA AGTGGTT
                                ||||||    ||| |||||||
                                TGTTTT    AGT TCACCAA
                                   _____  _
GAM1159 CYP4F3  3' ACAAAAACAGTCAGTGT     9449         C    A
                                ACAAAAACAG TCAG GT
                                |||||||||| |||| ||
                                TGTTTTTGTC AGTC CA
                                      _   A
GAM1159 DYRK1A  3' AAAAACAGCTTTGGT       38985        CAGAG
                                AAAAACAGCT    TGGT
                                ||||||||||    ||||
                                TTTTTGTCGA    ACCA
                                      A____
GAM1159 PRKG2   3' ACAAAAATGGCTCTGATTG   26519       CA   A  G
                                ACAAAAA  GCTC GA TG
                                |||||||  |||| || ||
                                TGTTTTT  CGAG CT AC
                                    AC   A  A
GAM1159 RP42    3' AAAAGCAGCTCATGGCT     33973     A     GAG
                                AAAA CAGCTCA   TGGTT
                                |||| |||||||   |||||
                                TTTT GTCGAGT   ACCGA
                                  C     ___
GAM1159 SELE    3' AAAAACACTCAGAACTTTAT   7800        G     TGG
                                AAAAACA CTCAGAG   TTAT
                                ||||||| |||||||   ||||
                                TTTTTGT GAGTCTT   AATA
                                    _     GA_
GAM1159 SH3BP4  3' CAGAAACAGCTCAGGGCACCT  30958    A        A  G
                                CA AAACAGCTCAG GTG TT
                                || ||||||||||| ||| ||
                                GT TTTGTCGAGTC CGT GA
                                 C         C  G
GAM1159 TAP2    3' CAAAATAGCAACTATGGTTAT  8079      A__    CAGA
                                CAAAA  CAGCT   GTGGTTAT
                                |||||  |||||   ||||||||
                                GTTTT  GTTGA   TACCAATA
                                   ATC    ____
GAM1159 TMPRSS3 3' ACAAAAAGCAGCTTGAAGGTT  37058       _    CA  T
                                ACAAAAA CAGCT  GAG GGTT
                                ||||||| |||||  ||| ||||
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                                TGTTTTT GTCGA  CTT CCAA
                                    C    A_  _
GAM1159  TNFRSF17  5'  CAAGAGCAGCTAGAATG     10164     AAA    C
                                CAA   CAGCT AGAGTG
                                |||   ||||| ||||||
                                GTT   GTCGA TCTTAC
                                  CTC    _
GAM1159  UBE2A     3'  AAACAGCACAACAGTTAT     17783        T  GA TG
                                AAACAGC CA  G  GTTAT
                                ||||||| ||  |  |||||
                                TTTGTCG GT  T  CAATA
                                    T  __ GT
GAM1159  ZNF140    3'  CAAAAAAATAAAAGAGTGGTTA 18340       CAGCTC
              T                  CAAAAA     AGAGTGGTTAT
                                ||||||     ||||||||||
                                GTTTTT     TCTCACCAATA
                                   TTATTT
GAM1160  CCNF      3'  CACATACGAACGCCTCTGG    12071        A     GTA
                                TACATAC AACGC   TGG
                                ||||||| |||||   |||
                                GTGTATG TTGCG   ACC
                                    C    GAG
GAM1160  DIRC1     3'  TGAGTACAAACGAATAAAGG   38126         TACA   C   T_
                                TGAGTACA    AACG GTA  GG
                                ||||||||    |||| |||  ||
                                ACTCATGT    TTGC TAT  CC
                                     _____    T   TT
GAM1160  BIN2      3'  TTTAACAATCTGAAAATGTGTT 32227        TTA         C
              C                  TTTAATG   CTGAAAATGTG TC
                                |||||||   |||||||||| ||
                                AAATTGT   GACTTTTACAC AG
                                    TA_         A
GAM1160  BMX       3'  TGCAGTCTGAAAATGTGCT    11891     TA_
                                TGT   CTGAAAATGTGCT
                                |||   ||||||||||||
                                ACG   GACTTTTACACGA
                                  TCA
GAM1160  HIVEP1    3'  ATGTCAGAAAAATGTGCT     13375       CT
                                ATGTTA  GAAAATGTGCT
                                ||||||  ||||||||||
                                TACAGT  TTTTTACACGA
                                   C_
GAM1160  TEL2      3'  TTTATTGTTACTGAGGCTGT   32047      A       AAA
                                TTTA TGTTACTGA   TGT
                                ||||  |||||||||   |||
                                AAAT ACAATGACT   ACA
                                  A        CCG
GAM1161  DLG5      5'  TTCAAGGCGTTGGTGTGCT    44474          ATACA  _  _
                                TTCAAGGCGTT     GG GT CT
                                ||||||||||     || || ||
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                                AAGTTCCGCAA    CC CA GA
                                      _____ A  C
GAM1161  FCER2    3'  GGGTCTTCAGGGTCTT     12816    C   ATA
                                GG GTT   CAGGGTCTT
                                || |||   |||||||||
                                CC CAG   GTCCCAGAA
                                 _   AA_
GAM1161  AGL      5'  AACCTTGATTTTTCAAT     8483         AAAAC
                                GACCTTGA    TTTCAAT
                                ||||||||    |||||||
                                TTGGAACT    AAAGTTA
                                     AA___
GAM1161  ARHGEF6  3'  CCTTAGGCCAACTTTCAAT   42798      AAA_
                                CCTTG   AACTTTCAAT
                                |||||   ||||||||||
                                GGAAT   TTGAAAGTTA
                                   CCGG
GAM1161  ARHGEF6  3'  GACCTTGAGACTCTCA      42799        AAA
                                GACCTTGA   ACTTTCA
                                ||||||||   |||||||
                                CTGGAACT   TGAGAGT
                                     C__
GAM1161  BCL2     3'  GACCCTGAAGGACAGCCA    8520         AA  TT
                                GACCTTGAA  AC  TCA
                                |||||||||  ||  |||
                                CTGGGACTT  TG  GGT
                                      CC  TC
GAM1161  BCL9     5'  GACCCTTGTCTTTCAAT     20239       GAAAAA
                                GACCTT     CTTTCAAT
                                ||||||     ||||||||
                                CTGGGA     GAAAGTTA
                                   ACA___
GAM1161  CAPZA1   3'  GACCTGAAAAGTCCCAAT    43714       T     AC TT
                                GACCT GAAAA  T  CAAT
                                ||||| |||||  |  ||||
                                CTGGA CTTTT  A  GTTA
                                   _    C_ GG
GAM1161  DAPP1    3'  CCTTGAAAAGTTTCTTTCA   30814         A___
                                CCTTGAAAA    CTTTCA
                                |||||||||    ||||||
                                GGAACTTTT    GAAAGT
                                     CAAA
GAM1161  FGF12    3'  GACCTTGAAATACGGCAAC   34298          A  TTT
                                GACCTTGAAA AC   CAAT
                                |||||||||| ||   ||||
                                CTGGAACTTT TG   GTTG
                                      A  CC_
GAM1161  HCRT     5'  AACCTTGAGGCTGTCAAT    11343         AAAA  T
                                GACCTTGA    CT TCAAT
                                ||||||||    || |||||
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                                TTGGAACT   GA AGTTA
                                    CC__  C
GAM1162 ADORA2A  3' TGGCTCGTTTTTATTTTATCT 8608     TC  ATTTC
                                TGG  TG    TTTATTTTATCT
                                |||  ||    ||||||||||||
                                ACC  GC    AAATAAAATAGA
                                  GA  AA___
GAM1162 PPP2R5E  3' TGGATTGAAGTCCTTATTTT  26480    TC   TT
                                TGG  TGA  TCTTTATTTT
                                |||  |||  ||||||||||
                                ACC  ACT  AGGAATAAAA
                                  TA   TC
GAM1162 PUM2     3' GGTACAGATTTTTATTTTATCT 31662    CT_    CT
                                GGT   GATTT  TTATTTTATCT
                                |||   |||||  ||||||||||
                                CCA   CTAAA  AATAAAATAGA
                                  TGT    __
GAM1163 MAP1A    3' CACAAGGTGGGCTCA       14339         AATAT  T
                                TACAAGGTG    GG CTTA
                                |||||||||    || ||||
                                GTGTTCCAC    CC GAGT
                                      _____  _
GAM1163 RGS5     3' TACAAGCTGAAGATATCTTAAT 18835       G    TATG
             T                   TACAAG TGAA    GTCTTAATT
                                ||||||| ||||    |||||||||
                                ATGTTC ACTT    TAGAATTAA
                                   G    CTA_
GAM1163 GOSR2    3' ACACCACGAAAAGATGTC    38287    _  T  C
                                AC CC TG GAAGATGTC
                                || || || |||||||||
                                TG GG GC TTTCTACAG
                                 T  T  T
GAM1163 INSRR    3' ACCCTTGCGGTAATAGTC    42843         AA  _
                                ACCCTTGCG  GAT GTC
                                |||||||||  ||| |||
                                TGGGAACGC  TTA CAG
                                     CA   T
GAM1163 KCNN3    5' ACCCTCGCTCCAAAGATGTC   13916         ___
                                ACCCTTGC   GAAGATGTC
                                ||||||||   |||||||||
                                TGGGAGCG   TTTCTACAG
                                    AGG
GAM1164 DDX6     3' TCTGCCAGCAATTTACAGTGC  20568     A         AC__
                                TCT CCAGCAATTTG    GC
                                ||| ||||||||||    ||
                                AGA GGTCGTTAAAT    CG
                                  C         GTCA
GAM1164 EXTL3    5' CCAACAATCAGGCCAT      11027         TGAC
                                CCAGCAATT    GCCAT
                                |||||||||    |||||
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                                GGTTGTTAG   CGGTA
                                     TC__
GAM1164 OPA1    3' TCTACCAGCGCATCTGTGC   39270       A_   AC
                                TCTACCAGC ATTTG GC
                                ||||||||| ||||| ||
                                AGATGGTCG TAGAC CG
                                     CG   A_
GAM1164 TRIM14  3' TCTGCAAGCAATTTGCCATA 37708    ACC     GAC
                                TCT  AGCAATTT  GCCATA
                                |||  |||||||  ||||||
                                AGA  TCGTTAAA  CGGTAT
                                  CGT     ___
GAM1164 FOXE1   5' TCAGGGGATCGTCGCGGGCTGG 20949    A T     TTATAA
                                TCA G GGATCGTC    CTGG
                                ||| | ||||||||    ||||
                                AGT C CCTAGCAG    GACC
                                  _ C     CGCCC_
GAM1165 CASP10  3' GAACCTTAAAATGCACCT   37383   T  GC
                                A ACC  AAAATGCACCT
                                | |||  ||||||||||
                                C TGG  TTTTACGTGGA
                                 T  AA
GAM1165 DDX11   3' CCACAGGCCTGGATGCACCT  36173     CC  AAA_
                                CCATA  GC   ATGCACCT
                                |||||  ||   ||||||||
                                GGTGT  CG   TACGTGGA
                                   C_  GACC
GAM1165 PLS3    3' TGACCTGCGAATCATGCACCT 22761   T  _  AAA__
                                A ACC GC    ATGCACCT
                                | ||| ||    ||||||||
                                A TGG CG    TACGTGGA
                                 C  A  CTTAG
GAM1165 XPA     3' ACCTACCACTTCTGCACCTA  7537     A    AAAA
                                ACC TACCGC   TGCACCTA
                                ||| ||||||   ||||||||
                                TGG ATGGTG   ACGTGGAT
                                  _    AAG_
GAM1165 CELSR2  3' TCCTTTTGGTGATGGCG    10855      TG   A   A
                                TCCTTT  TGGT ATGG CG
                                ||||||  |||| |||| ||
                                AGGAAA  ACCA TACC GC
                                   __   C   _
GAM1165 EPS8    3' TTTTATGGTGATAAATTACAT 20816       A   CG
                                TTTTGTGGT ATGGA  ACAT
                                ||||||||| |||||  ||||
                                AAAATACCA TATTT  TGTA
                                     C    AA
GAM1165 HIP12   3' CCTGAGGAGTAATGGGCGACAT 42398    TTTGT      A
                                CCT    GGTAATGG CGACAT
                                |||    |||||||| ||||||
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                                GGA    TCATTACC GCTGTA
                                  CTCC_      C
GAM1165 IL16    3' CCTTTTGCTGGGTGGCG    21095       _  TAA  A
                                CCTTTTG TGG   TGG CG
                                ||||||| |||   ||| ||
                                GGAAAAC ACC   ACC GC
                                    G  C__  _
GAM1165 OLFM1   3' TCCCTTTGTGGTGAGGACG   26781          AAT
                                TCCTTTTGTGGT   GGACG
                                ||||||||||||  |||||
                                AGGGAAACACCA   CCTGC
                                       CT_
GAM1166 BLAME   3' GGATCTGTTCAACA       33490        TGACAA
                                GGATTTGT    TCAACA
                                ||||||||    ||||||
                                CCTAGACA    AGTTGT
                                  _______
GAM1166 ITGA1   3' GGATCGGACAATCAGCA    41848      TGTT      A
                                GGATT   GACAATCA CA
                                |||||   |||||||| ||
                                CCTAG   CTGTTAGT GT
                                   C___      C
GAM1166 MSL3L1  3' GGGGTGACACAATCAACAAG  38593    ATT  TTG
                                GG  TG  ACAATCAACAAG
                                ||  ||  ||||||||||||
                                CC  AC  TGTTAGTTGTTC
                                 CC_  TG_
GAM1166 ATP8A2  3' TTGCTGGGTACTCTGATA   45274     CAAC
                                TTGC   TACTCTGATA
                                ||||   ||||||||||
                                AACG   ATGAGACTAT
                                  ACCC
GAM1166 B3GALT3 5' TTGTGAACTACTCTGAAACAGA 37673     CC         TAC
                                TTG  AACTACTCTGA   GCGGA
                                |||  ||||||||||   |||||
                                AAC  TTGATGAGACT   TGTCT
                                  AC         T__
GAM1166 PPP1R12B 3' TTGCTGATGACTCTGATGAGG  36985     CAACT      ACGC
                                TTGC    ACTCTGAT    GG
                                ||||    ||||||||   ||
                                AACG    TGAGACTA    CC
                                  ACTAC       CT__
GAM1167 CMRF35  3' CCAGAGGGGCTCTGTTGC    27432        T  ACG
                                CCAGAGGG GT   TTTGTTGC
                                |||||||| ||   ||||||||
                                GGTCTCCC CG   AGACAACG
                                   _ ____
GAM1167 FLRT2   3' CAGAGGATGTGTGATGC     29840          ACGTT  T
                                CAGAGGGTGT    TG TGC
                                ||||||||||    || |||
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                                GTCTCCTACA    AC ACG
                                     C____ T
GAM1167 GJB3    5' CAGAGGGTGTGGACGGGTG   35836        __  TT
                                CAGAGGGTGT  ACG  TG
                                ||||||||||  |||  ||
                                GTCTCCCACA  TGC  AC
                                     CC   CC
GAM1167 HSD17B1  5' CCAGAGGGTGACGTAACCCCA 7656         T   TTG  G
                                CCAGAGGGTG ACGT   TT CA
                                |||||||||| ||||   || ||
                                GGTCTCCCAC TGCA   GG GT
                                     _   TT_  G
GAM1167 LPIN1   3' AGGGTGTGCTGCTGCA     42631       AC   T
                                AGGGTGT  GTT GTTGCA
                                |||||||  ||| ||||||
                                TCCCACA  CGA CGACGT
                                   __  _
GAM1167 MBL2    3' CAGAGCACAGGTGTTTGTTG  6959      ____    ACGT
                                CAGAG   GGTGT   TTGTTG
                                |||||   |||||   ||||||
                                GTCTC   CCACA   AACAAC
                                  GTGT   ____
GAM1167 MGAT4B  5' CCGGGGGGTGGCTGCTGC   38265   AGA   TAC   T
                                CC   GGGTG   GTT GTTGC
                                ||   |||||   ||| |||||
                                GG   CCCAC   CGA CGACG
                                 CCC    ___  _
GAM1167 MUCDHL  3' CCAGAGGGTGGATGAGGGCCTG 34930        TAC____
            T                    CCAGAGGGTG      GTTTGT
                                ||||||||||      ||||||
                                GGTCTCCCAC      CGGACA
                                     CTACTCC
GAM1167 MYO10   3' CCAGAGGGTGGTGCGTTCA   29569        TA_
                                CCAGAGGGTG   CGTTTG
                                ||||||||||   ||||||
                                GGTCTCCCAC   GCAAGT
                                     CAC
GAM1167 MYO1D   3' CCAGCGGGATTCTTTGTTGCA 43489     A   TGTACG
                                CCAG GGG     TTTGTTGCA
                                |||| |||     |||||||||
                                GGTC CCC     AAACAACGT
                                  G   TAAG__
GAM1167 PMM2    3' GAGGGTGTATGGCTCAGTG   43552        C_   GT
                                GAGGGTGTA  GTTT  TG
                                |||||||||  ||||  ||
                                CTCCCACAT  CGAG  AC
                                     AC    TC
GAM1167 TCF2    3' CCAGAGGGTGATGGTGTG    27021        TAC  T
                                CCAGAGGGTG   GT TG
                                ||||||||||   || ||
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                                GGTCTCCCAC   CA AC
                                      TAC  C
GAM1167  UBE2V1   3'  AGAGGGCTGTTGTTGC      35341        GTACGT
                                AGAGGGT     TTGTTGC
                                |||||||     |||||||
                                TCTCCCG     AACAACG
                                   AC_____
GAM1167  XT3      3'  GAGGGTGTGCGTTCTCCCA   33665        A    G  G
                                GAGGGTGT CGTTT TT CA
                                |||||||| ||||| || ||
                                CTCCCACA GCAAG AG GT
                                     C    _  G
GAM1168  CARD4    5'  TCATCTTCAGCTGCGTGTG   25894     C  _      TAACC
                                TCA TCT CAGCTGC    TGTG
                                ||| ||| |||||||    ||||
                                AGT AGA GTCGACG    ACAC
                                  _  A     C____
GAM1168  F13A1    3'  TCATCTCAGCTTCCTGTG    44982     C       GCTAA
                                TCA TCTCAGCT    CCTGTG
                                ||| ||||||||    ||||||
                                AGT AGAGTCGA    GGACAC
                                  _      A____
GAM1168  GRM1     3'  TCACTCTCAGTTTTTGTG    9143          CTGCTAACC
                                TCACTCTCAG       TGTG
                                ||||||||||       ||||
                                AGTGAGAGTC       ACAC
                                     AAAA_____
GAM1168  MYO15A   3'  CCACTCTCAAACTTGT      32183         CT   AACC
                                TCACTCTCAG  GCT   TGT
                                ||||||||||  |||   |||
                                GGTGAGAGTT  TGA   ACA
                                     __  ____
GAM1168  NDUFA6   3'  TCAGTTCTTGAACCTGTG    14741      CTG  __
                                TCAG   CT  AACCTGTG
                                ||||   ||  ||||||||
                                AGTC   GA  TTGGACAC
                                  AA_  AC
GAM1168  TAF1C    3'  TCATCTTCAGCTGCCAAGTG  24991     C  _       CCT
                                TCA TCT CAGCTGCTAA   GTG
                                ||| ||| ||||||||||   |||
                                AGT AGA GTCGACGGTT   CAC
                                  _  A        ___
GAM1168  ZNF264   3'  TCACTCTCAGTTGTAAGATCTG 18275          C  C   C__
            T                  TCACTCTCAG TG TAA   CTGT
                               ||||||||||  || |||   ||||
                               AGTGAGAGTC AC ATT   GACA
                                     A  _   CTA
GAM1169  CLCA3    3'  CAAAAATTGCCAAACTGATT  22260        GATC
                               CAAGGAT    GCCAAACTGATT
                               |||||||    ||||||||||||
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                              GTTTTTA   CGGTTTGACTAA
                                 A___
GAM1169 DNM1    3' ACAAGGATAGCACAGTGACTGA 20603        AT  CAA_
           TT                 ACAAGGATG CGC   ACTGATT
                              ||||||||| |||   |||||||
                              TGTTCCTAT GTG   TGACTAA
                                 C_  TCAC
GAM1169 DPYD    3' ACAGAGAGTAGTCAAACTGATT 41289    AG TGATCGC
                              ACA GA     CAAACTGATT
                              ||| ||     ||||||||||
                              TGT CT     GTTTGACTAA
                                CT CATCA__
GAM1169 KCNC3   5' AGGAACCAAACTGAT     22488     TGATC
                              AGGA    GCCAAACTGAT
                              ||||    ||||||||||
                              TCCT    TGGTTTGACTA
                                _____
GAM1169 DISC1   3' GAGTACTGTGCTGCATTCCTG 33037   T  A___
                              GA TAT   CTGCATTCCTG
                              || |||   ||||||||||
                              CT ATG   GACGTAAGGAC
                               C  ACAC
GAM1169 M11S1   3' TTGGCGATTAAACATAATCCTG 25334        T TGCAT
                              TTGGCGATTA AC    TCCTG
                              |||||||||| ||    |||||
                              AACCGCTAAT TG    AGGAC
                                    T TATT_
GAM1169 RP42    3' TTGGTAAAACTGCATTC    33997     CG TTAT
                              TTGG A   ACTGCATTC
                              |||| |   |||||||||
                              AACC T   TGACGTAAG
                                AT T___
GAM1169 UNC5C   3' CTGGCTCCTGCTGCATTC   19009     GA ATA
                              TTGGC TT  CTGCATTC
                              ||||| ||  ||||||||
                              GACCG GA  GACGTAAG
                                 AG C__
GAM1169 ZNF35   3' TTGTGTCTTCTGCTGCATTCCT 18286    GCGA ATA
           G                  TTG   TT  CTGCATTCCTG
                              |||   ||  ||||||||||
                              AAC   AA  GACGTAAGGAC
                                ACAG GAC
GAM1170 AIM1    3' ACAAAATCACCCAAAA     45072        AT TG
                              GCAAAATCA CC CAAAA
                              ||||||||| || |||||
                              TGTTTTAGT GG GTTTT
                                     __ __
GAM1170 CA12    3' GCAGTAGGGATCCTGCAGAAG 10245    AAATCA     A
                              GCA     ATCCTGCA AAG
                              |||     |||||||| |||
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                                CGT     TAGGACGT TTC
                                  CATCCC      C
GAM1170  CRYGA    5'  GCAAAAACAACACAAAAG    31143       T   CCT
                                GCAAAA CAAT   GCAAAAG
                                |||||| ||||  |||||||
                                CGTTTT GTTG   TGTTTTC
                                   T   ____
GAM1170  HMGB2    3'  TTAGCAAAATAATTGCCTG   13409         CAAT_
                                TTAGCAAAAT    CCTG
                                ||||||||||    ||||
                                AATCGTTTTA    GGAC
                                      TTAAC
GAM1170  LANCL1   3'  GCAAAATCAGTTGCAAA     25853         ATCC
                                GCAAAATCA   TGCAAA
                                |||||||||   ||||||
                                CGTTTTAGT   ACGTTT
                                     CA__
GAM1170  NUFIP1   3'  TTAGCTGAATCAATCCTTTTAA 29597      AA        GC_
             AAG                   TTAGC  AATCAATCCT   AAAAG
                                |||||  ||||||||||  |||||
                                AATCG  TTAGTTAGGA   TTTTC
                                   AC        AAA
GAM1170  P23      3'  CTAGCAAAACCCTGCA      27340        ATCA
                                TTAGCAAA   ATCCTGCA
                                ||||||||   ||||||||
                                GATCGTTT   TGGGACGT
                                     _____
GAM1170  PCDHB16  3'  GCAAAATCTCATCGCTGCAAAA 34142        A_  _
             G                   GCAAAATC  ATC CTGCAAAAG
                                |||||||| ||| |||||||||
                                CGTTTTAG  TAG GACGTTTTC
                                     AG   C
GAM1170  PIM2     3'  TTAGCAAAATGAGAAGCAA   41030         CAATCCT
                                TTAGCAAAAT      GCAA
                                ||||||||||      ||||
                                AATCGTTTTA      CGTT
                                      CTCTT__
GAM1170  PIM2     3'  GCAAGAATCTGCAAAA      41024      AATC   C
                                GCAA   AATC TGCAAAA
                                ||||   |||| |||||||
                                CGTT   TTAG ACGTTTT
                                  C___   _
GAM1170  RLN2     3'  TCAGCAAAATCTAGCAA     39591          AATCCT
                                TTAGCAAAATC     GCAA
                                ||||||||||     ||||
                                AGTCGTTTTAG     CGTT
                                      AT_____
GAM1170  CALCB    3'  TGGAGCTGCATGATCAACAGGA 44715      _ ACA   A
             T                   TGGA CT   CAT GTCAACAGGAT
                                |||| ||   ||| ||||||||||
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                                ACCT GA   GTA TAGTTGTCCTA
                                  C  C__   C
GAM1170  DDX11    3'  TGGGTTTCACCTTTGTAACAGG 36181     ACTA   ATA_  C
              AT                   TGG    CAC    GT AACAGGAT
                                |||    |||    || ||||||||
                                ACC    GTG    CA TTGTCCTA
                                  CAAA   GAAA  _
GAM1170  FGF12    3'  TGGACTTGTAACAGG       34302       ACACATA  C
                                TGGACT      GT AACAGG
                                ||||||      || ||||||
                                ACCTGA      CA TTGTCC
                                   A_______ _
GAM1170  IL2RB    3'  TGGACTGAGGACCCTCAACAGG 9396        ACAC  AG
                                TGGACT    AT  TCAACAGG
                                ||||||    ||  ||||||||
                                ACCTGA    TG  AGTTGTCC
                                   CTCC  GG
GAM1171  C7       3'  TGATAGGCCTGAATGGAGCATT 8232      CAA     CGA
              CA                   TGA   GCCTGA   GAGCGTTCA
                                |||   ||||||   |||||||||
                                ACT   CGGACT   CTCGTAAGT
                                  ATC     TAC
GAM1171  DUSP5    3'  TGCAAGCCTGGTGACCACTCA  20663    A       ACGA  G
                                TG CAAGCCTG    GA CGTTCA
                                || ||||||||    || ||||||
                                AC GTTCGGAC    CT GTGAGT
                                 _       CA__  G
GAM1172  ABCB1    3'  TGATGATGTCTCTCACTC    9574      C        AC
                                TGA GATGTCTTT  CATTC
                                ||| |||||||||  |||||
                                ACT CTACAGAGA  GTGAG
                                  A       __
GAM1172  BSND     3'  TGTGTATTTCTTTACCATTC   38433      ACGATG
                                TGTG     TCTTTACCATTC
                                ||||     ||||||||||||
                                ACAC     AGAAATGGTAAG
                                   ATAA__
GAM1173  CCNT2    3'  CACAGTGTATATGACCATC    38492       TTA
                                TACGGT   TATATGACCATC
                                ||||||   ||||||||||||
                                GTGTCA   ATATACTGGTAG
                                   C__
GAM1173  F7       3'  CGTATCTCTGTGTGACCATC   33338    _   ATATA
                                CG GTTT     TGACCATC
                                || ||||     ||||||||
                                GC TAGA     ACTGGTAG
                                 A   GACAC
GAM1173  FAAH     3'  GGTTTATAAATAAGACCGTCC  11061        TAT__    A
                                GGTTTATA    GACC TCC
                                ||||||||    |||| |||
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                                CCAAATAT    CTGG AGG
                                    TTATT   C
GAM1173 HSD11B1  3' GGTTTAAAGAACCATCC    24360      TATAT
                                GGTTTA    GACCATCC
                                ||||||    ||||||||
                                CCAAAT    TTGGTAGG
                                   TTC__
GAM1173 ING1     3' ACACGGTTTATTTTGTCC    24394         ATA  A
                                ATACGGTTTAT   TG CC
                                ||||||||||   || ||
                                TGTGCCAAATA   AC GG
                                     AA_  A
GAM1173 MAP3K8   3' GGTTTACACAGTTTTATCC   23303        TGACC
                                GGTTTATATA    ATCC
                                |||||||||    ||||
                                CCAAATGTGT    TAGG
                                     CAAAA
GAM1174 DGUOK    3' TATCCAGCAAGTTTCCAAGAC  38962        C__  TG ACGT
                                TATCCAGCAA   TC  A   GAC
                                ||||||||||   || |   |||
                                ATAGGTCGTT   AG  T   CTG
                                     CAA  GT ____
GAM1174 GALNT2   3' TATCCAGCGTGGGGGCACGTGG 21009       AACTCTGA    A
           CC                     TATCCAGC      ACGTG CC
                                |||||||       ||||| ||
                                ATAGGTCG      TGCAC GG
                                    CACCCCCG    C
GAM1174 GGA3     3' CATCCAGCAGCTAGAGTG    39785       A  CT  AC
                                TATCCAGCA CT  GA  GTG
                                ||||||||| ||  ||  |||
                                GTAGGTCGT GA  CT  CAC
                                     C  T_  __
GAM1174 GNAL     3' CCAGCAGCGACTCTGAATGTGA 13171      ___      C
           C                     CCAGCA   ACTCTGAA GTGAC
                                ||||||   |||||||| |||||
                                GGTCGT   TGAGACTT CACTG
                                   CGC      A
GAM1174 KCNC3    3' ATCCAGCAACAGTGTGTGTG   22496       TC  AAC
                                ATCCAGCAAC  TG   GTG
                                ||||||||||  ||   |||
                                TAGGTCGTTG  AC   CAC
                                     TC  ACA
GAM1174 NIPSNAP1 3' TCCAGCAAGTGGGTGC      18874       CTC  AAC   A
                                TCCAGCAA   TG   GTG C
                                ||||||||   ||   ||| |
                                AGGTCGTT   AC   CAC G
                                    C__  C__   C
GAM1174 VCP      3' CATCCAGCAACTGTG       44008          CTGAAC
                                TATCCAGCAACT     GTG
                                ||||||||||||     |||
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                                GTAGGTCGTTGA     CAC
                                             _______
GAM1175 ATP7A    3' TTTGCCAACAGATAAACGC   6273      TA      GTCTT
                                TTTG CCAACAGG    ACGC
                                |||| ||||||||    ||||
                                AAAC GGTTGTCT    TGCG
                                  __      ATT__
GAM1175 E2F3     3' TTTGTACCAAGTCC       12636         ACAG
                                TTTGTACCA   GGTCT
                                |||||||||   |||||
                                AAACATGGT   TCAGG
                                             ____
GAM1175 IHPK3    5' CTTTGTACTGTGGGGTGAACCG 38370        CAACA   CTTA
              C                  CTTTGTAC    GGGT   CGC
                                |||||||    ||||   |||
                                GAAACATG    CCCA   GCG
                                    ACAC_   CTTG
GAM1175 NLGN1    3' CTTTATACTGACAGCACTTA  31385        CA   G T
                                CTTTGTAC  ACAG G CTTA
                                |||||||  |||| | ||||
                                GAAATATG  TGTC T GAAT
                                    AC   G _
GAM1175 PCDH9    5' CTTTGTATTGACAGGATC    44399       CCA
                                CTTTGTA   ACAGGGTC
                                |||||||   ||||||||
                                GAAACAT   TGTCCTAG
                                    AAC
GAM1176 COX15    3' TCGCCAGTGTTACTGTCTCCAT 38519    A     CCA  GA
                                TC CTAGTG   AC  GTCTCCAT
                                || ||||||   ||  |||||||||
                                AG GGTCAC   TG  CAGAGGTA
                                 C     AA_  A_
GAM1176 MTMR6    3' TCACTAGTGTACAGT       45279         CCA  G
                                TCACTAGTG   AC AGT
                                |||||||||   || |||
                                AGTGATCAC   TG TCA
                                    A__  _
GAM1176 TP63     3' CTAGTGCCAAATCCA       18997         CGAGTC
                                CTAGTGCCAA     TCCA
                                ||||||||||     ||||
                                GATCACGGTT     AGGT
                                     T_____
GAM1176 WRN      3' CTAGTGCAATTGGTCTCCAT   8138        CAACGA
                                CTAGTGC     GTCTCCAT
                                |||||||     ||||||||
                                GATCACG     CAGAGGTA
                                   TTAAC_
GAM1176 ZNF180   3' CCACTAGTGTTAGCATTCCAT  29935        CCAACG   C_
                                TCACTAGTG     AGT  TCCAT
                                |||||||||     |||  |||||
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                                GGTGATCAC     TCG  AGGTA
                                     AA____   TA
GAM1177 BCL7B    3' GGGAGCTTTCTAGAAACTG   11807     A       _
                                GGGA CTTTCTAGAG CTG
                                |||| |||||||||| |||
                                CCCT GAAAGATCTT GAC
                                  C        T
GAM1177 BLAME    3' TGGGAACTTTATTAGAGC    33501        C_
                                TGGGAACTTT  TAGAGC
                                ||||||||||  ||||||
                                ACCCTTGAAA  ATCTCG
                                     TA
GAM1177 CRY2     3' TGGAAACTTTTTAGATCTG   43589        C   G
                                TGGGAACTTT TAGA CTG
                                |||||||||| |||| |||
                                ACCTTTGAAA ATCT GAC
                                     A   A
GAM1177 DBH      3' TGGGCGTGCAGGGCTGTTCCA 8974     AACTTTC  A
                                TGGG      TAG GCTGTTCCA
                                ||||      ||| |||||||||
                                ACCC      GTC CGACAAGGT
                                  GCAC___  C
GAM1177 GABRE    5' TGGGGACTTTCTATGCTG    35079     A      GA
                                TGGG ACTTTCTA  GCTG
                                |||| ||||||||  ||||
                                ACCC TGAAAGAT  CGAC
                                  C       A_
GAM1177 GFPT2    3' TGGGATATTTCAAGCTGTT   23042     AC   TA
                                TGGGA  TTTC  GAGCTGTT
                                |||||  ||||  ||||||||
                                ACCCT  AAAG  TTCGACAA
                                  AT   __
GAM1177 ODF2     3' TGGGACTTTTCTAGAGCTA   14936     AC
                                TGGGA  TTTCTAGAGCTG
                                |||||  ||||||||||||
                                ACCCT  AAAGATCTCGAT
                                  GA
GAM1177 PCDHA1   3' GGGAACTTTCTGCAGATTTC  36398        AG  CTG
                                GGGAACTTTCT  AG   TTC
                                ||||||||||  ||   |||
                                CCCTTGAAAGA  TC   AAG
                                     CG  TA_
GAM1177 PCDHA10  3' GGGAACTTTCTGCAGATTTC  36565        AG  CTG
                                GGGAACTTTCT  AG   TTC
                                ||||||||||  ||   |||
                                CCCTTGAAAGA  TC   AAG
                                     CG  TA_
GAM1177 PCDHA11  3' GGGAACTTTCTGCAGATTTC  36577        AG  CTG
                                GGGAACTTTCT  AG   TTC
                                ||||||||||  ||   |||
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                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA12  3' GGGAACTTTCTGCAGATTTC  36597       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA13  3' GGGAACTTTCTGCAGATTTC  36605       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA2   3' GGGAACTTTCTGCAGATTTC  33139       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA3   3' GGGAACTTTCTGCAGATTTC  36476       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA4   3' GGGAACTTTCTGCAGATTTC  36489       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA5   3' GGGAACTTTCTGCAGATTTC  36498       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA6   3' GGGAACTTTCTGCAGATTTC  36512       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA7   3' GGGAACTTTCTGCAGATTTC  36520       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA8   3' GGGAACTTTCTGCAGATTTC  36529       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
                          CCCTTGAAAGA TC  AAG
                               CG TA_
GAM1177 PCDHA9   3' GGGAACTTTCTGCAGATTTC  36548       AG CTG
                          GGGAACTTTCT AG  TTC
                          ||||||||||| ||  |||
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                                CCCTTGAAAGA  TC   AAG
                                      CG  TA_
GAM1177  PCDHAC1   3'  GGGAACTTTCTGCAGATTTC   36620          AG  CTG
                                GGGAACTTTCT  AG   TTC
                                ||||||||||  ||   |||
                                CCCTTGAAAGA  TC   AAG
                                      CG  TA_
GAM1177  PCDHAC2   3'  GGGAACTTTCTGCAGATTTC   36631          AG  CTG
                                GGGAACTTTCT  AG   TTC
                                ||||||||||  ||   |||
                                CCCTTGAAAGA  TC   AAG
                                      CG  TA_
GAM1177  PDGFRB    3'  TGGGGGCTTTCCAGGACACC   42344      AA       AG TGTT
                                TGGG  CTTTCTAG  C    CC
                                ||||  ||||||||  |    ||
                                ACCC  GAAAGGTC  G    GG
                                   CC       CT T___
GAM1177  SHANK2    3'  TGTGTTCATTCTAGAGCTGTTC 29475    GGAACT
              CA                   TG     TTCTAGAGCTGTTCCA
                                ||     ||||||||||||||||
                                AC     AAGATCTCGACAAGGT
                                 ACAAGT
GAM1177  STK9      5'  TGGGAACTTTCACATATTTGTT 17196          _ GAGC
              C                    TGGGAACTTTC TA    TGTTC
                                ||||||||||| ||    |||||
                                ACCCTTGAAAG GT    ACAAG
                                      T  ATAA
GAM1177  TPO       3'  TGGGAACATGAAGCTGTTC    8100        TTTCTA
                                TGGGAAC     GAGCTGTTC
                                |||||||     |||||||||
                                ACCCTTG     TTCGACAAG
                                    TAC___
GAM1178  CYP24     3'  TTAAAGTCACACTGAATGTT   8952       _      T_
                                TTAAA TCACACTG  TGTT
                                ||||| ||||||||  ||||
                                AATTT AGTGTGAC  ACAA
                                   C       TT
GAM1178  DMRT1     3'  ACTTTAAATTGCACTGTTA    34979      _   CA
                                ACTT AAAT  CACTGTTG
                                |||| ||||  ||||||||
                                TGAA TTTA  GTGACAAT
                                   A   AC
GAM1178  GALNT1    3'  CTTAAATCACATTGCTGTT    33839          C
                                CTTAAATCACA TGTTGTT
                                |||||||||||| |||||||
                                GAATTTAGTGT ACGACAA
                                      A
GAM1178  GAP43     3'  TTAAGCCACACTGTTTGACT   13050      AT       GT
                                TTAA  CACACTGTT  TGACT
                                ||||  |||||||||  |||||
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                                AATT  GTGTGACAA  ACTGA
                                  CG       __
GAM1179  CNN2     3'  TGGAGGTGCAGTGAGCCAA   20408    AT      AGT
                                TG  GGTGCAGT   AGTTAA
                                ||  ||||||||   ||||||
                                AC  CCACGTCA   TCGGTT
                                 CT       C__
GAM1179  DSC3     3'  TGGTAGTGCAGTAGGGGT    35951    A        TA
                                TG TGGTGCAGTAG  GT
                                || ||||||||||  ||
                                AC ATCACGTCATC  CA
                                 C         CC
GAM1179  DYRK1A   3'  TGATGGTGGTGGTGGTGGT   39005        CA_  A  A
                                TGATGGTG   GT GT GT
                                ||||||||   || || ||
                                ACTACCAC   CA CA CA
                                     CAC  C  C
GAM1179  GGPS1    3'  TGATGGTAGTAGGATAGAGTTG 22111        CA___    T    AA
              GTG                  TGATGGTG    GTAG AGTT  TG
                                ||||||||    |||| ||||  ||
                                ACTACCAT    TATC TCAA  AC
                                     CATCC    _   CC
GAM1179  HEM1     5'  TGACTGGTAGTAGTTGGTGA   23742     GGTGCA       AA
                                TGAT     GTAGTAGTT  TGA
                                ||||     |||||||||  |||
                                ACTG     CATCATCAA  ACT
                                  AC____        CC
GAM1179  VEGF     3'  TGATGGTGTGGTGGCGGCAGC  17973        CA___ TA
                                TGATGGTG    G  GTAGT
                                ||||||||    |  |||||
                                ACTACCAC    C  CGTCG
                                     ACCAC GC
GAM1180  ACCN2    3'  GGAGAGAGTCCAACTCTT    33450    TAA  A     C
                                GG   AGA TCCAAC CTT
                                ||   ||| |||||| |||
                                CC   TCT AGGTTG GAA
                                 TC_  C     A
GAM1180  NBEA     3'  ATGGAGCCCAAATTCAACCCTT 45431      TAAA_    C
                                ATGG    GAAT CAACCCTT
                                ||||    |||| ||||||||
                                TACC    TTTA GTTGGGAA
                                  TCGGG    A
GAM1180  PIR51    3'  GACATGGTAATGGATTCC    27012         A_  A
                                GACATGGTAA  GA TCC
                                ||||||||||  || |||
                                CTGTACCATT  CT AGG
                                      AC  A
GAM1180  SAR1     3'  GACATGGTTGGAGAGCTTTCC  33551        AA_  A___
                                GACATGGT   AGA   TCC
                                ||||||||   |||   |||
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                                CTGTACCA  TCT   AGG
                                    ACC  CGAA
GAM1180 SERPINA5 3' CACAGCAAGAATCTGATCCTT 8410        A   CAAC
                                CATGGTAA GAATC   CCTT
                                |||||||| |||||   ||||
                                GTGTCGTT CTTAG   GGAA
                                    _    ACTA
GAM1180 SET7    3' TAGTAATTGTCAACCCTT   36158      AGAATC
                                TGGTAA    CAACCCTT
                                ||||||    ||||||||
                                ATCATT    GTTGGGAA
                                   AACA__
GAM1181 ACTN2   3' TGGAAAAACAGGGGGGAATTA 9954     C       TT_
                                TGG AAAACAGGGG  ATTA
                                ||| ||||||||||  ||||
                                ACC TTTTGTCCCC  TAAT
                                  T       CCT
GAM1181 AGER    3' TGGCAAGGTGGGGTTAT    10070      AACA
                                TGGCAA   GGGGTTAT
                                ||||||   ||||||||
                                ACCGTT   CCCCAATA
                                   CCA_
GAM1181 CCNT2   3' TGGCAAATTAGGTAATT    38498      ACAG   T
                                TGGCAAA   GGGT ATT
                                |||||||   |||| |||
                                ACCGTTT   TCCA TAA
                                    AA__   T
GAM1181 ISL1    3' TGGCAAAATAGAGGTAACC   13598       C    T
                                TGGCAAAA AGGGGT ATT
                                |||||||| |||||| |||
                                ACCGTTTT TCTCCA TGG
                                    A    T
GAM1181 SLC24A1 3' TAGCGAGGCAATTAAT     21822     AAAACA   T
                                TGGC    GGGGT ATTAAT
                                ||||    ||||| ||||||
                                ATCG    CTCCG TAATTA
                                  _______   T
GAM1182 GSTM1   3' AGTGCAGGGAAGGGTAATG  40444       TTCA  AA_
                                AGTGCAGG   GAA  TAATG
                                ||||||||   |||  |||||
                                TCACGTCC   CTT  ATTAC
                                    _____  CCC
GAM1182 GSTM2   3' AGTGCAGGGAAGGGTAATG  9193        TTCA  AA_
                                AGTGCAGG   GAA  TAATG
                                ||||||||   |||  |||||
                                TCACGTCC   CTT  ATTAC
                                    _____  CCC
GAM1182 SLC14A1 3' TGAGTGTGCAAAAAATAAT  31966     CAGGTT
                                TGAGTG    CAGAAAATAAT
                                ||||||    ||||||||||
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                                ACTCAC     GTTTTTTATTA
                                   AC____
GAM1182 YWHAZ    3' TGAGTGTAGCAAAAATAATG  18204       CA  TCA
                                TGAGTG  GGT   GAAAATAATG
                                ||||||  |||   ||||||||||
                                ACTCAC  TCG   TTTTTATTAC
                                   A_  ___
GAM1183 CYP2J2   3' AGACACCAGTGGTTTCAGAACA 8929         ACAAC_  TCC
             C                   AGGCACCA     TCA  GACAT
                                ||||||||     |||  |||||
                                TCTGTGGT     AGT  TTGTG
                                     CACCAA  C__
GAM1183 PRex1    3' AGGCACCAGCTGCTCCCA    34070        ACAA  AT
                                AGGCACCA    CTC  CCG
                                ||||||||    |||  |||
                                TCCGTGGT    GAG  GGT
                                     CGAC   __
GAM1184 HUNK     5' GGTGGGGCGCGGTCCGGCGGC 31074    ACGAGA      CACA
                                GG     CGCGGTTC    CGGC
                                ||     ||||||||    ||||
                                CC     GCGCCAGG    GCCG
                                 ACCCC_      CC__
GAM1184 WNT1     5' GGACGGGACGCGGCGGTGG   24084      A       TCCACAC
                                GGACG GACGCGGT      GG
                                ||||| ||||||||      ||
                                CCTGC CTGCGCCG      CC
                                   C       CCA____
GAM1185 CTGF     3' TGTTTTGACGGACTGTCA    12510        TACTTCT  C
                                TGTTTTGAC      GC GTCA
                                |||||||||      || ||||
                                ACAAAACTG      TG CAGT
                                     CC_____  A
GAM1185 HAP1     3' TGTTTTGACTGCTGCTGCC   19507         A  T
                                TGTTTTGACT CT CTGCC
                                |||||||||| || |||||
                                ACAAAACTGA GA GACGG
                                      C  C
GAM1185 SELE     3' TGTTTTGACTGTTGGCTTTGTC 7806          ACTT_  GCC
                                TGTTTTGACT    CT   GTC
                                ||||||||||    ||   |||
                                ACAAAACTGA    GA   CAG
                                     CAACC  AA_
GAM1185 SON      3' TGTTTTGACACTTGGC      38463         T   CT
                                TGTTTTGAC ACTT  GC
                                ||||||||| ||||  ||
                                ACAAAACTG TGAA  CG
                                      _   C_
GAM1186 ARHGEF12 3' AGTGGTGCCCTCTGTGAC    31635     CA  GCGAGA   C
                                AGTG  TGC     TCTG GAC
                                ||||  |||     |||| |||
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                                TCAC  ACG     AGAC CTG
                                  C_  GG____    A
GAM1186 CD8A    3' AGTGCATGTTTGGGACAGCA  12087        CGCGA  CT
                                AGTGCATG    GAT  GCG
                                ||||||||    |||  |||
                                TCACGTAC    CTG  CGT
                                    AAACC   T_
GAM1186 DGCR2   3' AGTGCATGTGGGATCCACGGCA 23085        CGCGA   TG  A
                                AGTGCATG    GATC  CG CA
                                ||||||||    ||||  || ||
                                TCACGTAC    CTAG  GC GT
                                    ACC__   GT  C
GAM1186 DNMT1   3' AGTGCATGTTGGGGATTCCTG  10713        CGC__  GA
                                AGTGCATG    GA  TCTG
                                ||||||||    ||  ||||
                                TCACGTAC    CT  GGAC
                                    AACCC  AA
GAM1187 ABCD4   3' GCCACCAAGTTGGACAGGCC   33746        CCC_   T
                                GCCACCAA    GACG GCC
                                ||||||||    |||| |||
                                CGGTGGTT    CTGT CGG
                                    CAAC    C
GAM1187 ADCY8   5' CGCCGCCGCGTGCCA       10003      ACCAAC   A
                                CGCC     CCG CGTGCCA
                                ||||     ||| |||||||
                                GCGG     GGC GCACGGT
                                  C_____  _
GAM1187 AKAP1   3' TCGCCACCAGGCCCCGT     40227         A_  GA
                                TCGCCACCA  CCC  CGT
                                |||||||||  |||  |||
                                AGCGGTGGT  GGG  GCA
                                    CC   __
GAM1187 ANKRA2  5' TCGCCACCGGCCAGCTGTGCC 35756        AA  CGAC
                                TCGCCACC  CC   GTGCC
                                ||||||||  ||   |||||
                                AGCGGTGG  GG   CACGG
                                    CC  TCGA
GAM1187 BTC     5' GCCACCAACCTGGAGGTA    45539         C_  C
                                GCCACCAACC  GA GTG
                                ||||||||||  || |||
                                CGGTGGTTGG  CT CAT
                                     AC  C
GAM1187 CACNA2D2 3' TCCCACCAACCCCTCGCC   25724    G        GACG
                                TC CCACCAACCC    TGCC
                                || ||||||||||    ||||
                                AG GGTGGTTGGG    GCGG
                                  _        GA__
GAM1187 COX10   3' GCCACCAAGTGCCA       10551         CCCGAC
                                GCCACCAA     GTGCCA
                                ||||||||     ||||||
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                              CGGTGGTT     CACGGT
                                       ______
GAM1187  CYP2B6   3'  TCACCACCAGCCTGGCCAACAT 8922          A _____
             G                  TCGCCACCA CC    CGACGTG
                                |||||||||  ||    |||||||
                                AGTGGTGGT GG    GTTGTAC
                                     C  ACCG
GAM1187  FBN1     5'  CCGCCACCGGCTCCCGCCGCC  42050        AA__    ACGT
                                TCGCCACC    CCCG    GCC
                                ||||||||    ||||    |||
                                GGCGGTGG    GGGC    CGG
                                     CCGA    GG__
GAM1187  GAS1     3'  TCGCCACCCACCCTCACC     13074         A    GACGT
                                TCGCCACC ACCC     GCC
                                ||||||||  ||||     |||
                                AGCGGTGG TGGG     TGG
                                     G    AG___
GAM1187  GNB1     5'  TCGCGGCCTGACGCGCC      13211      CACCAA  C
                                TCGC      CC GACGTGCC
                                ||||      ||  ||||||||
                                AGCG      GG CTGCGCGG
                                  CC_____  A
GAM1187  IL22RA2  3'  TCGCCACCCACCCCACTAC    38134         A    G  G
                                TCGCCACC ACCC AC TGC
                                ||||||||  |||| ||  |||
                                AGCGGTGG TGGG TG ATG
                                     G    G  _
GAM1187  KRAS2    5'  TCGCCGCCGCCACTGCCC     37887       A  AAC  G  G    A
                                TCGCC CC   CC AC TGCC C
                                |||||  ||   ||  ||  ||||  |
                                AGCGG GG   GG TG ACGG G
                                   C  C__  _  _    C
GAM1187  MN1      3'  TCGCTGATCAATTCATGCCACC 14594      CAC_   CCCGA
                                TCGC    CAA    CGTGCCACC
                                ||||    |||    |||||||||
                                AGCG    GTT    GTACGGTGG
                                  ACTA   AA___
GAM1187  MTM1     3'  GCCACAACCCGAAAACCA     7005        C      CGT
                                GCCAC AACCCGA   GCCA
                                |||||  |||||||   ||||
                                CGGTG TTGGGCT   TGGT
                                  _      TT_
GAM1187  PFKFB3   5'  TCGCCACCAGGCCCTGCTGC   44439         A_   GACG
                                TCGCCACCA  CCC    TGC
                                |||||||||  |||    |||
                                AGCGGTGGT  GGG    ACG
                                     CC   ACG_
GAM1187  RBM3     5'  TCTCACCAACCCCCAT      43258     GC       GA
                                TC  CACCAACCC  CGT
                                ||  |||||||||  |||
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                                AG  GTGGTTGGG  GTA
                                 A_        G_
GAM1187  SCA7     5'  TCACCACCTAAACGTGCCA   7310         AACCC
                                TCGCCACC    GACGTGCCA
                                ||||||||    |||||||||
                                AGTGGTGG    TTGCACGGT
                                    AT___
GAM1187  SIX6     3'  TCACCACCAGCCTGCATG    28903        AC  GA
                                TCGCCACCA  CC  CGTG
                                |||||||||  ||  ||||
                                AGTGGTGGT  GG  GTAC
                                     C_  AC
GAM1187  TEM5     3'  GCTTTGTCCCGGTGTGCCACC  37235    CACCAA   AC
                                GC     CCCG  GTGCCACC
                                ||     ||||  ||||||||
                                CG     GGGC  CACGGTGG
                                 AAACA_   CA
GAM1188  C11orf13 3'  GCTGTGTACACACAGTGAA   18485     C   TGA_
                                GCTG GTGC    AGTGAA
                                |||| ||||    ||||||
                                CGAC CATG    TCACTT
                                  A   TGTG
GAM1188  EDAR     3'  CTGCCTAAGACTGAAGTGGAAG 35306     G ___       A
                                CTGC T   GCTGAAGTG AAG
                                |||| |   |||||||| |||
                                GACG A   TGACTTCAC TTC
                                  G TTC        C
GAM1188  PTHLH    3'  CTCCCTTGAAGTGAAA      15854     G  GCGTGC
                                TTCC CT     TGAAGTGAAA
                                |||| ||     ||||||||||
                                GAGG GA     ACTTCACTTT
                                  _ _______
GAM1188  SLC19A2  5'  CTCCGCCAACTGGAGTGA    42887        CGT   A
                                TTCCGCTG   GCTG AGTGA
                                ||||||||   |||| |||||
                                GAGGCGGT   TGAC TCACT
                                    ___    C
GAM1188  SUPT5H   5'  TTCCGCTGCTGCTGGGAAA   17219         G    AAGT
                                TTCCGCTGC TGCTG   GAAA
                                ||||||||| |||||   ||||
                                AAGGCGACG ACGAC   CTTT
                                     _    C___
GAM1189  TNP1     3'  TGTGAAGCGCACCAGG      40477     C       TGCGAC
                                TGTG AAGCGCACC     GG
                                |||| |||||||||     ||
                                ACAC TTCGCGTGG     CC
                                  _       T_____
GAM1190  ASPA     3'  TATGATATCTTTAAAGATATAT 6255          ACAAA
             TA                   TATGATATCTT    ATATATTA
                                ||||||||||    ||||||||
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                                ATACTATAGAA    TATATAAT
                                     ATTTC
GAM1190  NCOA6IP  3'  TATATTACAAAATATATT    36053     C
                                TAT TTACAAAATATATT
                                ||| ||||||||||||||
                                ATA AATGTTTTATATAA
                                  T
GAM1191  KAL1     3'  ATTAGCAGCTTATTTCAT    6869        TT    AA
                                ATTAGCAG  CTTAT  CAT
                                ||||||||  |||||  |||
                                TAATCGTC  GAATA  GTA
                                    __    AA
GAM1191  NRXN1    3'  TTAGCAACACTTATAACAT   39854       TT
                                TTAGCAG  CTTATAACAT
                                |||||||  ||||||||||
                                AATCGTT  GAATATTGTA
                                    GT
GAM1192  RNF14    3'  GTATTAAAACATATATTTATAT 20184          _  C
                                GTATTAAAACAT TAT TATAT
                                |||||||||||| ||| |||||
                                CATAATTTTGTA ATA ATATA
                                      T  A
GAM1193  KIF5C    3'  TTATATATTTTAGTTCCCAGAC 21172          A   T_
              ATA                 TTATATGTTTTA TTTTT  GCATA
                                ||||||||||| |||||  |||||
                                AATATATAAAAT AAGGG  TGTAT
                                      C    TC
GAM1193  RNTRE    3'  TATATATATATTTTTTGCATA  31261       TTTA
                                TATATGT   ATTTTTTGCATA
                                |||||||   ||||||||||||
                                ATATATA   TAAAAAACGTAT
                                    TA__
GAM1194  CNGB3    3'  TACATACAATTAGAAGATATA  33309      T  CTA
                                TACAT CG   TAGAAGATATA
                                ||||| ||   ||||||||||
                                ATGTA GT   ATCTTCTATAT
                                   T  TA_
GAM1194  SHMT2    3'  CATTCATTCAGAAGATATA   24003      CTA
                                CATTCG   TAGAAGATATA
                                ||||||   ||||||||||
                                GTAAGT   GTCTTCTATAT
                                   AA_
GAM1195  ALDH2    3'  TACAAAGCAGGGTGTAGCA   40688      TA  AAA
                                TACAA  CA   TGTAGCA
                                |||||  ||   |||||||
                                ATGTT  GT   ACATCGT
                                   TC  CCC
GAM1195  CHAC     3'  CAATACAAAGCTATAAAATATA 37813        A_   C
              T                  CAATACAAA  TGTAG ATATAT
                                |||||||||  ||||| ||||||
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                                GTTATGTTT  ATATT TATATA
                                     CG    T
GAM1195 PIGA     3'  TACAAACAAAACACAAATATAT 33834      T     TG   C
                                TACAA ACAAAA  TAG ATATAT
                                ||||| ||||||  ||| ||||||
                                ATGTT TGTTTT  GTT TATATA
                                   _     GT   _
GAM1195 SLC10A2  3'  TACATATATAAAACATATACAT 7818       _  C       _
             ATAT                   TACA ATA AAAATGTA GCATATAT
                                ||||| ||| |||||||| ||||||||
                                ATGT TAT TTTTGTAT TGTATATA
                                  A  A       A
GAM1196 ADAMTS12 5'  GGAGTGATTCAGCTGACAGTGT 36288   A    C       __  C
             CCG                    A AGTGA TCGGCTGA  GTG TCCG
                                | ||||| ||||||||  ||| ||||
                                C TCACT AGTCGACT  CAC AGGC
                                 C    A       GT  _
GAM1196 GRB2     3'  GTGACCCGGCCAGGTGTTC   13287          GA   C
                                GTGACTCGGCT  GTG TC
                                ||||||||||  ||| ||
                                CACTGGGCCGG  CAC AG
                                      TC   A
GAM1196 HOXA3    3'  AAAGTGCTCGGCATCCTC    36188       A     TGA  G
                                AAAGTG CTCGGC   GT CTC
                                |||||| ||||||   || |||
                                TTTCAC GAGCCG   TA GAG
                                   _     ____  G
GAM1196 IGF1R    3'  GACTGGTTCTCAAGTGCTC    9327       C  __  _
                                GACT GG  CT GAGTGCTC
                                |||| ||  || ||||||||
                                CTGA CC  GA TTCACGAG
                                  _ AA  G
GAM1196 MAP3K4   5'  GGAGTGACTCGACTCCGCCTCC 25431    A          GA  G
             G                   A AGTGACTCGGCT  GT CTCCG
                                | ||||||||||||  || |||||
                                C TCACTGAGCTGA  CG GAGGC
                                 C          GG  _
GAM1196 OCLN     5'  GTGCGTTCGGTGCTCC      14907     ACT  GC  A
                                GTG   CG  TG GTGCTCC
                                |||   ||  || |||||||
                                CAC   GC  GC CACGAGG
                                  ____  AA  _
GAM1197 CCND2    3'  TGGAAAGTTACAGACTGTAAA  12053       TCAATA  T
                                TGGAAA      GC GACTGTAAA
                                ||||||      || ||||||||||
                                ACCTTT      TG CTGACATTT
                                   CAA___  T
GAM1197 DIBD1    3'  TGGAATCAATAGTTAAC     36027       A      C
                                TGGAA TCAATAG TGAC
                                ||||| ||||||| ||||
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                                ACCTT AGTTATC ATTG
                                  _      A
GAM1197 HCCS     5'  TGGAAACAGTGTTGACTGTAAA 23736       CAATAGC
                                TGGAAAT      TGACTGTAAA
                                |||||||      ||||||||||
                                ACCTTTG      ACTGACATTT
                                   TCACA__
GAM1197 SLC4A7   3'  TGGAAATCAAGGCATCTA    18827         TA  TGA
                                TGGAAATCAA  GC   CTG
                                ||||||||||  ||   |||
                                ACCTTTAGTT  CG   GAT
                                      C_  TA_
GAM1197 UBE3A    3'  TGGAAATCAGTAATGTAA    39285         A   CTGAC
                                TGGAAATCA TAG     TGTAA
                                |||||||||| |||     |||||
                                ACCTTTAGT ATT     ACATT
                                      C  _____
GAM1198 ATP6V0E  3'  GCACTGTAGAGCATGTCTTC   19486       T GA  C
                                GTATTGT G  CA GTCTTC
                                ||||||| |  || ||||||
                                CGTGACA C  GT CAGAAG
                                   T TC  A
GAM1198 CRP      3'  GTATTGCTGGGCTTC       43444          ACAC T
                                GTATTGTTGG    G CTTC
                                ||||||||||    | ||||
                                CATAACGACC    C GAAG
                                      _____ _
GAM1198 EGFL5    3'  GAAGTATTGTTGCTTTAGTTTT 44527    C        GACAC  C
             C                   A AGTATTGTTG     GT TTC
                                | ||||||||||     || |||
                                C TCATAACAAC     CA AAG
                                 T        GAAAT  A
GAM1198 SUV39H2  3'  ACAGTATTGTTAGGTACAGC   36008          _ _   C
                                ACAGTATTGTT GG ACA GT
                                |||||||||||| || ||| ||
                                TGTCATAACAA CC TGT CG
                                      T  A  _
GAM1198 XRCC2    3'  AGGATTGTTGGCCACAGATGTC 24088    T       A  _____
             TTC                   AG ATTGTTGG CAC    GTCTTC
                                || ||||||||| |||    ||||||
                                TC TAACAACC GTG    CAGAAG
                                 C       G   TCTA
GAM1199 B4GALT7  3'  TTCGAAAAATCAGAAGATC    28553         A     ATT
                                TTTGAAAAA TCAGAA   GGTC
                                ||||||||| ||||||   ||||
                                AAGCTTTTT AGTCTT   CTAG
                                      _    ____
GAM1199 B4GALT7  3'  AAAAAATCAGAAGATATCA    28541           ATTG
                                AAAAAATCAGAA    GTCA
                                ||||||||||||    ||||
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                                TTTTTTAGTCTT   TAGT
                                      CTA_
GAM1199  MTMR8    3'  TTTGAAAAACATTTCTATGGTC 31762        ATCAGAAAT
              A                  TTTGAAAAA       TGGTCA
                                 |||||||||       ||||||
                                 AAACTTTTT       ACCAGT
                                    GTAAAGAT_
GAM1199  PCMT1    3'  TTTGAAGAATCAGAAACC    23944       AA
                                 TTTGAA  AATCAGAAATT
                                 ||||||  ||||||||||
                                 AAACTT  TTAGTCTTTGG
                                    C_
GAM1199  RFX5     3'  TCTGAAAAGGTCAGAGGC    7797        AA    AATT
                                 TTTGAAAA  TCAGA   GGT
                                 ||||||||  |||||   |||
                                 AGACTTTT  AGTCT   CCG
                                     CC    _____
GAM1199  SHMT1    3'  TTTGAAATATAAAAATTGGT   20027       AAATC
                                 TTTGAAA    AGAAATTGGT
                                 |||||||    ||||||||||
                                 AAACTTT    TTTTTAACCA
                                     ATA__
GAM1199  STAU2    3'  TTTGAAAGAATCAGAAGGGT   30809       A       ATT
                                 TTTGAAA AATCAGAA   GGT
                                 ||||||| ||||||||   |||
                                 AAACTTT TTAGTCTT   CCA
                                     C       C__
GAM1200  C18orf1  3'  TGAAGGAAGACATTGCTTTCT  41233     A       _   CC
                                 TGAA GAGGACAT GCT  TCT
                                 |||| |||||||| |||  |||
                                 ACTT CTTCTGTA CGA  AGA
                                   C       A  A_
GAM1200  EXTL3    3'  GAGGAGGGCGTGCCCCTCAG   11034      CAT  T__
                                 GAGGA   GC   CCTCTCAG
                                 |||||   ||   ||||||||
                                 CTCCT   CG   GGGGAGTC
                                    CC_  CAC
GAM1200  FEZ1     3'  TGAAAGAGTACTTTTCTCA   35424       GACA   CC
                                 TGAAAGAG    TGCT  TCTCA
                                 ||||||||    ||||  |||||
                                 ACTTTCTC    ATGA  AGAGT
                                      _____    AA
GAM1200  GJA5     3'  GAGAGAGGACAACAGCTTCT  23582    A       T__   C
                                 GA AGAGGACA   GCT CT
                                 || ||||||||   ||| ||
                                 CT TCTCCTGT   CGA GA
                                   C       TGT   A
GAM1200  KCNMB4   3'  GAGGGATGAGCCTCTCA     30944     AC   CT
                                 GAGG  ATG  CCTCTCA
                                 ||||  |||  |||||||
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                                CTCC  TAC  GGAGAGT
                                  C_  TC
GAM1200  MAP3K7IP2 3'  AAGGCATTGTTCCTCTCAG   31517     A  GC_
                                GAGG CAT   TCCTCTCAG
                                |||| |||   |||||||||
                                TTCC GTA   AGGAGAGTC
                                  _  ACA
GAM1200  RGS19IP1  3'  GAGGGGGCTCCTCTCA     41697     ACAT
                                GAGG   GCTCCTCTCA
                                ||||   ||||||||||
                                CTCC   CGAGGAGAGT
                                  CC__
GAM1200  SH3BP5   3'  TGAAAGAGGGTTGCTTTTTTCT 22126         ACA   CC__
                                TGAAAGAGG   TGCT   TCT
                                |||||||||   ||||   |||
                                ACTTTCTCC   ACGA   AGA
                                     CA_   AAAA
GAM1200  TLL1     3'  TGAAAGAGACCTTTC      29740         ACATGCT   C
                                TGAAAGAGG      CCT TC
                                |||||||||      ||| ||
                                ACTTTCTCT      GGA AG
                                     ________  A
GAM1200  UFD1L    5'  AGACTCCGCTCCTCTCAG    43819     A_
                                GGAC  TGCTCCTCTCAG
                                ||||  ||||||||||||
                                TCTG  GCGAGGAGAGTC
                                  AG
GAM1201  FACL4    3'  TAACTATGGTTCAAGTGTGAAT 35684     A___     A
            A                    TAGC   GTTCAA TGTGAATA
                                ||||   |||||| ||||||||
                                ATTG   CAAGTT ACACTTAT
                                  ATAC     C
GAM1201  HTRA3    3'  GCAGTTTTGTGAATA      44831       CAAA
                                GCAGTT   TGTGAATA
                                ||||||   ||||||||
                                CGTCAA   ACACTTAT
                                   A___
GAM1201  MHC2TA   3'  TGAGCAGAATAAATGTGA    6989    T    TTC
                                A AGCAG   AAATGTGA
                                | |||||   ||||||||
                                A TCGTC   TTTACACT
                                 C    TTA
GAM1201  RNTRE    3'  TAGCTCTGTGTTCAAATGTG   31259     A____
                                TAGC    GTTCAAATGTG
                                ||||    ||||||||||
                                ATCG    CAAGTTTACAC
                                  AGACA
GAM1201  SALL1    3'  CAAATAGCAGTTCAAAATG    16454            T
                                TAAATAGCAGTTCAAA GTG
                                |||||||||||||| |||
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                                GTTTATCGTCAAGTTT TAC
                                                _
GAM1201  SPF30    3'  AATAGCAGTTATCAAATG    25235          __
                                AATAGCAGT  TCAAATG
                                |||||||||  |||||||
                                TTATCGTCA  AGTTTAC
                                     AT
GAM1201  TIAL1    3'  AGCACCCTTATGTGAATA    35294      G   AA
                                AGCA TTC  ATGTGAATA
                                |||| |||  |||||||||
                                TCGT GGG  TACACTTAT
                                  _  AA
GAM1201  TIMM17A  3'  CAAATGCAATTCAAGTGTGAAT 26788       A        A
              A                  TAAAT GCAGTTCAA TGTGAATA
                                |||||| ||||||||| ||||||||
                                GTTTA CGTTAAGTT ACACTTAT
                                  _       C
GAM1201  ADORA2A  3'  TCCTGGCACTCTCTCTCTTCT  8605      AACA    C
                                TCC    ATTC TCTCTCTTCT
                                |||    |||| ||||||||||
                                AGG    TGAG AGAGAGAAGA
                                  ACCG    _
GAM1201  AP2B1    3'  TCCACGATTCCTCCTCT     10493      ACA      T
                                TCCA   ATTCCTC CTCT
                                ||||   ||||||| ||||
                                AGGT   TAAGGAG GAGA
                                  GC_      _
GAM1201  BCL7B    3'  TCCACATCTCTCTCTTCT    11808      A  ATTC
                                TCCA CA    CTCTCTCTTCT
                                |||| ||    ||||||||||
                                AGGT GT    GAGAGAGAAGA
                                  _ A____
GAM1201  CALD1    3'  TCTAACAGTTCTAATCTCTCTT 37629    C    A   C__
              CT                  TC AACA TTC   TCTCTCTTCT
                                || |||| |||   ||||||||||
                                AG TTGT AAG   AGAGAGAAGA
                                 A    C   ATT
GAM1201  CBS      3'  TCCTGGACTCTTCTCTCTT    6309      AACA    C
                                TCC    ATTC TCTCTCTT
                                |||    |||| ||||||||
                                AGG    TGAG AGAGAGAA
                                  ACC_    A
GAM1201  CDC2L2   5'  TCCATTGAGTCTTCTCTTCT   37942      ACAATTC  C
                                TCCA      CT TCTCTTCT
                                ||||      || ||||||||
                                AGGT      GA AGAGAAGA
                                  AACTCA_  _
GAM1201  COL11A2  3'  CCATGTCCTTTCTCTTCT    38773     ACAAT    C
                                CCA     TCCT TCTCTTCT
                                |||     |||| ||||||||
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                                GGT    AGGA AGAGAAGA
                                  AC___   A
GAM1201  COX10    3'  CCCAGCAATTTCTCTTC    10547     A    CCTC
                                TCCA CAATT   TCTCTTC
                                |||| |||||   |||||||
                                GGGT GTTAA   AGAGAAG
                                  C    ____
GAM1201  CSF1R    5'  TCCTCTTCCTCTTCTCTCTTCT 23314    AACAA  C
                                TCC    TTC TCTCTCTTCT
                                |||    ||| ||||||||||
                                AGG    GAG AGAGAGAAGA
                                  AGAAG  A
GAM1201  DLG3     3'  TCCATCAGTCCTCCTCTT    34431     A AT    T
                                TCCA CA  TCCTC CTCTT
                                |||| ||  ||||| |||||
                                AGGT GT  AGGAG GAGAA
                                  A C_   _
GAM1201  EBI3     3'  CCCAACAACAATTCTTTTCT  25095       TCCTC  C
                                TCCAACAAT    TCT TTCT
                                |||||||||    ||| ||||
                                GGGTTGTTG    AGA AAGA
                                     TTA__   A
GAM1201  EPHA3    3'  CAACAATCCTCAACTTCT    23438      T   TCT
                                CAACAAT CCTC   CTTCT
                                ||||||| ||||   |||||
                                GTTGTTA GGAG   GAAGA
                                    _   TT_
GAM1201  ESRRG    3'  CCAACACCCATTTTCTCTTCT  42444      AT  TC__
                                CCAACA  TCC    TCTCTTCT
                                ||||||  |||    ||||||||
                                GGTTGT  GGG    AGAGAAGA
                                   __   TAAA
GAM1201  FEN1     3'  CAGCAGTTCCTCCCATCT    19956    A  A     _
                                CA CA TTCCTCTC TCT
                                || || |||||||| |||
                                GT GT AAGGAGGG AGA
                                 C  C       T
GAM1201  FMOD     3'  TCCAACAGTCCTTGCCCCT   12932      AT   CT
                                TCCAACA  TCCT  CTCTT
                                |||||||  ||||  |||||
                                AGGTTGT  AGGA  GGGGA
                                    C_   AC
GAM1201  FPRL1    3'  CCCACTGGTCTTTCTCTTCT  11148     ACAATTC  C
                                TCCA      CT TCTCTTCT
                                ||||      || ||||||||
                                GGGT      GA AGAGAAGA
                                  GACCA__  A
GAM1201  FZD3     3'  CCAGCATTTTTCTTTCTCTTCT 32628    A  ATTC_  C
                                CCA CA    CT TCTCTTCT
                                ||| ||    || ||||||||
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                                GGT GT    GA AGAGAAGA
                                  C  AAAAA  A
GAM1201  GNAZ    3'  TCCGGCAGTGCCTCTCCTC   13184    AA  ATT    T
                                TCC  CA   CCTCTC CTT
                                |||  ||   ||||||| |||
                                AGG  GT   GGAGAG GAG
                                  CC  CAC     _
GAM1201  GPR44   3'  TCAAACCTTTCCTCTCTCTTCT 21960    C   AA
                                TC AAC  TTCCTCTCTCTTCT
                                || |||  ||||||||||||||
                                AG TTG  AAGGAGAGAGAAGA
                                 T   GA
GAM1201  HRG     3'  TCCATTTGATCTCTCTTCT   7652      ACAATTCC
                                TCCA       TCTCTCTTCT
                                ||||       ||||||||||
                                AGGT       AGAGAGAAGA
                                  AAACT___
GAM1201  HSPD1   3'  TCCAGGGTCCTTCTCTTCT   41154     ACAAT   C
                                TCCA    TCCT TCTCTTCT
                                ||||    |||| ||||||||
                                AGGT    AGGA AGAGAAGA
                                  CCC__   _
GAM1201  IGF1    3'  TCTGACAGTCTTCTCTCTT   8353     CA   AT  C
                                TC  ACA  TC TCTCTCTT
                                ||  |||  || ||||||||
                                AG  TGT  AG AGAGAGAA
                                 AC   C_  A
GAM1201  IGF1    3'  CAACAATTTCTCATAAATTCT  8335         C   TCTC_
                                CAACAATT CTC     TTCT
                                |||||||| |||    ||||
                                GTTGTTAA GAG     AAGA
                                    A   TATTT
GAM1201  ITGA1   3'  CCAACAGCTCTTCCTCTCTTTT 41843       A___       C
            CT                    CCAACA    TTCCTCTCT TTCT
                                ||||||    ||||||||| ||||
                                GGTTGT    AAGGAGAGA AAGA
                                   CGAG        A
GAM1201  KIF5C   3'  TCCAATAATTTGCCTCCCTT   21163      C    CC
                                TCCAA AATT  TCTCTCTT
                                ||||| ||||  ||||||||
                                AGGTT TTAA  GGAGGGAA
                                  A    AC
GAM1201  KLF13   3'  CATCAAGTTCTCTCTCTTCT   44475    A   TTC
                                CA CAA   CTCTCTCTTCT
                                || |||   ||||||||||
                                GT GTT   GAGAGAGAAGA
                                 A   CAA
GAM1201  LMO7    3'  TCCAACAATTCATCACTCT   31916          C  T
                                TCCAACAATTC TC CTCT
                                |||||||||| || ||||
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                                AGGTTGTTAAG AG GAGA
                                      T  T
GAM1201  MTMR3    5'  TCCAACAAGGCTCTCTTCT   34399        TTCCT
                                TCCAACAA    CTCTCTTCT
                                ||||||||    |||||||||
                                AGGTTGTT    GAGAGAAGA
                                    CC___
GAM1201  MXI1     3'  TCCAATGTCCTCTTCT     25560      CAAT     C
                                TCCAA   TCCTCT TCT
                                |||||   |||||| |||
                                AGGTT   AGGAGA AGA
                                  AC__     _
GAM1201  PEA15    3'  ACAAGTATCTCTCTCTTCT   19075     TTC_
                                ACAA   CTCTCTCTTCT
                                ||||   ||||||||||
                                TGTT   GAGAGAGAAGA
                                  CATA
GAM1201  PIK3C2B  5'  ACAGTGAACCTCTCTCTTCT  15287     ATT__
                                ACA    CCTCTCTCTTCT
                                |||    ||||||||||||
                                TGT    GGAGAGAGAAGA
                                 CACTT
GAM1201  PKHD1    3'  TCCACATTCTCTCTTC     39806     A  ATTCC
                                TCCA CA    TCTCTCTTC
                                |||| ||    |||||||||
                                AGGT GT    AGAGAGAAG
                                  _ A_____
GAM1201  PKM2     3'  TCCAGCATTCCTCCTTCT    15338     ACA      TC
                                TCCA   ATTCCTC  TCT
                                ||||   |||||||  |||
                                AGGT   TAAGGAG  AGA
                                  CG_      GA
GAM1201  PROML1   3'  CAAGATCTCTCTCTCTCTT   25685     CAA  _
                                CAA   TTC CTCTCTCTT
                                |||   ||| |||||||||
                                GTT   GAG GAGAGAGAA
                                  CTA   A
GAM1201  PSA      3'  CCAATCAACTTTCTCTTCT   38453     _    CCTC
                                CCAA CAATT    TCTCTTCT
                                |||| |||||    ||||||||
                                GGTT GTTGA    AGAGAAGA
                                  A    A___
GAM1201  RNGTT    3'  TCCTCATTCCTCTTTCTTCT  19167     AACA      C
                                TCC    ATTCCTCT TCTTCT
                                |||    |||||||| ||||||
                                AGG    TAAGGAGA AGAAGA
                                  AG__       A
GAM1201  RUNX1    5'  CCTACATCTCTCTTTCTTCT  12017    A   A TC   C
                                CC ACA T  CTCT TCTTCT
                                || ||| |  |||| ||||||
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                                GG TGT A  GAGA AGAAGA
                                 A  _ GA   A
GAM1201  SERPIND1  3'  TCCAACAAGCCTCTCTTCT   6776        TTCC
                                TCCAACAA   TCTCTCTTCT
                                ||||||||   ||||||||||
                                AGGTTGTT   GGAGAGAAGA
                                    C___
GAM1201  SLC20A2   3'  CCAATGATTCCCCTGCTTCT  27569     CA      CT
                                CCAA  ATTCCTCT  CTTCT
                                ||||  ||||||||  |||||
                                GGTT  TAAGGGGA  GAAGA
                                  AC      C_
GAM1201  SORBS1    3'  ACAGGGGCCTCTCTCTTCT   31702     ATT_
                                ACA   CCTCTCTCTTCT
                                |||   ||||||||||||
                                TGT   GGAGAGAGAAGA
                                  CCCC
GAM1201  TOX       5'  CAAGCAACTCCTTTTCTT    31267     _      CTC
                                CAA CAATTCCT   TCTT
                                ||| ||||||||   ||||
                                GTT GTTGAGGA   AGAA
                                  C      AA_
GAM1201  TRIM34    5'  TCCTGAGGCTCTCCTCTCTCTT 38975     AACAA__
           CT                     TCC      TTCCTCTCTCTTCT
                                |||      ||||||||||||||
                                AGG      GAGGAGAGAGAAGA
                                  ACTCCGA
GAM1201  TRPV3     3'  TCCGGGAATTCCTCGACTTCT  45444     AAC      TCT
                                TCC   AATTCCTC   CTTCT
                                |||   ||||||||   |||||
                                AGG   TTAAGGAG   GAAGA
                                  CCC      CT_
GAM1201  USP14     3'  TCCAAAGATAATTTTCTCTTCT 23118      CA  TCCTC
                                TCCAA  AT    TCTCTTCT
                                |||||  ||    ||||||||
                                AGGTT  TA    AGAGAAGA
                                   TC  TTAAA
GAM1201  VEGF      3'  TCCAACAATGTGTCTCTTCT   17971        TCCTC
                                TCCAACAAT    TCTCTTCT
                                |||||||||    ||||||||
                                AGGTTGTTA    AGAGAAGA
                                     CAC__
GAM1202  ATP11B    3'  TAATATGCTAATAGTATCTAA  44309           GG
                                TAATATGCTAATAGTA  TAA
                                ||||||||||||||||  |||
                                ATTATACGATTATCAT  ATT
                                          AG
GAM1202  DISC1     3'  TAATATGCTAATGTGCA     33046          A  AG
                                TAATATGCTAAT GT  GTA
                                |||||||||||| ||  |||
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                                ATTATACGATTA CA  CGT
                                          _ __
GAM1202  DLX4     3'  TATGGTAAGTAGGTAAA     39620      CTAAT
                                TATG     AGTAGGTAAA
                                ||||     ||||||||||
                                ATAC     TCATCCATTT
                                  CAT__
GAM1202  FGF5     3'  TAATATGCTAATCAAATCAAAC 37590            AGTAGG
                C                TAATATGCTAAT      TAAACC
                                ||||||||||||     ||||||
                                ATTATACGATTA     GTTTGG
                                       GTTTA_
GAM1202  GAS1     3'  AATATGCTAATAGACAGC    13063            TA
                                AATATGCTAATAG  GGT
                                ||||||||||||  |||
                                TTATACGATTATC  TCG
                                       TG
GAM1202  HGF      3'  TAATATGCAATAATAAA     45322         T
                                TAATATGC AATAGTAGG
                                ||||||||| |||||||||
                                ATTATACG TTATTATTT
                                          _
GAM1202  IL12B    3'  TAATATACTAATAAATACATAA 13519             _  G
                A                TAATATGCTAATAG TA GTAAA
                                ||||||||||||| || |||||
                                ATTATATGATTATT AT TATTT
                                       T  G
GAM1202  ING1     5'  TAATATGCTAATGAAGT     24398           AGT
                                TAATATGCTAAT   AGGT
                                ||||||||||||   ||||
                                ATTATACGATTA   TTCA
                                       C__
GAM1202  KCNJ1    5'  TAATATGCTCAGTTTTTAGGT  6889          AATAG__
                                TAATATGCT      TAGGT
                                |||||||||      |||||
                                ATTATACGA      ATCCA
                                     GTCAAAA
GAM1202  KMO      3'  TAACATGCTAGTTAAGT     18956          ATAG
                                TAATATGCTA    TAGGT
                                ||||||||||    |||||
                                ATTGTACGAT    ATTCA
                                      CA__
GAM1202  NOTCH2   3'  TAACATGCTGGTAGG       35912          AATA
                                TAATATGCT    GTAGG
                                |||||||||    |||||
                                ATTGTACGA    CATCC
                                      C___
GAM1202  PHLDA3   3'  ATGCTAATGGCCAAACC     29609         AGTA  _
                                ATGCTAAT    GGT AAACC
                                ||||||||    ||| |||||
```

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                                TACGATTA   CCG TTTGG
                                    ____   G
GAM1202  ABCF1    3'  TGTAGGGTAAATCAGAGGCAG  9909     T     ATT   _ A
                                TGT AGGGTA   GATC GA GCAG
                                ||| ||||||   |||| || ||||
                                ACA TCCCAT   TTAG CT CGTC
                                  _    ___    T  C
GAM1202  IL18R1   3'  TGTTAGGGAGTGAAAGCA    19299        TAAT   TCG
                                TGTTAGGG   TGA   AAGCA
                                ||||||||   |||   |||||
                                ACAATCCC   ACT   TTCGT
                                     TC__   ___
GAM1202  JPH3     3'  TGTTAGGGGAAGTTGAGGCAG  34029        T _   TCGAA
                                TGTTAGGG AA TTGA    GCAG
                                |||||||| || ||||    ||||
                                ACAATCCC TT AACT    CGTC
                                     C  C    C____
GAM1202  PPT2     3'  TGTTAAGGAATTGAAGCA    39931        T     TCGA
                                TGTTAGGG AATTGA   AGCA
                                |||||||| ||||||   ||||
                                ACAATTCC TTAACT   TCGT
                                    _     ____
GAM1203  ARHGDIA  3'  GCACTGGTGGGCTGGGGA    20207        TAAC  TA   A
                                GCACTGGT   GG  CTG GGA
                                ||||||||   ||  ||| |||
                                CGTGACCA   CC  GAC CCT
                                    ____ C_   C
GAM1203  FCER2    3'  CTGGGGTGCTGAGGA      12811      TTAAC   A
                                CTGG    GGT CTGAGGA
                                ||||    ||| |||||||
                                GACC    CCA GACTCCT
                                  _____   C
GAM1203  KCNS2    3'  CTGGTTAACCGAACAAGAGGAG 42825         GGT  T_
                                CTGGTTAAC   AC  GAGGAG
                                |||||||||   ||  ||||||
                                GACCAATTG   TG  CTCCTC
                                     GCT  TT
GAM1203  KIP2     3'  GATTCCACGGTGTTGGGGAG   26889      A_    AC  A
                                GGTT  ACGGT  TG GGAG
                                ||||  |||||  || ||||
                                CTAA  TGCCA  AC CCTC
                                  GG    CA  C
GAM1203  MEF2D    3'  GCACTGAGTGTGCTGTTGAGG  25419       _ TAACG  AC
                                GCACTG GT    GT  TGAGG
                                ||||||  ||    ||  |||||
                                CGTGAC CA    CA  ACTCC
                                   T  CACGA  __
GAM1203  PPT2     3'  GCACTGGTTGGGGGCTCTGGG  39920         AAC   A   A
                                GCACTGGTT   GGT CTG GG
                                |||||||||   ||| ||| ||
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                                CGTGACCAA  CCG GAC CC
                                     CCC  A  _
GAM1203  RASA1    5'  ACTGGTTAGTTGGAGGA    35485       AAC  ACT
                                ACTGGTT  GGT  GAGGA
                                |||||||  |||  |||||
                                TGACCAA  TCA  CTCCT
                                   ___  AC_
GAM1203  TEGT     3'  GCACTGGTTGTGAATAGGGAG  42097        AAC   CT
                                GCACTGGTT  GGTA  GAG
                                |||||||||  ||||  |||
                                CGTGACCAA  TTAT  CTC
                                     CAC   CC
GAM1204  ACE2     3'  TGAGTGTCTGCTTTGTGCT   34762      TC    CTA
                                TGAGT  CTGCT  TGTT
                                |||||  |||||  ||||
                                ACTCA  GACGA  ACGA
                                   CA    AAC
GAM1204  TLR9     3'  TGAGTGCCTGCTCTGTGT    32662      T      A
                                TGAGT CCTGCTCT TGT
                                ||||| |||||||| |||
                                ACTCA GGACGAGA ACA
                                   C       C
GAM1205  ABCA1    3'  TGGCTTAGTGAATGAGGATGTG 24273     CAAATA   AA
                                TGGC    TGAG  AGGATGTG
                                ||||    ||||  ||||||||
                                ACCG    ACTT  TCCTACAC
                                  AATC__   AC
GAM1205  FBXL7    3'  TGGCAAAAGAGGATG      29417     CAAATAT   A
                                TGGC     GAGA AGGATG
                                ||||     |||| ||||||
                                ACCG     TTTT TCCTAC
                                  ________   C
GAM1205  HOXB5    5'  GGCCAAATATGGGGGGGGGGT  13448         AGAAA  AT
                                GGCCAAATATG    GG  GT
                                ||||||||||    ||  ||
                                CCGGTTTATAC    CC  CA
                                      CCCC_  CC
GAM1205  IFNA14   3'  TGGCTAAATATGAAGAACATA  13480     C      GAA
                                TGGC AAATATGA   AGGATGTG
                                |||| ||||||||   ||||||||
                                ACCG TTTATACT   TCTTGTAT
                                  A      ___
GAM1205  PNN      3'  TGGTTAAAATATGAGAAA    43404     CC_
                                TGG   AAATATGAGAAA
                                |||   ||||||||||||
                                ACC   TTTATACTCTTT
                                  AAT
GAM1206  BIN3     3'  CTGCAGCTTGCTCAGGCCGTGG 33078        _  A  _
                                CTGCAGCT GC C GGCCGTGG
                                |||||||| || | ||||||||
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                                GACGTCGA CG G CCGGCACC
                                     A  A T
GAM1206  CDC42    3'  TCTTCAGCTGCATTCTAGGA   12161     G       CGGCCGT
                                TCT CAGCTGCA      GGA
                                ||| ||||||||      |||
                                AGA GTCGACGT      CCT
                                  A       AAGAT__
GAM1206  DAP      3'  GACCTGCAGCAGATCGGCTGTG 43689          TGCA    C
              G                  GATCTGCAGC    CGGC GTGG
                                ||||||||||    |||| ||||
                                CTGGACGTCG    GCCG CACC
                                      TCTA    A
GAM1206  FGF23    3'  CTGTGGCTGCACAGAGG     33952     CA       CCGT
                                CTG  GCTGCACGG    GG
                                |||  |||||||||    ||
                                GAC  CGACGTGTC    CC
                                  AC        T___
GAM1206  ITSN1    3'  ACAGCATGTGTGGCCGTGG    16652       _  CAC
                                GCAGC TG   GGCCGTGG
                                ||||| ||   ||||||||
                                TGTCG AC   CCGGCACC
                                   T  ACA
GAM1206  NPR1     3'  CCTGTGCATGGCCGTGG     44578     CAGC    C
                                TCTG    TGCA GGCCGTGG
                                ||||    |||| ||||||||
                                GGAC    ACGT CCGGCACC
                                  ____    A
GAM1206  SCAMP1   3'  TGCAGCTGCGGTCTGGA     38067         AC  CCG
                                TGCAGCTGC  GG   TGGA
                                |||||||||  ||   ||||
                                ACGTCGACG  CC   ACCT
                                     __  AG_
GAM1207  ATP2B2   3'  CGTTGATATAGATACAAAG   11758          ATCTTT
                                CGTTGATATA     CAAAG
                                ||||||||||     |||||
                                GCAACTATAT     GTTTC
                                      CTAT__
GAM1207  AXL      3'  TCGTTGATATACAA        34888           ATCTTT
                                TCGTTGATATA     CAA
                                ||||||||||     |||
                                AGCAACTATAT     GTT
                                                _______
GAM1207  GRAF     5'  CGTCGATCTCATCTTTCA    31443        ATA
                                CGTTGAT   ATCTTTCA
                                |||||||   ||||||||
                                GCAGCTA   TAGAAAGT
                                    GAG
GAM1207  ALDOB    5'  GAGGCAGCAGCTGCCAAA    42770       C  AGATT
                                GAGGCA CA    CTGCCAAA
                                ||||||  ||    ||||||||
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                                CTCCGT GT    GACGGTTT
                                   C  C____
GAM1207  DHCR7    3'  AGGTACTGGACACCTGCCAA   10682     C  CAA  _
                                AGG AC   GAT TCTGCCAA
                                ||| ||   ||| ||||||||
                                TCC TG   CTG GGACGGTT
                                  A  AC_   T
GAM1207  FLOT2    3'  CAAGGCACCAGGATTCTG    20981          A
                                CGAGGCACCA GATTCTG
                                |||||||||| |||||||
                                GTTCCGTGGT CTAAGAC
                                      C
GAM1207  KIF3C    3'  GAGGCACCATCTGCCA      13951          AGAT
                                GAGGCACCA    TCTGCCA
                                |||||||||    |||||||
                                CTCCGTGGT    AGACGGT
                                             ____
GAM1207  LYN      3'  GAGGCAGCCACCCCTGCCAAAT 14285       _   AGAT
                                GAGGCA CCA    TCTGCCAAAT
                                |||||| |||    ||||||||||
                                CTCCGT GGT    GGACGGTTTA
                                   C   GG__
GAM1207  OVOL1    3'  GAGCATTAGAAGCCCTGCCA   21273     G  CC__   A
                                GAG CA    AAG TTCTGCCA
                                ||| ||    ||| ||||||||
                                CTC GT    TTC GGGACGGT
                                  _  AATC  _
GAM1207  SOLH     3'  CGGGGTCCTGAGATTCTG    24827    A  CA  A_
                                CG GG  CC  AGATTCTG
                                || ||  ||  ||||||||
                                GC CC  GG  TCTAAGAC
                                 _  CA  AC
GAM1208  CKTSF1B1 3'  CGTTTGTATACATGCATC    30085     CA  C
                                CGTT  TG TGTATGCATC
                                ||||  || ||||||||||
                                GCAA  AT ATGTACGTAG
                                  AC  _
GAM1208  EIF4E    3'  GCTAGAAAACTGTATGCATCAT 12694     CAT__
                                GTT    GCTGTATGCATCAT
                                |||    ||||||||||||||
                                CGA    TGACATACGTAGTA
                                  TCTTT
GAM1208  HIVEP2   3'  GTTTTGCTTTACATCAT     27552     CA   GTA
                                GTT  TGCT   TGCATCAT
                                |||  ||||   ||||||||
                                CAA  ACGA   ATGTAGTA
                                  A_   A__
GAM1208  MAN1A1   3'  CCCTTCAGTATATGCATC    45094    G   TGC
                                CC TTCA   TGTATGCATC
                                || ||||   ||||||||||
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                                GG AAGT   ATATACGTAG
                                 G   C__
GAM1208 EIF1A    3'  TATAAACATCTAAATTATC    44811          T
                                TATAGACATCTG AATTATC
                                |||||||||||| |||||||
                                ATATTTGTAGAT TTAATAG
                                          _
GAM1209 ANKH     3'  CACCCGCCTCCTGCATGTGTGG 38313         G ___ ACGA
            AGTAG                  CACCCGTCTC TG   GT    AGTAG
                                |||||||||| ||   ||    |||||
                                GTGGGCGGAG AC   CA    TCATC
                                      G  GTA  CACC
GAM1209 SIGLEC6  3'  CACTCGGTTTGTGGTACATTGC 40930     C  TCTC       AA
                                CAC CG    GTGGTACG  GT
                                ||| ||    ||||||||  ||
                                GTG GC    CACCATGT  CG
                                  A  CAAA       AA
GAM1210 PBP      3'  TTAATAATTTGATGACCCCATC 15020      A       A  A
                                TTAA AATTTGAT ACT CCATT
                                |||| |||||||| ||| |||||
                                AATT TTAAACTA TGG GGTAG
                                   A       C  _
GAM1210 RGR      3'  TTAAAAATAGAGCTACCATT   16306        TT  TAA
                                TTAAAAAT  GA   CTACCATT
                                ||||||||  ||   ||||||||
                                AATTTTTA  CT   GATGGTAA
                                     T_  C__
GAM1210 SRR      3'  TTAAGAATCTGATAACTA    34970      A
                                TTAA AATTTGATAACTA
                                |||| ||||||||||||
                                AATT TTAGACTATTGAT
                                   C
GAM1210 VSNL1    3'  TCATTAATTCTTCAAATTC    18038        TATT
                                TCATTAAT    TTTTCAAATTC
                                ||||||||    ||||||||||
                                AGTAATTA    AGAAGTTTAAG
                                          _____
GAM1211 DAP      5'  TGTCTCCTGTATGTGGGTGT   43693        A_____   C
                                TGTCTTCT    TGGG GT
                                ||||||||    |||| ||
                                ACAGAGGA    ACCC CA
                                     CATAC    A
GAM1211 TIAL1    3'  TACTTTCATGTCTTCAGAGTGT 35297     CTCA       TAT   C
                                TAC   ATGTCTTC   GGG GT
                                |||   ||||||||   ||| ||
                                ATG   TACAGAAG   CTC CA
                                  AAAG       T__   A
GAM1211 FGFRL1   3'  GTGCATACATGCATCCAG    34914      __    ATT
                                GTGC  GCATG   TCCAG
                                ||||  |||||   |||||
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                                CACG  TGTAC   AGGTC
                                  TA    GT_
GAM1211  PON2     3'  TACACATGCCATACATTTC   7164         G   _
                                TACACGTGC CATG ATTTC
                                ||||||||| |||| |||||
                                ATGTGTACG GTAT TAAAG
                                     _   G
GAM1211  ZNF41    3'  CATACCCAGTTGTGATTTCCAG 41913      G ____
                                CGTGC CA   TGATTTCCAG
                                ||||| ||   ||||||||||
                                GTATG GT   ACTAAAGGTC
                                  G  CAAC
GAM1212  NAP1L3   3'  TTTAATATTTATTTATTTT   21215
                                TTTAATATTTATTTATTTT
                                ||||||||||||||||||
                                AAATTATAAATAAATAAAA

GAM1213  A1BG     3'  CAGCCTGGGCAACATA     39089      GA   ATGTTT
                                CAGCC  GGCA    ACATA
                                |||||  ||||    |||||
                                GTCGG  CCGT    TGTAT
                                  AC   _______
GAM1213  ALOX15   3'  CAGCCTAGGCAACATA     10074      G    ATGTTT
                                CAGCC AGGCA    ACATA
                                ||||| |||||    |||||
                                GTCGG TCCGT    TGTAT
                                  A    _______
GAM1213  CASP10   3'  CAGCTTAGGCAACATA     37382      CG   ATGTTT
                                CAGC  AGGCA    ACATA
                                ||||  |||||    |||||
                                GTCG  TCCGT    TGTAT
                                  AA   _______
GAM1213  CD1D     3'  GAGGTGTCCCACATAGT     44299      CAA   _
                                GAGG   TGTTT ACATAGT
                                ||||   ||||| |||||||
                                CTCC   ACAGG TGTATCA
                                  ___    G
GAM1213  G6PC     3'  CAGCCTGGGCAACATA     6660       GA   ATGTTT
                                CAGCC  GGCA    ACATA
                                |||||  ||||    |||||
                                GTCGG  CCGT    TGTAT
                                  AC   _______
GAM1213  GRM6     3'  CAGCCTGGGCAACATA     9168       GA   ATGTTT
                                CAGCC  GGCA    ACATA
                                |||||  ||||    |||||
                                GTCGG  CCGT    TGTAT
                                  AC   _______
GAM1213  SCNN1G   3'  CAGCCTGGGCAACATA     9789       GA   ATGTTT
                                CAGCC  GGCA    ACATA
                                |||||  ||||    |||||
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                                GTCGG  CCGT     TGTAT
                                  AC   _______
GAM1214  FBXW1B   3'  TCAACAGGGCCTTCTTATT   37994      _    CC
                                TCAAC GGGCC  CTTATT
                                ||||| |||||  ||||||
                                AGTTG CCCGG  GAATAA
                                   T     AA
GAM1214  MAP3K14  3'  GGGCCCCCTTAACCTACG    19543          TTGTG
                                GGGCCCCCTTA     ACG
                                ||||||||||     |||
                                CCCGGGGGAAT     TGC
                                      TGGA_
GAM1214  PTCRA    3'  TCAAGGGGCCCCCTTTTGGA   39652      C        A   T
                                TCAA GGGCCCCCTT TTG GA
                                |||| |||||||||| ||| ||
                                AGTT CCCGGGGGAA AAC CT
                                  C        _  _
GAM1214  RAB7L1   3'  CAATGGGCCTCCTTACTG    19430     C    C
                                CAA GGGCC CCTTATTG
                                ||| ||||| ||||||||
                                GTT CCCGG GGAATGAC
                                  A    A
GAM1214  RBP3     3'  TCAGCAGGCCCCTTTGC     16196     A       CTTA
                                TCA CGGGCCCC    TTGT
                                ||| ||||||||    ||||
                                AGT GTCCGGGG    AACG
                                  C       A___
GAM1215  AGR2     3'  TCACACATGTACACTTGAAACC 26925         CAGGAAG
            A                    TCACACAT      TTGAAACCA
                                ||||||||      |||||||||
                                AGTGTGTA      AACTTTGGT
                                    CATGTG_
GAM1215  CCR2     3'  TCACACATCTGTGAAGCCA    8501          AG_
                                TCACACATC   GAAGTTG
                                |||||||||   |||||||
                                AGTGTGTAG   CTTCGGT
                                      ACA
GAM1215  CERD4    3'  TCCACATCAGGTGTGGGCTG   28955    A       AA___
                                TC CACATCAGG     GTTG
                                || |||||||||     ||||
                                AG GTGTAGTCC     CGAC
                                  _        ACACC
GAM1215  COL4A1   3'  TCACACATCAGTGCATTG     12308          GAA
                                TCACACATCAG   GTTG
                                ||||||||||   ||||
                                AGTGTGTAGTC   TAAC
                                      ACG
GAM1215  CYP27B1  3'  TCACACATTGGTCAGGGCCG   8956         ____    AA
                                TCACACA   TCAGG  GTTG
                                |||||||   |||||  ||||
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                                AGTGTGT   AGTCC  CGGC
                                   AACC   __
GAM1215  FGF2    3'  CACATCAGAGTAAAAA     12831       GA   T
                                CACATCAG  AGT GAAA
                                ||||||||  ||| ||||
                                GTGTAGTC  TCA TTTT
                                   __   T
GAM1215  G6PC    3'  TCACACATGGGAATAAGCC   6662        CA   GTTGAAA
                                TCACACAT  GGAA     CC
                                ||||||||  ||||     ||
                                AGTGTGTA  CCTT     GG
                                   C_   ATTC___
GAM1215  IFNG    5'  CCAAAGAAGTTGAAATCA    8366      _       C
                                TCAG GAAGTTGAAA CA
                                |||| |||||||||| ||
                                GGTT CTTCAACTTT GT
                                  T        A
GAM1215  IL1RN   3'  TCACACATTAGAAAGACC    8216       C     TTGAA
                                TCACACAT AGGAAG    ACC
                                |||||||| ||||||    |||
                                AGTGTGTA TCTTTC    TGG
                                   A    _____
GAM1215  KNS2    3'  ACACATGGGAAGGGAGCC    24469      CA    TT  AA
                                ACACAT  GGAAG  GA  CC
                                ||||||  |||||  ||  ||
                                TGTGTA  CCTTC  CT  GG
                                   C_    C_  C_
GAM1215  LTB4R   5'  ACACACAAAGTTGAGGCC    8877       CAG      AA
                                ACACAT   GAAGTTGA  CC
                                ||||||   ||||||||  ||
                                TGTGTG   TTTCAACT  GG
                                   ___       CC
GAM1215  M11S1   3'  ACCATCAGAACTGAAAC     25324    A      AG
                                AC CATCAGGA  TTGAAAC
                                || ||||||||  |||||||
                                TG GTAGTCTT  GACTTTG
                                  _      __
GAM1215  MLLT2   3'  TCACTTTCAGAGTTGAAAC   25508     ACA   GA
                                TCAC   TCAG  AGTTGAAAC
                                ||||   ||||  |||||||||
                                AGTG   AGTC  TCAACTTTG
                                  AA_   __
GAM1215  PDE4D   3'  TCATGTATCAGGAAGACTTGAA 43898     CAC       __
            A                    TCA   ATCAGGAAG  TTGAAA
                                 |||   |||||||||  ||||||
                                 AGT   TAGTCCTTC  AACTTT
                                   ACA       TG
GAM1215  PPP4R1  3'  TCACACACAGGGCTG       23076       T   AA
                                TCACACA CAGG  GTTG
                                ||||||| ||||  ||||
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                                AGTGTGT GTCC  CGAC
                                      _   __
GAM1215  RAF1     3'  TCCACATCAGGGCTG       44336    A        AA
                                TC CACATCAGG  GTTG
                                || |||||||||  ||||
                                AG GTGTAGTCC  CGAC
                                      _       __
GAM1215  TMPRSS2  3'  TCATGCACGGGGAAGCAAAACC 24937     CA   CA     T
              A                  TCA  CAT  GGAAGT GAAACCA
                                 |||  |||  |||||| |||||||
                                 AGT  GTG  CCTTCG TTTTGGT
                                   AC   CC     _
GAM1215  TPS1     3'  CACACCAGGGGCCCTCCGGAGT 41303          A__________
              CG                   CACATCAGG         AGTTG
                                   |||||||||         |||||
                                   GTGTGGTCC         TCAGC
                                        CCGGGAGGCC
GAM1215  TXNIP    3'  TCCTACATTAGGAAGTCAGA  26999    AC    C       _
                                 TC  ACAT AGGAAGTT GA
                                 ||  |||| |||||||| ||
                                 AG  TGTA TCCTTCAG CT
                                   GA    A       T
GAM1216  ATRN     3'  AGGTGAAACTCAGACATTGT  40264     A  TCA__
                                 AGG TG    TAGACATTGT
                                 ||| ||    ||||||||||
                                 TCC AC    GTCTGTAACA
                                   _  TTTGA
GAM1216  F8       3'  TCAAGAAGACATTGT       6570        ATGTCAT
                                 TCAAGG      AGACATTGT
                                 ||||||      |||||||||
                                 AGTTCT      TCTGTAACA
                                      ________
GAM1217  CHAC     3'  TATAAAATATATAAAAGCA   37817              _
                                 TATAAAATATATAAAA CA
                                 |||||||||||||||| ||
                                 ATATTTTATATATTTT GT
                                           C
GAM1217  JRKL     3'  TATAAAATATACAAAACAT   19091
                                 TATAAAATATATAAAACAT
                                 ||||||||||||||||||
                                 ATATTTTATATGTTTTGTA

GAM1217  TSG      3'  TATAAAATACAATAAACATAAA 34008          TA
              CT                   TATAAAATATA  AAACATAAACT
                                   ||||||||||  ||||||||||
                                   ATATTTTATGT  TTTGTATTTGA
                                          TA
GAM1218  ACADL    3'  TATTCTGTGTTCTCAGAT    11496         ATA
                                 TATTTTGTG   TCAGAT
                                 |||||||||   ||||||
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                                ATAAGACAC   AGTCTA
                                     AAG
GAM1218 KLRC4    3' TATTTTGTGATAAAAACAT   30237          TC
                                TATTTTGTGATA  AGATAT
                                ||||||||||||  ||||||
                                ATAAAACACTAT  TTTGTA
                                       T_
GAM1218 PLS1     3' CTTAATGTATCAGATAT     15411     T   A
                                TTT GTG TATCAGATAT
                                ||| ||| ||||||||||
                                GAA TAC ATAGTCTATA
                                  T  _
GAM1218 RELN     3' TATTTCCTGATATCAGAT    45358       G
                                TATTTT TGATATCAGAT
                                |||||| ||||||||||
                                ATAAAG ACTATAGTCTA
                                    G
GAM1218 SMP1     3' TTTTGGACCTCAGATAT     30721       T   A
                                TTTTG GAT TCAGATAT
                                ||||| ||| ||||||||
                                AAAAC CTG AGTCTATA
                                   _  G
GAM1219 MLLT7    3' TATTTATTGTCTGTAGTG    25532          A  GCGAC
                                TGTTTATTGTC TG    AGTG
                                |||||||||||  ||    ||||
                                ATAAATAACAG AC    TCAC
                                       _  A_____
GAM1220 GYS1     3' CTGGAGTGCAGGAACTG     44786       TA  ATC       C
                                TTGGA  GT   GCAGGAACT G
                                |||||  ||   ||||||||| |
                                GACCT  CA   CGTCCTTGA C
                                   __  ____       A
GAM1220 UBE2L3   3' TTGGATAGCTGACAGAA     17836         ATC
                                TTGGATAGT   GCAGGA
                                |||||||||   ||||||
                                AACCTATCG   TGTCTT
                                     AC_
GAM1221 SLA      3' TTACATTCATTTCTCATACG   27567         C  G  CC
                                TTATATTCAT TC CA  ACG
                                |||||||||| || ||  |||
                                AATGTAAGTA AG GT  TGC
                                      A  A  A_
GAM1222 ADORA1   3' TATGGCCTGGGGTCCA      8595       T   TTT  T
                                TATG CCTG   GG GTCCA
                                |||| ||||   || |||||
                                ATAC GGAC   CC CAGGT
                                  C   ____  _
GAM1222 EHF      3' TGTTTTGGTTTGTGTCCAAA  29118     CCT_    G
                                TGT    GTTTG TGTCCAAA
                                |||    ||||| ||||||||
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                                ACA   CAAAC ACAGGTTT
                                  AAAC    _
GAM1222 MGAT2    3' TATGTCCTGTTTGGACAAA   14454          TGTC
                                TATGTCCTGTTTGG   CAAA
                                ||||||||||||||  ||||
                                ATACAGGACAAACC   GTTT
                                       T___
GAM1222 PAX5     3' TGTCCATGGCAGGTGTCC    32525     _ TTT
                                TGTCC TG  GGTGTCC
                                ||||| ||  |||||||
                                ACAGG AC  CCACAGG
                                   T  CGT
GAM1222 RYR2     3' TGTTATGACAGTGTCCA     9769     CC  TT
                                TGT  TG  TGGTGTCCA
                                |||  ||  |||||||||
                                ACA  AC  GTCACAGGT
                                  AT  T_
GAM1222 SELPLG   3' TGTCCTGTTTGGGTGGCCA   40678          _ T
                                TGTCCTGTTTGG TG CCA
                                |||||||||||| || |||
                                ACAGGACAAACC AC GGT
                                       C  C
GAM1222 TNFSF8   3' TATGCCCTTTCTGTCCA     10330        GTTTGG
                                TATGTCCT     TGTCCA
                                ||||||||     ||||||
                                ATACGGGA     ACAGGT
                                     AAG___
GAM1223 ADRB1    3' TGGCTTTTCTCTTTG       8658      A    CCAAAT
                                TGGC TTTTC     TTTTTG
                                |||| |||||     ||||||
                                ACCG AAAAG     AGAAAC
                                  _    _______
GAM1223 B4GALT5  3' TGGCATTTTCCAGAATTC    21946          CA
                                TGGCATTTTCC  AATTT
                                ||||||||||  |||||
                                ACCGTAAAAGG  TTAAG
                                       TC
GAM1223 DBI      3' TGGTTATTTTCCCGAATTC   33926     C_      A
                                TGG  ATTTTCCC AATTT
                                |||  |||||||| |||||
                                ACC  TAAAAGGG TTAAG
                                  AA       C
GAM1223 GABRA2   5' CGGTGTTTTCTTCTTTTGCC  9042     CA    CCAAA
                                TGG  TTTTC    TTTTTTGCC
                                |||  |||||    |||||||||
                                GCC  AAAAG    AGAAAACGG
                                  AC    A____
GAM1223 IDE      3' TGACATTTGACAATTTTTTG   22474        TCCCA
                                TGGCATTT    AATTTTTTG
                                ||||||||    |||||||||
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                                ACTGTAAA    TTAAAAAAC
                                    CTG__
GAM1223 IFRD2    3' TGGCATTTGTCCAGATGC    27627       TC  AATTTTT
                                TGGCATTT CCA     TGC
                                |||||||| |||     |||
                                ACCGTAAA GGT     ACG
                                    CA  CT_____
GAM1223 OSBP     5' TGGCATTTCTCTCGGGCC    14989       CCCAAA   TT
                                TGGCATTTT    TTTT GCC
                                |||||||||    |||| |||
                                ACCGTAAAG    AGAG CGG
                                     _______  CC
GAM1223 PKHD1    3' TGGCATTTTTACATCTTTG   39811       CC  AAT
                                TGGCATTTT CA  TTTTTG
                                ||||||||| ||  ||||||
                                ACCGTAAAA GT  AGAAAC
                                     AT ___
GAM1223 SELPLG   3' TGGGTTTTCCCAGAGAGGTGCC 40677    CA      AATTTTT
                                TGG TTTTCCCA     TGCC
                                ||| |||||||     ||||
                                ACC AAAAGGGT     ACGG
                                  C_     CTCTCC_
GAM1224 ABCD2    5' TGAAAATGAGGAGAGAGC    23154       AC  CC
                                TGAAAATGAG AGA GT
                                |||||||||| ||| ||
                                ACTTTTACTC TCT CG
                                     C_  CT
GAM1224 PLAU     3' TGAAACTGAGACAGTGC     42881      A     GACC
                                TGAAA TGAGACA   GTGT
                                ||||| |||||||   ||||
                                ACTTT ACTCTGT   CACG
                                   G     ____
GAM1224 PUM1     3' TGGAAATGTACACCGTGTA   31242    A   AG AG
                                TG AAATG AC ACCGTGTA
                                || ||||| || ||||||||
                                AC TTTAC TG TGGCACAT
                                 C    A_ __
GAM1224 SLC26A4  3' TGAAAATGAGGCAGCATTATAA 7764         A  ACCG
                                TGAAAATGAG CAG   TGTAA
                                |||||||||| |||   |||||
                                ACTTTTACTC GTC   ATATT
                                     C  GTA_
GAM1224 STAC     3' TGAAAATGGAGACTTTTTGTG 17141       _  AGACC
                                TGAAAATG AGAC    GTG
                                |||||||| ||||    |||
                                ACTTTTAC TCTG    CAC
                                     C   AAAAA
GAM1224 UBE2V1   3' GAGACCCCAGGCCGTGTAA   35345     ___ A
                                GAGAC  AG CCGTGTAA
                                |||||  || ||||||||
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                                CTCTG   TC GGCACATT
                                   GGG  C
GAM1224  WNT5A    3'  GAGAATGAGACATGTG      18118    A       GACC
                                GA AATGAGACA    GTG
                                || |||||||||    |||
                                CT TTACTCTGT    CAC
                                 C       A___
GAM1224  ZNF42    5'  TGATAATGAGACAGAACC     18293     A        _
                                TGA AATGAGACAGA CC
                                ||| |||||||||| ||
                                ACT TTACTCTGTCT GG
                                  A         T
GAM1225  ACP1     5'  TCTGGGCTTTTCGA        28248         ACCTCA
                                TCTGGGCT     TTTTGA
                                ||||||||     ||||||
                                AGACCCGA     AAAGCT

                                      _______
GAM1225  ACP2     3'  TCTGAGCTATTTGCC       11510          CCTCAT    A
                                TCTGGGCTA     TTTG CC
                                |||||||||     |||| ||
                                AGACTCGAT     AAAC GG

                                      _______   _
GAM1225  APOBEC1  3'  TGGGGTACCTTGTGAACATTTC 25259      C    _______
                                TGGG TACCT     CATTTT
                                |||| |||||     ||||||
                                ACCC ATGGA     GTAAAG
                                   C    ACACTT
GAM1225  COL4A6   3'  TCTGGGCTACTTGGGTGGCACC 37977          CTCATTTTG
              C                  TCTGGGCTAC        ACCC
                                ||||||||||        ||||
                                AGACCCGATG        TGGG
                                     AACCCACCG
GAM1225  CXorf6   5'  TCTGGGCTCCTGAC        24242         A   CATTTT
                                TCTGGGCT CCT     GAC
                                |||||||| |||     |||
                                AGACCCGA GGA     CTG

                                      _  _______
GAM1225  CYLN2    3'  TCTGAGCTGCCTCTGCCC     18063         A    ATTT  A
                                TCTGGGCT CCTC    TG CCC
                                |||||||| ||||    || |||
                                AGACTCGA GGAG    AC GGG
                                     C    ____  _
GAM1225  DISC1    5'  CCTGGGCTGCCTCCTGCTCC   33034         A    ATT   AC
                                TCTGGGCT CCTC   TTG  CC
                                |||||||| ||||   |||  ||
                                GGACCCGA GGAG   GAC  GG
                                     C    ___   GA
GAM1225  DYRK1A   3'  TCTAGGCTTCTTTTGATCC    39001         ACC  A     C
                                TCTGGGCT   TC TTTTGA CC
                                ||||||||   || |||||| ||
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                                AGATCCGA   AG AAAACT GG
                                   ___ _     A
GAM1225  EPB42    5'  TCTGGGCTCCTTCTG       6517          A   CAT
                                TCTGGGCT CCT   TTTG
                                |||||||| |||   ||||
                                AGACCCGA GGA   AGAC
                                   _  ___
GAM1225  FZD7     3'  TCTGGGCTCCAGTTTGGCCCC  18636         A  TCAT   A
                                TCTGGGCT CC    TTTG CCCC
                                |||||||| ||    |||| ||||
                                AGACCCGA GG    AAAC GGGG
                                   _ TC__    C
GAM1225  GPR23    5'  TCTGGGCTGCCGCAGCTT    41317         A  T  T
                                TCTGGGCT CC CA TTT
                                |||||||| || || |||
                                AGACCCGA GG GT GAA
                                     C  C  C
GAM1225  HOXD4    5'  TGGGTACCTTTGCACC      31183      C    CATT  _
                                TGGG TACCT    TTG ACC
                                |||| |||||    ||| |||
                                ACCC ATGGA    AAC TGG
                                  _    ____  G
GAM1225  KCNA5    3'  TCTGGGCTATTTAGAGTCATTT 40683         CC_____
            T                    TCTGGGCTA      TCATTTT
                                |||||||||      |||||||
                                AGACCCGAT      AGTAAAA
                                     AAATCTC
GAM1225  KLHL3    3'  TCTCGGCTGCTTCTAACC    44647     G   ACCTCA
                                TCT GGCT     TTTTGACC
                                ||| ||||     ||||||||
                                AGA CCGA     AAGATTGG
                                  G   CG____
GAM1225  L1CAM    3'  TCTGGGCTCTCCAGATGGCC   35806         AC   ATTT  A
                                TCTGGGCT  CTC    TG CC
                                ||||||||  |||    || ||
                                AGACCCGA  GAG    AC GG
                                     __   GTCT  C
GAM1225  LNK      3'  TCTGGGCTTCCTGATGATCCC  24207         A   CATTT  _
                                TCTGGGCT CCT    TGA CCC
                                |||||||| |||    ||| |||
                                AGACCCGA GGA    ACT GGG
                                     A   CT___   A
GAM1225  LZTR1    3'  TCTGGGCACCCTGACC      27643         T   CATTT
                                TCTGGGC ACCT    TGACC
                                ||||||| ||||    |||||
                                AGACCCG TGGG    ACTGG
                                   _   _____
GAM1225  MLLT2    3'  TCTGGACTGTTTTTGA      25511         ACCTCA
                                TCTGGGCT     TTTTGA
                                ||||||||     ||||||
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                                AGACCTGA     AAAACT
                                    CA____
GAM1225 NINJ1    3'  TCTGGGCTATTGTGCCAGCCCC 19985        CCTCATT  GA
                                TCTGGGCTA     TT  CCCC
                                |||||||||      ||  ||||
                                AGACCCGAT     GG  GGGG
                                    AACAC__  TC
GAM1225 PPP1R8   3'  TGGGCTATTTCAACCC      39735       CCTCA   TG
                                TGGGCTA    TTT  ACCC
                                |||||||    |||  ||||
                                ACCCGAT    AAA  TGGG
                                    _____  GT
GAM1225 SCA7     3'  CTGGGCTATTTTGTCATGGTG  7306        CC___   TT
                                CTGGGCTA    TCAT  TG
                                ||||||||    ||||  ||
                                GACCCGAT    AGTA  AC
                                    AAAAC   CC
GAM1225 TNC      3'  TCTGGGCCGCCTTATTCC    13472       TA   C
                                TCTGGGC  CCT ATTTT
                                |||||||  ||| |||||
                                AGACCCG  GGA TAAGG
                                    GC   A
GAM1225 TRIM34   5'  TCTGGGCTCAACTTGACC    38977       TACC   T
                                TCTGGGC    TCA TTTGACC
                                |||||||    ||| |||||||
                                AGACCCG    AGT GAACTGG
                                    _____   T
GAM1225 VENTX2   3'  TCTGGGCACTTCCAGACC    30925       T  C  ATTTT
                                TCTGGGC AC TC    GACC
                                ||||||| || ||    ||||
                                AGACCCG TG AG    CTGG
                                    _  A  GT___
GAM1226 ARNT2    3'  GGACAGGGCCACACATTTTGG  31360       AA   GC
                                GGACAGG  TCG  CATTTTGG
                                |||||||  |||  ||||||||
                                CCTGTCC  GGT  GTAAAACC
                                    C_   GT
GAM1226 TNNC1    3'  GGAGGGAGTCGGGGGATTTGG  17618     CA   A   CCAT
                                GGA  GGA TCGG    TTTGG
                                |||  ||| ||||    |||||
                                CCT  CCT AGCC    AAACC
                                  C_   C    CCCT
GAM1227 GABRA2   3'  TCAAAGGATTCATCTAGGAAT  9043        G   C___
                                TCAAAGGA TTCA    GGAAT
                                |||||||| ||||    |||||
                                AGTTTCCT AAGT    CCTTA
                                    _    AGAT
GAM1227 PRPSAP2  3'  TCAAAAGAGGAGAATAAA    15738        TTCAC
                                TCAAAGGAG    GGAATAAA
                                |||||||||    ||||||||
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                                AGTTTTCTC    TCTTATTT
                                     C____
GAM1227 SIM2    3' TCACAAGGAGCTGTGAAT    28926    _      CACG
                                TCA AAGGAGTT   GAAT
                                ||| ||||||||   ||||
                                AGT TTCCTCGA   CTTA
                                  G       CA__
GAM1227 TRPS1   3' AAAGAAGTATGGAATAA     30451        TCAC
                                AAAGGAGT   GGAATAA
                                ||||||||   |||||||
                                TTTCTTCA   CCTTATT
                                     TA__
GAM1228 ADCY2   3' AACATTCTTGGAGACAGGA   42137          A  T
                                AACATTCTTGGA GAC AGGG
                                |||||||||||| ||| ||||
                                TTGTAAGAACCT CTG TCCT
                                      _  _
GAM1228 BCAT1   3' CAACATTTTTGGCACCAGGGA 42375       C   AAG
                                CAACATT TTGG  ACTAGGGA
                                ||||||| ||||  ||||||||
                                GTTGTAA AACC  TGGTCCCT
                                    A   G__
GAM1228 CA3     5' CATTCTTGGGGATGGG     23209        AA  CTA
                                CATTCTTGG  GA  GGG
                                |||||||||  ||  |||
                                GTAAGAACC  CT  CCC
                                     C_  A__
GAM1228 CEP2    3' ACGACATTCTTGAGGGCAAGG 28429    A       GA  AC
                                AC ACATTCTTG  AG  TAGGG
                                || |||||||||  ||  |||||
                                TG TGTAAGAAC  TC  GTTCC
                                 C        __  CC
GAM1228 CPNE3   3' ACATATATAGAGACTAGGG   19380     TCT   A
                                ACAT   TGGA GACTAGGG
                                ||||   |||| ||||||||
                                TGTA   ATCT CTGATCCC
                                  TAT   _
GAM1228 CXCR6   3' CAGCATTCTTGGAGATGGA   27293    A       A  CTA
                                CA CATTCTTGGA GA   GGG
                                || ||||||||| ||   |||
                                GT GTAAGAACCT CT   CCT
                                 C        _  A__
GAM1228 DNLC2A  3' AACATTCTTGGGGGG       30505         AAGACTA
                                AACATTCTTGG      GGG
                                ||||||||||       |||
                                TTGTAAGAACC      CCC
                                      _______
GAM1228 LGMN    3' TTCAGAAAAGACTGGGGA    24688    TT      A
                                TTC  GGAAGACT GGGA
                                |||  |||||||| ||||
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                                AAG  TTTTCTGA CCCT
                                  TC       C
GAM1228  RTN3     3'  CATTCTTGGAATCAGGA     43958          GACTA
                                CATTCTTGGAA    GGGA
                                ||||||||||    ||||
                                GTAAGAACCTT    TCCT
                                      AG___
GAM1228  SLC3A2   5'  CAGCATTCTTGGAAGCTAAGG  14398    A          A
                                CA CATTCTTGGAAG CTAGGG
                                || |||||||||||| ||||||
                                GT GTAAGAACCTTC GATTCC
                                 C          _
GAM1228  VANGL2   3'  TCTGGGAAAAGACTAGGGA   43463    T   __
                                TCT GGA  AGACTAGGGA
                                ||| |||  ||||||||||
                                AGA CCT  TCTGATCCCT
                                  C   TT
GAM1228  VEGF     3'  ACATTCTTGGGCAGGG      17937          AAGAC
                                ACATTCTTGG    TAGGG
                                ||||||||||    |||||
                                TGTAAGAACC    GTCCC
                                      C_____
GAM1229  CTSK     5'  TGATGGAAATCTGTTGTCTGG  7579         CTA  CCAC
                                TGATGGGG   TG    CTGG
                                ||||||||   ||    ||||
                                ACTACCTT   AC    GACC
                                     TAG  AACA
GAM1229  FANCE    3'  TTGATGAGGAGTGTGCCTGG   34899         CTA  CCA
                                TTGATGGGG   TG   CCTGG
                                |||||||||   ||   |||||
                                AACTACTCC   AC   GGACC
                                     TC_  AC_
GAM1229  GCK      3'  TGATGGGGTTGTCCCTTGG    37932         CTA  _  ACC
                                TGATGGGG   TG CC   TGG
                                ||||||||   || ||   |||
                                ACTACCCC   AC GG   ACC
                                     A__  A  GA_
GAM1229  ITGA11   3'  TCGGTGGGGCCACAGGCCTGG  29204     A         CCA
                                TTG TGGGGCTATG   CCTGG
                                ||| ||||||||||   |||||
                                AGC ACCCCGGTGT   GGACC
                                  C         CC_
GAM1229  MGAT5    5'  TGGTGGGGCTGTTCCAGCCTGG 14481    A      ATG  _
                                TG TGGGGCT   CCA CCTGG
                                || |||||||   ||| |||||
                                AC ACCCCGA   GGT GGACC
                                 C      CAA  C
GAM1229  NR5A2    3'  TTGGTGGAGCTACCACTGG    19239     A      AT    C
                                TTG TGGGGCT  GCCAC TGG
                                ||| |||||||  ||||| |||
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                                AAC ACCTCGA  TGGTG ACC
                                  C      __    _
GAM1229  PPP3CB   3'  GATGGTTCCGCTGCCTGG    34449      GG  AT  CA
                                GATGG  CT  GC  CCTGG
                                |||||  ||  ||  |||||
                                CTACC  GG  CG  GGACC
                                   AA  __  AC
GAM1229  SALL2    3'  CTGGTGGGGCCAGGCTTGG   41896     A       T  CACC
                                TTG TGGGGCTA GC    TGG
                                ||| ||||||| ||    |||
                                GAC ACCCCGGT CG    ACC
                                  C       C  A___
GAM1229  SLC12A7  3'  TTGATGGGGTTGATTCCCTTGG 27335         CTATG_  ACC
                                TTGATGGGG     CC   TGG
                                |||||||||     ||   |||
                                AACTACCCC     GG   ACC
                                     AACTAA  GA_
GAM1229  SON      3'  TTAATGGGGTTGTTTTGACACT 39891         CTA___  C   C
            TGG                   TTGATGGGG     TG CAC TGG
                                |||||||||     || ||| |||
                                AATTACCCC     AC GTG ACC
                                     AACAAA  T   A
GAM1230  SCN1A    3'  TATGTTATCCACTTAAAATGTA 44816       _      AATT
                                TATGT ATCCACT    GATGTA
                                ||||| |||||||    ||||||
                                ATACA TAGGTGA    TTACAT
                                   A      ATT_
GAM1231  BMPR1A   3'  TTGGCGAATCTTGGTCAGATAT 20256      TA    CCA  T
            T                   TTGG  AATC   GT CGGGTATT
                                ||||  ||||   || ||||||||
                                AACC  TTAG   CA GTCTATAA
                                  GC    AAC  _
GAM1232  ACATN    3'  TACTCCTGTGCACTGA      21841      AGTGGG
                                TGCT     TGTGCACTGA
                                ||||     ||||||||||
                                ATGA     ACACGTGACT
                                  GG_____
GAM1232  CYBA     3'  TATTGCAGGTGGGTGCACCTG  40780       TA      TG A
                                TATTGC  GTGGGTG  C CTG
                                ||||||  |||||||  | |||
                                ATAACG  CACCCAC  G GAC
                                    TC      GT _
GAM1232  F7       3'  TGCATCCGTGTGCACTGA    33345     TAGTGG
                                TGC     GTGTGCACTGA
                                |||     ||||||||||
                                ACG     CACACGTGACT
                                  TAGG__
GAM1232  FGFR2    3'  TGCTCTGTAAGTGTGTGCTGAC 35671      A_       CA
                                TGCT  GTGGGTGTG  CTGAC
                                ||||  |||||||||  |||||
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                                ACGA  CATTCACAC  GACTG
                                  GA        AC
GAM1232  SCG3     3'  TATTGCTAGCTACAGAGCGCTG 29891          GGGTGT  A
              A                    TATTGCTAGT      GC CTGA
                                   ||||||||||      || ||||
                                   ATAACGATCG      CG GACT
                                         ATGTCT  C
GAM1233  AMPD3    3'  TCCTAGTTCGGAATCTTG    7902      C      G
                                   TCC AGTTCGG AATTTTG
                                   ||| ||||||| |||||||
                                   AGG TCAAGCC TTAGAAC
                                     A      _
GAM1234  ADSL     3'  AGGAAAGCACCATGGGAAGAA  6182        A   AAGAATA
                                   GGGAAA CAT      GGAAGAA
                                   |||||| |||      |||||||
                                   TCCTTT GTG      CCTTCTT
                                      C   GTAC___
GAM1234  ATP6V1G2 3'  GGGAAATAGGAAAGGAGGAA   39628      AAC   A   T    A
                                   GGGAA   ATA GAA AGGA GAA
                                   |||||   ||| ||| |||| |||
                                   CCCTT   TAT CTT TCCT CTT
                                      ___  C   _    C
GAM1234  BLTR2    5'  GGGTAAGACAAGAATGGGGAG  33370     AAAAC       A  A
                                   GGG     ATAAGAAT GG AG
                                   |||     |||||||| || ||
                                   CCC     TGTTCTTA CC TC
                                     ATTC_       C  C
GAM1234  BMP6     3'  GGGAGGAGGGTAGGAAGA    11867      AAACATA  AA
                                   GGGA      AG  TAGGAAGA
                                   ||||      ||  ||||||||
                                   CCCT      TC  ATCCTTCT
                                     CC_____  CC
GAM1234  CARD4    3'  GGGAAAGTGCTGAGAAGGAAGA 25892       ACATAA  AT
              A                    GGGAAA     GA  AGGAAGAA
                                   ||||||     ||  ||||||||
                                   CCCTTT     CT  TCCTTCTT
                                      CACGA_  CT
GAM1234  CARKL    3'  GGGAAAACTTGGGAACTGTTTG 30000        ATAA    AG___
              AAGAA                  GGGAAAAC    GAAT     GAAGAA
                                   ||||||||    ||||     ||||||
                                   CCCTTTTG    CTTG     CTTCTT
                                        AACC    ACAAA
GAM1234  CD3G     3'  GGGAACTGAATAGGAGGA     6316       AACATAA       A
                                   GGGAA      GAATAGGA GA
                                   |||||      |||||||| ||
                                   CCCTT      CTTATCCT CT
                                      GA_____       C
GAM1234  CD83     3'  GGAAAACATGAGAAATGGA    20140         A   TA
                                   GGAAAACAT AGAA  GGA
                                   |||||||| ||||  |||
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                                CCTTTTGTA TCTT  CCT
                                     C    TA
GAM1234  EIF1A    3'  GGGAATAAGAGAGGA       44809      AAAC     AT
                                GGGA    ATAAGA  AGGA
                                ||||    ||||||  ||||
                                CCCT    TATTCT  TCCT
                                  _____     C_
GAM1234  GNB3     3'  GAGAAAGCATGAATAAGAAGA  13219        A   AA
                                GGGAAA CAT  GAATAGGAAGA
                                |||||| |||  ||||||||||
                                CTCTTT GTA  CTTATTCTTCT
                                   C   __
GAM1234  GRINL1A  3'  GGGAAGACAGAAAAAGGAGAA  43001       A  T   AT   A
                                GGGAA ACA AAGA  AGGA GAA
                                ||||| ||| ||||  |||| |||
                                CCCTT TGT TTTT  TCCT CTT
                                   C  C   __   _
GAM1234  IRF2     3'  GGGATGGGATGGGATAGGAAGA 13587      AAACATAA  A
                                GGGA       GA TAGGAAGA
                                ||||       || ||||||||
                                CCCT       CT ATCCTTCT
                                  ACCCTACC  _
GAM1234  KLHL3    3'  GGGAAAGCACAAGAAAAAGAA  44643        A       T
                                GGGAAA CATAAGAA AGGAA
                                |||||| |||||||| |||||
                                CCCTTT GTGTTCTT TTCTT
                                   C       T
GAM1234  LCP1     3'  GGGAGGCAGGGTAGGAAGA   14108      AAACATA  AA
                                GGGA      AG  TAGGAAGA
                                ||||      ||  ||||||||
                                CCCT      TC  ATCCTTCT
                                  CCG_____  CC
GAM1234  LIPE     5'  GGGAGGATTAGGAATAGGA   23813      AAACA  A
                                GGGA    TA GAATAGGA
                                ||||    || ||||||||
                                CCCT    AT CTTATCCT
                                  CCTA_  C
GAM1234  LOH11CR2A 5'  GGAAAGCATGCCTCATAGGAAG 31190       A   AAGA_
            A                    GGAAA CAT    ATAGGAAGA
                                |||||| |||    |||||||||
                                CCTTT GTA    TATCCTTCT
                                   C   CGGAG
GAM1234  MAML1    3'  GGGAGACATAATACTCCAGGA  31291      AA     GAA__
                                GGGA  ACATAA    TAGGA
                                ||||  ||||||    |||||
                                CCCT  TGTATT    GTCCT
                                  C_     ATGAG
GAM1234  MID1     3'  GGGAGCGGGAAATAGGAGAA   37785      AAACATAA       A
                                GGGA       GAATAGGA GAA
                                ||||       |||||||| |||
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                                CCCT       TTTATCCT CTT
                                  CGCCC___       _
GAM1234  MN1      3'  GGGAGGGGGTAAGAAAAGGA   14586      AAACA     T
                                GGGA     TAAGAA AGGA
                                ||||     |||||| ||||
                                CCCT     ATTCTT TCCT
                                  CCCCC      T
GAM1234  NR4A1    3'  GGAAGGAGGGTAGGAAGA    13417      AACATA  AA
                                GGAA     AG  TAGGAAGA
                                ||||     ||  ||||||||
                                CCTT     TC  ATCCTTCT
                                  CC____  CC
GAM1234  PAX4     3'  GGGAAAACATGATGGACAACAG 26199          AAG____
              AA                  GGGAAAACAT      AATAGGA
                                ||||||||||      |||||||
                                CCCTTTTGTA      TTGTCTT
                                      CTACCTG
GAM1234  PIM1     3'  GGAAGCTTGGAATAGGAAG    44969      AACATAA
                                GGAA      GAATAGGAAG
                                ||||      ||||||||||
                                CCTT      CTTATCCTTC
                                  CGAAC__
GAM1234  PKD2L1   5'  GGGAGAGGGGAGAATAGGAGGA 32020      AAACATA       A
                                GGGA      AGAATAGGA GA
                                ||||      ||||||||| ||
                                CCCT      TCTTATCCT CT
                                  CTCCCC_       C
GAM1234  PLA2G2D  3'  GGGAAAACAGGGGAAACAGA   29635        TAA_
                                GGGAAAACA    GAATAGG
                                |||||||||    |||||||
                                CCCTTTTGT    TTTGTCT
                                      CCCC
GAM1234  POLE2    5'  GGGAAAACAGACGGAG      15441        TAA  ATA   A
                                GGGAAAACA   GA   GGA G
                                |||||||||   ||   ||| |
                                CCCTTTTGT   CT   CCT C
                                      ___  G__   _
GAM1234  PPT1     3'  GAGAATGGAATAGGAAGA    41551      AACATAA
                                GGGAA      GAATAGGAAGA
                                |||||      ||||||||||
                                CTCTT      CTTATCCTTCT
                                  AC_____
GAM1234  PRX      3'  GGGAAAACTAAGGCGG      34130        A    AATA
                                GGGAAAAC TAAG    GG
                                |||||||| ||||    ||
                                CCCTTTTG ATTC    CC
                                      _   CG__
GAM1234  PXN      3'  GGGAGGAATAAGGATAAAAAGA 16028      AAAC    A
                                GGGA    ATAAG ATAGGAAGA
                                ||||    ||||| |||||||||
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                                CCCT   TATTC TATTTTTCT
                                  CCT_    C
GAM1234 RNH     3' GGGAGAGCAGCAGCAGGAAGA 40607     AAA  TA  AA
                                GGGA   CA  AG  TAGGAAGA
                                ||||   ||  ||  ||||||||
                                CCCT   GT  TC  GTCCTTCT
                                  CTC  CG  __
GAM1234 RPS6KA1  3' GGGAAAACTAAGGCTCAGG   40383       A   AA_
                                GGGAAAAC TAAG   TAGG
                                |||||||| ||||   ||||
                                CCCTTTTG ATTC   GTCC
                                     _   CGA
GAM1234 SEPN1    3' GGGAAAACAGGCAGGGAGA   42431       TAAGAA   A
                                GGGAAAACA     TAGG AGA
                                |||||||||     |||| |||
                                CCCTTTTGT     GTCC TCT
                                     CC_____   C
GAM1234 SGK     3' GGGAAAATAAAGAACTGAA   24742       CAT     A
                                GGGAAAA   AAGAAT GGA
                                |||||||   |||||| |||
                                CCCTTTT   TTCTTG CTT
                                    AT_     A
GAM1234 SLC1A4   3' GGGAAAACAAGGGAGTGAAGGA 16752        TAA  AT__
                                GGGAAAACA   GA    AGGA
                                |||||||||   ||    ||||
                                CCCTTTTGT   CT    TCCT
                                     TCC  CACT
GAM1234 SLC2A8   3' GGGAGCATGACAGGAAG     31031     AAA   AA  A
                                GGGA   CAT  GA TAGGAAG
                                ||||   |||  || |||||||
                                CCCT   GTA  CT GTCCTTC
                                  C__   __  _
GAM1234 SLC39A1  3' GGGTAGGCGCTAAGAAGAGTAG 30889     AAAACA_    ___
            GA                    GGG      TAAGAA   TAGGA
                                |||      ||||||   |||||
                                CCC      ATTCTT   ATCCT
                                  ATCCGCG     CTC
GAM1234 STK10    3' GGGAGAACAGGAGGA      25622      AAACATAA       A
                                GGGA       GAATAGGA GA
                                ||||       |||||||| ||
                                CCCT       CTTGTCCT CT
                                  _________       C
GAM1234 VANGL2   3' GGGAGGGGAATGGGAAGA    43461      AAACATAA    A
                                GGGA       GAAT GGAAGA
                                ||||       |||| ||||||
                                CCCT       CTTA CCTTCT
                                  CCC_____    C
GAM1234 WBSCR1   3' GGGAAAACAAGGAGCAGGAGAA 35270         TAA  A    A
                                GGGAAAACA   GA TAGGA GAA
                                |||||||||   || ||||| |||
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                                CCCTTTTGT   CT GTCCT CTT
                                     TC_  C    _
GAM1234  ZNF45    5'  GAGAAAACATGAGGGAAG    18294          A  AATA
                                GGGAAAACAT AG    GGAAG
                                |||||||||| ||    |||||
                                CTCTTTTGTA TC    CCTTC
                                     C  ____
GAM1235  EP300    5'  GAGAACTCGCGGCTCTAGAGG  10984         G T    CC
                                GAGAACTCG C GCTC  AGAGG
                                ||||||||| | ||||  |||||
                                CTCTTGAGC G CGAG  TCTCC
                                     _ C    A_
GAM1235  HMOX1    3'  TGAAACTCAGGGCTTTTGGAGG 13412       A    CT   CCCA
                                TGAGA CTCGG  GCT    GAGG
                                ||||| |||||  |||    ||||
                                ACTTT GAGTC  CGA    CTCC
                                   _    C_   AAAC
GAM1235  P3       3'  GAAAGCTTGACCCAGAG     33378     CTC    GCT
                                GAA   GGCT   CCCAGAG
                                |||   ||||   |||||||
                                CTT   TCGA   GGGTCTC
                                  ___    ACT
GAM1235  RXRA     3'  GGCTGTCCTTCCCAGAGG     16433       _ __
                                GGCTG C  TCCCAGAGG
                                ||||| |  |||||||||
                                CCGAC G  AGGGTCTCC
                                   A GA
GAM1235  SLC2A6   3'  AGCTGCCTGTTCCCAGAGG   32765       ____
                                GGCTGC    TCCCAGAGG
                                ||||||    |||||||||
                                TCGACG    AGGGTCTCC
                                   GACA
GAM1235  TNFSF15  3'  GAACTCGGTGGCAGAG      23052         C  CTCC
                                GAACTCGG TG    CAGAG
                                |||||||| ||    |||||
                                CTTGAGCC AC    GTCTC
                                     _  C___
GAM1235  TPR      5'  TGGGAACCCGAGCTCAGAG    17656    A       CT    CC
                                TG GAACTCGG  GCTC  AGAG
                                || ||||||||  ||||  ||||
                                AC CTTGGGCT  CGAG  TCTC
                                 C       __   __
GAM1235  VAT1     3'  TGGGAACTGGTCAAGCCCAGAG 26855    A     C  CT CT
              G                   TG GAACT GG  G  CCCAGAGG
                                || ||||| ||  |  ||||||||
                                AC CTTGA CC  T  GGGTCTCC
                                 C    _  AG TC
GAM1236  CD69     3'  TACACGATCATCCCA       12138          TAAATT
                                TACACGATC     ATCCCA
                                |||||||||     ||||||
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                                ATGTGCTAG     TAGGGT
                                          _______
GAM1236  MOCS2    3'  CACATTTAAATTATTCCAT   21204      ATC       C
                                CACG   TAAATTAT CCAT
                                ||||   |||||||| ||||
                                GTGT   ATTTAATA GGTA
                                  AA_       A
GAM1237  FANCF    3'  CAAGATGGCCTTCATGGATTA  35533      TAAAC  C
                                CAAG    CC TCATGGATTA
                                ||||    || ||||||||||
                                GTTC    GG AGTACCTAAT
                                  TACC_  A
GAM1237  CLTA     3'  TGAGGCTACTCTTGGGAAGCTT 12298      T    GTG
                                TGAG CTGCT   TTGGGAAGCTT
                                |||| |||||   ||||||||||
                                ACTC GATGA   AACCCTTCGAA
                                  C    G__
GAM1237  UC28     3'  GAGTCTTACACTTGGGAAG    34688       _  TGTG
                                GAGTCT GC    TTGGGAAG
                                |||||| ||    ||||||||
                                CTCAGA TG    AACCCTTC
                                   A  TG__
GAM1238  SYT4     3'  TGGCTAATCAGACAAACAATTA 41662    A     T    TGT
                                TG CTAATC AGATA   TAATTA
                                || |||||| |||||   ||||||
                                AC GATTAG TCTGT   GTTAAT
                                 C     _    TT_
GAM1239  BMPR1B   5'  CAGGCTTGTAAGTTTAACTTTT 10201     AAA__
           T                     CAG    TAAGTTTAACTTTTT
                                |||    ||||||||||||||
                                GTC    ATTCAAATTGAAAAA
                                  CGAAC
GAM1239  GPR85    3'  AAACAAAAATAATAACTTTTT  33253          GTT
                                AAACAGAAATAA   TAACTTTTT
                                ||||||||||||   |||||||||
                                TTTGTTTTTATT   ATTGAAAAA
                                          ____
GAM1239  ZNF265   3'  ACAACATAGTTTAACTTTT    24147      AAATA
                                ACAG    AGTTTAACTTTT
                                ||||    ||||||||||||
                                TGTT    TCAAATTGAAAA
                                  GTA__
GAM1240  EML1     3'  AGTTCATAGAAAAGTTACT    40720     C    TC
                                AGT CATA  GGAGTTACT
                                ||| ||||  |||||||||
                                TCA GTAT  TTTCAATGA
                                  A   CT
GAM1240  SRD5A2   3'  AGTCCATATCTCAGCACT     40456         GG   T
                                AGTCCATATC  AGT ACT
                                ||||||||||  ||| |||
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                                TCAGGTATAG  TCG TGA
                                     AG  _
GAM1241  SLC22A11  3'  CTGGCAGCTCTCTCAGC     32962      CCAG   C
                                TTGGT    AGC CTCTCAGC
                                |||||    ||| ||||||||
                                GACCG    TCG GAGAGTCG
                                   _____  A
GAM1242  SEL1L     3'  TTGGGATCGTTTTAAATTTTCT 22855     AA      TT
              TG                  TTG  ATTGTTTT  ATTTTCTTG
                                |||  ||||||||  |||||||||
                                AAC  TAGCAAAA  TAAAAGAAC
                                  CC       TT
GAM1243  ADH4      3'  CAAAACGTGGAGAGAAAAGTAT 8572        AACT
              AA                  TAAAAC    AGAGAAAAGTATAA
                                ||||||    ||||||||||||||
                                GTTTTG    TCTCTTTTCATATT
                                   CACC
GAM1243  BLTR2     5'  AACCTCTGAGAAAAGTATA    33360     AA  A
                                AAC  CT GAGAAAAGTATA
                                |||  || ||||||||||||
                                TTG  GA CTCTTTTCATAT
                                  GA  _
GAM1243  CSNK2A1   3'  TGAACTAAAAATAAAAGTATAA 12481    C       __
                                A AACTAGAGA  AAAGTATAA
                                | |||||||||  |||||||||
                                A TTGATTTTT  TTTCATATT
                                 C        AT
GAM1244  ACHE      3'  TGAGGAGGAAGGGAGCACTAGG 8566          AA    AA_
                                TGAGGAGGAG  GGAG   TGGG
                                ||||||||||  ||||   ||||
                                ACTCCTCCTT  CCTC   ATCC
                                      C_    GTG
GAM1244  ALMS1     5'  GGAGGAGGAGGAGGGGG     31532        A     AAT
                                GGAGGAG AGGAG   GGG
                                |||||||  |||||   |||
                                CCTCCTC TCCTC   CCC
                                    C     C__
GAM1244  ALMS1     5'  GAGGAGGAGGGGGGGAGGGA   31531         AA  A  ATG
                                GAGGAGGAG  GG GA   GGGA
                                |||||||||  || ||   ||||
                                CTCCTCCTC  CC CT   CCCT
                                     CC  C  ___
GAM1244  ALMS1     5'  GAGGAGGAGGAGGAGGGGG   31530         A     AAT
                                GAGGAGGAG AGGAG   GGGG
                                |||||||||  |||||   ||||
                                CTCCTCCTC TCCTC   CCCC
                                     C     ___
GAM1244  AMFR      3'  GAGGGGAGGGGACCCATGGGG  39936      A    AA   GA_
                                GAGG GGAG  GGA   ATGGGG
                                ||||  ||||  |||   ||||||
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```
                                CTCC CCTC  CCT   TACCCC
                                  _   C_  GGG
GAM1244 AR      5'  GAGGGGGGGAAGGCAGGGTGGG 6232      A  A    _  AA
             G                   GAGG GG GAAGG AG  TGGGG
                                 |||| || ||||| ||  |||||
                                 CTCC CC CTTCC TC  ACCCC
                                   C  C    G  CC
GAM1244 ARD1    3'  TGAGGAGGGGATGGGG     18576        AGAA  GAA
                                 TGAGGAGG   GGA  TGGGG
                                 ||||||||   |||  |||||
                                 ACTCCTCC   CCT  ACCCC
                                      _____  ___
GAM1244 ATP2B4   5'  GAGGAGGAAGAGGATGGGG   43198       GA   GAA
                                 GAGGAGGA  AGGA  TGGGG
                                 ||||||||  ||||  |||||
                                 CTCCTCCT  TCCT  ACCCC
                                      TC   ___
GAM1244 AXL     5'  TGAGGAGGGGGAAGGGGA    34890       AGAA  A   T
                                 TGAGGAGG   GG GAA GGGGA
                                 ||||||||   || ||| |||||
                                 ACTCCTCC   CC CTT CCCCT
                                      _____ _  _
GAM1244 BAK1    3'  GAGGAGCATGGAGGGTGGGG  45108      AA_   AA
                                 GAGGAG  GGAG  TGGGG
                                 ||||||  ||||  |||||
                                 CTCCTC  CCTC  ACCCC
                                    GTA   CC
GAM1244 BCAS1   3'  TGGGGAGGAGATGGAGTAAGGA 18926   A      A   AA
                                 TG GGAGGAGA GGAG  TGGGGA
                                 || ||||||| ||||  ||||||
                                 AC CCTCCTCT CCTC  ATTCCT
                                  C      A   __
GAM1244 BTG2    3'  TGGGGAGGAGAACCTGGGG   27624   A      GGAGAA
                                 TG GGAGGAGAA     TGGGG
                                 || |||||||||     |||||
                                 AC CCTCCTCTT     ACCCC
                                  C       GG____
GAM1244 C1orf6   5'  GAGGAGGAGGAGGGGCGGG   33528       A  AGAA
                                 GAGGAGGAG AGG   TGGG
                                 |||||||| |||   ||||
                                 CTCCTCCTC TCC   GCCC
                                      C  CC__
GAM1244 CACNA1D  5'  TGAGGCGGGGGCGGAATGGGGA 8768      A  AGAA  A_
                                 TGAGG GG   GG  GAATGGGGA
                                 ||||| ||   ||  |||||||||
                                 ACTCC CC   CC  CTTACCCCT
                                    G  C___  GC
GAM1244 CACNG7   3'  GAGGAGGAGGAGGAGGCAGGGG 36688       A    AAT
                                 GAGGAGGAG AGGAG   GGGG
                                 |||||||| |||||   ||||
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                                CTCCTCCTC TCCTC   CCCC
                                      C    CGT
GAM1244  CALU    3'  GAGGAGGAGGAATGGGG     10257         AAGGA
                                GAGGAGGAG    GAATGGGG
                                |||||||||    ||||||||
                                CTCCTCCTC    CTTACCCC
                                      _____
GAM1244  CAPN1   3'  TGGGAGGAGAGGGGACAGGA  23257    A      A  A  A
                                TG GGAGGAGA GG GA TGGGG
                                || |||||||| || || |||||
                                AC CCTCCTCT CC CT GTCCT
                                 _      C  _ _
GAM1244  CD34    3'  GGGGAGGGGGAGGTGGGA    12120    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  ACCCT
                                 _   CC   C_
GAM1244  CDK4    3'  TGGGAAGGAGAAGGAGAA    38143    A
                                TG GGAGGAGAAGGAGAA
                                || ||||||||||||||
                                AC CTTCCTCTTCCTCTT
                                 C
GAM1244  CDS1    5'  GAGGAGGAGAAGGGGCGGGGA  10398           AGAA
                                GAGGAGGAGAAGG   TGGGGA
                                ||||||||||||   ||||||
                                CTCCTCCTCTTCC   GCCCCT
                                      CC__
GAM1244  CELSR2  3'  TGAGGGGAGAAGACAGGGG   10857      A      AGAAT
                                TGAGG GGAGAAGG    GGGG
                                ||||| ||||||||    ||||
                                ACTCC CCTCTTCT    CCCC
                                   _      GT___
GAM1244  CELSR2  3'  GAGGAGAGGGGAGGAGAGGTGG 10849       ____     A_
            GGA                  GAGGAGA   AGGAGA  TGGGGA
                                |||||||   ||||||  ||||||
                                CTCCTCT   TCCTCT  ACCCCT
                                    CCCC    CC
GAM1244  CHAD    3'  AGAGGAGCTGGAGGGTGGGGA  10411       AA   AA
                                GGAGGAG  GGAG  TGGGGA
                                |||||||  ||||  ||||||
                                TCTCCTC  CCTC  ACCCCT
                                    GA   CC
GAM1244  CKTSF1B1 3'  TGAGGAGGAGGAGGAAAGGA  30092         A    AATG
                                TGAGGAGGAG AGGAG   GGGA
                                |||||||||| |||||   ||||
                                ACTCCTCCTC TCCTT   TCCT
                                      C   _____
GAM1244  CLTC    5'  GAGGAGGAGAAGGGGAGGGG  22151           A  AT
                                GAGGAGGAGAAGG GA  GGGG
                                |||||||||||| ||  ||||
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                                CTCCTCCTCTTCC CT  CCCC
                                      C  __
GAM1244  COL5A3   3'  TGAGGAGGCAGGCATTGGGG  31857        AGA  AGAA
                                TGAGGAGG  AGG   TGGGG
                                ||||||||  |||   |||||
                                ACTCCTCC  TCC   ACCCC
                                    G__  GTA_
GAM1244  CRY2     3'  TGAGGAGGGAGGGAAGGA   43588        A  A  A  T
                                TGAGGAGG GA GG GAA GGG
                                |||||||| || || ||| |||
                                ACTCCTCC CT CC CTT CCT
                                      _ _ _  _
GAM1244  CSF3R    3'  TGGGAGGAGAGGGAGATGCTGG 8910     A       A    A  G_
                                TG GGAGGAGA GGAGA TG  GG
                                || |||||||| ||||| ||  ||
                                AC CCTCCTCT CCTCT AC  CC
                                 _       C    _ GA
GAM1244  CX3CR1   3'  TGGGAAGGAGGAGGCAATGGGG 43301    A      A   AG
              A                  TG GGAGGAG AGG  AATGGGGA
                                || ||||||| |||  ||||||||
                                AC CTTCCTC TCC  TTACCCCT
                                 C      C   G_
GAM1244  DDX3     5'  GGAGGAGAGGGAGGG       35822         A   GAATG
                                GGAGGAGA GGA    GGG
                                |||||||| |||    |||
                                CCTCCTCT CCT    CCC
                                    C  ______
GAM1244  DMPK     3'  TGAGGAGGGGGGCGCGGGA   20625        AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   GCCCT
                                    CC__  GC__
GAM1244  DNM2     3'  GAGGAGGAGGAGGAGAGGA   22382         A     AT
                                GAGGAGGAG AGGAGA  GGG
                                ||||||||| ||||||  |||
                                CTCCTCCTC TCCTCT  CCT
                                     C     __
GAM1244  ESRRA    3'  GGAGGAGAGGGCGTGGGG    20833         A  AGAA
                                GGAGGAGA GG   TGGGG
                                |||||||| ||   |||||
                                CCTCCTCT CC   ACCCC
                                    C  GC__
GAM1244  FGFRL1   3'  AGGGGGAGAATGCAGTGGGGA  34900     A     GGAGAA
                                AGG GGAGAA     TGGGGA
                                ||| ||||||     ||||||
                                TCC CCTCTT     ACCCCT
                                  C     ACGTC_
GAM1244  FKBP10   3'  AGGGGCTGGGAGTGGGG     34956     A  AGAA   AA
                                AGG GG   GGAG  TGGGG
                                ||| ||   ||||  |||||
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                                TCC CC   CCTC  ACCCC
                                  _ GAC_   __
GAM1244  FOXD1    5'  TGAGGAGGGGGTGGCGGGG   20933        AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   GCCCC
                                     CCCA  ____
GAM1244  FOXF2    3'  TGAGGAGGGGAGAGGAGA    11130        A  _
                                TGAGGAGG GA AGGAGA
                                |||||||| || ||||||
                                ACTCCTCC CT TCCTCT
                                     C  C
GAM1244  GAB2     3'  TGGGAGCTGAAAGGGGAATGGG 38687    A   GA_    A
              G                  TG GGAG   GAAGG GAATGGGG
                                || ||||   ||||| ||||||||
                                AC CCTC   TTTCC CTTACCCC
                                 _   GAC    C
GAM1244  GPR86    3'  TGAGGAGGGTGGGGCAGGGG   35797        AGAA  AGAAT
                                TGAGGAGG   GG    GGGG
                                ||||||||   ||    ||||
                                ACTCCTCC   CC    CCCC
                                     CACC  GT___
GAM1244  GRB14    5'  GGGGAGAGGGGAGGAG     21048    A    A  A  AT
                                GG GGAGA GG GA  GGGG
                                || ||||| || ||  ||||
                                CC CCTCT CC CT  CCTC
                                 _    C  _  __
GAM1244  GRB14    5'  GAGGAGGAGGGTGGG      21035         AA  AGAA
                                GAGGAGGAG  GG   TGGG
                                |||||||||  ||   ||||
                                CTCCTCCTC  CC   ACCC
                                      __  _____
GAM1244  HDAC2    5'  TGGGAGGAGAGGAGGGG    44950    A      A   AAT
                                TG GGAGGAGA GGAG   GGG
                                || ||||||||  ||||   |||
                                AC CCTCCTCT CCTC   CCC
                                 _      _   ____
GAM1244  HHIP     5'  GAGGAGGAGAAGGAGTTGGA   35409            AA
                                GAGGAGGAGAAGGAG  TGGG
                                ||||||||||||||  ||||
                                CTCCTCCTCTTCCTC  ACCT
                                         A_
GAM1244  HMGA2    5'  GAGGAGGAGGAGGAGAGGA   18519         A     AT
                                GAGGAGGAG AGGAGA  GGG
                                |||||||||  ||||||  |||
                                CTCCTCCTC TCCTCT  CCT
                                     C     __
GAM1244  HOXA3    3'  GGGGGAAGGAGAGGA      36197    A  A      AT
                                GG GG GAAGGAGA  GGG
                                || || ||||||||  |||
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                                CC CC CTTCCTCT  CCT
                                 _ _     __
GAM1244  HOXB5    3'  TGAGGAGGGAGGAGGAGG    13453        A  A   AAT
                                TGAGGAGG GA GGAG   GGGG
                                |||||||| || ||||   ||||
                                ACTCCTCC CT CCTC   CTCC
                                   _ _   ___
GAM1244  IL13RA1  3'  TGAGGAGAGAAATGGGGTGGGG 11446       _   A  AGAA
                                TGAGGAG GAGA GG    TGGGG
                                ||||||| |||| ||    |||||
                                ACTCCTC CTTT CC    ACCCC
                                    T   A  CC__
GAM1244  ITGA3    3'  GGAGGAGGGGGTGGGA     24262        AA  AGAA
                                GGAGGAG  GG    TGGGG
                                |||||||  ||    |||||
                                CCTCCTC  CC    ACCCT
                                    CC  ____
GAM1244  JJAZ1    5'  GGAGGAGAGGGGAAGGGA    31691        A  A   T
                                GGAGGAGA GG GAA GGGG
                                |||||||| || ||| ||||
                                CCTCCTCT CC CTT CCCT
                                    C  _   _
GAM1244  KCNJ16   3'  TGAGGGGGAGGAGGGAA     33020      A    A   A
                                TGAGG GGAG AGG GAA
                                ||||| |||| ||| |||
                                ACTCC CCTC TCC CTT
                                   C    C   _
GAM1244  KCNK7    3'  TGGGGAGGAGAAGGTGCTGGGG 37861    A         AGAA
                                TG GGAGGAGAAGG    TGGGG
                                || ||||||||||    |||||
                                AC CCTCCTCTTCC    ACCCC
                                 C         ACG_
GAM1244  KLHL3    3'  TGAGGGGAGGGGAGGATGGGG  44651      A   AA   A
                                TGAGG GGAG  GGAG ATGGGG
                                ||||| ||||  |||| ||||||
                                ACTCC CCTC  CCTC TACCCC
                                   _   C_   C
GAM1244  LAG3     5'  TGAGGAGGTGGGGGCGGGG   14048        AGAA  AGAA
                                TGAGGAGG   GG   TGGGG
                                ||||||||   ||   |||||
                                ACTCCTCC   CC   GCCCC
                                    ACCC  ____
GAM1244  LIMK1    3'  TGAGGAGGGGCAGGGAGCCTTG 14173        AGAA_   AA_
            GGG                    TGAGGAGG    GGAG   TGGGG
                                ||||||||    ||||  |||||
                                ACTCCTCC    CCTC   ACCCC
                                    CCGTC   GGA
GAM1244  LPL      5'  TGAGGAGGAGGAAGAGGGG   6945         AA    AT
                                TGAGGAGGAG  GGAGA  GGGG
                                ||||||||||  |||||  ||||
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                                ACTCCTCCTC  CTTCT  CCCC
                                      __    __
GAM1244  LTF     3'  GGGGAGAAGAGCTGGGG     14262    A      AGAA
                                GG GGAGAAGG    TGGGG
                                || ||||||||    |||||
                                CC CCTCTTCT    ACCCC
                                 _       CG__
GAM1244  LY9     3'  TGAGAAGGAGGGGGAGGGG   43470          AA   GAAT
                                TGAGGAGGAG  GGA    GGGG
                                ||||||||||  |||    ||||
                                ACTCTTCCTC  CCT    CCCC
                                      CC  _____
GAM1244  MGAT5   5'  TGGGGAGGAGAGAGGGG     14480    A      AG   AAT
                                TG GGAGGAGA  GAG   GGG
                                || ||||||||  |||   |||
                                AC CCTCCTCT  CTC   CCC
                                 C       __   ____
GAM1244  MLLT7   3'  TGGGGTGGAGAAGGAGCCCCAG 25535    A  A        AA_
            A                    TG GG GGAGAAGGAG   TGGG
                                || || ||||||||||   ||||
                                AC CC CCTCTTCCTC   GTCT
                                 C  A         GGG
GAM1244  MN1     5'  TGGGGAGGGAAGGGGGTTGGGA 14600    A    A    AGAA
                                TG GGAGG GAAGG    TGGGG
                                || ||||| |||||    |||||
                                AC CCTCC CTTCC    ACCCT
                                 C    _    CCCA
GAM1244  MN1     5'  TAAGTGGGGGGAATGGGG    14590     GA  AGAA  A
                                TGAG  GG    GG GAATGGGG
                                ||||  ||    || ||||||||
                                ATTC  CC    CC CTTACCCC
                                  AC  _____  _
GAM1244  MUC3B   3'  TGAGGAGGAGGGAGACTGAGGG 45346          AA    AT__
            G                    TGAGGAGGAG  GGAGA    GGGG
                                ||||||||||  |||||    ||||
                                ACTCCTCCTC  CCTCT    CCCC
                                      __     GACT
GAM1244  MUC3B   3'  GAGGAGAGGAGGGAG       45338        A    AAT
                                GAGGAGA GGAG   GGG
                                ||||||| ||||   |||
                                CTCCTCT CCTC   CTC
                                    _    C__
GAM1244  MUC4    5'  TGGGAGGAGACATGGG      39678    A      AGGAGA
                                TG GGAGGAGA     ATGGG
                                || ||||||||     |||||
                                AC CCTCCTCT     TACCC
                                 _       G_____
GAM1244  NCALD   3'  TGGGGAAGAGAGGGGAGTGGG  36776    A      A  A  A
                                TG GGAGGAGA GG GA TGGG
                                || |||||||| || || ||||
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                                AC CCTTCTCT CC CT ACCC
                                 C       C _ C
GAM1244  NCALD    3'  TGGGAAGGAGAAGGAGAA    36775    A
                                TG GGAGGAGAAGGAGAA
                                || ||||||||||||||
                                AC CTTCCTCTTCCTCTT
                                 C
GAM1244  NEDD4    5'  GAGGAGGAGGAGGAGAAGCGGG 43101          A      _
              A                  GAGGAGGAG AGGAGAA TGGGG
                                |||||||||  |||||||  |||||
                                CTCCTCCTC TCCTCTT GCCCT
                                      C      C
GAM1244  NKX2H    5'  GAGGAGGGGAAGGAGGCGGGG  30759        A      AA
                                GAGGAGG GAAGGAG  TGGGG
                                |||||||  |||||||  |||||
                                CTCCTCC CTTCCTC  GCCCC
                                    C      C_
GAM1244  NPDC1    5'  GAGGAGGAGGAGGAAGAGGA   31727          A     AAT
                                GAGGAGGAG AGGAG   GGGGA
                                |||||||||  |||||   |||||
                                CTCCTCCTC TCCTT   CTCCT
                                     C    ___
GAM1244  NPR1     3'  TGGGGAGGGGAGGGGATCAGGA 44591    A    A  A  A  A G
                                TG GGAGG GA GG GA T GGGA
                                || ||||| || || || | ||||
                                AC CCTCC CT CC CT A TCCT
                                 C    C  C  _  _ G
GAM1244  NRXN2    3'  GAAGTAGGGAAGGAGGGTGGGG 31482      _  A      AA
              A                  GAGG AGG GAAGGAG  TGGGGA
                                ||||  |||  |||||||  ||||||
                                CTTC TCC CTTCCTC  ACCCCT
                                  A  _      CC
GAM1244  ODF2     5'  TGAGGGGAGAAGGGTGGA    14935       A       AGAA
                                TGAGG GGAGAAGG    TGGG
                                |||||  ||||||||    ||||
                                ACTCC CCTCTTCC    ACCT
                                   _       C____
GAM1244  OGDH     3'  GGGGAGGGAGTCCAAGA     45016    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  GTTCT
                                 _   __    AG
GAM1244  PCDH12   5'  TGAGGAGGATGAGGCCGGGG  32454         GA   AGAA
                                TGAGGAGGA  AGG    TGGGG
                                |||||||||  |||   |||||
                                ACTCCTCCT  TCC    GCCCC
                                     AC   G___
GAM1244  PCDHGA1  3'  TGAGGAGGAGGTGGGGGA    33151          AA  AGAAT
                                TGAGGAGGAG  GG    GGGG
                                ||||||||||  ||    ||||
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                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA10 3' TGAGGAGGAGGTGGGGGA   36875       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA11 3' TGAGGAGGAGGTGGGGGA   33152       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA12 3' TGAGGAGGAGGTGGGGGA   19026       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA2  3' TGAGGAGGAGGTGGGGGA   36740       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA3  3' TGAGGAGGAGGTGGGGGA   33163       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA4  3' TGAGGAGGAGGTGGGGGA   36824       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA5  3' TGAGGAGGAGGTGGGGGA   36833       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA6  3' TGAGGAGGAGGTGGGGGA   36840       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA7  3' TGAGGAGGAGGTGGGGGA   36849       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA8  3' TGAGGAGGAGGTGGGGGA   36858       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
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                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGA9  3' TGAGGAGGAGGTGGGGGA   36866       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB1  3' TGAGGAGGAGGTGGGGGA   36902       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB2  3' TGAGGAGGAGGTGGGGGA   36911       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB3  3' TGAGGAGGAGGTGGGGGA   36920       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB4  3' TGAGGAGGAGGTGGGGGA   36929       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB5  3' TGAGGAGGAGGTGGGGGA   36937       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB6  3' TGAGGAGGAGGTGGGGGA   36944       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGB7  3' TGAGGAGGAGGTGGGGGA   36952       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGC3  3' TGAGGAGGAGGTGGGGGA   37052       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
                                ACTCCTCCTC CC   CCCT
                                    CA _____
GAM1244 PCDHGC4  3' TGAGGAGGAGGTGGGGGA   37074       AA AGAAT
                                TGAGGAGGAG GG   GGGG
                                |||||||||| ||   ||||
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                                ACTCCTCCTC  CC    CCCT
                                     CA _____
GAM1244  PCDHGC5  3'  TGAGGAGGAGGTGGGGGA   37082        AA  AGAAT
                                TGAGGAGGAG  GG    GGGG
                                ||||||||||  ||    ||||
                                ACTCCTCCTC  CC    CCCT
                                     CA _____
GAM1244  PCOLN3   3'  TGAGGAGGGGAGGGCAGGA   15755       AGAA   AA
                                TGAGGAGG   GGAG  TGGGG
                                ||||||||   ||||  |||||
                                ACTCCTCC   CCTC  GTCCT
                                     ____   CC
GAM1244  PCTK1    5'  TGAGGAGGAGGAGGCGGCGG  37482        A  AGAA  _
                                TGAGGAGGAG AGG   TGG GG
                                |||||||||| |||   ||| ||
                                ACTCCTCCTC TCC   GCC CC
                                     C  ____  G
GAM1244  PIK3C2B  3'  TGGGGAGTGATGGATGGGG   15296   A   GA  A  GAA
                                TG GGAG  GA GGA   TGGGG
                                || ||||  || |||   |||||
                                AC CCTC  CT CCT   ACCCC
                                 C   A_  A  ___
GAM1244  PLAT     3'  GAGAGCCAGGGAGTGGGG   37448    G  A_  A  A
                                GAG AG  AGG GA TGGGG
                                ||| ||  ||| || |||||
                                CTC TC  TCC CT ACCCC
                                  _ GG  _ C
GAM1244  PLXNB3   3'  GGGGAGAGGGGGAAGGA    23950    A    A  A  T
                                GG GGAGA GG GAA GGG
                                || ||||| || ||| |||
                                CC CCTCT CC CTT CCT
                                 _   C  C  _
GAM1244  POU2F2   3'  GGAGGAGGAGGAGGATGAGGA  15462       A    A
                                GGAGGAG AGGAG ATGGGGA
                                ||||||| ||||| |||||||
                                CCTCCTC TCCTC TACTCCT
                                    C    C
GAM1244  PPP2R2B  5'  TGAGGAGGAGACGGGG     21339         AGGAGAA
                                TGAGGAGGAGA     TGGGG
                                ||||||||||      |||||
                                ACTCCTCCTCT     GCCCC
                                     _______
GAM1244  PPP3R1   5'  GGAGGGGGAGAGGGGG     44081      AGAA    AT
                                GGAGG   GGAGA  GGGG
                                |||||   |||||  ||||
                                CCTCC   CCTCT  CCCC
                                  C___    C_
GAM1244  PREB     3'  TGAGGGGAGGAGGAGAA    30145      A   A
                                TGAGG GGAG AGGAGAA
                                ||||| |||| |||||||
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                                ACTCC CCTC TCCTCTT
                                  _   C
GAM1244  PRKCM    5'  GAGGAGGAGGAGGAGGG     15643         A   GAAT
                                GAGGAGGAG AGGA   GGG
                                ||||||||| ||||   |||
                                CTCCTCCTC TCCT   CCC
                                    C   ____
GAM1244  PRKCM    5'  GGAGGAGGAGGAGGGCGAGGA 15644        A    AA
                                GGAGGAG AGGAG  TGGGGA
                                ||||||| |||||  ||||||
                                CCTCCTC TCCTC  GCTCCT
                                   C    CC
GAM1244  PROK1    3'  GGGGAGGGGAGGGGG       37102    A   AA   AAT
                                GG GGAG  GGAG   GGGG
                                || ||||  ||||   ||||
                                CC CCTC  CCTC   CCCC
                                 _   C_   ___
GAM1244  PSD      3'  GGGGAGGAAGGAGGGGA     15790    A   _     AAT
                                GG GGAG AAGGAG   GGGG
                                || |||| ||||||   ||||
                                CC CCTC TTCCTC   CCCT
                                 _   C     ___
GAM1244  RAD51L1  3'  TGGGAGGAGGGGGGAAATAGGA 39456    A      AA  AG
                                TG GGAGGAG  GG  AATGGGG
                                || |||||||  ||  |||||||
                                AC CCTCCTC  CC  TTATCCT
                                 _      C_  CT
GAM1244  RARA     3'  TGAGGAGGAGAACTGGGG    9716           GGAGAA
                                TGAGGAGGAGAA     TGGGG
                                ||||||||||||     |||||
                                ACTCCTCCTCTT     ACCCC
                                      G_____
GAM1244  RORA     5'  TGATGGGGAGGAGTATGGGG   39518     _ A   GAA   A
                                TGA GG GGA   GGAG ATGGGG
                                ||| || |||   |||| ||||||
                                ACT CC CCT   CCTC TACCCC
                                  A  _  ___    A
GAM1244  RORB     5'  TGAGGAGGAGGAGGAAGGG   27924         A   GAAT
                                TGAGGAGGAG AGGA   GGGG
                                |||||||||| ||||   ||||
                                ACTCCTCCTC TCCT   TCCC
                                    C   ____
GAM1244  SET7     5'  GAGGAGGAGGAGGAAGAGGA  36157         A    AAT
                                GAGGAGGAG AGGAG   GGGGA
                                ||||||||| |||||   |||||
                                CTCCTCCTC TCCTT   CTCCT
                                    C   ___
GAM1244  SIX3     3'  GAGGAGGGGAAGGAGAGGGA  24022         A       ATG
                                GAGGAGG GAAGGAGA   GGGA
                                ||||||| ||||||||   ||||
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                                CTCCTCC CTTCCTCT   CCCT
                                    C      ___
GAM1244  SIX3     5'  GAGGAGGAGAAGGAAAGG    24020           AATG
                                GAGGAGGAGAAGGAG   GGG
                                |||||||||||||||   |||
                                CTCCTCCTCTTCCTT   TCC
                                                 ____
GAM1244  SIX3     3'  GAGGAGGAGAAGGAAGAGGA  24021           AAT
                                GAGGAGGAGAAGGAG  GGGGA
                                |||||||||||||||  |||||
                                CTCCTCCTCTTCCTT  CTCCT
                                                  ___
GAM1244  SLC2A4   3'  TGGGGAGGAAAGGGGATGGGG 9802    A      A  A  A
                                TG GGAGGAGA GG GA TGGGG
                                || |||||||| || || |||||
                                AC CCTCCTTT CC CT ACCCC
                                 C       C  _  _
GAM1244  SLC5A1   3'  TGGGGAGGAGGACGGACAGGA 7364    A     AA_  GAA
                                TG GGAGGAG   GGA   TGGGG
                                || |||||||   |||   |||||
                                AC CCTCCTC   CCT   GTCCT
                                 C      CTG   ___
GAM1244  SLC9A1   3'  TGAGGAGGAGGATGAGG     43242         AAGGA  A
                                TGAGGAGGAG    GA TGGGG
                                ||||||||||    || |||||
                                ACTCCTCCTC    CT ACTCC
                                                _____  _
GAM1244  SMARCD1  3'  TGAGGAGGGGGTGGGGAAGCAG 40088        AGAA__   AAT
           GGG                    TGAGGAGG     GGAG   GGGG
                                |||||||||     ||||   ||||
                                ACTCCTCC     CCTT   CCCC
                                     CCCACC    CGT
GAM1244  SMCX     3'  TGGGGAGAGAAGGGAG      20075    A  AG      AGAAT
                                TG GG  GAGAAGG    GGG
                                || ||  |||||||    |||
                                AC CC  CTCTTCC    CTC
                                 _  CT      _____
GAM1244  SMCX     3'  AAAGAGGGGAGGAGAGTGGGG  20064       A  A    A
                                GAGGAGG GA GGAGA TGGGG
                                ||||||| || ||||| |||||
                                TTTCTCC CT CCTCT ACCCC
                                     C  _    C
GAM1244  SOX9     5'  GAGGAGGAGGAGGGGAGG    7374          A   AGAAT
                                GAGGAGGAG AGG    GGGG
                                ||||||||| |||    ||||
                                CTCCTCCTC TCC    CTCC
                                      C  C____
GAM1244  STAU     5'  GAGGAGGGGAAGGAAGAAGGA  32694        A     _   T
                                GAGGAGG GAAGGA GAA GGG
                                ||||||| |||||| ||| |||
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                                CTCCTCC CTTCCT CTT CCT
                                    C     T  _
GAM1244  TAF1C    3'  TGAGAAGGGGAGGGAG      24992        AGAA   AAT
                                TGAGGAGG   GGAG  GGG
                                ||||||||   ||||  |||
                                ACTCTTCC   CCTC  CTC
                                     _____   C__
GAM1244  TAF4     3'  TGGGAGGGGAAGGGAAGGA   17267    A    A    A  T
                                TG GGAGG GAAGG GAA GGG
                                || ||||| ||||| ||| |||
                                AC CCTCC CTTCC CTT CCT
                                 _    C    _  _
GAM1244  TBL1X    3'  GGAGGAGAGGGTGGGA      24889        A  AGAA
                                GGAGGAGA GG   TGGGG
                                |||||||| ||   |||||
                                CCTCCTCT CC   ACCCT
                                     C  _____
GAM1244  TBR1     3'  GGGGAGGCGGAGCTGGGG    27314    A   AA   AA
                                GG GGAG  GGAG  TGGGG
                                || ||||  ||||  |||||
                                CC CCTC  CCTC  ACCCC
                                 _   CG   G_
GAM1244  TCF7L2   5'  GAGGAGGGGAGGGGAAGGGGG  36250       A  A  A   T
                                GAGGAGG GA GG GAA GGGG
                                ||||||| || || ||| ||||
                                CTCCTCC CT CC CTT CCCC
                                    C  C  _  C
GAM1244  TEGT     3'  TGAGGGGTGGAAGGAGAGGA   42100      A  A_      AT
                                TGAGG GG  GAAGGAGA  GGG
                                ||||| ||  ||||||||  |||
                                ACTCC CC  CTTCCTCT  CCT
                                   _ AC       __
GAM1244  TNXB     5'  GGAGGAGAAGGGGAGG      37159          AGAAT
                                GGAGGAGAAGG    GGGG
                                ||||||||||    ||||
                                CCTCCTCTTCC    CTCC
                                      C_____
GAM1244  TRIM8    3'  TGGTGAGGAGAAGGAAGCAGGA 36283    AG         AAT
                                TG  GAGGAGAAGGAG   GGGG
                                ||  ||||||||||||   ||||
                                AC  CTCCTCTTCCTT   TCCT
                                 CA          CG_
GAM1244  TTC3     3'  TGGGGTGGGGAAGGAGAATGGT 17720    A  A  A         _
           GG                    TG GG GG GAAGGAGAATGG GG
                                || || || |||||||||||| ||
                                AC CC CC CTTCCTCTTACC CC
                                 C  A  C          A
GAM1244  UBE2V1   3'  GGGGGAGAGAAGATATGGGGA  35351    A    A    _
                                GG GGAGA GGAGA ATGGGGA
                                || ||||| ||||| |||||||
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                                CC CCTCT CTTCT TACCCCT
                                 C    _    A
GAM1244 UGCG    5' GAGGAAAGGGCGGAGGGGGGTG 17873       AGAA   AA___
           GGGA                  GAGGAGG   GGAG    TGGGGA
                                |||||||   ||||    ||||||
                                CTCCTTT   CCTC    ACCCCT
                                    CCCG   CCCCC
GAM1244 VAT1    3' GGAGGAGAAGGAGGTGGGA   26848          AA
                                GGAGGAGAAGGAG  TGGGG
                                ||||||||||||  |||||
                                CCTCCTCTTCCTC  ACCCT
                                       C_
GAM1244 VTN     5' TGAGGAAGGGAGGGAGAGG   8470        A  A    AT
                                TGAGGAGG GA GGAGA  GG
                                |||||||| || |||||  ||
                                ACTCCTTC CT CCTCT  CC
                                     C  C    __
GAM1244 ZNF278  5' CGGGGAGGAGAAGGAGGGG   36791    A         GAAT
                                TG GGAGGAGAAGGA   GGGG
                                || ||||||||||||   ||||
                                GC CCTCCTCTTCCT   CCCC
                                 C         ____
GAM1245 ABCC12  3' TCCGTGGATGGGAGGGG     37718        GTAGT  C
                                TCCGTGGA    GG GGGG
                                ||||||||    || ||||
                                AGGCACCT    CC CCCC
                                     AC___  T
GAM1245 ACVRL1  5' TCTGCGGGTGGCGGGG      6168     C   AGTA
                                TC GTGG   GTGGCGGGG
                                || ||||   |||||||||
                                AG CGCC   CACCGCCCC
                                 A  ____
GAM1245 ADD2    5' TCCGCGGCGGCGGG        32736        AGTAG
                                TCCGTGG    TGGCGGG
                                |||||||    |||||||
                                AGGCGCC    GCCGCCC
                                          _____
GAM1245 AF5Q31  5' TCCGGGAGGCGGCGGGG     30858     T   TA
                                TCCG GGAG  GTGGCGGGG
                                |||| ||||  |||||||||
                                AGGC CCTC  CGCCGCCCC
                                  _   __
GAM1245 APG5L   5' TCCGGTGGGGCGGCGGGG    22134     _  AGTA
                                TCCG TGG   GTGGCGGGG
                                |||| |||   |||||||||
                                AGGC ACC   CGCCGCCCC
                                  C  C___
GAM1245 BIN3    3' TCCGTGGAGGGCAGCAGG    33085         TA TG
                                TCCGTGGAG  G  GCGGG
                                |||||||||  |  |||||
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                                AGGCACCTC  C  CGTCC
                                     C_ GT
GAM1245 CDK2AP1  5' TCCGCGGAGCCGGCGGGG   21602        AG
                                TCCGTGGAGT  TGGCGGGG
                                ||||||||||  ||||||||
                                AGGCGCCTCG  GCCGCCCC
                                          __
GAM1245 CKMT1    5' TCCTGGAGTAGGCGCTGG    34190    G      TG  G
                                TCC TGGAGTAG  GC GG
                                ||| ||||||||  || ||
                                AGG ACCTCATC  CG CC
                                  _      CG  A
GAM1245 DIAPH2   3' TCCTGGAGTAATCTGGG     28681    G      GGC
                                TCC TGGAGTAGT   GGG
                                ||| |||||||||   |||
                                AGG ACCTCATTA   CCC
                                  _       GA_
GAM1245 DNCI1    5' TCCCGAAGGTGGCGGGG     44994    G    TA
                                TCC TGGAG  GTGGCGGGG
                                ||| |||||  |||||||||
                                AGG GCTTC  CACCGCCCC
                                  _    __
GAM1245 EGFL4    3' CCCAGCAGTGGTGGCGGGG   41563     TGG   A
                                TCCG   AGT GTGGCGGGG
                                ||||   ||| |||||||||
                                GGGT   TCA CACCGCCCC
                                  CG_   C
GAM1245 ENTPD6   3' TCCATGGAGGAGGTGGGG    10343        TAGT  C
                                TCCGTGGAG    GG GGGG
                                |||||||||    || ||||
                                AGGTACCTC    CC CCCC
                                     CT__  A
GAM1245 FASN     3' TCCGGTGGCAGGCGGGG     19944     _  AGTAGT
                                TCCG TGG     GGCGGGG
                                |||| |||     |||||||
                                AGGC ACC     CCGCCCC
                                  C   GT____
GAM1245 GNG5     5' CCGTGGGTCGGCGGGG      23608      A  AG
                                CCGTGG GT  TGGCGGGG
                                ||||||  ||  ||||||||
                                GGCACC CA  GCCGCCCC
                                     _ __
GAM1245 GPR30    5' TCCGTGGAGGCGAG        11317        GTAGT
                                TCCGTGGA    GGCGGG
                                ||||||||    ||||||
                                AGGCACCT    CCGCTC
                                          _____
GAM1245 LILRB1   3' TCCATGGAGTGTGGGG      27429          A   C
                                TCCGTGGAGT GTGG GG
                                |||||||||| |||| ||
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                                AGGTACCTCA CACC CC
                                      _  _
GAM1245  MAD2L2   3'  TCAGTGGGGTGGCAGG     26807    C   AGTA
                                TC GTGG   GTGGCGGG
                                || ||||   ||||||||
                                AG CACC   CACCGTCC
                                 T   C___
GAM1245  MYC      5'  TCCTGGCAGCGGCGGGG     14712    G   AG
                                TCC TGG  TAGTGGCGGGG
                                ||| |||  ||||||||||
                                AGG ACC  GTCGCCGCCCC
                                  _  __
GAM1245  NF2      3'  TCCTGGGGTGGCTGGG      7070     G   AGTA   _
                                TCC TGG   GTGGC GGG
                                ||| |||   ||||| |||
                                AGG ACC   CACCG CCC
                                  _  C___    A
GAM1245  NONO     3'  TCCTGGAGGAGCTGGGG     44360    G    T  GGC
                                TCC TGGAG AGT   GGGG
                                ||| ||||| |||   ||||
                                AGG ACCTC TCG   CCCC
                                  _    C  A__
GAM1245  PITX1    3'  TCCGCGGAGTGGGCCTCCGGGG 15329         AGT  ____
                                TCCGTGGAGT   GGC   GGGG
                                |||||||||   |||   ||||
                                AGGCGCCTCA   CCG   CCCC
                                      C__   GAGG
GAM1245  RAD23B   5'  TCTGTGGCCTGGCGGGG    16141    C   AGTAG
                                TC GTGG    TGGCGGGG
                                || ||||    ||||||||
                                AG CACC    ACCGCCCC
                                 A   GG___
GAM1245  RERE     5'  TCCGGGGAAAGTGGCGGGG   29037     T   T
                                TCCG GGAG AGTGGCGGGG
                                |||| |||| ||||||||||
                                AGGC CCTT TCACCGCCCC
                                  C   _
GAM1245  RFX2     3'  TCCGTGGAGCGGGACGCAGG  8460         AGTG_
                                TCCGTGGAGT    GCGGG
                                |||||||||    |||||
                                AGGCACCTCG    CGTCC
                                      CCCTG
GAM1245  ROR2     3'  CCTGTGGGGTCTCGGCGGGG  21258   _   A  AG
                                CC GTGG GT  TGGCGGGG
                                || |||| ||  ||||||||
                                GG CACC CA  GCCGCCCC
                                 A   C  GA
GAM1245  SCA1     3'  TCCGTGTGGTGACAGGG     7289       GAGTA
                                TCCGTG    GTGGCGGGG
                                ||||||    |||||||||
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                              AGGCAC    CACTGTCCC
                                 AC___
GAM1245 SELPLG   3' CCCGTGGAGGTGGGG      40672        TA   C
                              TCCGTGGAG  GTGG GG
                              |||||||||  |||| ||
                              GGGCACCTC  CACC CC
                                     __   _
GAM1245 SEZ6L    5' TCCGTGGAGGAGGAGAGG    34426        TAGT  C
                              TCCGTGGAG   GG GGGG
                              |||||||||   || ||||
                              AGGCACCTC   CC CTCC
                                   CT__  T
GAM1245 SLC17A7  3' TCCCTGGAATGGCGGGG    33697    G   GTA
                              TCC TGGA   GTGGCGGGG
                              ||| ||||   |||||||||
                              AGG ACCT   TACCGCCCC
                                G   ___
GAM1245 SLC24A1  3' TCCTGGGGTAGCGAG      21825    G   AGTA
                              TCC TGG    GTGGCGGG
                              ||| |||    ||||||||
                              AGG ACC    CATCGCTC
                                _  C___
GAM1245 SLC6A9   3' CGTGGAGCACGGGTGGGG    27985        GT  C
                              CGTGGAGTA  GG GGGG
                              |||||||||  || ||||
                              GCACCTCGT  CC CCCC
                                   GC  A
GAM1245 TBR1     3' TCCGGGCCGCGGCGGGG     27316     T  AGTA
                              TCCG GG    GTGGCGGGG
                              |||| ||    |||||||||
                              AGGC CC    CGCCGCCCC
                                _ GG__
GAM1245 TGFB1    5' TCCTCCCCGCAGTGGCGGGG  8553     GTGGA
                              TCC    GTAGTGGCGGGG
                              |||    ||||||||||||
                              AGG    CGTCACCGCCCC
                                AGGGG
GAM1245 TIRAP    5' GTGGAGCAGAGCCTGTGGGG  38092        T  _____
                              GTGGAGTAG GGC    GGGG
                              ||||||||| |||    ||||
                              CACCTCGTC TCG    CCCC
                                   _  GACA
GAM1245 VIPR2    3' CCTGTGGAGTTGGGTGGGG   18008   _     AGT  C
                              CC GTGGAGT   GG GGGG
                              || |||||||   || ||||
                              GG CACCTCA   CC CCCC
                               A      AC_  A
GAM1246 DMRT2    3' GCTTGGTGGTTCCACT      27263     _   ATTA
                              GCT GGTG   GTTCCACT
                              ||| ||||   ||||||||
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                                CGA CCAC    CAAGGTGA
                                  A   _____
GAM1246 EGF     3' AGTAGGTGATTAGTCGTAGA  12650    CT        CCAC
                                AG  GGTGATTAGTT    TAGA
                                ||  ||||||||||    ||||
                                TC  CCACTAATCAG    ATCT
                                 AT         C___
GAM1246 HTR2A   3' ATGATCGTTGGTTCCACTAGAC 8386        A___
                                GTGATT    GTTCCACTAGAC
                                ||||||    ||||||||||||
                                TACTAG    CAAGGTGATCTG
                                   CAAC
GAM1246 RU2     3' CTGGTCTTTCCACTAG      32292       GATTAG
                                CTGGT     TTCCACTAG
                                |||||     |||||||||
                                GACCA     AAGGTGATC
                                   GA____
GAM1246 ZNF278  3' AGCTGGTGGCTAGTTCCCAGGA 36815         AT      ACTA
                                AGCTGGTG  TAGTTCC    GA
                                ||||||||  |||||||    ||
                                TCGACCAC  ATCAAGG    CT
                                     CG      GTC_
GAM1247 LRRC2   3' TGTTAAAAAGAAAAAAATGTA  36004            __
                                TGTTAAAAGGAAAA  ATGTA
                                ||||||||||||||  |||||
                                ACAATTTTTCTTTT  TACAT
                                        TT
GAM1247 PPP1R2  3' CTAACTGAAAGGGAAAAATGTA 26417     _   TT   A
                                CTA TTG  AAA GGAAAAATGTA
                                ||| |||  ||| ||||||||||
                                GAT GAC  TTT CCTTTTTACAT
                                  T   __   C
GAM1247 BCAT1   3' CAGAGTTCACAATAGGA     42377          G  TCGGT
                                CAGAGTTCA CA     GGA
                                |||||||| ||     |||
                                GTCTCAAGT GT     CCT
                                     _  TAT__
GAM1247 C6      5' CAGAGCTTAGATGGAA      45400         C  CATCG
                                CAGAGTT AG     GTGGAA
                                |||||||  ||     ||||||
                                GTCTCGA TC     TACCTT
                                   A  _____
GAM1247 NPC1    3' TACAGAGTGTCAGTGAGCGGA  7078          _    CATC
                                TACAGAGT TCAG    GGTGGA
                                |||||||| ||||    ||||||
                                ATGTCTCA AGTC    TCGCCT
                                     C    AC__
GAM1247 NRL     3' CAGAGCTCAGCGTG        26133           ATCG
                                CAGAGTTCAGC    GTG
                                ||||||||||    |||
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                                GTCTCGAGTCG   CAC
                                      ____
GAM1247 TEL2    3' TACAGAGTCTGGCTGGGGA  32046       CA ATC T
                                TACAGAGTT GC  GG GGA
                                ||||||||| ||  || |||
                                ATGTCTCAG CG  CC CCT
                                     AC A__ _
GAM1248 FGF2    3' TCTAGGTAAGCTTCACTGGGT 12844         AGA CA
                                TCTAGGTAAGTTT  GCT GGT
                                |||||||||||||  ||| |||
                                AGATCCATTCGAA  TGA CCA
                                       G__  C_
GAM1248 FLT1    3' GGTTACTTAGAGCTCAGGT  12913    AAG
                                GGT  TTTAGAGCTCAGGT
                                |||  ||||||||||||||
                                CCA  GAATCTCGAGTCCA
                                  AT_
GAM1248 HMGA2   3' AGGTAAGTGGTATTCAGGT  18503       TTAGAGC
                                AGGTAAGT     TCAGGT
                                ||||||||     ||||||
                                TCCATTCA     AGTCCA
                                    CCATA__
GAM1249 CASP2   3' GCAGTGAGCTGAGATCGTGCC 37399    A_  CT      A
                                GCA GGGT TGAGATCGT CC
                                ||| |||| ||||||||| ||
                                CGT CTCG ACTCTAGCA GG
                                  CA  __      C
GAM1249 CLECSF12 3' GAGCCGAGATCGTGCC    44122     TT     A
                                GGGTC GAGATCGT CC
                                |||||  |||||||| ||
                                CTCGG CTCTAGCA GG
                                   __     C
GAM1249 F3      3' GCAGTGAGCCGAGATCGT   42551    A_   TT
                                GCA GGGTC GAGATCGT
                                |||  |||||  ||||||||
                                CGT CTCGG CTCTAGCA
                                  CA   __
GAM1249 FCAR    3' GCAGTGAGTCGAGATCGTGCC 39336    A_   TT     A
                                GCA GGGTC GAGATCGT CC
                                |||  |||||  |||||||| ||
                                CGT CTCAG CTCTAGCA GG
                                  CA   __      C
GAM1249 FHL2    5' GCAGTGAGCTGAGATCGTGCC 11110    A_  CT      A
                                GCA GGGT TGAGATCGT CC
                                |||  ||||  ||||||||| ||
                                CGT CTCG ACTCTAGCA GG
                                  CA   __      C
GAM1249 FOSB    3' GCAGGGTCTTGGGATAACAC  27541    A      A CG
                                GCA GGGTCTTG GAT  TAC
                                ||| |||||||| |||  |||
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                                CGT CCCAGAAC CTA  GTG
                                  _      C   TT
GAM1249  INMT     3'  GCAGTGAGCCGAGATCGTGCC  27676     A_    TT       A
                                GCA  GGGTC  GAGATCGT CC
                                |||  |||||  |||||||| ||
                                CGT  CTCGG  CTCTAGCA GG
                                  CA     __       C
GAM1249  LENG4    5'  AACAAGGGTCAACCCTCGTGCC 35873          TTGAGA    A
                                AGCAAGGGTC     TCGT CC
                                ||||||||||     |||| ||
                                TTGTTCCCAG     AGCA GG
                                      TTGGG_   C
GAM1249  LZTS1    5'  GCAGGGTCTTGGAAAGGC    34266     A       AG TC
                                GCA GGGTCTTG  A  GT
                                ||| ||||||||  |  ||
                                CGT CCCAGAAC  T  CG
                                  _      CT TC
GAM1249  MEFV     3'  GCAGTGAGCTGAGATCGTGCC  6970      A_   CT       A
                                GCA  GGGT  TGAGATCGT CC
                                |||  ||||  ||||||||| ||
                                CGT  CTCG  ACTCTAGCA GG
                                  CA   __       C
GAM1249  MPL      3'  GCAGTGAGCCGAGATCGTGCC  23881     A_    TT       A
                                GCA  GGGTC  GAGATCGT CC
                                |||  |||||  |||||||| ||
                                CGT  CTCGG  CTCTAGCA GG
                                  CA   __      C
GAM1249  MYBPH    3'  AAGCGGGGGTCTTGGGCATC  22646      AA       AG_
                                AAGC  GGGTCTTG   ATC
                                ||||  ||||||||   |||
                                TTCG  CCCAGAAC   TAG
                                  CC       CCG
GAM1249  MYO1E    5'  GCAAGAGTCCACTCGTAC    22655          TGAGA
                                GCAAGGGTCT    TCGTAC
                                ||||||||||    ||||||
                                CGTTCTCAGG    AGCATG
                                      TG___
GAM1249  PDE6B    3'  GCAGTGAGCTGAGATCGTGCC  7102      A_   CT       A
                                GCA  GGGT  TGAGATCGT CC
                                |||  ||||  ||||||||| ||
                                CGT  CTCG  ACTCTAGCA GG
                                  CA   __       C
GAM1249  PPP1R12B 5'  AGTGAGGGTCTTGACGT    36964    CA       GAT
                                AG  AGGGTCTTGA   CGT
                                ||  ||||||||||   |||
                                TC  TCCCAGAACT   GCA
                                 AC        ___
GAM1249  PTGIS    3'  GAGCTGAGATCGTGCC      9672       CT       A
                                GGGT  TGAGATCGT CC
                                ||||  ||||||||| ||
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                                CTCG  ACTCTAGCA GG
                                  __       C
GAM1249  SLA2     3'  GCAGTGAGCTGAGATCGTGCC  37014     A_   CT       A
                                GCA  GGGT  TGAGATCGT CC
                                |||  ||||  ||||||||| ||
                                CGT  CTCG  ACTCTAGCA GG
                                  CA   __       C
GAM1249  SLC15A1  3'  GCAGTGAGCTGAGATCGTGCC  22900     A_   CT       A
                                GCA  GGGT  TGAGATCGT CC
                                |||  ||||  ||||||||| ||
                                CGT  CTCG  ACTCTAGCA GG
                                  CA   __       C
GAM1249  SUOX     5'  AAGTGAGGAGTCTTGAGA    7836      CA  _
                                AAG  AGG GTCTTGAGA
                                |||  ||| |||||||||
                                TTC  TCC CAGAACTCT
                                  AC   T
GAM1249  TBXA2R   3'  GCAGTGAGCCGAGATCGTGCC  9857      A_    TT       A
                                GCA  GGGTC  GAGATCGT CC
                                |||  |||||  |||||||| ||
                                CGT  CTCGG  CTCTAGCA GG
                                  CA    __       C
GAM1249  THBD     3'  AAGCAAGGATTTTGCCTGTGT  7418          C   AGATC
                                AAGCAAGGGT TTG     GT
                                ||||||||||| |||     ||
                                TTCGTTCCTA AAC     CA
                                      A   GGACA
GAM1250  DTR      3'  TACATGGCTTCTCAATCTTTG  12616       AGATT        C
                                TACAT     CTTCTCGGTC TTG
                                |||||     |||||||||| |||
                                ATGTA     GAAGAGTTAG AAC
                                   CC___         A
GAM1250  FDFT1    3'  TAGGTTCTTCTCACCT      20896     A       GT
                                TAG TTCTTCTCG  CCT
                                |||  |||||||||  |||
                                ATC AAGAAGAGT  GGA
                                  C        __
GAM1250  FOXF1    3'  TACACAGATCGGTCT       11122         TTCTTC     C
                                TACATAGA     TCGGTC T
                                ||||||||     |||||| |
                                ATGTGTCT     AGCCAG A
                                     _______     A
GAM1250  STC1     3'  AATTGCTCTTGGTCCTTG    17169      C   C
                                GATT TTCT GGTCCTTG
                                ||||  ||||  ||||||||
                                TTAA GAGA CCAGGAAC
                                  C    A
GAM1250  TRHR     3'  CACAGATTCTCAATTTCTTTG  17679          CTCGG  C
                                CATAGATTCTT     TC TTG
                                ||||||||||     || |||
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                                GTGTCTAAGAG    AG AAC
                                     TTAA_  A
GAM1251  CD1D    3'  CAGGACTGAAGTCTTAGGA   44295       ACCATTAA
                                CAGGATT      TCTTAGGA
                                |||||||      ||||||||
                                GTCCTGA      AGAATCCT
                                   CTTC____
GAM1251  CD28    3'  AGGAGTACCATTAATTATAA  26014     T       CT
                                AGGA TACCATTAAT  TAG
                                |||| ||||||||||  |||
                                TCCT ATGGTAATTA  ATT
                                  C        AT
GAM1251  CPO     3'  AGGATTATTCTTAGTCTCAA  6427       CCA   A
                                AGGATTA   TTA TCTTAG
                                |||||||   ||| ||||||
                                TCCTAAT   AAT AGAGTT
                                   AAG   C
GAM1251  FADD    3'  AGGATTACCTTAGG       19242        ATTAATC
                                AGGATTACC     TTAGG
                                |||||||||     |||||
                                TCCTAATGG     AATCC
                                      _______
GAM1251  GPR44   3'  GGATTACCAGTGCCCAGAGG  21957        TTAA  TT
                                GGATTACCA   TC  AGG
                                |||||||||   ||  |||
                                CCTAATGGT   GG  TCC
                                     CACG  TC
GAM1251  KAL1    3'  AGGATAAAAATGATCTTAGGAA 6867      TACCATTA
                                AGGAT      ATCTTAGGAA
                                |||||      ||||||||||
                                TCCTA      TAGAATCCTT
                                  TTTTTAC_
GAM1251  MAB21L1  3'  CAGGATTGCTATAATCCTTTGA 24585       ACCAT     AG
                                CAGGATT    TAATCTT  GA
                                |||||||    |||||||  ||
                                GTCCTAA    ATTAGGA  CT
                                   CGAT_     AA
GAM1251  RHO     3'  GGATTTCCATTTTATAGGA   8064      A    AATCT
                                GGATT CCATT    TAGGA
                                ||||| |||||    |||||
                                CCTAA GGTAA    ATCCT
                                  A    AAT__
GAM1252  B3GALT5  5'  GAGGTGGGAGAGGAGACCCG  37682    A   C      G
                                GAG TGGG GAGGAGAT CTG
                                ||| |||| |||||||| |||
                                CTC ACCC CTCCTCTG GGC
                                 C   T      _
GAM1252  CADPS    5'  CGAGGTGGGCAAGGGG     42192     A       AGATGCT
                                CGAG TGGGCGAGG      GG
                                |||| |||||||||      ||
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                                GCTC ACCCGTTCC      CC
                                  C      _______
GAM1252 CENTD1   5' CGAGGTGAGGCGGCGCTGG   40137   T  C   AGA
                                A GGG GAGG   TGCTGG
                                | ||| ||||   ||||||
                                G TCC CTCC   GCGACC
                                 C   A   GCC
GAM1252 CHRNE    3' GATGGGCAGTGCTGG      6345        GAGG  A
                                GATGGGC    AG TGCTGG
                                |||||||    || ||||||
                                CTACCCG    TC ACGACC
                                     ____ _
GAM1252 CHST1    3' GAGGTGGGAGAGGGAGG     18906     A   C    A  TGCT
                                GAG TGGG GAGG GA    GG
                                ||| |||| |||| ||    ||
                                CTC ACCC CTCC CT    CC
                                  C   T   _ ____
GAM1252 DNMT3L   5' GAGGGGCGAGGAGCTGCGGG   30055     AT        A   T
                                GAG  GGGCGAGGAG TGC GGG
                                |||  |||||||||| ||| |||
                                CTC  CCCGCTCCTC ACG CCC
                                  __        G   _
GAM1252 DXF68S1E 5' GAGGTGGGTGACGGGCTGCGGG 41036     A   C  _  AGA   T
                                GAG TGGG GA GG   TGC GGG
                                ||| |||| || ||   ||| |||
                                CTC ACCC CT CC   ACG CCC
                                  C   A  G  CG_  _
GAM1252 EFNA1    3' GAGGTCTTGCTGGGAGATGCTG 20701     ATGG_  GA
            GG                    GAG    GC  GGAGATGCTGGG
                                |||    ||  ||||||||||||
                                CTC    CG  CCTCTACGACCC
                                  CAGAA  AC
GAM1252 ENG      5' TGGGCGGGGAGGGGGTGCTGGG 6509        A   A___
                                TGGGCG GGAG    TGCTGGG
                                |||||| ||||    |||||||
                                ACCCGC CCTC    ACGACCC
                                   C   CCCC
GAM1252 EPS8     5' CGAGGTGGGAGGGGACCGG   20810     A   CG   A AT
                                CGAG TGGG  AGG G  GCTGG
                                |||| ||||  ||| |  |||||
                                GCTC ACCC  TCC C  TGGCC
                                  C   __  C __
GAM1252 FOXI1    3' AGATGGGCAGTGCTG      29149        GAGG  A
                                AGATGGGC    AG TGCTG
                                ||||||||    || |||||
                                TCTACCCG    TC ACGAC
                                     ____ _
GAM1252 FSTL1    3' GAAGTGGAGAAGATGCTGGG  28217     A  GCG
                                GAG TGG   AGGAGATGCTGGG
                                ||| |||   ||||||||||||
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                                CTT ACC   TCTTCTACGACCC
                                  C  ___
GAM1252  GSTM1    3'  CGAGGAGGCAGGTGCTGG    40446     AT   G  AGA
                                CGAG  GGGC AGG   TGCTGG
                                ||||  |||| |||   ||||||
                                GCTC  TCCG TCC   ACGACC
                                  C_   _  ____
GAM1252  GSTM2    3'  CGAGGAGGCAGGTGCTGG    9195      AT   G  AGA
                                CGAG  GGGC AGG   TGCTGG
                                ||||  |||| |||   ||||||
                                GCTC  TCCG TCC   ACGACC
                                  C_   _  ____
GAM1252  GSTM4    3'  CGAGGAGGCAGGTGCTGG    9201      AT   G  AGA
                                CGAG  GGGC AGG   TGCTGG
                                ||||  |||| |||   ||||||
                                GCTC  TCCG TCC   ACGACC
                                  C_   _  ____
GAM1252  HD       3'  GGGCAGAAGGGATGCTGGG   13355     _   A
                                GGGC GAGG GATGCTGGG
                                |||| |||| |||||||||
                                CCCG CTTC CTACGACCC
                                  T   C
GAM1252  KCNK3    3'  GAGATGGGGGTGCTG       13905        CGA  AGA
                                GAGATGGG   GG   TGCTG
                                ||||||||   ||   |||||
                                CTCTACCC   CC   ACGAC
                                     ___  ___
GAM1252  MEN1     3'  CGAGATGGGCTGGACCTCTGGG 39173         GA   GATG
                                CGAGATGGGC  GGA   CTGGG
                                ||||||||||  |||   |||||
                                GCTCTACCCG  CCT   GACCC
                                     A_   GGA_
GAM1252  MIA      5'  TGAGCAAGGGGGTGCTGG    27210         AGA
                                TGGGCGAGG   TGCTGG
                                |||||||||   ||||||
                                ACTCGTTCC   ACGACC
                                     CCC
GAM1252  PAX5     3'  AGGCAAGTGGGGGATGCTGGG  32506       GA___
                                GGGCGAG    GATGCTGGG
                                |||||||    |||||||||
                                TCCGTTC    CTACGACCC
                                   ACCCC
GAM1252  PTGIR    3'  GAGATGGATGGGGAATCCAGG  9664         CGA  AG  G TG
                                GAGATGGG   GG  AT C  GG
                                ||||||||   ||  || |  ||
                                CTCTACCT   CC  TA G  CC
                                   AC_  CT  _ GT
GAM1252  SOX10    3'  GAGGTGGGCAAGGAACAGGG   28003     A         ATGCT
                                GAG TGGGCGAGGAG    GGG
                                ||| ||||||||||     |||
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                                CTC ACCCGTTCCTT    CCC
                                  C        GT___
GAM1253 BACH2    3' AAAATTATCATCAG       34766          TTAAGC
                                AAGATTATCATC     AG
                                ||||||||||||     ||
                                TTTTAATAGTAG     TC
                                         _______
GAM1253 SQLE     5' AGATTATCTGCTCGAGTGGGT 17105        AT  TA  CA
                                AGATTATC  CT  AG  GGT
                                ||||||||  ||  ||  |||
                                TCTAATAG  GA  TC  CCA
                                    AC  GC  AC
GAM1254 ADRBK1   3' ACCTGGCCGGCCCCGTCCTGGG 11521     CC   ATAA       A
            CA                    ACC  GCC    TCGTCCTGG CA
                                ||| |||    ||||||||| ||
                                TGG  CGG    GGCAGGACC GT
                                  AC   CCGG       C
GAM1254 ATSV     3' CCCCGTCCTGTCCTGG      20222       _ ATAATC
                                CCCCG CC     GTCCTGG
                                ||||| ||     |||||||
                                GGGGC GG     CAGGACC
                                  A  A_____
GAM1254 CPNE3    3' CCTCTTATCTTTCCTGGACA  19382    GCCATA  G_
                                CC     ATC  TCCTGGACA
                                ||     |||  |||||||||
                                GG     TAG  AGGACCTGT
                                 AGAA__   AA
GAM1254 GLI2     5' CCGCTCATCGTCCTGG      36116      CATA
                                CCGC    ATCGTCCTGG
                                ||||    ||||||||||
                                GGCG    TAGCAGGACC
                                  AG__
GAM1254 HDAC4    3' GCCATCTGCCCTGGAC      25768       AATC
                                GCCAT    GTCCTGGAC
                                |||||    |||||||||
                                CGGTA    CGGGACCTG
                                   GA__
GAM1254 KCNJ8    5' GCCTCTCCGTCCCTGGAC    22544     ATAA     _
                                GCC    TCGTCC TGGAC
                                |||    |||||| |||||
                                CGG    GGCAGG ACCTG
                                  AGA_     G
GAM1254 MGAT1    3' CCTGCCATGGCGTCCTG     14429    C    AAT
                                CC GCCAT   CGTCCTG
                                || |||||   |||||||
                                GG CGGTA   GCAGGAC
                                 A    CC_
GAM1254 MN1      5' ACCCCGCCTGATGTGAGGGAC 14569        ATAATC  CCT
                                ACCCCGCC     GT   GGAC
                                ||||||||     ||   ||||
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                                TGGGGCGG    CA  CCTG
                                    ACTA__  CTC
GAM1254 SLC9A3R1 3' CCACTGCCATGCCCTGGA   43246   CC_   AATC
                                CC  GCCAT   GTCCTGGA
                                ||  |||||   ||||||||
                                GG  CGGTA   CGGGACCT
                                 TGA   _____
GAM1255 MGAT2    5' CGTTACCTGCGCCTCCAGCG  14445      C A    A
                                TGTTACC GC CCTTTA CG
                                ||||||| || |||||| ||
                                GCAATGG CG GGAGGT GC
                                    A C    C
GAM1256 RUNX1    5' CAGCGCCGCCTTGGCTGTGGGT 12012     G     AACCGCA
                                CAGCG TCGTTTT     GGT
                                ||||| |||||||     |||
                                GTCGC GGCGGAA     CCA
                                  _     CCGACAC
GAM1256 SLC2A8   3' GGAGGGCTGACCGCAGGTC   31030   TC_  TTA
                                GG  GTT  ACCGCAGGTC
                                ||  |||  ||||||||||
                                CC  CGA  TGGCGTCCAG
                                 TCC  C__
GAM1257 CLN5     3' CAGATGCTGGTGATTG     27079       A    ACTACA
                                CAGATGCT GTGAT    TG
                                |||||||| |||||    ||
                                GTCTACGA CACTA    AC
                                    C   _______
GAM1257 KIR2DL1  3' CAGCTGCTGGTACATG     30569    A   A  GATACT
                                CAG TGCT GT    ACATG
                                ||| |||| ||    |||||
                                GTC ACGA CA    TGTAC
                                  G   C _______
GAM1257 KIR2DL2  3' CAGCTGCTGGTACATG     30571    A   A  GATACT
                                CAG TGCT GT    ACATG
                                ||| |||| ||    |||||
                                GTC ACGA CA    TGTAC
                                  G   C _______
GAM1257 KIR2DS2  3' CAGCTGCTGGTACATG     29479    A   A  GATACT
                                CAG TGCT GT    ACATG
                                ||| |||| ||    |||||
                                GTC ACGA CA    TGTAC
                                  G   C _______
GAM1257 KIR2DS4  3' CAGCTGCTGGTACATG     29484    A   A  GATACT
                                CAG TGCT GT    ACATG
                                ||| |||| ||    |||||
                                GTC ACGA CA    TGTAC
                                  G   C _______
GAM1258 AKAP2    3' TCTGCCTCTAAAGCCATTCCGC 28502   CA   CCCCCACA
                                TC  CCTT      CATTCCGC
                                ||  ||||      ||||||||
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                                AG  GGAG      GTAAGGCG
                                 AC   ATTTCG__
GAM1258 BCAS1   3' CTATACCCCACACATTCCG   18920   TC_
                                CT   CCCCACACATTCCG
                                ||   ||||||||||||||
                                GA   GGGGTGTGTAAGGC
                                 TAT
GAM1258 CACNA1D  3' ACTTTCCCCTGCACCCCGC   8763    C    CACA
                                AC TTCCCC   CATTCCGC
                                || ||||||   ||||||||
                                TG AAGGGG   GTGGGGCG
                                 A    AC__
GAM1258 CASP8   5' TCCACCCTTTCCTGGCACCATC 37884       __  CC_  A  TC
            GC                    TCCACCT  TCC   CAC CAT  CGC
                                |||||||  |||   ||| |||  |||
                                AGGTGGG  AGG   GTG GTA  GCG
                                    AA   ACC   _  __
GAM1258 CD1A    5' CACCTTCCCCTAATTCAAC   43406         CACAC   C
                                CACCTTCCCC    ATTC GC
                                ||||||||||    |||| ||
                                GTGGAAGGGG    TAAG TG
                                      AT___   T
GAM1258 CD79B   3' CCTCCCCCATCCCA       8421          CACA
                                CTTCCCCCA   TTCCG
                                |||||||||   |||||
                                GGAGGGGGT   AGGGT
                                      ____
GAM1258 CLDN14   5' TCCTGCCTTCCCTCTTCG    40324    A_     CCACACA  C
                                TCC  CCTTCCC      TTC G
                                |||  |||||||      ||| |
                                AGG  GGAAGGG      AAG C
                                  AC      AG_____   A
GAM1258 COG8    3' CCCACCTTCCTCCATACA    37038         C  C
                                TCCACCTTCC CCA ACA
                                |||||||||| ||| |||
                                GGGTGGAAGG GGT TGT
                                      A   A
GAM1258 EN1     5' TCCGCCCTCCCCCACCCG    10923    A        ACATT
                                TCC CCTTCCCCCAC    CCG
                                ||| ||||||||||    |||
                                AGG GGGAGGGGGTG    GGC
                                  C         _____
GAM1258 FKRP    3' TCCCCCTTCCCCTCTCCG    35898    A      CACACA
                                TCC CCTTCCCC     TTCCG
                                ||| ||||||||     |||||
                                AGG GGAAGGGG     GAGGC
                                  G       A_____
GAM1258 MAP1B   5' TCCGCCCTCTCCCAGCGCCGC  25398    A    C   CACATT
                                TCC CCTTC CCCA     CCGC
                                ||| ||||| ||||     ||||
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                                AGG GGGAG GGGT     GGCG
                                  C    A   CGC___
GAM1258 NTRK2    5' CCGCTTTCCCCCACCCG    26145    ACC       ACATT
                                CC   TTCCCCCAC    CCG
                                ||   |||||||||    |||
                                GG   AAGGGGGTG    GGC
                                 CGA       _____
GAM1258 OXTR     5' TCCACCCTCCTCTGAGCCAC  9531          C_____
                                TCCACCTTCC     CCAC
                                ||||||||||     ||||
                                AGGTGGGAGG     GGTG
                                      AGACTC
GAM1258 P2RY6    3' TCTCATCTTCCCTCACCCG   19993    _ C     C   ACATT
                                TC CA CTTCCC CAC     CCG
                                || || |||||| |||     |||
                                AG GT GAAGGG GTG     GGC
                                 A A     A  _____
GAM1258 PAFAH1B3 5' CTTCCCCCACGACGGCCGC   15077          _ ATT
                                CTTCCCCCAC AC   CCGC
                                |||||||||| ||   ||||
                                GAAGGGGGTG TG   GGCG
                                      C  CC_
GAM1258 RYR3     5' CTTCCCCCGGCAGCCGC     9771         ACA  TT
                                CTTCCCCC   CA  CCGC
                                ||||||||   ||  ||||
                                GAAGGGGG   GT  GGCG
                                     CC_  C_
GAM1258 TEM5     3' TCCCCTTTCCCCAGCATATTGC 37244     A   C    CA   TCC
                                TCC CCTT CCCCA  CAT   GC
                                ||| |||| |||||  |||   ||
                                AGG GGAA GGGGT  GTA   CG
                                  _   A    C_  TAA
GAM1258 TIMP3    3' TCCACCTCCCCTACTTTCCA  7468           CCAC  A
                                TCCACCTTCCC    AC TTCCG
                                ||||||||||    || |||||
                                AGGTGGAGGGG    TG AAGGT
                                      A___  A
GAM1258 TRPM7    5' TCCACCTCCTCCTCCTCCG   41621         _ _  ACACAT
                                TCCACCTTC CC CC     TCCG
                                |||||||| || ||     ||||
                                AGGTGGAGG GG GG     AGGC
                                     A  A  _______
GAM1258 VPREB1   3' TCCACCCTCTTCCATGACA   28323         CC   C_
                                TCCACCTTC  CCA  ACA
                                |||||||||  |||  |||
                                AGGTGGGAG  GGT  TGT
                                     AA   AC
GAM1258 WSX1     3' TCCACCTTCCATCCG       22119          CCCACACAT
                                TCCACCTTCC       TCCG
                                ||||||||||       ||||
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                                AGGTGGAAGG        AGGC
                                      T_________
GAM1258  YY1      5'  TCCCCCTTCCTCCTGCGCCTCC 18183     A     C  ACACA
              GC                     TCC CCTTCC CC     TTCCGC
                                ||| |||||| ||     ||||||
                                AGG GGAAGG GG     GAGGCG
                                  G     A  ACGCG
GAM1259  FLOT1    3'  TTGGGTAGCAAAGTT       25137          TCCCTT
                                TTGGGTAGC     AAGTT
                                |||||||||     |||||
                                AACCCATCG     TTCAA
                                      T_____
GAM1259  PPP3R1   3'  TGTTGGGTGGTACTCTCT    44087         A__    C
                                TGTTGGGT   GCTC CT
                                ||||||||   |||| ||
                                ACAACCCA   TGAG GA
                                     CCA    A
GAM1260  ITGAV    3'  TAAGGTCCAAATTTGGACTGCT 13631      A  GAT   GA
              T                  TAAG TC   GGT  GGACTGCTT
                                |||| ||   |||  |||||||||
                                ATTC AG   TTA  CCTGACGAA
                                  C  GT_   AA
GAM1261  AF1Q     3'  GAGGTAAGGCTAAAATAGG   27726            CTT
                                GAGGTAAGGCTAAA   GG
                                ||||||||||||||   ||
                                CTCCATTCCGATTT   CC
                                       TAT
GAM1261  AP2B1    3'  AGGGATAAGGCTACTACAGGTA 10479    A         AACTT
              AG                   AG GGTAAGGCTA     GGTAAG
                                || ||||||||||     ||||||
                                TC CTATTCCGAT     CCATTC
                                 C         GATGT
GAM1261  COG7     3'  AGGGGTGAGACTAAAGGCGG   42655    A   A       CT
                                AG GGT AGGCTAAA  TGG
                                || ||| ||||||||  |||
                                TC CCA TCTGATTT  GCC
                                 C   C       CC
GAM1261  DCK      3'  AGAGGTGGGACTAAACTGTTAA 8978         AA        TGG
              G                   AGAGGT  GGCTAAACT   TAAG
                                ||||||  |||||||||   ||||
                                TCTCCA  CTGATTTGA   ATTC
                                   CC        CA_
GAM1261  GPR86    3'  GAGGTAAGGCCAGAAAGGTA   35794           AACTT
                                GAGGTAAGGCTA     GGTA
                                ||||||||||||     ||||
                                CTCCATTCCGGT     CCAT
                                       CTTT_
GAM1261  PDE4D    3'  AGGTAAGGTCATTTGGT     43890         C  AAC
                                AGGTAAGG TA   TTGGT
                                ||||||||  ||   |||||
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                                TCCATTCC GT   AACCA
                                    A  A__
GAM1261  SLC22A5   3'  AGAGGCTAGGGCTGGTAA    16856       A   CTAAAC
                                AGAGGT AGG     TTGGTAA
                                ||||||| |||     |||||||
                                TCTCCG TCC     GACCATT
                                   A   C_____
GAM1261  SNX15    3'  GAGGTAGGGCCAGGCCCTGG   43935       A    AA_
                                GAGGTA GGCTA   CTTGG
                                |||||| |||||   |||||
                                CTCCAT CCGGT   GGACC
                                   C    CCG
GAM1261  TNS      3'  AGAGGTGGGAGCTAAGGCA   35463       AA_     ACTT
                                AGAGGT   GGCTAA    GGTA
                                ||||||   ||||||    ||||
                                TCTCCA   TCGATT    CCGT
                                   CCC     ____
GAM1262  CHN1     3'  TTTATCCATTTGTGT       12250          ACAAT
                                TTTATCCATT     TGTGT
                                ||||||||||     |||||
                                AAATAGGTAA     ACACA
                                               _____
GAM1262  EGLN1    5'  TCCATTACACCATACA      35177         ATTGT
                                TCCATTACA    GTACA
                                |||||||||    |||||
                                AGGTAATGT    TATGT
                                     GG___
GAM1262  EPHA3    3'  TTTATCCATTCTAGTGAC    23446         ACAATT   T
                                TTTATCCATT     GTG AC
                                ||||||||||     ||| ||
                                AAATAGGTAA     CAC TG
                                     GAT___   _
GAM1262  NEDD4    3'  TTTACCCATTGCAAATATG    43107          A   T
                                TTTATCCATT CAA TGTG
                                |||||||||| ||| ||||
                                AAATGGGTAA GTT ATAC
                                     C   T
GAM1263  GALNT7   3'  TTTTAATCTTCTGGATAA    32649       G_
                                TTTTAAT  TCTGGATAA
                                |||||||  |||||||||
                                AAAATTA  AGACCTATT
                                   GA
GAM1263  HHIP     3'  TTTTTTAATGACAGGATAA   35415         TCT
                                TTTTTTAATG   GGATAA
                                ||||||||||   ||||||
                                AAAAAATTAC   CCTATT
                                     TGT
GAM1263  KLRC1    3'  TTTTTTTTTCTGGATA      28799       AATG
                                TTTTTT    TCTGGATA
                                ||||||    ||||||||
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                              AAAAAA   AGACCTAT
                                 AA__
GAM1263 ORC3L   3' TTTTTTATACTCCTGGATAA  29608      ATG_
                              TTTTTTA   TCTGGATAA
                              |||||||   |||||||||
                              AAAAAAT   GGACCTATT
                                 ATGA
GAM1264 ABCC12  3' CATTTTCCCATGTTGT     37716        A  A
                              CATTTTTCCAT GT TGT
                              |||||||||||| || |||
                              GTAAAAGGGTA CA ACA
                                       _  _
GAM1264 CNTNAP2 3' ATTTTTCCATTTTAAATGTA  30482       AGT__
                              ATTTTTCCAT    ATGTA
                              ||||||||||    |||||
                              TAAAAAGGTA    TACAT
                                    AAATT
GAM1264 COL19A1 3' AACATTTATCTCCAAAATGTAC 12366      __    TAGT
           TT                  AACATT  TTTCCA   ATGTACTT
                              ||||||  ||||||   ||||||||
                              TTGTAA  AGAGGT   TACATGAA
                                 AT     TT__
GAM1264 FPRL1   3' CATTTTTCCTGAATAAATACTT 11147       AT   T
                              CATTTTTCC  AGTA GTACTT
                              |||||||||  |||| ||||||
                              GTAAAAAGG  TTAT TATGAA
                                    AC   T
GAM1264 HPGD    3' CATTTTTCCATACAGCAGT   9241         __   T
                              CATTTTTCCAT  AGTA GT
                              ||||||||||  |||| ||
                              GTAAAAAGGTA  TCGT CA
                                    TG   _
GAM1264 KLHL1   3' ACATTTTTCCTGTATA     34074        ATA
                              ACATTTTTCC   GTATG
                              ||||||||||   |||||
                              TGTAAAAAGG   CATAT
                                 A__
GAM1264 LAMR1   3' CATTTTTCCATGCTGC     14100        A  A
                              CATTTTTCCAT GT TGT
                              |||||||||||| || |||
                              GTAAAAAGGTA CG ACG
                                       _  _
GAM1265 MGAT5   5' TTGATCATTTCACAATGTA   14482       CGATT
                              TTGATCAT    CAATGTA
                              ||||||||    |||||||
                              AACTAGTA    GTTACAT
                                 AAGT_
GAM1265 NBEA    3' ACTTGATCAGTACAATGTA   45430       TCGATT
                              ACTTGATCA    CAATGTA
                              |||||||||    |||||||
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                                TGAACTAGT     GTTACAT
                                     CAT___
GAM1266  CBLB     3'  TGTTCAAAACTTTTTTAAAG   20336         G GTGG
                                TGTTCAGAA C    TTTTAAAG
                                |||||||||  |    ||||||||
                                ACAAGTTTT G    AAAATTTC
                                     _ AA__
GAM1266  KCNS2    3'  TGCTCAGAAGTGAGTAAAG    42838         GC    TTT
                                TGTTCAGAA  GTGG   TAAAG
                                |||||||||  ||||   |||||
                                ACGAGTCTT  CACT   ATTTC
                                     __    C__
GAM1266  KIF5C    3'  TGTTCAGAAGTGTGGTTTT    21169         C
                                TGTTCAGAAG GTGGTTTT
                                |||||||||| ||||||||
                                ACAAGTCTTC CACCAAAA
                                      A
GAM1266  RAB1A    3'  TTCAAATGGTTTTAGAG      43192       AAGC        A
                                TTCAG    GTGGTTTTA AG
                                |||||    |||||||||  ||
                                AAGTT    TACCAAAAT TC
                                   _____         C
GAM1266  SCNN1A   3'  TGTTCAGAGGCAGTACCAAG   9786          A C TG  TTTA
                                TGTTCAGA G G  GT    AAG
                                ||||||||  |  |  ||    |||
                                ACAAGTCT C C  CA    TTC
                                     _ _ GT  TGG_
GAM1266  SDC2     5'  GTTCAGTTTCTGGTTTTAAGGA 42573       AAGCG        A
                                GTTCAG    TGGTTTTAA GA
                                ||||||    |||||||||  ||
                                CAAGTC    ACCAAAATT CT
                                    AAAG_        C
GAM1266  WHSC1L1  3'  TGTTCAGAGTCTTGAA      35719         AGCGTG     A
                                TGTTCAGA     GTTTT AA
                                ||||||||     |||||  ||
                                ACAAGTCT     CAGAA TT
                                     _______     C
GAM1267  COL4A4   3'  TTCAATTGTTTGAGATAC     6412           T   A
                                TTCAATTGTTT AGA AC
                                ||||||||||| |||  ||
                                AAGTTAACAAA TCT TG
                                      C   A
GAM1267  MTMR1    3'  TTCAAGTTGTTTTAGAAACA   43162       _
                                TTCAA TTGTTTTAGAAACA
                                |||||  ||||||||||||||
                                AAGTT AACAAAATCTTTGT
                                   C
GAM1268  CLTCL1   3'  CGAAGCAGGTCATAGCAGG    41882         _ ATTT   T
                                CGAAGCAGG CG    GCG GG
                                |||||||||  ||    |||  ||
```

```
                                GCTTCGTCC GT    CGT CC
                                     A  AT__  _
GAM1268  FMO5     3'  AGTAAGCGATTTTATACCG   11142    C       GC   G
                                AG AGGCGATTT  GTG CG
                                || |||||||||  ||| ||
                                TC TTCGCTAAA  TAT GC
                                 A        A_   G
GAM1268  NLGN2    3'  ACGAGGCGGCCAGCGCGTGGCG 44743      A  A   GATT
                                ACGA GC GGC    TGCGTGGCG
                                |||| || |||    |||||||||
                                TGCT CG CCG    GCGCACCGC
                                  C  _   GTC_
GAM1269  ADRA1A   5'  GCTGGGGGGTGAGAGCGCGC   37810        A   T   _
                                GCTGGGG TGG GGGC CGC
                                ||||||| ||| |||| |||
                                CGACCCC ACT CTCG GCG
                                    C   _    C
GAM1269  NR3C1    3'  CTGCTGGGGGGAGGGC       6753          ATG T
                                TTGCTGGGGG   G GGGC
                                |||||||||   | ||||
                                GACGACCCC   C CCCG
                                     ___ T
GAM1270  ATP5J    5'  AGCCTCCGTTGCCTTG      11767         CGAGG
                                AGCCTTCGT     GCTTTG
                                |||||||||     ||||||
                                TCGGAGGCA     CGGAAC
                                     A____
GAM1270  ATRN     3'  AGTCCTTCTCCAGGCTTTG   40265    _    G  GA
                                AG CCTTC TC  GGGCTTTG
                                || ||||| ||  ||||||||
                                TC GGAAG AG  TCCGAAAC
                                 A    _  G_
GAM1270  BTEB1    5'  AGCTTGCGGAGCTTTG      10210     C  C T  A
                                AGC TT G CG GGGCTTTG
                                ||| || | || ||||||||
                                TCG AA C GC CTCGAAAC
                                  _ _ _  _
GAM1270  CAPN2    3'  GCCTCGTGTCCTTTGA      11967      C_   GAGGG
                                GCCTT  GTC    CTTTGA
                                |||||  |||    ||||||
                                CGGAG  CAG    GAAACT
                                   CA  ______
GAM1270  CASQ2    5'  GCCTTGTTGAGCAAGGAG    10283      C  CGA   TTT
                                GCCTT GT   GGGC   GAG
                                ||||| ||   ||||   |||
                                CGGAA CA   CTCG   CTC
                                   _ A__    TTC
GAM1270  CDKN2B   3'  AGCCTTCATCGAATTAGG    38539           ___
                                AGCCTTCGTCGA   GGG
                                ||||||||||||   |||
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                                TCGGAAGTAGCT  TCC
                                      TAA
GAM1270 CTNS    3' GCCTTCGCTGGGTGA     22347       CGA  CTT
                                GCCTTCGT  GGG  TGA
                                ||||||||  |||  |||
                                CGGAAGCG  CCC  ACT
                                    A__  ___
GAM1270 CXCL16  3' GCCTTCGTTGCGGGTACAGGAG 35201       CGA  CTTT_
                                GCCTTCGT  GGG   GAG
                                ||||||||  |||   |||
                                CGGAAGCA  CCC   CTC
                                    ACG  ATGTC
GAM1270 GRLF1   3' ACCTTCGTTGGCCATTGAG  44218       CGAG  _
                                GCCTTCGT   GGCT TTGAG
                                ||||||||   |||| |||||
                                TGGAAGCA   CCGG AACTC
                                    A___   T
GAM1270 H1F0    5' AGCCCTCGTCGGAGGCTGAG  23697        AG   TT
                                AGCCTTCGTCG  GGCT  GAG
                                ||||||||||  ||||  |||
                                TCGGGAGCAGC  CCGA  CTC
                                      CT   __
GAM1270 HMGN1   5' AGCCTTCGCGAAACTGGG   22446       T  ____
                                AGCCTTCG CGA   GGG
                                |||||||| |||   |||
                                TCGGAAGC GCT   CCC
                                    _  TTGA
GAM1270 PC      3' AGCTTCTGTTGAAGGCTT   9554     C  _ C
                                AGC TTC GT GAGGGCTT
                                ||| ||| || ||||||||
                                TCG AAG CA CTTCCGAA
                                  _  A  A
GAM1271 HOXB5   3' GGGGGTGGCACGGGCTCTTG  13451      T  CC  AA
                                GGGGGT GC  CGG  GCTCTTG
                                ||||||  ||  |||  |||||||
                                CCCCCA CG  GCC  CGAGAAC
                                   C  T_  __
GAM1271 LAPTM5  3' GGGGGTTGCCTGCTTT     27605        CCGGAA  C
                                GGGGGTTGCC     GCT TT
                                ||||||||||     ||| ||
                                CCCCCAACGG     CGA AA
                                    A_____  _
GAM1271 MADH7   3' GGGGGCTGCCCCGGCAGCCCTT 25373           A
            G                    GGGGGTTGCCCCGG AGCTCTTG
                                ||||||||||||| ||||||||
                                CCCCCGACGGGGCC TCGGGAAC
                                      G
GAM1271 SNCB    3' GGGGGTTGCCTCAGAGC    16932        C   A
                                GGGGGTTGCC CGGA GC
                                |||||||||| |||| ||
```

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                                CCCCCAACGG GTCT CG
                                     A   _
GAM1271  THY1     3'  GGGTCAGAGCTCTGGAAGCTCT 26626      ___  CCC
              TG                   GGGTT  GC  GGAAGCTCTTG
                                   |||||  ||  ||||||||||
                                   CCCAG  CG  CCTTCGAGAAC
                                     TCT  AGA
GAM1272  MUCDHL   3'  GGGGTCGTGCGTGGGG     36320       CT   AGC
                                   GGGGTCGT  GCGT  GG
                                   ||||||||  ||||  ||
                                   CCCCAGCA  CGCA  CC
                                       __   CC_
GAM1272  RAB18    3'  CGGGGTCGATGAGTGGGA    34573       TC  C  AGC
                                   CGGGGTCG  TG GT  GGA
                                   ||||||||  || ||  |||
                                   GCCCCAGC  AC CA  CCT
                                       T_  T  C__
GAM1273  AVPR1A   5'  ACAATGTTCTGTATGG     8721        ATCTC  C
                                   ACAATGTTC    GT ATGG
                                   |||||||||    || ||||
                                   TGTTACAAG    CA TACC
                                       A____  _
GAM1273  DDX3     3'  ACAATGTTCATCTTTGGCCA  10674         C__
                                   ACAATGTTCATCT  GTCA
                                   ||||||||||||  ||||
                                   TGTTACAAGTAGA  CGGT
                                         AAC
GAM1273  HPS1     3'  ACAGGAGGCTCTCGTCATGG  6799     ATGTTCA
                                   ACA     TCTCGTCATGG
                                   |||     ||||||||||
                                   TGT     AGAGCAGTACC
                                    CCTCCG_
GAM1273  PDE4B    3'  AATGTTCATCTCCACAGGG   15144         GT  T
                                   AATGTTCATCTC  CA GG
                                   ||||||||||||  || ||
                                   TTACAAGTAGAG  GT CC
                                         GT  C
GAM1273  RPP30    5'  ACAATGTTTGGTTCCCCCTGGA 26931       CATC  G  A
              G                    ACAATGTT   TC TC TGGAG
                                   ||||||||   || || |||||
                                   TGTTACAA   AG GG ACCTC
                                       ACCA  G  G
GAM1273  TRHDE    3'  ATGTTCATCATGTCAAGG    30102       TC   T
                                   ATGTTCATC  GTCA GG
                                   |||||||||  |||| ||
                                   TACAAGTAG  CAGT CC
                                       TA   T
GAM1274  DNCI1    3'  ATGCTGTGGTGAATTTTGG   44988      CGC  A
                                   GTGCTG  GGT AATTTTGG
                                   ||||||  ||| ||||||||
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                                TACGAC   CCA TTAAAACC
                                   A__   C
GAM1274  NCKAP1   3'  TGCTGCTGCTCTTAGAATTTTG 30259       _ GG_ _
                G                   TGCTGC GC   TA AATTTTGG
                                    |||||| ||   || ||||||||
                                    ACGACG CG   AT TTAAAACC
                                       A  AGA  C
GAM1274  PKD2     3'  GTGTTGCTAACTCAAATTTTGG 41076     C   GCGG_
                                    GTG TGC     TAAATTTTGG
                                    ||| |||     ||||||||||
                                    CAC ACG     GTTTAAAACC
                                      A   ATTGA
GAM1274  RAB3B    3'  GTGTGCGTGTCAAATTTTGG   16084     C    CGG
                                    GTG TGCG   TAAATTTTGG
                                    ||| ||||   ||||||||||
                                    CAC ACGC   GTTTAAAACC
                                      _    ACA
GAM1274  WHSC1    5'  CGTTGCTGTAAAATAATTTTGG 39402     _    CGC     A
                                    CGT GCTG   GGTAA TTTTGG
                                    ||| ||||   ||||| ||||||
                                    GCA CGAC   TTATT AAAACC
                                      A    ATT    _
GAM1275  MAPK4    3'  TGGGTGACACACAGTTTGCATG 15672          GAC  CC
                                    TGGGTGACGCG   GT  TGCATG
                                    ||||||||||   ||  ||||||
                                    ACCCACTGTGT   CA  ACGTAC
                                          GT_  A_
GAM1276  STAT1    3'  TCAGAGTAACTGATGTTTC    40218        CGAA     CA
                                    TTAGAGTA    ACTGA  TTTC
                                    ||||||||    |||||  ||||
                                    AGTCTCAT    TGACT  AAAG
                                         _____     AC
GAM1277  ATRN     3'  TGAGTCAGATGCTTTGAGGGT  40285          _     TT
                                    TGAGTCAGAT CTTTGG  GT
                                    |||||||||| ||||||  ||
                                    ACTCAGTCTA GAAACT  CA
                                          C     CC
GAM1277  CLC      3'  TGGGTCTGGTCTGGTCTGTCCC 29905    A   AGATC     _
                T                    TG GTC     TTTGGT TGTCCCT
                                     || |||     |||||| |||||||
                                     AC CAG     AGACCA ACAGGGA
                                      C   ACC__      G
GAM1277  COG6     3'  TGAGTAGATCATTGTTTC    43766       C     T   GTTG
                                    TGAGT AGATC TTG    TC
                                    ||||| ||||| |||    ||
                                    ACTCA TCTAG AAC    AG
                                       _     T   AA__
GAM1277  DIBD1    3'  AGTTAACAAGATGGTTGTCC   36026     C  ATCTT
                                    AGT AG     TGGTTGTCC
                                    ||| ||     |||||||||
```

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                                TCA TT    ACCAACAGG
                                  A  GTTCT
GAM1277  G6PT1    5'  TGAGTTGGGTTTTTTCTGCTCC 11170     CAGATC   GG  _
                CT                  TGAGT     TTT  TTG TCCCT
                                    |||||     |||  ||| |||||
                                    ACTCA     AAA  GAC AGGGA
                                      ACCCA_   AA   G
GAM1277  NEBL     3'  TGATCAGATCTTAATTCC    26912     G       TGGTTG
                                    TGA TCAGATCTT     TCC
                                    ||| |||||||||     |||
                                    ACT AGTCTAGAA     AGG
                                      _       TTA___
GAM1277  RNASE1   3'  TGAATCAGATTTACAGTT    16343         CTT
                                    TGAGTCAGAT   TGGTT
                                    ||||||||||   |||||
                                    ACTTAGTCTA   GTCAA
                                          AAT
GAM1277  SELP     3'  TGAGTCAGATGCTCCAGTC    16551         _  TG
                                    TGAGTCAGAT CTT  GTT
                                    |||||||||| |||  |||
                                    ACTCAGTCTA GAG  CAG
                                          C   GT
GAM1277  TAF4     3'  TGAGTTAAGATTTAATTGTCC  17266      C_   CT
                                    TGAGT  AGAT  TTGGTTGTCC
                                    |||||  ||||  ||||||||||
                                    ACTCA  TCTA  AATTAACAGG
                                      AT   __
GAM1277  TCF8     3'  TGGGTCAATCTTTGGCT     36243    A    A
                                    TG GTCAG TCTTTGGTT
                                    || ||||| |||||||||
                                    AC CAGTT AGAAACCGA
                                     C    _
GAM1278  ADH5     3'  TGTTTATTCTGTGATACGTC   8584          ATAAAC
                                    TGTTTATTC     GCGTC
                                    |||||||||     |||||
                                    ACAAATAAG     TGCAG
                                          ACACTA
GAM1278  KCNAB1   3'  TATGTTTATTTGTAAAGCTCAA 41406          CA   C  G
                                    TATGTTTATT  TAAA GC TCAA
                                    |||||||||  |||| || ||||
                                    ATACAAATAA  ATTT CG AGTT
                                          AC   _ _
GAM1278  SDC2     3'  TATGTCTATTCATAAGACTACA 42575             _ _
                                    TATGTTTATTCATAA AC GCG
                                    |||||||||||||| || |||
                                    ATACAGATAAGTATT TG TGT
                                              C  A
GAM1278  SFRP4    3'  ATGTTTATTCAGTATTGTCA   16582          TAAACGC
                                    ATGTTTATTCA      GTCA
                                    ||||||||||       ||||
```

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                                TACAAATAAGT      CAGT
                                      CATAA__
GAM1279  BARHL1   3'  CATTTGTAAGAAGTTTAT    33459            C
                                CATTTGTGAGAAGT TAT
                                |||||||||||||| |||
                                GTAAACATTCTTCA ATA
                                       A
GAM1279  LILRB2   3'  TTTATTGAGAAGTCTGTTGC   25245      _       ATC
                                TTTGT GAGAAGTCT   GC
                                ||||| |||||||||   ||
                                AAATA CTCTTCAGA   CG
                                   A        CAA
GAM1279  LILRB3   3'  TTGTTGAGAAGTCTGTTGC    27802      _       ATC
                                TTGT GAGAAGTCT   GC
                                |||| |||||||||   ||
                                AACA CTCTTCAGA   CG
                                   A        CAA
GAM1279  ZNF268   3'  CATTTATGAGGTTTTTGTCT   41759         AA____
                                CATTTGTGAG     GTCT
                                ||||||||||     ||||
                                GTAAATACTC     CAGA
                                      CAAAAA
GAM1280  ABAT     3'  TGGGATCCGGGCTTTCTCACTG 40779     A   ATGT   C
                                TGG ATC    CTT TCTCACTG
                                ||| |||    ||| ||||||||
                                ACC TAG    GAA AGAGTGAC
                                  C   GCCC   _
GAM1280  D12S2489E 3'  TGGGGTTGCACTCTCACTG    28886     AATCA   CTT
                                TGG    TGT   CTCTCACTG
                                |||    |||   |||||||||
                                ACC    ACG   GAGAGTGAC
                                  CCA__   T__
GAM1280  GCNT2    5'  TGGACTTGCCCTCTCT      11254      ATCA
                                TGGA    TGTCTTCTCT
                                ||||    ||||||||||
                                ACCT    ACGGGAGAGA
                                  GA__
GAM1280  PEX10    3'  TGGGGCTGCTGTTCTCACTG   15224     AATCA  T  TC
                                TGG    TG CT  TCTCACTG
                                |||    || ||  ||||||||
                                ACC    AC GA  AGAGTGAC
                                  CCG__  _  CA
GAM1280  SNTB1    3'  TGGAATCATTCTACACCA    34285         GTCT   CT
                                TGGAATCAT    TCT  CACTG
                                |||||||||    |||  |||||
                                ACCTTAGTA    AGA  GTGGT
                                      _____   T_
GAM1280  WHSC1    3'  TGGGACTGTCCCTCTCACTG   39393     AATCA    T
                                TGG    TGTCT CTCTCACTG
                                |||    ||||| |||||||||
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                                ACC    ACAGG GAGAGTGAC
                                  CTG__    _
GAM1281  GFRA1    3'  GGCAAAAAAGCTTGGCATCAA  23567      TCT_  ACC
                                GGCAA   GC   TGGCATCAA
                                |||||   ||  |||||||||
                                CCGTT   CG   ACCGTAGTT
                                   TTTT  A__
GAM1281  GNAI3    3'  GGTAATCTGCACAAACA    27098    C       CT
                                GG AATCTGCAC  GGCA
                                || |||||||||  ||||
                                CC TTAGACGTG  TTGT
                                 A       T_
GAM1281  ITPKA    3'  GGCAAAACCCCTGGCATC    13638      TCT  A
                                GGCAA   GC CCTGGCATC
                                |||||   || |||||||||
                                CCGTT   TG GGACCGTAG
                                   T__  G
GAM1281  PODXL    3'  TCGGCAATCTCACTGCA    23984         G   CTG
                                TCGGCAATCT CAC   GCA
                                |||||||||| |||   |||
                                AGCCGTTAGA GTG   CGT
                                      _   A__
GAM1281  PPP1R2   3'  AGCAATCTGTAAATCA     26416         CACC   C
                                GGCAATCTG    TGG ATCA
                                |||||||||    ||| ||||
                                TCGTTAGAC    ATT TAGT
                                      _____  _
GAM1281  PRX      3'  TCGGCAGCTGCACCTCGG    34135       AT       _
                                TCGGCA  CTGCACCT GG
                                ||||||  |||||||| ||
                                AGCCGT  GACGTGGA CC
                                   C_       G
GAM1281  UBE2B    3'  TCAGCAGGCCCTGGCAT     17796       ATCT  A
                                TCGGCA   GC CCTGGCAT
                                ||||||   || ||||||||
                                AGTCGT   CG GGACCGTA
                                   C___  _
GAM1282  AP1M1    3'  TCACCAAACCCCACCTCCCC   37174          AAC
                                TCACTAAGCC   CCACCTCCCC
                                ||||||||||   ||||||||||
                                AGTGGTTTGG   GGTGGAGGGG
                                      ___
GAM1282  AQP2     3'  ACCACCCACCTGCCTCCC    7930       A     _ _
                                GCCA CCCACCT CC CCC
                                |||| ||||||| || |||
                                TGGT GGGTGGA GG GGG
                                  _      C  A
GAM1282  ATP2A3   3'  CTAAGACCTCCCCACCTCCCCC 23193       _  AA
                                CTAAG CC  CCCACCTCCCCC
                                ||||| ||  ||||||||||||
```

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                                GATTC GG  GGGTGGAGGGGG
                                  T  AG
GAM1282  B3GAT1   3'  TCACCACCTGTGCCCACCTCCT 38304      AA  AA__      _
             CC                   TCACT  GCC   CCCACCTCC CC
                                  |||||  |||   |||||||| ||
                                  AGTGG  TGG   GGGTGGAGG GG
                                    __  ACAC       A
GAM1282  CD8A     3'  TCTCTGGGCTTTAGCCTCCCCC 12093    A  AA  CAACCCA
                                  TC CT  GC      CCTCCCCC
                                  || ||  ||      ||||||||
                                  AG GA  CG      GGAGGGGG
                                   A  CC  AAATC__
GAM1282  CDR2     3'  CCACTAGCCACCTCC       44018       A   AACCC
                                  TCACTA GCC    ACCTCC
                                  |||||| |||    ||||||
                                  GGTGAT CGG    TGGAGG
                                    _  _____
GAM1282  DPYSL3   3'  TCACCTGACCCACCCACCTCCC 10779      AA   A
                                  TCACT  GCC ACCCACCTCCC
                                  |||||  ||| ||||||||||
                                  AGTGG  TGG TGGGTGGAGGG
                                    AC   G
GAM1282  EHD4     3'  TCACTGCAGAGAACCACCTC   40208      A_  CC    C
                                  TCACT  AG  AACC ACCTC
                                  |||||  ||  |||| |||||
                                  AGTGA  TC  TTGG TGGAG
                                    CG  TC   _
GAM1282  KRT4     5'  CTAGGCTCACAGCACCTCCC   14003     A  _  ACC
                                  CTA GC CA   CACCTCCC
                                  ||| || ||   ||||||||
                                  GAT CG GT   GTGGAGGG
                                   C  A  GTC
GAM1282  MTA1L1   3'  CTACCTCTCAGCCCACCTCCC  21885     AGC__  A
                                  CTA    CA CCCACCTCCC
                                  |||    || ||||||||||
                                  GAT    GT GGGTGGAGGG
                                   GGAGA  C
GAM1282  NPTX2    3'  CTGAGCCCCCCTCCCC      45205    A   AAC  A
                                  CT AGCC   CC CCTCCCC
                                  || ||||   || |||||||
                                  GA TCGG   GG GGAGGGG
                                   C   ___  _
GAM1282  NRD1     5'  CCAGGACCCACCTCCTCC    14855     __        _
                                  CCA  ACCCACCTCC CC
                                  |||  |||||||||| ||
                                  GGT  TGGGTGGAGG GG
                                   CC         A
GAM1282  PPARA    3'  TCCTGAGATTAGCCACCTCCCC 22769    A  A  CCAAC
             C                     TC CT AG    CCACCTCCCCC
                                  || || ||    ||||||||||
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```
                                AG GA TC    GGTGGAGGGGG
                                 _ C  TAATC
GAM1282  PSCD4    3'  TCCTGAGCTCTGCCTTCCCC  30132    A  A   CAAC  ACC
                                TC CT AGC   CC   TCCCC
                                || || |||   ||   |||||
                                AG GA TCG   GG   AGGGG
                                 _ C   AGAC  A__
GAM1282  RFC2     3'  TCACTGCAACCTCCACCTCCTC 16282      A_   AAC      _
              C                  TCACT  AGCC   CCACCTCC CC
                                ||||| ||||  |||||||| ||
                                AGTGA  TTGG   GGTGGAGG GG
                                   CG   A__      A
GAM1282  SLC6A1   3'  ACTGTCCTCCCACCTCCCC   40484    AAG  AA
                                ACT   CC  CCCACCTCCCC
                                |||   ||  ||||||||||
                                TGA   GG  GGGTGGAGGGG
                                  CA_  A_
GAM1282  SPOCK    3'  TAAGCCAATGACTTCCC    41740       CCC  C
                                TAAGCCAA   AC TCCC
                                ||||||||   || ||||
                                ATTCGGTT   TG AGGG
                                     AC_  A
GAM1282  WHSC1    3'  CACTGGAGAGCCACCTCCCC  39355     AAGCCAAC
                                CACT       CCACCTCCCC
                                ||||       ||||||||||
                                GTGA       GGTGGAGGGG
                                  CCTCTC__
GAM1282  ZNF219   3'  TCACTAAGCTAATCGCCC    32336       C  CCCACC  _
                                TCACTAAGC AA     TC CCC
                                |||||||| ||     || |||
                                AGTGATTCG TT     AG GGG
                                     A _______  C
GAM1283  GPRK6    3'  GGAATGTTTGAGGGTTGACC  13271         AGATGC
                                GGAATGTTTGA     GCC
                                ||||||||||      |||
                                CCTTACAAACT     TGG
                                       CCCAAC
GAM1283  SEMG1    3'  TGGAAGTTTGAAGGCGC     16557      T      AT
                                TGGAA GTTTGAAG  GCGC
                                ||||| ||||||||  ||||
                                ACCTT CAAACTTC  CGCG
                                   _      __
GAM1283  SEMG2    3'  TGGAAGTTTGAAGGGGC     16558      T      AT
                                TGGAA GTTTGAAG  GC
                                ||||| ||||||||  ||
                                ACCTT CAAACTTC  CG
                                   _      CC
GAM1283  SOX9     3'  TGGAATGTCTTGAAGGTTAACT 7376          _   ATGC  C
              GC                   TGGAATGTTT GAAG    GC GC
                                |||||||||| ||||    || ||
```

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                                ACCTTACAGA CTTC   TG CG
                                     A   CAAT  A
GAM1284  TCN2    3'  GCGGACTCCGTTTTTTG    7406     AT      CC
                                GCG  GACTCCGT  TTTG
                                |||  ||||||||  ||||
                                CGC  CTGAGGCA  AAAC
                                  __       AA
GAM1285  NEU3    3'  GACTTCAGTAGCTTCTGT    27401     ATGTA TG     C
                                GACT    T  GTAGCT CTGT
                                ||||    |  |||||| ||||
                                CTGA    A  CATCGA GACA
                                  _____ GT     A
GAM1285  PAPSS1  3'  GACTATGTGGTCCCCT     24145       ATT   AG
                                GACTATGT   GGT  CTCCT
                                ||||||||   |||  |||||
                                CTGATACA   CCA  GGGGA
                                     ___   __
GAM1285  ATP7B   3'  AATGTGGACAGTAATAGCTA  6274       A__
                                AATGTG   AGTAATAGCTA
                                ||||||   ||||||||||||
                                TTACAC   TCATTATCGAT
                                   CTG
GAM1285  BACE2   3'  AATGTGATTTTCTTAATAGCT  39985       AG____
                                AATGTGA     TAATAGCT
                                |||||||     ||||||||
                                TTACACT     ATTATCGA
                                    AAAAGA
GAM1285  FUT6    5'  AGTACAAAGTGAAAAGGCT   6646        T     TAATA
                                AGTACAA GTGAAG    GCT
                                ||||||| ||||||    |||
                                TCATGTT CACTTT    CGA
                                    T     TC___
GAM1285  GEMIN5  5'  ATGTAGAAAGTAATAGCT    44842     __
                                ATGT  GAAGTAATAGCT
                                ||||  ||||||||||||
                                TACA  TTTCATTATCGA
                                  TC
GAM1285  ITGB1   3'  GCACAATGTGACCTTAGCT   38049          AGTAA
                                GTACAATGTGA    TAGCT
                                ||||||||||    |||||
                                CGTGTTACACT    ATCGA
                                      GGA__
GAM1285  PTER    3'  GCACAGTTGTAATAGCT     36216      AT  GAA
                                GTACA  GT   GTAATAGCT
                                |||||  ||   |||||||||
                                CGTGT  CA   CATTATCGA
                                  __  A__
GAM1285  RASGRP1 3'  AATATGAGATGGTAATAGCTA  25070       A___
                                AATGTGA   GTAATAGCTA
                                |||||||   ||||||||||
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                                TTATACT   CATTATCGAT
                                   CTAC
GAM1285 SPAG11   5' AAGGACAATGTGGACACGCTA 38478    T      AAGTAATA
                                AAG ACAATGTG      GCTA
                                ||| ||||||||      ||||
                                TTC TGTTACAC      CGAT
                                  C      CTGTG___
GAM1286 APP      3' TGAACAGGGATTCTTTTC    7922        AG  GCG
                                TGAGCAGG  TT   CTTTTC
                                ||||||||  ||   ||||||
                                ACTTGTCC  AA   GAAAAG
                                   CT  ___
GAM1286 CHRNB2   5' TGAGCAGGCGGAGGCTTTTC  8862        AGTTGC
                                TGAGCAGG     GCTTTTC
                                ||||||||     |||||||
                                ACTCGTCC     CGAAAAG
                                   GCCTC_
GAM1286 DUSP1    5' GCAGGGCGGCGCTTTTC     20656      A  T
                                GCAGG GT GCGCTTTTC
                                ||||| || |||||||||
                                CGTCC CG CGCGAAAAG
                                  _  C
GAM1286 FKRP     3' TGGGCAGAACACTTTT      35901    A    AGTT
                                TG GCAGG   GCGCTTTT
                                || |||||   ||||||||
                                AC CGTCT   TGTGAAAA
                                 C    _____
GAM1286 HD       3' TGAGCAGGGGCTCCCTTTC   13364        A   GCG
                                TGAGCAGG GTT   CTTTTC
                                |||||||| |||   ||||||
                                ACTCGTCC CGA   GGAAAG
                                   C   G__
GAM1286 IL20RA   3' TGAGAGGACACTTTT       30880     C   AGTT
                                TGAG AGG   GCGCTTTT
                                |||| |||   ||||||||
                                ACTC TCC   TGTGAAAA
                                  _  _____
GAM1286 LSP1     3' TGATCAGGAGTTTCTTTC    14244     G      GCG
                                TGA CAGGAGTT   CTTTT
                                ||| ||||||||   |||||
                                ACT GTCCTCAA   GAAAG
                                  A      A__
GAM1286 MAN2B1   5' GAGCAGAAGTGCTTTTC     8033          TGC
                                GAGCAGGAGT   GCTTTTC
                                ||||||||||   |||||||
                                CTCGTCTTCA   CGAAAAG
                                     ___
GAM1286 MLLT2    3' GAGCGGGGGTTGCCTTC     25500     A  A    G
                                GAGC GG GTTGC CTTT
                                |||| || ||||| ||||
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                                CTCG CC CAACG GAAG
                                  C  C    _
GAM1286  MTNR1B   3'  TGAGAAGGAGTTGGGCTC    25555     C       C
                                TGAG AGGAGTTG GCTT
                                |||| |||||||| ||||
                                ACTC TCCTCAAC CGAG
                                  T       C
GAM1286  MYO1C    3'  TGGCAGAGGCGCTTTT     41474    A   G  TT
                                TG GCAG AG  GCGCTTTT
                                || |||| ||  ||||||||
                                AC CGTC TC  CGCGAAAA
                                 _   _ __
GAM1286  NORE1    3'  AGCAGGAGACTTTT       36427        TTGC
                                AGCAGGAG   GCTTTT
                                ||||||||   ||||||
                                TCGTCCTC   TGAAAA
                                    ____
GAM1286  OLFM1    5'  TGGGCGGGAGCTGCGCCCTC  26785    A  A
                                TG GC GGAGTTGCGCTTTT
                                || || ||||||||||||||
                                AC CG CCTCGACGCGGGAG
                                 C  C
GAM1286  PMX1     3'  TAAGTAGCCATGGCGCTTTTC 35514     C  GA  T
                                TGAG AG  GT GCGCTTTTC
                                |||| ||  || |||||||||
                                ATTC TC  TA CGCGAAAAG
                                  A  GG  C
GAM1286  RHCE     3'  TGAACAGGCCTTGTTTTTC   39780       AG   CGC
                                TGAGCAGG  TTG   TTTTC
                                ||||||||  |||   |||||
                                ACTTGTCC  AAC   AAAAG
                                    GG   A__
GAM1286  RHD      3'  TGAACAGGCCTTGTTTTTC   32168       AG   CGC
                                TGAGCAGG  TTG   TTTTC
                                ||||||||  |||   |||||
                                ACTTGTCC  AAC   AAAAG
                                    GG   A__
GAM1286  THRB     5'  GAGCAGGAGGTCTCTTTTC   7857        TTGCG
                                GAGCAGGAG    CTTTTC
                                |||||||||    ||||||
                                CTCGTCCTC    GAAAAG
                                   CAGA_
GAM1287  EIF2AK3  3'  TGAGGGCTATAAAGCTTG    22109    A   CT  GATCT
                                TGA GGC  TA    GAGCTTG
                                ||| |||  ||    |||||||
                                ACT CCG  AT    TTCGAAC
                                  C   AT  _____
GAM1287  GFRA2    3'  AGCCTTGGTTAAGCTTGG    11261      AGATC
                                GGCCTT    TGAGCTTGG
                                ||||||    |||||||||
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                                TCGGAA    ATTCGAACC
                                   CCA__
GAM1287  NTF5    3'  GGTCCTTAGATCAGCTGG    26138   _      TG   T
                                GG CCTTAGATC  AGCT GG
                                || |||||||||  |||| ||
                                CC GGAATCTAG  TCGA CC
                                 A       __   _
GAM1287  ODF2    3'  TGAGAGGTTTGCACTGAGCTTG 14934    _  CCTTAGAT
           G                     TGA AGG       CTGAGCTTGG
                                ||| |||       ||||||||||
                                ACT TCC       GACTCGAACC
                                  C   AAACGT__
GAM1287  TNS     3'  TGAGGTGCCTTGGGTCTGAG   35481    AG_    AGA
                                TGA   GCCTT   TCTGAG
                                |||   |||||   ||||||
                                ACT   CGGAA   AGACTC
                                  CCA    CCC
GAM1287  ABCB11   5'  GAGGAAATAATGGACTCCAC   19044    AA       _  A
                                GA  AGATAATGG CT CCAT
                                ||  ||||||||| || ||||
                                CT  TTTATTACC GA GGTG
                                 CC       T  _
GAM1287  ADD2    3'  AGAGATAGCTCCATCCA    32721    TA     A
                                AGA  ATGGCT CCATCCA
                                |||  |||||| |||||||
                                TCT  TATCGA GGTAGGT
                                  C_     _
GAM1287  ATP1A2   3'  AAAGATAAACTTTTGTCCAC   8702         TG   ACCA
                                AAAGATAA  GCT    TCCAC
                                ||||||||  |||   |||||
                                TTTCTATT  TGA    AGGTG
                                     __  AAAC
GAM1287  CBFA2T1  3'  GAAAAGATATCTTTGTTATCCA 20299         ATGGCTACC
           C                     GAAAAGATA        ATCCAC
                                |||||||||        ||||||
                                CTTTTCTAT        TAGGTG
                                     AGAAACAA_
GAM1287  EGLN2    5'  AGAGGGCTGCCACCATCTAC   38813    TAATG       C
                                AGA    GCTACCATC AC
                                |||    ||||||||| ||
                                TCT    CGGTGGTAG TG
                                  CCCGA        A
GAM1287  LIPA    3'  GAAAAAATAGTGGTATAGTCTC 6937          A   CTACCA_
           CAC                   GAAAAGATA TGG      TCCAC
                                |||||||||  |||      |||||
                                CTTTTTTAT ACC      AGGTG
                                     C   ATATCAG
GAM1287  PSG4    3'  GAAATGGTGAGAGCCATCCAC  15799    T    CTA___
                                GA AATGG     CCATCCAC
                                || |||||     ||||||||
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                                CT TTACC     GGTAGGTG
                                 _    ACTCTC
GAM1287  PSG7     3'  GAAATGGTGAGAGCCATCCAC  15807    T    CTA___
                                GA AATGG     CCATCCAC
                                || |||||     ||||||||
                                CT TTACC     GGTAGGTG
                                 _    ACTCTC
GAM1287  SDC4     3'  AGAAAGGGTAGAACCATCCAC  16516     TAAT  CT__
                                AGA   GG   ACCATCCAC
                                |||   ||   |||||||||
                                TCT   CC   TGGTAGGTG
                                  TTC_  ATCT
GAM1287  SLC17A2  5'  GGAGAAATGACCATTGTCCAC  25182   A  T      CCA
                                A AGA AATGGCTA   TCCAC
                                | ||| ||||||||   |||||
                                C TCT TTACTGGT   AGGTG
                                 C  _       AAC
GAM1288  B4GALT5  3'  GTGTACTTGATGGTAATTATG  21941     _ A_  A
                                GTG AC  GAT GTAATTATG
                                ||| ||  ||| |||||||||
                                CAC TG  CTA CATTAATAC
                                  A  AA   C
GAM1288  DLG5     3'  TGATAGTGACAATAACCATTAT 44470           A   TA
           G                     TGATAGTGACAG TAG  ATTATG
                                ||||||||||| |||  ||||||
                                ACTATCACTGTT ATT  TAATAC
                                       _  GG
GAM1288  FGF12    3'  TGGTAGTGACAGGTGTA     34303    A       ATA
                                TG TAGTGACAG   GTA
                                || |||||||||   |||
                                AC ATCACTGTC   CAT
                                 C        CA_
GAM1288  CTSC     5'  GCTGAGAAAAGAGGTGAAGAAT 12239     A    TTATAA
           T                     GCT AGAG     TGAAGAATT
                                ||| ||||     |||||||||
                                CGA TCTT     ACTTCTTAA
                                  C    TTCTCC
GAM1288  FGF2     3'  TACTAGGTAAATGAAGAAT    12841       A A  TAT
                                TGCTA G GT   AATGAAGAAT
                                ||||| | ||   ||||||||||
                                ATGAT C CA   TTACTTCTTA
                                   _ _  T__
GAM1288  TCF2     3'  TGTTAAGAGTCATAATGA    7848     C
                                TG TAAGAGTTATAATGA
                                || ||||||||||||||
                                AC ATTCTCAGTATTACT
                                 A
GAM1289  CTNND2   5'  TTGCCCAACTGCAGCATC    10637        G    ACACC
                                TTGCCCAA TGCA     GTGTC
                                |||||||| ||||     |||||
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                                AACGGGTT ACGT    CGTAG
                                    G   _____
GAM1289  MAOB    3'  TTACCCAAGTGTGTACTGTCC  41033         CAAC  CG
                                TTGCCCAAGTG   AC  TGTCC
                                ||||||||||    ||  |||||
                                AATGGGTTCAC   TG  ACAGG
                                      ACA_  __
GAM1289  MRPL49   3'  TGCCCGAGTCATCTGTGT    43029      A   G  ACACC
                                TGCCC AGT CA    GTGT
                                ||||| ||| ||    ||||
                                ACGGG TCA GT    CACA
                                   C  _  AGA__
GAM1289  NAB2     5'  CCCCGCGCACGATGCCGTGTCC 25563     AA    ACA__
                                CCC  GTGCA    CCGTGTCC
                                |||  |||||    ||||||||
                                GGG  CGCGT    GGCACAGG
                                  G_    GCTAC
GAM1289  TFCP2    5'  TTGCCCCAGGAGACACCGTGTC 24924       A  TGCA
                                TTGCCC AG   ACACCGTGTC
                                ||||||  ||   ||||||||||
                                AACGGG TC   TGTGGCACAG
                                    G  CTC_
GAM1289  TRPS1    3'  TTGCCCAAGTTAACCA      30477         GCAAC
                                TTGCCCAAGT    ACCG
                                ||||||||||    ||||
                                AACGGGTTCA    TGGT
                                      AT___
GAM1289  ACPT     3'  TGCAAGGATAGCATTCAGCAG  38894     CAAACTCC  _
                                TGCA       GG ATTCAGCAG
                                ||||       ||  |||||||||
                                ACGT       TC TAAGTCGTC
                                  TCCTA___  G
GAM1289  CENPB    5'  TGCGCAGGTCCGGATTC     43019     A  AAC
                                TGC CA   TCCGGATTC
                                |||  ||   |||||||||
                                ACG GT   AGGCCTAAG
                                  C  CC_
GAM1289  DNASE1   5'  TGCTGGGCTCCGGATCCTGCA  23360     ACAAA        A
                                TGC    CTCCGGATTC GCA
                                |||    |||||||||| |||
                                ACG    GAGGCCTAGG CGT
                                  ACCC_        A
GAM1289  IFRD1    3'  TGCACAAAGTCTCATACAGCAG 41109        C  _  GATT
            A                    TGCACAAA TC CG    CAGCAGA
                                ||||||||  ||  ||    |||||||
                                ACGTGTTT AG GT    GTCGTCT
                                     C  A  AT__
GAM1289  IGF1R    3'  TGCACAGATTCAGGATCCAA   9331        AAC  C
                                TGCACA   TC GGATTCAG
                                ||||||   ||  ||||||||
```

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                                ACGTGT   AG CCTAGGTT
                                   CTA  T
GAM1289 ITGAM    3'  TGCGCAGGCTCCAGCAG     43521     A  AACTCC  A
                                TGC CA     GG TTCAGCAG
                                ||| ||     || ||||||||
                                ACG GT     CC AGGTCGTC
                                  C _______  G
GAM1289 LBR      3'  CACAAACTTTGGATCAAG    40427        CC    C
                                CACAAACT  GGATT AG
                                ||||||||  ||||| ||
                                GTGTTTGA  CCTAG TC
                                     AA    T
GAM1289 LILRB1   5'  TACACAAACTCCAGAAAGTAGA 27428             TTC  C
                                TGCACAAACTCCGGA   AG AGA
                                ||||||||||||||   || |||
                                ATGTGTTTGAGGTCT   TC TCT
                                         T__  A
GAM1289 LZTFL1   3'  TGCATAACTCAGCAGCAG    33772     CA    C  ATT
                                TGCA  AACTC GG   CAGCAG
                                ||||  ||||| ||   ||||||
                                ACGT  TTGAG TC   GTCGTC
                                  A_    _ ___
GAM1289 SLC26A4  3'  TGCACAAATTTTGGTAAATGCA 7766         CTCC  ATTCA
           G                     TGCACAAA   GG    GCAG
                                ||||||||   ||    ||||
                                ACGTGTTT   CC    CGTC
                                     AAAA  ATTTA
GAM1289 SNL      3'  TGCCAGACTCGCCCCGTGGCAG 16949    A  A   CGGATTCA
           A                     TGC CA ACTC       GCAGA
                                ||| || ||||       |||||
                                ACG GT TGAG       CGTCT
                                  _ C    CGGGGCAC
GAM1289 TNFRSF8  3'  TGTACAAGCCCCGGATCCCCTA 10327    C   A        AGC
           G                     TG ACAA CTCCGGATTC   AG
                                || |||| ||||||||||   ||
                                AC TGTT GGGGCCTAGG   TC
                                 A   C         GGA
GAM1289 WDR4     3'  TACACAGACTCAGTAGCGGA   38024       A   _____
                                TGCACA ACTC    CGGA
                                |||||| ||||    ||||
                                ATGTGT TGAG    GCCT
                                   C    TCATC
GAM1289 ZNF239   5'  TGCACAAATGCCCTGCAA    24980        CT  GGATTCA
                                TGCACAAA  CC     GCAG
                                ||||||||  ||     ||||
                                ACGTGTTT  GG     CGTT
                                     AC  GA_____
GAM1289 ZNF24    5'  GCGCAAACTCCGGCTCAG    28088    A        A
                                GC CAAACTCCGG TTCAG
                                || |||||||||| |||||
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                                CG GTTTGAGGCC GAGTC
                                 C       _
GAM1290  BACE    3'  TCTTTGTACTCCCTCTCCTTCT 39972    GGCAG  C      CC
                                TC    AC CCCTCTCC  CT
                                ||    || ||||||||  ||
                                AG    TG GGGAGAGG  GA
                                 AAACA  A       AA
GAM1290  BCL9    3'  GATCGGCACATCCCATCT    20240        GAC   C
                                GATCGGCA   CCC TCT
                                ||||||||   ||| |||
                                CTAGCCGT   GGG AGA
                                     GTA   T
GAM1290  CNP     3'  GGCACGTTTCCCTCTCCCC    37560      GACC_
                                GGCA    CCCTCTCCCC
                                ||||    ||||||||||
                                CCGT    GGGAGAGGGG
                                  GCAAA
GAM1290  GRAF    3'  GCCTCCCCTCTCTCCCT     31449    AGAC       C
                                GC    CCCCTCTC CCCT
                                ||    |||||||| ||||
                                CG    GGGGAGAG GGGA
                                 GA__       A
GAM1290  GRIA1   5'  GGTGTTTCCCCCCCTTTCCCT  9090     CAGA_      CC
                                GG    CCCCCTCT  CCCT
                                ||    ||||||||  ||||
                                CC    GGGGGGGA  GGGA
                                 ACAAA       AA
GAM1290  IL6R    5'  TCGGCTCCTCTCCCC       8187       AGACCC       C
                                TCGGC     CCTCTCCC C
                                |||||     |||||||| |
                                AGCCG     GGAGAGGG G
                                  A_____       A
GAM1290  INHBB   3'  AGCCCCCTCTTCTCTCCCT   13540    A     ___  C
                                AG CCCCCTC   TC CCCT
                                || |||||||   || ||||
                                TC GGGGGAG   AG GGGA
                                 _      AAG  A
GAM1290  JUNB    3'  GATCGCCCCCTCTTCCCC    13755      GCAGA       C
                                GATCG    CCCCCTCT CCCC
                                |||||    |||||||| ||||
                                CTAGC    GGGGGAGA GGGG
                                   _____       A
GAM1290  LEP     3'  GGCAGACCCCAAACCTCC    6916          C__
                                GGCAGACCCC   TCTCC
                                ||||||||||   |||||
                                CCGTCTGGGG   GGAGG
                                     TTT
GAM1290  MAL     3'  TCAGCAGAGGATCTTTCTTTCC 35336        CCCC  C  CC_
            T                    TCGGCAGA   CT TC   CCT
                                ||||||||   || ||   |||
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                                AGTCGTCT   GA AG   GGA
                                    CCTA  A  AAA
GAM1290  MYCL1    3'  TCGGCTTCTTCTCCCCCT    23891      AGACCCCC
                                TCGGC       TCTCCCCCT
                                |||||       |||||||||
                                AGCCG       AGAGGGGGA
                                   AAGA____
GAM1290  NEUD4    3'  GGCTTCCCCCTCTCCCCC    21622     AGA
                                GGC   CCCCCTCTCCCCC
                                |||   ||||||||||||
                                CCG   GGGGGAGAGGGGG
                                  AA_
GAM1290  WRN      5'  GAGCGGAGACCCCCTCTTCCCC 8140     T   C         C
              T                  GA CGG AGACCCCCTCT CCCCT
                                || ||| |||||||||| |||||
                                CT GCC TCTGGGGGAGA GGGGA
                                 C   _          A
GAM1291  DMD      5'  CTGACAGCTGTTTGCAGACCTC 19682          ___ _   TAA
              CT                   CTGACAGCTGT   CA ACC   TCCT
                                |||||||||||   || |||   ||||
                                GACTGTCGACA   GT TGG   AGGA
                                      AAC  C   ___
GAM1291  KRT16    5'  CCTGGCATTGTCAATCT     45450      A  GC     C
                                CCTG CA  TGTCAA CT
                                |||| ||  |||||| ||
                                GGAC GT  ACAGTT GA
                                  C  A_     A
GAM1291  PCDH9    5'  CTGGAGGCTGTCAAAACTCCT  44397     ACA       CCTAA
                                CTG   GCTGTCAA     TCCT
                                |||   ||||||||     ||||
                                GAC   CGACAGTT     AGGA
                                  CTC       TTG__
GAM1291  PPARGC1  3'  CCTGACAATTGTCATGCATCCT 29950         C     ACCTA
                                CCTGACAG TGTCA     ATCCT
                                |||||||| |||||     |||||
                                GGACTGTT ACAGT     TAGGA
                                     A     ACG__
GAM1291  PPEF1    3'  CTGACATTTAACCTAATC     26410       GCTGTC
                                CTGACA      AACCTAATC
                                ||||||      |||||||||
                                GACTGT      TTGGATTAG
                                   AAA___
GAM1291  EIF5A2   3'  TGACAGTTTTTGATAACATGA  33787       CTGTCAGG   T
                                TGACAG       GGT ACATGA
                                ||||||       ||| ||||||
                                ACTGTC       CTA TGTACT
                                   AAAAA___   T
GAM1291  FGFR2    3'  CGGCAGGTGAGAGGGGTTACAT 35660     A   C  TC
              G                   TG CAG TG  AGGGGTTACATG
                                || ||| ||  ||||||||||||
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                                GC GTC AC  TCCCCAATGTAC
                                 C   C  TC
GAM1291  GLTSCR1   3'  TGACAGCCTGTTGGGGGC    31840       _  CA
                                TGACAGC TGT  GGGGT
                                ||||||| |||  |||||
                                ACTGTCG ACA  CCCCG
                                    G   AC
GAM1291  LTB4R     5'  CGCAGCTGTCAGAGGATATGA  8882     A          TTAC
                                TG CAGCTGTCAGGGG   ATGA
                                || ||||||||||||   ||||
                                GC GTCGACAGTCTCC   TACT
                                 _          TA__
GAM1291  RSU1      3'  TGACATTTAAATGGTTACATGA 29678      GCTGTCAGG
                                TGACA       GGTTACATGA
                                |||||       ||||||||||
                                ACTGT       CCAATGTACT
                                   AAATTTA__
GAM1291  SCN1A     5'  TGAAGCTGTCAGGTCCTGGT   44818     C       ____
                                TGA AGCTGTCAGG   GGT
                                ||| ||||||||||   |||
                                ACT TCGACAGTCC   CCA
                                 _       AGGA
GAM1291  XRCC5     3'  TGACAGCTGTTGGAGGATCA   34493        CA_
                                TGACAGCTGT   GGGGTTA
                                ||||||||||   |||||||
                                ACTGTCGACA   TCCTAGT
                                      ACC
GAM1292  CTPS      3'  CAGAGACAGACATCTT      44797     C   GTCGT
                                CAG AGAT    AGACATCTT
                                ||| ||||    |||||||||
                                GTC TCTG    TCTGTAGAA
                                 _   _____
GAM1292  DYRK1A    3'  AACAGATGTTGTAATCTTGA   38987       C   GAC
                                AGCAGATGT GTA   ATCTTGA
                                ||||||||| |||   |||||||
                                TTGTCTACA CAT   TAGAACT
                                      A  ___
GAM1292  FCMD      3'  AGCTGACTCAGACATCTTGA   27510     A  GTCG
                                AGC GAT    TAGACATCTTGA
                                ||| |||    ||||||||||||
                                TCG CTG    GTCTGTAGAACT
                                  A  A___
GAM1292  GATA4     3'  CAGGGGACAAGGACATCTTG   13106     ATGT  TA
                                CAG    CG  GACATCTTG
                                |||    ||  |||||||||
                                GTC    GT  CTGTAGAAC
                                  CCCT  TC
GAM1292  IRS1      3'  CAGCAGATGAAATGTATCTTGA 24414        TCGTAGAC
                                CAGCAGATG       ATCTTGA
                                |||||||||       |||||||
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                                GTCGTCTAC       TAGAACT
                                     TTTACA__
GAM1292  KCNA3    3'  CAGATCAGGACATCTTG     13793      TG   TA
                                CAGA  TCG  GACATCTTG
                                ||||  |||  |||||||||
                                GTCT  AGT  CTGTAGAAC
                                  __   C_
GAM1292  MGEA5    3'  TGACAGATGTTATCTT      29219    A       CGTAGAC
                                C GCAGATGT      ATCTT
                                | ||||||||      |||||
                                A TGTCTACA      TAGAA
                                 C       A_______
GAM1292  MPP1     3'  ACAGATGTGTCATTTTG     14622         C  AGA   C
                                GCAGATGT GT   CAT TTG
                                |||||||| ||   ||| |||
                                TGTCTACA CA   GTA AAC
                                     _ ____   A
GAM1292  ZHX1     3'  CAGTAAATCAGACATCTTG   28516     A  TCG
                                CAG TG   TAGACATCTTG
                                ||| ||   ||||||||||
                                GTC AT   GTCTGTAGAAC
                                  _ TTA
GAM1292  CHGB     3'  GGTATATAAATGGTGTCT    12242         TG    AC
                                GGTATATG  GATG  GTCT
                                ||||||||  ||||  ||||
                                CCATATAT  TTAC  CAGA
                                     __   CA
GAM1292  KAL1     3'  TTCATGTATATGCATGTGTCT  6878       G       GG   AC
                                TTCA GTATATGT  ATG  GTCT
                                |||| ||||||||  |||  ||||
                                AAGT CATATACG  TAC  CAGA
                                  A       __   A_
GAM1292  LOXL2    3'  TTCAAGTATGTGTAAGTGTCT  14201          A    ATGAC
                                TTCAGGTAT TGTGG    GTCT
                                ||||||||| |||||    ||||
                                AAGTTCATA ACATT    CAGA
                                     C    CA___
GAM1293  MMP15    3'  TTTGCCGGCTGTACAATTTAT  14566       AGC     _
                                TTTGCC   GGTTGTA GATTTAT
                                ||||||   ||||||| |||||||
                                AAACGG   CCGACAT TTAAATA
                                   ___      G
GAM1293  RPS17    3'  TTTGCTGTTGTCCCAGATTTAT 9749       CAGCG   G
                                TTTGC    GTT TAGATTTAT
                                |||||    ||| |||||||||
                                AAACG    CAG GTCTAAATA
                                  ACAA_   G
GAM1293  SNX9     3'  ACATATTCTTTACAATTTGT   32146       CCG
                                ACATAT   TTACAATTTGT
                                ||||||   ||||||||||
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                                TGTATA   AATGTTAAACA
                                   AGA
GAM1293  TOX     5'  CACATCCGTTTGTGGTTTGTT  31268         ACAA_
                                CATATCCGTT    TTTGTT
                                ||||||||||    ||||||
                                GTGTAGGCAA    AAACAA
                                     ACACC
GAM1294  DRPLA    3'  GGGTGCTCCAAGGTCCAATGTA 12592     A    CATCA
                                GGGT CTCT    CCAATGTA
                                |||| ||||    ||||||||
                                CCCA GAGG    GGTTACAT
                                  C   TTCCA
GAM1294  FHL1     3'  GTGGGGGTTTTATCTCCTATGC 11097     A  CC  CC_   TT
                                GTGGG GT  TA   CCT  TGC
                                ||||| ||  ||   |||  |||
                                CACCC CA  AT   GGA  ACG
                                   C  AA  AGA   T_
GAM1294  GAS11    3'  TGTGGGAGACTTTTTCCCTTTT 11226        TCCTA__   C
             TGC                   TGTGGGAG      CCC TTTTGC
                                ||||||||      ||| ||||||
                                ACACCCTC      GGG AAAACG
                                     TGAAAAA   A
GAM1294  PDGFRB   3'  GCCCTCTTTGTCCCTTTTGC   42339      AC____
                                GTCCT     CCCTTTTGC
                                |||||     |||||||||
                                CGGGA     GGGAAAACG
                                   GAAACA
GAM1294  RRM2B    3'  TATGGCCTGCTCCTTTTG    42724      GAGT   ACC
                                TGTGG   CCT   CCTTTTG
                                |||||   |||   |||||||
                                ATACC   GGA   GGAAAAC
                                   _____  CGA
GAM1294  VIPR2    3'  GTGGGGGATGCTCCCTTTTG   18026      A_  C  AC
                                GTGGG  GT CT  CCCTTTTG
                                |||||  || ||  ||||||||
                                CACCC  TA GA  GGGAAAAC
                                   CC  C  __
GAM1295  AARS     3'  TAGCAGATGAAGAGCTCTT    11488        AAACA   G
                                TAGCAGAT    AGCT TT
                                ||||||||    |||| ||
                                ATCGTCTA    TCGA AA
                                     CTTC_   G
GAM1295  COL19A1  3'  GCAGATAAGTTGTAAGCGTTT  12377        AC___   T
                                GCAGATAA    AAGC GTTT
                                ||||||||    |||| ||||
                                CGTCTATT    TTCG CAAA
                                     CAACA   _
GAM1295  DNTT     3'  TAGAGATAGACAGTATTTCAG  43818     C    A   A C
                                TAG AGATA ACA G TGTTTCAG
                                ||| ||||| ||| | ||||||||
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                                ATC TCTAT TGT C ATAAAGTC
                                  _    C  _ _
GAM1295  TGIF     3'  TAACAGGAAGCTGTTT      17502       ATAAAC
                                TAGCAG     AAGCTGTTT
                                ||||||     |||||||||
                                ATTGTC     TTCGACAAA
                                   C_____
GAM1295  TMOD3    3'  TAGCAGAAAGTAGAAATGTTTC 30966        TAAACAAGC
              AG                  TAGCAGA       TGTTTCAG
                                |||||||       ||||||||
                                ATCGTCT       ACAAAGTC
                                    TTCATCTTT
GAM1295  ATP10C   3'  TGAAGTGGAGCCCAGCCCTCCT 35984      T  AAA       GGA
              G                   TGAA TG   CCCAGCCT   TG
                                |||| ||   ||||||||   ||
                                ACTT AC   GGGTCGGG   AC
                                  C  CTC       AGG
GAM1295  CENPE    3'  TGAATTGAAATTAAGCTG    12238         CCC   C
                                TGAATTGAAA   AGC TG
                                ||||||||||   ||| ||
                                ACTTAACTTT   TCG AC
                                     AAT   _
GAM1295  CYBB     3'  TGAATTGATACCTGAGGTG    44102        A   CAGCCT  A
                                TGAATTGA ACC     GG TG
                                |||||||| |||     || ||
                                ACTTAACT TGG     CC AC
                                     A   ACT___  _
GAM1295  PLA2G2D  3'  TGAATTGAGCACCTAGTATG   29640        AACCCA     _
                                TGAATTGA     GCCTGG ATG
                                ||||||||     |||||| |||
                                ACTTAACT     TGGATC TAC
                                     CG____     A
GAM1295  SHC1     3'  GATATGAAACCCAGAGTCCATG 16700    AT        CCTGG
              C                    GA  TGAAACCCAG    ATGC
                                ||  ||||||||||    ||||
                                CT  ACTTTGGGTC    TACG
                                 AT        TCAGG
GAM1295  SLC17A4  3'  TGAATTGAATCCTACTGAATG  24258         A  CAGC
                                TGAATTGAA CC    CTGGATG
                                |||||||| ||    |||||||
                                ACTTAACTT GG    GACTTAC
                                     A  AT__
GAM1295  SLC9A5   3'  TGAACTGAAGCCTGGCCCAG   21392         A  CA   TG
                                TGAATTGAA CC  GCC  G
                                ||||||||| ||  |||  |
                                ACTTGACTT GG  CGG  C
                                     C  AC   GT
GAM1296  CMAR     5'  TCCTCAGCTTGAGCCC      23296         CAAGCCC
                                TTCTCGGTT      GAGCCC
                                |||||||||      ||||||
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                                AGGAGTCGA      CTCGGG
                                    A_______
GAM1296 EZH1     3' CTCTTTCAGTTTGAGCCCT   12783     GG   AGCCC
                                CTC  TTCA    GAGCCCT
                                |||  ||||    |||||||
                                GAG  AAGT    CTCGGGA
                                  A_   CAAA_
GAM1296 FGFR1    3' TTCTGGGTTCAAGCAGTTAGC  31963      C       CCG_
                                TTCT GGTTCAAGC    AGC
                                |||| |||||||||    |||
                                AAGA CCAAGTTCG    TCG
                                  C       TCAA
GAM1297 PART1    3' AGAATATCTCATCTGTGTT   32455        ATGAT  _
                                AGAATGTCT    TC GTGTT
                                |||||||||    || |||||
                                TCTTATAGA    AG CACAA
                                    GT___  A
GAM1298 DPYSL2   3' GTGATGGAATGACCTACT    10755        CA
                                GTGATGGGG  GCCTACT
                                |||||||||  |||||||
                                CACTACCTT  TGGATGA
                                    AC
GAM1298 MME      3' TGTGATGGTGCCCTCTC     28607        GGCA   A
                                TGTGATGG   GCCT CTC
                                ||||||||   |||| |||
                                ACACTACC   CGGG GAG
                                    A___   A
GAM1298 PIK3R1   3' ACTGGGGTGGGGAAGCTTATTC 42858     TGA    C   C  C
                                ACTG   TGGGG AGC TA TC
                                ||||   ||||| ||| || ||
                                TGAC   ACCCC TCG AT AG
                                  CCC    T   A  A
GAM1298 PML      3' CTGTGATGGGTGGGGCCT    37754        GCA_
                                CTGTGATGGG    GCCT
                                ||||||||||    ||||
                                GACACTACCC    CGGA
                                    ACCC
GAM1298 DDX6     3' TGGGTTTGTACCGTGCAG    20570        CAGAAA  _
                                TGGGTTTG     TG GCAG
                                ||||||||     || ||||
                                ACCCAAAC     GC CGTC
                                    ATG___  A
GAM1298 GLP1R    3' CCTCTGGGCTCCTGGAAGTGGC 13139    _      GCA   A
          AG                      CC CTGGGTTT   GAA TGGCAG
                                || ||||||||   ||| ||||||
                                GG GACCCGAG   CTT ACCGTC
                                 A       GAC   C
GAM1298 HMGA2    3' CCTAACTTGCAGAAATGG    18506      G  T
                                CCTGG TT GCAGAAATGG
                                ||||| || ||||||||||
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                                GGATT AA CGTCTTTACC
                                  G  _
GAM1298 HMX1    5'  CCTCGGTCCGCTGGGGATGG  33209    G     AGAA_
                                CCT GGTTTGC    ATGG
                                ||| |||||||    ||||
                                GGA CCAGGCG    TACC
                                  G      ACCCC
GAM1298 IL6R    3'  GATCTCAGAAATGGCAG    8175      G
                                GGTTT CAGAAATGGCAG
                                ||||| ||||||||||||
                                CTAGA GTCTTTACCGTC
                                  _
GAM1298 LCP1    3'  CCCCTGGAGTTTAGGGGTGGCA 14104       _    CAGAAA
              G                  TCCCTGG GTTTG     TGGCAG
                                |||||||  |||||     ||||||
                                GGGGACC CAAAT     ACCGTC
                                   T    CCCC__
GAM1298 MUC4    3'  TCCCTGGGGGAATGG      39676       TTTGCA   A
                                TCCCTGGG     GAA TGG
                                ||||||||     ||| |||
                                AGGGACCC     CTT ACC
                                   C_____  _
GAM1298 NRXN3   3'  CCAGGCCTGCGGAAGTGG   39940   TG     A   A
                                C  GGTTTGC GAA TGG
                                |  ||||||| ||| |||
                                G  CCGGACG CTT ACC
                                 GT      C   C
GAM1298 OTP     3'  TCCCTGGTACGTAAAATGGC  37003      GTT  CA
                                TCCCTGG   TG  GAAATGGC
                                |||||||   ||  ||||||||
                                AGGGACC   GC  TTTTACCG
                                   AT_  A_
GAM1298 PCTK1   3'  CCCCTGCAACTGGGGATGGC  37468      GGT   CA  AA
                                TCCCTG   TTG  GA  TGGC
                                ||||||   |||  ||  ||||
                                GGGGAC   GAC  CT  ACCG
                                   GTT   CC  __
GAM1298 PREB    3'  CTCTGCTCTAGAGATGGCAG  30141   GG   GC   A
                                CT  GTTT  AGA ATGGCAG
                                ||  ||||  ||| |||||||
                                GA  CGAG  TCT TACCGTC
                                 GA   A_  C
GAM1298 RAB36   3'  TCCCAGGGGGAATGGC     22246     T   TTTGCA   A
                                TCCC GGG     GAA TGGC
                                |||| |||     ||| ||||
                                AGGG CCC     CTT ACCG
                                  T  C_____  _
GAM1298 SCA1    3'  TCTTTGGGTTTATAGGAACAG  7292     CC      C  A
                                TC  TGGGTTTG AG AATGG
                                ||  |||||||| || |||||
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                                AG  ACCCAAAT TC TTGTC
                                 AA       A  C
GAM1298  SLC35A2   3'  CCCTGGGTGGGGCAGGGGTGG  24951        TT_   AAA
                                CCCTGGGT   GCAG   TGG
                                ||||||||   ||||   |||
                                GGGACCCA   CGTC   ACC
                                     CCC    CCC
GAM1298  TXNIP    3'  TCCTTGGGTTTGAAGTCACAG  27000     C       C  AA
                                TCC TGGGTTTG AG  ATGG
                                ||| |||||||| ||  ||||
                                AGG ACCCAAAC TC  TGTC
                                  A       T  AG
GAM1298  VDR      3'  TCTCTGGGTTTTCAGGGAACTA 7529     C       G   A_   G
              C                  TC CTGGGTTT CAG  AAT GC
                                || |||||||| |||  ||| ||
                                AG GACCCAAA GTC  TTG TG
                                 A       A   CC   A
GAM1298  ZNF16    3'  GGTCTGGGAAGTGGCAG     28086       CA   A
                                GGTTTG  GAA TGGCAG
                                ||||||  ||| ||||||
                                CCAGAC  CTT ACCGTC
                                   C_   C
GAM1299  ABCB10   3'  AAAATGAGGTGCCATGCTA   28987         A  T AA
                                AAGATGAG GT G  ATGCTA
                                |||||||| || |  ||||||
                                TTTTACTC CA C  TACGAT
                                     _ _ GG
GAM1299  AEGL1    3'  TGGGAGTTGAACCACA      10062     A      AAT
                                TG GAGTTGA   GCTACA
                                || |||||||   ||||||
                                AC CTCAACT   TGGTGT
                                 C      ___
GAM1299  BSN      3'  AGATGAGACTTGTGGCT     18388         G   AAAT
                                AGATGAGA TTG    GCT
                                |||||||| |||    |||
                                TCTACTCT AAC    CGA
                                     G   AC__
GAM1299  CUGBP1   3'  AAAGGTGAGAGTTCAAGC    27275      A       G  AT
                                AAAG TGAGAGTT AA  GC
                                |||| |||||||| ||  ||
                                TTTC ACTCTCAA TT  CG
                                  C       G  __
GAM1299  GBE1     3'  AGACATTTTCTGAAATGCTACA 6685       GAGAG
                                AGAT    TTGAAATGCTACA
                                ||||    ||||||||||||
                                TCTG    GACTTTACGATGT
                                  TAAAA
GAM1299  ITGB1    3'  AGGTGAGAGCTGTTGC      38043     A       AAA
                                AG TGAGAGTTG   TGC
                                || |||||||||   |||
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                                TC ACTCTCGAC   ACG
                                 C        A__
GAM1299  MECP2    3'  AAAGTGACGCTTGAAATGCT   22564      A   GA   _
                                AAAG TGA  GTT GAAATGCT
                                |||| |||  ||| ||||||||
                                TTTC ACT  CGA CTTTACGA
                                  _  G_   A
GAM1299  PDGFRA   3'  AAAGATAGCAAAATGCTA    26283       GAG   T
                                AAAGAT   AGT GAAATGCTA
                                ||||||   ||| |||||||||
                                TTTCTA   TCG TTTTACGAT
                                   ___   _
GAM1299  PGK1     3'  AAGATGAGCTGAGATGCT    7112        GA    A
                                AAGATGA  GTTGA ATGCT
                                |||||||  ||||| |||||
                                TTCTACT  CGACT TACGA
                                   __    C
GAM1299  PIN4     3'  AAGATCAGAGTTGACTAAC   26326       G       AAT
                                AAGAT AGAGTTGA   GC
                                ||||| ||||||||   ||
                                TTCTA TCTCAACT   TG
                                   G       GAT
GAM1299  TCF12    3'  AAAAATGAGAGCAAGAGAAATG 17338           T___
            CTA                   AAAGATGAGAGT    GAAATGCTA
                                ||||||||||||    |||||||||
                                TTTTTACTCTCG    CTTTACGAT
                                      TTCT
GAM1299  RAD52    3'  TTCGTGGTCTTAGATGATT    39564         CGTTC
                                TTCGTGGTCT    GTGATT
                                ||||||||||    ||||||
                                AAGCACCAGA    TACTAA
                                      ATC__
GAM1300  COL4A3   3'  GAGGAAGCTACTGTATATG    6393      AAATT  AC
                                GAG    GT  CTGTATATG
                                |||    ||  |||||||||
                                CTC    CG  GACATATAC
                                  CTT__  AT
GAM1300  ELK1     3'  ACAGAGAAGTTGTGGAAGCTGT 23405        A    AC___
                                ATAGAGAA TTGT    CTGT
                                |||||||| ||||    ||||
                                TGTCTCTT AACA    GACA
                                    C    CCTTC
GAM1300  EIF4A2   3'  TATTTCTGATCCGTTATGA    12688      C       CCA
                                TATT CTGATCCG   ATGA
                                |||| ||||||||   ||||
                                ATAA GACTAGGC   TACT
                                  A       AA_
GAM1300  GALR1    3'  CAAATATTCCTGACCATATTGA 11195    T         CGCCA_
            TG                    CA ATATTCCTGATC     ATG
                                || ||||||||||||     |||
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                                GT TATAAGGACTGG     TAC
                                 T          TATAAC
GAM1300  MAP3K7IP2 3'  ATACATTCCTGATCATCTGA   31519            CGCCAA
                                ATATATTCCTGATC     TGA
                                ||||||||||||||     |||
                                TATGTAAGGACTAG     ACT
                                       TAG___
GAM1300  PYCS      3'  ATATTCCTCCAGCTCAGTG    16036        TGA  _ _  A
                                ATATTCC   TCC GC CA TG
                                |||||||   ||| || || ||
                                TATAAGG   AGG CG GT AC
                                    ___   T  A  C
GAM1301  ETV5      3'  CAATAGAGGAGAATCTCATGT  20842      _   TTTA
                                TAAT GAG    AGAATCTCATGT
                                |||| |||    ||||||||||||
                                GTTA CTC    TCTTAGAGTACA
                                  T   C___
GAM1302  AGM1      3'  TGACTGAATTGTATACTT    31816    A    TTCT
                                A ACTG    AATTGTATACTT
                                | ||||    ||||||||||||
                                A TGAC    TTAACATATGAA
                                 C   _____
GAM1302  CTNND2    3'  TAAACTATTCTGTGTCTTGTGC 10636          AA___    ATA
            TTA                   TAAACTGTTCT    TTGT   CTTA
                                ||||||||||     ||||   ||||
                                ATTTGATAAGA    AACA   GAAT
                                      CACAG    C__
GAM1302  PCDHA9    3'  CTGTGATCTTGTATACTTA    36545      TCTAA
                                CTGT    TTGTATACTTA
                                ||||    ||||||||||
                                GACA    AACATATGAAT
                                  CTAG_
GAM1302  BMP1      3'  GGGTATTCAGGGGAGGAGAAGT 25989    A   GC  AA    AAC
            T                    GG GTA  CA  GGAG   AAGTT
                                || |||  ||  ||||   |||||
                                CC CAT  GT  CCTC   TTCAA
                                 _   AA  CC    CTC
GAM1302  KCNN2     5'  GGAGCAGCAGGGACAGGT    34669        CAA   A  A  A
                                GGAGTAGC   AGG GA CA GT
                                |||||||   ||| || || ||
                                CCTCGTCG   TCC CT GT CA
                                    ___   _ _  C
GAM1302  MAP3K10   3'  GGGTACAAAGGAATAAGT    42759    A   GC       AAC
                                GG GTA  CAAAGGAG   AAGT
                                || |||  ||||||||   ||||
                                CC CAT  GTTTCCTT   TTCA
                                 _  __       A__
GAM1302  RGS16     3'  GGAGGGCCAAAGGGGAA     16323      TA       A
                                GGAG  GCCAAAGG GAA
                                ||||  |||||||| |||
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                                CCTC  CGGTTTCC CTT
                                  C_      C
GAM1302  WDR4     3'  GGATGCAGGGGAACAAGT    38021     _   CCAAA  A
                                GGA GTAG    GG GAACAAGT
                                ||| ||||    || ||||||||
                                CCT CGTC    CC CTTGTTCA
                                  A  _____  _
GAM1303  PCDH9    5'  TTTGATAGGGTTGGCTACTAT  44415       CGA   CGTC
                                TTTGAT   GTT   GCTACTAT
                                ||||||   |||   ||||||||
                                AAACTA   CAA   CGATGATA
                                   TCC   C___
GAM1303  C6       5'  GCATCTTTGCCAGT        45403         AACTC
                                GCATCTTT    GTCAGT
                                ||||||||    ||||||
                                CGTAGAAA    CGGTCA

                                  _____
GAM1304  ANXA11   3'  TTTGTTAGAAACAGACA     10105      CC       T
                                TTTG  AGAAACAGG CA
                                ||||  ||||||||| ||
                                AAAC  TCTTTGTCT GT
                                  AA       _
GAM1304  ANXA9    3'  TTTGCCAAAAGAATTCGAGTAT 18696          ACAGG  A
             C                   TTTGCCAGAA    TC AGTATC
                                ||||||||||    || ||||||
                                AAACGGTTTT    AG TCATAG
                                     CTTA_  C
GAM1304  DYRK2    3'  TTTGCCAGATAAAGTGTC    27045         AAC  _
                                TTTGCCAGA   AG GTC
                                |||||||||   || |||
                                AAACGGTCT   TC CAG
                                     ATT  A
GAM1304  ETV3     3'  TTTGTAGAAACAGGTTCCCAT  23481      CC        _ AA
                                TTTG  AGAAACAGGT C  GT
                                ||||  |||||||||| |  ||
                                AAAC  TCTTTGTCCA G  TA
                                  A_        A GG
GAM1304  MADH1    3'  CAGAGGTCAAGTAT       25337      AACA
                                CAGA    GGTCAAGTAT
                                ||||    ||||||||||
                                GTCT    CCAGTTCATA

                                  _____
GAM1304  OPA3     3'  TTTGCCAGAGTGCCCACGGT   36073         AA___  _
                                TTTGCCAGA    CA GGT
                                |||||||||    || |||
                                AAACGGTCT    GT CCA
                                     CACGG  G
GAM1304  PIAS3    3'  CCAGAAACAGACCCCAGT    25909          GT A_
                                CCAGAAACAG  C  AGT
                                ||||||||||  |  |||
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                                GGTCTTTGTC  G  TCA
                                      TG GG
GAM1304  TP53BP2  3'  TTTGCCAAAAATAATCGTAT  24066          CA   AA
                                TTTGCCAGAAA  GGTC  GTAT
                                ||||||||||  ||||  ||||
                                AAACGGTTTTT  TTAG  CATA
                                      A_   __
GAM1304  COMT     3'  TCAGGGCGCAGGCCTCGGCCGA 28695      ATAT         A
             G                   TCGG   CGGGCCTCGGCC AG
                                ||||   ||||||||||| ||
                                AGTC   GTCCGGAGCCGG TC
                                  CCGC         C
GAM1304  FRAP1    5'  TCGCGCGGCTTCGGCCAAG   22438    GATAT  _  C
                                TCG    CG GGC TCGGCCAAG
                                |||    || ||| |||||||||
                                AGC    GC CCG AGCCGGTTC
                                 _____  G  A
GAM1304  GTF2I    5'  CGGAGCAGCCTCGGCTGAG   37444     TATCG       CA
                                CGGA    GGCCTCGGC  AG
                                ||||    |||||||||  ||
                                GCCT    TCGGAGCCG  TC
                                  CG___       AC
GAM1305  ABCD4    3'  TCTTACAGATCTCACACTTCCA 33749        CCA_  CT  C
             G                   TCTTACGGA   GC  CT CCAG
                                |||||||||   ||  || ||||
                                AGAATGTCT   TG  GA GGTC
                                      AGAG  T_  A
GAM1305  AP1M1    3'  TCTTGAAGACCAGCCTCT    37175     AC
                                TCTT  GGACCAGCCTCT
                                ||||  ||||||||||||
                                AGAA  TCTGGTCGGAGA
                                  CT
GAM1305  CKTSF1B1 3'  CACACCAGCCTCTCCCAG    30081    G
                                CG ACCAGCCTCTCCCAG
                                || ||||||||||||||
                                GT TGGTCGGAGAGGGTC
                                 G
GAM1305  IL1R1    3'  TCTTAGGGAAAGTCTCCCAG   9370       C  CC  CC
                                TCTTA GGA  AG  TCTCCCAG
                                ||||| |||  ||  ||||||||
                                AGAAT CCT  TC  AGAGGGTC
                                   C  T_  __
GAM1305  ITPKB    3'  TCTTACAGGGCCAGGGCTGCT  13658        A_   C_  _
                                TCTTACGG  CCAG  CT CT
                                ||||||||  ||||  || ||
                                AGAATGTC  GGTC  GA GA
                                     CC   CC  C
GAM1305  LGALS3BP 5'  GACCCAGAAGCCTCTCCCAG   42930     ____
                                GACC   AGCCTCTCCCAG
                                ||||   ||||||||||||
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                                CTGG   TCGGAGAGGGTC
                                  GTCT
GAM1305 NCKAP1   5' CCTTCGCAGCAGCCTCTC   30255     A  GAC
                                TCTT CG   CAGCCTCTC
                                |||| ||   |||||||||
                                GGAA GC   GTCGGAGAG
                                  _  GTC
GAM1305 PLA2G5   3' CTTAGGAGCCTCTCTCA    9577      C   CCA     C
                                CTTA GGA   GCCTCTC CA
                                |||| |||   ||||||| ||
                                GAAT CCT   CGGAGAG GT
                                  _  ___     A
GAM1305 RAD54L   3' TCTTGATGATTTTCTCCCAG   18716     ACG  CCAGCC
                                TCTT   GA     TCTCCCAG
                                ||||   ||     ||||||||
                                AGAA   CT     AGAGGGTC
                                  CTA  AAA___
GAM1305 ROBO1    5' TCTTGCGGAGCCTCCC     39488     A    CCA
                                TCTT CGGA   GCCTCTC
                                |||| ||||   |||||||
                                AGAA GCCT   CGGAGGG
                                  C   ___
GAM1305 CEACAM6  3' TTGACATCTTGGGAAAAGC   14735          CT
                                TTGACATCTTGG  GAAGC
                                ||||||||||||  |||||
                                AACTGTAGAACC  TTTCG
                                      CT
GAM1305 CLIC3    5' GCCTTGACAAACAGCTGGAGC  21698        TCT     A
                                GCCTTGACA   TGGCTG AGC
                                |||||||||   |||||| |||
                                CGGAACTGT   GTCGAC TCG
                                     TT_     C
GAM1305 DUSP4    3' TGCCTTGACATCTGCATGCT   38429          TG__
                                TGCCTTGACATCT    GCT
                                ||||||||||||    |||
                                ACGGAACTGTAGA    CGA
                                       CGTA
GAM1305 EMP1     3' TGCCTTGGCTTTCAGCAAGAGG 10900       ACATC TG  T_  A
            CC                    TGCCTTG    T  GC  GA GCC
                                |||||||    |  ||  || |||
                                ACGGAAC    A  CG  CT CGG
                                   CGAA_ GT  TT  C
GAM1305 MEL      3' TGCCTTGTGTCTTGGCC     23875       ACA
                                TGCCTTG   TCTTGGCT
                                |||||||   ||||||||
                                ACGGAAC   AGAACCGG
                                   AC_
GAM1305 OSR1     3' TTGCACCAGCTGAAG       23040     A   TT
                                TTG CATC  GGCTGAAG
                                ||| ||||  ||||||||
```

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                                AAC GTGG  TCGACTTC
                                  _   __
GAM1305  PER2    3'  TGCTTGGCACGCGCTGAAGC  35622    C  A  CTTG
                                TGC TTG CAT   GCTGAAGC
                                ||| ||| |||   ||||||||
                                ACG AAC GTG   CGACTTCG
                                  _  C  CG__
GAM1305  SMOH    3'  CTTGCCTGGCTGAAGC     24813     ACAT
                                CTTG   CTTGGCTGAAGC
                                ||||   ||||||||||||
                                GAAC   GGACCGACTTCG
                                  ____
GAM1305  SNCA    3'  TTAACATCGTAGATTGAAGCC  28661       TT_ GC
                                TTGACATC   G  TGAAGCC
                                ||||||||   |  |||||||
                                AATTGTAG   C  ACTTCGG
                                     CAT TA
GAM1305  ZNF267  5'  TGCCCTGGCGTCTTAGCT   18259      ACA
                                TGCCTTG   TCTTGGCT
                                |||||||   ||||||||
                                ACGGGAC   AGAATCGA
                                    CGC
GAM1306  CXCL13  3'  TATTACTTATAACTGAATAAC  26951           T
                                TATTATTTATAACTGA GTAAC
                                |||||||||||||||| |||||
                                ATAATGAATATTGACT TATTG
                                                _
GAM1306  RASGRP1 3'  TATTATTTAAGCCACTGAT   25081       TA__
                                TATTATTTA   ACTGAT
                                |||||||||   ||||||
                                ATAATAAAT   TGACTA
                                     TCGG
GAM1307  ANKH    3'  TGTTGATTCTTAAGAGCGA   38329      GGCGC
                                TGTTGG    AAGAGCGA
                                ||||||    ||||||||
                                ACAACT    TTCTCGCT
                                   AAGAA
GAM1307  G1P3    3'  TGTTGGGGAGAGTGA      35642       CGCA   C
                                TGTTGGGG   AGAG GA
                                ||||||||   |||| ||
                                ACAACCCC   TCTC CT
                                     _____   A
GAM1307  HDAC4   3'  TGCTGGTGGGGCGTGGGCA  25787     T     CAAGA
                                TGCTG TGGGGCG    GCG
                                ||||| |||||||    |||
                                ACGAC ACCCCGC    CGT
                                   C      ACC__
GAM1307  NID     3'  TGTTGTTGGGGCTCAGGC   14801   C      GCA  A
                                TG TGTTGGGGC   AG GC
                                || |||||||||   || ||
```

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                                AC ACAACCCCG   TC CG
                                 A        AG_ _
GAM1307  SYN3     3'  GCTGTGAGGCGAGGGTGGCA   18565       T     CAAGA_
                                GCTGT GGGGCG      GCG
                                ||||| ||||||      |||
                                CGACA CTCCGC      CGT
                                   _      TCCCAC
GAM1307  CYP2F1   3'  CATCTGCCTCTGCCCTGC     8928         G     ___
                                CATCTGCC TCTGC   GC
                                |||||||| |||||   ||
                                GTAGACGG AGACG   CG
                                   _    GGA
GAM1307  FGD1     5'  CTGCCGTGCCAGGCATCGC    20903        _  C   ACAC
                                CTGCCGT CTG GCA    CGC
                                ||||||| ||| |||    |||
                                GACGGCA GGT CGT    GCG
                                    C   C   A___
GAM1307  GUCY1A2  5'  CTGCTGCTCGCGCGGCGCCGC  9218       C TC     AACA
                                CTGC G  TGCGC    CCGC
                                |||| |  |||||    ||||
                                GACG C  GCGCG    GGCG
                                  A GA     CCGC
GAM1307  MYOM2    3'  CATCTGCCGTCTACCC      19557            GCAACA
                                CATCTGCCGTCTGC     CC
                                ||||||||||||||     ||
                                GTAGACGGCAGATG     GG
                                                   _______
GAM1307  PTPN1    5'  TCTGCCGCTCTAGGCCGCGTCG 15906        _    C  AACAC
                C                TCTGCCG TCTG GC     CGC
                                |||||||| |||| ||     |||
                                AGACGGC AGAT CG     GCG
                                   G    C  GCGCA
GAM1307  TCF8     3'  TGCCGTCTGTATTACAGCAC   36242         C___   A
                                TGCCGTCTG    GCA CAC
                                |||||||||    ||| |||
                                ACGGCAGAC    TGT GTG
                                     ATAA   C
GAM1307  TSG      3'  CATCAGCCGTCTGCTGAAAAAC 34001      T       GC___     C
                ACTGC                CATC GCCGTCTGC     AACAC GC
                                |||| |||||||||     ||||| ||
                                GTAG CGGCAGACG     TTGTG CG
                                  T        ACTTT     A
GAM1308  CD2      3'  TGTGATGGAGCTCTCTGA     12085           AGCCTA   C
                                TGTGATGGGGC      CTC GA
                                ||||||||||      ||| ||
                                ACACTACCTCG      GAG CT
                                     A_____   A
GAM1308  CHRM1    3'  TGTGTGGGGCAGGGCCG     45427      A       CCTACT
                                TGTG TGGGGCAG      CCG
                                |||| ||||||||      |||
```

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                                ACAC ACCCCGTC     GGC
                                  _       CC____
GAM1308  INPP5A   3'  TGTGGGGCTGCTCCG      24413    A     A  CTAC
                                TG TGGGGC GC    TCCG
                                || |||||| ||    ||||
                                AC ACCCCG CG    AGGC
                                  _     A  _____
GAM1308  PIK3R1   3'  TGGGGAAGCTTATTCTGAA   42862      C   C  C  C
                                TGGGG AGC TA TC GAA
                                ||||| ||| || || |||
                                ACCCC TCG AT AG CTT
                                   T   A  A  A
GAM1308  SDC2     3'  GTGATGGGGCAGGAATCTGA   42572           CCTAC  C
                                GTGATGGGGCAG     TC GA
                                ||||||||||||     || ||
                                CACTACCCCGTC     AG CT
                                        CTT__  A
GAM1308  DDX6     3'  TGGGTTTGTACCGTGCAG    20570         CAGAAA  _
                                TGGGTTTG     TG GCAG
                                ||||||||     || ||||
                                ACCCAAAC     GC CGTC
                                     ATG___  A
GAM1308  GLP1R    3'  CCTCTGGGCTCCTGGAAGTGGC 13139    _       GCA   A
              AG                    CC CTGGGTTT   GAA TGGCAG
                                || ||||||||   ||| ||||||
                                GG GACCCGAG   CTT ACCGTC
                                 A       GAC   C
GAM1308  HMGA2    3'  CCTAACTTGCAGAAATGG     18506       G  T
                                CCTGG TT GCAGAAATGG
                                ||||| || ||||||||||
                                GGATT AA CGTCTTTACC
                                   G  _
GAM1308  HMX1     5'  CCTCGGTCCGCTGGGGATGG   33209     G      AGAA_
                                CCT GGTTTGC     ATGG
                                ||| |||||||     ||||
                                GGA CCAGGCG     TACC
                                  G      ACCCC
GAM1308  IL6R     3'  GATCTCAGAAATGGCAG     8175       G
                                GGTTT CAGAAATGGCAG
                                ||||| ||||||||||||
                                CTAGA GTCTTTACCGTC
                                  _
GAM1308  LCP1     3'  CCCCTGGAGTTTAGGGGTGGCA 14104        _    CAGAAA
              G                   TCCCTGG GTTTG     TGGCAG
                                ||||||| |||||     ||||||
                                GGGGACC CAAAT     ACCGTC
                                    T    CCCC__
GAM1308  MUC4     3'  TCCCTGGGGGAATGG       39676         TTTGCA   A
                                TCCCTGGG     GAA TGG
                                ||||||||     ||| |||
```

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                                AGGGACCC     CTT ACC
                                    C_____  _
GAM1308 NRXN3    3' CCAGGCCTGCGGAAGTGG    39940   TG     A  A
                                C  GGTTTGC GAA TGG
                                |  ||||||| ||| |||
                                G  CCGGACG CTT ACC
                                 GT      C  C
GAM1308 OTP      3' TCCCTGGTACGTAAAATGGC  37003       GTT  CA
                                TCCCTGG   TG  GAAATGGC
                                |||||||   ||  ||||||||
                                AGGGACC   GC  TTTTACCG
                                    AT_  A_
GAM1308 PCTK1    3' CCCCTGCAACTGGGGATGGC  37468      GGT   CA  AA
                                TCCCTG   TTG  GA  TGGC
                                ||||||   |||  ||  ||||
                                GGGGAC   GAC  CT  ACCG
                                   GTT   CC  __
GAM1308 PREB     3' CTCTGCTCTAGAGATGGCAG  30141    GG   GC   A
                                CT  GTTT  AGA ATGGCAG
                                ||  ||||  ||| |||||||
                                GA  CGAG  TCT TACCGTC
                                 GA   A_  C
GAM1308 RAB36    3' TCCCAGGGGGAATGGC      22246     T   TTTGCA   A
                                TCCC GGG     GAA TGGC
                                |||| |||     ||| ||||
                                AGGG CCC     CTT ACCG
                                  T  C_____  _
GAM1308 SCA1     3' TCTTTGGGTTTATAGGAACAG  7292     CC       C  A
                                TC  TGGGTTTG AG AATGG
                                ||  |||||||| || |||||
                                AG  ACCCAAAT TC TTGTC
                                 AA       A  C
GAM1308 SLC35A2  3' CCCTGGGTGGGGCAGGGGTGG 24951         TT_   AAA
                                CCCTGGGT   GCAG   TGG
                                ||||||||   ||||   |||
                                GGGACCCA   CGTC   ACC
                                     CCC    CCC
GAM1308 TXNIP    3' TCCTTGGGTTTGAAGTCACAG  27000     C       C  AA
                                TCC TGGGTTTG AG  ATGG
                                ||| |||||||| ||  ||||
                                AGG ACCCAAAC TC  TGTC
                                  A       T  AG
GAM1308 VDR      3' TCTCTGGGTTTTCAGGGAACTA 7529     C       G  A_  G
           C                     TC CTGGGTTT CAG  AAT GC
                                || |||||||| |||  ||| ||
                                AG GACCCAAA GTC  TTG TG
                                 A       A  CC   A
GAM1308 ZNF16    3' GGTCTGGGAAGTGGCAG     28086       CA   A
                                GGTTTG  GAA TGGCAG
                                ||||||  ||| ||||||
```

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                                CCAGAC  CTT ACCGTC
                                   C_  C
GAM1309  GPC6    5'  CGCGCTCCTCGCCGCTGCCCAG 25043         AA  CA__  A
             CGT                   CGCGCTCCTC  CGC   CG CGT
                                |||||||||  |||   || |||
                                GCGCGAGGAG  GCG   GT GCA
                                     CG  ACGG  C
GAM1309  HHIP    5'  CGCGCCCCTTGACGTCACCGC  35408         CA  C  GA
                                CGCGCTCCT  ACG CAC  CGT
                                |||||||||  ||| |||  |||
                                GCGCGGGGA  TGC GTG  GCG
                                     AC  A  __
GAM1309  HYAL3   5'  GCGTCCTGCGGCACGCCACGGC 18648    C   CA___      A
             GT                    GCG TCCT    ACGCCACG CGT
                                ||| ||||    |||||||| |||
                                CGC AGGA    TGCGGTGC GCA
                                  _   CGCCG       C
GAM1309  ACP1    5'  GGTACCTGGAGGAGGAAGGGCC 28244    _         CT  C
             G                     GG ACCTGGAGGAGGA  GG GCCG
                                || ||||||||||||  || ||||
                                CC TGGACCTCCTCCT  CC CGGC
                                 A          T_ _
GAM1309  ACTB    3'  GGACTTGGGAGAGGACTG    9926      C  AG
                                GGAC TGG  GAGGACTG
                                |||| |||  ||||||||
                                CCTG ACC  CTCCTGAC
                                  A  CT
GAM1309  ATP6V0C  3'  GGCCTGGAGGGGCGATGA    44558    A      A  AC_
                                GG CCTGGAGG GG   TGG
                                || ||||||||  ||   |||
                                CC GGACCTCC CC   ACT
                                 _       _  GCT
GAM1309  B3GAT1   3'  GGGTCTGAGGAGGAGGCTCC   38303    AC   G     CT   G
                                GG  CTG AGGAGGA  GGC CC
                                ||  ||| |||||||  ||| ||
                                CC  GAC TCCTCCT  CCG GG
                                 CA  _      __  A
GAM1309  BMP4    5'  GGCCGGGGACTGTGGCGC    10195    A_  A    __
                                GG  GG GGACT  GGCGC
                                ||  || |||||  |||||
                                CC  CC CCTGA  CCGCG
                                 GG  _    CA
GAM1309  BST1    3'  GGCTGGAGGAGGGTTAG     20266    AC       AC
                                GG  CTGGAGGAGG  TGG
                                ||  ||||||||||  |||
                                CC  GACCTCCTCC  ATC
                                 __        CA
GAM1309  CHIC2   5'  GGGCCTGACTCCCGGGGTTGGC 29053    A    AGGA_  AC_
             GCCG                  GG CCTGG    GG   TGGCGCCG
                                || |||||    ||   ||||||||
```

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                                CC GGACT    CC   ACCGCGGC
                                 C    GAGGG  CCA
GAM1309  CHST2    5'  GGCTGGCTGCTGGCGCC    41716    AC    AGGAGGA
                                GG  CTGG      CTGGCGCC
                                ||  ||||      ||||||||
                                CC  GACC      GACCGCGG
                                 __    GAC____
GAM1309  CNTN2    5'  GGACCTGGGGCGAGAGAAGG   22914         _______
                                GGACCTGG     AGGAGG
                                ||||||||     ||||||
                                CCTGGACC     TCTTCC
                                     CCGCTC
GAM1309  CYLN2    3'  GGACCTGGGGAGGGGACATGGC 18055         A  __   _
                                GGACCTGG GGA  GGAC TGGC
                                |||||||| |||  |||| ||||
                                CCTGGACC CCT  CCTG ACCG
                                     _  CC    T
GAM1309  DLX2     3'  GGCCGGGAGGAGGGAACCCCG  20592    A  T      ACT   G
                                GG CC GGAGGAGG   GGC CCG
                                || || ||||||||   ||| |||
                                CC GG CCTCCTCC   TTG GGC
                                 _ C       C__   G
GAM1309  DYSF     3'  GGTCTGGAGGAGCTCGCC    18582    AC       GACTGG
                                GG  CTGGAGGAG     CGCC
                                ||  |||||||||     ||||
                                CC  GACCTCCTC     GCGG
                                 A_       GA_____
GAM1309  EPHB2    3'  GGCTTGGAGGAAGAGGTGAGCC 32674    ACC        C_   C
              G                  GG   TGGAGGAGGA  TGG GCCG
                                ||   ||||||||||  ||| ||||
                                CC   ACCTCCTTCT  ACT CGGC
                                 GA_        CC   _
GAM1309  EPO      5'  GGCCTGGAGGAGAGGGCG    9034     A        ACT
                                GG CCTGGAGGAGG   GGCG
                                || ||||||||||   ||||
                                CC GGACCTCCTCT   CCGC
                                 _         C__
GAM1309  FBP1     5'  GGACCTGGCGGGAGGACTG   8004         A_
                                GGACCTGG  GGAGGACTG
                                ||||||||  |||||||||
                                CCTGGACC  CCTCCTGAC
                                     GC
GAM1309  GALNS    3'  GGTTGGGGGAGGACCG      8010     ACC   A
                                GG   TGG GGAGGACTG
                                ||   ||| |||||||||
                                CC   ACC CCTCCTGGC
                                 A__   C
GAM1309  HMGN3    5'  GGACTGGAACTGCTGGCGCCG  20162      C    GAGGA
                                GGAC TGGAG    CTGGCGCCG
                                ||||  |||||    |||||||||
```

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                                CCTG ACCTT    GACCGCGGC
                                  _    GAC__
GAM1309  KCNK7    5'  GGCCAGGAGGAGGTGCTG    37859    A  T      A_
                                GG CC GGAGGAGG  CTG
                                || || ||||||||  |||
                                CC GG CCTCCTCC  GAC
                                 _ T       AC
GAM1309  KLK4     3'  GGGTCTGGGGAAGGAGGGG   41754    AC   A     CT
                                GG  CTGG GGAGGA  GG
                                ||  |||| ||||||  ||
                                CC  GACC CTTCCT  CC
                                 CA   C     CC
GAM1309  KRT16    5'  GGATCTGGAGGAGGTGAACTG  45452     C        ___
                                GGA CTGGAGGAGG   ACTG
                                ||| ||||||||||   ||||
                                CCT GACCTCCTCC   TGAC
                                  A         ACT
GAM1309  LMO1     3'  GGCCTGGAGGCCAGGCGCCG   14183    A      AGGACT
                                GG CCTGGAGG     GGCGCCG
                                || ||||||||     |||||||
                                CC GGACCTCC     CCGCGGC
                                 _       GGT___
GAM1309  LZTR1    3'  GGATTTGGAGGAGGCTG     27639     CC       A
                                GGA  TGGAGGAGG CTG
                                |||  ||||||||| |||
                                CCT  ACCTCCTCC GAC
                                  AA       _
GAM1309  MADH3    3'  CTGGGGGGAGGGTGCCG     25347     A  A   CT  C
                                CTGG GG GGA  GG GCCG
                                |||| || |||  || ||||
                                GACC CC CCT  CC CGGC
                                  _ _   C_  A
GAM1309  MLC1     3'  GGCTCTGGAGGAGGGGCCCC  40151    AC       ACT   G
                                GG  CTGGAGGAGG   GGC CC
                                ||  ||||||||||   ||| ||
                                CC  GACCTCCTCC   CCG GG
                                 GA         ___   G
GAM1309  MMP25    5'  GGACCTGGGGGGAGGAGATCCG  35386        A     CTGGCG
                                GGACCTGG GGAGGA     CCG
                                |||||||| ||||||     |||
                                CCTGGACC CCTCCT     GGC
                                     C     CTA___
GAM1309  PAX9     3'  GGAATTGGGGGGAGGAGGTGC   26206     CC   A     CT  C
                                GGA  TGG GGAGGA  GG GC
                                |||  ||| ||||||  || ||
                                CCT  ACC CCTCCT  CC CG
                                  TA   C     __  A
GAM1309  PKM2     3'  GGGGCTGGAGGAGGGGGC     15337    AC       ACT
                                GG  CTGGAGGAGG   GGC
                                ||  ||||||||||   |||
```

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                                CC  GACCTCCTCC   CCG
                                 CC        ___
GAM1309  SNL      3'  GGCTGGGAGGAGGTGGC     16944    ACCT       AC
                                GG   GGAGGAGG  TGGC
                                ||   ||||||||  ||||
                                CC   CCTCCTCC  ACCG
                                 GAC_       __
GAM1309  SORCS2   3'  GGCCTGGAGGGTGGTGTGG   34059    A      A_  AC
                                GG CCTGGAGG  GG  TGG
                                || ||||||||  ||  |||
                                CC GGACCTCC  CC  ACC
                                 _       CA  AC
GAM1309  SRP46    5'  GGCCCGGAAACTGGCGC     36954    A     GGAG
                                GG CCTGGA    GACTGGCGC
                                || ||||||    |||||||||
                                CC GGGCCT    TTGACCGCG
                                 _     _____
GAM1309  TIMM17B  5'  GGAGCTGGAGGAAGTGCTG   25179    C        A_
                                GGA CTGGAGGAGG  CTG
                                ||| ||||||||||  |||
                                CCT GACCTCCTTC  GAC
                                  C         AC
GAM1309  UBE2L3   3'  GGACTGGAGGAGGGGTGTGGC  17828     C        AC__
                                GGAC TGGAGGAGG    TGGC
                                |||| |||||||||    ||||
                                CCTG ACCTCCTCC    ACCG
                                  _        CCAC
GAM1309  ZAP70    3'  GGACCTGGGGTGGGGC      43338         A  A  ACT
                                GGACCTGG GG GG   GGC
                                |||||||| || ||   |||
                                CCTGGACC CC CC   CCG
                                     _  A  ___
GAM1310  ETS2     3'  TCGCTCCTTTGAGAATCTCA   23472       AAGGAG   A
                                TCGCT     TTT AGAATCTCA
                                |||||     ||| |||||||||
                                AGCGA     AAA TCTTAGAGT
                                   GG____   C
GAM1310  SLC31A1  3'  TCCTTAAGAGAAATGGGAATCT 12397    G  A    TTTAA_
            CA                    TC CT AGGAG     GAATCTCA
                                || || |||||     ||||||||
                                AG GA TTCTC     CTTAGAGT
                                 _  A    TTTACC
GAM1310  TLR5     5'  TCCTGAGACTATAGGAATCTCA 44291    G  A   AGTT  A
                                TC CT AGG    TA GAATCTCA
                                || || |||    || ||||||||
                                AG GA TCT    AT CTTAGAGT
                                 _  C   GAT_  C
GAM1311  LAMP2    3'  GAAAAATTACATCTATAT    30385     TTTAGA
                                GAA     TACATCTATAT
                                |||     ||||||||||
```

```
                                CTT     ATGTAGATATA
                                  TTTA__
GAM1311  GBAS    3'  TGAGATTTATTCACACTT    11236    T      _
                                TG AGATTTAT CATATTT
                                || |||||||| |||||||
                                AC TCTAAATA GTGTGAA
                                  _       A
GAM1311  PARN    3'  TGTAGATTTGCACGATTTC    15094         AT  _
                                TGTAGATTT  CAT ATTTC
                                |||||||||  ||| |||||
                                ACATCTAAA  GTG TAAAG
                                     C_   C
GAM1311  PRKG1   3'  TGTGGATTCTTTTCTCCA    26518     A    ATCATA
                                TGT GATTT     TTTCTCCA
                                ||| |||||     ||||||||
                                ACA CTAAG     AAAGAGGT
                                  C    A_____
GAM1311  ZNF138  3'  TGTAGGGTTTTTCTCC      44345      AT  ATCATA
                                TGTAG  TT     TTTCTCC
                                |||||  ||     |||||||
                                ACATC  AA     AAAGAGG
                                   CC  _______
GAM1311  ZNF8    3'  TGTGGACTTACCACATTT    41967     A
                                TGT GATTTATCATATTT
                                ||| ||||||||||||||
                                ACA CTGAATGGTGTAAA
                                  C
GAM1312  EZH1    3'  TGGGACAGGTGGTCTACCT    12790     CGTC  C    C
                                TGG    GGC GGTGG CTACCT
                                |||    ||| ||||| ||||||
                                ACC    CTG CCACC GATGGA
                                  _____  T    A
GAM1312  TEM7    3'  TGGCGGCAGATGGCCT      33818      GTC   C
                                TGGC   GGC GGTGGCCT
                                ||||   ||| ||||||||
                                ACCG   CCG CTACCGGA
                                   ___   T
GAM1312  DDX3    3'  CAGGGCTGCTGATTGTTCC    35813     T   C    GG  GC
                                CAG GGC GCTG  TG  CC
                                ||| ||| ||||  ||  ||
                                GTC CCG CGAC  AC  GG
                                  _   A    TA  AA
GAM1312  HMGA1   5'  TGATGGCTGGGATGGCCTTCTT 44165     CC     _    CC
                                TGG  GCTGGG TGGCC  CTT
                                |||  |||||| |||||  |||
                                ACT  CGACCC ACCGG  GAA
                                  AC     T    AA
GAM1312  LTB4R   5'  GTGGCCACTGAGGTCCCTT    8886          _  GGCC
                                GTGGCCGCTG GGT    CCCTT
                                |||||||||| |||    |||||
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```
                                CACCGGTGAC CCA   GGGAA
                                      T  ____
GAM1312 PKLR    3' TGGTGCTGTTGGGTGGCC   7148     CC  ___
                                TGG  GCT   GGGTGGCC
                                |||  |||   ||||||||
                                ACC  CGA   CCCACCGG
                                  A_   CAA
GAM1312 PPP1R12B 3' ATGGCTACTCATGGTCTCCTT 36967     CG  GG   CCC
                                GTGGC  CT  GTGG   CCTT
                                |||||  ||  ||||   ||||
                                TACCG  GA  TACC   GGAA
                                   AT  G_   AGA
GAM1312 RET     3' AGTGGTGCTGGTGGCTCCTT  34152     CC   G   CC
                                AGTGG  GCTGG TGGC  CCTT
                                |||||  ||||| ||||  ||||
                                TCACC  CGACC ACCG  GGAA
                                   A_    _   A_
GAM1312 RHBDL   3' GTGGCTGGGACAGGGCCTCCTT 19554     CGC   T___   C
                                GTGGC   TGGG   GGCC CCTT
                                |||||   ||||   |||| ||||
                                CACCG   ACCC   CCGG GGAA
                                   ___   TGTC   A
GAM1312 TARBP2  3' CAGTGGCCGGCTGGGTGG   39527        _
                                CAGTGGCCG CTGGGTGG
                                ||||||||| ||||||||
                                GTCACCGGC GACCCACC
                                     C
GAM1313 ABCD4   3' TCTTACAGATCTCACACTTCCA 33749         A_  CT  C
           G                     TCTTACGGATC  GC  CT CCAG
                                ||||||||||  ||  || ||||
                                AGAATGTCTAG  TG  GA GGTC
                                      AG  T_  A
GAM1313 AP1M1   3' TCTTGAAGACCAGCCTCT   37175     AC
                                TCTT  GGATCAGCCTCT
                                ||||  ||||||||||||
                                AGAA  TCTGGTCGGAGA
                                  CT
GAM1313 CLASP1  3' CAACATCAGTCTTTCCCAG   42234    _   C  C
                                CGG ATCAG CT TCCCAG
                                ||| ||||| || ||||||
                                GTT TAGTC GA AGGGTC
                                  G    A  A
GAM1313 GAS7    3' TCTTGTGCATCAGTCTCC   25282     ACGG   CC
                                TCTT   ATCAG  TCTCC
                                ||||   |||||  |||||
                                AGAA   TAGTC  AGAGG
                                  CACG   __
GAM1313 IL1R1   3' TCTTAGGGAAAGTCTCCCAG  9370      C  TC  CC
                                TCTTA GGA  AG  TCTCCCAG
                                ||||| |||  ||  ||||||||
```

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                                AGAAT CCT  TC  AGAGGGTC
                                  C   T_  __
GAM1313  LGALS3BP  5'  CAGAAGCCTCTCCCAG     42929     TC
                                CGGA  AGCCTCTCCCAG
                                ||||  ||||||||||||
                                GTCT  TCGGAGAGGGTC
                                  __
GAM1313  NCKAP1   5'  CCTTCGCAGCAGCCTCTC    30255     A  GAT
                                TCTT CG   CAGCCTCTC
                                |||| ||   |||||||||
                                GGAA GC   GTCGGAGAG
                                  _  GTC
GAM1313  PLA2G5   3'  CTTAGGAGCCTCTCTCA     9577      C   TCA     C
                                CTTA GGA   GCCTCTC CA
                                |||| |||   ||||||| ||
                                GAAT CCT   CGGAGAG GT
                                  _  ___      A
GAM1313  RAD54L   3'  TCTTGATGATTTTCTCCCAG   18716     ACG   CAGCC
                                TCTT   GAT    TCTCCCAG
                                ||||   |||    ||||||||
                                AGAA   CTA    AGAGGGTC
                                  CTA   AA___
GAM1313  CEACAM6  3'  TTGACATCTTGGGAAAAGC    14735          CT
                                TTGACATCTTGG  GAAGC
                                ||||||||||||  |||||
                                AACTGTAGAACC  TTTCG
                                      CT
GAM1313  CLIC3    5'  GCCTTGACAAACAGCTGGAGC  21698        TCT     A
                                GCCTTGACA   TGGCTG AGC
                                |||||||||   |||||| |||
                                CGGAACTGT   GTCGAC TCG
                                     TT_     C
GAM1313  DUSP4    3'  TGCCTTGACATCTGCATGCT   38429          TG__
                                TGCCTTGACATCT    GCT
                                ||||||||||||    |||
                                ACGGAACTGTAGA    CGA
                                       CGTA
GAM1313  EMP1     3'  TGCCTTGGCTTTCAGCAAGAGG 10900       ACATC TG  T_  A
            CC                    TGCCTTG    T  GC  GA GCC
                                ||||||||    |  ||  || |||
                                ACGGAAC    A  CG  CT CGG
                                   CGAA_ GT  TT  C
GAM1313  MEL      3'  TGCCTTGTGTCTTGGCC     23875       ACA
                                TGCCTTG   TCTTGGCT
                                |||||||   ||||||||
                                ACGGAAC   AGAACCGG
                                   AC_
GAM1313  OSR1     3'  TTGCACCAGCTGAAG       23040     A   TT
                                TTG CATC  GGCTGAAG
                                ||| ||||  ||||||||
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                                AAC GTGG  TCGACTTC
                                  _   __
GAM1313  PER2     3'  TGCTTGGCACGCGCTGAAGC  35622     C   A   CTTG
                                TGC TTG CAT    GCTGAAGC
                                ||| ||| |||    ||||||||
                                ACG AAC GTG    CGACTTCG
                                  _   C   CG__
GAM1313  SMOH     3'  CTTGCCTGGCTGAAGC      24813      ACAT
                                CTTG    CTTGGCTGAAGC
                                ||||    ||||||||||||
                                GAAC    GGACCGACTTCG
                                  _____
GAM1313  SNCA     3'  TTAACATCGTAGATTGAAGCC  28661         TT_ GC
                                TTGACATC   G  TGAAGCC
                                ||||||||   |  |||||||
                                AATTGTAG   C  ACTTCGG
                                     CAT TA
GAM1313  ZNF267   5'  TGCCCTGGCGTCTTAGCT    18259        ACA
                                TGCCTTG   TCTTGGCT
                                |||||||   ||||||||
                                ACGGGAC   AGAATCGA
                                    CGC
GAM1314  SYCP1    3'  TCCAAAATATTTTAATAG    17233         TC_
                                TCCAAAAT   TTAATAG
                                ||||||||   |||||||
                                AGGTTTTA   AATTATC
                                     TAA
GAM1315  CA12     3'  TCCACAGGGTTCTCACCTGCGG 10252       ACA_____  T
                                TCCACA       AC CTGCGG
                                ||||||       || ||||||
                                AGGTGT       TG GACGCC
                                   CCCAAGAG  _
GAM1315  CARKL    3'  CCAAACCAAGCTCTGCGG    29989     CAA  _
                                CCA   CAA CTCTGCGG
                                |||   ||| ||||||||
                                GGT   GTT GAGACGCC
                                  TTG   C
GAM1315  COX15    5'  TCCACAACCCAGGGCTCTGTGG 38517         AA____    C
                                TCCACAAC     CTCTG GG
                                ||||||||     ||||| ||
                                AGGTGTTG     GAGAC CC
                                     GGTCCC     A
GAM1315  EGLN2    5'  TCCCCAAGTCCTCTGCGG    38836     A   CAA
                                TCC CAA   CTCTGCGG
                                ||| |||   ||||||||
                                AGG GTT   GAGACGCC
                                  G   CAG
GAM1315  ESRRBL1  5'  CCCACAGACCTCTGCGG     32838       ACAA
                                TCCACA    CTCTGCGG
                                ||||||    ||||||||
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                                GGGTGT   GAGACGCC
                                   CTG_
GAM1315 FANCG   5' TCCCAACCCCAGCGG      21559    A   AA  T
                                TCC CAAC  CTC GCGG
                                ||| ||||  ||| ||||
                                AGG GTTG  GGG CGCC
                                  _   __   T
GAM1315 FGFR2   3' TCCCCAACAACCATCCAG    35668    A      CTG
                                TCC CAACAACT   CGG
                                ||| ||||||||   |||
                                AGG GTTGTTGG   GTC
                                  G       TAG
GAM1315 MEN1    5' TCCACAACACACACCACGG   39231         _ T TG
                                TCCACAACA AC C  CGG
                                ||||||||| || |  |||
                                AGGTGTTGT TG G  GCC
                                     G  T GT
GAM1315 MMP14   3' TCCACAGCCCACCCTGTGG   22644       ACA_    C
                                TCCACA   ACTCTG GG
                                ||||||   |||||| ||
                                AGGTGT   TGGGAC CC
                                   CGGG     A
GAM1315 NDUFA1  5' TCCCAGCAAGCCCCGCGG    21230    A  A  _
                                TCC CA CAA CTCTGCGG
                                ||| || ||| ||||||||
                                AGG GT GTT GGGGCGCC
                                  _ C   C
GAM1315 PXF     3' TCCACCACAAGTCCTGG     16013      A   C   GC
                                TCCAC ACAA TCT  GG
                                ||||| |||| |||  ||
                                AGGTG TGTT AGG  CC
                                   G   C   A_
GAM1315 RTN2    3' TCCCAGCAGGCCCCGCGG    24727    A  A  A_
                                TCC CA CA  CTCTGCGG
                                ||| || ||  ||||||||
                                AGG GT GT  GGGGCGCC
                                  _ C  CC
GAM1315 SIAH1   5' CCCGCAACGGCCGCCCCGG   16710    A   AA  _  G
                                TCC CAAC  CT CT CGG
                                ||| ||||  || || |||
                                GGG GTTG  GG GG GCC
                                  C   CC  C  G
GAM1315 TFE3    3' TCCACAAGCACTAGCGG     27173       CA   CT
                                TCCACAA  ACT  GCGG
                                |||||||  |||  ||||
                                AGGTGTT  TGA  CGCC
                                    CG   T_
GAM1315 TOP3B   5' CCCACAGCAAGCCCCGCGG   19461       A  _
                                TCCACA CAA CTCTGCGG
                                |||||| ||| ||||||||
```

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                                GGGTGT GTT GGGGCGCC
                                   C   C
GAM1316 ADRA2B   3' AGAAAGGGAAGCCCAGACATTG 8645      C   AACT TA
            G                   AGA AGG   G  CAGACATTGG
                                ||| |||   |  ||||||||||
                                TCT TCC   C  GTCTGTAACC
                                 T  CTT_ GG
GAM1316 CLCN5    5' AGACAGGAGTTGATGTGCAATG 6356        AC  TACAGA  T
            G                   AGACAGGA  TG     CA TGG
                                ||||||||  ||     || |||
                                TCTGTCCT  AC     GT ACC
                                    CA  TACAC_  T
GAM1316 FOSB     3' GGGTGTGGGAGACATTGG    27543    AAC   AC_
                                GG   TGT   AGACATTGG
                                ||   |||   |||||||||
                                CC   ACA   TCTGTAACC
                                 C__   CCC
GAM1316 HPS1     3' GACAGGAACTTCTCGG      6803          GTACAGACA
                                GACAGGAACT       TTGG
                                ||||||||||       ||||
                                CTGTCCTTGA       AGCC
                                     AG_______
GAM1316 KIR2DL4  3' GGGACCTTAGACATTGG     13961    A   GTAC
                                GG ACT    AGACATTGG
                                || |||    |||||||||
                                CC TGG    TCTGTAACC
                                 C  AA__
GAM1316 KRTHA4   3' GAAGGAGTTGTCCAGACATTGG 34247    C    AC   A
                                GA AGGA  TGT CAGACATTGG
                                || ||||  ||| ||||||||||
                                CT TCCT  ACA GTCTGTAACC
                                 _   CA   G
GAM1316 LAMC1    3' CAGGAACTCGATAGCGTTGG   14079        GTAC  ACA
                                CAGGAACT   AG   TTGG
                                ||||||||   ||   ||||
                                GTCCTTGA   TC   AACC
                                     GCTA  GC_
GAM1316 SHOX2    3' GACAGGCGCGACATT       27839       AAC   ACA
                                GACAGG   TGT   GACATT
                                ||||||   |||   ||||||
                                CTGTCC   GCG   CTGTAA
                                   ___   ___
GAM1316 SLC19A1  3' GATGACAATGTGTCTGCC    16848        C  CCT A    T
                                GATGACAA GT   G TCTG CC
                                |||||||| ||   | |||| ||
                                CTACTGTT CA   C AGAC GG
                                     A ___ _    _
GAM1316 TSSC3    3' GATGAGGGTGTCCTGCCCG   17703      CAAC     A
                                GATGA   GTCCTG TCTG
                                |||||   |||||| ||||
```

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                                CTACT   CAGGAC GGGC
                                  CCCA    _
GAM1317 AOC3    3' CCTCAGGATTCGGGAGAAATTG 19016   _ A      TGCCA__
            CAGG                  CC CA GATTCGGGA     CAGG
                                || || |||||||||     ||||
                                GG GT CTAAGCCCT     GTCC
                                 A  C       CTTTAAC
GAM1317 DGUOK   3' CCAAGACTTTGGGCAGTGCAGG 38967       C_  ATGCCA
                                CCAAGATT  GGG    CAGG
                                ||||||||  |||    ||||
                                GGTTCTGA  CCC    GTCC
                                     AA   GTCAC_
GAM1317 MPP2    3' GACTCAGGGTGTCACAGG   40795       A  C
                                GATTCGGG TG CACAGG
                                |||||||| || ||||||
                                CTGAGTCC AC GTGTCC
                                     C  A
GAM1317 NEURL   3' TCCCAGGTGTGCCACA     20102     AGATTC  GA
                                TCCCA    GG  TGCCACA
                                |||||    ||  |||||||
                                AGGGT    CC  ACGGTGT
                                  _______  AC
GAM1317 NRXN2   3' CCCAGCGGGTGCCACAG    31473     AGATT   A
                                CCCA   CGGG TGCCACAG
                                ||||   |||| ||||||||
                                GGGT   GCCC ACGGTGTC
                                  C____   _
GAM1317 POU4F1  3' TCCCGGGATTGGAGAGCAGCCA 26398     AA   C   T__   C
            TAGG                  TCCC  GATT GGGA   GCCA AGG
                                |||| |||| ||||  |||| |||
                                AGGG  CTAA CTCT   CGGT TCC
                                  CC   C   CGT   A
GAM1317 PPP4R1  3' TCCCAAGAGTGGTCACAG   23077       TTCG  ATGC
                                TCCCAAGA   GG   CACAG
                                ||||||||   ||   |||||
                                AGGGTTCT   CC   GTGTC
                                     CA__  A___
GAM1317 RASD1   5' TCCCAGGATCTGGGCACAG   32014     A  TC  ATGC
                                TCCCA GAT  GGG   CACAG
                                ||||| |||  |||   |||||
                                AGGGT CTA  CCC   GTGTC
                                  C  GA  ____
GAM1317 CDR1    3' TTCCAATAATTTCAAGGTCT  19805       ____  C
                                TTCCGATAAT   GGG CT
                                ||||||||||   ||| ||
                                AAGGTTATTA   TCC GA
                                      AAGT   A
GAM1317 ERBB2IP 3' TTCCAATAAATCTTGCTGTCTT 33104       TGG__  C  C
            C                  TTCCGATAA    GC TG CTTC
                                |||||||||    || || ||||
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                                AAGGTTATT    CG AC GAAG
                                     TAGAA  _  A
GAM1317  FOXD2    5'  TTCCAATCCTGCCT      20976       AATGGG
                                TTCCGAT    CCTGCCT
                                |||||||    |||||||
                                AAGGTTA    GGACGGA
                                      _______
GAM1317  IL1F5    3'  CTCCGATCTCTGCCTT     29350       AATGGGC
                                TTCCGAT    CTGCCTT
                                |||||||    |||||||
                                GAGGCTA    GACGGAA
                                   GA_____
GAM1317  MGEA5    5'  TCCCGATAATCTTAGGTCT   29218         ___  C
                                TTCCGATAAT  GGG CT
                                ||||||||||  ||| ||
                                AGGGCTATTA  TCC GA
                                      GAA  A
GAM1317  UC28     3'  GATATGACTGCCTTC      34690     A  GC
                                GATA TGG  CTGCCTTC
                                |||| |||  ||||||||
                                CTAT ACT  GACGGAAG
                                  _  __
GAM1317  WISP3    5'  TTCTAATAACCTGCCTT    19305     CG  ATGG
                                TTC  ATA   GCCTGCCTT
                                |||  |||   |||||||||
                                AAG  TAT   TGGACGGAA
                                  AT  _____
GAM1317  ZNF2     3'  GAAGGTGGACCTGTCTTC   34379    TAA      C
                                GA  TGGGCCTG CTTC
                                ||  |||||||| ||||
                                CT  ACCTGGAC GAAG
                                 TCC       A
GAM1318  A1BG     3'  CAGCACCCTGGGCCCGCGGC  39088       CAAAC   TA
                                CGGCACCC    TCCG  GC
                                ||||||||    ||||  ||
                                GTCGTGGG    GGGC  CG
                                     ACCC_   GC
GAM1318  ADAM23   3'  CACCCCAACTTTAGCTCCGTAG 19200       A_____      C
            TCA                   CACCCCAA     CTCCGTAG CA
                                ||||||||     |||||||| ||
                                GTGGGGTT     GAGGCATC GT
                                     GAAATC       A
GAM1318  DIAPH2   3'  GGCTTCCTAAAAGACATAGCCA 28674     AC  C   CTC
            C                  GGC  CC AAA   CGTAGCCAC
                                |||  || |||   |||||||||
                                CCG  GG TTT   GTATCGGTG
                                  AA  A   TCT
GAM1318  FASN     3'  CAGCACCCCACGGGTGGC    19929         AACTCC  A
                                CGGCACCCCA     GT GC
                                ||||||||||     || ||
```

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                                GTCGTGGGGT     CA CG
                                      GCC___  C
GAM1318  FNTB     3'  CGGCACCCCACGCTGCCA    13004          AACTC   A
                                CGGCACCCCA    CGT GCCA
                                ||||||||||    ||| ||||
                                GCCGTGGGGT    GCG CGGT
                                      _____   A
GAM1318  GAMT     3'  CGACACCCTGGACTCCCGGC   6680         CAA    GTA
                                CGGCACCC   ACTCC   GC
                                ||||||||   |||||   ||
                                GCTGTGGG   TGAGG   CG
                                     ACC    GC_
GAM1318  IGFBP1   5'  CGGTGGCCCAAACTCTGGGC   8244      CAC        CGTA
                                CGG   CCCAAACTC    GC
                                |||   |||||||||    ||
                                GCC   GGGTTTGAG    CG
                                  ACC        ACC_
GAM1318  IL12RB2  3'  GCACTCCAATACAGTAGCCAC  11428      C    _  TCC
                                GCAC CCAA AC   GTAGCCAC
                                |||| |||| ||   ||||||||
                                CGTG GGTT TG   CATCGGTG
                                  A    A  T__
GAM1318  LIMK1    3'  CGGGCCCCAGACTCCCCA    14168     CA     A     G
                                CGG  CCCCA ACTCC TA
                                |||  ||||| ||||| ||
                                GCC  GGGGT TGAGG GT
                                  C_    C     G
GAM1318  LRP4     5'  GGCACTTCTGGGCACAGCCAC  42063      CCCAAACTC
                                GGCAC        CGTAGCCAC
                                |||||        |||||||||
                                CCGTG        GTGTCGGTG
                                   AAGACCC__
GAM1318  PREB     5'  CGGCACCCAGGACATGCCGC   30140        CAA  T__
                                CGGCACCC   AC   CCGT
                                ||||||||   ||   ||||
                                GCCGTGGG   TG   GGCG
                                     TCC  TAC
GAM1318  PSMD5    3'  GCATTCCAAACTCCTAGTTCCA 22780     CC        GTAG_
              C                  GCA  CCAAACTCC     CCAC
                                 |||  |||||||||     ||||
                                 CGT  GGTTTGAGG     GGTG
                                   AA        ATCAA
GAM1318  PTPN23   5'  CGGCCACTCCCGTAGC     41892      ACCC  AAC
                                CGGC    CA   TCCGTAGC
                                ||||    ||   ||||||||
                                GCCG    GT   GGGCATCG
                                  _____  GA_
GAM1318  RPIP8    5'  CGGAGCCCCAAACCCGTCGC   27451     CA       T    A
                                CGG  CCCCAAAC CCGT GC
                                |||  |||||||| |||| ||
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                                GCC  GGGGTTTG GGCA CG
                                  TC       _    G
GAM1318  SLC35A3   5'  CGGCTCCCGTCGCCGTAGCCAC 29277      A   CAAACT
                                CGGC CCC     CCGTAGCCAC
                                |||| |||     ||||||||||
                                GCCG GGG     GGCATCGGTG
                                  A   CAGC__
GAM1318  HSF4      5'  GGTGCAGTCTCGGCCCGGC    40769            ___
                                GGTGCAGTCTCGGC   GC
                                ||||||||||||||   ||
                                CCACGTCAGAGCCG   CG
                                         GGC
GAM1319  NFKBIL1   3'  TTTGAGATGTGGAACCAGGTCT 22674       C_   T   G
                T                TTTGAG  GTGG GAT TAGGTCTT
                                ||||||  |||| ||| ||||||||
                                AAACTC  CACC TTG GTCCAGAA
                                   TA   _  _
GAM1320  ATP6V0E   3'  TGAGATGGCTCTTCCCTCT    19487      AAGC   GAA
                                TGAGA    GGT   TTCCCTCT
                                |||||    |||   ||||||||
                                ACTCT    CCG   AAGGGAGA
                                   A___   AG_
GAM1320  BACH2     5'  AGAAAGCATGCTTTCTTCT    34768        G  AA   CC
                                AGAAAGCG TG  TTC  TCT
                                |||||||| ||  |||  |||
                                TCTTTCGT AC  AAG  AGA
                                     _ GA   A_
GAM1320  CABC1     5'  TGAGAAGTGGAACTCCCC     33691      AAGC   _
                                TGAGA    GGTG AATTCCCT
                                |||||    |||| ||||||||
                                ACTCT    TCAC TTGAGGGG
                                   _____    C
GAM1320  CPS1      3'  TGAGAAAGTTGTGAATCAGTTC 12422        CG      C___
                CT                 TGAGAAAG  GTGAATT    CCT
                                |||||||  |||||||    |||
                                ACTCTTTC  CACTTAG    GGA
                                     AA      TCAA
GAM1320  DPYS      3'  AGTGGTGAATTTTTTCTA    10738    C      CCC
                                AG GGTGAATT   TCTA
                                || ||||||||   ||||
                                TC CCACTTAA   AGAT
                                 A       AAA
GAM1320  EIF4E     3'  TAAGAAGTACAAATTCCTTCTA 12695       AGCG TG     C
                                TGAGAA    G  AATTCC TCTA
                                ||||||    |  |||||| ||||
                                ATTCTT    T  TTAAGG AGAT
                                   CA__ GT     A
GAM1320  ESRRG     3'  TGAGAAGACTTCCCTC      42449       AG GGTGAA
                                TGAGAA  C     TTCCCTC
                                ||||||  |     |||||||
```

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                                ACTCTT  G     AAGGGAG
                                   CT _______
GAM1320  GPC3     3'  TAAGAAAGTGGTTCCCT     21024         C   GAAT
                                TGAGAAAG GGT    TCCCT
                                |||||||| |||    |||||
                                ATTCTTTC CCA    AGGGA
                                     A  ____
GAM1320  IL12B    3'  TGAGAAAGGGATTCC       13521         C  TGA
                                TGAGAAAG GG   ATTCC
                                |||||||| ||   |||||
                                ACTCTTTC CC   TAAGG
                                     _ ___
GAM1320  MAN2A2   3'  GAGAAACAGTGATTCCTTCTA  25948       G     A   C
                                GAGAAA CGGTGA TTCC TCTA
                                |||||| |||||| |||| ||||
                                CTCTTT GTCACT AAGG AGAT
                                   _    _   A
GAM1320  PTGFR    3'  TGAGAAAGAGCCTTTGTTTCTC 9663         C   GAATTCC_
             TA                   TGAGAAAG GGT       CTCTA
                                |||||||| |||       |||||
                                ACTCTTTC TCG       GAGAT
                                     _  GAAACAAA
GAM1320  TFAP4    3'  TGGGAGAGTGGCGAATTC    17418    A  A  C
                                TG GA AG GGTGAATTC
                                || || || |||||||||
                                AC CT TC CCGCTTAAG
                                 C  C  A
GAM1320  TOP3A    3'  TGAGAAAGTGGCGTTCTCT   21465        C    AATTCC
                                TGAGAAAG GGTG     CTCT
                                |||||||| ||||     ||||
                                ACTCTTTC CCGC     GAGA
                                     A   AA____
GAM1320  UBE3A    5'  TGAGGAGCTGGTGAATTC    39284      AA  _
                                TGAG  AGC GGTGAATTC
                                ||||  ||| |||||||||
                                ACTC  TCG CCACTTAAG
                                  C_  A
GAM1320  VAV2     3'  GAGGTTGGTATTTCCCCTCT  17920     AAAGC   AA
                                GAG    GGTG  TTCCCTCT
                                |||    ||||  ||||||||
                                CTC    CCAT  AGGGGAGA
                                  CAA__    AA
GAM1320  FOXD2    5'  GTTTCTCGCTAGCCGGG     20973         TA  ATACA
                                GTTTCTCGCT  CT    GGG
                                ||||||||||  ||    |||
                                CAAAGAGCGA  GG    CCC
                                      TC  _____
GAM1321  ACCN2    3'  CACCCAGAGCCCTGCCTGCT  33431         _  GAT
                                CACCCAGA CTT   CCTGCT
                                |||||||| |||   ||||||
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                                GTGGGTCT GGG   GGACGA
                                     C   AC_
GAM1321  BCRP2    3'  CAGTGCCATCTGTCCTGCT   41651     CAC   GACT  A
                                CAG   CCA    TG TCCTGCT
                                |||   |||    || |||||||
                                GTC   GGT    AC AGGACGA
                                  AC_   AG__  _
GAM1321  CA7      3'  CAGCCCCAGGCTTGGACCCTG  41196     A     A   _
                                CAGC CCCAG CTTG ATCCTG
                                |||| ||||| |||| ||||||
                                GTCG GGGTC GAAC TGGGAC
                                  _    C   C
GAM1321  CD28     3'  CAGCACCCAAGTACTGCT    26017          ACTTGATC
                                CAGCACCCAG       CTGCT
                                ||||||||||       |||||
                                GTCGTGGGTT       GACGA
                                     CAT_____
GAM1321  CELSR2   3'  CAGAACCCAGACTTGAAACCTG 10845     C          T_
                                CAG ACCCAGACTTGA  CCTG
                                ||| ||||||||||||  ||||
                                GTC TGGGTCTGAACT  GGAC
                                  T          TT
GAM1321  CENTD2   3'  CAGCACCCGCTTTCTGCT    31590        AGA   GATC
                                CAGCACCC   CTT    CTGCT
                                ||||||||   |||    |||||
                                GTCGTGGG   GAA    GACGA
                                     C__   A___
GAM1321  COG4     3'  CCAGACTTTGTTTCTCTGCT   31721        GA__  _
                                CCAGACTT    TC CTGCT
                                ||||||||    || |||||
                                GGTCTGAA    AG GACGA
                                     ACAA  A
GAM1321  DMD      5'  CAGCACTGATCCTG       19679       CCAGACT
                                CAGCAC      TGATCCTG
                                ||||||      ||||||||
                                GTCGTG      ACTAGGAC
                                     ________
GAM1321  ELAC2    3'  AGACCCACTGATCCTG      32849    C    GAC
                                AG ACCCA   TTGATCCTG
                                || |||||   |||||||||
                                TC TGGGT   GACTAGGAC
                                  _    ____
GAM1321  GADD45B  3'  CAGCAACTCAACAGATTCTGCT 31826      CCCA   TT   C
                                CAGCA    GAC  GAT CTGCT
                                |||||    |||  ||| |||||
                                GTCGT    TTG  CTA GACGA
                                   TGAG   T_   A
GAM1321  HSPCB    3'  CAACATCCAATCCTGC      28876      C   GACTTG
                                CAGCA CCA     ATCCTGC
                                ||||| |||     |||||||
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                                GTTGT GGT     TAGGACG
                                  A  _______
GAM1321  HUNK     3'  GCCTTCAGGTAATCCCTGCTA  31070    ACC   ACT     _
                                GC   CAG   TGATCC TGCTA
                                ||   |||   |||||| |||||
                                CG   GTC   ATTAGG ACGAT
                                 GAA   C__     G
GAM1321  HYOU1    3'  CAGCCCTAGCTCCTGC      40631      A  C  A TTGA
                                CAGC CC AG C    TCCTGC
                                |||| || || |    ||||||
                                GTCG GG TC G    AGGACG
                                  _ A  _ ____
GAM1321  IL15RA   3'  GCAGTCCGTGAGATCCTGCT   13531     C_  AGACTT
                                GCA  CC     GATCCTGCT
                                |||  ||     |||||||||
                                CGT  GG     CTAGGACGA
                                  CA  CACT__
GAM1321  LFG      3'  GCATCTGAAATCCTGCT     44137     CCCA  CTT
                                GCA   GA   GATCCTGCT
                                |||   ||   |||||||||
                                CGT   CT   TTAGGACGA
                                  AGA_  ___
GAM1321  MIP      5'  CAGTGCCTGGGTCCCTGCTA   28931     A_   A__
                                CAG  CTTG   TCCTGCTA
                                |||  ||||   ||||||||
                                GTC  GGAC   GGGACGAT
                                  AC    CCA
GAM1321  MPP2     3'  AGCTCAGACCTGTGCCTGCT   40790     ACC      AT
                                AGC   CAGACTTG  CCTGCT
                                |||   ||||||||  ||||||
                                TCG   GTCTGGAC  GGACGA
                                  A__       AC
GAM1321  AGT      3'  CTGCTGGCCTTTGCCTCAAA   6189          GCTA   C
                                CTGCTGGCC    CTTC GA
                                |||||||||    |||| ||
                                GACGACCGG    GGAG TT
                                     AAAC    T
GAM1321  DBY      3'  TACTGCTGGCTGGTAAAACCGA 21660          CGCTACTT
              A                  TACTGCTGGC       CCGAA
                                 ||||||||||       |||||
                                 ATGACGACCG       GGCTT
                                      ACCATTTT
GAM1321  DFFA     3'  CACTGCCAATTACTTTTGAAC  20580       TG CCGC    CC
                                TACTGC  G    TACTT  GAAC
                                ||||||  |    |||||  ||||
                                GTGACG  T    ATGAA  CTTG
                                   GT A___     AA
GAM1321  DYRK1A   3'  ACTGCTGGTTCCATAGCTTC   38988         __   C  _
                                ACTGCTGG  CCG TA CTTC
                                ||||||||  ||| || ||||
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                                TGACGACC  GGT AT GAAG
                                    AA   _  C
GAM1321  HCS      3'  TACTACTGGGCTGATTACTTC  33233         CC   ____
                                TACTGCTGG  GCT   ACTTC
                                |||||||||  |||   |||||
                                ATGATGACC  CGA   TGAAG
                                    __   CTAA
GAM1321  ID4      3'  GCTATAACTGTTACTTCCGA   11382      GCC   ___
                                GCTG   GCT   ACTTCCGA
                                ||||   |||   ||||||||
                                CGAT   TGA   TGAAGGCT
                                  AT_   CAA
GAM1321  MAX      3'  TGCTGGCCTGCCCCGA      40365         _   ACTT
                                TGCTGGCC GCT    CCGA
                                |||||||| |||    ||||
                                ACGACCGG CGG    GGCT
                                    A   ____
GAM1321  PPP1R12B 3'  CTGCTGGCTGCTGGCCAA    36973         C   ACTT
                                CTGCTGGC GCT    CCGA
                                |||||||| |||    ||||
                                GACGACCG CGA    GGTT
                                    A   CC__
GAM1321  STAU     5'  CTGCTGGCTGCTGCTCCG    32693         C   A  T
                                CTGCTGGC GCT CT CCG
                                |||||||| ||| || |||
                                GACGACCG CGA GA GGC
                                    A   C  _
GAM1322  AK2      3'  TGAGAGGTTACTCATGAA    11562     A        GT
                                TGA AGGTTACTCG  TGAA
                                |||  ||||||||||  ||||
                                ACT TCCAATGAGT  ACTT
                                  C         __
GAM1322  C7orf2   3'  GAGGGGCCACGGTTGAATGGA  35370    AA     TC      CA
                                GA  GGTTAC  GGTTGAA  GA
                                ||  ||||||  |||||||  ||
                                CT  CCGGTG  CCAACTT  CT
                                 CC      __      AC
GAM1322  DYRK1A   3'  TGAAAGGTTGTTTCTTGAACAG 39002          ACTCGG
                                TGAAAGGTT     TTGAACAG
                                |||||||||     ||||||||
                                ACTTTCCAA     AACTTGTC
                                    CAAAG_
GAM1322  EPHB2    3'  TGAAGGTTATGAACA       32680      A    CTCGGT
                                TGAA GGTTA     TGAACA
                                |||| |||||     ||||||
                                ACTT CCAAT     ACTTGT
                                  _    _______
GAM1322  FKBP1A   3'  TGAAAGGATACTCAATACAGA  38284         T       TGA
                                TGAAAGG TACTCGGT   ACAGA
                                |||||||  ||||||||   |||||
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                                ACTTTCC ATGAGTTA   TGTCT
                                   T      ___
GAM1322 IGF1     3'  TGAAAGGTTTTGATATTTTGAA 8354          ACTCGG__    C
             TAGA                  TGAAAGGTT       TTGAA AGA
                                |||||||||       ||||| |||
                                ACTTTCCAA       AACTT TCT
                                     AACTATAA    A
GAM1322 MJD      3'  TGAAAGGTTAATTTGGTTAATA 36187          CTC_     AC
             AGA                   TGAAAGGTTA    GGTTGA  AGA
                                |||||||||||   ||||||  |||
                                ACTTTCCAAT    CCAATT  TCT
                                     TAAA     AT
GAM1322 PDGFRB   3'  TGAGGGGTAGCTGGCTGAACAG 42343     AA   TA  C
             A                    TGA  GGT  CT GGTTGAACAGA
                                |||  |||  || ||||||||||
                                ACT  CCA  GA CCGACTTGTCT
                                  CC   TC  _
GAM1322 PXN      3'  TGAGGGCTTACTCAGACAG    16032     AA   _     TTGA
                                TGA  GGTT ACTCGG    ACAG
                                |||  |||| ||||||    ||||
                                ACT  CCGA TGAGTC    TGTC
                                  C_    A     _____
GAM1322 NFRKB    5'  TTCACCGATATGGTTTGTGGA  26105         CCA    CCAT
                                TTCACCGAT   GTGG    TGGA
                                |||||||||   ||||    ||||
                                AAGTGGCTA   TACC    ACCT
                                     ___    AAAC
GAM1322 SOX11    3'  TTCACCAATTGCTCATTGG    17045         CCAGTG  _
                                TTCACCGAT     GC CATTGG
                                |||||||||     || ||||||
                                AAGTGGTTA     CG GTAACC
                                     A_____  A
GAM1322 TGFA     3'  TTCATTGTCTCCTGAGCCATTG 17450      CCGA_   AGT
             GA                    TTCA    TCC   GGCCATTGGA
                                ||||    |||   ||||||||||
                                AAGT    AGG   TCGGTAACCT
                                  AACAG   AC_
GAM1323 ABR      3'  GCCTTTGCTTCCCAGGT     35010      CCGAG  CA
                                GCCT    GT  TCCCAGGT
                                ||||    ||  ||||||||
                                CGGA    CG  AGGGTCCA
                                  AA___  A_
GAM1323 C4orf1   3'  TCCAAGGTCCCCACCCAGGT   40491         AT__
                                TCCGAGGTC    CCCAGGT
                                |||||||||    |||||||
                                AGGTTCCAG    GGGTCCA
                                     GGGT
GAM1323 FANCG    5'  CTCGCCTCTGGTTGGCCGGGT  21555         CGA   CATC  A
                                CTCGCCTC   GGT    CC GGT
                                ||||||||   |||    || |||
```

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                                GAGCGGAG  CCA   GG CCA
                                    A__   ACC_  C
GAM1323 GATA4   3' CCTCCAAGTCCCAGGT     13108       GTCA
                                CCTCCGAG   TCCCAGGT
                                ||||||||   ||||||||
                                GGAGGTTC   AGGGTCCA
                                    _____
GAM1323 GLRX2   5' CCCGCCTCTGGATTCTTTTAGG 32003       C_  GG  ATCCC
          T                      CTCGCCTC  GA  TC    AGGT
                                 ||||||||  ||  ||    ||||
                                 GGGCGGAG  CT  AG    TCCA
                                     AC  A_  AAAA_
GAM1323 GRB10   3' CTCGCTCTGGGTCCCCAGG   23654     C  CGA   AT
                                CTCGC TC   GGTC  CCCAGG
                                |||||  ||   ||||  ||||||
                                GAGCG AG   CCAG  GGGTCC
                                   _  AC_   ___
GAM1323 MEL     3' TCCCGATCACCCAGGT     23872     GA    T
                                TCC  GGTCA CCCAGGT
                                |||  ||||| |||||||
                                AGG  CTAGT GGGTCCA
                                  G_    _
GAM1323 RXRG    3' GCCCAGGGGTCATCCTGGGT   27941     CCGA      CA
                                GCCT    GGTCATCC  GGT
                                ||||    ||||||||  |||
                                CGGG    CCAGTAGG  CCA
                                  TCC_      AC
GAM1323 SLC6A6  3' CTCTTTTGGGTCCCCAGGT   16785    GCCTCCGA   AT
                                CTC       GGTC  CCCAGGT
                                |||       ||||  |||||||
                                GAG       CCAG  GGGTCCA
                                  AAAAC____   ___
GAM1323 SLC7A8  5' GCTTCCGCCTTTCCCAGGT   29290    C   AGGTCA
                                GC TCCG     TCCCAGGT
                                || ||||     ||||||||
                                CG AGGC     AGGGTCCA
                                 A   GGAA__
GAM1323 SMOH    3' CCTCTCTTTCCTGTCCCAGGT  24811     CGAGG  A__
                                CCTC    TC   TCCCAGGT
                                ||||    ||   ||||||||
                                GGAG    AG   AGGGTCCA
                                  AGAA_  GAC
GAM1323 TFCP2   5' CTCGTTCTTGGCTGCCCCAGGT 24922     CC  CGA   CA
                                CTCG  TC   GGT  TCCCAGGT
                                ||||  ||   |||  ||||||||
                                GAGC  AG   CCG  GGGGTCCA
                                  A_  AA_   AC
GAM1323 TRPV4   3' CTCGCCTCTGGGGCCAAAGCAG 41346       CGA    TCC
          G                     CTCGCCTC   GGTCA   CAGG
                                ||||||||   |||||   ||||
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                              GAGCGGAG  CCGGT  GTCC
                                  ACC    TTC
GAM1323 AF5Q31   3' ATGTTATGGCAGTTTTC    30851     CCA
                              ATGT  ATGGCAGTTTTC
                              ||||  ||||||||||||
                              TACA  TACCGTCAAAAG
                                A__
GAM1323 APPBP2   3' CATGTGTTCACTGCAGTTTTC 26876     C__ ATG
                              CATGT  CA  GCAGTTTTC
                              |||||  ||  |||||||||
                              GTACA  GT  CGTCAAAAG
                                 CAA GA_
GAM1323 CNTN3    3' CACGTCTTCAACAATTTT   42480      CAA
                              CATGTC  TGGCAGTTTT
                              ||||||  ||||||||||
                              GTGCAG  GTTGTTAAAA
                                 AA_
GAM1323 COL19A1  3' CATATCCAGTCCTGTGGTTTTC 12374       A___ GCA
                              CATGTCCA   TG  GTTTTC
                              ||||||||   ||  ||||||
                              GTATAGGT   AC  CAAAAG
                                   CAGG AC_
GAM1323 GPX1     5' CACGTGGCACAGGCAGTTTTC 8220      C_ AT
                              CATGT CA GGCAGTTTTC
                              ||||| || ||||||||||
                              GTGCA GT CCGTCAAAAG
                                 CC GT
GAM1323 HOXC11   3' CCACAGTCCAGTTT      41159     T   ATGGCA
                              CCACA GTCCA    GTTT
                              ||||| |||||    ||||
                              GGTGT CAGGT    CAAA
                                _   _______
GAM1323 HSPC126  3' ACTGTCAAATGGCAGTTTT  30504   A   C
                              AC TGTC AATGGCAGTTTT
                              || |||| ||||||||||||
                              TG ACAG TTACCGTCAAAA
                               _   T
GAM1323 KCNJ15   3' ATGTCCGTGCAGTTTT     13875      AATG
                              ATGTCC   GCAGTTTT
                              ||||||   ||||||||
                              TACAGG   CGTCAAAA
                                 CA__
GAM1323 PSMD5    3' CATGTCCATGAAAATTTT   22779       A  C
                              CATGTCCA TGG AGTTTT
                              |||||||| ||| ||||||
                              GTACAGGT ACT TTAAAA
                                   _  T
GAM1323 VBP1     3' CATGTCTCACAGTTTTC    17926      CAATG
                              CATGTC   GCAGTTTTC
                              ||||||   |||||||||
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                                GTACAG    TGTCAAAAG
                                  AG___
GAM1323 YWHAZ    3' ACCAGTATGTAGGCAGTTTTC 18198     C_   CCAAT
                                ACCA ATGT    GGCAGTTTTC
                                |||| ||||    ||||||||||
                                TGGT TACA    CCGTCAAAAG
                                  CA   T____
GAM1323 ZFX      3' CATGTTGCCAGTTTTC      18213      CCAA G
                                CATGT   TG CAGTTTTC
                                |||||   || ||||||||
                                GTACA   AC GTCAAAAG
                                  ____ G
GAM1324 IRS2     3' GGATAGAGGGCGAGTTAAAT  40707       TCTT A
                                GGATAGA   GC AGTTAAAT
                                |||||||   || ||||||||
                                CCTATCT   CG TCAATTTA
                                    CC__ C
GAM1324 TOMM22   3' AGGGCACAGTTGCAAGTT    33673     _   ATC
                                AGGG ATAG   TTGCAAGTT
                                |||| ||||  |||||||||
                                TCCC TGTC   AACGTTCAA
                                  G   ___
GAM1324 ZNF255   5' AGGGATAAAAAGCTACAAGTT 25099        TC_
                                AGGGATAGA   TTGCAAGTT
                                |||||||||  |||||||||
                                TCCCTATTT   GATGTTCAA
                                     TTC
GAM1325 DMD      5' GACTTGCTCAAGCTTTTCTT  19704    C       ATCG
                                GAC TGCTTAAGCT   TCTT
                                ||| ||||||||||   ||||
                                CTG ACGAGTTCGA   AGAA
                                  A        AA__
GAM1325 FBXL7    3' CCTGCTTAAGTACATCTT    29399         C  T
                                CCTGCTTAAG TA CGTCTT
                                |||||||||| || ||||||
                                GGACGAATTC AT GTAGAA
                                     _ _
GAM1326 CANX     3' TAATCAATACATTTGGGA    44667      TATAG
                                TAGTT    ACATTTGGGA
                                |||||    ||||||||||
                                ATTAG    TGTAAACCCT
                                   TTA__
GAM1326 MAX      3' TTTATAGTCTTATAGTAAAGGG 40366         _   ACATTT
                                TTTATAGTTT ATAG     GGG
                                |||||||||| ||||     |||
                                AAATATCAGA TATC     CCC
                                     A   ATTT__
GAM1327 ETS2     3' GCTCCTTTGAGAATCTC     23469     AAGGAG  A
                                GCT     TTT AGAATCTC
                                |||     ||| ||||||||
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                                CGA     AAA TCTTAGAG
                                  GG____  C
GAM1327  NAPB    3'  CAGCTCTCATTTAAGAATCTCA 43170      AAGGA
                                TAGCT    GTTTAAGAATCTCA
                                |||||    ||||||||||||||
                                GTCGA    TAAATTCTTAGAGT
                                   GAG__
GAM1327  RNF12   3'  TAGCTGAGAGTTCAGATCT   32039      AA      A  A
                                TAGCT  GGAGTTTA GA TCT
                                |||||  |||||||| || |||
                                ATCGA  TCTCAAGT CT AGA
                                   C_      _ _
GAM1327  STCH    3'  TAGTAAGAACTGGGAATCTCA  28081    C     GTTTAA
                                TAG TAAGGA     GAATCTCA
                                ||| ||||||     ||||||||
                                ATC ATTCTT     CTTAGAGT
                                  _     GACC__
GAM1327  TERF2   3'  GCTAAAGAGTTTTTAAAGGGAA 24911          AA_____
              TCT                  GCTAAGGAGTTT      GAATCT
                                |||||||||||      ||||||
                                CGATTTCTCAAA      CTTAGA
                                      AATTTCC
GAM1327  TRAM    3'  TAGCTATAAGAATCT      30703       AGGAGTT
                                TAGCTA      TAAGAATCT
                                ||||||      |||||||||
                                ATCGAT      ATTCTTAGA
                                  ________
GAM1328  DAB1    3'  CGAGCTCGCATCGATGCTATT  34350         __ CTA
                                CGAGTTCGT  CG   CTATT
                                |||||||||  ||   |||||
                                GCTCGAGCG  GC   GATAA
                                      TA  TAC
GAM1329  LAMP2   3'  GAAAAATTACATCTATAT    30385     TTTAGA
                                GAA     TACATCTATAT
                                |||     ||||||||||||
                                CTT     ATGTAGATATA
                                  TTTA__
GAM1329  GBAS    3'  TGAGATTTATTCACACTT    11236    T      _
                                TG AGATTTAT CATATTT
                                || |||||||| |||||||
                                AC TCTAAATA GTGTGAA
                                  _       A
GAM1329  PARN    3'  TGTAGATTTGCACGATTTC    15094        AT  _
                                TGTAGATTT  CAT ATTTC
                                |||||||||  ||| |||||
                                ACATCTAAA  GTG TAAAG
                                      C_   C
GAM1329  PRKG1   3'  TGTGGATTCTTTTCTCCA    26518     A    ATCATA
                                TGT GATTT     TTTCTCCA
                                ||| |||||     ||||||||
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                                ACA CTAAG     AAAGAGGT
                                  C    A_____
GAM1329 ZNF138   3' TGTAGGGTTTTTCTCC     44345      AT  ATCATA
                                TGTAG  TT     TTTCTCC
                                |||||  ||     |||||||
                                ACATC  AA     AAAGAGG
                                   CC  _______
GAM1329 ZNF8     3' TGTGGACTTACCACATTT    41967     A
                                TGT GATTTATCATATTT
                                |||  ||||||||||||||
                                ACA CTGAATGGTGTAAA
                                  C
GAM1330 MYLK     3' TGATGGCATAATAAACCAA   38167    T   A        TG
                                A ATG CATAATAAAT  G
                                | |||  ||||||||||  |
                                A TAC GTATTATTTG  T
                                 C   C         GT
GAM1330 NARS     3' TACATGACATGCATTTGGT   21218          AATAAA
                                TATATGACAT     TTGGT
                                ||||||||||     |||||
                                ATGTACTGTA     AACCA
                                      CGTA__
GAM1330 PCDHA9   3' TGATGACATAGTAAATGCTTAG 36553   T       A    ___
           TAA                    A ATGACATA TAAAT   TGGTAA
                                | ||||||||  |||||   ||||||
                                A TACTGTAT ATTTA   ATCATT
                                 C       C     CGA
GAM1330 PHYH     3' TATGACATAAAATTGGTA    26316          TA
                                TATGACATAA  AATTGGTA
                                ||||||||||  ||||||||
                                ATACTGTATT  TTAACCAT
                                      __
GAM1330 SMARCA2  3' TATATGACAAATGAACTCACTG 16894         T___   AA
           G                     TATATGACA    AAT  ATTGG
                                |||||||||    |||  |||||
                                ATATACTGT    TTG  TGACC
                                     TTAC   AG
GAM1330 SP3      3' TTTTATTAACTACCACACTGT  44387       C        AAT
                                TTTTA TAATTACTA   CTGT
                                |||||  |||||||||   ||||
                                AAAAT ATTGATGGT   GACA
                                   A        GT_
GAM1331 DUOX1    3' GCAGAAAAGTGATTTATTTG   32654      TTGCC_
                                GCAG     GATTTATTTG
                                ||||     ||||||||||
                                CGTC     CTAAATAAAC
                                  TTTTCA
GAM1331 SOX15    5' AGTCGTTGCCGAGGAACTTG   28019    CA      TTT
                                AG  GTTGCCGA   ATTTG
                                ||  ||||||||   |||||
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                                TC  CAACGGCT   TGAAC
                                 AG       CCT
GAM1331  ARAF1    3'  ACATTGATTGGCTGGTG     41907      C  C  CTACT
                                ACAT GA TG    GCTGGTG
                                |||| || ||    |||||||
                                TGTA CT AC    CGACCAC
                                  A  A  _____
GAM1331  MYOZ1    3'  GACTGTTACTGGTGG       34555       CTAC
                                GACTG   TGCTGGTGG
                                |||||   |||||||||
                                CTGAC   ATGACCACC
                                  A___
GAM1332  ADORA2B  5'  CCGGTCCAGGCGCCGTGCC   8612          AT   G  C
                                CCGGTCCAG  CGC GT GCC
                                |||||||||  ||| || |||
                                GGCCAGGTC  GCG CA CGG
                                     C_   G  _
GAM1332  AGTR1    5'  CCGGTCCAGACGTC       28909           CGCG
                                CCGGTCCAGAT   GTC
                                ||||||||||    |||
                                GGCCAGGTCTG   CAG
                                      ____
GAM1332  CMAR     5'  CCGGTCCAGTCGGCC      23292         ATCG
                                CCGGTCCAG   CGGTC
                                |||||||||   |||||
                                GGCCAGGTC   GCCGG
                                     A___
GAM1332  GCLC     5'  CCGGGCTGACGGCGGTCGCCCG 11296      TCCA   C
                                CCGG   GAT GCGGTCGCCCG
                                ||||   ||| ||||||||||
                                GGCC   CTG CGCCAGCGGGC
                                  CGA_  C
GAM1332  GP1BB    3'  CCGGTCCAGGTTGGCGC     7623          ATCGC  T
                                CCGGTCCAG    GG CGC
                                |||||||||    || |||
                                GGCCAGGTC    CC GCG
                                     CAA__  _
GAM1332  SCG3     5'  CGGCTTGGGTCACAGCCCG   29884      CCAGA    GTC
                                CGGT    TCGCG   GCCCG
                                ||||    |||||   |||||
                                GCCG    AGTGT   CGGGC
                                  AACCC    ___
GAM1332  WT1      5'  GGCCCAGATGCCGCCC      35964         CGCG
                                GGTCCAGAT   GTCGCCC
                                |||||||||   |||||||
                                CCGGGTCTA   CGGCGGG
                                      ____
GAM1332  AP1S1    5'  GCCTCCGGCTCGGCGCGTCC   10499     GATT     C
                                GCC   TCCGGC CGGCGCGTCC
                                |||   |||||| ||||||||||
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                                CGG    AGGCCG GCCGCGCAGG
                                 ____     A
GAM1332  EYA1     3'  GCTGATTTCCGGATTAGCATCG 7989     C       CCC   _
              T                   GC GATTTCCGG   GGCG CGT
                                  || |||||||||   |||| |||
                                  CG CTAAAGGCC   TCGT GCA
                                   A        TAA    A
GAM1333  BBOX1    3'  TGAGAGAAGTTACATGTTCAT  19603     A       _   G
                                  TGA AGAAGTTAC TGTT GT
                                  ||| ||||||||| |||| ||
                                  ACT TCTTCAATG ACAA TA
                                    C        T    G
GAM1333  C1QB     5'  TGTGAGAGGTTACCACCGTGGT 7946     AA   A    TG __
              GATC                    TG  AGA GTTAC  T  TGGTGATC
                                  ||  ||| |||||  |  ||||||||
                                  AC  TCT CAATG  G  ACCACTAG
                                   AC   C     GT GC
GAM1333  PPP2R2B  3'  TGGAAGAATTACTGTTAGC   21341    A    G
                                  TG AAGAA TTACTGTTGGT
                                  || ||||| ||||||||||
                                  AC TTCTT AATGACAATCG
                                   C    _
GAM1333  CALD1    3'  GCAATTTTAAACTTGGATC   37627        CCTT
                                  GCAATTT    ATTTGGATC
                                  |||||||    |||||||||
                                  CGTTAAA    TGAACCTAG
                                       ATT_
GAM1333  CALD1    3'  AGCAATTTTAAACTTGGATC  37624        CCTT
                                  AGCAATTT    ATTTGGATC
                                  ||||||||    |||||||||
                                  TCGTTAAA    TGAACCTAG
                                       ATT_
GAM1333  CLASP1   3'  AGCATTTTCCTTATGGA     42232      A       TT
                                  AGCA TTTCCTTA  TGGA
                                  |||| ||||||||  ||||
                                  TCGT AAAGGAAT  ACCT
                                    A       __
GAM1333  CRY1     3'  ACAATACCAATTTGGAT     19829       TT  TT
                                  GCAAT  CC  ATTTGGAT
                                  |||||  ||  ||||||||
                                  TGTTA  GG  TAAACCTA
                                     T_  T_
GAM1333  CYP1B1   3'  AGCAATTTGCTTATAGAG    6442         C     TT
                                  AGCAATTT CTTAT  GG
                                  |||||||| |||||  ||
                                  TCGTTAAA GAATA  TC
                                       C     TC
GAM1333  EPHB2    3'  GCAATTCCTCAAGGATC     32669        T     TTT
                                  GCAATT CCTTA   GGATC
                                  |||||| |||||   |||||
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                                CGTTAA GGAGT   CCTAG
                                   _    T__
GAM1333  GALR1    3'  AGGAATTTCCTAAATGGATC   11194    C      TATT
                                AG AATTTCCT    TGGATC
                                || ||||||||    ||||||
                                TC TTAAAGGA    ACCTAG
                                 C       TTT_
GAM1333  GPR44    3'  AGTCATTTCCCCCATTGGAT   21951    CA      AT
                                AG  ATTTCCTT  TTGGAT
                                ||  ||||||||  ||||||
                                TC  TAAAGGGG  AACCTA
                                 AG       GT
GAM1333  ID1      3'  AGCAATTTCCTCAGAAATC    43115          TTT
                                AGCAATTTCCTTA   GGATC
                                ||||||||||||   |||||
                                TCGTTAAAGGAGT   TTTAG
                                        C__
GAM1333  ING1     3'  AGTAATTTCCTGACCCAG    24395    C      T   TG
                                AG AATTTCCT ATT  G
                                || ||||||||  |||  |
                                TC TTAAAGGA TGG  C
                                 A       C   GT
GAM1333  LSP1     3'  GCAGTTTCCCCTTGGATC    14238    A     TA
                                GCA TTTCCT  TTTGGATC
                                |||  ||||||  ||||||||
                                CGT AAAGGG  GAACCTAG
                                  C     __
GAM1333  PCDHB9   3'  AGCAACTTCCACCTCCTGG    33318         _ TA
                                AGCAATTTCC T  TTTGG
                                ||||||||||  |  |||||
                                TCGTTGAAGG G  GGACC
                                      T GA
GAM1333  PPP2R5E  3'  AGCAATTTCATCAACAGATC   26465         C   TT
                                AGCAATTTC TTA  TGGATC
                                |||||||||  |||  ||||||
                                TCGTTAAAG AGT  GTCTAG
                                      T   T_
GAM1333  PTGFRN   3'  AGCAATTTGCCTTCAGG     42584         _   ATTT
                                AGCAATTT CCTT    GG
                                ||||||||  ||||    ||
                                TCGTTAAA GGAA    CC
                                     C    GT__
GAM1333  TADA2L   3'  AGCAATTCTCCTGGGAT     39426       _    TATTT
                                AGCAAT TTCCT     GGAT
                                ||||||  |||||     ||||
                                TCGTTA GAGGA     CCTA
                                   A     C_____
GAM1333  TAF15    3'  GCAATTTCACTATGGATC    40185         C   TT
                                GCAATTTC TTA  TGGATC
                                ||||||||  |||  ||||||
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                                CGTTAAAG GAT  ACCTAG
                                     T  __
GAM1333  UGDH     3'  AGCAATTTCATGGAT       17881          CTTATT
                                AGCAATTTC     TGGAT
                                |||||||||     |||||
                                TCGTTAAAG     ACCTA
                                     T_____
GAM1334  EPHA2    3'  TCCCTGGTCATCTCCTCAGT   20742       A         A
                                TCCCTG TCATCTCCTCA GT
                                |||||| |||||||||| ||
                                AGGGAC AGTAGAGGAGT CA
                                   C         _
GAM1334  GAB2     3'  TCCCTGATGTCAAGT       38684         CATCTCC
                                TCCCTGAT      TCAAGT
                                ||||||||      ||||||
                                AGGGACTA      AGTTCA
                                     C_______
GAM1334  GRIN2A   5'  CCTGGTCATCTCCAGGGC    9107       A       TCAA
                                CCTG TCATCTCC    GT
                                |||| ||||||||    ||
                                GGAC AGTAGAGG    CG
                                  C       TCC_
GAM1334  OSR1     3'  CTGATCATCTCACCTACT    23036           _  CAAG
                                CTGATCATCTC CT    TACT
                                |||||||||| ||    ||||
                                GACTAGTAGAG GG    ATGA
                                     T  _____
GAM1334  PLOD2    3'  CCTGATATAAAATTCAAGTACT 9595        CATCTCC
                                CCTGAT      TCAAGTACT
                                ||||||      |||||||||
                                GGACTA      AGTTCATGA
                                   TATTTTA
GAM1334  RAD54B   3'  CTGACCATCTCTCCATACT   29676           CT  AG
                                CTGATCATCTC  CA  TACT
                                |||||||||| ||  ||||
                                GACTGGTAGAG  GT  ATGA
                                     AG  __
GAM1334  SEL1L    3'  CTGATCATTTCTTACATACT   22846        C  CTCAA
                                CTGATCAT TC     GTACT
                                |||||||| ||     |||||
                                GACTAGTA AG     TATGA
                                     A  AATG_
GAM1334  IRTA2    3'  TGGAGTTTGTTCTGCCACTGTG 36350     GA        AGAAA
              C                   TGG  TTTGTTCTGC     GTGC
                                |||  ||||||||||    ||||
                                ACC  AAACAAGACG    CACG
                                  TC         GTGA_
GAM1334  LAMP1    3'  TGAGAAACGTTTGCAGAAAGTG 24511       TT    C
                                TGGGA  TGTT TGCAGAAAGTG
                                |||||  |||| ||||||||||
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                                ACTCT  GCAA ACGTCTTTCAC
                                  TT   _
GAM1334  MPZ     5'  TGGGGTTGAGAAAGT      8039      ATTT  TC  C
                                TGGG   GT  TG AGAAAGT
                                ||||   ||  || |||||||
                                ACCC   CA  AC TCTTTCA
                                  ____  __ _
GAM1334  MTCP1   5'  GGGCATCTGTTCTGTAGAAGGT 30584    _       C   A
           GC                     GGG ATTTGTTCTG AGAA GTGC
                                ||| |||||||||| |||| ||||
                                CCC TAGACAAGAC TCTT CACG
                                  G        A   C
GAM1334  TCF2    3'  TGGGGTTTCTTAGGGAGTGC  27033     ATTTG   GC  AA
                                TGGG   TTCT  AG  AGTGC
                                ||||   ||||  ||  |||||
                                ACCC   AAGA  TC  TCACG
                                  CA___   A_  CC
GAM1335  DUOX2   3'  GGAAGTCAATTAGAGATGTGGG 30446          TCGA   A
                                GGAGGTCAATT   AGAT TGGG
                                ||||||||||   |||| ||||
                                CCTTCAGTTAA   TCTA ACCC
                                      TC__   C
GAM1335  EPM2A   5'  GGCGGTTGATTTCCACCTGTGG 24971    A  CA    GAAGATA
           G                    GG GGT  ATTTC      TGGG
                                || |||  |||||      ||||
                                CC CCA  TAAAG      ACCC
                                 G  AC    GTGGAC_
GAM1335  KLK4    3'  GGGGTCAATTTCATG      41752    A       GAAGAT
                                GG GGTCAATTTC     ATG
                                || ||||||||||     |||
                                CC CCAGTTAAAG     TAC
                                 _       _______
GAM1335  EFNA1   3'  GCTGGTTGGCCTCCTTCCG   20703    CAA   A
                                GCT   TTG CCTTCTTCCG
                                |||   ||| ||||||||||
                                CGA   AAC GGAGGAAGGC
                                  CC_   C
GAM1336  FGF18   5'  TCCGGGCGTCCGTG       38010          AGAAGA
                                TCCGGGCGTTC     GTG
                                ||||||||||     |||
                                AGGCCCGCAGG     CAC
                                       _______
GAM1336  GSPT1   5'  CCCGGCCGGAGAGGAGTGGG   13306      G  TTC   A
                                TCCGG CG   AGA GAGTGGG
                                ||||| ||   ||| |||||||
                                GGGCC GC   TCT CTCACCC
                                   G  C__   C
GAM1336  M17S2   5'  CATTAGGGCGGAAAGAGTGGG  36587    CC    TTCA
                                CAT  GGGCG   GAAGAGTGGG
                                |||  |||||   ||||||||||
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                                GTA  CCCGC   TTTCTCACCC
                                  AT    C___
GAM1336  MADD     5'  CCGGGCGCGCGCGGGGAGTGGG 39065        TCAGAA_
                                CCGGGCGT      GAGTGGG
                                ||||||||      |||||||
                                GGCCCGCG      CTCACCC
                                    CGCGCCC
GAM1336  SLC30A4  5'  CGGCCGCAGGAGAGTG      30014     G  TT   A
                                CGG CG  CAG AGAGTG
                                ||| ||  ||| ||||||
                                GCC GC  GTC TCTCAC
                                  G  __  C
GAM1336  TBXA2R   5'  CGGGCGCCGAGGGTGGG     9850        TC  AAGA
                                CGGGCGT  AG   GTGGG
                                |||||||  ||   |||||
                                GCCCGCG  TC   CACCC
                                    GC  C___
GAM1336  APOB48R  3'  CCTGGCTCCCAGAGCACCGGGT 33089     AA_      T__   A
                                CC   CTCCCGGA   CCG GT
                                ||   ||||||||   ||| ||
                                GG   GAGGGTCT   GGC CA
                                 ACC       CGT   C
GAM1336  CTSZ     5'  TCCGGATCCCGCTCCGAGT   41615     AAC    GA
                                TCC   TCCCG  TCCGAGT
                                |||   |||||  |||||||
                                AGG   AGGGC  AGGCTCA
                                  CCT    G_
GAM1336  GC       3'  TCCAACTCTGGTCAAAGT    43094        CC  A  C
                                TCCAACTC  GG TC GAGT
                                ||||||||  || || ||||
                                AGGTTGAG  CC AG TTCA
                                    A_  _  T
GAM1336  HM13     5'  TCCGACTCCAGCTCCGGT    43111     A    C  A   A
                                TCC ACTCC GG TCCG GT
                                ||| ||||| || |||| ||
                                AGG TGAGG TC AGGC CA
                                  C    _  G   _
GAM1336  HOXD1    5'  TCCAACCCATGGCGAGT     35987        CC  ATC
                                TCCAACTC  GG   CGAGT
                                ||||||||  ||   |||||
                                AGGTTGGG  CC   GCTCA
                                    TA  ___
GAM1336  KCNA6    5'  CCCGGCTCCCGGACGCAGAG   13808     AA       C _
                                TCC  CTCCCGGAT C GAG
                                |||  ||||||||| | |||
                                GGG  GAGGGCCTG G CTC
                                  CC        C T
GAM1336  MTIF2    5'  TCTGACTCCCAGTACGGT    14685    CA      ATC  A
                                TC  ACTCCCGG   CG GT
                                ||  ||||||||   || ||
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                                AG  TGAGGGTC   GC CA
                                 AC       AT_ _
GAM1336  NEU3     3'  TCCAACTCCTAGTTCAGT    27408         CG A  CG
                                TCCAACTCC  G TC  AGT
                                |||||||||  | ||  |||
                                AGGTTGAGG  C AG  TCA
                                     AT A  __
GAM1336  NFE2L1   3'  TCCACTCCACCCGAGT      17333      A    CGG
                                TCCA CTCC   ATCCGAGT
                                |||| ||||   ||||||||
                                AGGT GAGG   TGGGCTCA
                                  _   ____
GAM1336  PRKAR1A  3'  TCCAATCTCCTGGAATCAGT   15613       _    C   TC G
                                TCCAA CTCC GGA  C AGT
                                ||||| |||| |||  | |||
                                AGGTT GAGG CCT  G TCA
                                   A    A   TA _
GAM1336  RAB2L    5'  TCCGGCCCCGGACCGAGT    21921     AAC      T
                                TCC   TCCCGGA CCGAGT
                                |||   ||||||| ||||||
                                AGG   GGGGCCT GGCTCA
                                  CC_      _
GAM1336  RAB7L1   3'  TCTAACTCCCAGGTTCAAGT   19438    C        ATC
                                TC AACTCCCGG   CGAGT
                                || |||||||||   |||||
                                AG TTGAGGGTC   GTTCA
                                 A        CAA
GAM1336  SMARCC1  3'  TCCACTCCCAAGAG        16904      A      ATCC
                                TCCA CTCCCGG    GAG
                                |||| |||||||    |||
                                AGGT GAGGGTT    CTC
                                  _     _____
GAM1336  SQLE     3'  TCCAAATCTTGGTCCAAG    17107       C  CC  A
                                TCCAA TC  GG TCCGAG
                                ||||| ||  || ||||||
                                AGGTT AG  CC AGGTTC
                                   T  AA  _
GAM1336  TNFSF15  3'  CAATCCTGACCCGAGT      23051     C   CG
                                CAA TCC  GATCCGAGT
                                ||| |||  |||||||||
                                GTT AGG  CTGGGCTCA
                                  _   A_
GAM1336  USP1     5'  TCCAACCCGAATGAG       17906      CT      CC
                                TCCAA  CCCGGAT  GAG
                                |||||  |||||||  |||
                                AGGTT  GGGCTTA  CTC
                                  __      __
GAM1337  MAN1A1   3'  ATCTGAACCAAATAGAATGCT  45090     G  CA  TT
                                ATC TG  GG  AAATAGAATGCT
                                ||| ||  ||  ||||||||||||
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                                TAG AC  TT  TTTATCTTACGA
                                  _ __  GG
GAM1337  MGAM     3'  GTGCACGTTGTAGTGC      43658       G   AAA   AA
                                GTGCA GTT   TAG  TGC
                                ||||| |||   |||  |||
                                CACGT CAA   ATC  ACG
                                   G   C__   __
GAM1337  MLLT4    3'  GTGCAGGCACCGGGATGCT   43681         TAAATA  A
                                GTGCAGGT     GA TGCT
                                ||||||||     || ||||
                                CACGTCCG     CT ACGA
                                     TGGCC_ _
GAM1337  NET1     3'  ATCGGCAGGTTAAATGAAT   25227      T         A
                                ATCG GCAGGTTAAAT GAAT
                                |||| |||||||||| ||||
                                TAGC CGTCCAATTTA CTTA
                                  _         _
GAM1337  RAB27A   3'  CATGTTAAATAGAATGCT    21360    G
                                CA GTTAAATAGAATGCT
                                || ||||||||||||||
                                GT CAATTTATCTTACGA
                                 A
GAM1337  RUNX3    3'  GTGCAGGCTGGTGGGATGCT   20325         AAATA  A
                                GTGCAGGTT    GA TGCT
                                |||||||||    || ||||
                                CACGTCCGA    CT ACGA
                                     CCACC  _
GAM1337  ADAMTS1  3'  TGCGTTATTTCACGTT      28114        CCGT  _
                                TGCGTTAT   TTC CGTT
                                ||||||||   ||| ||||
                                ACGCAATA   AAG GCAA
                                     _____  T
GAM1337  ZNF214   3'  CTGTGTGTTTCCATC       29910     C  TATCC
                                CTG GT    GTTTCCGTT
                                ||| ||    |||||||||
                                GAC CA    CAAAGGTAG
                                  A  ______
GAM1338  ABCD1    5'  GGGCAGAGGGGGCGTCTCTTC  6201         AAAATT  GG
                                GGGCAGAGG     TGT  CTTC
                                |||||||||     |||  ||||
                                CCCGTCTCC     GCA  GAAG
                                     CCC___   GA
GAM1338  CAPN1    3'  GGACAGAGGGGGCGTTGGCTTC 23253         AAAATTTG
                                GGGCAGAGG       TGGCTTC
                                |||||||||       |||||||
                                CCTGTCTCC       ACCGAAG
                                     CCCGCA__
GAM1338  CTBP2    5'  AGGCAGAGGAGAAGCT      35598          AAATTTGT
                                GGGCAGAGGA       GGCT
                                ||||||||||       ||||
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                                TCCGTCTCCT       TCGA
                                     CT_______
GAM1338  DAAM2    3'  GGACAGAGGCTGCTGTGGCTTC 45176          AAAAT
                                GGGCAGAGG     TTGTGGCTTC
                                |||||||||     ||||||||||
                                CCTGTCTCC     GACACCGAAG
                                     GAC__
GAM1338  DLEC1    3'  GGATGGAGTTTGTGGCTT    28830     CA   GAAAA
                                GGG  GAG     TTTGTGGCTT
                                |||  |||     ||||||||||
                                CCT  CTC     AAACACCGAA
                                  AC  _____
GAM1338  EIF2C1   3'  GGGCAGGGGGGGATGCTTGCTTC 29180        A  AAAATT   G_
                                GGGCAG GG      TGT  GCTTC
                                |||||| ||      |||  |||||
                                CCCGTC CC      ACG  CGAAG
                                   _  CCCT__   AA
GAM1338  HADH2    3'  GGGCAGAGGAGCGTGTG     21055          AAATT
                                GGGCAGAGGA     TGTG
                                ||||||||||     ||||
                                CCCGTCTCCT     ACAC
                                     CGC__
GAM1338  IGF2     5'  GGGCAGAGCGGGGGGGATGGCTT 8312          GAAAATTT
                                GGGCAGAG       GTGGCTT
                                ||||||||       |||||||
                                CCCGTCTC       TACCGAA
                                     GCCCCCC_
GAM1338  INPP5D   3'  GGGAGAGGGTCCAGTGGCTTC  44423     C     AAAATTT
                                GGG AGAGG      GTGGCTTC
                                ||| |||||      ||||||||
                                CCC TCTCC      CACCGAAG
                                  _    CAGGT__
GAM1338  KIF5C    3'  GGCCAGAGGAGGGTGACTTC   21154    G      AAATTT
                                GG CAGAGGA     GTGGCTTC
                                || |||||||     ||||||||
                                CC GTCTCCT     CACTGAAG
                                  G      CC____
GAM1338  NESH     5'  GGGCAGAGGGTGGGGGCTT    32341          AAAATTTGT
                                GGGCAGAGG        GGCTT
                                |||||||||        |||||
                                CCCGTCTCC        CCGAA
                                     CACCC____
GAM1338  ODF2     3'  GGGAGAGGAAAACCACCAGGCT 14932     C          TGT_
              TC                  GGG AGAGGAAAATT    GGCTTC
                                ||| ||||||||||    ||||||
                                CCC TCTCCTTTTGG    CCGAAG
                                  _          TGGT
GAM1338  PFKM     5'  GGGGGAAGGAGGAGAGGCTTC  41180     CA     AAATTTGT
                                GGG  GAGGA       GGCTTC
                                |||  |||||       ||||||
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                                CCC  TTCCT      CCGAAG
                                  CC    CCTCT___
GAM1338  SHC1     5'  GGGAGAGGGACAAGTGGCTTC  16703     C    AAA  TT
                                GGG AGAGG   AT  GTGGCTTC
                                ||| |||||   ||  ||||||||
                                CCC TCTCC   TG  CACCGAAG
                                  _    C__  TT
GAM1338  STIM1    3'  GGGCAGAGGAAAAATACCTT   41133          TTT   G
                                GGGCAGAGGAAAA   GTG CTT
                                ||||||||||||   ||| |||
                                CCCGTCTCCTTTT   TAT GAA
                                       ___   G
GAM1338  ZNF261   3'  GGGCAGAGAAGGCAGCT     22990         AAATTT TG
                                GGGCAGAGGA     G  GCT
                                ||||||||||     |  |||
                                CCCGTCTCTT     C  CGA
                                     C_____ GT
GAM1338  AMD1     3'  TTCAAACTACATTTCTC     11593         AC  CA
                                TTCAAACTA  CA  TCTC
                                |||||||||  ||  ||||
                                AAGTTTGAT  GT  AGAG
                                     __  AA
GAM1338  ATRN     3'  ATTTCAAAACATCTCC      40288         CTAACC
                                ATTTCAAA     ACATCTCC
                                ||||||||     ||||||||
                                TAAAGTTT     TGTAGAGG
                                     _______
GAM1338  BRCA1    3'  CTTCCATTGACCACATCTCC   28632      AAACTA
                                TTTC     ACCACATCTCC
                                ||||     ||||||||||
                                GAAG     TGGTGTAGAGG
                                  GTAAC_
GAM1338  CACNA2D2 3'  CTTCAAACTGGCCATCTC    25713         AACCA
                                TTTCAAACT    CATCTC
                                |||||||||    ||||||
                                GAAGTTTGA    GTAGAG
                                     CCG__
GAM1338  EZH1     3'  ATTTCAAATAGACCTAACTCC  12778        CTA   ACAT
                                ATTTCAAA   ACC    CTCC
                                ||||||||   |||    ||||
                                TAAAGTTT   TGG    GAGG
                                    ATC   ATT_
GAM1338  FCGR2B   3'  TTTGGAACTCGAGCATCTCCC  19659     CA    AACCA
                                TTT  AACT    CATCTCCC
                                |||  ||||    ||||||||
                                AAA  TTGA    GTAGAGGG
                                  CC   GCTC_
GAM1338  FHL2     3'  ATTTCAAACCATCTTCC     11105         TAACCA    _
                                ATTTCAAAC     CATCT CC
                                |||||||||     ||||| ||
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                                TAAAGTTTG     GTAGA GG
                                       _______    A
GAM1338  FZD1     3'  ATTTCAGGCGCTATCTCCCC   18611       AACTAACCAC
                                ATTTCA        ATCTCCCC
                                ||||||        ||||||||
                                TAAAGT        TAGAGGGG
                                   CCGCGA____
GAM1338  FZD1     3'  ATCTCAGTAACCACATCTTTCC 18610       AAC         CC
                                ATTTCA  TAACCACATCT  CC
                                ||||||  ||||||||||  ||
                                TAGAGT  ATTGGTGTAGA  GG
                                   C__         AA
GAM1338  JJAZ1    3'  CTACACCTACATCTCCCC    31688     _  _
                                CTA ACC ACATCTCCCC
                                ||| ||| ||||||||||
                                GAT TGG TGTAGAGGGG
                                  G   A
GAM1338  KCNA3    3'  ATTCCAAACACCATATTTTCC  13791        TA   CATC_
                                ATTTCAAAC  ACCA    TCC
                                |||||||||  ||||    |||
                                TAAGGTTTG  TGGT    AGG
                                     __   ATAAA
GAM1338  NFIB     3'  ATTTCAAACTGGGTTACACAC  24638        AAC___
                                ATTTCAAACT     CACAT
                                ||||||||||     |||||
                                TAAAGTTTGA     GTGTG
                                     CCCAAT
GAM1338  PSCDBP   3'  ATCTCAGACCACATCTTC    20179       AACTA       CC
                                ATTTCA    ACCACATCT  C
                                ||||||    |||||||||  |
                                TAGAGT    TGGTGTAGA  G
                                   C_____       AA
GAM1338  SH3BP2   3'  CTTCGGGTTAACCACAAGCCTC 16631      AAAC       __
                                TTTC   TAACCACA  TCTC
                                ||||   ||||||||  ||||
                                GAAG   ATTGGTGT  GGAG
                                  CCCA       TC
GAM1338  ZNF26    5'  ACTTCAAACTAAAGGCTTTCC  43792          CCACATC
                                ATTTCAAACTAA      TCC
                                ||||||||||||      |||
                                TGAAGTTTGATT      AGG
                                     TCCGAA_
GAM1339  ABCD1    3'  GGGAGCCGGGGCCCCAC     6200        T      GTGG
                                GGGAGC CGGGGCC   CCAC
                                |||||| |||||||   ||||
                                CCCTCG GCCCCGG   GGTG
                                  _     _____
GAM1339  ABP1     3'  GGAGTTCCCAGGTGTGGC    41792      __     GCC
                                GGAG  CTCGGG   GTGGC
                                ||||  ||||||   |||||
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                                CCTC  GGGTCC   CACCG
                                  AA     A__
GAM1339  ADAM23   5'  CGGGGCTCGGGGCTGGGC    19204      A       CGT
                                CGGG GCTCGGGGC   GGC
                                |||| |||||||||   |||
                                GCCC CGAGCCCCG   CCG
                                  _       AC_
GAM1339  ADRA2A   5'  GAGCTCGGGGGTCCTATG    8637          __ _
                                GAGCTCGGGG  CC GTG
                                ||||||||||  || |||
                                CTCGAGCCCC  GG TAC
                                      CA  A
GAM1339  AF1Q     5'  CGGGAGCTCCGGGGTCTGCG   27725         _   CC_
                                CGGGAGCTC GGGG   GTG
                                ||||||||| ||||   |||
                                GCCCTCGAG CCCC   CGC
                                     G    AGA
GAM1339  BCL10    5'  CGGGAGCTCGGGCTGCG     19405          G C
                                CGGGAGCTCGGG C GTG
                                |||||||||||| | |||
                                GCCCTCGAGCCC G CGC
                                      _ A
GAM1339  CACNA1C  3'  CGGGAGCTCGGCGTGGCC    8751           GGC
                                CGGGAGCTCGG   CGTGGCC
                                ||||||||||   |||||||
                                GCCCTCGAGCC   GCACCGG
                                        ___
GAM1339  DDX11    3'  CAGGAGCCTGTGGCCATG    36172        CGG
                                CGGGAGCT   GGCCGTG
                                ||||||||   |||||||
                                GTCCTCGG   CCGGTAC
                                     ACA
GAM1339  DDX11    3'  CAGGAGCCCTGTGGCCATG   36171        GG_
                                CGGGAGCTC   GGCCGTG
                                |||||||||   |||||||
                                GTCCTCGGG   CCGGTAC
                                     ACA
GAM1339  EDN3     5'  GGGGGTTCGAGGCCGGCC    6483      AGC      GT
                                GGG   TCGGGGCC  GGCC
                                |||   ||||||||  ||||
                                CCC   AGCTCCGG  CCGG
                                  CCA      __
GAM1339  EPB49    3'  GGAAGCTCGGGGTTTGCG    12733          CC_
                                GGGAGCTCGGGG   GTG
                                ||||||||||||   |||
                                CCTTCGAGCCCC   CGC
                                      AAA
GAM1339  HRB      5'  CGGGAGCCGGGCAGCGCTGC   21086        T   GC_  G
                                CGGGAGC CGGG   CGT GC
                                ||||||| ||||   ||| ||
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                                GCCCTCG GCCC  GCG CG
                                   _  GTC  A
GAM1339 IRS2    5' CGGGCGCTCGGGGTCCGCG  40701    A     _
                                CGGG GCTCGGGG CCGTG
                                |||| |||||||| |||||
                                GCCC CGAGCCCC GGCGC
                                  G      A
GAM1339 ITGA4   5' CGGGAGCTTCGGGTGCTCGCG 9423       _  _ _
                                CGGGAGCT CGGG GC CGTG
                                |||||||| |||| || ||||
                                GCCCTCGA GCCC CG GCGC
                                    A  A A
GAM1339 KCNJ10  5' CGGGGGCCGGGGCCGGGG  13868    A T     T
                                CGGG GC CGGGGCCG GG
                                |||| || |||||||| ||
                                GCCC CG GCCCCGGC CC
                                  C _     C
GAM1339 LHX5    5' GGGCGCACCGTGGCCA    35320    A TCGGG
                                GGG GC   GCCGTGGCCA
                                ||| ||   ||||||||||
                                CCC CG   TGGCACCGGT
                                 G _____
GAM1339 MBTPS1  5' CGGGAGCTCAGGGCCGGC  19132          GT
                                CGGGAGCTCGGGGCC GGC
                                |||||||||||||| |||
                                GCCCTCGAGTCCCGG CCG
                                                __
GAM1339 MECP2   3' CGGGAGCTGGGGGTTGTG  22584      C  CC
                                CGGGAGCT GGGG GTG
                                |||||||| |||| |||
                                GCCCTCGA CCCC CAC
                                    C  AA
GAM1339 NR2C2   5' CGGGAGCCGGGGGCCGCG  17670      C
                                CGGGAGCT GGGGCCGTG
                                |||||||| |||||||||
                                GCCCTCGG CCCCGGCGC
                                    C
GAM1339 PABPC4  5' CGGGGCTCGGGGCCCGAGC  19224    A      GT
                                CGGG GCTCGGGGCC GGC
                                |||| ||||||||| |||
                                GCCC CGAGCCCCGG TCG
                                  _      GC
GAM1339 PAX2    5' CGGGGCTCGGGGCTGGGC  19605    A      CGT
                                CGGG GCTCGGGGC  GGC
                                |||| ||||||||  |||
                                GCCC CGAGCCCCG  CCG
                                  _      AC_
GAM1339 PTPRO   5' CGGGGACTCGGGGGCACGGCTG 36222    AG    C    CA
            CG                  CGGG CTCGGGG CGTGGC CG
                                |||| ||||||| ||||||  ||
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                                GCCC  GAGCCCC GTGCCG  GC
                                  CT      C     AC
GAM1339  RYR2     5'  CGGGGGCTGGAGGGGGCCGCG  9767      A   C___
                                CGGG GCT    GGGGCCGTG
                                |||| |||    |||||||||
                                GCCC CGA    CCCCGGCGC
                                  C   CCTC
GAM1339  SBF1     3'  GGGGGCTCGGGGCCTCAATAC  42280     A        GTG__
                                GGG GCTCGGGGCC    GC
                                ||| ||||||||||    ||
                                CCC CGAGCCCCGG    TG
                                  C         AGTTA
GAM1339  SCRT1    5'  CGGGGCTTGGGGGGGCTGCG   36363     A   C___    C
                                CGGG GCT    GGGGC GTG
                                |||| |||    ||||| |||
                                GCCC CGA    CCCCG CGC
                                  _   ACCC    A
GAM1339  SOX11    3'  CGGGAGCCCGGGGCGCGCG    17018           _
                                CGGGAGCTCGGGGC CGTG
                                |||||||||||||| ||||
                                GCCCTCGGGCCCCG GCGC
                                        C
GAM1339  TLE1     5'  CGGGCGCTCGGGGACTGTG    22919     A      _ C
                                CGGG GCTCGGGG C GTG
                                |||| |||||||| | |||
                                GCCC CGAGCCCC G CAC
                                  G       T A
GAM1339  BDKRB2   3'  CAGATTCCAGCCCTCCAGGTT  8399      TC       GGA   A
                                CAG  TCCAGCCCT   CCG GTT
                                |||  |||||||||   ||| |||
                                GTC  AGGTCGGGA   GGT CAA
                                  TA        ___   C
GAM1339  DAAM2    3'  GTCCCAGCCCCAGGAGT     45177     T      TG ACC
                                GTC CCAGCCC  G   GAGT
                                ||| |||||||  |   ||||
                                CAG GGTCGGG  C   CTCA
                                  _      GT ___
GAM1339  DAPK1    5'  CAGTCTCCAGTCCCGGGCGCC  22354          _   T  A_
                                CAGTCTCCAG CCC GG  CC
                                |||||||||| ||| ||  ||
                                GTCAGAGGTC GGG CC  GG
                                      A   C  GC
GAM1339  DCN      3'  ATCTCCCAGTACTGGACCGGGT 39443       _  CC       A
              T                  GTCTCC AG  CTGGACCG GTT
                                 ||||||  ||  ||||||||  |||
                                 TAGAGG TC  GACCTGGC CAA
                                    G  AT       C
GAM1339  FKBP1B   3'  ATCTCCAGCCACCACCTTGAGT 38330          _  GG   __
              T                  GTCTCCAGCC CT  ACC  GAGTT
                                 ||||||||||  ||  |||  |||||
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                                TAGAGGTCGG GG  TGG  CTCAA
                                      T __   AA
GAM1339  FKBP1B   3'  ATCTCCAGCCACCTTGAGTT   38331          CTGG  __
                                GTCTCCAGCC    ACC  GAGTT
                                ||||||||||    |||  |||||
                                TAGAGGTCGG    TGG  CTCAA
                                      _____   AA
GAM1339  GBA      3'  CAGTCTCCAGTTTTGGGCC    44067          CCC   A
                                CAGTCTCCAG   TGG CC
                                ||||||||||   ||| ||
                                GTCAGAGGTC   ACC GG
                                      AAA   C
GAM1339  LRP1     3'  AGTCTCCAGCCCTGGGAACC   14206             __
                                AGTCTCCAGCCCTGG  ACC
                                ||||||||||||||  |||
                                TCAGAGGTCGGGACC  TGG
                                         CT
GAM1339  PPT2     3'  GTCTCTGGACCGAG       39924       CAGCCC
                                GTCTC     TGGACCGAG
                                |||||     |||||||||
                                CAGAG     ACCTGGCTC
                                  _______
GAM1339  PSMB9    3'  CAGGTTTTGGCCCTAGAGAGTT 15827     TCTCCA       CC
                                CAG     GCCCTGGA  GAGTT
                                |||     ||||||||  |||||
                                GTC     CGGGATCT  CTCAA
                                  CAAAAC       __
GAM1339  PTGDS    3'  CAGCTTCAGCCCTGGGGAGT   9632      T  C        ACC
                                CAG CT CAGCCCTGG   GAGT
                                ||| || |||||||||   ||||
                                GTC GA GTCGGGACC   CTCA
                                  _ A        C__
GAM1340  BRCA1    3'  TGACATTGAATGTTCCTCAAA  28651           A    G
                                TGACATTGAGT TTTCT GAA
                                |||||||||| ||||| |||
                                ACTGTAACTTA AAGGA TTT
                                      C    G
GAM1340  CD28     3'  TGATATTGAGCAGATGG     26025     C       TTTC
                                TGA ATTGAGTA    TGG
                                |||  ||||||||   |||
                                ACT TAACTCGT    ACC
                                  A       CT__
GAM1340  DDC      3'  TGAACATTGATTGCCCTGGAAA 8985    T       GTAT
            A                    A GACATTGA    TTCTGGAAAA
                                 | ||||||||    ||||||||||
                                 A TTGTAACT    GGGACCTTTT
                                 C       AAC_
GAM1340  ECM2     3'  ATGATACTGAGTATAACAGGA  10811      C        TTCT
                                ATGA ATTGAGTAT    GGA
                                ||||  |||||||||   |||
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                                TACT TGACTCATA    CCT
                                  A       TTGT
GAM1340 ITGAM    3' TGACTTGAATATCTGGAAA   43520     A     TT
                                TGAC TTGAGTA  TCTGGAAA
                                |||| |||||||  ||||||||
                                ACTG AACTTAT  AGACCTTT
                                  _      __
GAM1340 MFAP3    3' ATGACATTGGTGTGGAA     25452         A  ATTTC
                                ATGACATTG GT    TGGAA
                                ||||||||| ||    |||||
                                TACTGTAAC CA    ACCTT
                                     _ C_____
GAM1340 NSF      3' ATGATTGATTTTTCTGGA    41782     CA   GTA
                                ATGA  TTGA   TTTCTGGA
                                ||||  ||||   ||||||||
                                TACT  AACT   AAAGACCT
                                  __    AA_
GAM1340 PCM1     3' ATGCATTGAGTATGTAAGG   26225     A       TTCT
                                ATG CATTGAGTAT   GG
                                ||| ||||||||||   ||
                                TAC GTAACTCATA   CC
                                  _        CATT
GAM1340 PTGS2    3' TGACAATGAGATGTGGAAAA  9695       T   TATTTC
                                TGACA TGAG     TGGAAAA
                                ||||| ||||     |||||||
                                ACTGT ACTC     ACCTTTT
                                   T   TAC___
GAM1340 RAB38    3' ATTGAAATCTGGAAA      41264       TATT
                                ATTGAG   TCTGGAAA
                                ||||||   ||||||||
                                TAACTT   AGACCTTT
                                   T___
GAM1340 SLC2A5   3' GACAGGTATTTCTGGAAA   16767     TTGA
                                GACA   GTATTTCTGGAAA
                                ||||   ||||||||||||
                                CTGT   CATAAAGACCTTT
                                  C___
GAM1340 STAR     3' GACTATATTTCTGGAA     7388      ATTGA
                                GAC    GTATTTCTGGAA
                                |||    ||||||||||||
                                CTG    TATAAAGACCTT
                                  A____
GAM1340 ZNF134   3' TGACTTGGAGGCTGGAAA   18330     ATT   TATTT
                                TGAC   GAG    CTGGAAA
                                ||||   |||    |||||||
                                ACTG   CTC    GACCTTT
                                  AAC   C____
GAM1340 AIM1     5' CAATCTTCCGCTCTGGGAG   45078         T  CACCC
                                CAATCTTCC GC    GAG
                                ||||||||| ||    |||
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                                GTTAGAAGG CG    CTC
                                     _ AGACC
GAM1340 B4GALT2  3' CAATCTTCGGCACCGAGAGC  36136       CT  CAC
                                CAATCTTC  GC   CCGAGAGC
                                ||||||||  ||   ||||||||
                                GTTAGAAG  CG   GGCTCTCG
                                    C_  T__
GAM1340 EXT2     3' CAGTCTTCCTGTCCGTGAA   7586     A      CCAC   A
                                CA TCTTCCTG    CCG GAG
                                || ||||||||    ||| |||
                                GT AGAAGGAC    GGC CTT
                                 C       A___   A
GAM1340 INPP5B   3' ATCTTCCTGCTGGACAG     45470         CACCC  G
                                ATCTTCCTGC     GA AG
                                ||||||||||     || ||
                                TAGAAGGACG     CT TC
                                      AC___  G
GAM1340 MATK     5' TCTTCCTGCCACCCGCCGGC  40317            AGA
                                TCTTCCTGCCACCCG   GC
                                ||||||||||||||   ||
                                AGAAGGACGGTGGGC   CG
                                         GGC
GAM1340 NDRG3    3' ACAATCTTTCTAATGGCTGGGA 36744        C   CCACCCGA
           GC                     ACAATCTT CTG       GAGC
                                ||||||||  |||       ||||
                                TGTTAGAA GAT       CTCG
                                    A   TACCGACC
GAM1340 NUDT2    3' ACAACCTTCCCTGGACCTGAG  10113         GCC   C
                                ACAATCTTCCT   ACC GAG
                                ||||||||||   ||| |||
                                TGTTGGAAGGG   TGG CTC
                                      ACC   A
GAM1340 NYX      3' TCTTCCCACCCGAGGGC     35447       TGC       A
                                TCTTCC   CACCCGAG GC
                                ||||||   |||||||| ||
                                AGAAGG   GTGGGCTC CG
                                   ___        C
GAM1340 PIM1     3' ACAATCTTTTTGTATACTACCA 44959        C________
                                ACAATCTT       CTGCCA
                                ||||||||       ||||||
                                TGTTAGAA       GATGGT
                                     AAACATAT
GAM1340 SHANK2   3' ACCATCTTCCCTGGCCTCCGAG 29448    A      __   AC
           AGC                    AC ATCTTCCT  GCC  CCGAGAGC
                                || ||||||||  |||  ||||||||
                                TG TAGAAGGG  CGG  GGCTCTCG
                                 G       AC   A_
GAM1340 STIM1    3' ACAGCCTTCTTGCCAGCCA   41119     AT   C    C
                                ACA  CTTC TGCCA CCG
                                |||  |||| ||||| |||
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                                TGT  GAAG ACGGT GGT
                                  CG   A    C
GAM1340  TR2      3'  ACAGGCTCATTTTATCCGAGAG 43632     AT   CCTGCCAC
              C                    ACA  CTT       CCGAGAGC
                                   |||  |||       ||||||||
                                   TGT  GAG       GGCTCTCG
                                     CC   TAAAATA_
GAM1340  TRAF1    3'  ATCTTCCTAGCCCGAGAGC   24942         CCA
                                   ATCTTCCTG   CCCGAGAGC
                                   |||||||||   |||||||||
                                   TAGAAGGAT   GGGCTCTCG
                                        C__
GAM1341  ACVR1    5'  TACTCGGAGAGTAGAAGA    9961      CA       _
                                   TAC  GGAGAGTA AAGA
                                   |||  |||||||| ||||
                                   ATG  CCTCTCAT TTCT
                                     AG       C
GAM1341  ATP11A   3'  TACCAAGAAAAGAA       44182          GTAA
                                   TACCAGGAGA    AGAA
                                   ||||||||||    ||||
                                   ATGGTTCTTT    TCTT
                                          _____
GAM1341  CAPZA1   3'  TACCAGAAGTGCTTGGAAG   43718         A  AAA
                                   TACCAGGAG GT   GAAG
                                   |||||||||  ||   ||||
                                   ATGGTCTTC CG   CTTC
                                        A  AAC
GAM1341  CDH3     3'  CACCAGGAGGCCTAAGAAG   12171         A  A_
                                   TACCAGGAG GT  AAGAAG
                                   |||||||||  ||  ||||||
                                   GTGGTCCTC CG  TTCTTC
                                        _  GA
GAM1341  CDH6     3'  CACCAGGACAGCGGAAG     22321         G   AAA
                                   TACCAGGA AGT   GAAG
                                   ||||||||  |||   ||||
                                   GTGGTCCT TCG   CTTC
                                       G   C__
GAM1341  CLN6     3'  TACCAGAAGATGTCCGGGAAG  32828          _  AAA_
                                   TACCAGGAGA GT    GAAG
                                   ||||||||||  ||    ||||
                                   ATGGTCTTCT CA    CTTC
                                         A  GGCC
GAM1341  COMT     3'  CCAGTGTTAGTAAAGAAG    28691      GAG_
                                   CCAG    AGTAAAGAAG
                                   ||||    ||||||||||
                                   GGTC    TCATTTCTTC
                                     ACAA
GAM1341  FANCC    3'  CACCAGGAGTACCGAAG     43266         GA   AA
                                   TACCAGGA  GTA  GAAG
                                   ||||||||  |||  ||||
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                                GTGGTCCT  CAT  CTTC
                                   __  GG
GAM1341  HAP1    3'  TACCAGGACAGCACTAGA    19505        G   A_
                                TACCAGGA AGTA  AGA
                                |||||||| ||||  |||
                                ATGGTCCT TCGT  TCT
                                   G   GA
GAM1341  HSD3B1  5'  CACCAGGAAACAGAAG     9259         GTAA
                                TACCAGGAGA   AGAAG
                                ||||||||||   |||||
                                GTGGTCCTTT   TCTTC
                                    G___
GAM1341  ITPR1   3'  CACCAGCTTCAAAGAAG     13665       GAGAG
                                TACCAG    TAAAGAAG
                                ||||||    ||||||||
                                GTGGTC    GTTTCTTC
                                  GAA__
GAM1341  MAP4    5'  CCAGGAGAGCGCCGGGAAG   14352         AAA__
                                CCAGGAGAGT    GAAG
                                ||||||||||    ||||
                                GGTCCTCTCG    CTTC
                                    CGGCC
GAM1341  MHC2TA  3'  GGAGAGCAGGGTGGAGAAGC   6986         A_____    III
                                GGAGAGTA     AGAAG  C
                                ||||||||     |||||  |
                                CCTCTCGT     TCTTC  G
                                   CCCACC    III
GAM1341  MLF2    3'  ACCAGGAGATTAAAGAAG    24141         G
                                ACCAGGAGA TAAAGAAG
                                ||||||||| ||||||||
                                TGGTCCTCT ATTTCTTC
                                    A
GAM1341  NHLH1   3'  CACCAGGAGTTGAAGAAG    24650         AGTA
                                TACCAGGAG   AAGAAG
                                |||||||||   ||||||
                                GTGGTCCTC   TTCTTC
                                    AAC_
GAM1341  PIK3R3  5'  CCAGGAGATATATAGAAG    41438         _  A
                                CCAGGAGA GTA AGAAG
                                |||||||| ||| |||||
                                GGTCCTCT TAT TCTTC
                                   A  A
GAM1341  PIK4CB  3'  ACCAGGAGGGGCAGGGAAG   15311         A_  AA
                                ACCAGGAG  GTA  GAAG
                                ||||||||  |||  ||||
                                TGGTCCTC  CGT  CTTC
                                   CC  CC
GAM1341  PKHD1   3'  CACCAGATGCCTAAAGAAG   39803         AGAG
                                TACCAGG   TAAAGAAG
                                |||||||   ||||||||
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                                GTGGTCT   ATTTCTTC
                                    ACGG
GAM1341  PKNOX1   3'  TACCAGGAAACAGAAG     21310        GTAA
                                TACCAGGAGA   AGAAG
                                ||||||||||   |||||
                                ATGGTCCTTT   TCTTC
                                     G___
GAM1341  SQLE     5'  TACCAAGAGGAGCACGGA    17106        _   AA
                                TACCAGGAG AGTA  GA
                                ||||||||| ||||  ||
                                ATGGTTCTC TCGT  CT
                                     C   GC
GAM1341  TRIM14   3'  ACCAGGAACTGCTAAGAAG   37693        A_  A
                                ACCAGGAG  GT AAGAAG
                                ||||||||  || ||||||
                                TGGTCCTT  CG TTCTTC
                                     GA  A
GAM1341  TYRP1    3'  ACCAGATAAAAAAGAAG     43641       A   T
                                ACCAGG GAG AAAGAAG
                                ||||||| ||| |||||||
                                TGGTCT TTT TTTCTTC
                                    A   _
GAM1341  ZNF83    5'  TACCAAGAGTCCTTAGAAG   32891        AGTAA
                                TACCAGGAG    AGAAG
                                |||||||||    |||||
                                ATGGTTCTC    TCTTC
                                     AGGAA
GAM1341  HS2ST1   3'  TCATGGTTAGTTGAAAAAATGC 29341          C  TCC
                                TCGTGGTTAGT GA   GGTGC
                                ||||||||||| ||   |||||
                                AGTACCAATCA CT   TTACG
                                      A  TTT
GAM1341  PLA2G4C  5'  GTGCTCCGGAATCCGGTGC   43860     G  AGTC
                                GTG TT    GATCCGGTGC
                                ||| ||    ||||||||||
                                CAC AG    TTAGGCCACG
                                  G  GCC_
GAM1342  GPX4     3'  GCAGGTTTGCAGGCAGGCCGT  13282      C___
                                GCGG    GCAGGCAGGCCGT
                                ||||    ||||||||||||||
                                CGTC    CGTCCGTCCGGCA
                                   CAAA
GAM1342  HDAC7A   3'  ACTGTCAAAGCAGGCAGGCTGT 32465    A  _  C        C
                                GC TG CGG GCAGGCAGGC GT
                                || || ||| |||||||||| ||
                                TG AC GTT CGTCCGTCCG CA
                                 _  A  T        A
GAM1342  HR       5'  GCGCGGGCGGTGGCGGTCG   32923    A  C    CA   A  C
                                GC TG GGCG  GGC GG CG
                                || || ||||  ||| || ||
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                                CG GC CCGC  CCG CC GC
                                 C  _   CA  _ A
GAM1342 LEF1    3' GCGTCGACTGGGCAGGCCGT  32212   ATG   GCA
                                GC  CGGC  GGCAGGCCGT
                                ||  ||||  ||||||||||
                                CG  GCTG  CCGTCCGGCA
                                 CA_   AC_
GAM1342 NUP50   5' CGCAGCGGCGCAGGGG     28406     T       CA
                                CGCA GCGGCGCAGG  GG
                                |||| ||||||||||  ||
                                GCGT CGCCGCGTCC  CC
                                  _       __
GAM1342 SFRP1   3' TGCGGGGGAACAGGCAGGCTGT 16577      C___       C
                                TGCGG   GCAGGCAGGC GT
                                |||||   |||||||||| ||
                                ACGCC   TGTCCGTCCG CA
                                   CCCT        A
GAM1342 AKAP13  3' CTCCGGACTGCAGCACAG   28480    ____
                                CTT   CTGCAGCACAG
                                |||   ||||||||||||
                                GAG   GACGTCGTGTC
                                  GCCT
GAM1342 DISC1   3' CATGAGTTCTTAGCCAG    33030      C   GC  A
                                CATGAG TTCT  AGC CAG
                                |||||| ||||  ||| |||
                                GTACTC AAGA  TCG GTC
                                   _   A_  _
GAM1342 DMD     5' CATAGCCAAGCACAGA     19680    G   TCTGC
                                CAT AGCT    AGCACAGA
                                ||| ||||    ||||||||
                                GTA TCGG    TCGTGTCT
                                  _   T____
GAM1342 EGLN2   5' CATGGCATCAGCACAGC    38816     A TTCTG      A
                                CATG GC    CAGCACAG C
                                |||| ||    |||||||| |
                                GTAC CG    GTCGTGTC G
                                  _ TA___      C
GAM1342 FRAT2   3' TGACCTTGAACACAGA     28977    G TC  C
                                TGA CT  TG AGCACAGA
                                ||| ||  || ||||||||
                                ACT GA  AC TTGTGTCT
                                  G  __  _
GAM1342 IL2RA   3' GAGCTTCCAAAACGCAGGCA  7671         C  A  A
                                GAGCTTCTG AGC CAG CA
                                ||||||||| ||| ||| ||
                                CTCGAAGGT TTG GTC GT
                                     T  C  C
GAM1342 KRTHA2  3' TGAGGCAGCACAGAC      14017     CTTCT
                                TGAG    GCAGCACAGAC
                                ||||    ||||||||||
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                              ACTC    CGTCGTGTCTG
                                      _____
GAM1342  NUP98    3'  GAGCTTCCCACAGAC      32232       GCAG
                              GAGCTTCT    CACAGAC
                              ||||||||    |||||||
                              CTCGAAGG    GTGTCTG
                                      ____
GAM1342  STK10    3'  TGAGCTGGCACAGAC      25624       TCTGCA
                              TGAGCT     GCACAGAC
                              ||||||     ||||||||
                              ACTCGA     CGTGTCTG
                                 C_____
GAM1342  TCL1A    3'  TGAGTCCTGAGCACAGA     35031     C    C
                              TGAG TTCTG AGCACAGA
                              |||| ||||| ||||||||
                              ACTC AGGAC TCGTGTCT
                                _    _
GAM1343  BACE     3'  TCACTTGCTCTGTGGGTA    39971      CAGGC       AA
                              TCGCT    TGTTCTGTG  TA
                              |||||    |||||||||  ||
                              AGTGA    ACGAGACAC  AT
                                _____       CC
GAM1343  BCLG     3'  AGGCTGTTTACTAACGTGAAATA 39819        C_____       III
           GC                   AGGCTGTT     TGTGAATAG   C
                              ||||||||     |||||||||   |
                              TCCGACAA     GCACTTATC   G
                                   ATGATT        III
GAM1343  COL4A3   3'  GGTGATATTTTGTGAATAG   36382    C__    C
                              GG   TGTT TGTGAATAG
                              ||   |||| |||||||||
                              CC   ATAA ACACTTATC
                               ACT    A
GAM1343  CYP4F3   3'  TCGTTTGGGCTACTGTGAATAG 9455     CTCA    TT
                              TCG    GGCTG  CTGTGAATAG
                              |||    |||||  ||||||||||
                              AGC    CCGAT  GACACTTATC
                                AAAC    __
GAM1343  PTGIS    3'  GCCAGCTCCCTGTGA      9673      CA    G
                              GCT  GGCT TTCTGTGA
                              |||  |||| ||||||||
                              CGG  TCGA GGGACACT
                                __    _
GAM1343  SYN3     3'  TCGCTCAGGCCTGTTTTGA   18569          GTTCTG
                              TCGCTCAGGCT     TGA
                              ||||||||||     |||
                              AGCGAGTCCGG     ACT
                                    ACAAA_
GAM1343  WHSC1    3'  TCGCATGGTACTGTGAATA   39383      TCA  CTGTT
                              TCGC   GG    CTGTGAATA
                              ||||   ||    |||||||||
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                                AGCG  CC   GACACTTAT
                                  TA_ AT___
GAM1343 ATP12A   3' GAGACATAGGAAGGGAGGTGG 11726      CGTGTCT    C
                                GAGACA     GGGAGG GG
                                ||||||     |||||| ||
                                CTCTGT     CCCTCC CC
                                   ATCCTT_    A
GAM1343 DPYD     5' TGAGACAGTGTTGGTGGC   41296      C  C  GA
                                TGAGACA GTGT TGG  GGC
                                ||||||| |||| |||  |||
                                ACTCTGT CACA ACC  CCG
                                   _  _  A_
GAM1343 EGR1     5' TGAGAAGCGTGCAGGCGG   12669     CA   CTGGG
                                TGAGA  CGTGT   AGGCGG
                                |||||  |||||   ||||||
                                ACTCT  GCACG   TCCGCC
                                  TC   _____
GAM1343 FAAH     3' TGAGGCACTGAGAGGTGG   11062    A  GTGTC    C
                                TGAG CAC   TGGGAGG GG
                                |||| |||   ||||||| ||
                                ACTC GTG   ACTCTCC CC
                                  C  _____     A
GAM1343 FASN     3' GAGGTGCCGTGGGAGGCGGC  19937    ACAC   _
                                GAG   GTGTC TGGGAGGCGGC
                                |||   ||||| ||||||||||
                                CTC   CACGG ACCCTCCGCCG
                                  ____   C
GAM1343 GHR      3' TGAGTATGTGTCTGGTTATAGG 6719     ACAC     G___
              C                  TGAG   GTGTCTGG   AGGC
                                ||||   ||||||||   ||||
                                ACTC   CACAGACC   TCCG
                                  ATA_     AATA
GAM1343 HOXD3    3' TGAGACCCGGGAGGCG     27901      ACGTGT
                                TGAGAC    CTGGGAGGCG
                                ||||||    ||||||||||
                                ACTCTG    GGCCCTCCGC
                                  _____
GAM1343 KCNQ3    5' GTGCGTGAACGAGGCGGC   21130    C  __
                                GTGT TGG  GAGGCGGC
                                |||| |||  ||||||||
                                CACG ACT  CTCCGCCG
                                  C  TG
GAM1343 LDB1     3' GAGGCAAATGCCCTGGGGGGTG 19337    A  C   _   A  C
              G                  GAG CA GTGTC TGGG GG GG
                                ||| || ||||| |||| || ||
                                CTC GT TACGG ACCC CC CC
                                  C  T   G   C  A
GAM1343 LSS      3' TGAGGCCGTGCCCAGAGGTGGC 14249    ACA    TG G   C
                                TGAG   CGTGTC  G AGG GGC
                                ||||   ||||||  | ||| |||
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                                ACTC   GCACGG  C TCC CCG
                                  CG_     GT _   A
GAM1343  PTMA     5'  GAGGCGCGCGGCGGAGGCGGC  15867     ACA    CTG
                                GAG   CGTGT   GGAGGCGGC
                                |||   |||||   |||||||||
                                CTC   GCGCG   CCTCCGCCG
                                  C__     CCG
GAM1343  TLE2     3'  AGGCAGGGCTGGGAGGCGGC   17556    A  CGT T
                                AG CA   G CTGGGAGGCGGC
                                || ||   | ||||||||||||
                                TC GT   C GACCCTCCGCCG
                                 C  CC_ _
GAM1344  APP      3'  TGTGTGCACATAAAACAGG    7925       _    AAC
                                TGTG GCACA   AAAACAGG
                                |||| |||||   ||||||||
                                ACAC CGTGT   TTTTGTCC
                                  A     A__
GAM1344  ATSV     3'  CGTGTGGCACAGGTCCCCGGGC 20226     T       AACAAAACA
                                CGT GTGGCACA        GGC
                                ||| ||||||||        |||
                                GCA CACCGTGT        CCG
                                  _       CCAGGGGC_
GAM1344  CPO      3'  TTGTGGCACAAATGAAAAC    6428            C_
                                TTGTGGCACAAA  AAAAC
                                ||||||||||||  |||||
                                AACACCGTGTTT  TTTTG
                                       AC
GAM1344  DMD      5'  GCCAAGCACAGATAAAGCAGGC 19685    TGT     AAC   A
                                GT   GGCACA   AAA CAGGC
                                ||   ||||||   ||| |||||
                                CG   TCGTGT   TTT GTCCG
                                 GT_     CTA   C
GAM1344  INSRR    3'  TTGTTGGCAGCAAGGTAGGC   42850     _   CAAA   AAC
                                TTGT GGCA    CAA   AGGC
                                |||| ||||    |||   ||||
                                AACA CCGT    GTT   TCCG
                                  A    C___   CCA
GAM1344  JUP      3'  CGTTGCTGGGGGAAAACAGA   13772       _  CACAAAC
                                CGTTG TGG      AAAACAGG
                                ||||| |||      ||||||||
                                GCAAC ACC      TTTTGTCT
                                   G   CCC_____
GAM1344  PKNOX1   3'  TATAGCAAATGAAACAGGC   21311        CAAACA
                                TGTGGCA     AAACAGGC
                                |||||||     ||||||||
                                ATATCGT     TTTGTCCG
                                    TTAC__
GAM1344  REQ      3'  GTTGTGTTAAAAAACAGG    26548       GCACAAAC
                                GTTGTG       AAAACAGG
                                ||||||       ||||||||
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                                CAACAC       TTTTGTCC
                                   AATT____
GAM1344  CDH11    5'  GAGGGTGGCCTCCCGGACGC   38031      A       GCA
                                GAGG TGGCCTCC   ATGT
                                |||| ||||||||   ||||
                                CTCC ACCGGAGG   TGCG
                                  C       GCC
GAM1344  COG2     3'  GAGGATGGCTTCCCGCAGCC   28880         C_     AT
                                GAGGATGGC  TCCGCA  GTC
                                |||||||||  ||||||  |||
                                CTCCTACCG  GGGCGT  CGG
                                     AA     __
GAM1344  CSTB     3'  GAGGATGACTTTGTCA      6437          CTCCGCAA
                                GAGGATGGC       TGTCA
                                |||||||||       |||||
                                CTCCTACTG       ACAGT
                                     AA_______
GAM1345  PLAG1    3'  TCCGTGTTTGGTGACCTAAC   15357       C  _____
                                TCCGTG TTG    CCTAGC
                                |||||| |||    ||||||
                                AGGCAC AAC    GGATTG
                                   A   CACT
GAM1345  REST     5'  TCCGCTGCTGCGCCGCGAGCTC 24711      _   _    TA    A
                                TCCG TGCT TGCC  GCGA CTC
                                |||| |||| ||||  |||| |||
                                AGGC ACGA GCGG  CGCT GAG
                                  G   C    __    C
GAM1345  ABCC3    3'  GAGCTCACAAACGTGTGCA   33421         TCGGC   CA
                                GAGTTCAC     ACG  TGCA
                                ||||||||     |||  ||||
                                CTCGAGTG     TGC  ACGT
                                     TT___   AC
GAM1345  ALCAM    3'  GAGAGTTCGCTGGTGGCA    11566         A  C__
                                GAGAGTTC CT   GGCA
                                |||||||| ||   ||||
                                CTCTCAAG GA   CCGT
                                     C  CCA
GAM1345  CYP3A4   3'  GAGAGCTCAATGCATG      32714         CTCGGCAC
                                GAGAGTTCA       GCATG
                                |||||||||       |||||
                                CTCTCGAGT       CGTAC
                                     TA_______
GAM1345  EN2      5'  GAGAGCTGCGCGCATG      10951         CACTCG  A
                                GAGAGTT     GC CGCATG
                                |||||||     || ||||||
                                CTCTCGA     CG GCGTAC
                                   _______  C
GAM1345  GRIN2C   5'  GAGGGTCACTCGGGC       9124      A  T      CAC
                                GAG GT CACTCGG   GC
                                ||| || |||||||   ||
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                                CTC CA GTGAGCC   CG
                                  C _      ___
GAM1345 HOXB5    3' GAGAGTTCACATTAAACATGC  13447          TCGGCAC
                                GAGAGTTCAC      GCATGC
                                ||||||||||      ||||||
                                CTCTCAAGTG      TGTACG
                                     TAATT__
GAM1345 OGT      5' GTTCATTCGCACGCAATGC    18784      C   G     _
                                GTTCA TCG CACGCA TGC
                                ||||| ||| |||||| |||
                                CAAGT AGC GTGCGT ACG
                                   A   _     T
GAM1346 CHRNA2   5' AGCTGCTGCTGGATTCTGTGAG 8829          CA    G  CA
                                AGCTGTTGC  GGGT CT  TGAG
                                |||||||||  |||| ||  ||||
                                TCGACGACG  CCTA GA  ACTC
                                     A_    A  C_
GAM1346 COLQ     3' AGCTGCTGCCAGTTCT      38691           GGTG
                                AGCTGTTGCCAG    CT
                                ||||||||||||    ||
                                TCGACGACGGTC    GA
                                      AA__
GAM1346 CYP1A2   3' AGCAGTTGCCAGGGCTGGTGAG 8911      T         GCTCA
                                AGC GTTGCCAGGGT     TGAG
                                ||| ||||||||||     ||||
                                TCG CAACGGTCCCG     ACTC
                                  T         ACC__
GAM1346 KIR2DL3  3' ACTGTGGTGCTCATG       30951       TGCCAG
                                GCTGT     GGTGCTCATG
                                |||||     ||||||||||
                                TGACA     CCACGAGTAC
                                  _______
GAM1346 NCYM     5' TGTCTGCGTGCTCGTGAG     26747     _  CAGG     A
                                TGT TGC    GTGCTC TGAG
                                ||| |||    |||||| ||||
                                ACA ACG    CACGAG ACTC
                                  G  ____     C
GAM1346 PPP1R12B 3' GCTGCCTGGGGTGCTCATGAG  36976       A_
                                GTTGCC  GGGTGCTCATGAG
                                ||||||  ||||||||||||
                                CGACGG  CCCACGAGTACTC
                                   AC
GAM1346 PSG4     3' AGCTGTTGTTATGGTGTC     15797        CCAG    C
                                AGCTGTTG    GGTG TC
                                ||||||||    |||| ||
                                TCGACAAC    CCAC AG
                                     AATA   _
GAM1346 ABCB9    3' GGGCAAGATGCAGGAAGCGGTG 33356      C        _ __   C
             ATCCA                  GGGC AGATGCAGGA GC  TGA CCA
                                ||||| |||||||||| ||  ||| |||
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                                CCCG TCTACGTCCT CG  ACT GGT
                                  T        T  CC   A
GAM1346  ACK1     3'  GGGCCAGAGGCAGGTCATACCC 25117         T    AGCTG
             A                   GGGCCAGA GCAGG     ACCCA
                                 |||||||| |||||     |||||
                                 CCCGGTCT CGTCC     TGGGT
                                     C     AGTA_
GAM1346  ANXA8    3'  AGGCCAGGGCAGCTGACC     11571        ATGCA  _
                                 GGGCCAG     GG AGCTGACC
                                 |||||||     || ||||||||
                                 TCCGGTC     CC TCGACTGG
                                     _____  G
GAM1346  CABC1    5'  GGGCTGGCTGCAGGAAGCTG   33688      CAGA      _
                                 GGGC    TGCAGGA GCTG
                                 ||||    ||||||| ||||
                                 CCCG    ACGTCCT CGAC
                                   ACCG      T
GAM1346  CASQ2    3'  AGGCTAGGAAGCCAGCTGACCC 10280      C  AT_  AGG
             A                   GGGC AG   GC   AGCTGACCCA
                                 |||| ||   ||   ||||||||||
                                 TCCG TC   CG   TCGACTGGGT
                                   A  CTT  G__
GAM1346  CLASP1   3'  GGGTCAGGGCAGAGGGGTCTG  42243     C   AT     AG___
                                 GGG CAG  GCAGG     CTG
                                 ||| |||  |||||     |||
                                 CCC GTC  CGTCT     GAC
                                   A  C_     CCCCA
GAM1346  EN1      5'  GGGCGGGTGCAGGAAAAAAGCT 10920      CAGA      _____
                                 GGGC    TGCAGGA     GCT
                                 ||||    |||||||     |||
                                 CCCG    ACGTCCT     CGA
                                   CCC_      TTTTT
GAM1346  HLCS     5'  GGGCCAGGCGCGGTGGCT     7643         A   A  A_
                                 GGGCCAG TGC GG  GCT
                                 ||||||| ||| ||  |||
                                 CCCGGTC GCG CC  CGA
                                     C   _  AC
GAM1346  IFITM2   3'  GGGCTGATGCAGGACT      26973      CA        G
                                 GGGC  GATGCAGGA CT
                                 ||||  ||||||||| ||
                                 CCCG  CTACGTCCT GA
                                   A_        _
GAM1346  IL12A    5'  GGCTGGGAGGCTGACCC      9403      CAGA  CA   _
                                 GGC    TG  GGAG CTGACCC
                                 |||    ||  |||| |||||||
                                 CCG    AC  CCTC GACTGGG
                                   _____ __    C
GAM1346  IMPDH1   3'  GGGCCAGAGCAGGGCCA      9412         T    A
                                 GGGCCAGA GCAGG GCTG
                                 |||||||| ||||| ||||
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                                CCCGGTCT CGTCC CGGT
                                      _   _
GAM1346  MYLK2    3'  GGGCCAGATGGTGTGGGCT   37528          CA__  A
                                GGGCCAGATG   GG GCT
                                ||||||||||   || |||
                                CCCGGTCTAC   CC CGA
                                     CACA  _
GAM1346  PRKCH    5'  GGGACAGGTGCAGGAGTCG   26511     C  A      C
                                GGG CAG TGCAGGAG TG
                                ||| ||| |||||||| ||
                                CCC GTC ACGTCCTC GC
                                  T  C       A
GAM1346  RAMP3    3'  GGGCTGGTGCAGGAGCCA    25203      CAGA
                                GGGC   TGCAGGAGCTG
                                ||||   ||||||||||
                                CCCG   ACGTCCTCGGT
                                  ACC_
GAM1346  RERE     3'  GGCCTGGATGCAGGAGTCTG  29030      A_        _
                                GGCC  GATGCAGGAG CTG
                                ||||  |||||||||| |||
                                CCGG  CTACGTCCTC GAC
                                  AC         A
GAM1346  SLC7A8   3'  GGGCTGGATGCAGGAGGC    29292      CA        _
                                GGGC  GATGCAGGAG C
                                ||||  |||||||||| |
                                CCCG  CTACGTCCTC G
                                  AC         C
GAM1347  MET      3'  GGACAAAGTGTGGACTGTTGCT 43414          C_  AC___
           T                     GGACAAAGTG  GA    GCTT
                                ||||||||||  ||    ||||
                                CCTGTTTCAC  CT    CGAA
                                     AC  GACAA
GAM1347  CELSR2   3'  TATAAAAAAAATGAATCCCTGA 10854             AACGC
           AG                    TATAAAAAAAGTGAG    GAAG
                                ||||||||||||||    ||||
                                ATATTTTTTTTTACTT    CTTC
                                       AGGGA
GAM1347  STAU2    3'  TAAAAAAAGGGAGAACTGA   30803         T     GC
                                TAAAAAAAG GAGAAC  GA
                                |||||||| ||||||  ||
                                ATTTTTTTC CTCTTG  CT
                                     C     A_
GAM1348  ADAM17   3'  CAAACCACACAAGAACTGT   34830           _ G
                                TAAACCACACAAGG C GT
                                |||||||||||||| | ||
                                GTTTGGTGTGTTCT G CA
                                       T A
GAM1348  DLG4     3'  CAGAAGGCGGCAGCATTT    10702    C       _
                                CA AAGGCGGTA CGTTT
                                || |||||||| |||||
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                                GT TTCCGCCGT GTAAA
                                 C       C
GAM1348  MEN1    3'  AAACCATGCAACACGTT    39137      CACAAG  GG
                                AAACCA    GC  TACGTT
                                ||||||    ||  ||||||
                                TTTGGT    CG  GTGCAA
                                   A_____  TT
GAM1348  RPL15   3'  ACCACACAGTATGTT      16389       AGGCG   C
                                ACCACACA    GTA GTT
                                ||||||||    ||| |||
                                TGGTGTGT    CAT CAA
                                    _____  A
GAM1348  RPP30   3'  TAAATCACACAAAGGT     26939     C      GC
                                TAAA CACACAAG  GGT
                                |||| ||||||||  |||
                                ATTT GTGTGTTT  CCA
                                  A      __
GAM1348  UGT1A1  3'  TAAACACACAAGGTGGCAC   7867      C      C
                                TAAAC ACACAAGG GGTAC
                                ||||| |||||||| |||||
                                ATTTG TGTGTTCC CCGTG
                                   _       A
GAM1348  UGT1A4  3'  TAAACACACAAGGTGGCAC   28296     C      C
                                TAAAC ACACAAGG GGTAC
                                ||||| |||||||| |||||
                                ATTTG TGTGTTCC CCGTG
                                   _       A
GAM1348  UGT1A9  3'  TAAACACACAAGGTGGCAC   34290     C      C
                                TAAAC ACACAAGG GGTAC
                                ||||| |||||||| |||||
                                ATTTG TGTGTTCC CCGTG
                                   _       A
GAM1348  GAD1    5'  GTTCCCTCTCGCACC      9052      TTAT    A  A
                                GTTCT   TTCTC CAC C
                                |||||   ||||| ||| |
                                CAAGG   GAGAG GTG G
                                   _____    C  C
GAM1348  PRX     3'  CTCTTCGGCCACTTCTCGTACA 34117    G  T_      AC
            CG                   CTC TTC  TTATTTCTC  ACACG
                                ||| |||  |||||||||  |||||
                                GAG AAG  GGTGAAGAG  TGTGC
                                  _  CC       CA
GAM1349  ATRN    3'  TGGGGATGCGTTTCTTGGG   40287    A  TCA  C C
                                TG GG   GC G TTCTTGGG
                                || ||   || | ||||||||
                                AC CC   CG C AAGAACCC
                                 C  TA_  _ A
GAM1349  EGFL5   5'  TGGAGGTCAAAGTGGTTTTGGG 44542    T      CCGCTTC
            C                    TG GAGGTCAG      TTGGGC
                                || ||||||||      ||||||
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                                AC CTCCAGTT      AACCCG
                                 _       TCACCAA
GAM1349 ENTPD6   3' GTGGGGTCAGCCCGAGGTGGGC 10340     A       GCTTCT
                                GTG GGTCAGCC     TGGGC
                                ||| ||||||||     |||||
                                CAC CCAGTCGG     ACCCG
                                  C       GCTCC_
GAM1349 LAMA5    3' TGTGAGGCAGCTGCAGGGG   24502        T    C  TTCTT
                                TGTGAGG CAGC GC    GGG
                                ||||||| |||| ||    |||
                                ACACTCC GTCG CG    CCC
                                    _   A  TC___
GAM1349 USP1     3' TGAGATTCTGCTTCTTGGG   17907       CAGCC
                                TGAGGT    GCTTCTTGGG
                                ||||||    ||||||||||
                                ACTCTA    CGAAGAACCC
                                   AGA__
GAM1349 AES      3' GGAAGGGGAGGGGGAATCC   10056         A  CC__
                                GGAAGGGGA GG    TCC
                                ||||||||| ||    |||
                                CCTTCCCCT CC    AGG
                                     C  CCTT
GAM1349 AK1      3' CGCAGGAAGGGTTCTCC     7874           GAAGGC
                                CGCAGGAAGGG     CTCC
                                ||||||||||      ||||
                                GCGTCCTTCCC     GAGG
                                      AA____
GAM1349 ALDOA    3' GAGGAGGCGGCCTCCTC     6211     A    AA
                                GA GGGG  GGCCTCCTC
                                || ||||  |||||||||
                                CT CCTC  CCGGAGGAG
                                 _    CG
GAM1349 ALPP     3' CACGGGGAGGGGAAGGTTCC  42867     A  A       CC
                                CGC GG AGGGGAAGG  TCC
                                ||| || |||||||||  |||
                                GTG CC TCCCCTTCC  AGG
                                  C  C        A_
GAM1349 ALS2     3' AGGAAGGGATATCCTCTTC   34089         AAGG   C
                                AGGAAGGGG    CCTC TC
                                |||||||||    |||| ||
                                TCCTTCCCT    GGAG AG
                                     ATA_    A
GAM1349 ANKTM1   3' GCAGGAAGGTGGAGGTAACC  28804          _  A  CCT
                                GCAGGAAGG GGA GG   CC
                                ||||||||| ||| ||   ||
                                CGTCCTTCC CCT CC   GG
                                     A   _  ATT
GAM1349 ARHGEF12 3' GGTGGGGAAGGCTTCCT     31641    AA       C
                                GG  GGGGAAGGC TCCT
                                ||  ||||||||| ||||
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                                CC  CCCCTTCCG AGGA
                                 A_       A
GAM1349  AXL     5'  TGAGGAGGGGGAAGGGGACC   11790   C   A      CCT
                                G AGGA GGGGAAGG   CC
                                | |||| ||||||||   ||
                                A TCCT CCCCTTCC   GG
                                 C   C       CCT
GAM1349  BCR     5'  CGCAGGAAGGGAGGGCC     34633          AA
                                CGCAGGAAGGGG  GGCC
                                ||||||||||||  ||||
                                GCGTCCTTCCCT  CCGG
                                       C_
GAM1349  BIN3    3'  CCCAGGAAGGGGTTTCCTC   33075   G       AAGG
                                C CAGGAAGGGG   CCTC
                                | ||||||||||   ||||
                                G GTCCTTCCCC   GGAG
                                 G        AAA_
GAM1349  CA1     3'  TGAGGAAGGACAAGTTTCTTC  11934   C      G   GCC  C
                                G AGGAAGGG AAG   TC TC
                                | |||||||| |||   || ||
                                A TCCTTCCT TTC   AG AG
                                 C       G   AA_  A
GAM1349  CACNA1C  3'  CGCCCCTGGAGGCCTCCTCC   8749     AGGAAGG   A
                                CGC      GGA GGCCTCCTCC
                                |||      ||| ||||||||||
                                GCG      CCT CCGGAGGAGG
                                  GGGA___   _
GAM1349  CDH15    3'  GCAGGAAGGGGCCTCTTC    22334         GAAG    C
                                GCAGGAAGGG    GCCTC TC
                                ||||||||||    ||||| ||
                                CGTCCTTCCC    CGGAG AG
                                      ____     A
GAM1349  CENTD1   5'  GCCGGAGGCGCCAGGCCTCCTC 40142    A   A  GGA_
                                GC GGA GG    AGGCCTCCTC
                                || ||| ||    ||||||||||
                                CG CCT CC    TCCGGAGGAG
                                 G   _  GCGG
GAM1349  CHRNA3   3'  AGGAAGCAGCCTCCTC      8833        GGGAA
                                AGGAAG    GGCCTCCTC
                                ||||||    |||||||||
                                TCCTTC    TCGGAGGAG
                                   G____
GAM1349  CHST1    5'  GGGGAGAAAGTCTTCT      18913    AA       C  C
                                GG  GGGGAAGG CT CT
                                ||  |||||||| || ||
                                CC  CCTCTTTC GA GA
                                 __       A  A
GAM1349  CYFIP2   5'  CGGGGAGGGGAAGCTCTTC   43908    CA   A     GC   C
                                CG  GGA GGGGAAG  CTC TC
                                ||  ||| |||||||  ||| ||
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                                GC  CCT CCCCTTC  GAG AG
                                 C_  _      __   A
GAM1349  EGLN2    5'  CGCAGAGGGCAGCGCCTCCTCC 38823      GAA   A  _
                                CGCAG   GGGG AG GCCTCCTCC
                                |||||   |||| || |||||||||
                                GCGTC   TCCC TC CGGAGGAGG
                                   ____   G  G
GAM1349  ENSA     3'  GCAGGGAGGGGAAGCGTC    20760      A      G C
                                GCAGG AGGGGAAG C TC
                                ||||| |||||||| | ||
                                CGTCC TCCCCTTC G AG
                                   C       _ C
GAM1349  ENTPD6   3'  GCAGGAAGGGGAGCTC      10338          AG  C
                                GCAGGAAGGGGA  GC TC
                                ||||||||||||  || ||
                                CGTCCTTCCCCT  CG AG
                                          __  _
GAM1349  ESRRB    5'  CCCAGGAAGGGGAGGATGCCTC 42628   G        AG__
              C                  C CAGGAAGGGGA   GCCTCC
                                | ||||||||||    ||||||
                                G GTCCTTCCCCT    CGGAGG
                                 G          CCTA
GAM1349  FCMD     3'  CAGGAAGGGGAGAGACTTC   27513          _   C
                                CAGGAAGGGGA AGGC TC
                                |||||||||| |||| ||
                                GTCCTTCCCCT TCTG AG
                                      C    A
GAM1349  FGF2     3'  GCAGGTTTGCAAGGCTTCCTC  12839      AAGGGG    C
                                GCAGG     AAGGC TCCTC
                                |||||     ||||| |||||
                                CGTCC     TTCCG AGGAG
                                   AAACG_    A
GAM1349  GATA3    5'  CGCGGGGAGGGAAGGGCGGTCC 13094     A  A     A   C_
                                CGC GG AGGGGA GGC  TCC
                                ||| || |||||| |||  |||
                                GCG CC TCCCTT CCG  AGG
                                  C  C     C   CC
GAM1349  GYS1     5'  CGCAGGAAGGGGGGCTCC    44783          AA   C
                                CGCAGGAAGGGG  GGC TCC
                                ||||||||||||  ||| |||
                                GCGTCCTTCCCC  CCG AGG
                                          __  _
GAM1349  HBA1     3'  GCAGGAAGGGGAGGAGGGGC  8151           A____
                                GCAGGAAGGGGA    GGC
                                ||||||||||||    |||
                                CGTCCTTCCCCT    CCG
                                      CCTCC
GAM1349  HTRA3    3'  CGTGGGAAGGGGAAGCC     44828    CA        G
                                CG  GGAAGGGGAAG CC
                                ||  |||||||||| ||
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                                GC  CCTTCCCCTTC GG
                                 AC         _
GAM1349  IFITM2   5'  GCTCAGAGGGGCTTCCTC    26972    AGGA    AA  C
                                GC   AGGGG  GGC TCCTC
                                ||   |||||  ||| |||||
                                CG   TCTCC  CCG AGGAG
                                 AG__    __  A
GAM1349  IGSF8    3'  GGAAGGGGAGGCACGTCTCC  38081        A  ____
                                GGAAGGGGA GGC   CTCC
                                ||||||||| |||   ||||
                                CCTTCCCCT CCG   GAGG
                                      _  TGCA
GAM1349  MAP3K5   5'  GCGGGAAGGGACGGAGCTTCCT 25442    A      AA_  C
                                GC GGAAGGGG   GGC TCCT
                                || ||||||||   ||| ||||
                                CG CCTTCCCT   TCG AGGA
                                 C       GCC   A
GAM1349  MBD1     3'  AGGAAGGGCACCAGCTTCTTC  31919       GAA_  C  C
                                AGGAAGGG    GGC TC TC
                                ||||||||    ||| || ||
                                TCCTTCCC    TCG AG AG
                                     GTGG   A  A
GAM1349  MNT      3'  GGAAGGGGAAGGACAGCC    33718         _ CT
                                GGAAGGGGAAGG C  CC
                                |||||||||||| |  ||
                                CCTTCCCCTTCC G  GG
                                       T TC
GAM1349  POU2AF1  3'  AGGAAGGAGGCCTTTTCC    26362       GGA    CC
                                AGGAAGG   AGGCCT  TCC
                                |||||||   ||||||  |||
                                TCCTTCC   TCCGGA  AGG
                                    ___     AA
GAM1349  PRDM2    3'  GAAGGGGAACTCGGCCTCCTCC 31970        ___
                                GAAGGGGAA   GGCCTCCTCC
                                |||||||||   ||||||||||
                                CTTCCCCTT   CCGGAGGAGG
                                     GAG
GAM1349  PTGFRN   3'  GCAGGAGGGGCCTCCTC     42592      A  GAAG
                                GCAGGA GGG    GCCTCCTC
                                |||||| |||    ||||||||
                                CGTCCT CCC    CGGAGGAG
                                   _  ____
GAM1349  PVR      5'  GGAAGGGGAATACCCACT    27110        G  TC
                                GGAAGGGGAA GCC  CT
                                |||||||||| |||  ||
                                CCTTCCCCTT TGG  GA
                                      A  GT
GAM1349  RALBP1   5'  AGGAAGGGACGAGGTCTTCTC  27697        A_  C  C
                                AGGAAGGGG  AGG CT CTC
                                |||||||||  ||| || |||
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                                TCCTTCCCT  TCC GA GAG
                                     GC   A  A
GAM1349  RFC1     3'  GGAAAAAACAAGGCTTTCTC   16274        _     CTC
                                GGAAGGGG AAGGC   CTC
                                |||||||| |||||   |||
                                CCTTTTTT TTCCG   GAG
                                     G     AAA
GAM1349  RHBG     3'  GGAAAGGGGCCTCCT       33821         AAG
                                GGAAGGGG   GCCTCCT
                                ||||||||   |||||||
                                CCTTTCCC   CGGAGGA
                                     ____
GAM1349  SLC13A3  3'  GCAGAAGGGGACAATCT     41300      G      AG C
                                GCAG AAGGGGA  G CT
                                |||| |||||||  | ||
                                CGTC TTCCCCT  T GA
                                  _      GT A
GAM1349  SLC14A1  3'  GCAGGAAGTGGGGACTGAGCTC 31965        __     A_ GC
                                GCAGGAA  GGGGA  G  CTC
                                |||||||  |||||  |  |||
                                CGTCCTT  CCCCT  C  GAG
                                     CA     GA TC
GAM1349  SLC22A12 5'  CGCGAGGGAGGTGCAGCCTCCT 40332     _   A   GGAA
           C                     CGC AGG AGG    GGCCTCCTC
                                |||  ||| |||    |||||||||
                                GCG TCC TCC    TCGGAGGAG
                                  C   C   ACG_
GAM1349  SLC6A1   5'  CAGCTCCAGAAGGCCTCCT   40487     GAAGG
                                CAG     GGAAGGCCTCCT
                                |||     ||||||||||||
                                GTC     TCTTCCGGAGGA
                                  GAGG_
GAM1349  SLC7A8   3'  GGAGGGGGAAAGCACCCT    29291     A        C
                                GGA GGGGAAGGC TCCT
                                ||| |||||||| ||||
                                CCT CCCCTTTCG GGGA
                                  C         T
GAM1349  SNAI1    3'  GGCCATGGGAAGGCCTCTTCC  25608    AAG_         C
                                GG    GGGAAGGCCTC TCC
                                ||    |||||||||| |||
                                CC    CCCTTCCGGAG AGG
                                 GGTA          A
GAM1349  SOX4     3'  GCAGGAAGGGGGAGACTCCT   16985           A    C
                                GCAGGAAGGGG AGGC TCCT
                                |||||||||| |||| ||||
                                CGTCCTTCCCC TCTG AGGA
                                       C   _
GAM1349  SOX4     3'  GGAAGGGGGAGGGGGTCTC    16989         A   CCTC
                                GGAAGGGG AGG    CTC
                                |||||||| |||    |||
```

```
                                CCTTCCCC TCC   GAG
                                    C  CCCA
GAM1349  TCP11    3'  CAGGAAGATGATGGGCCTCCTC 33071       GG  A_
                                CAGGAAG  GA  GGCCTCCTC
                                |||||||  ||  |||||||||
                                GTCCTTC  CT  CCGGAGGAG
                                    TA  AC
GAM1349  TGM2     3'  GGAGGGGGCTGCCTCCTC    21440     A   AAG
                                GGA GGGG   GCCTCCTC
                                |||  ||||   ||||||||
                                CCT CCCC   CGGAGGAG
                                  C   GA_
GAM1349  TNFRSF1B 3'  GGAGGGGGAAGGCTGACTC   9873      A       CTC
                                GGA GGGGAAGGC   CTC
                                |||  |||||||||   |||
                                CCT CCCCTTCCG   GAG
                                  C        ACT
GAM1349  TNP2     5'  TGAGGGCAGGGCCTCCTC    24057   A   AA_
                                A GGGG   GGCCTCCTC
                                |  ||||   |||||||||
                                A TCCC   CCGGAGGAG
                                 C   GTC
GAM1349  TNXB     3'  CGCTGGCAGAGAAGGCTTCCTC 37154     A  AA       C
              C                  CGC GG  GGGGAAGGC TCCTCC
                                 |||  ||  |||||||||  ||||||
                                 GCG CC  TCTCTTCCG AGGAGG
                                   A  G_       A
GAM1349  TULP3    3'  GCAGGGAGGGGAAGGGGAGGCC 17736      A    _____
                                GCAGG AGGGGA    AGGCC
                                |||||  ||||||    |||||
                                CGTCC TCCCCT    TCCGG
                                   C     TCCCC
GAM1349  YWHAG    3'  AGGAGGGGGCCTCC       29786     A   AAG
                                AGGA GGGG   GCCTCC
                                ||||  ||||   ||||||
                                TCCT CCCC   CGGAGG
                                   _   ____
GAM1349  ZNF278   5'  CGCGGGGAGGAGAAGGAGGGGT 36788    A  A       CC___
              CC                  CGC GG AGGGGAAGG    TCC
                                  |||  ||  |||||||||    |||
                                  GCG CC TCCTCTTCC    AGG
                                    C  C        TCCCC
GAM1350  CASP8    3'  TGGTAGTGTGGAATTTAGC   37881       G      GGGC
                                TGGTAG TGTGGAA   GC
                                ||||||  |||||||   ||
                                ACCATC ACACCTT   CG
                                   _      AAAT
GAM1350  CDH5     3'  GGTGGGTGTGGAGGTGGCC   12191     A       A  GCGC
                                GGT GGTGTGGA GG   GCC
                                |||  ||||||| ||   |||
```

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                                CCA CCACACCT CC    CGG
                                  C       _ AC__
GAM1350  CPNE7    3'  GGTGGGTGTGGGGGCAC     30871     A      AA
                                GGT GGTGTGG  GGGCGC
                                ||| |||||||  ||||||
                                CCA CCACACC  CCCGTG
                                  C      __
GAM1350  FOSB     3'  GGTGGGTGTGGGAGACA     27544     A      AA
                                GGT GGTGTGG  GGGCG
                                ||| |||||||  |||||
                                CCA CCACACC  TCTGT
                                  C      C_
GAM1350  GRM1     3'  TGGAGGTGTGGGAGATCGG   9146      T      A _______
                                TGG AGGTGTGG AG     GG
                                ||| |||||||| ||     ||
                                ACC TCCACACC TC     CC
                                  _       C  TAGIII
GAM1350  MSN      3'  TGGGGGTGTGGAAGGGAC    41252     TA          C
                                TGG  GGTGTGGAAGGG GC
                                |||  |||||||||||| ||
                                ACC  CCACACCTTCCC TG
                                  C_          _
GAM1350  PIM1     5'  TGGCGGCGGGAGGGCGCGCC  44974      A   T   A
                                TGGT GGTG GGA GGGCGCGCC
                                |||| |||| ||| |||||||||
                                ACCG CCGC CCT CCCGCGCGG
                                  _   _  _
GAM1350  PPP3CB   3'  TGGAGGTGTGGATGC       34452     T       AGG
                                TGG AGGTGTGGA   GC
                                ||| |||||||||   ||
                                ACC TCCACACCT   CG
                                  _       A__
GAM1350  RASAL1   5'  TGGTGGGTGGGAGGCG      21655     A   T   AG
                                TGGT GGTG GGA  GGCG
                                |||| |||| |||  ||||
                                ACCA CCAC CCT  CCGC
                                  C   _  __
GAM1350  SELL     3'  TGCTAGGTGTGGAAGTCGG   8513      G          _____
                                TG TAGGTGTGGAAG    GG
                                || ||||||||||||    ||
                                AC ATCCACACCTTC    CC
                                  G          AGIII
GAM1350  TIMP3    5'  GGTGGGCTGGGGCGCGCC    7464      T  AA_
                                GGTG GG   GGGCGCGCC
                                |||| ||   |||||||||
                                CCAC CC   CCCGCGCGG
                                  _ GAC
GAM1350  AGPS     3'  GATTACTAGTATAACCACAG  18931           T   T
                                GATTACTAGTAT ACC TGG
                                |||||||||||| ||| |||
```

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                                CTAATGATCATA TGG GTC
                                      T   T
GAM1351 ANGPT2   3' CAGTGCGCAGCCGTGACTTTCA 10086          TCTGCG
          G                    CAGTGCGTAGCCGT     TCAG
                               ||||||||||||||     ||||
                               GTCACGCGTCGGCA     AGTC
                                     CTGAA_
GAM1351 CDKN1C   5' GTGGTGGACTCTTCTGCGTC  6337     C  A_  CG
                               GTG GT  GC  TTCTGCGTC
                               ||| ||  ||  |||||||||
                               CAC CA  TG  AAGACGCAG
                                 _  CC  AG
GAM1351 VNN1     3' CAGTGCATGGCTGTTATCG   21683       A  C   CTG
                               CAGTGCGT GC GTT   CG
                               |||||||| || |||   ||
                               GTCACGTA CG CAA   GC
                                    C  A   TA_
GAM1351 ADAMTS13 3' GCGCAGCGGCTGGCCGTC   40037       T     GTT
                               GCGCAGCG GCTGGC   CGTT
                               |||||||| ||||||   ||||
                               CGCGTCGC CGACCG   GCAG
                                  _     ____
GAM1351 CNGB1    3' GCTGGCGTGCTGGCGGGACG  10532    GCA        TT_
                               GC   GCGTGCTGGCG   CG
                               ||   ||||||||||   ||
                               CG   CGCACGACCGC   GC
                                AC_         CCT
GAM1351 POLS     3' GCGGGGTGCTGGTCTCG     28120     CAGC      CG
                               GCG    GTGCTGG  TTCG
                               |||    |||||||  ||||
                               CGC    CACGACC  GAGC
                                 CC__      A_
GAM1352 ABAT     5' GGATGCGCGCCCCGAGTTCCGG 40776    CAC     G_ TC    A
          C                     GG   GCGCGC  TG  TTCC GC
                               ||   ||||||  ||  |||| ||
                               CC   CGCGCG  GC  AAGG CG
                                TA_     GG  TC    C
GAM1352 ACP1     5' GGCAGCGCGTGTGAGAG     28240      C    C   TCTTCC
                               GGCA GCGCG GTG     AG
                               |||| ||||| |||     ||
                               CCGT CGCGC CAC     TC
                                 _    A   TC_____
GAM1352 CDKN2A   3' AGGCATCGCGCACGTCCAG   38466      _      TGTCT
                               AGGCA CGCGCGCG    TCCAG
                               ||||| ||||||||    |||||
                               TCCGT GCGCGTGC    AGGTC
                                 A       ______
GAM1352 CDKN2B   3' AGGCATCGCGCACGTCCAG   38540      _      TGTCT
                               AGGCA CGCGCGCG    TCCAG
                               ||||| ||||||||    |||||
```

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                                TCCGT GCGCGTGC    AGGTC
                                  A      _____
GAM1352  CSHL1    3'  AGGTGGCTGCCGTCTTCCAGC  35454    CAC  GC  G
                                AGG   GC  GC TGTCTTCCAGC
                                |||   ||  || ||||||||||
                                TCC   CG  CG GCAGAAGGTCG
                                  AC_  A_  _
GAM1352  FLRT2    5'  GGCGTATCACTGTGTCTTCTAG 29853    ACG_  GC      C
              C                  GGC   CGC  GTGTCTTC AGC
                                |||   |||  |||||||| |||
                                CCG   GTG  CACAGAAG TCG
                                  CATA  A_      A
GAM1352  G6PD     5'  AGGTGCGCGCGCATCCCAGGCC 7595     CAC         ___
              AGC                  AGG   GCGCGCGTGTCTT   CCAGC
                                |||   ||||||||||||   |||||
                                TCC   CGCGCGCGTAGGG   GGTCG
                                  A__          TCC
GAM1352  INPP5D   3'  GGTGTGCGTTTTTCTTCCAGC  44424    CAC   CGCGTG
                                GG   GCG    TCTTCCAGC
                                ||   |||    |||||||||
                                CC   CGC    AGAAGGTCG
                                 ACA   AAAA__
GAM1352  ITPKB    3'  GGGCGCGTGTGTGACCTTTAGC 13649    CAC    C   CTT  ___
                                GG   GCGCG GTGT   CC   AGC
                                ||   ||||| ||||   ||   |||
                                CC   CGCGC CACA   GG   TCG
                                  ___    A    CT_  AAA
GAM1352  LDHB     5'  AGCTGCGTGCGTCTCCTCCGGC 14114    AC   C    G     A
                                GGC  GCG GCGT TCTTCC GC
                                |||  ||| |||| |||||| ||
                                TCG  CGC CGCA AGGAGG CG
                                  A_   A    G     C
GAM1352  MUC4     3'  GCACGCGCGCGTGCACAG    39667            CTTC
                                GCACGCGCGCGTGT    CAG
                                ||||||||||||||    |||
                                CGTGCGCGCGCACG    GTC
                                          T___
GAM1352  PTPRN    3'  GGCAGGCGTGCCCCTTCTGGC  15981     CGC   C  G    CA
                                GGCA   GCG GT TCTTC  GC
                                ||||   ||| || |||||  ||
                                CCGT   CGC CG GGAAG  CG
                                  C__   A  G    AC
GAM1352  SLC25A11 5'  GGCGCGCGCACGCCCCTCCAGC 18678     A       G
                                GGC CGCGCGCGT TCTTCCAGC
                                ||| ||||||||| |||||||||
                                CCG GCGCGTGCG GGGAGGTCG
                                  C       _
GAM1352  SOST     5'  GGCACGCCACCTTCCAG     36107        G   GTGT
                                GGCACGC CGC    CTTCCAG
                                |||||||  |||    |||||||
```

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                                CCGTGCG GTG    GAAGGTC
                                   _  _____
GAM1352  SOX12    3'  AGGCGCGTGCGTTGCCACCCGG 28024      AC   C   _  T   A
              C                    AGGC  GCG GCGT GTC TCC GC
                                   ||||  ||| |||| ||| ||| ||
                                   TCCG  CGC CGCA CGG GGG CG
                                     __  A   A   T   C
GAM1352  CYFIP1   3'  ACGGAGTGCAGCGCGT     42457     A   CCA   CGC
                                   ACG AGT   GCA   GCGCGT
                                   ||| |||   |||   ||||||
                                   TGC TCA   CGT   CGCGCA
                                    C  ___   ___
GAM1352  GPC6     5'  CGAGTGTGTATGCGCGCGTG   25041     A  CCAGCAC
                                   CGA GT      GCGCGCGTG
                                   ||| ||      |||||||||
                                   GCT CA      CGCGCGCAC
                                    _  CACATA_
GAM1352  PARK2    3'  GTGCGCGCGCGCGCGTG     30373    CCA  A
                                   GT   GC CGCGCGCGTG
                                   ||   || ||||||||||
                                   CA   CG GCGCGCGCAC
                                    CG_  C
GAM1352  STK10    3'  CGGGGGCCAGCACGCATCGC   25618    AAGT        _
                                   CG    CCAGCACGCG CGC
                                   ||    |||||||||| |||
                                   GC    GGTCGTGCGT GCG
                                    CCCC         A
GAM1353  CLECSF12 3'  TAAAATTGCTCTGACTGT    44125          GT_
                                   TAAAATTGTTT   CTGT
                                   ||||||||||   ||||
                                   ATTTTAACGAG   GACA
                                         ACT
GAM1354  CACNB2   3'  TTTTGGGGATGCTGTTAGT    8799         _   CCG  CC
                                   TTTTGGGG TGC   GT  AGT
                                   |||||||| |||   ||  |||
                                   AAAACCCC ACG   CA  TCA
                                        T   A__   A_
GAM1354  GCK      5'  TTTGGGGTTTGAGGTTCAGTC  37933        GCCC   C
                                   TTTGGGGT    GGT CAGTC
                                   ||||||||    ||| |||||
                                   AAACCCCA    CCA GTCAG
                                        AACT   A
GAM1354  GSK3B    5'  TATGTTGGGGTGTTAGGT    13303     T       CCC
                                   TAT TTGGGGTG   GGT
                                   ||| ||||||||   |||
                                   ATA AACCCCAC   CCA
                                     C       AAT
GAM1354  RGR      3'  CAAAAAATTACAGATATTG   16303          CTC
                                   CAAAAAATT   TAGATATTG
                                   |||||||||   |||||||||
```

```
                                GTTTTTTAA  GTCTATAAC
                                     T__
GAM1355 ACTN2   5' GGCGGGCGGCGGGCGGCGGGC 9950       A TCT T  A
                                GGCGGGC GC  GC GGC GGC
                                ||||||| ||  || ||| |||
                                CCGCCCG CG  CG CCG CCG
                                    C CC_ _  C
GAM1355 ALX3    3' GGTGGGCAGCTCATTCTGCAGG 27065   C      TG_  G
                                GG GGGCAGCTC  CTG CAGG
                                || |||||||||  ||| ||||
                                CC CCCGTCGAG  GAC GTCC
                                 A       TAA  _
GAM1355 AP2A1   5' TGGCGGGCGGGCGGGCGGG  39108       AGCTCT T  A
                                TGGCGGGC    GC GGC GG
                                ||||||||    || ||| ||
                                ACCGCCCG    CG CCG CC
                                    CC_____ C  C
GAM1355 AP2A1   5' GGCGGGCGGGCGGGCTGGCAGG 39106      A_ TCT
            C                    GGCGGGC GC  GCTGGCAGGC
                                ||||||| ||  ||||||||||
                                CCGCCCG CG  CGACCGTCCG
                                    CC CC_
GAM1355 BGN     5' GGCGGGCTGGGGTGGTGGGC  11821      AGCTC C__  CA
                                GGCGGGC   TG  TGG GGC
                                |||||||   ||  |||  |||
                                CCGCCCG   AC  ACC CCG
                                    _____ CCC  AC
GAM1355 C1orf6  5' GGCGGGCGGTCGGGCGGG   33530      AGC TGCT  A
                                GGCGGGC  TC   GGC GG
                                |||||||  ||   ||| ||
                                CCGCCCG  AG   CCG CC
                                    CC_ C___  C
GAM1355 CD7     3' TGGGGGCCTGCTGGTGGG   26006   C  AGCT    CA
                                TGG GGGC  CTGCTGG GG
                                ||| ||||  ||||||| ||
                                ACC CCCG  GACGACC CC
                                  _  ____     AC
GAM1355 CRHR1   5' GGCGGGCGGCTGCGGGC    20447      A  CT T
                                GGCGGGC GCT GC GGC
                                ||||||| |||  || |||
                                CCGCCCG CGA  CG CCG
                                    C  __ C
GAM1355 GFAP    3' GGTGGGTGCCGTCTGGCAGGC 13125   C  CA  CTG
                                GG GGG  GCT  CTGGCAGGC
                                || |||  |||  |||||||||
                                CC CCC  CGG  GACCGTCCG
                                 A  A_  CA_
GAM1355 NLGN2   5' TGGCGGGCAGCGCCCCGTGCAG 44764         T G  _
            G                    TGGCGGGCAGC CT CTG GCAGG
                                ||||||||||| || ||| |||||
```

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                                ACCGCCCGTCG GG GGC CGTCC
                                      C  _  A
GAM1355 RAI14   3' TGGTGGCAGCTCATATTAGG  31809    CG     TGCTGGC
                                TGG  GGCAGCTC     AGG
                                |||  ||||||||      |||
                                ACC  CCGTCGAG     TCC
                                  A_      TATAA__
GAM1355 VARS2   5' GGTGGGCGGCTCTCCAGG   26662   C   A   G TGG
                                GG GGGC GCTCT C   CAGG
                                || |||| ||||| |   ||||
                                CC CCCG CGAGA G   GTCC
                                 A   C    _ ___
GAM1355 VASP    5' GGCGGGCGGCTCGCCCACGGGC 17917      A   T  G  A
                                GGCGGGC GCTC GCT GC GGC
                                ||||||| |||| ||| || |||
                                CCGCCCG CGAG CGG TG CCG
                                    C   _  G  C
GAM1355 WBSCR5  5' TGGCGGGCGGGCAGGGCGGGC 37131       A_  TCT  T
                                TGGCGGGC  GC   GC GGC
                                ||||||||  ||   || |||
                                ACCGCCCG  CG   CG CCG
                                     CC  TCC  C
GAM1355 ZFP103  5' TGGCGGGCGGCGCCTCTCAGGC 24963       A  TCT   GG_
                                TGGCGGGC GC   GCT   CAGGC
                                |||||||| ||   |||   |||||
                                ACCGCCCG CG   CGG   GTCCG
                                     C  ___   AGA
GAM1355 EPHA8   3' TGCTGGTGTCCCCGCGG    33903    C  C   TCTTC
                                TGC GG GTCC    CCGCGG
                                ||| || ||||    ||||||
                                ACG CC CAGG    GGCGCC
                                  A  A   _____
GAM1355 SORCS2  3' TTGCTGGTGGTTCTGTGCCCTC 34069     C  C_  C  ___  TC   C
           CGTGG                TTGC GG  GT CT   CT  CCG GG
                                |||| ||  || ||   ||  ||| ||
                                AACG CC  CA GA   GG  GGC CC
                                  A  AC  A  CAC  GA   A
GAM1356 ABCG2   3' TTCATGTTTAATTCAGTTT   22096      TA
                                TTCAT  TTTAATTTAGTTT
                                |||||  ||||||||||||
                                AAGTA  AAATTAAGTCAAA
                                   C_
GAM1356 TARDBP  3' ATTATTTAAATCAGTTTTATT  28904        T
                                ATTATTTAA TTAGTTTTATT
                                ||||||||| ||||||||||
                                TAATAAATT AGTCAAAATAA
                                      T
GAM1357 ANK1    3' TAGAGCACCAAGTTCACT    33874     A GT    C
                                TAGA T  CAAGT CACT
                                |||| |  ||||| ||||
```

```
                                ATCT G  GTTCA GTGA
                                  C TG    A
GAM1357  BMP1    3'  CAGCTGTGAGTCCACT     25975     AA   CA
                                TAG  TGT  AGTCCACT
                                |||  |||  ||||||||
                                GTC  ACA  TCAGGTGA
                                  G_   C_
GAM1357  DSP     3'  TAGAATGTCCTATCACT     20646         AA   C
                                TAGAATGTC  GTC ACT
                                |||||||||  ||| |||
                                ATCTTACAG  TAG TGA
                                     GA   _
GAM1357  FPRL1   3'  TAAAATGCAAAGTCCACT    11149         C
                                TAGAATGT AAGTCCACT
                                ||||||||| |||||||||
                                ATTTTACG TTCAGGTGA
                                     T
GAM1357  GNAS    3'  CAGGATGTAGTCCACT      38656     A    CA
                                TAG ATGT  AGTCCACT
                                |||  ||||  ||||||||
                                GTC TACA  TCAGGTGA
                                  C    __
GAM1357  HIP2    3'  TAGGTGTCAAATTCACT     23771     AA       C
                                TAG  TGTCAAGT CACT
                                |||  |||||||| ||||
                                ATC  ACAGTTTA GTGA
                                  C_       A
GAM1357  HMMR    3'  TAAAATGTCAAAAGACACT   29808           TC_
                                TAGAATGTCAAG   CACT
                                ||||||||||||   ||||
                                ATTTTACAGTTT   GTGA
                                       TCT
GAM1357  KCNJ15  3'  TACAATTCAGTCCACT      13878    G   G   A
                                TA AAT TCA GTCCACT
                                || ||| ||| |||||||
                                AT TTA AGT CAGGTGA
                                 G   _   _
GAM1357  LTB4R   5'  CAGAATGCCAATTACT      8878           GTCC
                                TAGAATGTCAA    ACT
                                ||||||||||    |||
                                GTCTTACGGTT    TGA
                                      AA__
GAM1357  MADH5   3'  TAAAACAAGTCCACT       25356       TGT
                                TAGAA   CAAGTCCACT
                                |||||   ||||||||||
                                ATTTT   GTTCAGGTGA
                                        ____
GAM1357  MAN2A2  3'  TAGAATGCCATCACT       25954          AGTC
                                TAGAATGTCA    CACT
                                |||||||||    ||||
```

```
                                ATCTTACGGT   GTGA
                                     A___
GAM1357 MFAP2    3' CAGGGCTGCAGTCCACT    32706    AA_  CA
                                TAG  TGT  AGTCCACT
                                |||  |||  ||||||||
                                GTC  ACG  TCAGGTGA
                                  CCG  __
GAM1357 PTGFRN   3' TAGAACGTCCCTCTGTCACT  42595       AA___  C
                                TAGAATGTC    GTC ACT
                                |||||||||    ||| |||
                                ATCTTGCAG    CAG TGA
                                     GGAGA  _
GAM1357 PTPRG    3' TAGAATGCAACCACT      15943       T  GT
                                TAGAATG CAA  CCACT
                                ||||||| |||  |||||
                                ATCTTAC GTT  GGTGA
                                   _  __
GAM1357 SCAMP3   5' TAGCCCTCAGAGTCCACT   25033    AATG  _
                                TAG   TCA AGTCCACT
                                |||   ||| ||||||||
                                ATC   AGT TCAGGTGA
                                  GGG_  C
GAM1357 SLC24A1  3' TAGAATGTCTAATCCCT    21821       A   A
                                TAGAATGTC AGTCC CT
                                ||||||||| ||||| ||
                                ATCTTACAG TTAGG GA
                                     A   _
GAM1357 SOCS5    3' TAAAATGTAAGCCACT     30423       C  T
                                TAGAATGT AAG CCACT
                                |||||||| ||| |||||
                                ATTTTACA TTC GGTGA
                                   _  _
GAM1357 ST7      3' TAGAATATCTTCATCCACT  32939       AA_
                                TAGAATGTC  GTCCACT
                                |||||||||  |||||||
                                ATCTTATAG  TAGGTGA
                                     AAG
GAM1357 TFG      3' TAGAAAGTCAAGTCAATCACT 25874     T     ___
                                TAGAA GTCAAGTC  CACT
                                ||||| ||||||||  ||||
                                ATCTT CAGTTCAG  GTGA
                                   T      TTA
GAM1357 TIMM23   3' TAAAATGTCAGAGGTACACT  26752       A__  C
                                TAGAATGTCA  GT CACT
                                ||||||||||  || ||||
                                ATTTTACAGT  CA GTGA
                                     CTC  T
GAM1357 WHSC1    3' TAGGATGAGCCCACT      39378    A  TCA
                                TAG ATG  AGTCCACT
                                ||| |||  ||||||||
```

```
                                ATC TAC   TCGGGTGA
                                  C  ___
GAM1357 BAT3    5' TCCGTTTCCCCGATAGTATT  21585    AC     TCTCG
                                TCC  TTCTCT    AGTATT
                                |||  ||||||    ||||||
                                AGG  AAGGGG    TCATAA
                                  CA     CTA__
GAM1357 CCKAR   3' TCCGTTCTTTCTTCTCTGC   8810     A__  C      GA
                                TCC   CTT TCTTCTC  GT
                                |||   ||| |||||||  ||
                                AGG   GAA AGAAGAG  CG
                                  CAA  _      A_
GAM1357 EDAR    3' CTCCACTTTCTTTTTGCTC   35305       C   ____
                                CTCCACTT TCTT    CTC
                                ||||||||| ||||    |||
                                GAGGTGAA AGAA    GAG
                                     _    AAAC
GAM1357 EFNA1   3' CTCCACTTCTTTCTCCGT    20700        C    GA
                                CTCCACTTCT TTCTC  GT
                                |||||||||| |||||  ||
                                GAGGTGAAGA AAGAG  CA
                                     _    G_
GAM1357 FCGR2A  3' CTCTAATTCTCTTCTCAAAT  44277    CAC
                                CTC   TTCTCTTCTCGAGT
                                |||   ||||||||||||||
                                GAG   AAGAGAAGAGTTTA
                                  ATT
GAM1357 FCGR2B  3' CTCTGATTTTCTTCTCAAAT  19658    CACTTC
                                CTC     TCTTCTCGAGT
                                |||     ||||||||||
                                GAG     AGAAGAGTTTA
                                  ACTAAA
GAM1357 GAP43   5' CTCCACCTCTTTTCTGGAAT  13046        C   C
                                CTCCACTTCT TTCT GAGT
                                |||||||||| |||| ||||
                                GAGGTGGAGA AAGA CTTA
                                      A   C
GAM1357 GHR     3' TCTACTTCTCTTAGCATGTATT 6718    C       CT  A
                                TC ACTTCTCTT  CG GTATT
                                || |||||||||  || |||||
                                AG TGAAGAGAA  GT CATAA
                                  A        TC  A
GAM1357 GPM6B   3' TCCATTTCATCTTCAGCACT  42543     C  _    TCG
                                TCCA TTC TCTTC   AGTATT
                                |||| ||| |||||   ||||||
                                AGGT AAG AGAAG   TCGTGA
                                  A  T    ___
GAM1357 HGF     3' CCCACTTCTTGACAGTGTTC  45319        CTTCT G   A
                                TCCACTTCT    C AGT TTC
                                |||||||||    | ||| |||
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                                GGGTGAAGA    G TCA AAG
                                     ACT__ _   C
GAM1357  MEIS2    3'  TTCTCTTCTAAAACTATT    33548        C_  G
                                TTCTCTTCT  GA TATT
                                |||||||||  || ||||
                                AAGAGAAGA  TT ATAA
                                     TT  G
GAM1357  NIPSNAP1  3'  CTCTGTTCTTCTTCCCAA    18870    CAC   _
                                CTC   TTCT CTTCTCGA
                                |||   |||| ||||||||
                                GAG   AAGA GAAGGGTT
                                  AC_    A
GAM1357  OGN      5'  ACTTCTCTATCAGAAATTC    37456        _  TC   T
                                ACTTCTCT TC  GAG ATTC
                                |||||||| ||  ||| ||||
                                TGAAGAGA AG  CTT TAAG
                                     T  T_  _
GAM1357  PPARBP   3'  CTCCCTTTCTTAAGCAAGTATT 21927     A   C    CT_
                                CTCC CTT TCTT   CGAGTATT
                                |||| ||| ||||   ||||||||
                                GAGG GAA AGAA   GTTCATAA
                                  _  _    TTC
GAM1357  RASA1    5'  TCCACTTCTTTTCTGGAGC    35488        C    C
                                TCCACTTCT TTCT GAGT
                                ||||||||| |||| ||||
                                AGGTGAAGA AAGA CTCG
                                     A    C
GAM1357  RXRA     3'  TTCTCCTCTCACACTTC     16438          AGTA
                                TTCTCTTCTCG    TTC
                                ||||||||||    |||
                                AAGAGGAGAGT    AAG
                                     GTG_
GAM1357  SPAG9    5'  TCTGCTTCTCTTTCTTCAAGT  19562    CA      _ _
                                TC  CTTCTCTT CT CGAGT
                                ||  |||||||| || |||||
                                AG  GAAGAGAA GA GTTCA
                                 AC       A  A
GAM1357  TEC      3'  CTTCTCTTCAGGCATATT    17386        TCGA
                                CTTCTCTTC    GTATT
                                |||||||||    |||||
                                GAAGAGAAG    TATAA
                                     TCCG
GAM1357  TM7SF3   3'  CTTCTCTTTTTGTATTC     40654        CTCGA
                                CTTCTCTT     GTATTC
                                ||||||||     ||||||
                                GAAGAGAA     CATAAG
                                     AAA__
GAM1357  TRPS1    3'  TCCACTTCTTTATTTCAGT    30467         CTTC_  G
                                TCCACTTCT     TC AGT
                                |||||||||     || |||
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                                AGGTGAAGA    AG TCA
                                     AATAA  _
GAM1357  UCP3    3'  TCTACTTCTGTTTCTTGAAT  17856   C    C_   C
                                TC ACTTCT  TTCT GAGT
                                || |||||||  |||| ||||
                                AG TGAAGA  AAGA CTTA
                                 A     CA    A
GAM1357  WNT15   3'  CTTCTCTTTGTTGAGTATC   18147       CTC_
                                CTTCTCTT   GAGTATT
                                ||||||||   |||||||
                                GAAGAGAA   CTCATAG
                                     ACAA
GAM1357  ZNF136  3'  CTTCTCTTCAGTGAGTATT   40876       TC_
                                CTTCTCTTC  GAGTATT
                                |||||||||  |||||||
                                GAAGAGAAG  CTCATAA
                                     TCA
GAM1358  AFG3L2  3'  GATGGTGTAGAGCAAGAAG   45543    T  _  CTGAA
                                GATG TG AGA    GCAAGAAG
                                |||| || |||    ||||||||
                                CTAC AC TCT    CGTTCTTC
                                  C  A  _____
GAM1358  ANKTM1  3'  TGTTGGGGACAGCAAGAAG   28809     A_  TGA
                                TGTTG  GAC  AGCAAGAAG
                                |||||  |||  |||||||||
                                ACAAC  CTG  TCGTTCTTC
                                   CC  ___
GAM1358  CDKN2C  3'  TGTTGAGATTGGCAAAA     38572       C  AA
                                TGTTGAGA TG  GCAAGA
                                |||||||| ||  ||||||
                                ACAACTCT AC  CGTTTT
                                     A  __
GAM1358  CYP3A4  3'  TGTTGAGGATGGAATGCAAGA  32716       ACT_  _
                                TGTTGAG   GAA GCAAGA
                                |||||||   ||| ||||||
                                ACAACTC   CTT CGTTCT
                                     CTAC   A
GAM1358  FMR2    3'  GATGTGGGATTTCAAGAAG   12966     T A  CTGAAG
                                GATGT G GA     CAAGAAG
                                ||||| | ||     |||||||
                                CTACA C CT     GTTCTTC
                                  _ C  AAA___
GAM1358  FUT6    5'  ATGTTGAGGAACTGCAGGAGGA 6649        __  GAA   A  A
                                ATGTTGAG  ACT   GCA GA GA
                                ||||||||  |||   ||| || ||
                                TACAACTC  TGA   CGT CT CT
                                     CT   ___   C  C
GAM1358  HIP2    3'  GATGTTGGTGCTCCTCAAGAAG 23767       AGA  GAAG
            A                 GATGTTG   CT    CAAGAAGA
                                |||||||   ||    ||||||||
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                                CTACAAC  GA   GTTCTTCT
                                    CAC  GGA_
GAM1358 PAX9     3' TGCTGAGACAGGGAGA     26208        TGA  CA
                                TGTTGAGAC  AG  AGA
                                |||||||||  ||  |||
                                ACGACTCTG  TC  TCT
                                     ___  CC
GAM1358 PIK3CD   3' GAGGCTGAGGCAAGAAGA    22728    A   A
                                GAG CTGA GCAAGAAGA
                                ||| |||| |||||||||
                                CTC GACT CGTTCTTCT
                                  C   C
GAM1358 PTPN7    3' GATGTTGAGACTTGGAGATCAG 38714          GA_  CA_
                                GATGTTGAGACT  AG  AG
                                ||||||||||||  ||  ||
                                CTACAACTCTGA  TC  TC
                                      ACC  TAG
GAM1358 RFC1     3' GTTGAGACTCCAGAAG     16276        GAAGCA
                                GTTGAGACT     AGAAG
                                |||||||||     |||||
                                CAACTCTGA     TCTTC
                                     GG____
GAM1358 SAS      3' GAGACTGAGGCAGGAGGA    25587        A  A  A
                                GAGACTGA GCA GA GA
                                |||||||| ||| || ||
                                CTCTGACT CGT CT CT
                                    C  C  C
GAM1358 TNFRSF9  3' GAGACTGAGGCAGGAGGA    11452        A  A  A
                                GAGACTGA GCA GA GA
                                |||||||| ||| || ||
                                CTCTGACT CGT CT CT
                                    C  C  C
GAM1358 UMPS     3' TGAGAGACTGAGGCAGGAGGA  7504     TT      A  A  A
                                TG  GAGACTGA GCA GA GA
                                ||  |||||||| ||| || ||
                                AC  CTCTGACT CGT CT CT
                                 T_      C  C  C
GAM1358 HSF2BP   3' AGAGAGAGAATGAAT      28141      CTCGAC
                                AGAGG     GAGAATGAAT
                                |||||     ||||||||||
                                TCTCT     CTCTTACTTA
                                     _______
GAM1358 PDGFRA   3' CAGAGACTTGGAACACTGAATT 26285        CGAC  AA_
           G                     CAGAGGCT   GAG  TGAATTG
                                 ||||||||   |||  |||||||
                                 GTCTCTGA   CTT  ACTTAAC
                                     AC__   GTG
GAM1358 TAF4     3' GGTGCAACGATGAATTG     17264    CT     GAA
                                GG CGACGA  TGAATTG
                                ||  ||||||  |||||||
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                                CC  GTTGCT   ACTTAAC
                                 AC     ___
GAM1359  STMN1    3'  TCATTTGTGCGTTGGGT     24517        AACATT
                                TCGTTTG     CGTTGGGT
                                |||||||     ||||||||
                                AGTAAAC     GCAACCCA
                                   AC_____
GAM1359  RAB5A    3'  TACATTGTTTATTATGGTTCTA 20012    G      TTCAAGC
                                TA ATTGTTT      GGTTCTA
                                || |||||||      |||||||
                                AT TAACAAA      CCAAGAT
                                 G      TAATA__
GAM1360  USP9X    5'  CAATTTTGTCTGCTTATGTA   21636       ATAA
                                TAATTT    TTTGCTTATGTA
                                ||||||    ||||||||||||
                                GTTAAA    AGACGAATACAT
                                   AC__
GAM1361  MXI1     3'  TGTTTTATCATTATCAAATGC  39025          ATTTC
                                TGTTTTATTAT     TCAAATGC
                                ||||||||||     ||||||||
                                ACAAAATAGTA     AGTTTACG
                                      AT___
GAM1362  ACYP1    3'  CCATCATACAGGTAATATATAA 9963               C
                                TCGTTATACAGGTAATA ATAA
                                |||||||||||||||| ||||
                                GGTAGTATGTCCATTAT TATT
                                         A
GAM1362  B3GALT3  3'  TGTCATTATGCAGTACATA    37672         A   GTAA
                                TGTCGTTAT CAG    TACATA
                                ||||||||| |||    ||||||
                                ACAGTAATA GTC    ATGTAT
                                   C  _____
GAM1362  GNRHR    5'  TGTTATTACACATTAATGCATA 7618      CG      GG    A
            A                    TGT  TTATACA  TAAT CATAA
                                |||  |||||||  |||| |||||
                                ACA  AATGTGT  ATTA GTATT
                                  AT      A_   C
GAM1362  AIM1     3'  TATAGTCCCAGCTACTTGG    45085       GA   A
                                TATAGT  CTA CTACTTGG
                                ||||||  ||| ||||||||
                                ATATCA  GGT GATGAACC
                                   G_   C
GAM1362  CDH1     3'  GCCTGTGGTCCCAGCTACTTGG 20365    ATA   A__   A
                                GT   GTG   CTA CTACTTGG
                                ||   |||   ||| ||||||||
                                CG   CAC   GGT GATGAACC
                                 GA_   CAG   C
GAM1362  DISC1    3'  GCCTGTAACCCCAGCTACTTGG 33042    ATA     AA__
                                GT   GTGACT    CTACTTGG
                                ||   ||||||    ||||||||
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                                CG  CATTGG   GATGAACC
                                 GA_    GGTC
GAM1362  FANCE    3'  CATGTAGTCCCAGCTACTTGG  34896    A   GA  A
                                CGT TAGT  CTA CTACTTGG
                                ||| ||||  ||| ||||||||
                                GTA ATCA  GGT GATGAACC
                                  C   G_  C
GAM1362  GLTSCR1  5'  GCCTGTGGTCTTAGCTACTTGG 31837    ATA  A_  AA_
                                GT  GTG  CT  CTACTTGG
                                ||  |||  ||  ||||||||
                                CG  CAC  GA  GATGAACC
                                 GA_  CA  ATC
GAM1362  KLRD1    3'  GCCTGCAGTCCTAGCTACTTGG 28810    A__   GA  A
                                GT  TAGT  CTA CTACTTGG
                                ||  ||||  ||| ||||||||
                                CG  GTCA  GAT GATGAACC
                                 GAC   G_  C
GAM1362  UGDH     3'  GCCTGTAGTCCCAGCTACTTGG 17883    A__   GA  A
                                GT  TAGT  CTA CTACTTGG
                                ||  ||||  ||| ||||||||
                                CG  ATCA  GGT GATGAACC
                                 GAC   G_  C
GAM1362  VENTX2   3'  GTCTGTAATCCTAGCTACTTGG 30917    ATA   __  A
                                GT  GTGA  CTA CTACTTGG
                                ||  ||||  ||| ||||||||
                                CA  CATT  GAT GATGAACC
                                 GA_   AG  C
GAM1363  MDM1     3'  TATAAATAGTATCTTTTTTCA  33518              _
                                TATAAATAGTATTTTTTT CA
                                |||||||||||||||||| ||
                                ATATTTATCATAGAAAAA GT
                                          A
GAM1363  MAPRE2   3'  TATTAATAAGGTCTTCACTTCT 30692              A
            AG                    TATTAATAAGGTCTTCAT TTTAG
                                |||||||||||||||||| |||||
                                ATAATTATTCCAGAAGTG AGATC
                                          A
GAM1364  APM1     3'  TATTAAATATAAATTGTCTAAA 22017          T   A
                                TATTAAATAT AAATT TCTAAA
                                |||||||||| ||||| ||||||
                                ATAATTTATA TTTAA AGATTT
                                      _   C
GAM1364  PPAT     3'  TAAATATTAAATTTCTAAAT  15484           A
                                TAAATATTAAATT TCTAAAT
                                |||||||||||| |||||||
                                ATTTATAATTTAA AGATTTA
                                          _
GAM1364  BCAT1    3'  TTTTTCCTAGACTACTATA   42389       A
                                TTTTTC TAGACTGTTATA
                                |||||| ||||||||||||
```

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                                AAAAAG ATCTGATGATAT
                                   G
GAM1364  DKK1     3'  TTTTCATAGCATCTATTATA  29274        A__
                                TTTTCATAG  CTGTTATA
                                |||||||||  ||||||||
                                AAAAGTATC  GATAATAT
                                    GTA
GAM1364  RAP1A    3'  TTTTCACATCTGTTATA    16156       GA
                                TTTTCATA  CTGTTATA
                                ||||||||  ||||||||
                                AAAAGTGT  GACAATAT
                                    A_
GAM1365  ITGB1    3'  GTAGATCAACTATTTCA    38053         CA
                                GTAGATCAACTA  TTCA
                                ||||||||||||  ||||
                                CATCTAGTTGAT  AAGT
                                      A_
GAM1365  KRAS2    3'  AATCAACTGCATGCACCAAAA  37885       A  T
                                GATCAACT CAT CATTAAAA
                                |||||||| ||| ||||||||
                                TTAGTTGA GTA GTGGTTTT
                                    C  C
GAM1365  PPAT     3'  GATCAAGCACTTCATTAAAA  15483      C  A
                                GATCAA TAC TTCATTAAAA
                                |||||| ||| ||||||||||
                                CTAGTT GTG AAGTAATTTT
                                   C  _
GAM1365  ZNF174   3'  GTAGATCACTCATCTTTATTAA 18364       A A   C__
            A                    GTAGATCA CT CATT   ATTAAA
                                |||||||| || ||||   ||||||
                                CATCTAGT GA GTAG   TAATTT
                                    _ _    AAA
GAM1365  IFNGR1   3'  TTTACATATTCCATTAATTCTA 43543       TC   T
            T                    TTTACAT  TTCT TTAATTCTAT
                                |||||||  |||| ||||||||||
                                AAATGTA  AAGG AATTAAGATA
                                    T_   T
GAM1365  OXTR     3'  TTTACTTCTTCTTTTCCTA   9538       A      TAA
                                TTTAC TTCTTCTTT   TTCTA
                                |||||| |||||||||   |||||
                                AAATG AAGAAGAAA   AGGAT
                                   _      ____
GAM1365  PDE1A    3'  TTTATGTTCTTCTTAATTCC   22711     CA     TT
                                TTTA  TTCTTCT  TAATTCT
                                ||||  |||||||  |||||||
                                AAAT  AAGAAGA  ATTAAGG
                                  AC      __
GAM1366  CNR1     3'  TGGTTACAAAGGCATTAT    32005     GA
                                TGGT  TGCGAGGGCATTAT
                                ||||  ||||||||||||||
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                                ACCA  ATGTTTCCGTAATA
                                  __
GAM1366  NELL2    3'  CATGGTGATGTGAGACAC    26047          C    G
                                TATGGTGATG GAGG CAT
                                |||||||||| |||| |||
                                GTACCACTAC CTCT GTG
                                     A   _
GAM1366  DDEF2    3'  TATAATGATAGCTGCAACCTC  19324          CAA  A G
                                TATAATGATA   CT C AACCTC
                                ||||||||||   || | ||||||
                                ATATTACTAT   GA G TTGGAG
                                     C__  C _
GAM1366  HSPA9B   3'  TATAATGATCAATTCATCCTAC 19975          A   CTACGA__
              CTC                  TATAATGAT CAA       ACCTC
                                |||||||| |||       |||||
                                ATATTACTA GTT       TGGAG
                                     _  AAGTAGGA
GAM1367  AGL      3'  CATATAGCATTTACATA     8494           GATCA
                                CATATAGCG    ACATA
                                |||||||||    |||||
                                GTATATCGT    TGTAT
                                     AAA__
GAM1367  APC4     3'  TTTACATAAGTGAGCCACATAC 45500         T  C GA   A
                                TTTACATA AG G  TCA CATAC
                                |||||||| || |  ||| |||||
                                AAATGTAT TC C  GGT GTATG
                                     _  A TC  _
GAM1367  HK2      3'  ACATAACAAATTAACATA    6783           C
                                ATATAGCGGAT AACATA
                                |||||||||||| ||||||
                                TGTATTGTTTA TTGTAT
                                      A
GAM1367  PFN2     3'  TTACATACAGTGGTTAACATAC 38163          C  ATC
                                TTACATATAG GG   AACATAC
                                |||||||||| ||   |||||||
                                AATGTATGTC CC   TTGTATG
                                     A  AA_
GAM1367  PTP4A2   3'  CACATAGCCGGTCAACAT    38623          _  A
                                CATATAGC GG TCAACAT
                                |||||||| || |||||||
                                GTGTATCG CC AGTTGTA
                                     G  _
GAM1367  ROR2     3'  TTTACAAATAGGACCAACA   21266        T   GC
                                TTTACA ATA  GGATCAACA
                                |||||| |||  |||||||||
                                AAATGT TAT  CCTGGTTGT
                                   T  __
GAM1367  WT1      3'  TTTACATTAGCAGACACATAC  35973        A       CA
                                TTTACAT TAGCGGAT  ACATAC
                                ||||||| ||||||||  ||||||
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                                AAATGTA ATCGTCTG  TGTATG
                                  _     __
GAM1368  CAV3     3'  GAACCCAGGCCCTTCCCTCAGT 37846          CTGA_ TG
                 G                 GAATCCAGGCCC    T  GTG
                                   ||||||||||||    |  |||
                                   CTTGGGTCCGGG    A  CAC
                                         AAGGG GT
GAM1368  CDH12    5'  GAATCCAGGTTTGAGGT     19775        CCCC   TT
                                   GAATCCAGG   TGA  GGT
                                   |||||||||   |||  |||
                                   CTTAGGTCC   ACT  CCA
                                        AA__   __
GAM1368  FGD1     3'  GAATCCAGGTCTCCTACCTCTG 20904        CC_   AT__
                 GTG                  GAATCCAGG   CCTG   TGGTG
                                      |||||||||   ||||   |||||
                                      CTTAGGTCC   GGAT   ACCAC
                                           AGA    GGAG
GAM1368  FSTL3    3'  CCGAATCCGGGCTCTAAGGAGT 25217        A   CC   TT
                 G                    TCGAATCC GGC  CTGA  GGTG
                                      ||||||||| |||  ||||  ||||
                                      GGCTTAGG CCG  GATT  TCAC
                                           C   A_   CC
GAM1368  NPY2R    3'  TCAATCCAGGTCCTAACGT   9501     G      CC     TG
                                      TC AATCCAGG  CCTGAT  GT
                                      || ||||||||  ||||||  ||
                                      AG TTAGGTCC  GGATTG  CA
                                       _       A_     __
GAM1368  PLOD     3'  GAATCTCTTTGATTGGTG    7157       CAGGCCCC
                                      GAATC       TGATTGGTG
                                      |||||       |||||||||
                                      CTTAG       ACTAACCAC
                                         AGAA____
GAM1368  PTPRF    3'  TCTAGGCTCTCTGATTGGT   39038    C   CC_
                                      TC AGGC   CTGATTGGT
                                      || ||||   |||||||||
                                      AG TCCG   GACTAACCA
                                       A    AGA
GAM1368  RRP22    3'  TCCAATCCAGGTCCCTGATTG  27009    G      C
                                      TC AATCCAGG CCCTGATTG
                                      || |||||||| |||||||||
                                      AG TTAGGTCC GGGACTAAC
                                       G       A
GAM1368  SCG3     3'  GAATCCTGCTGATTGGTG    29887       AG  CCC
                                      GAATCC  GC   TGATTGGTG
                                      ||||||  ||   |||||||||
                                      CTTAGG  CG   ACTAACCAC
                                         A_  ____
GAM1368  SVIL     5'  TCGAATCCAGCTTTTGAT    34735         GCCC  GA
                                      TCGAATCCAG    CT  TTGGT
                                      ||||||||||    ||  |||||
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                                AGCTTAGGTC   GA  AACTA
                                     _____  A_
GAM1368  CLN5    3'  CTGGATTTGCCACATCTAG   27080          _  A_
                                CTGGATTTGCC CA  TAG
                                ||||||||||| ||  |||
                                GACCTAAACGG GT  ATC
                                      T  AG
GAM1368  FMO4    3'  CCTGAATTTGGCTAATAG    12924          CCC
                                CCTGGATTTG   AATAG
                                |||||||||   |||||
                                GGACTTAAAC   TTATC
                                     CGA
GAM1368  LTF     5'  CCTGTTGCCCAATAG      14259      GAT
                                CCTG   TTGCCCAATAG
                                ||||   ||||||||||
                                GGAC   AACGGGTTATC
                                  ___
GAM1368  MEN1    5'  CCTGGATTCTGCACACAG    39171        _   CCA
                                CCTGGAT TTGC   ATAG
                                ||||||| ||||  ||||
                                GGACCTA GACG   TGTC
                                    A   TG_
GAM1368  NLGN3   3'  CCTGGGGGCCCAATAG     33282       ATTT
                                CCTGG   GCCCAATAG
                                |||||   |||||||||
                                GGACC   CGGGTTATC
                                  CC__
GAM1368  NSF     5'  CTATTTCTTGCCCAATAG    41783     GA_
                                CTG   TTTGCCCAATAG
                                |||   ||||||||||||
                                GAT   GAACGGGTTATC
                                 AAA
GAM1368  PTGFR   3'  CCTGAATCTGACAATAG     9659          CC
                                CCTGGATTTG  CAATAG
                                |||||||||  ||||||
                                GGACTTAGAC  GTTATC
                                     T_
GAM1368  RBBP9   3'  CCTAGACCAATGTTGTCCAATA 43137        _____  C      III
           GC                    CCTGGAT    TTG CCAATAG   C
                                |||||||    ||| |||||||  |
                                GGATCTG    AAC GGTTATC   G
                                    GTTAC   A      III
GAM1368  RERE    3'  CCTGAATTTGAGCCAGTAG   29024         C_  A
                                CCTGGATTTG  CCA TAG
                                |||||||||  ||| |||
                                GGACTTAAAC  GGT ATC
                                     TC   C
GAM1368  TXK     3'  CCTGGATTTCCGAAACAAT   17765         G  ____
                                CCTGGATTT CC    CAAT
                                |||||||| ||    ||||
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                                GGACCTAAA GG    GTTA
                                    _ CTTT
GAM1369  EGLN3    3'  TATTTTAGGTGCTGAGAGTATG 35209     G    A   GG
              T                  TAT TTAG TGC  GGGAGTATGT
                                 ||| |||| |||  ||||||||||
                                 ATA AATC ACG  CTCTCATACA
                                   A   C   A_
GAM1369  GRM1     3'  GTTAGATGTTACTGTATGT    9138         CGGGGGA
                                 GTTAGATG      GTATGT
                                 ||||||||      ||||||
                                 CAATCTAC      CATACA
                                     AATGA__
GAM1369  GPR61    3'  AGGGAAGTAGGATGGACAGG   44263         T     ATT
                                 AGGGAAGTA GATGGA   GG
                                 ||||||||| ||||||   ||
                                 TCCCTTCAT CTACCT   CC
                                     C     GT_
GAM1369  GPRC5B   3'  TAAGGGAATAAAATTG      32176        AGTATG
                                 TAAGGGA     ATGGAATTG
                                 |||||||     |||||||||
                                 ATTCCCT     TATTTTAAC
                                     _______
GAM1369  SCA7     5'  GACTCTGTGGTGGAATTGGG   7307     AGTA_  A
                                 GA     TG TGGAATTGGG
                                 ||     || ||||||||||
                                 CT     AC ACCTTAACCC
                                   GAGAC  C
GAM1369  SH3BP2   3'  TAAGGGGATGGATTG       16638       AAGTAT     A
                                 TAAGGG      GATGGA TTG
                                 ||||||      |||||| |||
                                 ATTCCC      CTACCT AAC
                                     _______     _
GAM1369  TERF2    3'  AAGGAAGGGAATTG        24905        TATGAT
                                 AGGGAAG     GGAATTG
                                 |||||||     |||||||
                                 TTCCTTC     CCTTAAC
                                     _______
GAM1370  PPP2R5B  5'  AGGTGCTGGGTGAGA       26444        CGTCGTA
                                 AGGTGCT      GGTGAGA
                                 |||||||      |||||||
                                 TCCACGA      CCACTCT
                                     C_______
GAM1370  CAPN10   3'  TCAAGCATTTGCCCTGCC    35778    C      CGCG
                                 TC AGCATTT   GTCCTGCC
                                 || |||||||   ||||||||
                                 AG TCGTAAA   CGGGACGG
                                   T     _____
GAM1370  COL19A1  3'  CCCAGCATTTCTTGCTGCCC  12375          GCGGTC
                                 TCCAGCATTTC     CTGCCC
                                 ||||||||||      ||||||
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                                GGGTCGTAAAG     GACGGG
                                      AAC___
GAM1370 COX15    3'  TCCAGCATCTCTTTTTGC    38518          GCGGTCC
                                TCCAGCATTTC      TGC
                                ||||||||||      |||
                                AGGTCGTAGAG      ACG
                                      AAAA___
GAM1370 CYP21A2  3'  CCCGGCTGGCATCGGTCCTGCC 7982      A  ATTTCG
              C                  TCC GC     CGGTCCTGCCC
                                ||| ||     ||||||||||
                                GGG CG     GCCAGGACGGG
                                  C  ACCGTA
GAM1370 FAAH     3'  CAGGAGGGCGGTCCTGCC    11048     CATTTC
                                CAG     GCGGTCCTGCC
                                |||     ||||||||||
                                GTC     CGCCAGGACGG
                                  CTCC__
GAM1370 HOXC4    5'  TCCTGCATTCCTCCTGCC    31161     A      GCGG
                                TCC GCATTTC    TCCTGCC
                                ||| |||||||    |||||||
                                AGG CGTAAGG    AGGACGG
                                  A      _____
GAM1370 IRAK1    3'  TCCAGCGATCCTCCTGCC    11475       AT   GCGG
                                TCCAGC  TTC    TCCTGCC
                                ||||||  |||    |||||||
                                AGGTCG  AGG    AGGACGG
                                    CT   _____
GAM1370 KCNQ1    3'  CAGCGTGGGCTGGTCCTGCCC  6883      ATTTC  _
                                CAGC    GC GGTCCTGCCC
                                ||||    || ||||||||||
                                GTCG    CG CCAGGACGGG
                                  CACC_  A
GAM1370 PIG8     3'  GCAGAGCGGGTCCTGCC     22188     TTT  C
                                GCA   CG GGTCCTGCC
                                |||   || |||||||||
                                CGT   GC CCAGGACGG
                                  CTC  _
GAM1370 RAD51L1  3'  TCCAAGCAGTACGGTCCTG   39455      _   TTTC
                                TCCA GCA    GCGGTCCTG
                                |||| |||    |||||||||
                                AGGT CGT    TGCCAGGAC
                                  T   CA__
GAM1370 TGFBR3   3'  CAGCCATTGGTCCTGCCC    17488     ATTTCGC
                                CAGC      GGTCCTGCCC
                                ||||      ||||||||||
                                GTCG      CCAGGACGGG
                                  GTAA___
GAM1370 TRAF1    3'  TCCACCCGGTCCTG       24947      GCATT  G
                                TCCA    TC CGGTCCTG
                                ||||    || ||||||||
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                                AGGT    GG GCCAGGAC
                                  _____ _
GAM1370 TSG     3' CCCAGCATTTTCACCCTGTCC 34002        _  GGT   _
                                TCCAGCATTT CGC  CCTG CC
                                |||||||||| |||  |||| ||
                                GGGTCGTAAA GTG  GGAC GG
                                     A  ___   A
GAM1370 UBE2V1  3' CAGCATTTAGTGGTCCTG   35343       CGC
                                CAGCATTT  GGTCCTG
                                ||||||||  |||||||
                                GTCGTAAA  CCAGGAC
                                    TCA
GAM1370 USP6    5' CCCAGCATTTCCATCCACTTGC 45026         G  G  ___
                                TCCAGCATTTC CG TCC  TGC
                                |||||||||| || |||  |||
                                GGGTCGTAAAG GT AGG  ACG
                                      _ _  TGA
GAM1370 VHL     3' TCCACCTGGTCCTGC      8117      GCATT  GC
                                TCCA   TC  GGTCCTGC
                                ||||    ||  ||||||||
                                AGGT   GG  CCAGGACG
                                  _____ A_
GAM1370 WBSCR1  3' CCAGGCTGTGGTCCTGC    35267     CATTTC ___
                                CCAG    GC  GGTCCTGC
                                ||||    ||  ||||||||
                                GGTC    CG  CCAGGACG
                                  ______ ACA
GAM1370 ZNF136  3' TCCAGCATCTCCTG       40878        TCGCGG
                                TCCAGCATT    TCCTG
                                |||||||||    |||||
                                AGGTCGTAG    AGGAC
                                     _______
GAM1371 AKAP13  3' TGAGGAGCAGTGGGCGTCC  28487   T  C  GCG  C
                                TG GGA GC  AG GGGCGTCC
                                || ||| ||  || ||||||||
                                AC CCT CG  TC CCCGCAGG
                                 T  _ ___  A
GAM1371 HDAC4   5' GTGGACCGGCGGCGTCC    25778      G  CGA   G
                                GTGGAC CG  GCGG CGTCC
                                |||||| ||  |||| |||||
                                CACCTG GC  CGCC GCAGG
                                   _ ___   _
GAM1372 C8orf1  3' TACAATTTTCGAAGTACTTACC 20274      CCTC      GGG
            A                    TATAA   CGAAGTAC  ACCA
                                |||||   ||||||||  ||||
                                ATGTT   GCTTCATG  TGGT
                                   AAAA      AA_
GAM1372 PODXL   3' CTCCCACGGGACCA       23970     GAAG
                                CTCC   TACGGGACCA
                                ||||   ||||||||||
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                              GAGG   GTGCCCTGGT
                                ____
GAM1372 RLBP1   5' ACTTCCTGTCAGGACCA    7256    C  GAA  A
                              AC TCC   GT CGGGACCA
                              || |||   || ||||||||
                              TG AGG   CA GTCCTGGT
                               A  A__  _
GAM1373 CCNF    3' TGGATGAGGGGACAGTG    12079       TAATGT
                              TGGATGAGG     CAGTG
                              |||||||||     |||||
                              ACCTACTCC     GTCAC
                                   CCT___
GAM1373 ENAM    3' TGGTATAGAATGTCAGTGAT  36679    A  A  T
                              TGG TG GG AATGTCAGTGAT
                              ||| || || ||||||||||||
                              ACC AT TC TTACAGTCACTA
                                _  A  _
GAM1373 LILRB4  3' CTGGCTGGGGTTCAGTGA   27776    A  A   AATG
                              CTGG TG GGT    TCAGTGA
                              |||| || |||    |||||||
                              GACC AC CCA    AGTCACT
                                G  C  _____
GAM1373 PDE4B   5' CTGGATGAGGTGTCGGTGAT  15147         AAT   A
                              CTGGATGAGGT   GTC GTGAT
                              ||||||||||   ||| |||||
                              GACCTACTCCA   CAG CACTA
                                    ___  C
GAM1373 THBD    3' ACTGGATGGGGTGGAGCCTAGG 7419        A   AAT   _  T
           AT                   ACTGGATG GGT   GTC AG GAT
                              |||||||| |||   ||| || |||
                              TGACCTAC CCA   CGG TC CTA
                                  C   CCT   A  _
GAM1373 ADRA1B  3' CCCCCCACGATGTTTT     8619        AATGA  C  C
                              TCCCCCAC     GA GT TTT
                              ||||||||     || || |||
                              GGGGGGTG     CT CA AAA
                                   _____  A  _
GAM1373 BACH2   3' TCTGCCACAATGAGACTTTTC 34810    CC        GTC
                              TC  CCACAATGAGAC   TTTC
                              ||  ||||||||||||   ||||
                              AG  GGTGTTACTCTG   AAAG
                               AC          A__
GAM1373 CFL1    3' TCCCCCACAACTGGGGTGCC  24286         GAGAC_
                              TCCCCCACAAT     GTC
                              ||||||||||     |||
                              AGGGGGTGTTG     CGG
                                    ACCCCA
GAM1373 COLQ    3' CACCTTGGAGATGTCTTTCC  38693    AAT_   C
                              CAC    GAGA GTCTTTCC
                              |||    |||| ||||||||
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                                GTG   CTCT CAGAAAGG
                                  GAAC   A
GAM1373  CYP4F3   3'  CCGCACAAGCGTCTTTC    9454    C   ATG  A
                                CC CACA   AG CGTCTTTC
                                || ||||   || ||||||||
                                GG GTGT   TC GCAGAAAG
                                 C   ___  _
GAM1373  DAG1     3'  TCCCCCACAGGGGGACTGC   20527        ATGA  _
                                TCCCCCACA   GAC GT
                                |||||||||   ||| ||
                                AGGGGGTGT   CTG CG
                                     CCCC   A
GAM1373  GPR63    5'  CCACAAGAGTCCTT      36265      ATG   C
                                CCACA   AGA GTCTTT
                                |||||   ||| ||||||
                                GGTGT   TCT CAGGAA
                                  ___   _
GAM1373  GRP58    3'  TCCTCCCCAATGGTTTTC   23678    _  A    AGAC  C
                                TCC CCC CAATG   GT TTTC
                                ||| ||| |||||   || ||||
                                AGG GGG GTTAC   CA AAAG
                                  A  _    ____  _
GAM1373  GRPR     5'  CCCACAGCGTCTTTC      23682       ATGA A
                                CCCACA   G CGTCTTTC
                                ||||||   | ||||||||
                                GGGTGT   C GCAGAAAG
                                  ____ _
GAM1373  LFNG     3'  TCCCCTGCAATGAGCAT    45220      CA     A
                                TCCCC  CAATGAG CGT
                                |||||  ||||||| |||
                                AGGGG  GTTACTC GTA
                                   AC     _
GAM1373  OLFM1    3'  CCCCAGGTGAGCCCTTC    26766      CAA   GAC
                                CCCCA   TGA   GTCTTTC
                                |||||   |||   |||||||
                                GGGGT   ACT   CGGGAAG
                                   CC_   ___
GAM1373  OXCT     3'  TCCCCCACAAGAGGCATTC   7746         T   A   CTT
                                TCCCCCACAA GAG CGT   TC
                                |||||||||| ||| |||   ||
                                AGGGGGTGTT CTC GTA   AG
                                      _   C   ___
GAM1373  PCYT1A   3'  TCCCCAGTTGTCTTTC     22705      CACAATG  AC
                                TCCCC      AG  GTCTTTC
                                |||||      ||  |||||||
                                AGGGG      TC  CAGAAAG
                                   ________  AA
GAM1373  PYGM     5'  TCCCCTGCAATGGGAGGGTCT 24700      CA    A  C_
                                TCCCC  CAATG GA  GTCT
                                |||||  ||||| ||  ||||
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                                AGGGG  GTTAC CT  CAGA
                                  AC    C  CC
GAM1373 RERE    5' TCCCTGCCGTGACCTTTC   29036     CCACAA  A   GT
                                TCCC     TG GAC  CTTTC
                                ||||     || |||  |||||
                                AGGG     GC CTG  GAAAG
                                  ACG___  A  __
GAM1373 SERPINE1 3' CCCAGATGAAGGCGTCTTTCC 8286      CA    A_
                                CCCA  ATGAG  CGTCTTTCC
                                ||||  |||||  |||||||||
                                GGGT  TACTT  GCAGAAAGG
                                  C_    CC
GAM1373 SLC22A12 5' TCCCCCACGGTGGTGCCC   40336       AA  AGAC
                                TCCCCCAC  TG   GTCT
                                ||||||||  ||   ||||
                                AGGGGGTG  AC   CGGG
                                    CC  CA__
GAM1373 TBXAS1   5' CCCCCACAATGTGCTCTTTC  36290         AGACG
                                CCCCCACAATG    TCTTTC
                                ||||||||||    ||||||
                                GGGGGTGTTAC    AGAAAG
                                     ACG__
GAM1373 TEM8    3' TCCCTCCTGATGTTTCTTTCC 38192     _ ACAA   GACG
                                TCCC CC    TGA    TCTTTCC
                                |||| ||    |||    |||||||
                                AGGG GG    ACT    AGAAAGG
                                  A _____   ACAA
GAM1373 UBE2H    3' TCCTCCCCAAGTTTTT     17808    _   A   TGAGAC  C
                                TCC CCC CAA     GT TTT
                                ||| ||| |||     || |||
                                AGG GGG GTT     CA AAA
                                  A  _  _______  A
GAM1373 XK      3' CCAGCAATGAGAGGAAGTCT  34358    _      C___
                                CCA CAATGAGA    GTCT
                                ||| ||||||||    ||||
                                GGT GTTACTCT    CAGA
                                  C       CCTT
GAM1374 OPA1    3' TTAGAATCATTTCTGACTT   39271       ATCCTAAA
                                TTAGAAT       TCTGACTT
                                |||||||       ||||||||
                                AATCTTA       AGACTGAA
                                    GTAA_____
GAM1374 PTPN12   3' GAATACTATAAATCTGGCTTT  15921       CC       A
                                GAATAT  TAAATCTG CTTT
                                ||||||  |||||||| ||||
                                CTTATG  ATTTAGAC GAAA
                                    AT       C
GAM1374 RB1CC1   3' TCTGCATTTGAAATGGTTAG   31318     A        A
                                TCT TATTTGAAAT GTTAG
                                ||| |||||||||| |||||
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                                AGA GTAAACTTTA CAATC
                                  C         C
GAM1375 NCK2     3'  CGGGCAGCTCCACCG       44304     TGAAGC   A
                                CGG      GCA CTCCACCG
                                |||      ||| ||||||||
                                GCC      CGT GAGGTGGC
                                 _______  C
GAM1375 SHMT2    3'  TCGGTGAAGAGCTTCTGCTTCA 24011         C  AA  C___
             CCGTG                   TCGGTGAAG GC  CT    CACCGTG
                                |||||||||  ||  ||    |||||||
                                AGCCACTTC CG  GA    GTGGCAC
                                     T  AA  CGAA
GAM1375 SORBS1   3'  TCGGTGAAATGCTGCCGT    31715         C  AACTCCA
                                TCGGTGAAG GC      CCGT
                                |||||||||  ||      ||||
                                AGCCACTTT CG      GGCA
                                     A  AC_____
GAM1375 BSCL2    5'  GCGATCCAGACGCTGATACC   37218         A    AGC_
                                GTGATCCA ACGC    ACC
                                ||||||||  ||||    |||
                                CGCTAGGT TGCG    TGG
                                     C    ACTA
GAM1375 BTG2     3'  GCAGTGATTCACAGC       27617         CCAAA
                                GCAGTGAT    CGCAGC
                                ||||||||    ||||||
                                CGTCACTA    GTGTCG
                                     A____
GAM1375 COL4A5   3'  GCAGGATTAGTAGCACCG    37898      T   CCAAACGC
                                GCAG GAT       AGCACCG
                                ||||  |||       |||||||
                                CGTC CTA       TCGTGGC
                                  _   ATCA____
GAM1375 CXorf6   3'  GCTGTGACCCATGCAGCA    24241    A       AAC
                                GC GTGATCCA   GCAGCA
                                ||  ||||||||   ||||||
                                CG CACTGGGT   CGTCGT
                                 A       A__
GAM1375 D1S155E  3'  GCAGTGATCTAAGCAGCAGCA  28389         C  A _
                                GCAGTGATC AA C GCAGCA
                                |||||||||  ||  |  ||||||
                                CGTCACTAG TT G CGTCGT
                                     A  C T
GAM1375 RRM2B    3'  GCAATGATTTAAATACATGTAC 42721         CC   CG  GC_  C
             TGT                   GCAGTGAT  AAA  CA   AC GT
                                |||||||  |||  ||   ||  ||
                                CGTTACTA  TTT  GT   TG CA
                                     AA   AT  ACA  A
GAM1376 ZNF175   3'  TTTAATCTTGGATTTTCAGA   28370         CC    GCG
                                TTTAATCT  GGATT   TGGA
                                ||||||||  |||||   ||||
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                                AAATTAGA  CCTAA   GTCT
                                    A_    AA_
GAM1377 ACVR1B   3' AGCGCTACGATTACAGG    33757    A        ATGTG
                                AGC CTACGATTACA    GG
                                ||| ||||||||||    ||
                                TCG GATGCTAATGT    CC
                                  C        _____
GAM1377 GABRP    3' TAGCACCATTGGATGTGGG   30558       CGATTACA
                                TAGCACTA      ATGTGGG
                                ||||||||      |||||||
                                ATCGTGGT      TACACCC
                                    AACC____
GAM1377 CBR1     3' TATTTTCATCAATTACAATTTT 12039         CT   C
                                TATTTTCATCAA  TTAT GTTTT
                                ||||||||||||  |||| |||||
                                ATAAAAGTAGTT  AATG TAAAA
                                      __   T
GAM1377 FGF23    3' TTTTCATCAACTTGCCCCATT  33961          TA_
                                TTTTCATCAACTT   TCGTT
                                ||||||||||||   |||||
                                AAAAGTAGTTGAA   GGTAA
                                       CGG
GAM1378 TMEPAI   3' GGTCAGATTGCGAATACCTGGG 33617    _ T  ATA       AA
          GC                      GG CG GT   CGAATACCTG  GC
                                || || ||   ||||||||||  ||
                                CC GT TA   GCTTATGGAC  CG
                                 A  C  AC_        CC
GAM1378 ARHGEF12 3' TACTTCAAAAAATATATAC   31643            C
                                TATTTCAAAAAATATA AC
                                ||||||||||||||| ||
                                ATGAAGTTTTTTATAT TG
                                       A
GAM1379 BST2     3' CCGGAGGGAGGCTCTGGAG   20268     T      AG  GT
                                CCG GAGGGAGG  TC  GAG
                                ||| ||||||||  ||  |||
                                GGC CTCCCTCC  AG  CTC
                                  _       G_  AC
GAM1379 MAD      3' CGTGCAAGGGAGTTGTG     14308     AG  A    C
                                CGTG  GG GGAGT GTG
                                ||||  || ||||| |||
                                GCAC  TC CCTCA CAC
                                  GT  _    A
GAM1379 RARB     5' CACTCGAGGGGGAGGAAGTG  32057     C  TGA      TC
                                CAC CG   GGGAGGAG  GTG
                                ||| ||   ||||||||  |||
                                GTG GC   CCCTCCTT  CAC
                                  A  TCC       __
GAM1379 ADAT1    3' ACAGGTGTGCGCCACCATGC  28992    C   ACAT      C
                                AC GGT    CGTCGCCA GC
                                || |||    |||||||| ||
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                              TG CCA   GCGGTGGT CG
                               T  CAC_      A
GAM1379 CRACC   3' ACAGGTGCACACCACCACGC  34514   C  A  T GT
                              AC GGT CA C  CGCCACGC
                              || ||| || |  ||||||||
                              TG CCA GT G  GTGGTGCG
                               T  C  _ TG
GAM1379 CRAT    5' CACCGGGCAAAGTCCGCGC   19660      TA  TC  CG  A
                              CACCGG  CA  GT  CC CGC
                              ||||||  ||  ||  || |||
                              GTGGCC  GT  CA  GG GCG
                                 C_  TT  __  C
GAM1379 CRK     5' GGTGCCGCCGCCGCGC     40828    ACA      A
                              GGT   TCGTCGCC CGC
                              |||   |||||||| |||
                              CCA   GGCGGCGG GCG
                                C__      C
GAM1379 DMC1    3' ACAGGTGTGAGCCACCACGC  28197   C  ACATC
                              AC GGT    GTCGCCACGC
                              || |||    ||||||||||
                              TG CCA    CGGTGGTGCG
                               T  CACT_
GAM1379 DUSP7   5' CCTGCCCCCGTCGCCGCGC   42268   G  ACA      A
                              CC GT   TCGTCGCC CGC
                              || ||   |||||||| |||
                              GG CG   GGCAGCGG GCG
                               A  GG_      C
GAM1379 FOXE1   3' CACCGGGTGCCTACGC     20938      TACATC  C  _
                              CACCGG     GT GCC ACGC
                              ||||||     || ||| ||||
                              GTGGCC     CA CGG TGCG
                                 _______ _  A
GAM1379 GALNT7  3' ACAGGTATGCGCCACCATGC  38350   C   CAT      C
                              AC GGTA   CGTCGCCA GC
                              || ||||   |||||||| ||
                              TG CCAT   GCGGTGGT CG
                               T   AC_      A
GAM1379 IL10    3' ACAGGTGCGCGCCACCATGC  8192    C  ACAT     C
                              AC GGT    CGTCGCCA GC
                              || |||    |||||||| ||
                              TG CCA    GCGGTGGT CG
                               T  CGC_      A
GAM1379 ITGAL   3' ACAGGTGTGTGCCACCACGC  13615   C  ACATC
                              AC GGT    GTCGCCACGC
                              || |||    ||||||||||
                              TG CCA    CGGTGGTGCG
                               T  CACA_
GAM1379 LUZP1   3' ACAGGTGTGAGCCACCACGC  37954   C  ACATC
                              AC GGT    GTCGCCACGC
                              || |||    ||||||||||
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                              TG CCA    CGGTGGTGCG
                               T  CACT_
GAM1379 MSH3    3' ACAGGTGTGCGCCACCATGC  14629   C  ACAT     C
                              AC GGT   CGTCGCCA GC
                              || |||   |||||||| ||
                              TG CCA   GCGGTGGT CG
                               T  CAC_     A
GAM1379 MYH11   3' CACAGGTGTGTACCACCACGC 35625    C  ACATCG
                              CAC GGT    TCGCCACGC
                              ||| |||    |||||||||
                              GTG CCA    GGTGGTGCG
                                T  CACAT_
GAM1379 RAB7L1  3' ACAGGTGTGAGCCACCACGC  19428   C  ACATC
                              AC GGT   GTCGCCACGC
                              || |||   ||||||||||
                              TG CCA   CGGTGGTGCG
                               T  CACT_
GAM1379 TAF1    3' ACAGGTGTGAGCCACCACGC  39885   C  ACATC
                              AC GGT   GTCGCCACGC
                              || |||   ||||||||||
                              TG CCA   CGGTGGTGCG
                               T  CACT_
GAM1379 TSN     3' ACAGGTGTGAGCCACCACGC  21489   C  ACATC
                              AC GGT   GTCGCCACGC
                              || |||   ||||||||||
                              TG CCA   CGGTGGTGCG
                               T  CACT_
GAM1380 ADAR    3' TTCCCAGCTGCCGGAG     31914       CA  ACG
                              TTCCCAGT TGT  CGGAG
                              |||||||| |||  |||||
                              AAGGGTCG ACG  GCCTC
                                   __  ___
GAM1380 AFG3L2  3' TTCCCAGTGCCTGGAG     45544       CAT ACGC
                              TTCCCAGT  GT   GGAG
                              |||||||  ||   ||||
                              AAGGGTCA  CG   CCTC
                                   ___ GA__
GAM1380 ASTN    3' TTCCCAGTCATGAGGGTGGGGA 42962          TACGC A
                              TTCCCAGTCATG    GG GA
                              ||||||||||||    || ||
                              AAGGGTCAGTAC    CC CT
                                     TCCCA  C
GAM1380 ASTN    3' TTCCCAATCATGCAGATGGAGA 42961          CGC
                              TTCCCAGTCATGTA  GGAGA
                              ||||||||||||||  |||||
                              AAGGGTTAGTACGT  CCTCT
                                     CTA
GAM1380 C2      3' TTCCCAGCTTGTGTGCG    6298        CA  AC
                              TTCCCAGT TGT GCG
                              |||||||| ||| |||
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                                AAGGGTCG  ACA  CGC
                                    A_   CA
GAM1380 CA12    3' TTCTCAGTCATGGCACTGA   10253    C      TA  G
                                TTC CAGTCATG  CGC GA
                                ||| ||||||||  ||| ||
                                AAG GTCAGTAC  GTG CT
                                  A      C_   A
GAM1380 CA5B    5' TTCCCAGTTAAGTTGCAG    28514       CAT  AC
                                TTCCCAGT   GT  GCGG
                                ||||||||   ||  ||||
                                AAGGGTCA   CA  CGTC
                                    ATT  A_
GAM1380 CAPN2   3' TTCCCAGTTGGCTCATGGGA  11972       CAT  A  C  A
                                TTCCCAGT   GT CG GG GA
                                ||||||||   || || || ||
                                AAGGGTCA   CG GT CC CT
                                    AC_  A  A  _
GAM1380 COL4A5  3' TTCCCAGTTCTGTACAAGCAGA 37900       CA   __
                                TTCCCAGT  TGTAC  GCGGA
                                ||||||||  |||||  |||||
                                AAGGGTCA  ACATG  CGTCT
                                    AG    TT
GAM1380 CRHR1   3' TTCCCAGTGGTGTCGGA    20454       CA   ACG
                                TTCCCAGT  TGT   CGGA
                                ||||||||  |||   ||||
                                AAGGGTCA  ACA   GCCT
                                    CC  ___
GAM1380 DXS1283E 3' TCCTCAGTCATGTGGA     43356    _      ACGC
                                TCC CAGTCATGT   GGA
                                ||| |||||||||   |||
                                AGG GTCAGTACA   CCT
                                  A      _____
GAM1380 EPS15   5' TTCCATCATGCAAGGGAG    12750     CA      CGC
                                TTCC  GTCATGTA  GGAG
                                ||||  ||||||||  ||||
                                AAGG  TAGTACGT  CCTC
                                  __      TC_
GAM1380 GATA4   3' TTCCCAGTTGTTGTTCTGGA  13113       CA_  ACGC
                                TTCCCAGT  TGT   GGA
                                ||||||||  |||   |||
                                AAGGGTCA  ACA   CCT
                                    ACA  AGA_
GAM1380 ICAM1   3' TTCCCAGTTGTATGTCCTCA  43439       C__   ACG
                                TTCCCAGT  ATGT  CG
                                ||||||||  ||||  ||
                                AAGGGTCA  TACA  GT
                                    ACA   GGA
GAM1380 ICMT    3' TTCCCAGCATGACAGAG     29663       T   TAC
                                TTCCCAG CATG  GCGGAG
                                ||||||| ||||  ||||||
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                                AAGGGTC GTAC   TGTCTC
                                    _   ___
GAM1380 LARGE    3' TCCCCAGTTATGATGGGA    21867       C   TACGC
                                TTCCCAGT ATG    GGA
                                |||||||| |||    |||
                                AGGGGTCA TAC    CCT
                                    A   TAC__
GAM1380 LEF1     5' TTCCCGCTTCGCGGAG     32215      A  CATGTA
                                TTCCC GT     CGCGGAG
                                ||||| ||     |||||||
                                AAGGG CG     GCGCCTC
                                   _ AA____
GAM1380 MAP1A    3' TTCCCAGTCGTTTGGCAGAGA  14351        ATGTAC
                                TTCCCAGTC     GCGGAGA
                                |||||||||     |||||||
                                AAGGGTCAG     CGTCTCT
                                    CAAAC_
GAM1380 MUC4     3' TCCCCAGTCAGGTTTGGAG   39675        T  ACGC
                                TTCCCAGTCA GT    GGAG
                                |||||||||| ||    ||||
                                AGGGGTCAGT CA    CCTC
                                    C  AA__
GAM1380 NDUFB3   5' TTCCCAGTATATGTGCA     14745       C    AC
                                TTCCCAGT ATGT  GCG
                                |||||||| ||||  |||
                                AAGGGTCA TATA  CGT
                                    _   CA
GAM1380 NDUFB9   5' TCCCCGGCCGCGCGGAGA    22673      A   ATGTA
                                TTCCC GTC    CGCGGAGA
                                ||||| |||    ||||||||
                                AGGGG CGG    GCGCCTCT
                                   C   C____
GAM1380 STARD4   3' TTCCCAGCTATTCAGGAG    40127       CA   A  C
                                TTCCCAGT  TGT CG GGAG
                                ||||||||  ||| || ||||
                                AAGGGTCG  ATA GT CCTC
                                    __   A  _
GAM1380 SULT2B1  5' CTCCCAGTTACTCCGGAG    21417       CATG   G_
                                TTCCCAGT    TAC  CGGAG
                                ||||||||    |||  |||||
                                GAGGGTCA    ATG  GCCTC
                                    _____   AG
GAM1380 TFAP2C   3' TTCCCAGTCTGTGCGGTGGAGA 17407        A   A  C_
                                TTCCCAGTC TGT CG  GGAGA
                                ||||||||| ||| ||  |||||
                                AAGGGTCAG ACA GC  CCTCT
                                    _  C  CA
GAM1380 TLR4     5' TTCTGGTCTCACGCAGGAGA   17568     CCA   ATG    _
                                TTC   GTC   TACGC GGAGA
                                |||   |||   ||||| |||||
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                                AAG  CAG  GTGCG CCTCT
                                  AC_  A__    T
GAM1380  TLX1    5'  CTCCTGGCTGCGCGGAG    24333     CA  CA  TA
                                TTCC  GT  TG  CGCGGAG
                                ||||  ||  ||  |||||||
                                GAGG  CG  AC  GCGCCTC
                                  AC  __  __
GAM1380  TLX1    5'  CCATTGGCTGTGCGCGGAGA  24330    GTCA_  A
                                CCA    TGT CGCGGAGA
                                |||    ||| ||||||||
                                GGT    ACA GCGCCTCT
                                  AACCG  C
GAM1380  EXTL2   5'  CTCCATTAGCTGGATTAA    11019           ACCT
                                CTCCATTGGCTGGG   TTAA
                                ||||||||||||||   ||||
                                GAGGTAATCGACCT   AATT
                                         ____
GAM1380  IL17R   3'  CCTTCATGGCTGGGGCC    30740    C  T     A
                                CCT CAT GGCTGGG CC
                                ||| ||| ||||||| ||
                                GGA GTA CCGACCC GG
                                  A  _     C
GAM1380  PROML1  3'  CTTCATTGCTGATCACTTT   25686   C    G   GAC
                                CT CATTG CTGG  CTTT
                                || ||||| ||||  ||||
                                GA GTAAC GACT  GAAA
                                 A    _   AGT
GAM1380  PXN     3'  TCCATGGCCCCTTT      16031      T   GGGA
                                TCCAT GGCT   CCTTT
                                ||||| ||||   |||||
                                AGGTA CCGG   GGAAA
                                   _  ____
GAM1380  TMSB4Y  3'  CCTCCATTGTCAGCAGGTCTTT 20087        ___  T  AC
                                CCTCCATTG  GC GGG  CTTT
                                |||||||||  || |||  ||||
                                GGAGGTAAC  CG TCC  GAAA
                                     AGT  _  A_
GAM1380  WWP2    3'  CCTTCATTGGCTGAGAATGAAT 41452    C        CCT__
           TAAC                  CCT CATTGGCTGGGA    TTAAC
                                ||| ||||||||||||    |||||
                                GGA GTAACCGACTCT    AATTG
                                  A          TACTT
GAM1381  ACPT    3'  CGGGCCGGGGCAGTCAGC    38889   A  TAC  A
                                CG GGC  CG GGGCAGTCAGC
                                || |||  || ||||||||||
                                GC CCG  GC CCCGTCAGTCG
                                 _  ___  _
GAM1381  ATF5    5'  CGAGGCTACAGAGCCATGGCC  28936        CG    AGTCA
                                CGAGGCTAC  AGGGC    GCC
                                |||||||||  |||||    |||
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                                GCTCCGATG  TCTCG    CGG
                                    __    GTAC_
GAM1381  ATP6V1G2  3'  CGAGGCTACCAAGTTAAGTAGC 39626          GGC   C
                                CGAGGCTACCGAG   AGT AGC
                                |||||||||||||   ||| |||
                                GCTCCGATGGTTC   TCA TCG
                                      AAT   _
GAM1381  CD79A    3'  CGAGGCTGCTACAATCAGC   34646       ACCGAGG
                                CGAGGCT      GCAGTCAGC
                                |||||||      |||||||||
                                GCTCCGA      TGTTAGTCG
                                   CGA____
GAM1381  CH25H    3'  CAAGGCTATTGAGGTGAGC   19550        CC   GC
                                CGAGGCTA  GAGG  AGT
                                ||||||||  ||||  |||
                                GTTCCGAT  CTCC  TCG
                                     AA   AC
GAM1381  CYFIP2   5'  GAGGCTACCGCAGGGCCCCGCG 43909         _    AGTCA
              CC                  GAGGCTACCG AGGGC    GCC
                                |||||||||| |||||    |||
                                CTCCGATGGC TCCCG    CGG
                                     G    GGGCG
GAM1381  ITGA2    3'  AGGTTACTGCCAGTCAGCC   13599    C  CGAGGG
                                AGG TAC     CAGTCAGCC
                                |||  |||     |||||||||
                                TCC ATG     GTCAGTCGG
                                  A  ACG___
GAM1381  MNT      5'  CGAGAGCTGCCGGGGGCGCGCC 33711     _  A  A   A_
                                CGAG GCT CCG GGGC  GTC
                                |||| ||| ||| ||||  |||
                                GCTC CGA GGC CCCG  CGG
                                  T  C  C   CG
GAM1381  NDUFA10  3'  GGCTGCCGAGAGCTGGCC    21234     A      A_
                                GGCT CCGAGGGC  GTC
                                |||| ||||||||  |||
                                CCGA GGCTCTCG  CGG
                                  C       AC
GAM1381  OSM      3'  CAAGGCAGGGGGGCAGTCAGCC 33910      TACCGA
                                CGAGGC     GGGCAGTCAGCC
                                ||||||     ||||||||||||
                                GTTCCG     CCCGTCAGTCGG
                                   TCCC__
GAM1381  PCDH11X  5'  GAGGCTATTCAGGCAGCC    37303       CCGA
                                GAGGCTA    GGGCAGTC
                                |||||||    ||||||||
                                CTCCGAT    TCCGTCGG
                                    AAG_
GAM1381  PCDH11Y  5'  GAGGCTATTCAGGCAGCC    37343       CCGA
                                GAGGCTA    GGGCAGTC
                                |||||||    ||||||||
```

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                                CTCCGAT   TCCGTCGG
                                   AAG_
GAM1381  PHB     3'  CGGGGCTGTGGCCCAGTCAGCC 15263    A   ACCGAG  __
                                CG GGCT    GGC  AGTCAGCC
                                || ||||     |||  ||||||||
                                GC CCGA    CCG  TCAGTCGG
                                 C   CA____  GG
GAM1381  SEZ6L   5'  CGGGGCTCCTGAGGGCAG   34420   A   A  _
                                CG GGCT CC GAGGGCAG
                                || |||| || ||||||||
                                GC CCGA GG CTCCCGTC
                                 C   _ A
GAM1381  SHOX    5'  CGGGGCTGGCGAGCAGCC   27819   A   ACCGA
                                CG GGCT    GGGCAGTC
                                || ||||    ||||||||
                                GC CCGA    CTCGTCGG
                                 C   CCG__
GAM1381  TLL2    5'  CGAGGCAACCGGGAAGCAGCC  29749      T   A   C  T
                                CGAGGC ACCG GGG AG CAGCC
                                |||||| |||| ||| || |||||
                                GCTCCG TGGC CCT TC GTCGG
                                   T   _  _ _
GAM1381  CASP8   5'  TCCCTCCATGGCCTCACTTCC  37880      GAC     TCG
                                TCCCTC   GGCCTCG   TCC
                                ||||||   |||||||   |||
                                AGGGAG   CCGGAGT   AGG
                                   GTA     GA_
GAM1381  HHEX    3'  ACGAGGTCAGTCGTCCCA    15564     CC  _
                                ACGG  TC GTCGTCCCA
                                ||||  || |||||||||
                                TGCT  AG CAGCAGGGT
                                  CC  T
GAM1381  LYL1    3'  CCTTGACGGCCCTGGGCCG   24578    C      C__
                                CCT GACGGCCT   GTCG
                                ||| ||||||||   ||||
                                GGA CTGCCGGG   CGGC
                                  A       ACC
GAM1381  NFE2L2  5'  TCCCCGACGGCGGCCCTGTTCC 26088     T     __  GTCG
                                TCCC CGACGGC  CTC    TCC
                                |||| |||||||  |||    |||
                                AGGG GCTGCCG  GGG    AGG
                                  _      CC   ACA_
GAM1381  OGG1    5'  CTCCTCGGATTGTCGTCCC   32563    GA   CCTC
                                CTC  CGG   GTCGTCCC
                                |||  |||   ||||||||
                                GAG  GCC   CAGCAGGG
                                  GA   TAA_
GAM1382  ADCY8   5'  GGGGCGGAGCTGGGGGCGG   10014     A    G    A
                                GGGG GGAGC GGGGG GG
                                |||| ||||| ||||| ||
```

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                                CCCC CCTCG CCCCC CC
                                  G    A    G
GAM1382 AQP5     5' GGGGGGGCAGGGGGCGG     11636      A A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ _       G
GAM1382 AR       5' GGGGGGCGGGTGGGGAGAAGGG 6244      A A    __       C
                                GGG GG GCGGG  GGGAGGAG GG
                                ||| || |||||  |||||||| ||
                                CCC CC CGCCC  CCCTCTTC CC
                                  _ _    AC      _
GAM1382 ARHG     5' GGGGGAGCTGGGGGCGG     11686     A    G    A
                                GGG GGAGC GGGGG GG
                                ||| ||||| ||||| ||
                                CCC CCTCG CCCCC CC
                                  _    A    G
GAM1382 ARHGDIA  3' GGGGAGGGGCTGGGGGGG    20213       A G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCCC CC
                                    C A    _
GAM1382 B3GAT1   5' GGAGAGGGGCGGCCACGGGCGG 33005       A   GGGGA A
                                GGGGAGG GCGG    GG GCGG
                                ||||||| ||||    || ||||
                                CCTCTCC CGCC    CC CGCC
                                    C   GGTG_ _
GAM1382 C1orf6   5' GAGGAGGAGGAGGGGCGG    33527         C    A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CTCCTCCTC CTCCCC CC
                                     _    G
GAM1382 C1QG     3' GGGGAGGGGGTGCAGTGGGGGT 41689       A___  __    A
             GG                   GGGGAGG   GCG  GGGGG GG
                                ||||||    |||  ||||| ||
                                CCCCTCC    CGT  CCCCC CC
                                    CCCA   CA    A
GAM1382 CACNA2D2 5' GGGGAGGGGGGGGCAG      25720       AGC    G
                                GGGGAGG   GGGGG AG
                                |||||||   ||||| ||
                                CCCCTCC   CCCCC TC
                                    ___    G
GAM1382 CACNG6   5' GGGCGGGAGCGAGGAGCG    36698    A     _
                                GG GCGGGGG GAGGAGCG
                                || ||||||| ||||||||
                                CC CGCCCTC CTCCTCGC
                                  _     G
GAM1382 CALM3    3' GGGGTGGGGTGGGGAGG     23242     A AGC  _
                                GGGG GG   GG GGGGAGG
                                |||| ||   || |||||||
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                                CCCC CC   CC CCCCTCC
                                  A ___ A
GAM1382 CALR     3' GGGGAGGGGGTGGGGGAGAGTG 41774       AGCG     G  C
                G                GGGGAGG   GGGGGAG AG GG
                                 ||||||| ||||||| || ||
                                 CCCCTCC   CCCCCTC TC CC
                                    CCCA     _ A
GAM1382 CAPON    5' GGGGAGCGGTGGGGCTTGCGG 41931    A    _   AGGA
                                 GG GGAGCGG GGGG   GCGG
                                 || ||||||| ||||   ||||
                                 CC CCTCGCC CCCC   CGCC
                                  _     A  GAA_
GAM1382 CAPON    5' GGGGAGGAGGTGGCGGCGGGAG 41933        CG  G  A_
                CGG                 GGGGAGGAG  GG GG  GGAGCGG
                                 |||||||||  || ||  |||||||
                                 CCCCTCCTC  CC CC  CCTCGCC
                                      CA  G  GC
GAM1382 CDC25B   5' GGGCGAGGGGTGGGGGGGG   34856    _   AGC    A
                                 GGG GAGG   GGGGGG GG
                                 ||| ||||   |||||| ||
                                 CCC CTCC   CCCCCC CC
                                   G   CCA    _
GAM1382 COL11A2  3' GGGGAGGACAGGGGTGG    38778       G    GA
                                 GGGGAGGA CGGGGG  GG
                                 |||||||| ||||||  ||
                                 CCCCTCCT GTCCCC  CC
                                     _     A_
GAM1382 COL1A1   3' GGGCAGGAGCGGGCTGAGG   6377     G       GG
                                 GGG AGGAGCGGG  GAGG
                                 ||| |||||||||  ||||
                                 CCC TCCTCGCCC  CTCC
                                   G        GA
GAM1382 CSNK1G2  3' GGGGCAGGAGTGGGGTAGGGCG 10619     _    C   GG   A
                G                 GGGG AGGAG GGGG  AGG GCGG
                                  |||| ||||| ||||  ||| ||||
                                  CCCC TCCTC CCCC  TCC CGCC
                                    G    A   A_  _
GAM1382 CST1     3' GGGTGGGAGTGGGTGGTGG   12495    GA   C  G  A
                                 GGG  GGAG GGG GG GG
                                 |||  |||| ||| || ||
                                 CCC  CCTC CCC CC CC
                                   AC    A   A  A
GAM1382 CTRL     3' GGAGGAGGGGTGGGGGCCCCGG 12523       C  _  A  AG_
                                 GGAGGAG GGG GGG GG   CGG
                                 ||||||| ||| ||| ||   |||
                                 CCTCCTC CCC CCC CC   GCC
                                     _  A  _  GGG
GAM1382 DES      3' GGGGAGGGCGTGGGGAGG    43573       A  G
                                 GGGGAGG GCG GGGGAGG
                                 ||||||| ||| |||||||
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                                CCCCTCC CGC CCCCTCC
                                   _  A
GAM1382 DLX2    3' GGGGAGGGCGGGCAGGCG   20595       A   G  AGGA
                                GGGGAGG GCGGG GG   GCG
                                ||||||| ||||| ||   |||
                                CCCCTCC CGCCC TC   CGC
                                   _   G ____
GAM1382 DNMT3L  5' GGGGAGGGGCGGGGGCGG   30068       A     GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                   C     G_
GAM1382 DNMT3L  5' GGGGGCGGGGAGGGGCG    30072     AGGA      A  A
                                GGGG   GCGGGGGG GG GCG
                                ||||   |||||||| || |||
                                CCCC   CGCCCCTC CC CGC
                                  ____      _ _
GAM1382 ED1     5' AGGGAGGAGGAGGGGCGG   10819        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                TCCCTCCTC CTCCCC CC
                                   _    G
GAM1382 EGFL5   3' GGGGGGGGCAGGGGGCGG   44531     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ C      G
GAM1382 EGLN1   5' GGGGAGGGCCGAGGGGCGG  35174       A  G    AGGA
                                GGGGAGG GC GGGGG   GCGG
                                ||||||| || |||||   ||||
                                CCCCTCC CG CTCCC   CGCC
                                   _ G   ____
GAM1382 EIF4G1  3' GGGGAGGAGAGGGACACCTGGC 22409        C   GGAGGA
           GG                    GGGGAGGAG GGGG    GCGG
                                |||||||| ||||    ||||
                                CCCCTCCTC CCCT    CGCC
                                     T   GTGGAC
GAM1382 EMX2    5' GGGTGGGGGTGGGGGGAAG  44695    GA  AGC
                                GGG  GG  GGGGGGAGG
                                |||  ||  |||||||||
                                CCC  CC  CCCCCCTTC
                                  AC  CCA
GAM1382 EPS15   5' GGGGAGGAGGCGGAGGGAGCGG 12747        _      GGA
                                GGGGAGGAG CGGGGGGA  GCGG
                                |||||||| ||||||||  ||||
                                CCCCTCCTC GCCTCCCT  CGCC
                                     C     ___
GAM1382 FBXL11  3' GGGGCGGGGTGGGGGGAAG  29438     A  AGC
                                GGGG GG  GGGGGGAGG
                                |||| ||  |||||||||
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                                CCCC CC   CCCCCCTTC
                                  G  CCA
GAM1382  FCN2     3'  GGGAGGAGTGTGGGGGTGG   31892        CG_    A
                                GGGAGGAG   GGGGG GG
                                ||||||||   ||||| ||
                                CCCTCCTC   CCCCC CC
                                     ACA    A
GAM1382  FHIT     3'  GGGGAGAGGCGGGGGGGCG   12875       GA      AGGA
                                GGGGAG  GCGGGGGG   GCG
                                ||||||  ||||||||   |||
                                CCCCTC  CGCCCCCC   CGC
                                   TC      _____
GAM1382  FOS      5'  GGGCGAGGGGCCGAGGGGCGG  23519     _   A  G    AGGA
                                GGG GAGG GC GGGGG   GCGG
                                ||| |||| || |||||   ||||
                                CCC CTCC CG CTCCC   CGCC
                                  G   C  G   _____
GAM1382  FOXG1B   5'  GGGGGGGCGGCGGGCGG    23512     A  A   G   A
                                GGGG GG GCGG GGG GG
                                |||| || |||| ||| ||
                                CCCC CC CGCC CCC CC
                                  _ _   G   G
GAM1382  FXR2     5'  GGGGAGCCGCGGGGGGCGG   22166       GA      A
                                GGGGAG  GCGGGGGG GG
                                ||||||  |||||||| ||
                                CCCCTC  CGCCCCCC CC
                                   GG       G
GAM1382  FXYD1    3'  GGGAAGGGGCGGCGGAGGGGGC 34865       A   G  GA  A
            GG                    GGGGAGG GCGG GG  GG GCGG
                                ||||||| |||| ||  || ||||
                                CCCTTCC CGCC CC  CC CGCC
                                   C   G  TC  C
GAM1382  GAP43    3'  GGGGAGGGTGGGGATGTGG   13048       AGC    GA_
                                GGGGAGG   GGGGG   GG
                                |||||||   |||||   ||
                                CCCCTCC   CCCCT   CC
                                   CA_    ACA
GAM1382  GDF2     5'  GGGGAGGAGCTGGGAAGGAGCG 32129         GG
            G                    GGGGAGGAGC  GGGGAGGAGCGG
                                ||||||||||  ||||||||||||
                                CCCCTCCTCG  CCCTTCCTCGCC
                                     A_
GAM1382  GNA15    3'  GGGCAGGAGTACCCTGGGGGGC 40907    G    C_____     A
            GG                    GGG AGGAG     GGGGGG GG
                                |||  |||||     |||||| ||
                                CCC TCCTC     CCCCCC CC
                                  G    ATGGGA     G
GAM1382  GRB14    5'  GGGGAGGAGCGGCCGGTGG   21051          GG  A
                                GGGGAGGAGCGG  GG GG
                                ||||||||||||  || ||
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                                CCCCTCCTCGCC  CC CC
                                      GG  A
GAM1382  GRB14    5'  GGGGAGAGGGGAGGAGCGG   21050       GAGCG
                                GGGGAG    GGGGGAGGAGCGG
                                ||||||    ||||||||||||
                                CCCCTC    TCCCCTCCTCGCC
                                  _____
GAM1382  GRB7     3'  GGAGAGGGGTCAGGAGG     23640     C   GG    C
                                GGAG GGGG  AGGAG G
                                |||| ||||  ||||| |
                                CCTC CCCC  TCCTC C
                                  T   AG    A
GAM1382  GTF2IRD1 5'  GGAGAGGAGCGGAGAGCGG   32261             A
                                GGGGAGGAGCGGGGGG GG
                                |||||||||||||| ||
                                CCTCTCCTCGCCTCTC CC
                                       G
GAM1382  HNRPDL   5'  GAGGAGGGGCGGGGGCTGG   24174       A     GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CTCCTCC CGCCCCC  CC
                                    C      GA
GAM1382  HOXC4    3'  GGGGAGGGTGGGGGCATGG   31155       AGC    GA_
                                GGGGAGG   GGGGG   GG
                                |||||||   |||||   ||
                                CCCCTCC   CCCCC   CC
                                    CA_    GTA
GAM1382  HYOU1    3'  GGGGTGGGGTGAGGGGTGG   40638     A  AGC     A
                                GGGG GG   GGGGGG GG
                                |||| ||   |||||| ||
                                CCCC CC   CTCCCC CC
                                  A  CCA     A
GAM1382  IGFBP2   3'  GGAGAGGGGCGGGGGGCAGG   8260        A      _
                                GGGGAGG GCGGGGGG AGG
                                ||||||| |||||||| |||
                                CCTCTCC CGCCCCCC TCC
                                    C       G
GAM1382  INSR     3'  GGGGGCGGGTGGGGGGAACG   43380     AGGA    _  A
                                GGGG   GCGGG GGG GGAGCG
                                ||||   ||||| ||| ||||||
                                CCCC   CGCCC CCC CCTTGC
                                  ____    A   C
GAM1382  ITGA6    5'  GGAGGGGAGCGGGGACCTGCAG 6832      A        GAGG_
            CGG                   GGGG GGAGCGGGGG    AGCGG
                                ||||| ||||||||||    |||||
                                CCTC CCTCGCCCCT    TCGCC
                                  C         GGACG
GAM1382  JAM2     5'  GGGCGAGGAGCTGGGGGCGG   34546    _     G    A
                                GGG GAGGAGC GGGGG GG
                                ||| ||||||| ||||| ||
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                                CCC CTCCTCG CCCCC CC
                                  G      A    G
GAM1382  JUNB     3'  GGGGAGGGCAGGGGGCGG    13760        A       A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGTCCCCC CC
                                   _       G
GAM1382  KCNC3    3'  GGGAAGGGGCGGGGGGGACCG  22508        A       AG  G
                                GGGGAGG GCGGGGGG  GA CG
                                ||||||| ||||||||  || ||
                                CCCTTCC CGCCCCCC  CT GC
                                   C       __ G
GAM1382  KCNC3    5'  GGGGGGCGGGGCGGGAGGGGCG 22517     A  A     __     A
            G                    GGG GG GCGGGG  GGAGG GCGG
                                ||| || ||||||  ||||| ||||
                                CCC CC CGCCCC  CCTCC CGCC
                                  _ _     GC    C
GAM1382  KCNC3    5'  GGGAGGGGCGGGGACGCAGGGG 22511       A      G__   A
            CGG                    GGGAGG GCGGGGG   AGG GCGG
                                |||||| |||||||   ||| ||||
                                CCCTCC CGCCCCT   TCC CGCC
                                   C      GCG   C
GAM1382  KCNC3    3'  GGGGGGGGGGTGGGGGGGG    22520      A  AGC     A
                                GGGG GG   GGGGGG GG
                                |||| ||   |||||| ||
                                CCCC CC   CCCCCC CC
                                  C  CCA     _
GAM1382  KCNF1    3'  GGGGAGGGTTGGGGGGACACAG 13837        AGC      GGA
                                GGGGAGG   GGGGGGA   GCGG
                                |||||||   |||||||   ||||
                                CCCCTCC   CCCCCCT   TGTC
                                   CAA      G__
GAM1382  KCNK3    3'  GGGGATGAGGAAGGGGAG    13909      G   CG
                                GGGGA GAG  GGGGGAG
                                ||||| |||  |||||||
                                CCCCT CTC  TCCCCTC
                                  A   CT
GAM1382  KCNQ2    5'  GGGGCGGAGCGCGGGGGGCGG  41512      A    _    AGGA
                                GGGG GGAGCG GGGGG   GCGG
                                |||| |||||| |||||   ||||
                                CCCC CCTCGC CCCCC   CGCC
                                  G     G   _____
GAM1382  LASS1    3'  GGAGGGGGTGGAGGGGCG    34609      C   _    A
                                GGAG GGGG GGAGG GCG
                                |||| |||| ||||| |||
                                CCTC CCCC CCTCC CGC
                                  _   A    C
GAM1382  LBX1     3'  GGGGAGGAGGCGGGAGTGG   27288          _     GA
                                GGGGAGGAG CGGGGG  GG
                                ||||||||| ||||||  ||
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                                CCCCTCCTC GCCCTC  CC
                                     C     A_
GAM1382  LRP1    5'  GGAGGGGGGGTGGGGGGCG   14216     C     A__ A
                                GGAG GGGGGG   GG GCG
                                |||| ||||||   || |||
                                CCTC CCCCCC   CC CGC
                                  _     ACC  C
GAM1382  LRP1    5'  GGCGGGGAGGGGGGGTGG    14217    _ A   C     A
                                GG GG GGAG GGGGGG GG
                                || || |||| |||||| ||
                                CC CC CCTC CCCCCC CC
                                 G  _   _     A
GAM1382  LSP1    3'  GGGGAGGGCGGGGGCGG     14239        A      GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                   _      G_
GAM1382  MAP3K10  5'  GGGGAGGGGCCGGGGGCTGCGG 42758        A  G    AGGA
                                GGGGAGG GC GGGGG    GCGG
                                ||||||| || |||||    ||||
                                CCCCTCC CG CCCCC    CGCC
                                    C  G    GA__
GAM1382  MGMT    5'  GGGGCGGCGGGGGGGGGCG    14493      AGGA       A GA
                                GGGG   GCGGGGGG G  GCG
                                ||||   |||||||| |  |||
                                CCCC   CGCCCCCC C  CGC
                                  GC__       _ __
GAM1382  MGMT    5'  GGGGGGGGGCGGGGGGGG     14495     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  _ C       _
GAM1382  MIC2    5'  GGGGGCGGGTGAGGGGAGCGG  14508     AGGA    _  A
                                GGGG   GCGGG GGG GGAGCGG
                                ||||   ||||| ||| |||||||
                                CCCC   CGCCC CTC CCTCGCC
                                  ____    A  C
GAM1382  MKPX    5'  GAGGAGGAGCGGCGGGGCGG   33638           _   A
                                GGGGAGGAGCGG GGGG GG
                                |||||||||||| |||| ||
                                CTCCTCCTCGCC CCCC CC
                                       G   G
GAM1382  MNT     3'  GGGGAGGGGCAGCGGGTGG   33721        A   G   A
                                GGGGAGG GCGG GGG GG
                                ||||||| |||| ||| ||
                                CCCCTCC CGTC CCC CC
                                    C   G   A
GAM1382  MSL3L1  5'  GGCGGGGGCGGGGAGGCG    38588    _ A  A      AGGA
                                GG GG GG GCGGGGGG   GCG
                                || || || ||||||||   |||
```

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                                CC CC CC CGCCCCTC    CGC
                                 G  _  _      _____
GAM1382  MSL3L1   5'  GGGGAGGGCGGGCGGGGGCGG  38592        A    G  A  A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                   _    G  _  _
GAM1382  NAGA     5'  GGAGGGGCGGGGCTGCG     7040        A     GGAGGA
                                GGAGG GCGGGGG     GCG
                                ||||| ||||||      |||
                                CCTCC CGCCCC      CGC
                                  C     GA____
GAM1382  NCALD    3'  GGGGAAGAGAGGGGAGTGG   36769         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTTCTC CCCCTC CC
                                     T     A
GAM1382  NCOA6IP  5'  GGGAAGGGGCGGGACCACGGGC 36052        A     GGA_  A
              GG                  GGGGAGG GCGGGG    GG GCGG
                                ||||||| ||||||    || ||||
                                CCCTTCC CGCCCT    CC CGCC
                                   C     GGTG  _
GAM1382  NEUROD2  5'  GGGGAGGGGAGGGGGGGAGG   26064      __    C
                                GGGGA  GGAG GGGGGGAGG
                                |||||  ||||  |||||||||
                                CCCCT  CCTC CCCCCCTCC
                                  CC   _
GAM1382  NFIA     5'  GGGGGGAGGGGGTGTGG     43219      A   C    GGA
                                GGGG GGAG GGGG   GG
                                |||| |||| ||||   ||
                                CCCC CCTC CCCC   CC
                                  _   _    ACA
GAM1382  NGFR     3'  GGGAAGGGGTGGGGGTCTGG   14784        AGC    GA_
                                GGGGAGG   GGGGG   GG
                                |||||||   |||||   ||
                                CCCTTCC   CCCCC   CC
                                    CCA    AGA
GAM1382  NPR1     5'  GGGAAGGAGCAGGAGC      44585          GGGGGG
                                GGGGAGGAGC     AGGAGC
                                ||||||||||     ||||||
                                CCCTTCCTCG     TCCTCG
                                       _______
GAM1382  NRXN1    5'  GGGGAGCGGGCGGCGCGGAGTG 39847    A       G  A__    C
              G                   GG GGAGCGGG GG   GGAG GG
                                || ||||||||  ||   |||| ||
                                CC CCTCGCCC CC   CCTC CC
                                  _      G  GCG   A
GAM1382  NTSR1    3'  GGGGAGGGGTGGGGAGGAG   14890        AGC  _
                                GGGGAGG   GG GGGGAGGAG
                                |||||||   || |||||||||
```

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                                CCCCTCC   CC CCCCTCCTC
                                   ___  A
GAM1382  PACSIN1   3'  GGGGAGGGGCGGCAGTGG    45163       A   G  GA
                                GGGGAGG GCGG GG  GG
                                ||||||| |||| ||  ||
                                CCCCTCC CGCC TC  CC
                                    C   G  A_
GAM1382  PAFAH1B1  5'  GGGGGAGGGGAGGGGAGCG   7717     A   C     A
                                GGG GGAG GGGGGG GGAGCG
                                ||| |||| |||||| ||||||
                                CCC CCTC CCCTCC CCTCGC
                                  _   _    _
GAM1382  PAX2      3'  GGGAGGGGATGGGAGGAGTGG  19633       AGC  _      C
                                GGGAGG   GGG GGGAGGAG GG
                                ||||||   ||| |||||||| ||
                                CCCTCC   CCT CCCTCCTC CC
                                   ___  A       A
GAM1382  PAX2      3'  GGGGAGGGGCGGCAGGCGG   19636       A   G  A
                                GGGGAGG GCGG GGG GG
                                ||||||| |||| ||| ||
                                CCCCTCC CGCC TCC CC
                                    C   G  G
GAM1382  PCTK3     3'  GGGGAGGAGTGGAGGGTGG   43784        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCCTC CCTCCC CC
                                     A     A
GAM1382  PDE4A     3'  AGGGGAGTGAGGGGAGGAGTGG 26247     A   C        C
                                GGG GGAG GGGGGGGAGGAG GG
                                ||| |||| |||||||||| ||
                                TCC CCTC CTCCCCTCCTC CC
                                  _   A         A
GAM1382  PDE4A     3'  GGGGAGGAGTGGAGGGGAACAG 26267        CG    A
                                GGGGAGGAG  GGGGG GGAGCGG
                                |||||||||  ||||| |||||||
                                CCCCTCCTC  CCTCC CCTTGTC
                                     A_    _
GAM1382  PDE4A     3'  GGGGGGCGGGGGGGGTGAGTGG  26275    A  A      AG   C
                                GGG GG GCGGGGGGG  GAG GG
                                ||| || ||||||||  ||| ||
                                CCC CC CGCCCCCC  CTC CC
                                  _ _       CA   A
GAM1382  PLOD3     5'  GGGGAGGGGCGGCGGCTCGG   9897        A   G  GA_
                                GGGGAGG GCGG GG   GG
                                ||||||| |||| ||   ||
                                CCCCTCC CGCC CC   CC
                                    C   G  GAG
GAM1382  PLOD3     5'  GGGAGGCGGGGGAGGGGCGG   9895        AGCG       A
                                GGGAGG   GGGGGAGG GCGG
                                ||||||   |||||||| ||||
```

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                                CCCTCC   CCCCCTCC CGCC
                                   G___      C
GAM1382  PML     3'  GGCGAGGAGTGGGCTGGCGAGG 37732    G    C  __ _    C
              AGTGG                  GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA G     A
GAM1382  PPP2R1A  3'  GGGGAGGACGGGAGGTGG    30600        G     A
                                GGGGAGGA CGGGGGG GG
                                |||||||| ||||||| ||
                                CCCCTCCT GCCCTCC CC
                                   _     A
GAM1382  PRDM16   3'  GGGGAGGATGCTGAGGAGTGG  35246        _ _    A
                                GGGGAGGA GC GGGGGG GG
                                |||||||| || |||||| ||
                                CCCCTCCT CG CTCCTC CC
                                    A A     A
GAM1382  PRDM2    3'  GGGGAGAGAGGGGTGG      31973        AGC    A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCT   CTCCCC CC
                                   ___     A
GAM1382  PRKCA    3'  GGGGAGGGCTGGGGGCTGG   15626        A _    GA
                                GGGGAGG GC GGGGG  GG
                                ||||||| || |||||  ||
                                CCCCTCC CG CCCCC  CC
                                   _ A    GA
GAM1382  PROC     3'  GGGGGGGGGCGGGGGGGG    7194       A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  C  C      _
GAM1382  PRODH    3'  GGCGGGGGCGGGGGGTGCTGG  32279    _  A  A      AGGA  _
                                GG GG GG GCGGGGGG   GC GG
                                || || || ||||||||   || ||
                                CC CC CC CGCCCCCC   CG CC
                                 G  _  _      A___  A
GAM1382  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   39036    A   C    A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _     _
GAM1382  PTPRG    5'  GGGGAGAGGCAGGGGGAGCGG  15940       GA       GGA
                                GGGGAG  GCGGGGGGA   GCGG
                                ||||||  |||||||||   ||||
                                CCCCTC  CGTCCCCCT   CGCC
                                   TC       ___
GAM1382  PXN      3'  GGGGAGGATGGAGAGTGG    16030        GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
```

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                                CCCCTCCT  CCTCTC CC
                                    A_     A
GAM1382  RAB13    5'  GGGGAGGGGTGGGGAGCGC   16117       AGC  _     GA
                                GGGGAGG   GG GGGGAG  GC
                                |||||||   || ||||||  ||
                                CCCCTCC   CC CCCCTC  CG
                                   ___  A     G_
GAM1382  RAB13    5'  GGGGGAGCCGGGGGGAGG     16118     A    G
                                GGG GGAGC GGGGGGAGG
                                ||| ||||| ||||||||
                                CCC CCTCG CCCCCTCC
                                  _    G
GAM1382  RAB3A    3'  GGGGGGGGGGGGGGGTCCCAG   16074     A  AGC     A  AG_
                                GGGG GG   GGGGGG GG   CGG
                                |||| ||   |||||| ||   |||
                                CCCC CC   CCCCCC CC   GTC
                                  _ ___     _ AGG
GAM1382  RANBP3   3'  GGGAGGGGGGTTTGGGGGGCGG 28762       AGC  ___   A  A
                                GGGAGG   GGG   GGG GG GCGG
                                ||||||   |||   ||| || ||||
                                CCCTCC   CCC   CCC CC CGCC
                                   C__   AAA  _ _
GAM1382  REST     5'  GGGGAGAGGTGGGGGAGG    24710       G  CG
                                GGGGAG AG  GGGGGAGG
                                |||||| ||  ||||||||
                                CCCCTC TC  CCCCCTCC
                                   _ CA
GAM1382  RHCG     3'  GGGGAGGGCAGGGGTGG     32243       A      GA
                                GGGGAGG GCGGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGTCCCC  CC
                                   _      A_
GAM1382  RNH      5'  GGGGAGGGGTGGGTGGGGTGG  40608       AGC_ _   A
                                GGGGAGG    GG GGGG GG
                                |||||||    || |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM1382  RPA1     3'  GGGGATGGGGGGGGGGTGG    16371      _ AGC     A
                                GGGGA GG   GGGGGG GG
                                ||||| ||   |||||| ||
                                CCCCT CC   CCCCCC CC
                                   A  CC_     A
GAM1382  SALL1    3'  GGGGCGGGGTGGGGGGCAAGG  16460     A  AGC     __
                                GGGG GG   GGGGGG  AGG
                                |||| ||   ||||||  |||
                                CCCC CC   CCCCCC  TCC
                                  G  CCA     GT
GAM1382  SCRT1    3'  GGGGAGGGGAGGGGGCTCGG   36370       AGC     A  AG
                                GGGGAGG   GGGGGG GG  CGG
                                |||||||   |||||| ||  |||
```

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                                CCCCTCC   CCTCCC CC  GCC
                                   ___     _ GA
GAM1382  SF1      5'  GGGGCGGGCCGGGGGCGG    21568      A  A  G    A
                                GGGG GG GC GGGGG GG
                                |||| || || ||||| ||
                                CCCC CC CG CCCCC CC
                                  G _ G    G
GAM1382  SIAT8E   5'  GGGGAGGGGGAGGGGCG     40837      GGAGCG       A
                                GGGGA     GGGGGAGG GCG
                                |||||     |||||||| |||
                                CCCCT     CCCCCTCC CGC
                                  _______       C
GAM1382  SLC9A1   3'  GGGGAGGAGCTGTGCTGGGGTG 43238          GG____    A
              G                  GGGGAGGAGC     GGGG GG
                                ||||||||||     |||| ||
                                CCCCTCCTCG     CCCC CC
                                     ACACGA    A
GAM1382  SLC9A3R2 5'  GGGGGAGCTCGGGGGCGG    41532     A    G_    A
                                GGG GGAGC  GGGGG GG
                                ||| |||||  ||||| ||
                                CCC CCTCG  CCCCC CC
                                  _    AG    G
GAM1382  SMG1     3'  GGGGAGGAGTAGGGAACGATGG 31511          CG     G  GC
                                GGGGAGGAG  GGGGGA GA  GG
                                |||||||||  ||||| ||  ||
                                CCCCTCCTC  TCCCTT CT  CC
                                     A_     G  A_
GAM1382  SOX11    3'  GGGGGGCCGGGGGAGG      17029     A  A  G
                                GGG GG GC GGGGGAGG
                                ||| || || ||||||||
                                CCC CC CG CCCCCTCC
                                  _ _  G
GAM1382  SPI1     3'  GGGGAGGGGCGGGTGACGG    17080        A    G GA
                                GGGGAGG GCGGG G  GG
                                ||||||| ||||| |  ||
                                CCCCTCC CGCCC C  CC
                                    C     A TG
GAM1382  SPI1     3'  GGAGTGGGGGGAGGGGCGG    17077      C        A
                                GGAG GGGGGGAGG GCGG
                                |||| |||||||| ||||
                                CCTC CCCCCCTCC CGCC
                                  A        C
GAM1382  SPTB     3'  GGGGAGGATGGAGGGCGG     7384          GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CCTCCC CC
                                     A_     G
GAM1382  SRD5A1   5'  GAGGAGGGGCGGCTACCGGAGG 9827         A    GG___     A
              GGCGG                  GGGGAGG GCGG    GGAGG GCGG
                                ||||||| ||||    ||||| ||||
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                                CTCCTCC CGCC    CCTCC CGCC
                                   C   GATGG    C
GAM1382 TCF3    3' GGGGGGGACGGGGGGGCTCAGG 43325     A AG     _____
                                GGGG GG  CGGGGGG   AGG
                                |||| ||  |||||||   |||
                                CCCC CC  GCCCCCC   TCC
                                  _ CT     CGAG
GAM1382 TFAP2A  3' GGTGAGGCGTGGGAGGGGCGG 17399   GA A  GG    A
                                GG  GG GCG  GGGAGG GCGG
                                ||  || |||  |||||| ||||
                                CC  TC CGC  CCCTCC CGCC
                                 AC _  A_    C
GAM1382 TNFRSF11A 3' GGGGGGAGTCGGGGGGAGG   19276     A   _
                                GGGG GGAG CGGGGGGAGG
                                |||| |||| ||||||||||
                                CCCC CCTC GCCCCCCTCC
                                  _   A
GAM1382 TNFSF5  3' GGGGGGGGGGGGGGGGTTTCGG 6331     A AGC    A AG_
                                GGGG GG   GGGGGG GG   CGG
                                |||| ||   |||||| ||   |||
                                CCCC CC   CCCCCC CC   GCC
                                  _ C__     _ AAA
GAM1382 TNFSF5  3' GGGGGGGGGGGGGGGG      6329      A AGC    A
                                GGGG GG   GGGGGG GG
                                |||| ||   |||||| ||
                                CCCC CC   CCCCCC CC
                                  _ C__     _
GAM1382 TSLP    5' GGGGAGGAAGGTCAGGGAGGAG 39700         C __
           CGG                   GGGGAGGAG GG  GGGGAGGAGCGG
                                |||||||||  ||  ||||||||||||
                                CCCCTCCTT CC  TCCCTCCTCGCC
                                     _ AG
GAM1382 TULP1   3' GGGGAGGAGGGGGGGCACAGCGG 17731        GC    AGG
                                GGGGAGGA  GGGGGG   AGCGG
                                ||||||||  ||||||   |||||
                                CCCCTCCT  CCCCCC   TCGCC
                                    __     GTG
GAM1382 UGCG    5' GGGGGGTGGGGACGGAAGGGGC 17877     A AGC  __    A
           GG                    GGGG GG   GGG  GGGAGG GCGG
                                |||| ||   |||  |||||| ||||
                                CCCC CC   CCC  CCTTCC CGCC
                                  _ AC_   TG     C
GAM1382 VAT1    3' GGGGAGGGGCAGGGGAGAGCGG 26851       A     GA
                                GGGGAGG GCGGGGG  GGAGCGG
                                |||||||  |||||||  |||||||
                                CCCCTCC CGTCCCC  TCTCGCC
                                   C     __
GAM1382 WSX1    5' AGGGGGAGTGGGGAGGCG    22114     A   C    AGGA
                                GGGG GGAG GGGGGG   GCG
                                |||| |||| ||||||   |||
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                                TCCC CCTC CCCCTC    CGC
                                  _    A     ____
GAM1382  YWHAE    3'  GGGGAGGAGTGAGGGGAAG   27598         C
                                GGGGAGGAG GGGGGGAGG
                                ||||||||| |||||||||
                                CCCCTCCTC CTCCCCTTC
                                     A
GAM1382  ABR      5'  GCGGGCGGGAGCCGGGGGAGG  35011      G  AG    G
                                GCGGG GG  GAGC GGGGGAGG
                                ||||| ||  |||| ||||||||
                                CGCCC CC  CTCG CCCCCTCC
                                   G  __   G
GAM1382  AGL      5'  CGGGGGGAGGGGACGGGG    8495          A_
                                CGGGGGGAGG  GCGGGG
                                ||||||||||  ||||||
                                GCCCCCCTCC  TGCCCC
                                     CC
GAM1382  ANP32A   3'  AGGGGGGGGGGAGAGGGG    26706    C     A    C
                                AG GGGGGG GGAG GGGG
                                || |||||| |||| ||||
                                TC CCCCCC CCTC CCCC
                                 _     C    T
GAM1382  AP2M1    3'  GGGGGAGGGAGCGGCACCTGG  19822      GA      GG___
                                GGGGG  GGAGCGG    GG
                                |||||  |||||||    ||
                                CCCCC  CCTCGCC    CC
                                   TC      GTGGA
GAM1382  AR       5'  GCGGGGGGGCGGGTGGG     6233         AGGA    _
                                GCGGGGGG    GCGGG GGG
                                ||||||||    ||||| |||
                                CGCCCCCC    CGCCC CCC
                                     _____     A
GAM1382  ARIH1    5'  GCGGCGGGGAGGGCGCGGAGG  25091     _      A_
                                GCGG GGGGAGG  GCGGGGG
                                |||| |||||||  |||||||
                                CGCC CCCCTCC  CGCCTCC
                                  G      CG
GAM1382  ARSD     3'  GCGGTGGGGCCTGGGGGGAGG  28928     _   AGGAGC
                                GCGG GGGG     GGGGGGAGG
                                |||| ||||     |||||||||
                                CGCC CCCC     CCCCCCTCC
                                  A   GGA___
GAM1382  ARVCF    3'  AGTGGGGTGGGGGGGGCAGGAGG 11699    C   _  A  A
                                AG GGGG GG GG GCGGGGGG
                                || |||| || || ||||||||
                                TC CCCC CC CC CGTCCTCC
                                 A   A  C  C
GAM1382  ASNS     5'  GCGGGGTGAGAGGGGAG     11716       G   GAGCG
                                GCGGGG GAG    GGGGGAG
                                |||||| |||    |||||||
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                                CGCCCC CTC    TCCCCTC
                                   A  _____
GAM1382 ATRX    3' AGTGGGGGAGAGGGGCGTGG  39603   C   _   A  G
                                AG GGGGG GAGG GCG GG
                                || ||||| |||| ||| ||
                                TC CCCCC CTCC CGC CC
                                 A    T   C  A
GAM1382 AXIN1   3' GCCGGGGGATGGGGGGGGG  41379   G    _ AGC
                                GC GGGGGA GG  GGGGGG
                                || |||||| ||  ||||||
                                CG CCCCCT CC  CCCCCC
                                 G    A C__
GAM1382 AXL     5' AGCGGGGGAGGGGGA      34879        AGGAGC   G
                                AGCGGGGGGG    GGGGG A
                                |||||||||     ||||| |
                                TCGCCCCCT     CCCCC T
                                     _______   G
GAM1382 B3GAT1  3' GCGGGGAGCTCTGGGGAGG  38299       AGGAGCGG
                                GCGGGGGG      GGGGAGG
                                ||||||||      |||||||
                                CGCCCCTC      CCCCTCC
                                    GAGA____
GAM1382 B4GALT1 3' GAAAGAAGGGGGTGGGGGGAGG 11282   GG    AGC_
                                G  GGGAGG   GGGGGGAGG
                                |  ||||||   |||||||||
                                C  TCTTCC   CCCCCCTCC
                                 TT    CCCA
GAM1382 BACE2   5' GCGGCGGGGAGGACGGGAGG  39991    _     G
                                GCGG GGGGAGGA CGGGGGG
                                |||| |||||||| |||||||
                                CGCC CCCCTCCT GCCCTCC
                                  G      _
GAM1382 BACH2   5' GCGAGGGGAGGCCGGGGGG  34792         AG
                                GCGGGGGGAGG  CGGGGGG
                                ||||||||||  |||||||
                                CGCTCCCCTCC  GCCCCCC
                                     G_
GAM1382 BAZ1B   5' GGGGTGGGGGAAGGGAGG   37093    _ A   C
                                GGGG GG GGAG GGGGGG
                                |||| || |||| ||||||
                                CCCC CC CCTT CCCTCC
                                  A  C   _
GAM1382 BCL11B  5' GGGGGGAGCCGGGGGAGG   39753    A   G
                                GGGG GGAGC GGGGGAGG
                                |||| ||||| ||||||||
                                CCCC CCTCG CCCCCTCC
                                  _    G
GAM1382 BRAF    5' GCGGGGAGGGGGCCGGGAGG  20262       A  AG
                                GCGGGGGG GG  CGGGGGG
                                |||||||| ||  |||||||
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                                CGCCCCTC CC  GCCCTCC
                                     C  CG
GAM1382  BRF1     3'  AGCGGGGAGGGGGGGTCTGGAGG 11325         A  AGC   G__
                                AGCGGGGGGG GG   GGG   GGAGG
                                ||||||||| ||   |||   |||||
                                TCGCCCCTC CC   CCC   CCTCC
                                     _ ___   AGA
GAM1382  CALM3    3'  GGGGGGTGGGGTGGGGAGG    23236       A  AGC  _
                                GGGGGG GG   GG GGGGAGG
                                |||||| ||   || |||||||
                                CCCCCC CC   CC CCCCTCC
                                   A  ___  A
GAM1382  CALM3    3'  GGTGGGGAGGTGGTGGGGGG   23244    _      AGC_
                                GG GGGGAGG    GGGGGG
                                || |||||||    ||||||
                                CC CCCCTCC    CCCCCC
                                 A       ACCA
GAM1382  CALR     3'  GCGGGGAGGGGGTGGGGG    41770         A  AGCG
                                GCGGGGGG GG    GGGGG
                                |||||||| ||    |||||
                                CGCCCCTC CC    CCCCC
                                     _  CCA_
GAM1382  CD34     3'  AGTGGGGGCAGGGGTGGG    12111    C    G   AGC  _
                                AG GGGGG AGG   GG GGG
                                || ||||| |||   || |||
                                TC CCCCC TCC   CC CCC
                                 A    G   ___  A
GAM1382  CDC25B   5'  GCAGCGGGCGAGGGGTGGGGGG 34842      _  _   AGC     A
              GG                  GCGG GGG GAGG   GGGGGG GG
                                |||| ||| ||||   |||||| ||
                                CGTC CCC CTCC   CCCCCC CC
                                  G  G   CCA    _
GAM1382  CDC25B   5'  GGGGGGGGGGGGGAAGGAGG    34857       A  AGC
                                GGGGGG GG   GGGGGGGAGG
                                |||||| ||   |||||||||
                                CCCCCC CC   CCTTCCTCC
                                   _  CC_
GAM1382  CKM      3'  GCGGGGCGAGGAGTGAGG     12260       G     C
                                GCGGGG GAGGAG GGGG
                                |||||| |||||| ||||
                                CGCCCC CTCCTC CTCC
                                   G     A
GAM1382  COL1A1   3'  AGTGGAGGGGAGGCCAAGGGGG 6364     C  _      AGC_
              G                  AG GG GGGGAGG    GGGGGG
                                || || |||||||    ||||||
                                TC CC CCCCTCC    CCCCCC
                                 A  T      GGTT
GAM1382  CSK      5'  GCGGGAGGGAGTCGGGGGGAGG 20462         AG  _
                                GCGGGGGG  GAG CGGGGGGAGG
                                ||||||||  ||| ||||||||||
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                                CGCCCTCC  CTC GCCCCCCTCC
                                    __  A
GAM1382  CSK     5'  GCGGGGGAAGGGGGCGGGAGG  20464          A_
                                GCGGGGGGAGG  GCGGGGGG
                                ||||||||||  ||||||||
                                CGCCCCCTTCC  CGCCCTCC
                                      CC
GAM1382  DACH    5'  GGGGGTGGGGCGGGGAG     38873      GA  A
                                GGGGG  GG GCGGGGGG
                                |||||  || ||||||||
                                CCCCC  CC CGCCCCTC
                                  AC  _
GAM1382  DLG4    3'  GGGAGGGAGGCCGGGGGG    10707     _     AG
                                GGG GGGAGG  CGGGGGG
                                |||  ||||||  |||||||
                                CCC CCCTCC  GCCCCCC
                                  T     G_
GAM1382  DRPLA   3'  GGGGGGAGGGTGGGGG      12591         AGCG
                                GGGGGGAGG   GGGGG
                                |||||||||   |||||
                                CCCCCCTCC   CCCCC
                                     CA__
GAM1382  EGFL3   5'  GCGGGCGGGAGGGGGCGAGG  41707      _     AGCG  G
                                GCGGG GGGAGG   GGG GAGG
                                |||||  ||||||   |||  ||||
                                CGCCC CCCTCC   CCC CTCC
                                  G     _____  G
GAM1382  EGLN1   5'  GCGGAGGGAGGGCCGGGAGG  35169          AG
                                GCGGGGGGAGG  CGGGGGG
                                ||||||||||  |||||||
                                CGCCTCCCTCC  GCCCTCC
                                      CG
GAM1382  ELAVL3  3'  GGGGGCAGGAGGATGGGG    10886      G    C  _
                                GGGGG AGGAG GG GGGG
                                |||||  |||||  ||  ||||
                                CCCCC TCCTC CT CCCC
                                  G    _  A
GAM1382  ENG     3'  AGCGGGGGCAGGGGCGGAGG  6490         G  A
                                AGCGGGGG AGG GCGGGGG
                                ||||||||  |||  |||||||
                                TCGCCCCC TCC CGCCTCC
                                     G  C
GAM1382  EPHA8   3'  GGGGTGGGGTGGGGAG      33898      A  AGC  _
                                GGGG GG   GG GGGGAG
                                ||||  ||   ||  ||||||
                                CCCC CC   CC CCCCTC
                                  A  ___  A
GAM1382  FAAH    5'  GCGGGGGGCGGAGCGGGGG   11057         A
                                GCGGGGGG GGAGCGGGGG
                                ||||||||  ||||||||||
```

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                                CGCCCCCC CCTCGCCCCC
                                     G
GAM1382  FBXL11   3'  GCGGGGTGGGGGGGAAGAG   29431      GGA  AGC
                                GCGGGG  GG  GGGGGGAG
                                ||||||  ||  ||||||||
                                CGCCCC  CC  CCCTTCTC
                                   AC_  ___
GAM1382  FBXL11   3'  GCGGGGCGGGGTGGGGGG   29430      _  A  AGC
                                GCGGGG GG GG  GGGGGG
                                |||||| || ||  ||||||
                                CGCCCC CC CC  CCCCCC
                                   G  _  A__
GAM1382  FE65L2   3'  AGCAGGGGGAGGGGCAGGGG  39315         A
                                AGCGGGGGGAGG GCGGGGG
                                |||||||||||| |||||||
                                TCGTCCCCCTCC CGTCCCC
                                      C
GAM1382  FGFR1    5'  GGAGGCGGGGCGGGGGGAG   31946     A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
                                CCTCC CC CGCCCCCCTC
                                   G  C
GAM1382  FKBP2    5'  AGCGGGGGGAGGGGGTCAGGGG 38388          AGCG_
           AGG                  AGCGGGGGGAGG    GGGGGAGG
                                ||||||||||||    ||||||||
                                TCGCCCCCCTCC    TCCCCTCC
                                      CCCAG
GAM1382  FOXD2    5'  GCGGGGAGGGGGGCGGGGG   20969       A  A
                                GCGGGGGGG GG GCGGGGG
                                |||||||| || |||||||
                                CGCCCCTC CC CGCCCCC
                                     _  C
GAM1382  FZD7     3'  GCGGGAGGGGGGCAGGGGAGG  18633       A  A     G
                                GCGGGGGGG GG GCGGGGG AGG
                                |||||||| || ||||||| |||
                                CGCCCTCC CC CGTCCCC TCC
                                     _  _     _
GAM1382  GABRB3   5'  GCGGAGGGGGGAGGGGAGG   34874       A   C
                                GCGGGGGG GGAG GGGGGG
                                |||||||| |||| ||||||
                                CGCCTCCC CCTC CCCTCC
                                     _   _
GAM1382  GPC1     3'  AGTGGGAGGAGGCGGGGAG   13235   C      GA
                                AG GGGGGGAG  GCGGGGGG
                                || ||||||||  ||||||||
                                TC CCCTCCTC  CGCCCCTC
                                 A      ___
GAM1382  GRB14    5'  GCGGCGGGGGAGGGGAGG   21042     G  A   C
                                GCGG GGG GGAG GGGGGG
                                |||| ||| |||| ||||||
```

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                                CGCC CCC CCTC CCCTCC
                                  G  _  _
GAM1382  GRB14    5'  GCGGGGGAGGGGAGGGGG   21043       GA  AGC
                                GCGGGGG  GG   GGGGGG
                                |||||||  ||   ||||||
                                CGCCCCC  CC   TCCCCC
                                    TC  C__
GAM1382  GTF2IRD1  5'  GCGGGGAGGGGGCGCGGGGGGG 32260        A  A_      A
              G                  GCGGGGGG GG  GCGGGGGG GG
                                ||||||||  ||  ||||||||  ||
                                CGCCCCTC CC  CGCCCCCC CC
                                    C  CG       _
GAM1382  HIP12    3'  GGTGGGGGGGAGCAGGAGG    42405    _   A
                                GG GGGG GGAGCGGGGGG
                                ||  ||||  ||||||||||
                                CC CCCC CCTCGTCCTCC
                                 A   _
GAM1382  HIP2     3'  GGGGGGGGTGAAGGGGG     23769       A  AGC
                                GGGGGG GG   GGGGGG
                                ||||||  ||   ||||||
                                CCCCCC CC   TCCCCC
                                   _  ACT
GAM1382  HLX1     5'  GCGGGCGGGGGAGCCAGG    34989       _  A    G
                                GCGGG GGG GGAGC GGG
                                |||||  |||  |||||  |||
                                CGCCC CCC CCTCG TCC
                                  G  _    G
GAM1382  HOXB2    5'  GGGGGAGGGGGCTGCTGGGGGG 13436        A_  _____     A
              GG                  GGGGGAGG  GC    GGGGGG GG
                                ||||||||  ||    ||||||  ||
                                CCCCCTCC  CG    CCCCCC CC
                                    CC  ACGA     _
GAM1382  HOXC6    3'  GCGGGGGTGGGGGCGTCGAAGG 21074        GA  A   GGG
                                GCGGGGG  GG GCG   GGAGG
                                |||||||  ||  |||   |||||
                                CGCCCCC  CC CGC   CTTCC
                                    AC  C   AG_
GAM1382  HYOU1    3'  GGTGGGGTGAGGGGTGGG    40640    _   AG   C   _
                                GG GGGG  GAG GGG GGG
                                ||  ||||  |||  |||  |||
                                CC CCCC  CTC CCC CCC
                                 A   A_  _   A
GAM1382  IGF2     5'  AGGGGGGGAGGGAGTCGGAGG  8309     C        _  _
                                AG GGGGGGAGG AG CGGGGG
                                ||  |||||||||  ||  ||||||
                                TC CCCCCCTCC TC GCCTCC
                                 _       C  A
GAM1382  IGFBP2   3'  GCGGGGGGCAGGGGCGCCAGG  8259          _   A   GG
                                GCGGGGGG AGG GCG  GGG
                                ||||||||  |||  |||  |||
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                                CGCCCCCC TCC CGC  TCC
                                     G  C  GG
GAM1382 IHPK2   5' GCGGGGAGATGGGGGAG    41590        GGAGCG
                                GCGGGGGGA    GGGGGAG
                                |||||||||    |||||||
                                CGCCCCTCT    CCCCCTC
                                     A_____
GAM1382 ILF1    5' GGCGGGAGGAGGGGAGGAG  21114   G     C
                                GG GGGAGGAG GGGGGGAG
                                || |||||||| ||||||||
                                CC CCCTCCTC CCCTCCTC
                                 G      _
GAM1382 KCNC3   3' AGTGGGGGGGGGGGTGGGGGGGG 22495   C    A AGC    A
                                AG GGGGGG GG   GGGGGG GG
                                || |||||| ||   |||||| ||
                                TC CCCCCC CC   CCCCCC CC
                                 A    _ CCA    _
GAM1382 KCNJ3   5' GGAGGTGGGGGGCGGGGGGAGG 13847     GA A
                                GGGGG  GG GCGGGGGGAGG
                                |||||  || ||||||||||
                                CCTCC  CC CGCCCCCCTCC
                                   AC  C
GAM1382 KCNJ3   5' GCGGGGGGAGGAAAGGGGG   13846          C
                                GCGGGGGGAGGAG GGGGG
                                |||||||||||| |||||
                                CGCCCCCCTCCTT CCCCC
                                        T
GAM1382 KCNN4   5' GCGGGGAGGGGCAGGGGAGG  13925       A A     G
                                GCGGGGGG GG GCGGGGG AGG
                                |||||||| || ||||||| |||
                                CGCCCCTC CC CGTCCCC TCC
                                    _ _     _
GAM1382 KPNB1   5' GCGGGGGAGGGACCCTGGGGG 13969       GA  GCG_
                                GCGGGGG  GGA   GGGGG
                                |||||||  |||   |||||
                                CGCCCCC  CCT   CCCCC
                                     TC  GGGA
GAM1382 LAG3    5' AGTGGTGGGGGGGTGGGGGG   14042   C _   A AGC
                                AG GG GGGG GG   GGGGGG
                                || || |||| ||   ||||||
                                TC CC CCCC CC   CCCCCC
                                 A  A   _ A__
GAM1382 LRP1    5' GCGGGGAGGGGGGGGTGGGGGG 14212       A AGC_
                                GCGGGGGG GG   GGGGGG
                                |||||||| ||   ||||||
                                CGCCCCTC CC   CCCCCC
                                     C  CCCA
GAM1382 LU      3' GCGGGGTGAGGGGGGGGG    24563       G   AGC
                                GCGGGG GAGG   GGGGGG
                                |||||| ||||   ||||||
```

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                                CGCCCC CTCC   CCCCCC
                                   A   ___
GAM1382  MAP3K7IP1 3'  GGTGGGAGGAGGGGTGGG    25933    G      C  _
                                GG GGGAGGAG GGG GGG
                                || |||||||| ||| |||
                                CC CCCTCCTC CCC CCC
                                 A      _  A
GAM1382  MAX     5'  GCGGCGGGGAGGGGAAGGGG  40363     _     AGC
                                GCGG GGGGAGG   GGGGGG
                                |||| |||||||   ||||||
                                CGCC CCCCTCC   TTCCCC
                                  G      CC_
GAM1382  MDM4    5'  GGTGGGGGGAGGGGTGGCAG   14395    _   A   C   _  G
                                GG GGGG GGAG GGG GG AG
                                || |||| |||| ||| || ||
                                CC CCCC CCTC CCC CC TC
                                 A   _   _  A  G
GAM1382  MDS1    3'  GCTTCGGGTGGGGGGAGG    22563    GGG   AGGAGC
                                GC   GGG     GGGGGGAGG
                                ||   |||     |||||||||
                                CG   CCC     CCCCCCTCC
                                 AAG   A_____
GAM1382  MGMT    5'  GCGGCGGGGGGGGCGGGGGGGG 14489      _   A  A      A
                                GCGG GGGG GG GCGGGGGG GG
                                |||| |||| || |||||||| ||
                                CGCC CCCC CC CGCCCCCC CC
                                  G   _ C       _
GAM1382  MKPX    5'  GCGGGGCGGGCGGGGAG     33640       GGA  A
                                GCGGGG   GG GCGGGGGG
                                ||||||   || ||||||||
                                CGCCCC   CC CGCCCCTC
                                   G__  _
GAM1382  MSL3L1   5'  GCGGGCGGGGGCGGGGAG    38586      G  A  A
                                GCGGG GG GG GCGGGGGG
                                ||||| || || ||||||||
                                CGCCC CC CC CGCCCCTC
                                  G  _  _
GAM1382  MUC4    5'  AGTGGCGGGAGGGATGGGAGG  39662    C  G     AGC
                                AG GG GGGAGG   GGGGGG
                                || || ||||||   ||||||
                                TC CC CCCTCC   CCCTCC
                                 A  G     CTA
GAM1382  NCOR2    3'  GCGGAGGGAGGGCGCGGGGG   26739          A_
                                GCGGGGGGAGG  GCGGGGG
                                ||||||||||  |||||||
                                CGCCTCCCTCC  CGCCCCC
                                       CG
GAM1382  NDST2    5'  GCGGGGGGAGGAAGGGAGG   18879           C
                                GCGGGGGGAGGAG GGGGGG
                                |||||||||||| ||||||
```

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                                CGCCCCCCTCCTT CCCTCC
                                          _
GAM1382  NFATC4   5'  GGGGGGAGTTCAGGAGG     21246        GAG
                                GGGGGGAG  CGGGGGG
                                ||||||||  |||||||
                                CCCCCCTC  GTCCTCC
                                    AA_
GAM1382  NHLH1    5'  GGTGGGAGGGGGAGG      24656    G     AGC
                                GG GGGAGG  GGGGGG
                                || ||||||  ||||||
                                CC CCCTCC  CCCTCC
                                 A    ___
GAM1382  NHLH1    5'  AGGGGGAGGAAGGGGGAGG   24648         GC
                                GGGGGGAGGA GGGGGGAGG
                                |||||||||| |||||||||
                                TCCCCCTCCT TCCCCCTCC
                                          __
GAM1382  NOTCH3   3'  GGTGGGGTGGGGAGGA     7739     _   A  AGCG
                                GG GGGG GG   GGGGGA
                                || |||| ||   ||||||
                                CC CCCC CC   CCTCCT
                                 A   A ____
GAM1382  NPDC1    5'  AGCGGGGGAGGACGCAGGAGG 31724        G   _
                                AGCGGGGG AGGA GCGGGGGG
                                |||||||| |||| ||||||||
                                TCGCCCCC TCCT CGTCCTCC
                                    _   G
GAM1382  NRGN     3'  GCGGGGGGGGAGGGCGGG    26128        A   C  G
                                GCGGGGGG GGAG GG GGG
                                |||||||| |||| || |||
                                CGCCCCCC CCTC CC CCC
                                    _   _ G
GAM1382  NT5M     5'  AGCGGGGCGGGGAGCGCAGG  33643       _ A     G
                                AGCGGGG GG GGAGCG GGG
                                ||||||| || |||||| |||
                                TCGCCCC CC CCTCGC TCC
                                    G _     G
GAM1382  PABPC4   5'  GGGGCCCGAGCGGGGGGAG   19229     AG_
                                GGGG  GAGCGGGGGGAG
                                ||||  ||||||||||||
                                CCCC  CTCGCCCCCCTC
                                  GGG
GAM1382  PAFAH1B1 5'  GCGGGGGAGGGGGA       7711         GAGGAGC
                                GCGGGGG     GGGGGGA
                                |||||||     |||||||
                                CGCCCCC     TCCCCCT
                                          _______
GAM1382  PAPOLA   5'  GCGGGAGGGAGGGGGGGG   37206      _     AGC
                                GCGGG GGGAGG  GGGGGG
                                ||||| ||||||  ||||||
```

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                                CGCCC CCCTCC  CCCCCC
                                  T    ___
GAM1382 PAX2    3' GCGGGGCGGGGCGGAGGGGGAG 19630      _ A AGC
                G                  GCGGGG GG GG  GGGGGGAGG
                                   |||||| || ||  |||||||||
                                   CGCCCC CC CC  TCCCCCTCC
                                     G _ GCC
GAM1382 PAX7    5' GGGGTGGAGGTTGGGGGGAGG 30334    _   AGC
                                   GGGG GGAGG  GGGGGGAGG
                                   |||| |||||  |||||||||
                                   CCCC CCTCC  CCCCCCTCC
                                     A   AA_
GAM1382 PCBP1   5' GGCGGCTGGCGGGGGGAG   26222   G AGGA
                                   GG GG   GCGGGGGGAG
                                   || ||   ||||||||||
                                   CC CC   CGCCCCCCTC
                                    G GAC_
GAM1382 PCBP1   5' GCGGGGGGAGGGGAGGTGTAGG 26220        AGC   G__
                                   GCGGGGGGAGG  GGGGG  AGG
                                   ||||||||||  |||||  |||
                                   CGCCCCCCTCC  CCTCC  TCC
                                         ___   ACA
GAM1382 PCDHGA1  3' AGTGGGGTGGGGAGGAGG   36728   C  _ A  C
                                   AG GGGG GG GGAG GGGG
                                   || |||| || |||| ||||
                                   TC CCCC CC CCTC CTCC
                                    A  A _  _
GAM1382 PCDHGA10 3' AGTGGGGTGGGGAGGAGG   36869   C  _ A  C
                                   AG GGGG GG GGAG GGGG
                                   || |||| || |||| ||||
                                   TC CCCC CC CCTC CTCC
                                    A  A _  _
GAM1382 PCDHGA11 3' AGTGGGGTGGGGAGGAGG   36878   C  _ A  C
                                   AG GGGG GG GGAG GGGG
                                   || |||| || |||| ||||
                                   TC CCCC CC CCTC CTCC
                                    A  A _  _
GAM1382 PCDHGA12 3' AGTGGGGTGGGGAGGAGG   36887   C  _ A  C
                                   AG GGGG GG GGAG GGGG
                                   || |||| || |||| ||||
                                   TC CCCC CC CCTC CTCC
                                    A  A _  _
GAM1382 PCDHGA2  3' AGTGGGGTGGGGAGGAGG   36735   C  _ A  C
                                   AG GGGG GG GGAG GGGG
                                   || |||| || |||| ||||
                                   TC CCCC CC CCTC CTCC
                                    A  A _  _
GAM1382 PCDHGA3  3' AGTGGGGTGGGGAGGAGG   33158   C  _ A  C
                                   AG GGGG GG GGAG GGGG
                                   || |||| || |||| ||||
```

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                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGA4  3' AGTGGGGTGGGGAGGAGG   36819   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGA5  3' AGTGGGGTGGGGAGGAGG   36827   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGA6  3' AGTGGGGTGGGGAGGAGG   36835   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGA7  3' AGTGGGGTGGGGAGGAGG   36843   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGA8  3' AGTGGGGTGGGGAGGAGG   36852   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGA9  3' AGTGGGGTGGGGAGGAGG   36861   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGB1  3' AGTGGGGTGGGGAGGAGG   33172   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGB2  3' AGTGGGGTGGGGAGGAGG   33173   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGB3  3' AGTGGGGTGGGGAGGAGG   36914   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A  _   _
GAM1382  PCDHGB4  3' AGTGGGGTGGGGAGGAGG   19027   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
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                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PCDHGB5  3' AGTGGGGTGGGGAGGAGG   36932   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PCDHGB6  3' AGTGGGGTGGGGAGGAGG   36939   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PCDHGB7  3' AGTGGGGTGGGGAGGAGG   33178   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PCDHGC3  3' AGTGGGGTGGGGAGGAGG   37047   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PCDHGC4  3' AGTGGGGTGGGGAGGAGG   37069   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PCDHGC5  3' AGTGGGGTGGGGAGGAGG   37076   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM1382 PDE4A    3' GCGGGGGGGTGAGTGGATCAG 26258       AG  C  G_
                                GCGGGGGG  GAG GGG  GG
                                ||||||||  ||| |||  ||
                                CGCCCCCC  CTC CCT  TC
                                     CA  A  AG
GAM1382 PDE4A    3' AGTGAGGGGAGGAGTGGAGG  26250   C       C
                                AG GGGGGGAGGAG GGGGG
                                || ||||||||||| |||||
                                TC CTCCCCTCCTC CCTCC
                                 A         A
GAM1382 PDE4A    3' GGGGGCAGGGGGAAAGG    26271     G  AGCG  GG
                                GGGGG AGG   GGG  AGG
                                ||||| |||   |||  |||
                                CCCCC TCC   CCC  TCC
                                   G  ____  TT
GAM1382 PDE4A    3' AGTGGGGGAAGGTGAGGGGAGG 26252   C       AGC
                                AG GGGGGGAGG  GGGGGGAGG
                                || |||||||||  |||||||||
```

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                                TC CCCCCTTCC   CTCCCCTCC
                                 A        A__
GAM1382  PDE4A    3'  AGTGGGGCGGGGGGGCGGGGGG  26251    C   _  A  A
                                AG GGGG GG GG GCGGGGGG
                                || |||| || || ||||||||
                                TC CCCC CC CC CGCCCCCC
                                 A   G  _  C
GAM1382  PFN1     5'  GGCTGGCGGGCGGGGGGAG   22719    GG  A  A
                                GG  GG GG GCGGGGGGAG
                                ||  || || ||||||||||
                                CC  CC CC CGCCCCCCTC
                                 GA  G  _
GAM1382  PLOD3    5'  GCGGGGGAGGGGCGGCGG    9892        GA  A   G
                                GCGGGGG  GG GCGG GG
                                |||||||  || |||| ||
                                CGCCCCC  CC CGCC CC
                                    TC  _   G
GAM1382  PNUTL1   3'  GCGGGGGAAGGGCAAGGGAGG  15433          A     G
                                GCGGGGGGAGG GCGGGGG AGG
                                |||||||||| ||||||| |||
                                CGCCCCCTTCC CGTTCCC TCC
                                          _     _
GAM1382  PPT2     5'  GCGGGGGGAAGGGTGAG     39921         GGAGC   G
                                GCGGGGGGA    GGGG GAG
                                |||||||||    |||| |||
                                CGCCCCCCT    TCCC CTC
                                     _____   A
GAM1382  PROC     3'  GCAGGGGGGGGGGGGCGGGGGGG 7191         A  A_      A
           G                     GCGGGGGG GG  GCGGGGGG GG
                                |||||||| ||  |||||||| ||
                                CGTCCCCC CC  CGCCCCCC CC
                                    C  CC      _
GAM1382  PRODH    3'  GCGGGGGCGGGGGGGTGCTGGAG 32278        GA  AGC   ____
           G                     GCGGGGG  GG   GGGG   GGAGG
                                |||||||  ||   ||||   |||||
                                CGCCCCC  CC   CCCC   CCTCC
                                    G_  ___   ACGA
GAM1382  PTPRA    3'  AGTGGTGGGGATGGGGGAG   38905    C  _   GGAGCG
                                AG GG GGGGA     GGGGGAG
                                || || |||||     |||||||
                                TC CC CCCCT     CCCCCTC
                                 A  A    A_____
GAM1382  RAB13    5'  AGCCGGGGGAGGGGTGGGG   16111     G      AGC  _
                                AGC GGGGGAGG   GG GGGG
                                ||| ||||||||   || ||||
                                TCG CCCCCTCC   CC CCCC
                                  G       ___  A
GAM1382  RAB3A    3'  GCGGGGGGGGGGGGGGG      16065        A  AGC
                                GCGGGGGG GG   GGGGGG
                                |||||||| ||   ||||||
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                                CGCCCCCC CC   CCCCCC
                                   _ ___
GAM1382  RAB3A    3'  GCGGGGGGGGGGGTTCAGGAGG  16067        A  AG_
                                GCGGGGGG GG   CGGGGGG
                                |||||||| ||   |||||||
                                CGCCCCCC CC   GTCCTCC
                                    C  CAA
GAM1382  RCE1     3'  GGGGGGTGGGGAGAG       23068       AGGAGC
                                GGGGGG     GGGGGGAG
                                ||||||     ||||||||
                                CCCCCC     CCCCTCTC
                                  A_____
GAM1382  RFX1     3'  GCGGGTGGGGCGGGGAG     16291       _  AGGA
                                GCGGG GGG    GCGGGGGG
                                ||||| |||    ||||||||
                                CGCCC CCC    CGCCCCTC
                                  A  _____
GAM1382  RPA1     3'  AGCGGGGATGGGGGGGGG    16366        GA  AGC
                                AGCGGGGG  GG   GGGGGG
                                ||||||||  ||   ||||||
                                TCGCCCCT  CC   CCCCCC
                                    AC  ___
GAM1382  RREB1    5'  GGGGGGGGGTGAGGGGGAGG   16400       A  AGC
                                GGGGGG GG   GGGGGGAGG
                                |||||| ||   |||||||||
                                CCCCCC CC   TCCCCCTCC
                                   _  AC_
GAM1382  SALL1    3'  GCGGGGTGGGGGGGCAAGG    16456       _  A  A
                                GCGGGG GG GG GCGGGG
                                |||||| || || ||||||
                                CGCCCC CC CC CGTTCC
                                   A  _  C
GAM1382  SALL1    3'  GCGGGGCGGGGTGGGGGG     16455       _  A  AGC
                                GCGGGG GG GG   GGGGGG
                                |||||| || ||   ||||||
                                CGCCCC CC CC   CCCCCC
                                   G  _  A__
GAM1382  SLC21A3  3'  GGTGGGGGAAGGGGGGAG    39577    G   A   C
                                GG GGG GGAG GGGGGGAG
                                || ||| |||| ||||||||
                                CC CCC CCTT CCCCCCTC
                                 A  _   _
GAM1382  SMG1     3'  AGTGGTGGGGAGGAGTAGG    31504    C  _       CG
                                AG GG GGGGAGGAG  GG
                                || || |||||||||  ||
                                TC CC CCCCTCCTC  CC
                                 A  A        AT
GAM1382  SMOH     3'  AGCGAGGGGAGGGGGTTAGAGG 24807           AGC  GG
                                AGCGGGGGGAGG   GG  GGAGG
                                ||||||||||||   ||  |||||
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                                TCGCTCCCCTCC  CC  TCTCC
                                      C__  AA
GAM1382  SOX11    3'  GCCGGGGGAGGGGTGGTGG   17022    G      AGC  _  _
                                GC GGGGGAGG  GG GG GG
                                || ||||||||  || || ||
                                CG CCCCCTCC  CC CC CC
                                 G      ___  A  A
GAM1382  SOX11    3'  AGTCGGGGGGCCGGGGGAG   17002   _    GAGGA  G
                                AG CGGGGG    GC GGGGGAG
                                || ||||||    || |||||||
                                TC GCCCCC    CG CCCCCTC
                                 A     _____  G
GAM1382  SOX4     3'  AGGGGGGGAGGGGTGCGCTGGG 16975    C       A__  GG
                                AG GGGGGGAGG  GCG  GGG
                                || |||||||||  |||  |||
                                TC CCCCCCTCC  CGC  CCC
                                 _       CCA  GA
GAM1382  SPI1     3'  AGTGGGGGGAGGGGCGGG    17073    C       A
                                AG GGGGGGAGG GCGGG
                                || ||||||||| |||||
                                TC CCCCCCTCC CGCCC
                                 A       C
GAM1382  SPI1     3'  GGGGGCCTGGAGTGGGGGGAGG 17083      GA_   C
                                GGGGG  GGAG GGGGGGAGG
                                |||||  |||| |||||||||
                                CCCCC  CCTC CCCCCCTCC
                                   GGA   A
GAM1382  SPTBN2   3'  GCGGGGGTGGGAGAGGGGG   28070       GA   C
                                GCGGGGG  GGAG GGGGG
                                |||||||  |||| |||||
                                CGCCCCC  CCTC CCCCC
                                    AC   T
GAM1382  SPTBN2   3'  GGGGGTGGGGAGGGAG     28072      A  AGC
                                GGGGG GG  GGGGGGAG
                                ||||| ||  ||||||||
                                CCCCC CC  CCTCCCTC
                                   A  ___
GAM1382  SRD5A1   5'  GGCGGCGGCGCGGGGGGAG   9829    G  A  A
                                GG GG GG GCGGGGGGAG
                                || || || ||||||||||
                                CC CC CC CGCCCCCCTC
                                 G  G  G
GAM1382  SSRP1    5'  GCTGGGGGGACGCGGGGGGGG  17125   _     GGA      A
                                GC GGGGGGA  GCGGGGGG GG
                                || |||||||  |||||||| ||
                                CG CCCCCCT  CGCCCCCC CC
                                 A     G__      _
GAM1382  SSRP1    5'  GCGGGGGGGGGCGCGGGGAG   17124       A  A
                                GCGGGGGG GG GCGGGGGG
                                |||||||| || ||||||||
```

```
                                CGCCCCCC CC CGCCCCTC
                                     _ G
GAM1382 SSRP1    5' GCGGGGAGGGGGATGGGGGG  17123      _ A  GC
                                GCGGGG GG GGA  GGGGGG
                                |||||| || |||  ||||||
                                CGCCCC CC CCT  CCCCCC
                                   T  C   A_
GAM1382 SYT5     3' GGTGGAAGGTGGGGGGAG    17242    G     AGC
                                GG GGGAGG   GGGGGGAG
                                || ||||||   ||||||||
                                CC CCTTCC   CCCCCCTC
                                 A     A__
GAM1382 TCF3     3' GGGGGGGGGGGACGGGGGG    43326       A  AG
                                GGGGGG GG  CGGGGGG
                                |||||| ||  |||||||
                                CCCCCC CC  GCCCCCC
                                   C  CT
GAM1382 TNFRSF11A 3' GGGGGGGGGGAGTCGGGGGGAGG 19278       A   _
                                GGGGGG GGAG CGGGGGGAGG
                                |||||| |||| ||||||||||
                                CCCCCC CCTC GCCCCCCTCC
                                   C   A
GAM1382 TNFSF5   3' GAGGGTGGCGGGGGGG      6325       GAGGA      A
                                GGGGG    GCGGGGGG G
                                |||||    |||||||| |
                                CTCCC    CGCCCCCC C
                                  AC____      _
GAM1382 TNFSF5   3' GCGGGGGGGGGGGGGGGGG   6327         A  AGC     A
                                GCGGGGGG GG   GGGGGG GG
                                |||||||| ||   |||||| ||
                                CGCCCCCC CC   CCCCCC CC
                                     _  C__     _
GAM1382 TULP1    3' GCGCGGGGAGGAGGGGGG    17728     G       C
                                GCG GGGGAGGAG GGGGG
                                ||| ||||||||| |||||
                                CGC CCCCTCCTC CCCCC
                                  G       _
GAM1382 UNC5C    5' CGGGGGGAGGGGAGGGGG    19007          AGC
                                CGGGGGGAGG   GGGGGG
                                ||||||||||   ||||||
                                GCCCCCCTCC   TCCCCC
                                      CC_
GAM1382 VDR      3' AGTGGGGGGAGGTGCAGG    7512     C       A
                                AG GGGGGGAGG GCGGG
                                || |||||||| |||||
                                TC CCCCCCTCC CGTCC
                                 A       A
GAM1382 VDR      3' AGCGGGGCCTGCAGTGGGGGGA 7510         GGAGG  C
             GG                   AGCGGGG    AG GGGGGGAGG
                                |||||||    || |||||||||
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                                TCGCCCC    TC CCCCCCTCC
                                    GGACG  A
GAM1382  WNT7A    5'  AGCGGGAGGAGGGAGGGAG   21521          AGCG
                                AGCGGGGGGAGG   GGGGGAG
                                ||||||||||||   |||||||
                                TCGCCCTCCTCC   CTCCCTC
                                          ____
GAM1382  YY1      5'  AGCGGGCGGGGGGAGAGGGGG  18163       _  A   C
                                AGCGGG GGG GGAG GGGGG
                                |||||| ||| |||| |||||
                                TCGCCC CCC CCTC CCCCC
                                   G  C   T
GAM1382  ZIC3     5'  GCGGGGGGAGGAGGAGG     18248           C
                                GCGGGGGGAGGAG GGGG
                                |||||||||||| ||||
                                CGCCCCCCTCCTC CTCC
                                          _
GAM1382  ZIC3     5'  GGGGGTGTTGGCGGGGGGAGG  18253      GAGGA
                                GGGGG    GCGGGGGGAGG
                                |||||    ||||||||||
                                CCCCC    CGCCCCCCTCC
                                   ACAAC
GAM1382  ZNF216   5'  AGTGGGAGGAGGGAAGCGAGGG 25651    C       __       A
            GGG                   AG GGGGGGAGG  AGCGGGGGG GG
                                || |||||||||  |||||||||  ||
                                TC CCCTCCTCC  TCGCTCCCC CC
                                 A        CT       _
GAM1383  AK3      3'  CCTTTTGAAAGGCAGAGGAG  30180    CG      ATCT
                                CC  TTGAAAGG    GGGAG
                                ||  ||||||||    |||||
                                GG  AACTTTCC    TCCTC
                                 AA       GTC_
GAM1383  ALDH3B2  3'  ACCCGTTGGAGGCGGGTGGGA  8680         AA   ATC_
                                ACCCGTTG  AGG    TGGGA
                                ||||||||  |||   |||||
                                TGGGCAAC  TCC    ACCCT
                                     C_   GCCC
GAM1383  ASGR2    5'  GTGAAAGGTGTGGAGA      10141    T     ATC  _
                                GT GAAAGG   TG GGAGA
                                || ||||||   || |||||
                                CA CTTTCC   AC CCTCT
                                 _     ___  A
GAM1383  C7       3'  TCGATTCAGATTTGGGAGAA  8231       AA_   C
                                TTGA   GGAT TGGGAGAA
                                ||||   |||| ||||||||
                                AGCT   TCTA ACCCTCTT
                                  AAG    A
GAM1383  CAPN10   3'  GCAGAGGATCTGGGAG      35785    TGAA
                                GT    AGGATCTGGGAG
                                ||    ||||||||||||
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                                CG   TCCTAGACCCTC
                                 TC__
GAM1383 CELL    3' ACCCGTTGCAGGGACGGGGG  12221       AAA   CT
                                ACCCGTTG  GGAT GGG
                                ||||||||  |||| |||
                                TGGGCAAC  CCTG CCC
                                    GTC   CC
GAM1383 ELAVL3  3' CCTGGGCAAGGGGGTCTGGGAG 10883   GTTGA   A__
                                CC    AAGG  TCTGGGAG
                                ||    ||||  ||||||||
                                GG    TTCC  AGACCCTC
                                 ACCCG   CCC
GAM1383 EXTL1   3' ACCCATTGGGGGCGGAGGGGGA 20862       AAA__  TCT
            G                    ACCCGTTG    GGA  GGGAG
                                ||||||||    |||  |||||
                                TGGGTAAC    CCT  CCCTC
                                    CCCCG   CC_
GAM1383 EZH1    3' CCGTTGGGGCCTGGGAG    12780      AAA  AT
                                CCGTTG  GG CTGGGAG
                                ||||||  ||  |||||||
                                GGCAAC  CC GACCCTC
                                   ___  CG
GAM1383 FUT1    3' TTGGAGGACCCAGGGGAGAA  6637     AA     __
                                TTG  AGGATCT  GGGAGAA
                                |||  |||||||  |||||||
                                AAC  TCCTGGG  CCCTCTT
                                 C_      TC
GAM1383 GAS7    3' TTGGGGGGTCCTAGGAGAA   25291    AAA  A
                                TTG   GG TCTGGGAGAA
                                |||   || ||||||||||
                                AAC   CC GGATCCTCTT
                                 CCC  A
GAM1383 IHPK1   3' CCCTTGAGCCCTGGGAG    45485    G   AAGGA
                                CCC TTGA    TCTGGGAG
                                ||| ||||    ||||||||
                                GGG AACT    GGACCCTC
                                  _   CG___
GAM1383 NUMB    3' CACCAAAAGGGGGTTTGGGGGA 19049   TT    ATC__   A
            A                    CG  GAAAGG    TGGG GAA
                                ||  ||||||    |||| |||
                                GT  TTTTCC    ACCC CTT
                                 GG     CCCAA   C
GAM1383 PGLS    3' TTGAAAGGAGAGCCCGGAGA  28986       T__  G
                                TTGAAAGGA   CT GGAGA
                                |||||||||   || |||||
                                AACTTTCCT   GG CCTCT
                                    CTC  G
GAM1383 POU4F1  3' GTTGAAAGGTTCTACCAGGA  26394       A  ___
                                GTTGAAAGG TCT   GGGA
                                ||||||||| |||   ||||
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                                CAACTTTCC AGA   TCCT
                                     A   TGG
GAM1383  PSG7     3'  TTGAGGTTCCATGGGAGAA   15810      AA  A   __
                                TTGA  GG TCT  GGGAGAA
                                ||||  || |||  |||||||
                                AACT  CC AGG  CCCTCTT
                                  __  A   TA
GAM1383  RET      3'  CCCAGGAGGGGTCTGGGGGAA  33930      TT  AA  A     A
                                CCCG  GA  GG TCTGGG GAA
                                ||||  ||  || ||||||  |||
                                GGGT  CT  CC AGACCC CTT
                                  C_  CC  _     C
GAM1383  SNAPAP   3'  GTGAAAGGAAGCAAGAG     29698    T      TC
                                GT GAAAGGA  TGGGAG
                                || |||||||  ||||||
                                CA CTTTCCT  GTTCTC
                                 _      TC
GAM1383  SOX4     3'  CGTTGGAAGGGGGAG       16982      A    ATCT
                                CGTTG AAGG    GGGAG
                                ||||| ||||    |||||
                                GCAAC TTCC    CCCTC
                                   C    ____
GAM1383  SYNGR3   3'  CCTGTGAGAGAAAGTGGAGA   20094    GT   A    TCTG
                                CC  TGA AGGA    GGAGA
                                ||  ||| ||||    |||||
                                GG  ACT TCTT    CCTCT
                                 AC   C    TCA_
GAM1383  WNT8B    3'  CCCTAGGTCTGGGAGA      40585     GTTGAA   A
                                CCC      AGG TCTGGGAGA
                                |||      ||| |||||||||
                                GGG      TCC AGACCCTCT
                                 A_____   _
GAM1383  BMP1     3'  TCATCCCTGGCCAGTGT     25991          A  CT  GA
                                TCATCCTTG CC  GG  GT
                                |||||||| ||  ||  ||
                                AGTAGGGAC GG  TC  CA
                                     C  __  A_
GAM1383  SMG1     3'  TCACCCTTGACCCTGGGGT   31512              A
                                TCATCCTTGACCCTGGG GT
                                |||||||||||||||| ||
                                AGTGGGAACTGGGACCC CA
                                                 _
GAM1384  B4GALT2  3'  GGCAAAGTGGCGGGGTG     36141      TTAC     A   C
                                GGCGG    GTGGCG GGT G
                                |||||    |||||| ||| |
                                CCGTT    CACCGC CCA C
                                   T___      C   A
GAM1384  CYP24    5'  GGGTGGGGCGAGGTG       8948      C  TTACGT       C
                                GGG GG     GGCGAGGT G
                                ||| ||     |||||||| |
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                                CCC CC     CCGCTCCA C
                                  A _______       A
GAM1384 KPNB1    5' TGGGGGTTGGGGGTC      13979     C  TACG  CGA
                                TGGG GGT   TGG  GGTC
                                |||| |||   |||  ||||
                                ACCC CCA   ACC  CCAG
                                  _  ____  C__
GAM1384 RTN4     5' GGGCGGTTGTGGGGGTG    42492       AC   CGA  C
                                GGGCGGTT  GTGG  GGT G
                                ||||||||  ||||  ||| |
                                CCCGCCAA  CACC  CCA C
                                    __   C__  A
GAM1384 CRSP8    3' TTCCTGCGTGTCTGGGAAGGTG 44340          __________
            CTG                   TTCCTGCGTGTC       GCTG
                                ||||||||||||       ||||
                                AAGGACGCACAG       CGAC
                                      ACCCTTCCA
GAM1384 NEUROD1  5' TTCCTCGTGTCGTGGCC    14759     G     C
                                TTCCT CGTGTCG TGGCT
                                ||||| ||||||| |||||
                                AAGGA GCACAGC ACCGG
                                  _     _
GAM1384 SON      3' CTGCGTGTTGCTCACTCA    38459       C  G
                                CTGCGTGT GCT GCTCG
                                |||||||| ||| |||||
                                GACGCACA CGA TGAGT
                                    A  G
GAM1384 UPF3A    3' CTGCGTGTTTCTACGTCA    35693       CG  GC
                                CTGCGTGT  CTG  TCG
                                ||||||||  |||  |||
                                GACGCACA  GAT  AGT
                                    AA  GC
GAM1385 ABCD1    3' GGGGCGGGGCAGGGGCCGG   6202      A_   T
                                GGGG  GGGC GGGGCCGG
                                ||||  |||| ||||||||
                                CCCC  CCCG CCCCGGCC
                                  GC   T
GAM1385 ACP1     5' GGGCGGGGAGGGTCCGCGGG  28242     C      _  _
                                GGGC GGGGAGGG CTG GGG
                                |||| |||||||| ||| |||
                                CCCG CCCCTCCC GGC CCC
                                  _      A  G
GAM1385 ADCY7    5' GGGCTGGGGAGAGGGCCTCTGG 9988      C     GGCT    ___
            G                   GGGC GGGGAG   GGGGCC  GGG
                                |||| ||||||   ||||||  |||
                                CCCG CCCCTC   TCCCGG  CCC
                                  A     _____     AGA
GAM1385 ADORA2B  5' GGGCTGGGGCGCTGGTGGCCGG 8614      C   AGG   _
            G                   GGGC GGGG  GCTGG GGCCGGG
                                |||| ||||  ||||| |||||||
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                                CCCG CCCC   CGACC CCGGCCC
                                  A   G__    A
GAM1385 AGRN    3' GGACTGGGCTGGGGCTGG    44253    GA       C
                                GGG  GGGCTGGGGC GG
                                |||  |||||||||| ||
                                CCT  CCCGACCCCG CC
                                  GA        A
GAM1385 ANK1    3' GGGTTGGGGAGGGTGGGCAG   33872    CC      C   GC
                                GGG  GGGGAGGG TGGG  CGG
                                |||  |||||||| ||||  |||
                                CCC  CCCCTCCC ACCC  GTC
                                  AA      _   __
GAM1385 AOC3    3' GGGCTGGGGGAGTACCAGGGGC 19019     C_    GG _    C
            TGGG                  GGGC  GGGGAG  CT GGGGC GGG
                                ||||  ||||||  || ||||| |||
                                CCCG  CCCCTC  GG CCCCG CCC
                                  AC     AT  T    A
GAM1385 ARAF1   5' GGGCTGAGGTGGGGCTGGG   41911     C   A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CCCG CTCC  CCCGACCC
                                  A   AC
GAM1385 ARHGDIA  3' GGGTGGGGGAGGGCTGAGG   20216    CC
                                GGG  GGGGAGGGCTGGGG
                                |||  ||||||||||||||
                                CCC  CCCCTCCCGACTCC
                                  AC
GAM1385 ARIX    5' GGGCGGGGGCGGGGGCCGGG   23183     CGG  A   T
                                GGGC   GG GGGC GGGGCCGGG
                                ||||   || |||| |||||||||
                                CCCG   CC CCCG CCCCGGCCC
                                  ___  _   C
GAM1385 ASGR2   5' GCTCTGAGGGCTGGGGCTGGG  38954    CGGG        C
                                GC   GAGGGCTGGGGC GGG
                                ||   ||||||||||||| |||
                                CG   CTCCCGACCCCG CCC
                                 AGA_         A
GAM1385 ASPH    3' GGGCTGGGAGGGCTGGAGAGG  37138     CG         CC
                                GGGC  GGGAGGGCTGGGG  GG
                                ||||  ||||||||||||||  ||
                                CCCG  CCCTCCCGACCTC  CC
                                  A_          T_
GAM1385 ASPH    5' GGGCTGGTGAGGGCTGGTGG   37139     C  G      _
                                GGGC GG GAGGGCTGG GG
                                |||| || |||||||| ||
                                CCCG CC CTCCCGACC CC
                                  A  A       A
GAM1385 ATP2B4   5' AGGCCGGGGAGTGGGCTGGG   43195         __
                                GGGCCGGGGA  GGGCTGGG
                                |||||||||  ||||||||
```

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                                TCCGGCCCCT  CCCGACCC
                                     CA
GAM1385  B4GALT2   3'  GGGCTAGGGGGAGGGGGTCGGG 36143      CG   A   CT    C
                                GGGC  GGG GGG  GGGG CGGG
                                ||||  ||| |||  |||| ||||
                                CCCG  CCC CCT  CCCC GCCC
                                  AT   _   C_    A
GAM1385  BACE2     5'  GGGCTCGGGGGGGCGCCGGG    39993      _     A  _
                                GGGC CGGGG GG GCTGGG
                                |||| ||||| || ||||||
                                CCCG GCCCC CC CGGCCC
                                  A     _ G
GAM1385  BAIAP3    3'  GGCCTGGGGAAGGGTTGGG    19456      _     _  C
                                GGCC GGGGA GGG TGGG
                                |||| ||||| ||| ||||
                                CCGG CCCCT CCC ACCC
                                  A     T   A
GAM1385  BAIAP3    3'  GGGGTGGGGGCCAGGGCCGGG  19457     CCGG  A    TG
                                GGG    GG GGGC  GGGCCGGG
                                |||    || ||||  ||||||||
                                CCC    CC CCCG  CCCGGCCC
                                  CA__  _    GT
GAM1385  BARHL1    3'  GGGCCGGGCAGGGCCCCCTCCC 33470         G      GGGG_
           GGG                    GGGCCGGG AGGGCT     CCGGG
                                |||||||| ||||||     |||||
                                CCCGGCCC TCCCGG     GGCCC
                                     G      GGGAG
GAM1385  BARHL1    3'  GGGCTGAGGCTGGGGGCTGGGG 33471      C    A___        C
           TCGGG                    GGGC GGGG    GGGCTGGGG CGGG
                                |||| ||||    |||||||||| ||||
                                CCCG CTCC    CCCGACCCC GCCC
                                  A   GACC        A
GAM1385  BCL2L2    3'  GGGCAGGGGAAAGGAGGGGTTG 19747      C       CT    CC
           GG                     GGGC GGGGAGGG  GGGG  GGG
                                |||| ||||||||  ||||  |||
                                CCCG CCCCTTTC  CCCC  CCC
                                  T       CT    AA
GAM1385  BGN       3'  GAGTCGGGGAGGGTTGAAAGG  11819     C       C  GG CC
                                GGG CGGGGAGGG TG  G  GG
                                ||| |||||||| ||  |  ||
                                CTC GCCCCTCCC AC  T  CC
                                  A        A  TT __
GAM1385  BRAF      5'  GGGCGGGGAGGGGGCCGG    20264      C       CTGG
                                GGGC GGGGAGGG    GGCCGG
                                |||| ||||||||    ||||||
                                CCCG CCCCTCCC    CCGGCC
                                  _      _____
GAM1385  C21orf2   3'  GGGCTGGGGAAGACGCTGGG   22304      C      __
                                GGGC GGGGAGG  GCTGGG
                                |||| |||||||  ||||||
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                                CCCG CCCCTTC  CGACCC
                                  A      TG
GAM1385  CHAD     5'  GGCTGGGACGCCTGGGGCCGGG 10417     C    AGGG
                                GGC GGGG    CTGGGGCCGGG
                                ||| ||||    ||||||||||
                                CCG CCCT    GACCCCGGCCC
                                  A   GCG_
GAM1385  COL6A2   3'  GGGCCTGGGGAGACCTGGGGCT 38445       _      G      C
              GGG                   GGGCC GGGGAGG CTGGGGC GGG
                                ||||| ||||||| ||||||| |||
                                CCCGG CCCCTCT GACCCCG CCC
                                  A      G      A
GAM1385  COL6A2   3'  GGGCTGGGCGGGGGCCGG    38447     GA    T
                                GGG  GGGC GGGGCCGG
                                |||  |||| ||||||||
                                CCC  CCCG CCCCGGCC
                                  GA   C
GAM1385  COPE     3'  GGGTGGGGAGGGCTGCAGGG   28576     CC         G  CC
                                GGG  GGGGAGGGCTG GG  GG
                                |||  |||||||||| ||  ||
                                CCC  CCCCTCCCGAC TC  CC
                                  A_          G  __
GAM1385  COX7A1   5'  CGGGGCTGGGGCTGGGGCTGGG 12408       A__        C
                                CGGGG   GGGCTGGGGC GGG
                                |||||   |||||||||| |||
                                GCCCC   CCCGACCCCG CCC
                                   GAC         A
GAM1385  COX7A1   5'  CGGCGGGGCTGGGGCTGG    12407     GGA        C
                                CGG   GGGCTGGGGC GG
                                |||   |||||||||| ||
                                GCC   CCCGACCCCG CC
                                  GC_         A
GAM1385  COX7A1   5'  GGGCTGGGGCTGGGGCTGGGGC 12411      C    A__        C
              TGGG                  GGGC GGGG   GGGCTGGGGC GGG
                                |||| ||||   |||||||||| |||
                                CCCG CCCC   CCCGACCCCG CCC
                                  A   GAC         A
GAM1385  CSK      3'  GGGCCGGAGGGGTGCAGGCTGG 20468          A   C  _   C
              G                   GGGCCGGGG GGG TG GGGC GGG
                                |||||||| ||| || |||| |||
                                CCCGGCCTC CCC AC TCCG CCC
                                     _  _ G   A
GAM1385  CYP11B1  3'  GGGCCAGGTGGGGCTGGG    41629         GA
                                GGGCCGGG  GGGCTGGG
                                ||||||||  ||||||||
                                CCCGGTCC  CCCGACCC
                                    AC
GAM1385  DAG1     3'  GGGCAGGGGAGAGGGGCTGGG  20525      C      GCT    C
                                GGGC GGGGAGG   GGGGC GGG
                                ||||  |||||||   ||||| |||
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                                CCCG CCCCTCT   CCCCG CCC
                                  T      ___     A
GAM1385  DES      3'  GGGCTGGGGAGGTCTGCGGG   43572      C      G   _
                                GGGC GGGGAGG CTG GGG
                                |||| ||||||| ||| |||
                                CCCG CCCCTCC GAC CCC
                                  A      A   G
GAM1385  DGUOK    3'  GGGCTGGGGATGGAAAGGTGGT 38961      C    _   CT  _  CC
              TGGG                  GGGC GGGGA GGG  GG GG  GGG
                                |||| ||||| |||  || ||  |||
                                CCCG CCCCT CCT  CC CC  CCC
                                  A    A   TT  A  AA
GAM1385  DLEC1    3'  GGGCCTGGGGCTGAGGGCTGGG 28834       _    ___
                                GGGCC GGGG   AGGGCTGGG
                                ||||| ||||   |||||||||
                                CCCGG CCCC   TCCCGACCC
                                   A    GAC
GAM1385  DMPK     5'  GGGTGAGGGCTGGGGGTTGGG  20621     _         CC_
                                GGG GAGGGCTGGGG   GGG
                                ||| ||||||||||   |||
                                CCC CTCCCGACCCC   CCC
                                  A          CAA
GAM1385  DMPK     5'  GGGCTAGGGGGGTGAGGGCTGGG 20619      C___   _
                                GGGC    GGG GAGGGCTGGG
                                ||||    ||| ||||||||||
                                CCCG    CCC CTCCCGACCC
                                  ATCC   A
GAM1385  DNMT3A   5'  GGGCTGGGGGGCTGCTGGG   35432      C    A  __
                                GGGC GGGG GG  GCTGGG
                                |||| |||| ||  ||||||
                                CCCG CCCC CC  CGACCC
                                  A    _  GA
GAM1385  DOC1     5'  GGGCGGGGGCCGGGCCGG    40482      CGG  A       G
                                GGGC   GG GGGCTGGG CCGG
                                ||||   || ||||||| ||||
                                CCCG   CC CCCGGCCC GGCC
                                   ___  _       _
GAM1385  DOC1     5'  GGGCCGGGCGGGGGCCGG    40481       GGGGA    T
                                GGGCC    GGGC GGGGCCGG
                                |||||    |||| ||||||||
                                CCCGG    CCCG CCCCGGCC
                                   _____    C
GAM1385  DRIL1    5'  GGGCCGCGGGGGGAGCCGG    23370       G  A   CTGG
                                GGGCCG GG GGG    GGCCGG
                                |||||| || |||    ||||||
                                CCCGGC CC CCC    TCGGCC
                                   G  _  _____
GAM1385  DUSP7    5'  GGCCCGGGGCCGGGGCCGG   42274      G   AGG
                                GGCC GGG   GCTGGGGCCGG
                                |||| |||   ||||||||||
```

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                                CCGG CCC   CGGCCCCGGCC
                                  G  ___
GAM1385  EGFL4    3'  GGGCTGGGGGGTGGCTGGA    41577      C    AG
                                GGGC GGGG  GGCTGGG
                                |||| ||||  |||||||
                                CCCG CCCC  CCGACCT
                                  A    CA
GAM1385  EGFL6    5'  GGCCTGGGGAGGGGCTGGG    31777      _      _
                                GGCC GGGGAGGG CTGGG
                                |||| |||||||| |||||
                                CCGG CCCCTCCC GACCC
                                  A       C
GAM1385  EGLN1    5'  GGGCCGGGAGGGCCGGG     35173         G
                                GGGCCGGG AGGGCTGGG
                                |||||||| |||||||||
                                CCCGGCCC TCCCGGCCC

                                  _
GAM1385  EIF4A1   3'  GAGCCCTGGCTGGGGCTGG   10868       GGGGAG        C
                                GGGCC     GGCTGGGGC GG
                                |||||     ||||||||| ||
                                CTCGG     CCGACCCCG CC
                                   GA____        A
GAM1385  EN1      3'  GGGCCGGCGATGCGGGTCGGG  10919        G  GG  T   GC
                                GGGCCGG GA  GC GGG  CGGG
                                ||||||| ||  || |||  ||||
                                CCCGGCC CT  CG CCC  GCCC
                                    G  A_  _   A_
GAM1385  ENG      5'  GGGCGGGGAGGGGGTGCTGGG  6503       C       CT  G  C
                                GGGC GGGGAGGG  GG GC GGG
                                |||| ||||||||  || || |||
                                CCCG CCCCTCCC  CC CG CCC
                                  _       __  A  A
GAM1385  ERBB3    3'  GGACTGGGGAAAAGGGGCTGGG 12755       C     _____
                                GGGC GGGGA    GGGCTGGG
                                |||| |||||    ||||||||
                                CCTG CCCCT    CCCGACCC
                                  A     TTTC
GAM1385  ESPN     3'  GGGCCTGGCTGGCTGGGGCTGG 36447       GG  AG        C
            G                    GGGCC  GG  GGCTGGGGC GGG
                                |||||  ||  ||||||||| |||
                                CCCGG  CC  CCGACCCCG CCC
                                  A_  GA        A
GAM1385  FAAH     3'  GGGTCGGGAAGGGGCCAGGGCC 11060     C        _ TG
            GGG                    GGG CGGGGAGGG C  GGGCCGGG
                                ||| |||||||| |  ||||||||
                                CCC GCCCTTCCC G  CCCGGCCC
                                  A        C GT
GAM1385  FDXR     3'  GGGCCGGGGCTGGGGCTGGG   35929         GAGG       C
                                GGGCCGGG    GCTGGGGC GGG
                                ||||||||    |||||||| |||
```

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                                CCCGGCCC   CGACCCCG CCC
                                     ____      A
GAM1385 GA      5' GGGTGGGGCTGGGGCTGGG  29970    GA       C
                                GGG  GGGCTGGGGC GGG
                                |||  |||||||||| |||
                                CCC  CCCGACCCCG CCC
                                  AC        A
GAM1385 GAS11   3' GGGCTGGAGGGGGCTGAGG  11218    C   A
                                GGGC GGGG GGGCTGGGG
                                |||| |||| |||||||||
                                CCCG CCTC CCCGACTCC
                                  A   C
GAM1385 GDI1    3' GGGCTGGGAGGGGCTGGG   41015    C   GA
                                GGGC GGG  GGGCTGGG
                                |||| |||  ||||||||
                                CCCG CCC  CCCGACCC
                                  A  TC
GAM1385 GNB2    5' GGGCCGCGGGACGGGGGCTGGG 23602      _   ___
                                GGGCCG GGGA  GGGCTGGG
                                |||||| ||||  ||||||||
                                CCCGGC CCCT  CCCGACCC
                                   G   GCC
GAM1385 GNB2    5' GGGTTGGGGGCGGCTGGG   23603    CC   AG
                                GGG  GGGG  GGCTGGG
                                |||  ||||  |||||||
                                CCC  CCCC  CCGACCC
                                  AA   CG
GAM1385 GNB2    3' GGCCCGGGGAAGGGGGCTGGG 23601   G       CTG   C
                                GG CCGGGGAGGG  GGGC GGG
                                || ||||||||||  |||| |||
                                CC GGCCCCTTCC  CCCG CCC
                                 G        ___   A
GAM1385 GPI     3' GGGCTGGGGGTTAGGCTGGG  6750     C   A__
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CCCG CCCC  TCCGACCC
                                  A   CAA
GAM1385 GUCY1A2 5' GGGCGGGGAGGGCTGCGG   9223     C       G
                                GGGC GGGGAGGGCTG GG
                                |||| |||||||||| ||
                                CCCG CCCCTCCCGAC CC
                                  _        G
GAM1385 HOXB5   3' GGGCTGGGGGTGGCACGGG  13450    C   AG  _
                                GGGC GGGG  GGC TGGG
                                |||| ||||  ||| ||||
                                CCCG CCCC  CCG GCCC
                                  A   CA  T
GAM1385 HSD11B2 5' GGGCGGGGGCCGGGCCGG   6806     CGG A     G
                                GGGC  GG GGGCTGGG CCGG
                                ||||  || |||||||| ||||
```

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                                CCCG   CC CCCGGCCC GGCC
                                  ___  _      _
GAM1385  IKBKB    5'  GGGCGGGGAAGGCGGGGCTGGG 41810      C       T    C
                                GGGC GGGGAGGGC GGGGC GGG
                                |||| ||||||||| ||||| |||
                                CCCG CCCCTTCCG CCCCG CCC
                                  _       _    A
GAM1385  IL12RB2  5'  GGGCGGGGGTCGGGGCTGGG  11433     C   A__
                                GGGC GGGG   GGGCTGGG
                                |||| ||||   ||||||||
                                CCCG CCCC   CCCGACCC
                                  C   AGC
GAM1385  IL12RB2  5'  GGGCCGGGGCGGGGGTCGGG  11432         AGGGCT   C
                                GGGCCGGGG     GGGG CGGG
                                |||||||||     |||| ||||
                                CCCGGCCCC     CCCC GCCC
                                     GC____   A
GAM1385  INPPL1   5'  GGGCTGAGGCTGGGGCCGGG  11465     C GGGA
                                GGGC G    GGGCTGGGGCCGGG
                                |||| |    ||||||||||||||
                                CCCG C    TCCGACCCCGGCCC
                                  A _____
GAM1385  ITGA3    3'  GGAAGGGGCTGGGGCTGG    24261        _      C
                                GGGAGGG CTGGGGC GG
                                ||||||| ||||||| ||
                                CCTTCCC GACCCCG CC
                                    C      A
GAM1385  ITPKB    3'  GGGCCAGGGAGGGCGTGGG   13648             _
                                GGGCCGGGGAGGGC TGGG
                                |||||||||||||| ||||
                                CCCGGTCCCTCCCG ACCC
                                       C
GAM1385  JAK3     3'  GGGCCAGGGCTTAAGGGGTTGG 6863          AGGGCT   CC
           G                     GGGCCGGGG     GGGG  GGG
                                |||||||||     ||||  |||
                                CCCGGTCCC     CCCC  CCC
                                     GAATT_   AA
GAM1385  JUNB     5'  GGTCTGGGGAGGGTCCCTGCGG 13764    GCC      _ GGG  C
           G                     GG   GGGGAGGG CT   GC GGG
                                ||   |||||||| ||   || |||
                                CC   CCCCTCCC GG   CG CCC
                                 AGA       A  GA_ _
GAM1385  JUP      5'  GGGTCGGGGTCGGGCCGGG   13780     C    A_
                                GGG CGGGG  GGGCTGGG
                                ||| |||||  ||||||||
                                CCC GCCCC  CCCGGCCC
                                  A    AG
GAM1385  JUP      5'  GGGCCGGGTCGGGGTCGG    13778        GAGGGCT   C
                                GGGCCGGG     GGGG CGG
                                ||||||||     |||| |||
```

```
                                CCCGGCCC      CCCC GCC
                                    AG_____   A
GAM1385 KCNJ10   5' GGGCCGGGGCCGGGGTCGGG  13873       GAGG     C
                                GGGCCGGG   GCTGGGG CGGG
                                ||||||||   ||||||| ||||
                                CCCGGCCC   CGGCCCC GCCC
                                    _____     A
GAM1385 KCNK4    5' GGGCCGGGCGGGGGGCTCCTGG 37837       GA  CT  G_ _
           G                     GGGCCGGG  GGG  GGG  CC GGG
                                ||||||||  |||  |||  || |||
                                CCCGGCCC  CCC  CCC  GG CCC
                                    G_  __  GA  A
GAM1385 KIF5C    5' GGGTGGGGGGCCGGGGCCGGG  21158    CCG  A
                                GGG  GGG GGGCTGGGGCCGGG
                                |||  ||| ||||||||||||||
                                CCC  CCC CCCGGCCCCGGCCC
                                  A__  _
GAM1385 KIFC3    5' GGCCGGGCTGGCTGGGGCTGGG 24463       GAG       C
                                GGCCGGG  GGCTGGGGC GGG
                                |||||||  |||||||| |||
                                CCGGCCC  CCGACCCCG CCC
                                    GA_       A
GAM1385 KLK4     3' GGTCTGGGGAAGGAGGGGTTGG 41755    GCC      CT   CC
           G                     GG  GGGGAGGG  GGGG  GGG
                                ||  ||||||||  ||||  |||
                                CC  CCCCTTCC  CCCC  CCC
                                  AGA      T_   AA
GAM1385 KPNB1    5' GGGATGGGGGTTGGGGGTCGGG 13975    CCG  A  GCT   C
                                GGG  GGG GG  GGGG CGGG
                                |||  ||| ||  |||| ||||
                                CCC  CCC CC  CCCC GCCC
                                  TA_  _ AAC   A
GAM1385 L1CAM    3' GGCTGGGGAGTGGCTGGG   35803    C    _
                                GGC GGGGAG GGCTGGG
                                ||| |||||| |||||||
                                CCG CCCCTC CCGACCC
                                  A     A
GAM1385 LFG      3' GGGTGGGGAGGGATGGGGCTGG 44145    CC      C    C
           G                     GGG  GGGGAGGG TGGGGC GGG
                                |||  |||||||| |||||| |||
                                CCC  CCCCTCCC ACCCCG CCC
                                  A_       T     A
GAM1385 LIMK1    5' GGGCTGGGGGGCGGCCGGG    14171     C   AG
                                GGGC GGGG  GGCTGGG
                                ||||| ||||  |||||||
                                CCCG CCCC  CCGGCCC
                                  A   CG
GAM1385 LIMK1    5' GGGCCCGGCGGGGCTGGGGCTG 14170      G  GA       C
           GG                    GGGCC GG  GGGCTGGGGC GGG
                                |||||| ||  ||||||||||| |||
```

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                                CCCGG CC  CCCGACCCCG CCC
                                  G  GC        A
GAM1385  LOXL2    3'  GGGTGGGGGCCGGGCTGGG   14198    CC   A_
                                GGG  GGGG  GGGCTGGG
                                |||  ||||  ||||||||
                                CCC  CCCC  CCCGACCC
                                  AC   GG
GAM1385  MADH3    5'  GGCTGGGGAGGGCGTGCGGG  25348    C      _ _
                                GGC GGGGAGGGC TG GGG
                                ||| ||||||||| || |||
                                CCG CCCCTCCCG AC CCC
                                  A       C  G
GAM1385  MAML1    5'  GGGCCGGGCCCGGGGCCGG   31293       GAGGG
                                GGGCCGGG    CTGGGGCCGG
                                ||||||||    ||||||||||
                                CCCGGCCC    GGCCCCGGCC
                                    G____
GAM1385  MAP3K10  3'  GGGCTGGGGCAGGGCCTGGG  42757    C   _    _
                                GGGC GGGG AGGGC TGGG
                                |||| |||| ||||| ||||
                                CCCG CCCC TCCCG ACCC
                                  A   G    G
GAM1385  MAX      3'  GGGCTGGGAAGGGTCCGCACTG 40364     C      _  GG  C
           GG                   GGGC GGGGAGGG CTG  GC GGG
                                |||| |||||||| |||  || |||
                                CCCG CCCTTCCC GGC  TG CCC
                                  A       A  G_  A
GAM1385  MECP2    3'  GGGCCGGGAGGGGTAGACCTGG 22603       G   CTG    _
           G                    GGGCCGGG AGGG   GGGCC GGG
                                |||||||| ||||   ||||| |||
                                CCCGGCCC TCCC   TCTGG CCC
                                    _   CA_    A
GAM1385  MFI2     5'  GGCTGGGGCCGGGCTGGGGCTG 25468    C   A_       C
           GG                   GGC GGGG  GGGCTGGGGC GGG
                                |||  ||||  |||||||||| |||
                                CCG CCCC  CCCGACCCCG CCC
                                  A   GG        A
GAM1385  MFI2     5'  GGGGCTGGCTGGGGCCGG    25470     AG
                                GGGG  GGCTGGGGCCGG
                                ||||  ||||||||||||
                                CCCC  CCGACCCCGGCC
                                  GA
GAM1385  MIC2     5'  GGGCCGGGTGGGGCGAAGCCCG 14506       GA   TG  G
           GG                   GGGCCGGG  GGGC  GG CCGGG
                                ||||||||  ||||  || |||||
                                CCCGGCCC  CCCG  TC GGCCC
                                    AC   CT  G
GAM1385  MYLK2    3'  GAGCTGGGGAGGGAACCGGG  37522     C      CTGG
                                GGGC GGGGAGGG   GGCCGGG
                                |||| ||||||||   |||||||
```

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                                CTCG CCCCTCCC    TTGGCCC
                                  A      ____
GAM1385  NGFR     3'  GGGCTGGGGGAACCCTGGGCTG 14786      C    A    G_   C
                GG                  GGGC GGGG GGGCT  GGGC GGG
                                    |||| |||| |||||  |||| |||
                                    CCCG CCCC CTTGG  CCCG CCC
                                      A   _    GA   A
GAM1385  NGFR     3'  GGGCTGAGGGAGGGTTGAGG   14785      C _      C
                                    GGGC G GGGAGGG TGGGG
                                    |||| | ||||||| |||||
                                    CCCG C CCCTCCC ACTCC
                                      A T      A
GAM1385  NR1D1    3'  GGGCCAGGGGAGGGTTGTGGG  34703       _       C _
                                    GGGCC GGGGAGGG TG GGG
                                    ||||| |||||||| || |||
                                    CCCGG CCCCTCCC AC CCC
                                       T       A  A
GAM1385  NRIP1    5'  GGGCGGGCGTGGGGCCGG    40967     A   _
                                    GGG GGGC TGGGGCCGG
                                    ||| |||| |||||||||
                                    CCC CCCG ACCCCGGCC
                                      G    C
GAM1385  NTSR1    3'  GGGTGGGGAGGAGTTGGG    14891     CC      _ C
                                    GGG  GGGGAGG G TGGG
                                    |||  ||||||| | ||||
                                    CCC  CCCCTCC C ACCC
                                      A_      T A
GAM1385  OLFM1    5'  GGGCTGGGCAGGGCTGGGCTGG 26777      C   G        G C
                G                    GGGC GGG AGGGCTGGG C GGG
                                    |||| ||| ||||||||| | |||
                                    CCCG CCC TCCCGACCC G CCC
                                      A  G        _ A
GAM1385  OTOF     3'  GGGCTGGGGAGCGGCTGGCGGG 22062      C     _     GGC
                                    GGGC GGGGAG GGCTGG   CGGG
                                    |||| |||||| ||||||   ||||
                                    CCCG CCCCTC CCGACC   GCCC
                                      A     G     ___
GAM1385  PACE     3'  GGCTGGGGCCGGGGCCGG    15036     C   GAGG
                                    GGC GGG    GCTGGGGCCGG
                                    ||| |||    ||||||||||
                                    CCG CCC    CGGCCCCGGCC
                                      A  _____
GAM1385  PACSIN1  3'  GGGCTGGGAGGGCTGGCACAG  45160      CG         G  C
                                    GGGC  GGGAGGGCTGG GC GG
                                    ||||  |||||||||| || ||
                                    CCCG  CCCTCCCGACC TG TC
                                      A_          G  _
GAM1385  PAH      5'  GGGCTGAGGGAGGGTGTGGG   7094       C _      C  _
                                    GGGC G GGGAGGG TG GGG
                                    |||| | ||||||| || |||
```

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                                CCCG C CCCTCCC AC CCC
                                  A T      _ A
GAM1385  PEA15    3'  GGGTGGGGAGGGGCATCTTGGG 19079     CC       _ ____
                                GGG  GGGGAGGG C    TGGG
                                |||  |||||||| |    ||||
                                CCC  CCCCTCCC G    ACCC
                                  A_       C TAGA
GAM1385  PEX14    3'  GGGCTGGGGAGGGGCTTGGG   41875     C       _ _
                                GGGC GGGGAGGG CT GGG
                                |||| |||||||| || |||
                                CCCG CCCCTCCC GA CCC
                                  A       C  A
GAM1385  PEX14    3'  GGGCCTGGGGCTGGGGCTGGG  41874      GGGGA        C
                                GGGCC    GGGCTGGGGC GGG
                                |||||    |||||||||| |||
                                CCCGG    CCCGACCCCG CCC
                                   AC___         A
GAM1385  PEX14    3'  GGGGCTGGGGCTGGGGCTGGG  41876     A__         C
                                GGGG   GGGCTGGGGC GGG
                                ||||   |||||||||| |||
                                CCCC   CCCGACCCCG CCC
                                  GAC         A
GAM1385  PFKFB4   3'  GGGCTGGGGTGGGGGCTCTGGG 21293      C    A__     G_
                                GGGC GGGG   GGGCT  GGG
                                |||| ||||   |||||  |||
                                CCCG CCCC   CCCGA  CCC
                                  A   ACC     GA
GAM1385  PFKL     3'  GGGCTGGGGAGGGGCGTGGG   15238      C       _ _
                                GGGC GGGGAGGG C TGGG
                                |||| |||||||| | ||||
                                CCCG CCCCTCCC G ACCC
                                  A       C C
GAM1385  PIK3R2   5'  GGGCTGGGAGGGTCCGCTGGG  22750      CG     ____
                                GGGC  GGGAGG    GCTGGG
                                ||||  ||||||    ||||||
                                CCCG  CCCTCC    CGACCC
                                  A_      CAGG
GAM1385  PKD1     3'  GAGCTGGGGAGGGGACCCTGGG 7137       C       _____
                                GGGC GGGGAGGG    CTGGG
                                |||| ||||||||    |||||
                                CTCG CCCCTCCC    GACCC
                                  A       CTGG
GAM1385  PKM2     3'  GGGCTGGAGGAGGGGCTCTGGG 15335      C  _     ___
                                GGGC GG GGAGGG   CTGGG
                                |||| || ||||||   |||||
                                CCCG CC CCTCCC   GACCC
                                  A  T     CGA
GAM1385  PLD2     3'  GGGCTGGGAGGGCCCTGGG    15384      CG       G_
                                GGGC  GGGAGGGCT  GGG
                                ||||  |||||||||  |||
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                                CCCG  CCCTCCCGG  CCC
                                  A_       GA
GAM1385  POLR2E   3'  GAGCTGGGGTGGGGCTGGG   40920     C   A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CTCG CCCC  CCCGACCC
                                  A   AC
GAM1385  PPP1R8   5'  GAGGTAGGGTTGGGGCCGGG   39728     _   C
                                GGGG AGGG TGGGGCCGGG
                                |||| |||| ||||||||||
                                CTCC TCCC ACCCCGGCCC
                                  A   A
GAM1385  PPP2R4   3'  GGGATGGGGAGGGGCCACTGCT 41331     CC      _  GG  C
            GGG                   GGG  GGGGAGGG CTG  GC GGG
                                ||| |||||||| |||  || |||
                                CCC  CCCCTCCC GGT  CG CCC
                                  TA       C   GA  A
GAM1385  PPP3CB   5'  GGGCCGGGCGGGGTTGGG    34450        GA   C
                                GGGCCGGG  GGG TGGG
                                ||||||||  ||| ||||
                                CCCGGCCC  CCC ACCC
                                     GC   A
GAM1385  PPP4C    3'  GGGTTGGAGGGGGCAGGGGCCG 15536     CC    A    T
            GG                    GGG  GGGG GGGC GGGGCCGGG
                                |||  |||| |||| |||||||||
                                CCC  CCTC CCCG CCCCGGCCC
                                  AA   C   T
GAM1385  PRKACA   3'  GGGCTGGGAGGGCTGAGGGGCT 15585     CG       __    C
            GGG                   GGGC  GGGAGGGCT  GGGGC GGG
                                ||||  |||||||||  ||||| |||
                                CCCG  CCCTCCCGA  CCCCG CCC
                                  A_       CT    A
GAM1385  PSD      5'  GGGCCAGGGAGTGGGCCGG   15788          GGCTG
                                GGGCCGGGGAG    GGGCCGG
                                ||||||||||    |||||||
                                CCCGGTCCCTC    CCCGGCC
                                     A____
GAM1385  PSD      5'  GGGCTGGGGTGGGCCTGGG   15789     C   A   _
                                GGGC GGGG GGGC TGGG
                                |||| |||| |||| ||||
                                CCCG CCCC CCCG ACCC
                                  A   A   G
GAM1385  PTMS     5'  GGTGCCGGGGCCGGGGCCGGG  15897   _     GAGG
                                GG GCCGGG   GCTGGGGCCGGG
                                || ||||||   ||||||||||||
                                CC CGGCCC   CGGCCCCGGCCC
                                 A    _____
GAM1385  PTPRJ    3'  GGGCAGGGGAAGCGGGGCCGGG 15961     C      G T
                                GGGC GGGGAGG C GGGGCCGGG
                                |||| ||||||| | |||||||||
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                                CCCG CCCCTTC G CCCCGGCCC
                                  T     _ _
GAM1385  PVRL2    5'  GGGCCCGGGAGGGGACTGGG   16003      G     __
                                GGGCC GGGAGGG  CTGGG
                                ||||| |||||||  |||||
                                CCCGG CCCTCCC  GACCC
                                   G      CT
GAM1385  PYCR1    3'  GGGCCGGGAGGGGGCGTGGG   43127        _ A   _
                                GGGCCGGG G GGGC TGGG
                                |||||||| | |||| ||||
                                CCCGGCCC C CCCG ACCC
                                     T C   C
GAM1385  RAB3B    5'  GGGCCGGGGCGGGGCGCTGCGG 16083         A  C  GG  C
            G                    GGGCCGGGG GGG TG  GC GGG
                                |||||||| ||| ||  || |||
                                CCCGGCCCC CCC GC  CG CCC
                                     G  C  GA  _
GAM1385  RAB7     5'  GCGCTGGGGGCTCCGGGCCGGG 21577    CGG  A    G_
                                GC   GG GGGCT  GGGCCGGG
                                ||   || |||||  ||||||||
                                CG   CC CCCGA  CCCGGCCC
                                 CGA  _    GG
GAM1385  RAD21    5'  GGCCCGGGGAGGGGAAAAGGGT 26526    G        CT__   C
            CGGG                   GG CCGGGGAGGG    GGGG CGGG
                                || ||||||||||    |||| ||||
                                CC GGCCCCTCCC    TCCC GCCC
                                 G        CTTT    A
GAM1385  RFX1     3'  GGGCTGGGGAGAAGACGCTGGG 16293      C     ____
                                GGGC GGGGAGG    GCTGGG
                                |||| |||||||    ||||||
                                CCCG CCCCTCT    CGACCC
                                  A      TCTG
GAM1385  ROR2     5'  GGGCCGGGGCGCGGGGTCGGG  21264         AGG  T    C
                                GGGCCGGGGG   GC GGGG CGGG
                                |||||||||   || |||| ||||
                                CCCGGCCCC   CG CCCC GCCC
                                     G__  _    A
GAM1385  RPIP8    5'  AGGCCGGGGAGGGAGCTCTCCG 27449           CTGGGG
            GG                   GGGCCGGGGAGGG     CCGGG
                                ||||||||||||     |||||
                                TCCGGCCCCTCCC     GGCCC
                                       TCGAGA
GAM1385  RXRA     3'  AGGCTGGGGAGGGGCCGG    16412      C    GGGCT
                                GGGC GGGGA    GGGGCCGG
                                |||| |||||    ||||||||
                                TCCG CCCCT    CCCCGGCC
                                  A    _____
GAM1385  RYR1     5'  GGGCTGGGGGCGGGCTGGG    8072       C   A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
```

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                                CCCG CCCC  CCCGACCC
                                  A   CG
GAM1385  RYR1     5'  GGGCGGGAGGGCTGGG     8070      CG
                                GGGC  GGGAGGGCTGGG
                                ||||  ||||||||||||
                                CCCG  CCCTCCCGACCC
                                  __
GAM1385  SCRT1    5'  GGGCTTGGGGGGGCTGCGG   36369     C_   A     G
                                GGGC  GGGG GGGCTG GG
                                ||||  |||| |||||| ||
                                CCCG  CCCC CCCGAC CC
                                  AA   _     G
GAM1385  SF1      5'  GGGCCGGGGGCGGCGGGGCCGG 21566         AG   T
             G                   GGGCCGGGG  GGC GGGGCCGGG
                                |||||||||  ||| |||||||||
                                CCCGGCCCC  CCG CCCCGGCCC
                                    CG  _
GAM1385  SLC6A8   5'  GGGCCGGGGGGCGGCCGG    24779        AG   TGG
                                GGGCCGGGG  GGC   GGCCGG
                                |||||||||  |||   ||||||
                                CCCGGCCCC  CCG   CCGGCC
                                    __  ___
GAM1385  SLC8A2   3'  GGGCTGGGGGGAAGGGCTGGG  42418      C___
                                GGGC   GGGGAGGGCTGGG
                                ||||   ||||||||||||
                                CCCG   CCCTTCCCGACCC
                                  ACCC
GAM1385  SLC9A5   3'  GCTGGGGAGGGAGTTGGG    21389    C      C__
                                GC GGGGAGGG   TGGG
                                || ||||||||   ||||
                                CG CCCCTCCC   ACCC
                                 A       TCA
GAM1385  SMARCB1  5'  GGGCTGGGGCGGGGCCGG    42315     C    AGGGC
                                GGGC GGGG    TGGGGCCGG
                                |||| ||||    |||||||||
                                CCCG CCCC    GCCCCGGCC
                                  A   ______
GAM1385  SNL      3'  GGGCTGGGAGGAGGTGGCTGGG 16945     CG      CT  _   C
                                GGGC  GGGAGGG  GG GGC GGG
                                ||||  |||||||  || ||| |||
                                CCCG  CCCTCCT  CC CCG CCC
                                  A_      __  A   A
GAM1385  SOX10    3'  AGGCTGGGGGGCAGGGGCTGGG  27994     CGG  A    T    C
                                GGGC   GG GGGC GGGGC GGG
                                ||||   || |||| ||||| |||
                                TCCG   CC CCCG CCCCG CCC
                                  A__  _    T    A
GAM1385  SPI1     3'  GGGCCGGCGGGGGGCTGCGGG   17079        _  A     _
                                GGGCCGGG GG GGGCTG GGG
                                ||||||| || |||||| |||
```

```
                                CCCGGCC CC CCCGAC CCC
                                   G _     G
GAM1385  TAGLN    3'  GAGCTGGGGGAGGGCCGGG   40617      C_
                                GGGC  GGGGAGGGCTGGG
                                ||||  |||||||||||||
                                CTCG  CCCCTCCCGGCCC
                                  AC
GAM1385  TBR1     3'  GGGCCGCGGCGGGGCCGG    27312       G  AGGGC
                                GGGCCG GG    TGGGGCCGG
                                |||||| ||    |||||||||
                                CCCGGC CC    GCCCCGGCC
                                   G _____
GAM1385  TEM8     3'  GGGTTGGGGAGAGGCTGGG   38186     CC     _
                                GGG  GGGGAG GGCTGGG
                                |||  |||||| |||||||
                                CCC  CCCCTC CCGACCC
                                  AA     T
GAM1385  TFDP1    5'  GGGCTGGGGCCGGGCCGGG   28285      C    A_
                                GGGC GGGG  GGGCTGGG
                                |||| ||||  ||||||||
                                CCCG CCCC  CCCGGCCC
                                  A    GG
GAM1385  TFDP1    5'  AGGCGCGGGCTGGGGCCGGG   28274      CGGGGA
                                GGGC     GGGCTGGGGCCGGG
                                ||||     ||||||||||||||
                                TCCG     CCCGACCCCGGCCC
                                  CG____
GAM1385  TGFB1    3'  GGGGCGGGGTGGGGCCGG    8547       A   C
                                GGGG GGG TGGGGCCGG
                                |||| ||| |||||||||
                                CCCC CCC ACCCCGGCC
                                  G   C
GAM1385  THY1     3'  GGTGGGGGCTGGGGGTTGGG   26629    _  A       CC_
                                GG GG GGGCTGGGG   GGG
                                || || |||||||||   |||
                                CC CC CCCGACCCC   CCC
                                 A  _        CAA
GAM1385  TMPRSS2  3'  GGGTTAGGGAGAGCAGGCTGGG 24936     CC        TG    C
                                GGG  GGGGAGGGC  GGGC GGG
                                |||  |||||||||  |||| |||
                                CCC  TCCCTCTCG  TCCG CCC
                                  AA        __    A
GAM1385  TPSB1    3'  GGGCAGGGGAGGGCTGGAGGG  17658      C           CC
                                GGGC GGGGAGGGCTGGGG  GG
                                |||| ||||||||||||||  ||
                                CCCG CCCCTCCCGACCTC  CC
                                  T           __
GAM1385  TRAF5    5'  GGCCTGGGGCGGGGCCGG    21473      GGGGA   T
                                GGCC    GGGC GGGGCCGG
                                ||||    |||| ||||||||
```

```
                                CCGG    CCCG CCCCGGCC
                                  AC___   _
GAM1385 VASP    5' GGGCCGGGGCGGGTCTCCGGG 17918        A  _ GGGG
                                GGGCCGGGG GGG CT   CCGGG
                                ||||||||| ||| ||   |||||
                                CCCGGCCCC CCC GA   GGCCC
                                     G  A ____
GAM1385 WDR4    3' GGGCTACGGCTGGGGCTGGG  38023     CGGGGAG      C
                                GGGC     GGCTGGGGC GGG
                                ||||     ||||||||| |||
                                CCCG     CCGACCCCG CCC
                                  ATG____       A
GAM1385 WNT3A   5' GCCGGGGGGGGGCCG       37545       AGGGCT
                                GCCGGGG    GGGGCCG
                                |||||||    |||||||
                                CGGCCCC    CCCCGGC

                                  _______
GAM1385 ASGR2   5' GAGGGCTGGGGCTGGGGCAG  38953          C   A
                                GAGGGCTGGGGC GGGG GG
                                |||||||||||| |||| ||
                                CTCCCGACCCCG CCCC TC
                                      A   G
GAM1385 ATP7B   3' GGGCTGGAGTCGGGGGGCTG  6278         C    AG
                                GGGCTGGGG CGGGG  GGCTG
                                ||||||||| |||||  |||||
                                CCCGACCTC GCCCC  CCGAC
                                     A   __
GAM1385 BGN     3' GGGCTGGGTTGGACGCAGCTG 11822       GCCG  AG_
                                GGGCTGGG   GGG  GGCTG
                                ||||||||   |||  |||||
                                CCCGACCC   CCT  TCGAC
                                    AA__  GCG
GAM1385 BGN     3' GAGCCGCAGAGTCGGGGAGGG 11817      __  C
                                GGGCTG  GGG CGGGGAGGG
                                ||||||  ||| |||||||||
                                CTCGGC  CTC GCCCCTCCC
                                   GT  A
GAM1385 CCND1   5' GAGGGCTGTGGGTCCTGGCTG 38206       _  _ GGGGAG
                                GAGGGCTG GGG CC     GGCTG
                                |||||||| ||| ||     |||||
                                CTCCCGAC CCC GG     CCGAC
                                    A  A  A_____
GAM1385 CCND1   5' GGGCAGCTGGGGAGGGCT   38214     TGG  C
                                GGGC  GGC GGGGAGGGCT
                                ||||  ||| ||||||||||
                                CCCG  TCG CCCCTCCCGA
                                  ___  A
GAM1385 COX7A1  5' GGGGCTGGGGCTGGGGCTGGG 12412   A       C   A_
                                G GGGCTGGGGC GGGG  GGG
                                | |||||||||| ||||  |||
```

```
                                C CCCGACCCCG CCCC  CCC
                                _       A   GA
GAM1385  COX7A1   5'  GGGGCTGGGGCTGGGGCTGGGG 12413   A       C   A__
             CTG                  G GGGCTGGGGC GGGG  GGGCTG
                                | ||||||||| ||||  ||||||
                                C CCCGACCCCG CCCC  CCCGAC
                                _       A   GAC
GAM1385  DACH    5'  GGGGGCTGGGATCGAGGGCTG  38872   A      GC GGG
                                G GGGCTGGG  C  GAGGGCTG
                                | ||||||||  |  ||||||||
                                C CCCGACCC  G  CTCCCGAC
                                 C      TA ___
GAM1385  DBH     3'  AGGGCTGGCGGAGGGCT    8966        GGCCGG
                                AGGGCTGG    GGAGGGCT
                                ||||||||    ||||||||
                                TCCCGACC    CCTCCCGA
                                    G_____
GAM1385  DLEC1   3'  GGGCCTGGGGCTGAGGGCTG  28833    _    CGGG
                                GGGC TGGGGC   GAGGGCTG
                                |||| ||||||   ||||||||
                                CCCG ACCCCG   CTCCCGAC
                                  G    A___
GAM1385  DMPK    5'  GAGGGCTGGGGGTTGGGGCTG  20612         CCG GGA
                                GAGGGCTGGGG  G  GGGCTG
                                ||||||||||  |  ||||||
                                CTCCCGACCCC  C  CCCGAC
                                    ___ AAC
GAM1385  DMPK    5'  GGGCTAGGGGGTGAGGGCTG  20618       CC  G
                                GGGCTGGGG  GG GAGGGCTG
                                |||||||||  || ||||||||
                                CCCGATCCC  CC CTCCCGAC
                                    __  A
GAM1385  FDXR    3'  GGGGCCGGGGCTGGGGCT   35930        A__
                                GGGGCCGGGG  GGGCT
                                ||||||||||  |||||
                                CCCCGGCCCC  CCCGA
                                    GAC
GAM1385  GA      5'  GGGGCTGGGGCTGGGGCAG  29969   A       C   A
                                G GGGCTGGGGC GGGG GG
                                | ||||||||| |||| ||
                                C CCCGACCCCG CCCC TC
                                _       A   G
GAM1385  GGA1    3'  TGGGGTTGGGGCTGGGCC   30052     CC   A_
                                TGGGG  GGGG  GGGCT
                                |||||  ||||  |||||
                                ACCCC  CCCC  CCCGG
                                  AA   GA
GAM1385  HIC1    5'  GGGGCTCGGGTCCCGGGCTG  44568     _   GA__
                                GGGGC CGGG   GGGCTG
                                ||||| ||||   ||||||
```

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                                CCCCG GCCC   CCCGAC
                                  A   AGGG
GAM1385  ITGA3    3'  GGGCTGGGGCTGGGGAGTGGGC 24266          C    __
                TG                  GGGCTGGGGC GGGGA  GGGCTG
                                    |||||||||| |||||  ||||||
                                    CCCGACCCCG CCCCT  CCCGAC
                                       A    CA
GAM1385  LFG      3'  GAGGGCTGGGCTGGGC      44135          G CGGGGA
                                    GAGGGCTGGG C     GGGC
                                    |||||||||| |     ||||
                                    CTCCCGACCC G     CCCG
                                       _ A_____
GAM1385  NRAP     3'  GGGCTGGGGCAGGGGCT     40196          CGG  A
                                    GGGCTGGGGC   GG GGGCT
                                    ||||||||||   || |||||
                                    CCCGACCCCG   TC CCCGA
                                       ___ _
GAM1385  PCOLCE   3'  GAGGGCTAGGGGCCGGGG    45237        _
                                    GAGGGCT GGGGCCGGGG
                                    ||||||| ||||||||||
                                    CTCCCGA CCCCGGCCCC
                                       T
GAM1385  PEX14    3'  GGGGCTGGGGCTGGGGCTGGGG 41877   A        C    A__
                CTG                   G GGGCTGGGGC GGGG   GGGCTG
                                    | ||||||||| ||||   ||||||
                                    C CCCGACCCCG CCCC   CCCGAC
                                    _        A   GAC
GAM1385  PLXNB2   3'  GGGGCTGGGGCTGGTGCT    29648   A        C  GGAGG
                                    G GGGCTGGGGC GG    GCT
                                    | ||||||||| ||    |||
                                    C CCCGACCCCG CC    CGA
                                    _        A  A____
GAM1385  PNUTL2   3'  GGACTTGGTTGGGGAGGG    38649       G  GCC
                                    GGGCT GG   GGGGAGGG
                                    ||||| ||   ||||||||
                                    CCTGA CC   CCCCTCCC
                                       A  AA_
GAM1385  PRKACA   3'  GAGGGCTGAGGGGCTGGGGGGC 15577        __    CG   A
                TG                    GAGGGCT  GGGGC  GGG GGGCTG
                                    ||||||| |||||  ||| ||||||
                                    CTCCCGA  CCCCG  CCC CCCGAC
                                       CT    A_  _
GAM1385  PRKCA    3'  GAGGGCTGGGGGCTGGGGAGG  15624          _ C
                                    GAGGGCTGGGG C GGGGAGG
                                    |||||||||| | |||||||
                                    CTCCCGACCCC G CCCCTCC
                                          C A
GAM1385  PYGB     3'  GAGGGCAGGGGGCAGGGGGCTG 16049       T_    CG   A
                                    GAGGGC  GGGGC  GGG GGGCTG
                                    ||||||  |||||  ||| ||||||
```

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                                CTCCCG  CCCCG  TCC CCCGAC
                                   TC    __  _
GAM1385  RFNG     3'  GGGCTGGGAGAGGGGGGGCTG  44775        CC    A
                                GGGCTGGGG  GGGG GGGCTG
                                |||||||||  |||| ||||||
                                CCCGACCCT  CCCC CCCGAC
                                     CT   _
GAM1385  RYR1     5'  GAGGGCTGGGGGGCGGGCT    8067          CCGGGGA
                                GAGGGCTGGGGG      GGGCT
                                ||||||||||       |||||
                                CTCCCGACCCC      CCCGA
                                      CG_____
GAM1385  RYR1     5'  GGGCTGGGCGGGAGGGCTG    8071         G CG
                                GGGCTGGG C  GGGAGGGCTG
                                ||||||||  |  ||||||||||
                                CCCGACCC G  CCCTCCCGAC

                                  _ __
GAM1385  SLC30A3  3'  GGGGCTGGGGCTGAGGCT    18432    A        C GGGA
                                G GGGCTGGGGC G    GGGCT
                                | ||||||||||  |    |||||
                                C CCCGACCCCG C    TCCGA
                                 _         A _____
GAM1385  SLC8A2   3'  GAGGGCTGGGGGGGAAGGGCTG  42414          CCG
                                GAGGGCTGGGG   GGGAGGGCTG
                                ||||||||||   ||||||||||
                                CTCCCGACCCC   CCTTCCCGAC

                                     ___
GAM1385  SLC9A1   5'  GGGCTGGGAGCCCAGGCTG   43236        _   GGGGA
                                GGGCTGGG GCC     GGGCTG
                                ||||||||  |||     ||||||
                                CCCGACCC CGG     TCCGAC
                                     T   G_____
GAM1385  SUOX     5'  AGGCTGGGGCGCTGGGGCTG  7838          CGGGGA
                                GGGCTGGGGC      GGGCTG
                                ||||||||||      ||||||
                                TCCGACCCCG      CCCGAC
                                      CGAC__
GAM1385  TBXA2R   5'  GAGGGTGGGGCGAGGGCT    9855       C     CGGG
                                GAGGG TGGGGC    GAGGGCT
                                |||||  ||||||    |||||||
                                CTCCC ACCCCG    CTCCCGA

                                  _     _____
GAM1385  TCFL4    3'  GAGGGCTGGTGGCTGGGG    41828          _  C
                                GAGGGCTGG GGC GGGG
                                |||||||||  ||| ||||
                                CTCCCGACC CCG CCCC
                                      A   A
GAM1385  TRPV3    3'  GGGCTGGGGTTGGGGCT     45442         CCG   AGG
                                GGGCTGGGG   GGG   GCT
                                |||||||||   |||   |||
```

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                                CCCGACCCC  CCC  CGA
                                     AA_  ___
GAM1385 ZFP36L1  3' GAGGTGCTGGGGGAAAGGG  22286    _     CCG GG
                                GAGG GCTGGGG  G  AGGG
                                |||| |||||||  |  ||||
                                CTCC CGACCCC  C  TCCC
                                  A     ___ TT
GAM1386 EFNB2    3' TCCATGAGTGATGCAGATGTG  19884       A  _  _
                                TCCATGAGT ATG AGA GTG
                                ||||||||| ||| ||| |||
                                AGGTACTCA TAC TCT CAC
                                     C  G  A
GAM1386 EHF      3' CCATGAGTGGATACTGCTGA  29114       AAT  GAG  C
                                CCATGAGT  GA  TGC GA
                                ||||||||  ||  ||| ||
                                GGTACTCA  CT  ACG CT
                                    C__  ATG  A
GAM1386 EYA2     3' TCCGGAGTAATGAGACTA    23486    AT       G
                                TCC  GAGTAATGAGA TG
                                |||  |||||||||||  ||
                                AGG  CTCATTACTCT AT
                                  C_        G
GAM1386 HIF1A    3' TCCATGAGTAACTGC       11352          GAGAG
                                TCCATGAGTAAT    TGC
                                ||||||||||||    |||
                                AGGTACTCATTG    ACG
                                      _____
GAM1386 HOXC11   3' TCCGGAATGGAGTGCCG     41161    AT  GTA  A
                                TCC  GA  ATG GAGTGCCG
                                |||  ||  ||| ||||||||
                                AGG  CT  TAC CTCACGGC
                                  C_  ___  _
GAM1386 PKD1     3' TGGGGTGATGAGAGTGCC    7144     A_  A
                                TG  GT ATGAGAGTGCC
                                ||  || ||||||||||
                                AC  CA TACTCTCACGG
                                 CC  C
GAM1386 STAU2    3' TCCATAAAGGAGTGCG      30805       TAATGA    C
                                TCCATGAG    GAGTGC G
                                ||||||||    |||||| |
                                AGGTATTT    CTCACG C
                                    C_____    A
GAM1386 CMRF35   3' GGTATTGCTGACGGCCC    27436    AC       ATCAT
                                GG  ATTGCTGAT    GGCCC
                                ||  |||||||||    |||||
                                CC  TAACGACTG    CCGGG
                                 A_       _____
GAM1386 CRHR1    3' GGCATTGCTGGTGGC       20446    A      ATATCA
                                GG CATTGCTG     TGGC
                                || ||||||||     ||||
```

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                                CC GTAACGAC     ACCG
                                 _      C_____
GAM1386 DAZ     3' GGCATTAGTAATATGGCCCA  19853    A    C    TCA
                                GG CATTG TGATA   TGGCCCA
                                || ||||| |||||   |||||||
                                CC GTAAT ATTAT   ACCGGGT
                                 _    C    ___
GAM1386 KCNJ10   3' GGATATGTTGATATCAGATTCC 13870     CAT  C      TGG_
                                GGA   TG TGATATCA    CC
                                |||   || ||||||||    ||
                                CCT   AC ACTATAGT    GG
                                  AT_  A       CTAA
GAM1386 PRKAR2B  3' GGCATGCTGATAAGGATCCCA  15621    A   T     TCATGG
                                GG CAT GCTGATA     CCCA
                                || ||| |||||||     ||||
                                CC GTA CGACTAT     GGGT
                                 _  _      TCCTA_
GAM1386 PUM2     3' GGACATGCTGATGACC      31661       T    TATCA
                                GGACAT GCTGA     TGGCC
                                |||||| |||||     |||||
                                CCTGTA CGACT     ACTGG
                                   _    _____
GAM1386 ZNF136   3' GGACATTGCTTATATTCA    40877          G   _
                                GGACATTGCT ATAT CA
                                |||||||||| |||| ||
                                CCTGTAACGA TATA GT
                                      A   A
GAM1387 NOTCH3   3' GGCTATGGAACATGTCCAATCT 7737           C_  GCT  A
             GG                   GGCTATGGAAC  GTC   GT TGG
                                ||||||||||  |||   || |||
                                CCGATACCTTG  CAG   TA ACC
                                      TA   GT_  G
GAM1387 PRKCG    3' GGCTGTAGAGGCTGTATG    15628      A    ACCGTC
                                GGCT TGGA     GCTGTATG
                                |||| ||||     ||||||||
                                CCGA ATCT     CGACATAC
                                  C   C_____
GAM1387 ADARB1   3' AGTCATGGTCGAGTCGGACCTG 31869    C        _  TGTGC
                                AG CATGGTCGGG CG     CCTG
                                || ||||||||| ||     ||||
                                TC GTACCAGCTC GC     GGAC
                                 A        A  CT___
GAM1387 FGFR3    3' AGCCATGTCGGGCCCAGCTCCC 6611        G     G _  G
             TG                   AGCCATG TCGGGC T GT CCCTG
                                ||||||| |||||| | || |||||
                                TCGGTAC AGCCCG G CG GGGAC
                                    _     G T  A
GAM1387 GAL      5' GCCGGGTCGGGTGGGCTCTG   45049     AT      CG  T  C
                                GCC  GGTCGGG  TG GC CTG
                                |||  |||||||  || || |||
```

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                                CGG  CCAGCCC  AC CG GAC
                                  C_      __ C  A
GAM1387  GOT2     3'  AGCCATGGATGCCTCTGCCCTG 45233        TCGG  GTG
                                AGCCATGG   GC   TGCCCTG
                                ||||||||   ||   |||||||
                                TCGGTACC   CG   ACGGGAC
                                    TA__  GAG
GAM1387  RIMS1    3'  AGCAGTGGTCAATCTGTGCCCT 43726     CA      GCG
             G                   AGC  TGGTCGG   TGTGCCCTG
                                |||  |||||||  |||||||||
                                TCG  ACCAGTT   ACACGGGAC
                                  TC      AG_
GAM1387  TFDP1    5'  GCCGTGGCGGGGTCCCT     28278     A  T    C  GTG
                                GCC TGG CGGG GT   CCCT
                                ||| ||| |||| ||   ||||
                                CGG ACC GCCC CA   GGGA
                                  C  _   _ ___
GAM1387  TPD52L2  3'  GCTGGGTTGCGTGTGCTCTG   17639    CA   TCGG      C
                                GC  TGG    GCGTGTGC CTG
                                ||  |||    |||||||| |||
                                CG  ACC    CGCACACG GAC
                                 __   CAA_       A
GAM1388  CAV1     3'  TTCAATTCATAAATTGTTGCTG 12001         TCAACATAC
                                TTCAATTC        GTTGCTG
                                ||||||||        |||||||
                                AAGTTAAG        CAACGAC
                                    TATTTAA__
GAM1388  SP1      5'  TTCAATTTTCACCACAGCTG   41478        C   A    C
                                TTCAATT TCA CATA GTTG
                                ||||||| ||| |||| ||||
                                AAGTTAA AGT GTGT CGAC
                                   A   G    _
GAM1388  DVL3     3'  TTTGGGAATCACCAGCATATC  20693      A     TG TT
                                TTTG GGAAT  T  CAGCATATC
                                |||| |||||  |  |||||||||
                                AAAC CCTTA  G  GTCGTATAG
                                  _    GT __
GAM1388  GRIN2A   3'  TTTGAGGAATTTTTCCTACAT  9117           G    A
                                TTTGAGGAATT TTTC GCAT
                                |||||||||||| |||| ||||
                                AAACTCCTTAA AAGG TGTA
                                      A   A
GAM1388  LOH11CR2A 3'  TTTAAGGGACAGCATA      31196        AATTGTTT
                                TTTGAGG       CAGCATA
                                |||||||       |||||||
                                AAATTCC       GTCGTAT
                                   CT_______
GAM1389  ACYP1    3'  ATCATACAGGTAATATATAA   9962         A     C
                                GTTATACA GTAATA ATAA
                                |||||||| |||||| ||||
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                                TAGTATGT CATTAT TATT
                                    C     A
GAM1389 COG6    3' TTGTTATATACAACACATAA  43769       CAAG
                                TTGTTATA   TAATACATAA
                                ||||||||   ||||||||||
                                AACAATAT   GTTGTGTATT
                                    AT__
GAM1389 PTGFR   3' GTTGTTATAACAAACCATCAT 9660        _   TA  A
                                GTTGTTATA CAAG  AT CAT
                                ||||||||| ||||  || |||
                                CAACAATAT GTTT  TA GTA
                                     T   GG  _
GAM1389 DAF     5' CAAGGACGCGCCGCCGG    8206        A  AT
                                TAAGGACGC CC  TCGG
                                ||||||||| ||  ||||
                                GTTCCTGCG GG  GGCC
                                     C  C_
GAM1389 FBN2    3' AGGACGCAGCGCACCCTGG  12804       C__   _
                                AGGACGCA   CATTC GG
                                ||||||||   ||||| ||
                                TCCTGCGT   GTGGG CC
                                    CGC    A
GAM1389 HOXD3   3' AAGGACGCCCATGGA      27892       A   TC
                                AAGGACGC CCAT  GGA
                                ||||||||| ||||  |||
                                TTCCTGCG GGTA  CCT
                                    _   __
GAM1389 LAMP1   3' CAAGGACGTGCCGCCACTGGA 24504      __ A_   C
                                TAAGGAC  GC  CCATT GGA
                                |||||||  ||  ||||| |||
                                GTTCCTG  CG  GGTGA CCT
                                   CA  GC   _
GAM1389 RANBP2L1 3' TAAGAACAACACAGTTTGGA  37026      _  CA  C
                                TAAGGACG CAC  TT GGA
                                |||||||| |||  || |||
                                ATTCTTGT GTG  AA CCT
                                    T   TC  A
GAM1389 SPN     5' TAAGGACGCAGCACTGGG    17089        C   C
                                TAAGGACGCA CATT GG
                                |||||||||| |||| ||
                                ATTCCTGCGT GTGA CC
                                     C   C
GAM1390 AKAP13  3' GACTGGGCCTTCTTCTGGC   28482    C   A  CC  _
                                GAC GGGCC TCT  CTG C
                                ||| ||||| |||  ||| |
                                CTG CCCGG AGA  GAC G
                                  A    A  A_  C
GAM1390 FLRT2   3' CGGGCCATTTCTTGTT     29847       C  CCTGC
                                CGGGCCAT TC    TGTT
                                |||||||| ||    ||||
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```
                                GCCCGGTA AG    ACAA
                                    A  A____
GAM1390  GDF2    5'  GGGCCGGCATCTCCCTGCTGTT 32127      ___
             T                   GGGCC   ATCTCCCTGCTGTTT
                                 |||||   ||||||||||||||||
                                 CCCGG   TAGAGGGACGACAAA
                                    CCG
GAM1390  MYLK    5'  ACCGTCTTCTCTGTTGTT    38170    A  _ C   C
                                 GCC TCT C CTG TGTT
                                 ||| ||| | ||| ||||
                                 TGG AGA G GAC ACAA
                                   C   A A   A
GAM1390  ORC5L   3'  GCTCAAACCCTGCTGTTT    14979    _  TCT
                                 GC CA   CCCTGCTGTTT
                                 || ||   ||||||||||
                                 CG GT   GGGACGACAAA
                                  A  TT_
GAM1390  RASGRP2  5'  GACCGGGCGTCTTCCTGC    25174        CA   C
                                 GACCGGGC  TCT CCTGC
                                 ||||||||  ||| |||||
                                 CTGGCCCG  AGA GGACG
                                     C_   A
GAM1390  ST5     3'  GGGCCTTCTCCCCAGGCT    40120      A     __
                                 GGGCC TCTCCCT  GCT
                                 ||||| |||||||  |||
                                 CCCGG AGAGGGG  CGA
                                    A      TC
GAM1390  TBL1X   3'  GGGCCATCTTCCTCAGCCCTT  24892        C   __   G
                                 GGGCCATCT CCT  GCT TT
                                 |||||||||  |||  ||| ||
                                 CCCGGTAGA GGA  CGG AA
                                      A   GT   G
GAM1390  CLCN1   5'  CCAGGCCTTGGCCTGCTT    6351      C   GGTC   C
                                 CCAG CCT    GCCT GCTT
                                 |||| |||    |||| ||||
                                 GGTC GGA    CGGA CGAA
                                   C   AC__   _
GAM1390  DNASE1L1 3'  GACCAGCCTTGGCTGGACTT   27494        C   CGCCTC
                                 GACCAGCC TGGT     GCTT
                                 |||||||| ||||     ||||
                                 CTGGTCGG ACCG     TGAA
                                     A   ACC____
GAM1390  LAMA4   5'  GCGGCGGTGCCTCGCTTA    14060    CC   C
                                 GC  TGGT GCCTCGCTTA
                                 ||  |||| ||||||||||
                                 CG  GCCA CGGAGCGAAT
                                  CC   _
GAM1390  TRIM14   3'  GACTAGCCCTGGTCACACA   37701     C         CT
                                 GAC AGCCCTGGTCGC  CG
                                 ||| ||||||||||||  ||
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                                CTG TCGGGACCAGTG  GT
                                  A         T_
GAM1391 LMAN1    3' TTGTCTTTGCTTTAAGGT    24529      CCGCACAT
                                TTGTC      CTTTAAGGT
                                |||||      |||||||||
                                AACAG      GAAATTCCA
                                   AAAC____
GAM1391 PCDHB9   3' ATTGATCCTTATTTTAAGGTC 33320     TC  GCACATC
                                ATTG  CC     TTTAAGGTC
                                ||||  ||     |||||||||
                                TAAC  GG     AAATTCCAG
                                  TA  AATA___
GAM1391 RAB36    3' TTGTTCTGCACATCCTGGC   22251     CCC       TAA
                                TTGT   GCACATCTT   GGT
                                ||||   |||||||||   |||
                                AACA   CGTGTAGGA   CCG
                                  AGA        ___
GAM1391 SNX9     3' TCCCGTAATTATTAAGGTC   32159     CAC  CT
                                TCCCG   AT  TTAAGGTC
                                |||||   ||  ||||||||
                                AGGGC   TA  AATTCCAG
                                   AT_  AT
GAM1391 ATP6V1A1 3' AGGCTTCCAAGATGTTTAA   11776     A   TGAT
                                AGGC TCC    GGTGTTTAA
                                |||| |||    |||||||||
                                TCCG AGG    CTACAAATT
                                  A  TT__
GAM1391 COX10    3' AGCATTTTGGGTAATATTTAAA 10545      CC  A_
           AA                    GGCAT  TG  TGGTGTTTAAAAA
                                |||||  ||  ||||||||||||
                                TCGTA  AC  ATTATAAATTTTT
                                   AA  CC
GAM1391 MAPK14   3' AGGCACTTGAATAATATTT   10603      CCT
                                AGGCAT   GATGGTGTTT
                                ||||||   ||||||||||
                                TCCGTG   TTATTATAAA
                                   AAC
GAM1391 OXCT     3' GGCATCTGTTTAAA       7745       CTGATGG
                                GGCATC     TGTTTAAA
                                ||||||     ||||||||
                                CCGTAG     ACAAATTT
                                  ________
GAM1391 PPP1R12B 3' AGCATCCTGATGTCACCTTAA 36963          GTG_
                                GGCATCCTGATG   TTTAA
                                ||||||||||||   |||||
                                TCGTAGGACTAC   GAATT
                                      AGTG
GAM1391 SYK      3' AGGCATCCTTGGGCATTT    17234        GAT
                                AGGCATCCT   GGTGTTT
                                |||||||||   |||||||
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                                TCCGTAGGA  CCGTAAA
                                     AC_
GAM1391  TEC      3'  AGGCATATTTGATGTTCA    17383       CCTGA
                                AGGCAT    TGGTGTTTA
                                ||||||    |||||||||
                                TCCGTA    ACTACAAGT
                                   TAA__
GAM1391  TEM5     3'  GGGTGCTGGTGTTTAAAA    37238    CATCC  A
                                GG    TG TGGTGTTTAAAA
                                ||    || ||||||||||||
                                CC    AC ACCACAAATTTT
                                 C____  G
GAM1391  TTID     3'  AAGCATTAGATGTGTTTAAAAA 27710       CCT    G
                                AGGCAT   GATG TGTTTAAAAA
                                ||||||   |||| ||||||||||
                                TTCGTA   CTAC ACAAATTTTT
                                   AT_   _
GAM1391  USP21    3'  GGCTTAAGGGTGTTTAAA    32445     ATCC   T
                                GGC    TGA GGTGTTTAAA
                                |||    ||| ||||||||||
                                CCG    ATT CCACAAATTT
                                  A___   C
GAM1391  ZNF261   3'  AGGCATTTGGAAGATTTTAAAA 22986       CCT  T   G
            A                    AGGCAT   GA GGT TTTAAAAA
                                ||||||   || ||| |||||||
                                TCCGTA   CT CTA AAATTTTT
                                   AAC  T   _
GAM1392  CYP1A2   3'  GCTTGAACCTGCGAGGTGGAG  42901    CC       T  TTTATA
                                GC  TGAACCTG CG     GAG
                                ||  |||||||| ||     |||
                                CG  ACTTGGAC GC     CTC
                                 A_       _  TCCAC_
GAM1392  DISC1    3'  GCTTGAACCTGGGAGGTAGAG  33045    CC       TCGTTTA
                                GC  TGAACCTG      TAGAG
                                ||  ||||||||      |||||
                                CG  ACTTGGAC      ATCTC
                                 A_       CCTCC__
GAM1392  FOXD2    3'  GCCCCGGGCCTGTCGCCCTGAG 20966       AA        ATA
                                GCCCTG  CCTGTCGTTT   GAG
                                ||||||  ||||||||||   |||
                                CGGGGC  GGACAGCGGG   CTC
                                   CC         A__
GAM1392  GHR      3'  CCTGAACCTGTGGGAGGTGGAG 6712           CGTTTATA
                                CCTGAACCTGT       GAG
                                ||||||||||        |||
                                GGACTTGGACA       CTC
                                      CCCTCCAC
GAM1392  HDAC4    3'  GCCCTGGACGCTTGCTGT    25769       A  _  _  C
                                GCCCTG AC CT GT GT
                                |||||| || || || ||
```

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                                CGGGAC TG GA CG CA
                                   C  C  A  A
GAM1392 ITGA2    3' GACTCTGAAGTTTATAGA   13601    AC  TC
                                GA  CTG  GTTTATAGA
                                ||  |||  |||||||||
                                CT  GAC  CAAATATCT
                                 GA   TT
GAM1392 B29      3' TCTCAGGGTTGTCGCAAGTA  36710        CA  AGCT
                                TTTCAGGGT  TCG   GTA
                                |||||||||  |||   |||
                                AGAGTCCCA  AGC   CAT
                                     AC   GTT_
GAM1392 COL19A1  3' TTTCCTTTGTTGAGCTGTAC  12392     AGG_  CATC
                                TTTC   GT   GAGCTGTAC
                                ||||   ||   |||||||||
                                AAAG   CA   CTCGACATG
                                  GAAA  A___
GAM1392 HMGCR    3' TTTCAGAGTCATCTCTAC    9240          GA_
                                TTTCAGGGTCATC   GC
                                ||||||||||||   ||
                                AAAGTCTCAGTAG   TG
                                       AGA
GAM1392 HTRA3    3' TTTCAGGATCATCTGTA     44840          GAGC
                                TTTCAGGGTCATC   TGTA
                                ||||||||||||   ||||
                                AAAGTCCTAGTAG   ACAT
                                      ____
GAM1392 KCNMB3   5' TTTCAGGGATATTGCA     30840        TC  CGAGC
                                TTTCAGGG  AT    TGTA
                                ||||||||  ||    ||||
                                AAAGTCCC  TA    ACGT
                                    TA  _____
GAM1392 MGP      5' TCTCAGGGTTCTTGTGT     9464         CA  GAGC
                                TTTCAGGGT  TC   TGT
                                |||||||||  ||   |||
                                AGAGTCCCA  AG   ACA
                                     __  AAC_
GAM1392 MOX2     3' TTTCAGGGTGCTGT       42527         CATCGA
                                TTTCAGGGT    GCTGT
                                |||||||||    |||||
                                AAAGTCCCA    CGACA
                                      _______
GAM1392 PRKACB   3' TTTCTGGGTCTAGCTGTAC   15598     A    ATCG
                                TTTC GGGTC   AGCTGTAC
                                |||| |||||   ||||||||
                                AAAG CCCAG   TCGACATG
                                  A    A___
GAM1392 TAF1     3' TTTCAGGATCAGATACTGTAC  39888          TC  _
                                TTTCAGGGTCA  GA GCTGTAC
                                ||||||||||  ||  |||||||
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                                AAAGTCCTAGT  CT TGACATG
                                      __ A
GAM1392  TCF3     3'  TTTCAGAGAGCTGT       43335        GTCATC
                                TTTCAGG     GAGCTGT
                                |||||||     |||||||
                                AAAGTCT     CTCGACA
                                      _______
GAM1392  TEM8     3'  TTCCAGGGTTGTCATTGTAC  38196         CA   AGC
                                TTTCAGGGT  TCG   TGTAC
                                |||||||||  |||   |||||
                                AAGGTCCCA  AGT   ACATG
                                     AC   A__
GAM1393  KIF2     3'  TACAAAAATTGAACTGAGTTAA 21135          _    CT_
              AAGG                   TACAAAAATT AATT   TTAAAAGG
                                |||||||||| ||||   ||||||||
                                ATGTTTTTAA TTGA   AATTTTCC
                                      C    CTC
GAM1393  NAPB     3'  ACAAAAATTAATTCTTAACCCC 43164              TAAAA_
              GG                   ACAAAAATTAATTCTT     GG
                                ||||||||||||||||     ||
                                TGTTTTTAATTAAGAA     CC
                                        TTGGGG
GAM1394  CACNG3   5'  CTGCGGGCACCACTGGA     27236      AGAT   _
                                CTGC    GGGC TCACTGGA
                                ||||    |||| ||||||||
                                GACG    CCCG GGTGACCT
                                  ____    T
GAM1394  CCND1    3'  TCACTGGATGGTTTGTTGG   38222       CA    GCTCAC
                                TTACTG  GATGG     TGG
                                ||||||  |||||     |||
                                AGTGAC  CTACC     ACC
                                   __     AAACA_
GAM1394  DLEC1    3'  CTGCAGATGGGGTGAGTCTGG  28826          CTCA__
                                CTGCAGATGGG     CTGG
                                ||||||||||     ||||
                                GACGTCTACCC     GACC
                                       CACTCA
GAM1394  DTR      3'  TTACTACAGATGGGTCACAGAA 12621            C    T
                                TTACTGCAGATGGG TCAC GGAA
                                |||||||||||||| |||| ||||
                                AATGATGTCTACCC AGTG TCTT
                                      _   _
GAM1394  HIP12    3'  CTGCAGATTCCAGCTGGAA   42400         GGGC  _
                                CTGCAGAT    TCA CTGGAA
                                ||||||||    ||| ||||||
                                GACGTCTA    GGT GACCTT
                                     A___   C
GAM1394  KCNA6    3'  TACAGGGCACTGGA       13819      GAT    TC
                                TGCA   GGGC  ACTGGA
                                ||||   ||||  ||||||
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                                ATGT  CCCG  TGACCT
                                  ___   __
GAM1394 KIF5C   3' TACTGCAGATGGCTGGA    21161          GCTCA
                                TACTGCAGATGG   CTGGA
                                ||||||||||||   |||||
                                ATGACGTCTACC   GACCT
                                      _____
GAM1394 KLK13   3' TGAGATGGGCTGATGGAA   31813   C      CAC
                                TG AGATGGGCT  TGGAA
                                || |||||||||  |||||
                                AC TCTACCCGA  ACCTT
                                 _       CT_
GAM1394 LMO2    3' TTACTATGGATGGGCTGTGG  24554     CA     CAC
                                TTACTG  GATGGGCT  TGG
                                ||||||  ||||||||  |||
                                AATGAT  CTACCCGA  ACC
                                    AC      C__
GAM1394 SLC4A2  3' TTACTGCAGGGGCAGTGG   16776       AT   TCAC
                                TTACTGCAG  GGGC   TGG
                                |||||||||  ||||   |||
                                AATGACGTC  CCCG   ACC
                                     __   TC__
GAM1394 SMURF1  3' CTGCAGATGGCGGGTGG    45194        G TCAC
                                CTGCAGATGG C   TGG
                                |||||||||| |   |||
                                GACGTCTACC G   ACC
                                     _ CCC_
GAM1394 TRPS1   3' TTACTGCAATTAACTGG    30476       A  GGCTC
                                TTACTGCAG TG   ACTGG
                                |||||||||  ||   |||||
                                AATGACGTT AT   TGACC
                                     A  _____
GAM1394 ADORA2A 3' TCTGGGCCCAGCAGCTCCTGAA 8606    A       A_  TA
                                TC TGGGCCCAGCA  TT  GAA
                                || ||||||||||  ||  |||
                                AG ACCCGGGTCGT  AG  CTT
                                 _        CG  GA
GAM1394 ARNT2   3' TCATGGGCTCAGAGGTCAG  31365       C   CAAT
                                TCATGGGC CAG   TTAG
                                ||||||| |||   ||||
                                AGTACCCG GTC   AGTC
                                    A  TCC_
GAM1394 ATRN    3' TGGGCCTGGCTATCTAGAAAC 40292      CA  A
                                TGGGCC  GC ATTTAGAAAC
                                ||||||  || ||||||||||
                                ACCCGG  CG TAGATCTTTG
                                   AC  A
GAM1394 CALD1   3' CATGGGTTTCTTTAGAAA   37626      CCCAGCAA
                                CATGGG      TTTAGAAA
                                ||||||      ||||||||
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                                GTACCC       AAATCTTT
                                   AAAG____
GAM1394  CLN6     3'  TCATGGGCCTGAGCCTGGGCAG 32830         C_   AATT_
                                TCATGGGCC  AGC     TAG
                                |||||||||  |||     |||
                                AGTACCCGG  TCG     GTC
                                     AC   GACCC
GAM1394  COLQ     3'  TCATAGGCCTAGAGA       38695         C  CAATTT
                                TCATGGGCC AG      AGA
                                |||||||||  ||      |||
                                AGTATCCGG TC      TCT
                                     A  _______
GAM1394  MYO15A   5'  TCACGGGCTCAGGGACTTGGA  32185         C   CA    A
                                TCATGGGC CAG  ATTT GA
                                ||||||||  |||  |||| ||
                                AGTGCCCG GTC  TGAA CT
                                     A   CC    C
GAM1394  SELPLG   5'  TCGTGGGCCCAGAAGAA     40676    A       CAATTT
                                TC TGGGCCCAG      AGAA
                                || |||||||||      ||||
                                AG ACCCGGGTC      TCTT
                                 C        T_____
GAM1394  WNT11    3'  TGGGCCCAGCAGGCTCAGA    21544           A_
                                TGGGCCCAGCA  TTTAGA
                                ||||||||||  ||||||
                                ACCCGGGTCGT  GAGTCT
                                      CC
GAM1395  SKP2     5'  AGCCAGACCCGCTAAGCCTAG  25598       TTA  G
                                AGCCG   AC CCGCTAAGCCTAG
                                |||||   || ||||||||||||
                                TCGGT   TG GGCGATTCGGATC
                                   C__  _
GAM1395  ACVRL1   3'  CCACTGCCCCCCACCCCCC    6162       _   AG_
                                CCAC GCC   CACCCCCC
                                ||||  |||   ||||||||
                                GGTG CGG   GTGGGGGG
                                  A   GGG
GAM1395  ADAM19   3'  CACCACACGGCCCTCC      37763         CA  A  C
                                CACCACGC  GC CC CC
                                ||||||||  || || ||
                                GTGGTGTG  CG GG GG
                                     C_  _  A
GAM1395  BAP1     3'  CACTTGCCAGCACCCCCC    21643     CAC
                                CAC   GCCAGCACCCCCC
                                |||   ||||||||||||
                                GTG   CGGTCGTGGGGGG
                                  AA_
GAM1395  BAPX1    3'  CACCACACTTGGAGGCTCCCC  10159         CA____  A
                                CACCACGC     GC CCCC
                                ||||||||     || ||||
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                                GTGGTGTG     CG GGGG
                                     AACCTC  A
GAM1395  BMP6     3'  CACCACGACACCCCCC      11859       CCA
                                CACCACG   GCACCCCCC
                                |||||||   |||||||||
                                GTGGTGC   TGTGGGGGG
                                     ___
GAM1395  CAP2     5'  CACCATCCTAGTTGCCTCCC  26837      CG  _  CA_  _
                                CACCA  CC AG   CC CCC
                                |||||  || ||   || |||
                                GTGGT  GG TC   GG GGG
                                   A_  A  AAC  A
GAM1395  CD68     3'  CACCACACCCCAACCCCC    40783        AGC
                                CACCACGCC   ACCCCC
                                |||||||||   ||||||
                                GTGGTGTGG   TGGGGG
                                     GGT
GAM1395  COL5A1   5'  ACCTCGGCACCCCCC      6413     A  CCA
                                ACC CG   GCACCCCCC
                                ||| ||   |||||||||
                                TGG GC   CGTGGGGGG
                                  A  ___
GAM1395  CRIM1    3'  CACCACCCTCCCACCCATTTCC 32370       G  AG_    ____
            C                    CACCAC CC   CACCC    CCC
                                ||||||  ||   |||||    |||
                                GTGGTG GG   GTGGG    GGG
                                   _  AGG     TAAA
GAM1395  CYLN2    5'  CACCGGCTGCACCCCC      18045     AC  CA
                                CACC  GC  GCACCCCC
                                ||||  ||  ||||||||
                                GTGG  CG  CGTGGGGG
                                  C_  A_
GAM1395  DLG5     3'  CACCAACAAGAACCTCCC    44445      C  C  C  _
                                CACCA GC AG ACC CCC
                                ||||| || || ||| |||
                                GTGGT TG TC TGG GGG
                                   _  T  T   A
GAM1395  DNM2     3'  CAACACCCCAGCGCCCCC    22377    C   G    A
                                CA CAC CCAGC CCCCC
                                || ||| ||||| |||||
                                GT GTG GGTCG GGGGG
                                 T   G    C
GAM1395  DSS1     5'  CCGCGCCCAACACCTCCC    26704    A   _    _
                                CC CGCC AGCACC CCC
                                || |||| |||||| |||
                                GG GCGG TTGTGG GGG
                                 C   G     A
GAM1395  EFNB1    3'  CACCTCCCTCCACCCCCC    20709     ACG  AG
                                CACC   CC  CACCCCCC
                                ||||   ||  ||||||||
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                                GTGG  GG GTGGGGGG
                                  AG_ AG
GAM1395 EYA2    3' CATCACCAGGCACCCCCC   23484   _    _
                                CA CGCCAG CACCCCCC
                                || |||||| ||||||||
                                GT GTGGTC GTGGGGGG
                                 A     C
GAM1395 FN14    3' CACCGCCCCCCACCCCCC   32489    AC  AG_
                                CACC  GCC  CACCCCCC
                                ||||  |||  ||||||||
                                GTGG  CGG  GTGGGGGG
                                  __  GGG
GAM1395 GLTSCR1 3' CCAGCTCCCAGCACCCTCC  31833    CG__      _
                                CCA   CCAGCACCC CC
                                |||   ||||||||| ||
                                GGT   GGTCGTGGG GG
                                  CGAG       A
GAM1395 HCK     3' CACCACCTGGGCACCCCC   40938     GCCA
                                CACCAC   GCACCCCC
                                ||||||   ||||||||
                                GTGGTG   CGTGGGGG
                                   GACC
GAM1395 HEXA    3' CCTACAGCCAGCACCCTCC   8013   _ _       _
                                CC AC GCCAGCACCC CC
                                || || |||||||||| ||
                                GG TG CGGTCGTGGG GG
                                 A T        A
GAM1395 HOXC10  3' CACCACACCCCACATCCC   41486       A_  C
                                CACCACGCC  GCA CCC
                                |||||||||  ||| |||
                                GTGGTGTGG  TGT GGG
                                     GG  A
GAM1395 HOXC10  3' CACCAGCCACACTCCC     41487     C   G  C
                                CACCA GCCA CAC CCC
                                ||||| |||| ||| |||
                                GTGGT CGGT GTG GGG
                                  _   _  A
GAM1395 IGF2R   3' CACCAGCAGCGCCTCCC    9334     C  C  A  _
                                CACCA GC AGC CC CCC
                                ||||| || ||| || |||
                                GTGGT CG TCG GG GGG
                                  _ _  C  A
GAM1395 IGFBP2  3' CACCACCCAAGCACTCTCC   8254      G  _  CC_
                                CACCAC CCA GCAC   CC
                                |||||| ||| ||||   ||
                                GTGGTG GGT CGTG   GG
                                   _  T   AGA
GAM1395 ITGA2   3' CACCTCCCCCACCCCCC    13600    ACG  AG
                                CACC   CC  CACCCCCC
                                ||||   ||  ||||||||
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                                GTGG  GG  GTGGGGGG
                                  A__  GG
GAM1395  KCNK5    5'  CCCGCAAGCACCGCTCCCC   19033    A  C    ___
                                CC CGC AGCACC  CCCC
                                || ||| ||||||  ||||
                                GG GCG TCGTGG  GGGG
                                 _  T    CGA
GAM1395  KCNQ2    3'  CACCCCGTCATCACTCCC    41505     A  C  G  C
                                CACC CG CA CAC CCC
                                |||| || || ||| |||
                                GTGG GC GT GTG GGG
                                  G  A  A  A
GAM1395  KIF3B    3'  CACCACACCAGGCAAACC    22029          _  CC
                                CACCACGCCAG CA  CC
                                |||||||||| ||  ||
                                GTGGTGTGGTC GT  GG
                                      C  TT
GAM1395  KIF3C    3'  CACCTCCCACACCCCCC     13946     ACG  A
                                CACC  CC GCACCCCCC
                                ||||  || |||||||||
                                GTGG  GG TGTGGGGGG
                                  A__  G
GAM1395  KLHL3    3'  CACACACGCTCACCCCCC    44639    _    CAG
                                CAC CACGC  CACCCCCC
                                ||| |||||  ||||||||
                                GTG GTGCG  GTGGGGGG
                                  T    A__
GAM1395  LIMK1    3'  CCTTGCCCAGCACCTCCC    32531    AC  _    _
                                CC  GCC AGCACC CCC
                                ||  ||| |||||| |||
                                GG  CGG TCGTGG GGG
                                 AA  G    A
GAM1395  LTB4R    5'  CCATCTTCCAGCACCCCC    8881     CG__
                                CCA   CCAGCACCCCC
                                |||   ||||||||||
                                GGT   GGTCGTGGGGG
                                  AGAA
GAM1395  MAPK14   3'  CACGCACGCACACCCCC     40010    _    CA
                                CAC CACGC  GCACCCCC
                                ||| |||||  ||||||||
                                GTG GTGCG  TGTGGGGG
                                  C   __
GAM1395  MAT2A    3'  CACCAGCCAGACCCCC      25402     C    C
                                CACCA GCCAG ACCCCC
                                ||||| ||||| ||||||
                                GTGGT CGGTC TGGGGG
                                     _   _
GAM1395  MGAT3    3'  CACACTCCAGTGGCACCTCC  14455    C  G  ___    C
                                CAC AC CCA   GCACC CC
                                ||| || |||   ||||| ||
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                                GTG TG GGT   CGTGG GG
                                  _ A   CAC    A
GAM1395  MYBL2    3'  CACCCCTGGCCACATCCCCC   14701     AC__   G _
                                CACC   GCCA CA CCCCC
                                ||||   |||| || |||||
                                GTGG   CGGT GT GGGGG
                                  GGAC   _ A
GAM1395  NRL      3'  CACCACACTTCCACCCCCC   26132       CAG
                                CACCACGC   CACCCCCC
                                ||||||||   ||||||||
                                GTGGTGTG   GTGGGGGG
                                     AAG
GAM1395  PFKFB3   3'  CAGCACTCATCACCCTCC    44432    C   GC  G    _
                                CA CAC  CA CACCC CC
                                || |||  || ||||| ||
                                GT GTG  GT GTGGG GG
                                 C   A_  A    A
GAM1395  PPARBP   3'  CACCCCTCCCACCCCCC     21926     ACG  AG
                                CACC   CC  CACCCCCC
                                ||||   ||  ||||||||
                                GTGG   GG  GTGGGGGG
                                  GGA  __
GAM1395  PRPS1    3'  ACCACCCCCCACCCCCC     15725      G  AG
                                ACCAC CC  CACCCCCC
                                |||||  ||  ||||||||
                                TGGTG GG  GTGGGGGG
                                   G  G_
GAM1395  PRX      3'  CAGCACCCTCGCCCCCC     34106    C   G  A_  A
                                CA CAC CC  GC CCCCC
                                || ||| ||  || |||||
                                GT GTG GG  CG GGGGG
                                 C   _  AG  _
GAM1395  PTP4A2   3'  CACACACACACACCCCC     38622     _    CA
                                CAC CACGC  GCACCCCC
                                ||| |||||  ||||||||
                                GTG GTGTG  TGTGGGGG
                                  T    __
GAM1395  PTPRS    3'  CACCATCCCCCCACCCCCC   39300      CG  AG
                                CACCA  CC  CACCCCCC
                                |||||  ||  ||||||||
                                GTGGT  GG  GTGGGGGG
                                   AG  GG
GAM1395  RAB36    3'  CACCACACCCACCCCC      22233        AG
                                CACCACGCC  CACCCCC
                                |||||||||  |||||||
                                GTGGTGTGG  GTGGGGG
                                     __
GAM1395  RCN1     5'  CACCAGCGCCAGCAGCAGCCCC 16199       _      C___
                                CACCA CGCCAGCA    CCCC
                                ||||| ||||||||    ||||
```

```
                                GTGGT GCGGTCGT   GGGG
                                  C      CGTC
GAM1395 RENT1   3' CACCACACCCTCAGTCCC   16248       AG  CC
                                CACCACGCC  CA  CCC
                                |||||||||  ||  |||
                                GTGGTGTGG  GT  GGG
                                     GA  CA
GAM1395 RUNX1   3' CACCAGCTTGACAGTTCCCC  12011     C ____  CA
                                CACCA GC   CAG  CCCC
                                |||||  ||   |||  ||||
                                GTGGT CG   GTC  GGGG
                                  _ AACT   AA
GAM1395 RUNX1   5' CACCACGCTGCGAAACCC   12010       CA ___
                                CACCACGC  GC   ACCC
                                ||||||||  ||   ||||
                                GTGGTGCG  CG   TGGG
                                    A_  CTT
GAM1395 RXRA    3' CACCAGCTTGCGCCCCC    16414     C  CA  A
                                CACCA GC  GC CCCCC
                                |||||  ||  ||  |||||
                                GTGGT CG  CG GGGGG
                                  _ AA  C
GAM1395 SCNN1A  3' CCAGGGCCAGCACCCTCC   9781     C_       _
                                CCA  GCCAGCACCC CC
                                |||  ||||||||||  ||
                                GGT  CGGTCGTGGG GG
                                  CC        A
GAM1395 SCNN1G  3' CACCACTGCCTCGGCTCCC  9788       _  A__  A
                                CACCAC GCC   GC CCC
                                ||||||  |||   ||  |||
                                GTGGTG CGG   CG GGG
                                   A  AGC  A
GAM1395 SDC1    3' CACTCAGCGGCCACCCCCC  16500    _  C  CAG
                                CAC CA GC   CACCCCCC
                                |||  ||  ||   ||||||||
                                GTG GT CG   GTGGGGGG
                                  A  _  CCG
GAM1395 SDHC    3' CACCAACCCACCCCCC     42975      C   AG
                                CACCA GCC  CACCCCCC
                                |||||  |||  ||||||||
                                GTGGT TGG  GTGGGGGG
                                   _  __
GAM1395 SIGLEC11 3' CACACCAGTGCGACTCCC   38083       __  _  C
                                CACGCCA  GC AC CCC
                                |||||||  ||  ||  |||
                                GTGTGGT  CG TG GGG
                                    CA  C  A
GAM1395 SLC8A2  3' CACCCATCCCCACCCCCC   42411     ACG  AG
                                CACC   CC  CACCCCCC
                                ||||   ||  ||||||||
```

```
                                GTGG  GG GTGGGGGG
                                  GTA G_
GAM1395 SMCX    3' ACCCGCCCACCCCCC      20065    A   AG
                                ACC CGCC CACCCCCC
                                ||| |||| ||||||||
                                TGG GCGG GTGGGGGG
                                  _   __
GAM1395 SNX5    3' CACCGCCCTCACCCCCC    30863    AC  AG
                                CACC GCC CACCCCCC
                                |||| ||| ||||||||
                                GTGG CGG GTGGGGGG
                                  __ GA
GAM1395 SOX11   3' CACCCGCCACCCCC       17006    A   AGC
                                CACC CGCC  ACCCCC
                                |||| ||||  ||||||
                                GTGG GCGG  TGGGGG
                                  _  ____
GAM1395 SPTBN4  3' CACCGCCCCACACCCCC    36083    AC  A_
                                CACC GCC GCACCCCC
                                |||| ||| ||||||||
                                GTGG CGG TGTGGGGG
                                  __ GG
GAM1395 SURF6   3' CACCACGCCTGGACGTGCTCCC 27586        A______ A
          C                      CACCACGCC     GC CCCC
                                |||||||||     || ||||
                                GTGGTGCGG     CG GGGG
                                    ACCTGCA A
GAM1395 SWAP70  3' CACCACGCCCGGCCCCC    43421        AGCA
                                CACCACGCC   CCCCC
                                |||||||||   |||||
                                GTGGTGCGG   GGGGG
                                    GCC_
GAM1395 TCF3    3' CACTCAGATCACACCCCCC  43317    _ CGCCA
                                CAC CA    GCACCCCCC
                                ||| ||    |||||||||
                                GTG GT    TGTGGGGGG
                                 A CTAG_
GAM1395 TNFSF8  3' CACCACACTACATTGCTTCCC 10328       __ __ AC
                                CACCACGC CA GC CCC
                                |||||||| || || |||
                                GTGGTGTG GT CG GGG
                                    AT AA AA
GAM1395 UPF3B   3' CACCAGCACAGCGGCTCCC  38764     C _   ACC_
                                CACCA GC CAGC   CCC
                                ||||| || ||||   |||
                                GTGGT CG GTCG   GGG
                                  _ T   CCGA
GAM1395 WBSCR1  3' CAGCACCAGCACCACCCC   35266   _       _
                                CA CGCCAGCACC CCCC
                                || |||||||||| ||||
```

```
                                GT GTGGTCGTGG GGGG
                                 C        T
GAM1395 ZFP36L1  5' CACGCCAGTTCCCGGCGCCCC 22281        CA_ ____
                                CACGCCAG  CC   CCCC
                                ||||||||  ||   ||||
                                GTGCGGTC  GG   GGGG
                                    AAG  CCGC
GAM1395 ZNF179   3' CACCTCATCAGTGCTCCCC   28372     A  C  __  A
                                CACC CG CA  GC CCCC
                                |||| || ||  || ||||
                                GTGG GT GT  CG GGGG
                                  A  A  CA  A
GAM1396 ITGA2    3' TGGTGTTTCTCAAAGTGT    13604       CCCATAA
                                TGGTGT      TAAAGTGT
                                ||||||      ||||||||
                                ACCACA      GTTTCACA
                                   AAGA___
GAM1396 TSN      3' CTGGTGTCTTTTGGTTAGTGTA 21493        CCATAATAA
                                CTGGTGTC       AGTGTA
                                ||||||||       ||||||
                                GACCACAG       TCACAT
                                    AAAACCAA_
GAM1396 ZNF140   3' TGGTGAATAAAGTG       18343      TCCCAT
                                TGGTG     AATAAAGTG
                                |||||     |||||||||
                                ACCAC     TTATTTCAC
                                  _______
GAM1396 ZNF22    5' ACTAGTGTTTCATTTCCTAGAG 45043        CC   AA__  AA_
            GTGTA                  ACTGGTGT  CAT   TA  GTGTA
                                |||||||| |||   ||  |||||
                                TGATCACA GTA   AT   CACAT
                                    AA  AAGG  CTC
GAM1396 ABCD4    3' TGTCAGTCCTCCTGGTGT    33751     ACTGA
                                TGT    CTTCCTGGTGT
                                |||    ||||||||||
                                ACA    GGAGGACCACA
                                  GTCA_
GAM1396 ACTG2    5' TGACTGAGGGCTGGTGT     11518    T    CTTC
                                TG ACTGA   CTGGTGT
                                || |||||   |||||||
                                AC TGACT   GACCACA
                                 _    CCC_
GAM1396 CA3      3' TGACTGACTTCTTGCTGGTGT  23220    T       ___
                                TG ACTGACTTC   CTGGTGT
                                || |||||||||   |||||||
                                AC TGACTGAAG   GACCACA
                                 _       AAC
GAM1396 CBS      5' TGTCATGGGATCCTGGTGT   6312      AC  ACT
                                TGT  TG   TCCTGGTGT
                                |||  ||   |||||||||
```

```
                                ACA  AC   AGGACCACA
                                  GT  CCT
GAM1396  CEP2     3'  TGGGCTGACTTCAGGATGT   28444    TA      CT
                                TG  CTGACTTC  GGTGT
                                ||  ||||||||  |||||
                                AC  GACTGAAG  CTACA
                                 CC       TC
GAM1396  EDN3     3'  TGTATCGGCCTGGTGT      6485      C  ACTT
                                TGTA TG    CCTGGTGT
                                ||||  ||    ||||||||
                                ACAT GC    GGACCACA
                                  A  C___
GAM1396  EXTL3    3'  TGTGGCTGACTTCAAGAT    11042     A_      CT
                                TGT  CTGACTTC  GGT
                                |||  ||||||||  |||
                                ACA  GACTGAAG  CTA
                                  CC       TT
GAM1396  FLT1     3'  TGACTGACTTCCTGTGT     12915    T         G
                                TG ACTGACTTCCTG TGT
                                ||  ||||||||||||  |||
                                AC TGACTGAAGGAC ACA
                                 _          _
GAM1396  GAN      3'  TGTACTGACTTCCAGCA     35156             T
                                TGTACTGACTTCC GGTG
                                ||||||||||||  ||||
                                ACATGACTGAAGG TCGT
                                           _
GAM1396  IL10RA   3'  TGAGCTGACTTCAGCCTGGT  40628    TA      ___
                                TG  CTGACTT   CCTGGT
                                ||  |||||||   ||||||
                                AC  GACTGAA   GGACCA
                                 TC      GTC
GAM1396  ITGA1    3'  TGCACTATTGTCCTGGTGT   41859       ACT
                                TGTACTG   TCCTGGTGT
                                |||||||   |||||||||
                                ACGTGAT   AGGACCACA
                                    AAC
GAM1396  LFG      3'  TGACGCCTCTCCTGGTGT    44154     _____
                                TGAC    TTCCTGGTGT
                                ||||    ||||||||||
                                ACTG    GAGGACCACA
                                  CGGA
GAM1396  LNK      3'  TGCTCTACCTGGTGT       24208     A   ACTT
                                TGT CTG    CCTGGTGT
                                |||  |||    ||||||||
                                ACG GAT    GGACCACA
                                  A  _____
GAM1396  MUC4     3'  TACTGACTTCCCTCGTGT    39674           G_
                                TACTGACTTCCT  GTGT
                                ||||||||||||  ||||
```

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                                ATGACTGAAGGG  CACA
                                      AG
GAM1396  NGFR     3'  GTACCATCCCTGGTGT      14791       AC
                                GTACTG  TTCCTGGTGT
                                ||||||  ||||||||||
                                CATGGT  AGGGACCACA
                                   __
GAM1396  PAX3     3'  TGTTTTGATTCCTAGTGT    30328     AC   C
                                TGT  TGA TTCCTGGTGT
                                |||  ||| ||||||||||
                                ACA  ACT AAGGATCACA
                                  AA   _
GAM1396  PCLO     3'  TGTGCTGCTTCCTGGCAT    45312     A   A
                                TGT CTG CTTCCTGGTGT
                                ||| ||| ||||||||||
                                ACA GAC GAAGGACCGTA
                                  C  _
GAM1396  TPT1     3'  TGTCTTAAGTCCTGGTGT    17663     A  GACT
                                TGT CT    TCCTGGTGT
                                ||| ||    |||||||||
                                ACA GA    AGGACCACA
                                  _ ATTC
GAM1396  ZNF175   3'  TGTTGACTCCTGGTGT      28368     AC    T
                                TGT  TGACT CCTGGTGT
                                |||  ||||| ||||||||
                                ACA  ACTGA GGACCACA
                                   __    _
GAM1397  C4B      3'  CCCAGGTTCAGGTT        8235       TCAC
                                CCCGG    GTTCAGGTT
                                |||||    |||||||||
                                GGGTC    CAAGTCCAA
                                   _____
GAM1397  CARKL    3'  CCTCCGGTCACATGGTTC    29990    C        TCA
                                CC CCGGTCACGT   GGTTC
                                || ||||||||||   |||||
                                GG GGCCAGTGTA   CCAAG
                                  A        ___
GAM1397  CDKN2B   3'  CCTCAGTCTTCAGGTT      38543    C    ACG
                                CC CGGTC   TTCAGGTT
                                || |||||   ||||||||
                                GG GTCAG   AAGTCCAA
                                  A   ___
GAM1397  DXYS155E 3'  CCTCGGCCACGCTCCCGTTC  22949    C        AG
                                CC CGGTCACGTTC  GTTC
                                || ||||||||||  ||||
                                GG GCCGGTGCGAG  CAAG
                                  A         GG
GAM1397  EGLN2    5'  CCTGGTCTCAGGTTC       38821    C   ACGT
                                CC GGTC    TCAGGTTC
                                || ||||    ||||||||
```

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                                GG CCAG    AGTCCAAG
                                 A   _____
GAM1397  EXTL3    3'  CCCGGCCAGCCGGGTGGGTTC  11031        C   CA___
                                CCCGGTCA GTT     GGTTC
                                |||||||| |||     |||||
                                GGGCCGGT CGG     CCAAG
                                     _   CCCAC
GAM1397  FCMD     3'  CCCTCAGACATTCAGGTT    27516     C   TC
                                CCC CGG  ACGTTCAGGTT
                                ||| |||  ||||||||||
                                GGG GTC  TGTAAGTCCAA
                                  A   __
GAM1397  GALGT    3'  CCCTACTGGGCATCAGGTTC   11180     CCC_  T  CGT
                                CCC    GG CA   TCAGGTTC
                                |||    || ||   ||||||||
                                GGG    CC GT   AGTCCAAG
                                  ATGA  C  ___
GAM1397  GGA1     3'  CCCCCCAGTCACTGGGTTC   30046          GTTCA
                                CCCCCCGGTCAC    GGTTC
                                ||||||||||||    |||||
                                GGGGGGTCAGTG    CCAAG
                                      AC___
GAM1397  GP9      3'  CCCCCTGGCTGGAGCCAGGTTC 6746       C   CACGT
                                CCCCC GGT     TCAGGTTC
                                ||||| |||     ||||||||
                                GGGGG CCG     GGTCCAAG
                                   A   ACCTC
GAM1397  HS3ST3A1 5'  CCGCCCGAGTTCAGGTTC    25803    _    TCAC
                                CC CCCGG    GTTCAGGTTC
                                || |||||    ||||||||||
                                GG GGGCT    CAAGTCCAAG
                                 C    _____
GAM1397  IHPK3    3'  CCTCCGTCCTCCAGGTTC    38369    C   GT ACG
                                CC CCG  C   TTCAGGTTC
                                || |||  |   |||||||||
                                GG GGC  G   AGGTCCAAG
                                 A   AG ___
GAM1397  LZTS1    3'  CCCTCTGGTTCACGGTGGTT   34262     CCC   _   TTCA
                                CCC   GGT CACG    GGTT
                                |||   ||| ||||    ||||
                                GGG   CCA GTGC    CCAA
                                  AGA   A    CA__
GAM1397  MSF      5'  CCTCCCGGGCGGATCAGGTTC  44722    _    TCA  T_
                                CC CCCGG   CG  TCAGGTTC
                                || |||||   ||  ||||||||
                                GG GGGCC   GC  AGTCCAAG
                                 A    C__  CT
GAM1397  PCSK2    3'  CCTTCAGGCCTCAGGTTC    15126    GG   C  _
                                CC  TCA GT TCAGGTTC
                                ||  ||| || ||||||||
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                                GG  AGT CG AGTCCAAG
                                 A_   C  G
GAM1397 SLC30A4  5' CCCCAGGTCTGACAGGTTC   30011     C    ACGTT
                                CCCC GGTC     CAGGTTC
                                |||| ||||     |||||||
                                GGGG CCAG     GTCCAAG
                                  T    ACT__
GAM1397 SLC7A6   3' CCTGGCATTCAGGTTC      19590    C   CAC
                                CC GGT   GTTCAGGTTC
                                || |||   ||||||||||
                                GG CCG   TAAGTCCAAG
                                 A   ___
GAM1397 TLR5     5' CCTGTCTCCAGGTTC       44289    G   ACG
                                CC GTC   TTCAGGTTC
                                || |||   |||||||||
                                GG CAG   AGGTCCAAG
                                 A   ___
GAM1397 UPK1B    3' CCCGGTCAAGTGATTC      28082        C  TCA
                                CCCGGTCA GT   GGTTC
                                |||||||| ||   |||||
                                GGGCCAGT CA   CTAAG
                                     T  ___
GAM1397 WEE1     5' CCTCAGGTCCAGTCTCAGGTTC 18087    C _    ACG_
                                CC C GGTC    TTCAGGTTC
                                || | ||||    |||||||||
                                GG G CCAG    GAGTCCAAG
                                 A T    GTCA
GAM1397 ARHGDIA  3' CCGTCGTCCGTCCGTCAGTCTG 20201     CA     ACC   G_  A
                                CCG  CGTCC   CCG  GG TCTG
                                |||  |||||   |||  || ||||
                                GGC  GCAGG   GGC  TC AGAC
                                  A_    CA_   AG  _
GAM1397 EZH1     3' GTCTGTTCCCAGGAATCTG    12786     CAC_
                                GTC    CCCGGGGATCTG
                                |||    ||||||||||||
                                CAG    GGGTCCTTAGAC
                                  ACAA
GAM1397 GNLY     3' ACGTTCCCGGGATCT       29803      CCAC     G
                                ACGT    CCCGGG ATCT
                                ||||    |||||| ||||
                                TGCA    GGGCCC TAGA
                                  A___     _
GAM1397 IRF6     5' GTCCACAGGGATCTG       26037       CCC
                                GTCCAC   GGGGATCTG
                                ||||||   |||||||||
                                CAGGTG   TCCCTAGAC
                                    ___
GAM1397 KCNMB3   5' GCACGTCCCTCCTGAAAAT   30838        AC  C GG
                                GCACGTCC  CC G  GAT
                                ||||||||  || |  |||
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```
                                CGTGCAGG  GG C  TTA
                                    GA  A TT
GAM1397  MYLK2    3'  ACGAGGCTGCCCTGGGGATCTG 37517     TCCA__  C
                                ACG     CCC GGGGATCTG
                                |||     ||| |||||||||
                                TGC     GGG CCCCTAGAC
                                  TCCGAC   A
GAM1397  SHOX     5'  CCGCCTGTCCACCCTCCCATTT 27816      AC       CGGGGA_
             CTG                  CCGC  GTCCACCC      TCTG
                                ||||  ||||||||      ||||
                                GGCG  CAGGTGGG      AGAC
                                  GA       AGGGTAA
GAM1397  SLC14A2  3'  GTCTCTTATCCTGGGGATCTG  28400     CAC___  C
                                GTC     CC GGGGATCTG
                                |||     || |||||||||
                                CAG     GG CCCCTAGAC
                                  AGAATA  A
GAM1398  IL1R1    3'  AAATGGCTCAATACCTTTTATT 9350       TAT    __
                                AAATG   GTTCA  ACCTTTTATT
                                |||||   |||||  ||||||||||
                                TTTAC   CGAGT  TGGAAAATAA
                                   ___     TA
GAM1398  PROS1    3'  GGATGTATGTTCATTCTT    44613    A        AC
                                A ATGTATGTTCA  CTT
                                | ||||||||||  |||
                                C TACATACAAGT  GAA
                                 C          AA
GAM1398  ROCK2    3'  TGTATGTATCAGTCTCTCA    42366       _  AC
                                TGTATGT TCA  CTTTTA
                                |||||||  |||  ||||||
                                ACATACA AGT  GAGAGT
                                    T   CA
GAM1398  TRPM8    3'  GTATGTTCAATACATTATT    35860         CCTT
                                GTATGTTCAA    TTATT
                                ||||||||||    |||||
                                CATACAAGTT    AATAA
                                      ATGT
GAM1398  CXCR6    3'  TGTGGGTATATACATTTAC    27296     AACT
                                TGTG    TATACATTTGC
                                ||||    ||||||||||
                                ACAC    ATATGTAAATG
                                  CCAT
GAM1398  TM4SF4   3'  TGTGACTTTATACATTTTACAT 21460      AC       _ _
             TTGT                   TGTGA  TTATACATTT GC TTTGT
                                |||||  |||||||||| || |||||
                                ACACT  AATATGTAAA TG AAACA
                                   GA        A  T
GAM1399  ARG2     3'  TGTTAGGGATGTGGATAGAATA 10124          GTCTACA
                                TGTTAGGGATG      AGAATA
                                ||||||||||      ||||||
```

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                                ACAATCCCTAC      TCTTAT
                                     ACCTA__
GAM1399  KLRG1    3'  TATCTTGAAATTAATATGCAGG 25153           C  CCA
                                TATCTTGAAATTGA AT   CAGG
                                |||||||||||||| ||   ||||
                                ATAGAACTTTAATT TA   GTCC
                                      A  C__
GAM1400  CD5      3'  CCTGCCACTCGGGGCAGCAG   30544         CACTC  A
                                CCTGTCACTT     CA CAG
                                ||||||||||     || |||
                                GGACGGTGAG     GT GTC
                                     CCCC_  C
GAM1400  CTRL     3'  CTGCCATTCATTCCAACAG    12522       C    C
                                CTGTCA TTCA TCCAACAG
                                |||||| |||| ||||||||
                                GACGGT AAGT AGGTTGTC
                                   _    A
GAM1400  CUL4B    3'  CCTAACGGCTCCAACAG     18723      TC  TTCA
                                CCTG  AC    CTCCAACAG
                                ||||  ||    |||||||||
                                GGAT  TG    GAGGTTGTC
                                  __ CC__
GAM1400  IHPK1    3'  CAACCTGTCACGTGCCAACAG  45481          TTCACT
                                TAACCTGTCAC     CCAACAG
                                ||||||||||      |||||||
                                GTTGGACAGTG     GGTTGTC
                                     CAC___
GAM1400  ITGA1    3'  ACCTGTCATTTTCCAA      41841         C  CAC
                                ACCTGTCA TT   TCCAA
                                |||||||| ||   |||||
                                TGGACAGT AA   AGGTT
                                    A  ___
GAM1400  KITLG    3'  CTGTCACTCCAGACA       19644          CTCCA
                                CTGTCACTTCA     ACA
                                ||||||||||     |||
                                GACAGTGAGGT     TGT
                                     C_____
GAM1400  MASP1    3'  ACCTGGAATTACTCCAACAG   40092       TCACTTC
                                ACCTG      ACTCCAACAG
                                |||||      ||||||||||
                                TGGAC      TGAGGTTGTC
                                  CTTAA__
GAM1400  PPP1R8   3'  TGTTTTCATTCCAACA      39736     CAC    C
                                TGT   TTCA TCCAACA
                                |||   |||| |||||||
                                ACA   AAGT AGGTTGT
                                  A__    A
GAM1400  SLC1A3   3'  TAACCTGCACTTTGCTCACAG  20045        T    CA   CA
                                TAACCTG CACTT  CTC  ACAG
                                ||||||| |||||  |||  ||||
```

```
                                ATTGGAC GTGAA  GAG  TGTC
                                   _    AC   __
GAM1400  TRPM8    3'  CCTTGTCACCTCCTCTGACAG  35857     _      A   CA
                                CCT GTCACTTC CTC  ACAG
                                ||| |||||||| |||  ||||
                                GGA CAGTGGAG GAG  TGTC
                                  A       _  AC
GAM1400  WASF1    5'  TGCAACTTTACTCCAACA    19447     C    C
                                TGT ACTT ACTCCAACA
                                ||| |||| |||||||||
                                ACG TGAA TGAGGTTGT
                                  T   A
GAM1400  ZNF217   5'  ACTTGTCACTCACCCCTCTAAC 27188    C      T     ___
              AG                  AC TGTCACT CACTCC   AACAG
                                || ||||||| ||||||   |||||
                                TG ACAGTGA GTGGGG   TTGTC
                                 A      _     AGA
GAM1400  FCN3     5'  TCTGATTGAAACTAATAT    18943     A    ACAG
                                TCT GATT    GAGACTAATAT
                                ||| ||||    ||||||||||
                                AGA CTAA    CTTTGATTATA
                                  _   _____
GAM1401  SEPN1    3'  GTGGAGGATGGGACAGTGCT   42436     ATA  AC       A
                                GTG   GA  GGACGGTG CT
                                |||   ||  |||||||| ||
                                CAC   CT  CCTGTCAC GA
                                  CTC  AC       _
GAM1401  GBF1     3'  TGCCGGGCTGGAGGCAGAGGCT 20081       AT  CGCACA
              G                   TGCCG  CT     CAGAGGCTG
                                |||||  ||     |||||||||
                                ACGGC  GA     GTCTCCGAC
                                   CC  CCTCC_
GAM1401  GOT1     3'  GCCGGTTTAAACAGAGGCTG   13225      ATCTCGCAC
                                GCCG        ACAGAGGCTG
                                ||||        ||||||||||
                                CGGC        TGTCTCCGAC
                                  CAAATT___
GAM1401  KCNK4    3'  GCCAATGTGTGTGCAGAGGCTG 37833        CTCGCACA
                                GCCGAT       CAGAGGCTG
                                ||||||       |||||||||
                                CGGTTA       GTCTCCGAC
                                   CACACAC_
GAM1402  HGF      3'  GATGCCAGCACATATCT     45320      ACG   AA
                                GATG   CGG  CACATATCT
                                ||||   |||  |||||||||
                                CTAC   GTC  GTGTATAGA
                                  G__   __
GAM1402  FMR1     3'  GATTATTATGCATACATGGAAA 12941    GTTAG  AG
              T                   GA    AT  ATACATGGAAAT
                                ||    ||  ||||||||||||
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                                CT    TA  TATGTACCTTTA
                                 AATAA  CG
GAM1402  IL2RB    3'  AGAGTTAGCTGGGACTGG    9377        ATA_   ACA
                                AGAGTTAG   GAT   TGG
                                ||||||||   |||   |||
                                TCTCAATC   CTG   ACC
                                    GACC  ___
GAM1402  MAN2A2   3'  GTTCAGGTACATGGA      25953     AGA   A
                                GTT   TAG TACATGGA
                                |||   ||| ||||||||
                                CAA   GTC ATGTACCT
                                  ___  C
GAM1402  SLC16A7  3'  AGAGTCAGGTATGGAA      21836        ATAGATAC
                                AGAGTTAG       ATGGAA
                                ||||||||       ||||||
                                TCTCAGTC       TACCTT
                                    CA_______
GAM1402  SOX13    3'  AGAGTTAGGTGACAATGG    25006        ATA    C
                                AGAGTTAG   GATA ATGG
                                ||||||||   |||| ||||
                                TCTCAATC   CTGT TACC
                                    CA_   _
GAM1403  ATF7     3'  TCAGCGGGTAATATGTCAT   27794      TAA
                                TTAGT   TAATATGTCAT
                                |||||   ||||||||||||
                                AGTCG   ATTATACAGTA
                                  CCC
GAM1403  SLC4A7   3'  ACATTAGTTAATAAATAGT   18816           TAT
                                ACATTAGTTAATAA   GT
                                ||||||||||||||   ||
                                TGTAATCAATTATT   CA
                                       TAT
GAM1403  TEM7     3'  ACTTTAGTTAACCTGTGTCAT  33797    A       AATA
                                AC TTAGTTAAT    TGTCAT
                                || |||||||||    ||||||
                                TG AATCAATTG    ACAGTA
                                 A        GAC_
GAM1404  ALPI     3'  CAGGTGCAGGGGTGTGGAA   11576       CGCT    C_
                                TAGGTGC    GGGTG  GAA
                                |||||||    |||||  |||
                                GTCCACG    CCCAC  CTT
                                    TC__     AC
GAM1404  COL4A2   3'  TAAGTGCTGCTGCTGGAT    12321       C___
                                TAGGTGC    GCTGGGT
                                |||||||    |||||||
                                ATTCACG    CGACCTA
                                    ACGA
GAM1404  EZH1     3'  CAGGAGTTGCTGGGTGCG    12779     TGCC
                                TAGG    GCTGGGTGCG
                                ||||    ||||||||||
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                                GTCC    CGACCCACGC
                                  TCAA
GAM1404  IHPK3    3'  GGTGCAGAGCAGGTGAGA    38372      C__  T    C
                                GGTGC   GC GGGTG GA
                                |||||   || ||||| ||
                                CCACG   CG TCCAC CT
                                   TCT  _    T
GAM1404  KLF8     5'  GGTTCGCTGGGCCGAA     28537     GC       G
                                GGT  CGCTGGGT CGAA
                                |||  |||||||| ||||
                                CCA  GCGACCCG GCTT
                                 A_       _
GAM1404  LTB4R    5'  TAGGTGCTGTTTGCTAAAT   8888        CGC  GG   G
                                TAGGTGC   TG  TGC AAAT
                                |||||||   ||  ||| ||||
                                ATCCACG   AC  ACG TTTA
                                    ___  AA   A
GAM1404  ZNF266   3'  TAGGGTTGCTGTACAAAAT   44779     TGCC   GG
                                TAGG    GCT  GTGCGAAAT
                                ||||    |||  |||||||||
                                ATCC    CGA  CATGTTTTA
                                  CAA_   __
GAM1404  ALP      3'  GCTAGCCCCAAAAA       30929      TCT  T
                                GCTA   GC CCCAAAAA
                                ||||   || ||||||||
                                CGAT   CG GGGTTTTT
                                  ___  _
GAM1404  ATP7B    3'  TCTACTAGTTTGCTCCCAAA  6281     G    TC_
                                TC GCTA   TGCTCCCAAA
                                || ||||   ||||||||||
                                AG TGAT   ACGAGGGTTT
                                 A    CAA
GAM1404  CHRNB4   3'  CATCGGCCACAACCCAGAAAG  8868          CTGCT    A
                                CATCGGCTAT    CCCA AAAG
                                ||||||||||    |||| ||||
                                GTAGCCGGTG    GGGT TTTC
                                      TT___    C
GAM1404  LDB3     3'  CCGGGCTCCCAAGAA      44108      CTATCT       A
                                TCGG     GCTCCCAA AA
                                ||||     |||||||| ||
                                GGCC     CGAGGGTT TT
                                  _______       C
GAM1404  PRSS11   3'  CATCGTGCTCCCAA       15764       GCTATC
                                CATCG     TGCTCCCAA
                                |||||     |||||||||
                                GTAGC     ACGAGGGTT
                                  _______
GAM1404  SRGAP1   5'  CCGTGCATTTCCCAAAAAG   43599     _  TATCTGC
                                TCG GC      TCCCAAAAAG
                                ||| ||      ||||||||||
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                                GGC CG      AGGGTTTTTC
                                  A  TAA____
GAM1404  STARD5   3'  CATCAGCTTGTTCCAAA     36122         ATC  CTC
                                CATCGGCT   TG   CCAAA
                                ||||||||   ||   |||||
                                GTAGTCGA   AC   GGTTT
                                     ___  AA_
GAM1405  B3GALT3  3'  GTAATCCACATAAGATATA    37670           CA
                                GTAATCTATATA  AGATATA
                                ||||||||||||  |||||||
                                CATTAGGTGTAT  TCTATAT
                                      __
GAM1405  IL1RAP   3'  GTGGATTTATATACACAGATAT 13503    A_  C       _
           A                     GT  AT TATATACA AGATATA
                                ||  || |||||||| |||||||
                                CA  TA ATATATGT TCTATAT
                                 CC  A       G
GAM1405  PPP1R2   3'  GTATCTATATATAAAATATA   26421     A       C
                                GTA TCTATATA AAGATATA
                                ||| |||||||| ||||||||
                                CAT AGATATAT TTTTATAT
                                  _       A
GAM1405  WASF3    3'  TACATAATCTATAGTAAGATAT 27390            TAC
           A                     TACGTAATCTATA   AAGATATA
                                ||||||||||||   ||||||||
                                ATGTATTAGATAT   TTCTATAT
                                      CA_
GAM1406  HPS4     3'  TGACTATAACGTAATAGAACTG 35218          _____      III
           C                     TGATTATGAT    AGAACTG   C
                                ||||||||||    |||||||  |
                                ACTGATATTG    TCTTGAC   G
                                     CATTA      III
GAM1406  TEM7     3'  TGATTATGACCCCCCACTG   33816          AGA__
                                TGATTATGAT    ACTG
                                ||||||||||    ||||
                                ACTAATACTG    TGAC
                                     GGGGG
GAM1406  TIMP3    5'  TGATATATGATAGAAGACTG   7469       _       __
                                TGAT TATGATAGA  ACTG
                                ||||  |||||||||  ||||
                                ACTA ATACTATCT  TGAC
                                  T        TC
GAM1406  SCNN1G   3'  TCAATTTATTCATCCACAAAAT 9790        A         GT_
           T                     TCAAT TTATTCATCTA   GATT
                                |||||  ||||||||||   ||||
                                AGTTA AATAAGTAGGT   TTAA
                                  _         GTT
GAM1407  WFS1     3'  TCCACGCAATCTACACATGGTC 25642       A       T  GAGA
           G                     TCCAC TAATCTAT TA    TCG
                                |||||  |||||||  ||    |||
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                                AGGTG GTTAGATG GT    AGC
                                  C       T  ACC_
GAM1408  CBLB     3'  TGCCTTTAAATTCTGA      20335          GGATT
                                TGTCTTTAAG    TTCTGA
                                ||||||||||    ||||||
                                ACGGAAATTT    AAGACT
                                      _____
GAM1408  CNGB3    3'  CTGCTGGGGATTTTTTGA    33305     T  TTAA      C
                                CTG CT    GGGATTTT TGA
                                ||| ||    |||||||| |||
                                GAC GA    CCCTAAAA ACT
                                  _ C___       A
GAM1408  NR4A2    3'  TGTCAGGATTTTCTGA      26168      TTTAA
                                TGTC    GGGATTTTCTGA
                                ||||    ||||||||||||
                                ACAG    TCCTAAAAGACT
                                  _____
GAM1408  PTPN18   3'  TCTGTCTTTTGGGGGCTCTG   30772         AA   ATT
                                TCTGTCTTT  GGG   TTCTG
                                |||||||||  |||   |||||
                                AGACAGAAA  CCC   GAGAC
                                     AC   C__
GAM1408  PTPN7    5'  TCTGTCTTTGAGGGCTGA    38718         A    ATTTT
                                TCTGTCTTT AGGG    CTGA
                                |||||||||  ||||    ||||
                                AGACAGAAA TCCC    GACT
                                     C   _____
GAM1408  STK38    3'  TCTGTCTTAGGGATTTTCTG   28580        TA
                                TCTGTCTT  AGGGATTTTCTG
                                ||||||||  ||||||||||||
                                AGACAGAA  TCCCTAAAAGAC
                                     __
GAM1408  TMPRSS4  3'  TCTGACTTTGGGGGATCCCC   33394      T    AA     TT
                                TCTG CTTT  GGGATT  C
                                |||| ||||  ||||||  |
                                AGAC GAAA  CCCTAG  G
                                  T    CC     GG
GAM1408  CBFB     3'  TAGAAAAAATGATTAGA     35635           T
                                TAGAAAAAATGATT AGA
                                |||||||||||||| |||
                                ATCTTTTTTACTAA TCT
                                     _
GAM1408  LYAAT1   3'  CAGAAAAGGTGAAAACATGA   38527        AA   TTT
                                TAGAAAA  TGA   AGACATGA
                                |||||||  |||   ||||||||
                                GTCTTTT  ACT   TTTGTACT
                                    CC   ___
GAM1408  MDM1     3'  AAAAAATGCATAACATGAA    33511        ATTTA
                                AAAAAATG    GACATGAA
                                ||||||||    ||||||||
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                                TTTTTTAC    TTGTACTT
                                    GTA__
GAM1408 NCL     3' GAAAAAATGGTTTTGTACATG 41052        A  AG_
                                GAAAAAATG TTT  ACATG
                                ||||||||| |||  |||||
                                CTTTTTTAC AAA  TGTAC
                                    C  ACA
GAM1408 NOVA1   3' GACGAAATTCAGACATG    27060    AAAAAT
                                GA    GATTTAGACATG
                                ||    ||||||||||||
                                CT    TTAAGTCTGTAC
                                 GCT___
GAM1408 NPC2    3' CAGAAAAAGAGACATG     26961        ATGATTT
                                TAGAAAAA     AGACATG
                                ||||||||     |||||||
                                GTCTTTTT     TCTGTAC
                                    C_______
GAM1408 NRCAM   3' GAAAAATGAATATAGAGACATG 22692      A  TTT___
            AA                   GAAAAA TGA     AGACATGAA
                                |||||| |||     |||||||||
                                CTTTTT ACT     TCTGTACTT
                                   _  TATATC
GAM1408 PMS1    3' GAAAAAATGGGCGACCATGAA  8047        ATTTA  _
                                GAAAAAATG    GAC ATGAA
                                |||||||||    ||| |||||
                                CTTTTTTAC    CTG TACTT
                                     CCG__  G
GAM1408 RAF1    3' TAGAAAAGAAGGCAACATGAA  44335       AAT  TTTA
                                TAGAAAA  GA   GACATGAA
                                |||||||  ||   ||||||||
                                ATCTTTT  CT   TTGTACTT
                                   ___ TCCG
GAM1408 RCN1    3' TAGAAAAACAAACAAAGACATG 40615       AT  TT
                                TAGAAAAA GAT  AGACATG
                                ||||||||  |||  |||||||
                                ATCTTTTT TTG  TCTGTAC
                                     GT  TT
GAM1408 WASF3   3' GAAAGGGGATGCAGACATGA  27385     AAAT  T
                                GAAA   GAT TAGACATGA
                                ||||   ||| |||||||||
                                CTTT   CTA GTCTGTACT
                                  CCC_  C
GAM1409 ABR     3' GGCTGGGCAGCCGGCTT    35014          GACA
                                GGCTGGGTAGCT   GGCTT
                                ||||||||||||   |||||
                                CCGACCCGTCGG   CCGAA
                                       _____
GAM1409 BARHL1  3' AGGCTGGGGGCTGGGGTC   33458        TA   ACA  CT
                                AGGCTGGG  GCTG  GG  TC
                                ||||||||  ||||  ||  ||
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                                TCCGACCC CGAC  CC AG
                                    C_   C__ __
GAM1409 CUL3    5' GGCTGGGGAGCTGGCC     18741       T  GACA
                                GGCTGGG AGCT  GGCT
                                ||||||| ||||  ||||
                                CCGACCC TCGA  CCGG
                                    C  ____
GAM1409 DNMT3A  5' GGCTGGGGGGCTGCTGGGCTT 35431      TA  ACA
                                GGCTGGG GCTG  GGCTT
                                ||||||| ||||  |||||
                                CCGACCC CGAC  CCGAA
                                    CC  GAC
GAM1409 EPHA8   3' GGCTGGGCAGCTGGGCTC   33896         ACA
                                GGCTGGGTAGCTG  GGCTT
                                ||||||||||||  |||||
                                CCGACCCGTCGAC  CCGAG
                                              ___
GAM1409 MAN2A2  3' GGATGGGTAGCTGGTAGA   25952   C      AC
                                GG TGGGTAGCTG  AGG
                                || ||||||||||  |||
                                CC ACCCATCGAC  TCT
                                 T       CA
GAM1409 NEURL   3' GGCTGGGTATGAGCTT     20100       GC  CAG
                                GGCTGGGTA  TGA  GCTT
                                |||||||||  |||  ||||
                                CCGACCCAT  ACT  CGAA
                                          __  ___
GAM1409 NTF5    5' GGCTGGGAGTCCCCAGGCTTCG 26137      T _ GA
                                GGCTGGG AG CT  CAGGCTTCG
                                ||||||| || ||  |||||||||
                                CCGACCC TC GG  GTCCGAAGC
                                    _ A  G_
GAM1409 TAC3    5' GGCTGGGTGGTCTGGCAG   29920       AG_  A
                                GGCTGGGT  CTG CAG
                                ||||||||  ||| |||
                                CCGACCCA  GAC GTC
                                     CCA  C
GAM1410 APM1    3' TGATGGAAAAAGATATACCA  22020     T__
                                TGATG  GGGGATATACCA
                                |||||  ||||||||||||
                                ACTAC  TTTCTATATGGT
                                  CTT
GAM1410 CNTNAP2 3' TGATATGGGAGAACCA     30496        ATAT
                                TGATGTGGGG   ACCA
                                ||||||||||   ||||
                                ACTATACCCT   TGGT
                                      CT__
GAM1410 DAZL    3' TGAGTGTGATTTACCA     42781    T  GG  A
                                TGA GTG  GAT TACCA
                                ||| |||  ||| |||||
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                                ACT CAC  CTA ATGGT
                                  _  A_  A
GAM1410 EXT2    3' TGATTTAAATATACCA     7593      GTGG
                                TGAT   GGATATACCA
                                ||||   ||||||||||
                                ACTA   TTTATATGGT
                                  AA__
GAM1410 FABP2   3' TGAATGGAAATATACCA    6587     T   GG
                                TGA GTGG  ATATACCA
                                ||| ||||  ||||||||
                                ACT TACC  TATATGGT
                                  _   TT
GAM1410 HLA-DMB 5' TGATGTGGGGATACCCA    13384           A
                                TGATGTGGGGATAT CCA
                                |||||||||||||| |||
                                ACTACACCCCTATG GGT
                                                _
GAM1410 KCNS3   5' TGAGGTGGAGATGCCA     13935    T      ATA
                                TGA GTGGGGAT   CCA
                                ||| ||||||||   |||
                                ACT CACCTCTA   GGT
                                  C       C__
GAM1410 LAMP2   3' TGATGTGTTAACTACCA    30391       GG   A
                                TGATGTG  GAT TACCA
                                |||||||  ||| |||||
                                ACTACAC  TTG ATGGT
                                    AA  _
GAM1410 NONO    3' TGATTAAACAATATACCA   44361     GT  G
                                TGAT  GG GATATACCA
                                ||||  || |||||||||
                                ACTA  TT TTATATGGT
                                  AT  G
GAM1410 PLA2G2D 3' TGAGGTGGGGATGCCA     29641    T      ATA
                                TGA GTGGGGAT   CCA
                                ||| ||||||||   |||
                                ACT CACCCCTA   GGT
                                  C       C__
GAM1410 RUNX3   3' TGATGTGAGAATCCA      20329          ATA
                                TGATGTGGGGAT   CCA
                                ||||||||||||   |||
                                ACTACACTCTTA   GGT
                                               ___
GAM1410 SLC26A4 3' TGAACAGAGATATGCCA    7765     T TG     A
                                TGA G  GGGATAT CCA
                                ||| |  ||||||| |||
                                ACT T  CTCTATA GGT
                                  _ GT      C
GAM1410 SVIL    5' TGACGTGGGAATCCA      17228          ATA
                                TGATGTGGGGAT   CCA
                                ||||||||||||   |||
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                                ACTGCACCCTTA  GGT
                                      ___
GAM1410  TP63     3'  TAATATAAAATATACCA     19001         G
                                TGATGTGGG ATATACCA
                                ||||||||| ||||||||
                                ATTATATTT TATATGGT
                                      _
GAM1410  UBE1     3'  TGATGAGGGAACACCA      17782       T    T
                                TGATG GGGGA ATACCA
                                ||||| ||||| ||||||
                                ACTAC TCCCT TGTGGT
                                  _   _
GAM1411  IL2RB    3'  GTTTTGGAAAGCACGCTCA   9393          ATAG  A
                                GTTTTGGAAA   AC CTCA
                                ||||||||||   || ||||
                                CAAAACCTTT   TG GAGT
                                     CG__  C
GAM1411  PIK3CD   3'  AGTTTTGGAAGACCT      22724         AAAT   A
                                AGTTTTGGA   AGAC CT
                                |||||||||   |||| ||
                                TCAAAACCT   TCTG GA
                                     ____  _
GAM1411  PMSCL1   5'  AGTTTTGGAGACAC       22763         AAATA
                                AGTTTTGGA    GACAC
                                |||||||||    |||||
                                TCAAAACCT    CTGTG
                                     _____
GAM1411  PPM1D    3'  TAAGTTTGGAAAAACCTC    18839       T    ATA   A
                                TAAGTTT GGAAA   GAC CTC
                                ||||||| |||||   ||| |||
                                ATTCAAA CCTTT   TTG GAG
                                  _   ___  _
GAM1411  SDC2     3'  TAAGCTTCAGTAGACA      42574       TG AAAA
                                TAAGTTT  G   TAGACA
                                |||||||  |   ||||||
                                ATTCGAA  C   ATCTGT
                                    GT ____
GAM1412  ETV5     3'  ATACATAGAGAATCTAAGCTT  20841       TT___
                                ATATGT    ATCTAAGCTT
                                ||||||    ||||||||||
                                TATGTA    TAGATTCGAA
                                   TCTCT
GAM1412  LAMC1    3'  TACAAGCTGCCATCTAAG    14093      TA   T
                                TACAA  TGTT ATCTAAG
                                |||||  |||| |||||||
                                ATGTT  ACGG TAGATTC
                                  CG   _
GAM1412  TCTE1L   3'  CAATATTAACGCTAAGCTT   43372       GTTTAT
                                CAATAT     CTAAGCTT
                                ||||||     ||||||||
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                                GTTATA     GATTCGAA
                                   ATTGC_
GAM1413  ATF7     3'  TCAGCGGGTAATATGTCAT   27794      TAA
                                TTAGT   TAATATGTCAT
                                |||||   ||||||||||
                                AGTCG   ATTATACAGTA
                                   CCC
GAM1413  SLC4A7   3'  ACATTAGTTAATAAATAGT   18816           TAT
                                ACATTAGTTAATAA   GT
                                ||||||||||||||   ||
                                TGTAATCAATTATT   CA
                                         TAT
GAM1413  TEM7     3'  ACTTTAGTTAACCTGTGTCAT  33797    A       AATA
                                AC TTAGTTAAT    TGTCAT
                                || |||||||||    ||||||
                                TG AATCAATTG    ACAGTA
                                 A        GAC_
GAM1414  AKAP13   3'  AAGCATCAACTCTGTGCCAG   28465     G         TTAT
                                AAG ATCAACTCTGT    CTAG
                                ||| ||||||||||    ||||
                                TTC TAGTTGAGACA    GGTC
                                  G         C___
GAM1414  APG5L    3'  AAGGATGATTCTGTTCA     22128       CAAC
                                AAGGAT    TCTGTTTA
                                ||||||    ||||||||
                                TTCCTA    AGACAAGT
                                   CTA_
GAM1414  CDC27    3'  GGTCAGTTACTCTGTTTATCTG 10367    A  ___          A
            GA                    GG TCA   ACTCTGTTTATCT GA
                                || |||   |||||||||||||| ||
                                CC AGT   TGAGACAAATAGA CT
                                 _  CAA          C
GAM1414  EPB41    3'  AAGGATCAATGAGATCTAG   20762         CTC  TTT
                                AAGGATCAA   TG   ATCTAG
                                |||||||||   ||   ||||||
                                TTCCTAGTT   AC   TAGATC
                                      ___  TC_
GAM1414  GPR4     3'  GGAGATCGCTGTTTATCTAGA  40886   A    AACT
                                A GGATC    CTGTTTATCTAGA
                                | |||||    ||||||||||||||
                                C TCTAG    GACAAATAGATCT
                                 C    C___
GAM1414  LARGE    3'  AAGGATCAGATTTTCTATTT   21856        AC___
                                AAGGATCA     TCTGTTT
                                ||||||||     |||||||
                                TTCCTAGT     AGATAAA
                                     CTAAA
GAM1414  MS4A7    5'  GGATCAGCTCACCT       34528       ACTCT
                                GGATCA     GTTTATCT
                                ||||||     ||||||||
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                                CCTAGT    CGAGTGGA
                                      _____
GAM1414  TEM7    3'  AAGGACCAGCTTGTGAGTCTAG 33795        A  C   TTA
                                AAGGATCA CT TGT   TCTAG
                                |||||||| || |||   |||||
                                TTCCTGGT GA ACA   AGATC
                                     C  _   CTC
GAM1415  ACK1    3'  TGATGTCCTCCAGGGGCTGC  25121     AC       ATGA
                                TGAT  TCCTCCGGG   GC
                                ||||  |||||||||   ||
                                ACTA  AGGAGGTCC   CG
                                  C_       CCGA
GAM1415  BMP8    3'  TGACACTCCTGCTTGAGC    11886         CCGGGA
                                TGATACTCCT     TGAGC
                                ||||||||||     |||||
                                ACTGTGAGGA     ACTCG
                                      CGA___
GAM1415  DAG1    3'  TGGCACTCCTCCCCAGCC    20531    A       GGGATG
                                TG TACTCCTCC     AGCC
                                || |||||||||     ||||
                                AC GTGAGGAGG     TCGG
                                 C       GG____
GAM1415  POLR2G  3'  GATGCCTTCTGGGATGAG    15457     ACT   _ C
                                GAT   CCT C GGGATGAG
                                |||   ||| | ||||||||
                                CTA   GGA G CCCTACTC
                                  C__   A A
GAM1415  RNH     5'  TGGCACTCCTCTCCCCGGGGCT 40612    A      ____     A_
           G                     TG TACTCCT    CCGGG  TG
                                || |||||||    |||||  ||
                                AC GTGAGGA    GGCCC  AC
                                 C      GAGG    CG
GAM1415  SHMT2   3'  GATGCCTTCTGGGATGAG    24006     ACT   _ C
                                GAT   CCT C GGGATGAG
                                |||   ||| | ||||||||
                                CTA   GGA G CCCTACTC
                                  C__   A A
GAM1415  SLC19A2 3'  TGAGCTTCTCTGGGAAGC    42894     TA  C   C    TG
                                TGA  CT CTC GGGA  AGC
                                |||  || ||| ||||  |||
                                ACT  GA GAG CCCT  TCG
                                  C_  A   A   __
GAM1415  SURF5   3'  TGATGACTCGGAATGA      39509      _   CTCC
                                TGAT ACTC    GGGATGA
                                |||| ||||    |||||||
                                ACTA TGAG    CCTTACT
                                  C    _____
GAM1415  TCP10   3'  CCGTGCCTGGGGTGGGCCAC  21427    T__  _   A  A
                                CC   CC GGG TG GCCAC
                                ||   || ||| || |||||
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                                GG   GG CCC AC CGGTG
                                 CAC  A   C  C
GAM1415  TUBA2    5'  TGAGCTCCTCCGCTGCC     38617     TA       GGATGA
                                TGA  CTCCTCCG     GCC
                                |||  ||||||||      |||
                                ACT  GAGGAGGC     CGG
                                  C_       GA____
GAM1416  PTX3     3'  CCTTGTAGTATAAATATG    15990         _    C
                                CCTTGTAG ATGAG ATG
                                |||||||| ||||| |||
                                GGAACATC TATTT TAC
                                     A     A
GAM1416  ZNF217   3'  CCTTGCAGATTCCTCATA    27191          GAG_
                                CCTTGTAGAT    CATG
                                ||||||||||    ||||
                                GGAACGTCTA    GTAT
                                      AGGA
GAM1417  ABL1     5'  CCCGCCGCCCCGCGCCC      28705          CCCTA
                                CCCGCCGCTC    GCCC
                                ||||||||||     ||||
                                GGGCGGCGGG    CGGG
                                      CG___
GAM1417  ABL2     5'  CCCAGCCCAGGCCCTGGCCC   28723     _  GCTC    A
                                CCC GCC    CCCT GCCC
                                ||| |||    |||| ||||
                                GGG CGG    GGGA CGGG
                                  T   GTCC    C
GAM1417  ACCN2    3'  CCCCCACACTAGCCC       33436     G    TCCC
                                CCC CCGC    CTAGCCC
                                ||| ||||    |||||||
                                GGG GGTG    GATCGGG
                                  _    T___
GAM1417  ADAM12   5'  CCGCCGCTGAGCTCTTCTAGCC 18468       _____    CC
                                CCGCC    GCTC  CTAGCC
                                |||||    ||||  ||||||
                                GGCGG    CGAG  GATCGG
                                   CGACT    AA
GAM1417  ADCY8    5'  CCCGCCTCGCCCTAGCCC    10001       GC  _
                                CCCGCC  TC CCCTAGCCC
                                ||||||  ||  |||||||||
                                GGGCGG  AG GGGATCGGG
                                   __  C
GAM1417  AMD1     5'  CCCGCCGCTGCCGCC       11588         C  CTA
                                CCCGCCGCT CC   GCC
                                |||||||| ||   |||
                                GGGCGGCGA GG   CGG
                                      C  ___
GAM1417  ARF3     3'  CCCCGCTCCCCCCGGCCC    11671     G        A_
                                CC CCGCTCCCCT  GCCC
                                || ||||||||||  ||||
```

```
                                GG GGCGAGGGGG  CGGG
                                 _        GC
GAM1417  ARSB     5'  CCCGCCGCCTCCGACCC     6250         TC  CTA
                                CCCGCCGC  CC   GCCC
                                ||||||||  ||   ||||
                                GGGCGGCG  GG   TGGG
                                    GA  C__
GAM1417  ATBF1    5'  CCCGCCGCCGCCGCC       27845         C  CTA
                                CCCGCCGCT CC   GCC
                                |||||||||  ||   |||
                                GGGCGGCGG GG   CGG
                                     C  ___
GAM1417  ATP2C1   5'  CCCCCGCTCCCGGCC       30785     G       CTA
                                CCC CCGCTCCC   GCC
                                |||  ||||||||   |||
                                GGG GGCGAGGG   CGG
                                 _       C__
GAM1417  ATSV     3'  CCCCGCTCCCTCCTGGTCC    20221    G       _  AG__
                                CC CCGCTCCC CT    CC
                                ||  ||||||||  ||    ||
                                GG GGCGAGGG GG    GG
                                 _       A  ACCA
GAM1417  AXUD1    3'  CCCCCTCCCCCTAGTCC     37484     G  GC       _
                                CCC CC  TCCCCTAG CC
                                |||  ||  ||||||||  ||
                                GGG GG  GGGGGATC GG
                                 _  A_       A
GAM1417  BAALC    5'  CCCGCCGCCCCTAGTCC     36037         TC     _
                                CCCGCCGC  CCCTAG CC
                                ||||||||  ||||||  ||
                                GGGCGGCG  GGGATC GG
                                     __     A
GAM1417  BACE     3'  CCCCACTACCTAGCCC      39955    G    CC
                                CC CCGCT  CCTAGCCC
                                ||  |||||  ||||||||
                                GG GGTGA  GGATCGGG
                                 _    T_
GAM1417  BCL2L2   3'  CCTAGCCCCACCTGGCCC    19738    GCC    _  A
                                CC   GCTCC CCT GCCC
                                ||   |||||  |||  ||||
                                GG   CGGGG GGA CGGG
                                  AT_     T   C
GAM1417  BCL2L2   3'  CCCAGCCACACCTAGCCC    19736     _    TCC
                                CCC GCCGC   CCTAGCCC
                                |||  |||||   ||||||||
                                GGG CGGTG   GGATCGGG
                                  T     T__
GAM1417  BMP8     5'  CCGCCACTCATAGGGAGCCC   11876          CCCT__
                                CCGCCGCTC     AGCCC
                                |||||||||     |||||
```

```
                                GGCGGTGAG     TCGGG
                                     TATCCC
GAM1417 BTG3     5' CCCGCCGCTGCCGCC      27714        C  CTA
                                CCCGCCGCT CC   GCC
                                ||||||||| ||   |||
                                GGGCGGCGA GG   CGG
                                     C ___
GAM1417 C7orf2   5' CCCGCCGCCGCGCCGCCC    35367        CC_  TA
                                CCCGCCGCT   CC  GCCC
                                |||||||||   ||  ||||
                                GGGCGGCGG   GG  CGGG
                                     CGC __
GAM1417 CAPN1    5' CCCGCCGCCCCTCCGCCC    23250          _  TA
                                CCCGCCGCTCC CC  GCCC
                                |||||||||| ||  ||||
                                GGGCGGCGGGG GG  CGGG
                                      A __
GAM1417 CAPN10   3' CCCGCCGCTTCTCTACC     35767        CCC   G
                                CCCGCCGCT   CTA CC
                                |||||||||   ||| ||
                                GGGCGGCGA   GAT GG
                                     AGA  _
GAM1417 CAPN10   3' CCCGCCGCTTCTCTACC     35767        CCC   G
                                CCCGCCGCT   CTA CC
                                |||||||||   ||| ||
                                GGGCGGCGA   GAT GG
                                     AGA  _
GAM1417 CAV2     5' CCCTCGCCTCGCCTAGCCC   10289     GC  _  C
                                CCC  CGC TC CCTAGCCC
                                |||  ||| || ||||||||
                                GGG  GCG AG GGATCGGG
                                  A_   G  C
GAM1417 CCND1    3' CCCGCCGCCCAGACCC      38201        TCC  TA
                                CCCGCCGC   CC  GCCC
                                |||||||   ||  ||||
                                GGGCGGCG   GG  TGGG
                                     ___  TC
GAM1417 CDC34    3' CCGGCCGCTCCCACCC      20351    C       CTA
                                CC GCCGCTCCC   GCCC
                                || |||||||||   ||||
                                GG CGGCGAGGG   TGGG
                                  C        ___
GAM1417 CDH23    5' CCCGCGCTCCATGCCC      38071      C    CCTA
                                CCCGC GCTCC    GCCC
                                ||||| |||||    ||||
                                GGGCG CGAGG    CGGG
                                   _    TA__
GAM1417 CDKN2A   5' CCCGCCGCCCGCTGCC      38469        T  C  A
                                CCCGCCGC CC CT GCC
                                |||||||| || || |||
```

```
                                GGGCGGCG GG GA CGG
                                    _ C _
GAM1417 CDKN2A   3' CCCCCCTGAGCTTCCCTAG   38468    G ___  C
                                CCC CC   GCT CCCTAG
                                ||| ||   ||| ||||||
                                GGG GG   CGA GGGATC
                                  G  ACT   A
GAM1417 CEBPA    3' CCCTGCTCCCAGCCC      20390    GCC    CT
                                CCC   GCTCCC  AGCCC
                                |||   ||||||  |||||
                                GGG   CGAGGG  TCGGG
                                  A__     __
GAM1417 CEBPD    5' CCCGCCGCCTTTTCTAGCCC  45514       CCC_
                                CCCGCCGCT    CTAGCCC
                                |||||||||    |||||||
                                GGGCGGCGG    GATCGGG
                                     AAAA
GAM1417 CELSR3   5' CCCGCCGCTCGGGCCC     10830        CCCTA
                                CCCGCCGCTC    GCCC
                                ||||||||||    ||||
                                GGGCGGCGAG    CGGG
                                     CC___
GAM1417 CHN1     5' CCCGCCGCACCCACACC     12244       T  CTA
                                CCCGCCGC CCC   GCC
                                |||||||| |||   |||
                                GGGCGGCG GGG   TGG
                                     T  TG_
GAM1417 CHN2     5' CCCGGCCGCTCGCAGCC     19806    _    CCC
                                CCCG CCGCTC   TAGCC
                                |||| ||||||   |||||
                                GGGC GGCGAG   GTCGG
                                  C     C__
GAM1417 CHRNE    3' CCCCCCTCTCCTCTTCTAGCCC 6342     G  G   C___
                                CCC CC CTCC    CTAGCCC
                                ||| || ||||    |||||||
                                GGG GG GAGG    GATCGGG
                                  G  A    AGAA
GAM1417 COL9A1   5' CCCGCCGCTAATCCCTTGGCCC 38533       C__   A_
                                CCCGCCGCT   CCCT  GCCC
                                |||||||||   ||||  ||||
                                GGGCGGCGA   GGGA  CGGG
                                     TTA    AC
GAM1417 CORO2A   5' CCCGCCGACTCCCGGCGCCC  38062      _    CTA
                                CCCGCCG CTCCC   GCCC
                                ||||||| |||||   ||||
                                GGGCGGC GAGGG   CGGG
                                    T    CCG
GAM1417 CRKL     5' CCCGCCTGCTCCGGGGCC    23305      _    CCTA
                                CCCGCC GCTCC    GCC
                                |||||| |||||    |||
```

```
                                GGGCGG CGAGG   CGG
                                   A    CCC_
GAM1417 CSF3R   5' CCCAGCCCCTGCTTGGCC   8906     CC    C_ A_
                                CCCG  GCTCC  CT  GCC
                                ||||  |||||  ||  |||
                                GGGT  CGGGG  GA  CGG
                                  __    AC  AC
GAM1417 CSNK1D  5' CCCGCCGCTCCCAGCGCC   40063          CTA
                                CCCGCCGCTCCC   GCC
                                ||||||||||||   |||
                                GGGCGGCGAGGG   CGG
                                       TCG
GAM1417 CSPG4   3' CCCAGCTGCCTGCCCTAGTCC 12493    _ C   C_    _
                                CCC GC GCT  CCCTAG CC
                                ||| || |||  |||||| ||
                                GGG CG CGG  GGGATC GG
                                  T  A   AC     A
GAM1417 DDEF2   5' CCGCCGCTCCGGCCC      19315         CCTA
                                CCGCCGCTCC    GCCC
                                ||||||||||    ||||
                                GGCGGCGAGG    CGGG
                                      C___
GAM1417 DDX26   5' CCCCGCTCCCCGGCCC     29086    G       TA
                                CC CCGCTCCCC  GCCC
                                || |||||||||  ||||
                                GG GGCGAGGGG  CGGG
                                  _       C_
GAM1417 DGAT1   5' CCGGCCGCCGTAGCCC     42072    C     CCCC
                                CC GCCGCT    TAGCCC
                                || ||||||    ||||||
                                GG CGGCGG    ATCGGG
                                  C     C___
GAM1417 DMPK    5' CCCGCCTCCCAGCC       20608       GC    CT
                                CCCGCC  TCCC  AGCC
                                ||||||  ||||  ||||
                                GGGCGG  AGGG  TCGG
                                   __    __
GAM1417 DSCAM   5' CCTGCCGCTCCCCGGCC    10796    C        TA
                                CC GCCGCTCCCC  GCC
                                || ||||||||||  |||
                                GG CGGCGAGGGG  CGG
                                  A        C_
GAM1417 DUSP7   5' CCCGCCGCCCCGGCC      42264          CCTA
                                CCCGCCGCTCC    GCC
                                ||||||||||    |||
                                GGGCGGCGGGG    CGG
                                      C___
GAM1417 DXYS155E 5' CCGCCGCCGCCGCTGGCCC   22946        C  _  A
                                CCGCCGCT CC CT GCCC
                                |||||||| || || ||||
```

```
                                GGCGGCGG GG GA CGGG
                                    C  C  C
GAM1417  EGLN2    5'  CCACTCCCATCCTGGCCC    38817        ___  A
                                CCGCTCCC   CT GCCC
                                ||||||||   || ||||
                                GGTGAGGG   GA CGGG
                                    TAG  C
GAM1417  EMX2     5'  CCGCCGCCCGCTGCCC      44681        T  C  A
                                CCGCCGC CC CT GCCC
                                ||||||| || || ||||
                                GGCGGCG GG GA CGGG
                                   _  C  _
GAM1417  EN1      5'  CCCGCCGCCCCGGCC       10906          CCTA
                                CCCGCCGCTCC    GCC
                                ||||||||||    |||
                                GGGCGGCGGGG    CGG
                                    C___
GAM1417  EPB49    3'  CCTGCCCCTCCCAACCC     12726    C   G    CT
                                CC GCC CTCCC  AGCCC
                                || ||| |||||  |||||
                                GG CGG GAGGG  TTGGG
                                 A   G    __
GAM1417  EPIM     5'  CCCGCCGCTCAAGCC       12739          CCCT
                                CCCGCCGCTC    AGCC
                                |||||||||    ||||
                                GGGCGGCGAG    TCGG
                                    T___
GAM1417  EVC      5'  CCCGCCGCATCCCGCCGCC   30975        _   _  A
                                CCCGCCGC TCCC CT GCC
                                |||||||| |||| || |||
                                GGGCGGCG AGGG GG CGG
                                    T   C  _
GAM1417  EZH1     3'  ACCAGGCTCCCCTAGTCC    12776     __         _
                                GCC  GCTCCCCTAG CC
                                |||  ||||||||||  ||
                                TGG  CGAGGGGATC GG
                                  TC         A
GAM1417  F2R      5'  CCGCCGCTCGCAAGCCC     12794          CCCT
                                CCGCCGCTC    AGCCC
                                |||||||||    |||||
                                GGCGGCGAG    TCGGG
                                    CGT_
GAM1417  FBN1     5'  CCCGCCGCCTCTTGCC      42048          CCC  A
                                CCCGCCGCT   CT GCC
                                |||||||||   || |||
                                GGGCGGCGG   GA CGG
                                    A__  A
GAM1417  FOXD2    5'  CCGCCGCTCCTGCACCC     20959          CCTA
                                CCGCCGCTCC    GCCC
                                ||||||||||    ||||
```

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                                GGCGGCGAGG   TGGG
                                     ACG_
GAM1417 FOXF2   5' CCTGCGAGCGCCCTAGCCC   11128   C  C_  TC
                                CC GC  GC  CCCTAGCCC
                                || ||  ||  |||||||||
                                GG CG  CG  GGGATCGGG
                                 A  CT  C_
GAM1417 GABRB3  5' CCGCCGCCGCGCTGGCCC   9047       CCC  A
                                CCGCCGCT   CT GCCC
                                ||||||||   || ||||
                                GGCGGCGG   GA CGGG
                                     CGC  C
GAM1417 GML     5' CCCGCCGCCTCCAGCC     13159       CCC
                                CCCGCCGCT   CTAGCC
                                |||||||||   ||||||
                                GGGCGGCGG   GGTCGG
                                     A__
GAM1417 GNA11   5' CCAGCCGCCCAGCCC      44030   C     CCCT
                                CC GCCGCTC   AGCCC
                                || |||||||   |||||
                                GG CGGCGGG   TCGGG
                                 T    _____
GAM1417 GNB2    5' CCCGCCGCCAGCGCTGCC   23597       CCC_  A
                                CCCGCCGCT   CT GCC
                                |||||||||   || |||
                                GGGCGGCGG   GA CGG
                                     TCGC  _
GAM1417 GNGT2   3' CCCACCCAACCCTGGCCC   36481     GCTC   A
                                CCCGCC   CCCT GCCC
                                ||||||   |||| ||||
                                GGGTGG   GGGA CGGG
                                   GTT_   C
GAM1417 GSTM5   3' CCCCATCAGCCTAGCCC    9205    G  C  C_
                                CC CCG TC  CCTAGCCC
                                || ||| ||  ||||||||
                                GG GGT AG  GGATCGGG
                                 _  _  TC
GAM1417 HCK     3' CCTGGGCACCCCCTGGCCC   40939   GCC  _    A
                                CC   GC TCCCCT GCCC
                                ||   || |||||| ||||
                                GG   CG GGGGGA CGGG
                                 ACC  T     C
GAM1417 HDAC7A  3' CCCACTCCCCCCTAGCCC   32468     CG
                                CCCGC  CTCCCCTAGCCC
                                |||||  ||||||||||||
                                GGGTG  GGGGGGATCGGG
                                  A_
GAM1417 HNRPM   5' CCCGGCTGCCTCCTTGGCCC  25567    CC  _  _  A_
                                CCCG  GCT CC CCT  GCCC
                                ||||  ||| || |||  ||||
```

```
                                GGGC  CGA GG GGA  CGGG
                                  __  C A  AC
GAM1417  HNRPM    5'  CCCCCGCTCCCGGCTGCC    25566     G      __ A
                                CCC CCGCTCCC  CT GCC
                                ||| ||||||||  || |||
                                GGG GGCGAGGG  GA CGG
                                  _      CC  _
GAM1417  ID4      5'  CCGCGCTCCCCTAGCCC     11379     C
                                CCGC GCTCCCCTAGCCC
                                |||| ||||||||||||
                                GGCG CGAGGGGATCGGG
                                  _
GAM1417  IER3     3'  CCCACCGGGCCTAGCCC     19352       CTCC
                                CCCGCCG   CCTAGCCC
                                |||||||   ||||||||
                                GGGTGGC   GGATCGGG
                                   CC__
GAM1417  IER3     3'  CCCACCGGCCTAGCCC      19351       CTCC
                                CCCGCCG   CCTAGCCC
                                |||||||   ||||||||
                                GGGTGGC   GGATCGGG
                                   C___
GAM1417  IGFBP4   3'  CCCCACCTCCCTAGCCC     11396    G   TC
                                CC CCGC  CCCTAGCCC
                                || ||||  |||||||||
                                GG GGTG  GGGATCGGG
                                 _   GA
GAM1417  INPPL1   5'  CCCGCCGCCCCGCGCC      11462         CCTA
                                CCCGCCGCTCC   GCC
                                ||||||||||   |||
                                GGGCGGCGGGG   CGG
                                     CG__
GAM1417  ITPR2    3'  CCTGCCGCTCCCTGCCC     13676    C       CTA
                                CC GCCGCTCCC  GCCC
                                || |||||||||  ||||
                                GG CGGCGAGGG  CGGG
                                 A       A__
GAM1417  JAG2     5'  CCCGCCGCCGCCGCCC      13706        C  CTA
                                CCCGCCGCT CC  GCCC
                                ||||||||| ||  ||||
                                GGGCGGCGG GG  CGGG
                                   C  ___
GAM1417  JTB      5'  CCCGACGCAGCCATCTAGCCC  27442     C  TC __
                                CCCG CGC  CC  CTAGCCC
                                |||| |||  ||  |||||||
                                GGGC GCG  GG  GATCGGG
                                  T  TC  TA
GAM1417  JUN      5'  CCGCCGCTGTCAACAGCGCC  13740       CCCC_  _
                                CCGCCGCT    TAGC CC
                                ||||||||    |||| ||
```

```
                                GGCGGCGA    GTCG GG
                                    CAGTT    C
GAM1417 JUND     5' CCCGTCCGCTCGGCCC     23799     _     CCCTA
                                CCCG CCGCTC    GCCC
                                |||| ||||||    ||||
                                GGGC GGCGAG    CGGG
                                  A     C____
GAM1417 KCNA6    5' CCAGCCGCTCCGGACCC     13807    C      CCTA
                                CC GCCGCTCC    GCCC
                                || ||||||||    ||||
                                GG CGGCGAGG    TGGG
                                 T       CC__
GAM1417 KCND3    3' CCCTCCCTTCCTCTGGCCC   22532    G  GC   C  A
                                CCC CC  TCC CT GCCC
                                ||| ||  ||| || ||||
                                GGG GG  AGG GA CGGG
                                  A  GA   A  C
GAM1417 KCNK1    5' CCCGCCGCCTCTTCTGGCCC   13883       _  CC  A
                                CCCGCCGC TC  CT GCCC
                                |||||||| ||  || ||||
                                GGGCGGCG AG  GA CGGG
                                    G  AA  C
GAM1417 KCNK1    5' CCCGCCGCCCCCGCCC      13882          CTA
                                CCCGCCGCTCCC   GCCC
                                ||||||||||||   ||||
                                GGGCGGCGGGGGG   CGGG
                                          ___
GAM1417 KCNK1    5' CCCCCGCCCGGGCCTGGC    13880    G     C__   A
                                CCC CCGCTC   CCT GC
                                ||| ||||||   ||| ||
                                GGG GGCGGG   GGA CG
                                  _     CCC   C
GAM1417 KCNK5    5' CCCAGCTGCTACCAGTCC    19032    _ C   CCC   _
                                CCC GC GCT   CTAG CC
                                ||| || |||   |||| ||
                                GGG CG CGA   GGTC GG
                                  T  A   T__    A
GAM1417 KCNS2    5' CCCGCCGCTCCCGGAGCCC   42822          CT
                                CCCGCCGCTCCC  AGCCC
                                ||||||||||||  |||||
                                GGGCGGCGAGGG  TCGGG
                                      CC
GAM1417 KIAA0857 5' CCCGCCGCCCCAACC      42469          CCT
                                CCCGCCGCTCC   AGCC
                                ||||||||||   ||||
                                GGGCGGCGGGG   TTGG
                                          ___
GAM1417 KIF5C    5' CCGGCCGCTCCGAGCCC     21148    C      CCT
                                CC GCCGCTCC   AGCCC
                                || ||||||||   |||||
```

```
                                GG CGGCGAGG   TCGGG
                                 C       C__
GAM1417  LASS2    5'  CCCTCCGCTCCCGGCCC     42668     G       CTA
                                CCC CCGCTCCC   GCCC
                                ||| ||||||||   ||||
                                GGG GGCGAGGG   CGGG
                                  A       C__
GAM1417  LGR6     5'  CCCGGCAGCCTAGCCC      44477     CC  TCC
                                CCCG  GC   CCTAGCCC
                                ||||  ||   ||||||||
                                GGGC  CG   GGATCGGG
                                  __  TC_
GAM1417  LOXL2    5'  CCGCCGCCGCTGAGCCC     14196        CCC  _
                                CCGCCGCT   CT AGCCC
                                ||||||||   || |||||
                                GGCGGCGG   GA TCGGG
                                     C__  C
GAM1417  LRP8     5'  CCGCCGCTGCCGCCC       37791        C  CTA
                                CCGCCGCT CC   GCCC
                                |||||||| ||   ||||
                                GGCGGCGA GG   CGGG
                                     C  ___
GAM1417  MGAT1    5'  CCCGCCGCGCCCCGCCC     14426        T    TA
                                CCCGCCGC CCCC  GCCC
                                |||||||| ||||  ||||
                                GGGCGGCG GGGG  CGGG
                                     C   __
GAM1417  MMP25    3'  CCCGCCGCCGCCGCCC      35381        C  CTA
                                CCCGCCGCT CC   GCCC
                                ||||||||| ||   ||||
                                GGGCGGCGG GG   CGGG
                                      C  ___
GAM1417  MNT      3'  CCTCGCCGCCCAGCCC      33709    _      CCCT
                                CC CGCCGCTC    AGCCC
                                || ||||||||    |||||
                                GG GCGGCGGG    TCGGG
                                 A       ____
GAM1417  MTMR1    5'  CCCGCCGCCCTCGCAGCCC   43151          CCC
                                CCCGCCGCTC   TAGCCC
                                ||||||||||   ||||||
                                GGGCGGCGGG   GTCGGG
                                      AGC
GAM1417  MXI1     5'  CCTGCCGCCCCAGCC       39017    C       CCT
                                CC GCCGCTCC   AGCC
                                || ||||||||   ||||
                                GG CGGCGGGG   TCGG
                                 A       ___
GAM1417  MYBL2    5'  CCGGCCGCTCCGGGCCC     14703    C       CCTA
                                CC GCCGCTCC    GCCC
                                || ||||||||    ||||
```

```
                                GG CGGCGAGG   CGGG
                                 C       CC__
GAM1417  NCKAP1   5'  CCCGCCGCCCTTCCGCCC    30252          CC  A
                                CCCGCCGCTC  CT GCCC
                                ||||||||||  || ||||
                                GGGCGGCGGG  GG CGGG
                                      AA  _
GAM1417  NOTCH3   3'  CCCCCGACCCCTGGCCC     7734      G   CT    A
                                CCC CCG  CCCCT GCCC
                                ||| |||  ||||| ||||
                                GGG GGC  GGGGA CGGG
                                  _  T_    C
GAM1417  NRAP     3'  CCCCGCTCTGTAGCTCC     40190    G     CCC   _
                                CC CCGCTC   TAGC CC
                                || ||||||   |||| ||
                                GG GGCGAG   ATCG GG
                                 _     AC_   A
GAM1417  NRG1     5'  CCGCCGCTCAGCTCCTGGCC   30340         C___   A
                                CCGCCGCTC    CCT GCC
                                |||||||||    ||| |||
                                GGCGGCGAG    GGA CGG
                                      TCGA   C
GAM1417  NRIP1    5'  CCTGCCGCCCCGTCCTGGCCC  40958    C       __   A
                                CC GCCGCTCC  CCT GCCC
                                || ||||||||  ||| ||||
                                GG CGGCGGGG  GGA CGGG
                                 A       CA   C
GAM1417  OGDH     3'  CCTCCTGCTCCCCCCGGCC    45009    G  _      A_
                                CC CC GCTCCCCT  GCC
                                || || ||||||||  |||
                                GG GG CGAGGGGG  CGG
                                 A  A       GC
GAM1417  OTX1     3'  CCTCCGGCGGGCCTAGCCC    30984    G   _ TCC
                                CC CCG C   CCTAGCCC
                                || ||| |   ||||||||
                                GG GGC G   GGATCGGG
                                 A   C CCC
GAM1417  PAPOLA   5'  CCGCCGCTGCCGCCC       37204         C  CTA
                                CCGCCGCT CC   GCCC
                                |||||||| ||   ||||
                                GGCGGCGA GG   CGGG
                                     C  ___
GAM1417  PAX6     5'  CCACCGCTCCTCACTGGCCC   11484          C__  A
                                CCGCCGCTCC   CT GCCC
                                ||||||||||   || ||||
                                GGTGGCGAGG   GA CGGG
                                      AGT  C
GAM1417  PCDHGA1  3'  CCCGCCGCCCGCTGCCC     36729         T  C  A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
```

```
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA10 3' CCCGCCGCCCGCTGCCC    36871      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA11 3' CCCGCCGCCCGCTGCCC    36880      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA12 3' CCCGCCGCCCGCTGCCC    36889      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA2  3' CCCGCCGCCCGCTGCCC    36736      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA3  3' CCCGCCGCCCGCTGCCC    36742      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA4  3' CCCGCCGCCCGCTGCCC    36820      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA5  3' CCCGCCGCCCGCTGCCC    36829      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA6  3' CCCGCCGCCCGCTGCCC    33168      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA7  3' CCCGCCGCCCGCTGCCC    36845      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGA8  3' CCCGCCGCCCGCTGCCC    36855      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
```

```
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGA9   3' CCCGCCGCCCGCTGCCC    33171      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB1   3' CCCGCCGCCCGCTGCCC    36898      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB2   3' CCCGCCGCCCGCTGCCC    36907      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB3   3' CCCGCCGCCCGCTGCCC    36916      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB4   3' CCCGCCGCCCGCTGCCC    36925      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB5   3' CCCGCCGCCCGCTGCCC    36934      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB6   3' CCCGCCGCCCGCTGCCC    36940      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGB7   3' CCCGCCGCCCGCTGCCC    36948      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGC3   3' CCCGCCGCCCGCTGCCC    37049      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417  PCDHGC4   3' CCCGCCGCCCGCTGCCC    37070      T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
```

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                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PCDHGC5  3' CCCGCCGCCCGCTGCCC    37078       T C A
                                CCCGCCGC CC CT GCCC
                                |||||||| || || ||||
                                GGGCGGCG GG GA CGGG
                                    _ C _
GAM1417 PEX7    5' CCCGCCGCCCCCGGCCC    7109          CTA
                                CCCGCCGCTCCC  GCCC
                                ||||||||||||  ||||
                                GGGCGGCGGGGG  CGGG
                                      C__
GAM1417 PHKG1   3' CCCACCTGCCCCCTAGCCC   26311      _ T
                                CCCGCC GC CCCCTAGCCC
                                |||||| || ||||||||||
                                GGGTGG CG GGGGATCGGG
                                   A _
GAM1417 PIK3R2  3' CCCGCCGCCGCAGCC      22742       CCCC
                                CCCGCCGCT   TAGCC
                                |||||||||   |||||
                                GGGCGGCGG   GTCGG
                                     C___
GAM1417 PIM2    3' GCCTTATTTCCCCTAGCCC   41027    GC___
                                GCC    TCCCCTAGCCC
                                |||    ||||||||||
                                CGG    AGGGGATCGGG
                                  AATAA
GAM1417 PITX3   5' CCCCCTGCTCCCGGGCC    22756    G _    CTA
                                CCC CC GCTCCC  GCC
                                ||| || ||||||  |||
                                GGG GG CGAGGG  CGG
                                  _ A    CC_
GAM1417 PIWIL1  3' CCCATACAACCTAGCCC    43752    CC  TCC
                                CCCG  GC  CCTAGCCC
                                ||||  ||  ||||||||
                                GGGT  TG  GGATCGGG
                                  A_  TT_
GAM1417 PKIA    5' CCCGCCGCGCCCGCC      27738       T  CTA
                                CCCGCCGC CCC  GCC
                                |||||||| |||  |||
                                GGGCGGCG GGG  CGG
                                     C  ___
GAM1417 PMM2    3' GCCTGGGCTCCCCTGGCCC   43553    ___     A
                                GCC  GCTCCCCT GCCC
                                |||  |||||||| ||||
                                CGG  CGAGGGGA CGGG
                                  ACC      C
GAM1417 PPP2R1A 3' CCCGTGCTCCCCTAGCCC   30598    CC
                                CCCG  GCTCCCCTAGCCC
                                ||||  ||||||||||||
```

```
                                GGGC  CGAGGGGATCGGG
                                  A_
GAM1417  PPP3CA   5'  CCGCCGCTGCCGCCAGCCC   9611        C  _
                                CCGCCGCT CC CTAGCCC
                                |||||||| || |||||||
                                GGCGGCGA GG GGTCGGG
                                    C  C
GAM1417  PPP5C    3'  CCTGCTCTGCCCCTAGCCC   26488    C  CG  _
                                CC GC  CT CCCCTAGCCC
                                || ||  || ||||||||||
                                GG CG  GA GGGGATCGGG
                                 A  A_  C
GAM1417  PPT2     3'  CCAGCCGCTCCAGGCGCCC   39916    C       CCTA
                                CC GCCGCTCC    GCCC
                                || ||||||||    ||||
                                GG CGGCGAGG    CGGG
                                 T       TCCG
GAM1417  PRDM16   3'  CCCGGCTGCCCAGCCC      35243     CC   C   T
                                CCCG  GCT CCC AGCCC
                                ||||  ||| ||| |||||
                                GGGC  CGA GGG TCGGG
                                  __   C   _
GAM1417  PRKAG1   3'  CCCCCATACCTTCCCTAGC   15604     G   ___  C
                                CCC CCG   CT CCCTAGC
                                ||| |||   || |||||||
                                GGG GGT   GA GGGATCG
                                  _   ATG  A
GAM1417  PRKY     5'  CCCGCCGCTTCCTCCAGC    15690        C  _
                                CCCGCCGCT CC CTAGC
                                ||||||||| || |||||
                                GGGCGGCGA GG GGTCG
                                     A  A
GAM1417  PRX      3'  CCTCGCCCCCCACCCTAGC   34111    _   G  _
                                CC CGCC CTC CCCTAGC
                                || |||| ||| |||||||
                                GG GCGG GGG GGGATCG
                                 A   G   T
GAM1417  PSCD4    3'  CCCCTGACCCCTAGCCC     30123    G  GCT
                                CC CC   CCCCTAGCCC
                                || ||   ||||||||||
                                GG GG   GGGGATCGGG
                                 _  ACT
GAM1417  PTEN     5'  CCGGCGTTCCCAGCCC      7206      C  C   CT
                                CCG CG TCCC  AGCCC
                                ||| || ||||  |||||
                                GGC GC AGGG  TCGGG
                                  C  A   __
GAM1417  PTPRA    5'  CCCGCGGCTCCGAGCCC     38907      C    CCT
                                CCCGC GCTCC   AGCCC
                                ||||| |||||   |||||
```

```
                                GGGCG CGAGG   TCGGG
                                  C    C__
GAM1417  PTPRF    5'  CCGCCGCCTCCACCTGGTCC  39032       _  _  AG_
                                CCGCCGC TCC CCT   CC
                                ||||||| ||| |||   ||
                                GGCGGCG AGG GGA   GG
                                   G   T   CCA
GAM1417  PURA     5'  CCTGCCGCTCCGCCC      25206    C      CCTA
                                CC GCCGCTCC    GCCC
                                || ||||||||    ||||
                                GG CGGCGAGG    CGGG
                                 A      _____
GAM1417  PXR1     3'  CCCCGCTCCCACCC       7233     G      CTA
                                CC CCGCTCCC   GCCC
                                || ||||||||   ||||
                                GG GGCGAGGG   TGGG
                                 _      ____
GAM1417  PYGO2    3'  CCCGCCGCATCCCCTACCC   41949       _     G
                                CCCGCCGC TCCCCTA CC
                                |||||||| ||||||| ||
                                GGGCGGCG AGGGGAT GG
                                    T      G
GAM1417  RAB1A    5'  CCCTGCTCCCCTCCC      43184     GCC      AG
                                CCC   GCTCCCCT  CCC
                                |||   ||||||||  |||
                                GGG   CGAGGGGA  GGG
                                  A__       __
GAM1417  RABL2A   3'  CCACCCACCCCTAGCCC     30196      GCT
                                CCGCC   CCCCTAGCCC
                                |||||   ||||||||||
                                GGTGG   GGGGATCGGG
                                   GT_
GAM1417  RABL2B   3'  CCACCCACCCCTAGCCC     28202      GCT
                                CCGCC   CCCCTAGCCC
                                |||||   ||||||||||
                                GGTGG   GGGGATCGGG
                                   GT_
GAM1417  RALB     5'  CCCGCCGCCTCCGCCGTCC   16145       TC  _  AG
                                CCCGCCGC  CC CT  CC
                                ||||||||  || ||  ||
                                GGGCGGCG  GG GG  GG
                                    GA  C  CA
GAM1417  RGS3     3'  CCCCCCAGGCTGCCTTAGTCC  39123     G  __   C  C   _
                                CCC CC  GCT CC TAG CC
                                ||| ||  ||| || ||| ||
                                GGG GG  CGA GG ATC GG
                                  G  TC   C  A   A
GAM1417  RHEB2    5'  CCCGCCGCCTCCGCCC      24715       TC  CTA
                                CCCGCCGC  CC   GCCC
                                ||||||||  ||   ||||
```

```
                                GGGCGGCG  GG   CGGG
                                    GA  ___
GAM1417  RIMS1    5'  CCCTCTGCTCGCTCTCTGGC   43729     ___  _    CC  A
                                CCC   GC CGCTC  CT GC
                                |||   || |||||  || ||
                                GGG   CG GCGAG  GA CG
                                  AGA  A    A_  C
GAM1417  RNF12    5'  CCGCCGCTCTCAAGCCC     32035        CCCT
                                CCGCCGCTC    AGCCC
                                |||||||||    |||||
                                GGCGGCGAG    TCGGG
                                     AGT_
GAM1417  ROCK2    5'  CCCACCGCCTGCCTCTAGC   42352        C_  _
                                CCCGCCGCT  CC CTAGC
                                |||||||||  || |||||
                                GGGTGGCGG  GG GATCG
                                     AC  A
GAM1417  RRAS2    5'  CCGCCGCTGCCGCCC       29306        C  CTA
                                CCGCCGCT CC   GCCC
                                |||||||| ||   ||||
                                GGCGGCGA GG   CGGG
                                    C  ___
GAM1417  SFRP1    3'  CCCCCCGCTCCCACCC      16569     G      CTA
                                CCC CCGCTCCC   GCCC
                                ||| ||||||||   ||||
                                GGG GGCGAGGG   TGGG
                                  G       ____
GAM1417  SLC12A4  5'  CCCGCCGCACCCGCCGTCC   22890        T  _  AG
                                CCCGCCGC CCC CT  CC
                                |||||||| ||| ||  ||
                                GGGCGGCG GGG GG  GG
                                    T   C  CA
GAM1417  SLC12A4  5'  CCCGCCGTCCCAGCCGCCC   22891        C    CTA_
                                CCCGCCG TCCC    GCCC
                                ||||||| ||||    ||||
                                GGGCGGC AGGG    CGGG
                                   _    TCGG
GAM1417  SLC22A3  5'  CCCGCCGCCCGCCGCCC     35046        C  TA
                                CCCGCCGCTC CC  GCCC
                                |||||||||| ||  ||||
                                GGGCGGCGGG GG  CGGG
                                     C  __
GAM1417  SLC22A7  3'  CCTTCTGCTCTCCCAGCCC   27430    GCC_   C
                                CC    GCTC CCTAGCCC
                                ||    |||| ||||||||
                                GG    CGAG GGGTCGGG
                                 AAGA   A
GAM1417  SLC6A6   3'  CCCACCACTCCCCTAGTCC   16782             _
                                CCCGCCGCTCCCCTAG CC
                                |||||||||||||||| ||
```

```
                                GGGTGGTGAGGGGATC GG
                                          A
GAM1417 SMARCD2  3' CCTCCTCTTCCTAGCCC    16913    G  G  CC
                                CC CC CT  CCTAGCCC
                                || || ||  ||||||||
                                GG GG GA  GGATCGGG
                                 A  A  A_
GAM1417 SMURF1   5' CCTCGCCGCTTCCGCC     45190   _     C  CTA
                                CC CGCCGCT CC   GCC
                                || ||||||| ||   |||
                                GG GCGGCGA GG   CGG
                                 A      A ___
GAM1417 SMURF1   5' CCCGCCGCCGCCGCC      45188         C  CTA
                                CCCGCCGCT CC   GCC
                                |||||||| ||   |||
                                GGGCGGCGG GG   CGG
                                     C ___
GAM1417 SOX11    3' CCCGCCGCGCCCCGCGCCC   17010        T   TA
                                CCCGCCGC CCCC  GCCC
                                |||||||| ||||  ||||
                                GGGCGGCG GGGG  CGGG
                                    C   CG
GAM1417 SOX11    3' CCCCCTGCTCCCCACGCCC   17009    G _     TA
                                CCC CC GCTCCCC  GCCC
                                ||| || |||||||  ||||
                                GGG GG CGAGGGG  CGGG
                                  _ A      TG
GAM1417 SPARC    3' CCCACCACTGAGCCTCTAGTCC 17066        C__ _   _
                                CCCGCCGCT   CC CTAG CC
                                |||||||||   || |||| ||
                                GGGTGGTGA   GG GATC GG
                                     CTC  A   A
GAM1417 SRRM2    5' CCCGCCGCCTCCGCCC      32272        TC  CTA
                                CCCGCCGC  CC   GCCC
                                ||||||||  ||   ||||
                                GGGCGGCG  GG   CGGG
                                    GA ___
GAM1417 T        5' CCCGCCGTCCCCGAAGCCC   17244        C    T_
                                CCCGCCG TCCCC  AGCCC
                                ||||||| |||||  |||||
                                GGGCGGC AGGGG  TCGGG
                                   _    CT
GAM1417 TAZ      3' CCCCCTGCTCCCCTAGCC    6487     G _
                                CCC CC GCTCCCCTAGCC
                                ||| || ||||||||||||
                                GGG GG CGAGGGGATCGG
                                  _ A
GAM1417 TBX1     5' CCGCCGCCTCCGCTGGCCC   25625        TC  _  A
                                CCGCCGC  CC CT GCCC
                                |||||||  || || ||||
```

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                                GGCGGCG  GG GA CGGG
                                    GA  C  C
GAM1417  TCAP     3'  CCCCCCTCCCCTAGCCCG    18947     G  G          III
                                CCC CC CTCCCCTAGCCC   G
                                ||| || ||||||||||||   |
                                GGG GG GAGGGGATCGGG   C
                                  _ _          III
GAM1417  TCF8     3'  CCCAGCTGCCCAGCCC      36236     CC   C   T
                                CCCG  GCT CCC AGCCC
                                ||||  ||| ||| |||||
                                GGGT  CGA GGG TCGGG
                                  __  C  _
GAM1417  TMEPAI   3'  CCCGCCGCTCCTGGCC      33595          CCTA
                                CCCGCCGCTCC    GCC
                                ||||||||||    |||
                                GGGCGGCGAGG    CGG
                                      AC__
GAM1417  TNFRSF8  3'  CCTGCTGCCCTCCTAGCCC    10317    C  C    C
                                CC GC GCTC CCTAGCCC
                                || || |||| ||||||||
                                GG CG CGGG GGATCGGG
                                 A  A    A
GAM1417  TULP3    5'  CCCGCCACCGAGGAAGCCC    17735         CCCCT
                                CCCGCCGCT    AGCCC
                                |||||||||    |||||
                                GGGCGGTGG    TCGGG
                                     CTCCT
GAM1417  UBE3A    5'  CCCGCCGCCTCCGCCC      7859         TC  CTA
                                CCCGCCGC  CC   GCCC
                                ||||||||  ||   ||||
                                GGGCGGCG  GG   CGGG
                                    GA  ___
GAM1417  WIF1     3'  CCCGCCGCTCCTCGGCC     41164          CCTA
                                CCCGCCGCTCC    GCC
                                ||||||||||    |||
                                GGGCGGCGAGG    CGG
                                      AGC_
GAM1417  ZNF219   5'  CCCGCCCCCGGCCCTGGCCC   32316       G  C_   A
                                CCCGCC CT  CCCT GCCC
                                |||||| ||  |||| ||||
                                GGGCGG GG  GGGA CGGG
                                   G  CC   C
GAM1417  ZNF219   3'  CCGCGCCTTCCACCTCTGGTCC 32321    _   GC   _  AG___
                                CC CGCC  TCC CCT    CC
                                || ||||  ||| |||    ||
                                GG GCGG  AGG GGA    GG
                                 C   A_   T  GACCA
GAM1418  HTRA3    3'  CATGGCCGCCTTGGGGAG    44824          CA__
                                CATGGCCGCTT    GAG
                                ||||||||||    |||
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                                GTACCGGCGGA  CTC
                                     ACCC
GAM1418 HYAL1   3' GCTGCAGTTCAAAGA     37643   C  TTCAG
                                GC GC    AGTTCAAAGA
                                || ||    ||||||||||
                                CG CG    TCAAGTTTCT
                                 A _____
GAM1418 MMP14   3' CCTGAGGTCAGAGTTCAGAG  22636   GCT__       A
                                CC    TCAGAGTTCA AG
                                ||    |||||||||| ||
                                GG    AGTCTCAAGT TC
                                 ACTCC        C
GAM1418 MMP25   5' GGCCGCCGGCGGGGTTCGAAG 35388       TCAGA_   A
                                GGCCGCT    GTTC AAG
                                |||||||    |||| |||
                                CCGGCGG    CAAG TTC
                                    CCGCCC   C
GAM1418 SERPINB3 3' GGTTGCTAAATTCAAAG    27946   CC   TCA
                                GG  GCT   GAGTTCAAAG
                                ||  |||   ||||||||||
                                CC  CGA   TTTAAGTTTC
                                 AA  ___
GAM1418 TP53    3' GCAAGCAAGGGTTCAAAGA   8096    C_  TTC  A
                                GC  GC   AG GTTCAAAGA
                                ||  ||   || |||||||||
                                CG  CG   TC CAAGTTTCT
                                 TT  T__  C
GAM1419 BCL6    5' CAGGGGAGGACTTGGTGT    39905       A   C_
                                CGGGGGAG ACT  GTGT
                                |||||||| |||  ||||
                                GTCCCCTC TGA  CACA
                                     C   AC
GAM1419 HLA-C   3' CGGGGAGGGAACACAGGT    45133     _ A   T  T
                                CGGGG G GAAC CG GT
                                ||||| | |||| || ||
                                GCCCC C CTTG GT CA
                                   T C   T  C
GAM1419 P4HB    3' CGGGGGTGAACGGACGGTGT  9546       A   TC___
                                CGGGGG GAAC    GTGT
                                |||||| ||||    ||||
                                GCCCCC CTTG    CACA
                                   A   CCTGC
GAM1419 PTP4A2  3' CGGGGGAAAAGGGAGATGT   38628        CTC__
                                CGGGGGAGAA    GTGT
                                ||||||||||    ||||
                                GCCCCCTTTT    TACA
                                      CCCTC
GAM1419 SF3B2   3' CGGGAGAGGTGGTTCTTGTGT 27764        AA____  C
                                CGGGGGAG     CT GTGT
                                ||||||||     || ||||
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                                GCCCTCTC     GA CACA
                                     CACCAA  A
GAM1419  TAF7     5'  CGGGAGAGAGCCGAGCGT    24862         A  C_
                                CGGGGGAGA CT  GTGT
                                ||||||||| ||  ||||
                                GCCCTCTCT GG  CGCA
                                     C  CT
GAM1419  TMEPAI   3'  CAGGGGAGGACGGGCTGTGT   33592         A  TC___
                                CGGGGGAG AC    GTGT
                                |||||||| ||    ||||
                                GTCCCCTC TG    CACA
                                     C  CCCGA
GAM1419  TRPV1    5'  GGGAGAGCTGGGCTCGTGT    38799         AA___
                                GGGGGAG    CTCGTGT
                                |||||||    |||||||
                                CCCTCTC    GAGCACA
                                     GACCC
GAM1419  ZNF179   3'  CAGGGGAGAAAGGATGTGT    28373         CTC__
                                CGGGGGAGAA    GTGT
                                ||||||||||    ||||
                                GTCCCCTCTT    CACA
                                      TCCTA
GAM1420  ATRN     3'  TCCGTCCCGCACCGCACA    40291          ____
                                TCCGTCCCGT    CACA
                                |||||||||    ||||
                                AGGCAGGGCG    GTGT
                                      TGGC
GAM1420  TGFB3    3'  CCCTCTGTCTGCGTCACA    17459       C  C_
                                CCCTC GTC  CGTCACA
                                ||||| |||  |||||||
                                GGGAG CAG  GCAGTGT
                                   A  AC
GAM1421  DDX3     5'  GACCGTAGGTGTCGCGTG    35817          A
                                GGCCGTAGGTGTC CGTG
                                |||||||||||| ||||
                                CTGGCATCCACAG GCAC
                                       C
GAM1422  CD209L   3'  CAACCAGCAAGTCCCCAG    30682          ATAA
                                CAACCAGCGAG    CCCAG
                                ||||||||||    |||||
                                GTTGGTCGTTC    GGGTC
                                      AG__
GAM1422  IGFBP6   3'  TCCAACCAGCGGTGAGGGGCC  13487          A_  TAAC
                                TCCAACCAGCG  GA    CC
                                |||||||||| ||    ||
                                AGGTTGGTCGC  CT    GG
                                      CA  CCCC
GAM1422  NEURL    3'  CCAACCATGATAACCCAGC    20099        GCGA
                                CCAACCA    GATAACCCAGC
                                |||||||    ||||||||||
```

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                                GGTTGGT   CTATTGGGTCG
                                   A___
GAM1422 OSCAR   3' CAACCCAGGAAGTCCAGC   39306      _ C  ATAAC
                                CAACC AG GAG    CCAGC
                                ||||| || |||    |||||
                                GTTGG TC TTC    GGTCG
                                   G  C  A____
GAM1422 PFKFB4  3' CCAGACACTTTCTGACCCAGCC 21288     _ AGATA__
                                CCAG CG      ACCCAGCC
                                |||| ||      ||||||||
                                GGTC GT      TGGGTCGG
                                  T  GAAAGAC
GAM1422 TGFB3   3' TCCAGTCTGGCCCTGACCCAGC 17461     ACCA_ GAGATA
            C                    TCCA    GC    ACCCAGCC
                                ||||    ||    ||||||||
                                AGGT    CG    TGGGTCGG
                                  CAGAC  GGAC__
GAM1422 UQCRB   3' TCCAACCAGTGAGGAAAAC   26657        C  AT_
                                TCCAACCAG GAG   AAC
                                ||||||||| |||   |||
                                AGGTTGGTC CTC   TTG
                                     A   CTT
GAM1422 ZNF76   3' CCAGCATGGTGTGGGACCCAGC 18304      AGATA____
            C                    CCAGCG       ACCCAGCC
                                ||||||       ||||||||
                                GGTCGT       TGGGTCGG
                                   ACCACACCC
GAM1423 ARHGEF6 3' TCCTGTGGATGGTGTAATTTCT 42804    CAATA     _____
            G                    TCC    GATGGTG    TCTG
                                |||    |||||||    ||||
                                AGG    CTACCAC    AGAC
                                  ACAC_      ATTAA
GAM1423 BCL2L10 3' CAGATAAAAACGTCTGGG    33789       ___
                                TAGATGG   TGTCTGGG
                                |||||||   ||||||||
                                GTCTATT   GCAGACCC
                                     TTT
GAM1423 CLASP1  3' TCCCAGTGAGGTGGTGG     42248      ATA  T   TC
                                TCCCA   GA GGTG  TGG
                                |||||   || ||||  |||
                                AGGGT   CT CCAC  ACC
                                   CA_  _   C_
GAM1423 LTK     3' CCCCATGGACACCTGGG     14265      ATAGA  _ GT
                                TCCCA    TGG T  CTGGG
                                |||||    ||| |  |||||
                                GGGGT    ACC G  GACCC
                                   _____  T TG
GAM1423 PDE1B   3' TCCTGATGGATGGTGCTGA   9567     CA  A     T
                                TCC  AT GATGGTG CTGG
                                |||  || ||||||| ||||
```

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                                AGG  TA CTACCAC GACT
                                  AC  C      _
GAM1423  PSCD4    3'  TCCCATCTGTCTGGGA      30131       ATAGATGG
                                TCCCA       TGTCTGGGA
                                |||||       |||||||||
                                AGGGT       ACAGACCCT
                                  AG_______
GAM1423  RANBP3   3'  CAGGGGTGGCCTCCTGGGACG  28753     A__    G_
                                TAG   TGGT  TCTGGGACG
                                |||   ||||  |||||||||
                                GTC   ACCG  GGACCCTGC
                                  CCC    GA
GAM1423  SPOCK    3'  TAAATGGTCAATTTGGGA     41739         __  C
                                TAGATGGT  GT TGGGA
                                ||||||||  || |||||
                                ATTTACCA  TA ACCCT
                                     GT  A
GAM1423  UGDH     3'  TCCTGAAGGATGAGACCTGGGA 17886     CAATA     TG
                                TCC    GATGG  TCTGGGA
                                |||    |||||  |||||||
                                AGG    CTACT  GGACCCT
                                  ACTTC    CT
GAM1424  APBA2    3'  CCCCAAACTTTCATTACAAGTC 24278         C     AG  G
                                CCCCAAGC TTCAT  AC AAGTC
                                |||||||| |||||  || |||||
                                GGGGTTTG AAGTA  TG TTCAG
                                     A    A_ _
GAM1424  BRCA1    5'  CCCCACAGCCTGGTGCGGGGTC 28624       _     TCATAGA  AA
                                CCCCA AGCCT      CG  GTC
                                ||||| |||||      ||  |||
                                GGGGT TCGGA      GC  CAG
                                   G    CCAC___  CC
GAM1424  CCNT2    3'  CAAGCCTTCAGAAAGT      38491           TAGAC
                                CAAGCCTTCA    GAAGT
                                ||||||||||    |||||
                                GTTCGGAAGT    TTTCA
                                      C_____
GAM1424  FGF7     3'  CCTCAAGCCTTCATGACA    12858    _        A
                                CC CAAGCCTTCAT GACG
                                || ||||||||||| ||||
                                GG GTTCGGAAGTA CTGT
                                  A         _
GAM1424  GNGT2    5'  CCCCACAGTTTCACCTTACGAA 36482      AGCC    AG_
              GT                  CCCCA   TTCAT   ACGAAGT
                                |||||   |||||   |||||||
                                GGGGT   AAGTG   TGCTTCA
                                   GTCA    GAA
GAM1424  HAS3     3'  CCAGCCTTCATGGGTTGGGTC  39769     A       AGACGAA
                                CCA GCCTTCAT      GTC
                                ||| ||||||||      |||
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                                GGT CGGAAGTA      CAG
                                  _       CCCAACC
GAM1424  MDFI     3'  CAAGCCTTGTGTGACAGTC   24610        CATA   GA
                                CAAGCCTT    GAC  AGTC
                                ||||||||    |||  ||||
                                GTTCGGAA    CTG  TCAG
                                    CACA   __
GAM1424  MUSK     5'  CCAGGCTCACGCAGGACGAAGT 24629     A  CT    A___
                                CCA GC  TCAT    GACGAAGT
                                ||| ||  ||||    ||||||||
                                GGT CG  AGTG    CTGCTTCA
                                  C __    CGTC
GAM1424  SOX5     3'  CCAAGCCTTTTGAGGCTGAGGT 27990         CAT  AC_  A
              C                  CCAAGCCTT   AG   GA GTC
                                ||||||||||   ||   || |||
                                GGTTCGGAA   TC   CT CAG
                                     AAC  CGA  C
GAM1424  TGFA     3'  CCCCAAGCAGACGGAG      17442        CTTCAT     A
                                CCCCAAGC     AGACG AG
                                ||||||||     ||||| ||
                                GGGGTTCG     TCTGC TC
                                    _______     C
GAM1424  TRIM8    3'  CCCCAAGCTTTCAGGGAAGCC  36281        C    TAGAC
                                CCCCAAGC TTCA     GAAGTC
                                |||||||| ||||    ||||||
                                GGGGTTCG AAGT     CTTCGG
                                    A    CC___
GAM1425  ADORA1   3'  CCCAACACAGGGGCTCCAGGC  8590          AGACCC  T
                                TCCAACACAG     CC GGT
                                ||||||||||     || |||
                                GGGTTGTGTC     GG CCG
                                     CCCGA_  T
GAM1425  BECN1    3'  TCTAACACAGAGCAGAGTC   19070    C       ACCCCCT
                                TC AACACAGAG      GGTC
                                || |||||||||      ||||
                                AG TTGTGTCTC      TCAG
                                  A        GTC_____
GAM1425  PPT2     3'  TCCAGCAGCAGCACCTGGTCG  23124     A  _   AGACCC
                                TCCA CA CAG     CCTGGTCG
                                |||| || |||     ||||||||
                                AGGT GT GTC     GGACCAGC
                                  C  C   GT_____
GAM1425  RBBP2    5'  CAACACAGAAACCCCAGAATCG 22801            CT
                                CAACACAGAGACCCC  GGTCG
                                ||||||||||||||  |||||
                                GTTGTGTCTTTGGGG  TTAGC
                                          TC
GAM1425  SLC2A6   3'  CCAACACAGAGGCCCAGCCA   32766          A   CCT
                                CCAACACAGAG CCC   GGTCG
                                |||||||||| |||   |||||
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                                GGTTGTGTCTC GGG   TCGGT
                                      C  ___
GAM1426 ADAMTS13 3' CAGCATCTTCCTGGAGGGGTCC 40028     G      CTAA_  C
            CCA                   CAG ATCTTCCT    GG CCCCA
                                  ||| ||||||||    || |||||
                                  GTC TAGAAGGA    CC GGGGT
                                    G       CCTCC  A
GAM1426 APXL    3' AGAATCTTTGGGTCCCC     11615        CCTCTAA  C
                                  AGGATCTT      GG CCCC
                                  ||||||||      || ||||
                                  TCTTAGAA      CC GGGG
                                       AC_____  A
GAM1426 ATP5B   3' CAGGATCTTTTGCACCCC    40647        CCTCTAAG  _
                                  CAGGATCTT       GC CCCC
                                  |||||||||       || ||||
                                  GTCCTAGAA       CG GGGG
                                       AA______  T
GAM1426 CIAS1   3' GGTGTCTTCCTCACCC     22208    A_      TAAG
                                  GG  TCTTCCTC    GCCC
                                  ||  ||||||||    ||||
                                  CC  AGAAGGAG    TGGG
                                   AC       _____
GAM1426 COPEB   3' CAGGACCTTTTTAGCCCC    44430        CCTCTAA    C
                                  CAGGATCTT      GGCCC C
                                  |||||||||      ||||| |
                                  GTCCTGGAA      TCGGG G
                                       AAA____    A
GAM1426 DRPLA   5' CAGGATCTCCAAGTTTCC    12585       TTCC     GCCC
                                  CAGGATC    TCTAAG   CC
                                  |||||||    ||||||   ||
                                  GTCCTAG    AGGTTC   GG
                                       ____     AAA_
GAM1426 DUSP4   5' CAGAATCTCCAGGGCTCT    38408         ____
                                  CAGGATCTTC    CTCT
                                  ||||||||||    ||||
                                  GTCTTAGAGG    GAGA
                                        TCCC
GAM1426 EFNA4   3' CAGGTCTTCAGCCTGGGGCCCC 23390     A    C_   AA
            CA                    CAGG TCTTC  TCT  GGCCCCCA
                                  |||| |||||  |||  ||||||||
                                  GTCC AGAAG  GGA  CCGGGGGT
                                    _    TC   CC
GAM1426 EGFL5   5' GGACTTTTCTACCCC      44530     T   CC   AAG
                                  GGA CTT  TCT   GCCCC
                                  ||| |||  |||   |||||
                                  CCT GAA  AGA   TGGGG
                                    _  A_  ___
GAM1426 EPHA8   3' AGGATCCTCTGGTCCC      33889      TCT     AA  _
                                  AGGA   TCCTCT  GG CCC
                                  ||||   ||||||  || |||
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                                TCCT   AGGAGA  CC GGG
                                  ___     __ A
GAM1426  FGF23    3'  GGATCTTTCACTGAGGAGCCTC 33956        _ _  CTAA    C
              CA                    GGATCTT C CT    GGCC CCA
                                    ||||||| | ||    |||| |||
                                    CCTAGAA G GA    TCGG GGT
                                       A T  CTCC    A
GAM1426  FLRT2    5'  CAGGATCTTGCTCTGTTGC    29841         C    AAG
                                    CAGGATCTT CTCT   GC
                                    ||||||||| ||||   ||
                                    GTCCTAGAA GAGA   CG
                                          C    CAA
GAM1426  GALR1    5'  GGCGGTTTTCCCTGGCTCCC   11204    ATC__    T  AA   C
                                    GG     TTCC CT  GGC CCC
                                    ||     |||| ||  ||| |||
                                    CC     AAGG GA  CCG GGG
                                     GCCAA   _ __   A
GAM1426  GSTM4    5'  GACCTCCTCTGGGGTTCCC    9202       T    AA  CC
                                    GATCT CCTCT  GG  CCC
                                    ||||| |||||  ||  |||
                                    CTGGA GGAGA  CC  GGG
                                       _    CC  AA
GAM1426  HCR      3'  CAGGATCCTCCCAGCCCCC    44952          CTAA
                                    CAGGATCTTCCT    GGCCCCC
                                    ||||||||||||    |||||||
                                    GTCCTAGGAGGG    TCGGGGG
                                                 ____
GAM1426  HMOX2    3'  AGGCCTCTGAGGCTTCC     42171     ATCTT    A    CC
                                    AGG     CCTCT AGGC  CC
                                    |||     ||||| ||||  ||
                                    TCC     GGAGA TCCG  GG
                                      ______    C    AA
GAM1426  HPS1     3'  GGGGCTTCCTCCCCATCTCCCA 6804     AT       AAGGCC
                                    GG  CTTCCTCT     CCCA
                                    ||  ||||||||     ||||
                                    CC  GAAGGAGG     GGGT
                                     CC       GGTAGA
GAM1426  ICA1     5'  GGGTCTCTCCTCGACCCCCA   22467    A  _    TAA
                                    GG TCT TCCTC   GGCCCCCA
                                    || ||| |||||   ||||||||
                                    CC AGA AGGAG   CTGGGGGT
                                     C   G    ___
GAM1426  IL2RA    3'  CAGGATCTTGCTCTGTTGCCC  7669         C    AAG
                                    CAGGATCTT CTCT   GCCC
                                    ||||||||| ||||   ||||
                                    GTCCTAGAA GAGA   CGGG
                                          C    CAA
GAM1426  LIM2     3'  CAGGATTTCAGGCC        36184        C   CTCTA
                                    CAGGAT TTC     AGGCC
                                    |||||| |||     |||||
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                                GTCCTA AAG    TCCGG
                                  _  _____
GAM1426  MBD1    3'  CAGGATCATCCTTTCAGC    31920       T   CTAA
                                CAGGATC TCCT   GGC
                                ||||||| ||||   |||
                                GTCCTAG AGGA   TCG
                                    T   AAG_
GAM1426  MPP2    3'  AGATCTTCCCCTGCC      40789          AAG
                                GGATCTTCCTCT   GCC
                                ||||||||||||  |||
                                TCTAGAAGGGGA  CGG
                                      ___
GAM1426  MSN     3'  AGGATCTTCTACTCAGCC    41239        CT  AA
                                AGGATCTTC  CT  GGCC
                                |||||||||  ||  ||||
                                TCCTAGAAG  GA  TCGG
                                     AT  G_
GAM1426  NFRKB   5'  CAGGATCCTCCAGAAGGTCC   26092         TCT   _
                                CAGGATCTTCC   AAGG CC
                                ||||||||||   |||| ||
                                GTCCTAGGAGG   TTCC GG
                                      TC_   A
GAM1426  PCOLN3  3'  CAGAGTCTGAAGGCCCCC    15747    GA   TCCTCT
                                CAG  TCT     AAGGCCCCC
                                |||  |||     |||||||||
                                GTC  AGA     TTCCGGGGG
                                  TC   C_____
GAM1426  PTPRH   3'  CAGGATCCTTCCTGCC      15947       _    CTAAG
                                CAGGATC TTCCT    GCC
                                ||||||| |||||    |||
                                GTCCTAG AAGGA    CGG
                                    G   _____
GAM1426  RARG    3'  CAGGGTCTTCCTCTTGCCC   9721      A       AAG
                                CAGG TCTTCCTCT   GCCC
                                |||| |||||||||   ||||
                                GTCC AGAAGGAGA   CGGG
                                  C       A__
GAM1426  RENT1   3'  AGGGTCTTCCTCCCTCC     16247     A       AAGG
                                AGG TCTTCCTCT   CC
                                ||| |||||||||   ||
                                TCC AGAAGGAGG   GG
                                  C       GA__
GAM1426  RGS16   3'  AGGATCCTTTTCTGCC      16318        CC   AAG
                                AGGATCTT  TCT   GCC
                                ||||||||  |||   |||
                                TCCTAGGA  AGA   CGG
                                    AA  ___
GAM1426  RNASE1  5'  AGGTCTTCCTCCCC        16340     A      CTAAGGC
                                AGG TCTTCCT     CCCC
                                ||| |||||||     ||||
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                                TCC AGAAGGA      GGGG
                                  _     _______
GAM1426 SLC21A9  3' AGGATTCCTGGGGCCCCCA   28558      CT   CTAA
                                AGGAT  TCCT   GGCCCCCA
                                |||||  ||||   ||||||||
                                TCCTA  AGGA   CCGGGGGT
                                  ___   CC__
GAM1426 SRGAP1   3' GGTGTCTTCCTCTCCTTTCCC  43601    A_       AAGG_
                                GG  TCTTCCTCT    CCC
                                ||  |||||||||    |||
                                CC  AGAAGGAGA    GGG
                                 AC       GGAAA
GAM1427 BACE     3'  AGAGCTAAAAAAGAGCTCTTT  39946        TTTGT  A
                                AGAGCTAAA    GA CTCTTT
                                |||||||||    || ||||||
                                TCTCGATTT    CT GAGAAA
                                     TTT__  C
GAM1427 CDH19    3'  TAGAGCCAGGGCACAAAACTCT 34501        AATTTGT
                TT                  TAGAGCTA      GAACTCTTT
                                |||||||||      |||||||||
                                ATCTCGGT      TTTGAGAAA
                                    CCCGTGT
GAM1427 COL19A1  3'  TAGAGTGGGTGTGAACTCTTT  12380      CTAAATT
                                TAGAG      TGTGAACTCTTT
                                |||||      ||||||||||||
                                ATCTC      ACACTTGAGAAA
                                  ACCC___
GAM1427 TSG      3'  GAGCTAAATCTCAACT      34005          GTG
                                GAGCTAAATTT   AACT
                                ||||||||||   ||||
                                CTCGATTTAGA   TTGA
                                     G__
GAM1428 APBA1    3'  TGGTTGATAACTTGAG      43091     A      AAA
                                TGG TTGATAAC   GAG
                                |||  ||||||||   |||
                                ACC AACTATTG   CTC
                                  _       AA_
GAM1428 DBY      3'  TGAATTGATGACTCCTGTTAAA 21664         A  AAAGA
                G                   TGGATTGAT AC     GTTAAAG
                                |||||||||  ||    |||||||
                                ACTTAACTA TG     CAATTTC
                                     C  AGGA_
GAM1428 GCLM     3'  TGGATTGATATGGAGGCAA    13136         ACAAA   T
                                TGGATTGATA     GAG TAA
                                ||||||||||     ||| |||
                                ACCTAACTAT     CTC GTT
                                     AC___   C
GAM1428 RAD50    3'  GGATTGATGGTGAAGCCA     39438         AACAAA
                                GGATTGAT      GAGTTA
                                ||||||||      ||||||
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                                CCTAACTA     TTCGGT
                                    CCAC__
GAM1428 RAD52    3' TGGATTGATACAAAGTAG    39567         A    _
                                TGGATTGATA CAAAG AG
                                |||||||||| ||||| ||
                                ACCTAACTAT GTTTC TC
                                      _    A
GAM1428 RPL10    3' TGGATTGGTAAGAATCA     25674       ATAACA
                                TGGATTG     AAGAGTTA
                                |||||||     ||||||||
                                ACCTAAC     TTCTTAGT
                                    CA____
GAM1428 SERPINH2 3' TGGATTGATAGCAACAAAG   10300         ___
                                TGGATTGATA   ACAAAG
                                ||||||||||   ||||||
                                ACCTAACTAT   TGTTTC
                                      CGT
GAM1429 LASS1    3' TGGCCGCAGGGACCTTGCTG   34620      TATTA
                                TGGTT    GACCTTGCTG
                                |||||    ||||||||||
                                ACCGG    CTGGAACGAC
                                   CGTCC
GAM1429 LDHB     5' ATGGTGTATGGGGGCCTTGCTG 14116      T   TAGA_
                                ATGGT TAT    CCTTGCTG
                                ||||| |||    ||||||||
                                TACCA ATA    GGAACGAC
                                   C   CCCCC
GAM1429 SHANK2   3' GGCTGGCAGGGCCTTGCTG   29463     TAT   A_
                                GGTT   TAG  CCTTGCTG
                                ||||   |||  ||||||||
                                CCGA   GTC  GGAACGAC
                                  CC_   CC
GAM1430 GLUD1    3' GTGGTTACATGTAAACT     23590        C   AC
                                GTGGTTAC GTG  AAGCT
                                |||||||| |||  |||||
                                CACCAATG TAC  TTTGA
                                     _   A_
GAM1430 HDAC4    3' CCCGTGGCTGTTGCACGCT   25751         ACCG  A  A
                                CCCGTGGTT    TG CA GCT
                                |||||||||    || || |||
                                GGGCACCGA    AC GT CGA
                                     CA__  _  G
GAM1430 SVIL     5' CGTGGTTAGCGAGC       34727        CC    CAA
                                CGTGGTTA  GTGA   GC
                                ||||||||  ||||   ||
                                GCACCAAT  CGCT   CG
                                     __   ____
GAM1431 ANKH     3' AAGGCCTCTTTCATTAC     33375      AG   A
                                AAGG  CTC TTTCATTAC
                                ||||  ||| |||||||||
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                                TTCC  GAG AAAGTAATG
                                  G_  _
GAM1431  EGFL6    3'  AGAAGCTCATCAACTTAC    31774          TCA
                                AGGAGCTCATT   TTAC
                                ||||||||||   ||||
                                TCTTCGAGTAG   AATG
                                      TTG
GAM1431  FTSJ2    3'  AAGGAGCTAATGACCATTA   30163        CATT_
                                AAGGAGCT    TCATTA
                                ||||||||    ||||||
                                TTCCTCGA    GGTAAT
                                    TTACT
GAM1431  KRTHA5   5'  AGGAGCCCCATTAC       14019        ATTT
                                AGGAGCTC    CATTAC
                                ||||||||    ||||||
                                TCCTCGGG    GTAATG

                                ____
GAM1431  SMARCC2  3'  AAGGAGCTTTCCTTAC     40070        CA   A
                                AAGGAGCT  TTTC TTAC
                                ||||||||  |||| ||||
                                TTCCTCGA  AAGG AATG

                                __   _
GAM1432  JAM3     3'  CCGATGAAGTAAGGCTGCT   37262        ____   C
                                TCGATGA    AGGC GCT
                                |||||||    |||| |||
                                GGCTACT    TCCG CGA
                                    TCAT    A
GAM1432  OA1      3'  GAGCAAGGTTTGGGGGCCGCTA 7082       ACTCGA  AA
                                GAGCAA     TG  GGCCGCTA
                                ||||||     ||  ||||||||
                                CTCGTT     AC  CCGGCGAT
                                   CCAA__  CC
GAM1432  PDGFB    3'  GGGCAAGACCGGAGGCCGCT   15190   A   AC   ATGA
                                G GCAA  TCG    AGGCCGCT
                                | ||||  |||    ||||||||
                                C CGTT  GGC    TCCGGCGA
                                 C    CT   C___
GAM1432  SNCB     5'  GGCAGACGCGGGGGCCGCTA   16930   A   A  T  ATGAA
                                G GCA AC CG     GGCCGCTA
                                | ||| || ||     ||||||||
                                C CGT TG GC     CCGGCGAT
                                _   C  C  CC___
GAM1432  TF       3'  GCAAACTCATGGATCATCT    9865         G   AA GC  _
                                GCAAACTC ATG  G  CG CT
                                |||||||| |||  |  || ||
                                CGTTTGAG TAC  C  GT GA
                                     _   __ TA  A
GAM1432  VIPR2    3'  GAGCAGCCGCTAGGGCTGCT   18014      AAC   ATGAA   C
                                GAGCA   TCG    GGC GCT
                                |||||   |||    ||| |||
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                                CTCGT  GGC   CCG CGA
                                  C__  GATC_  A
GAM1433 ADD1    3' GACAGATCGGGGAGAGTTGGC 30519       ____ CAT
                                GACAGATC   AG  TTGGC
                                ||||||||   ||  |||||
                                CTGTCTAG   TC  AACCG
                                    CCCC  TC_
GAM1433 CDC7L1  3' AGACAGATCAATGGTAATGG  18600        CATT__
                                AGACAGATCAG    TGG
                                ||||||||||    |||
                                TCTGTCTAGTT    ACC
                                      ACCATT
GAM1433 COL10A1 5' AGATGGTGCCTTGGCAGC   7961     CA_ A
                                AGAT  GC TTTGGCAGC
                                ||||  || |||||||||
                                TCTA  CG GAACCGTCG
                                  CCA  _
GAM1433 CYP1A1  3' CAGATCAGTGTCTATGAG   7972       CA   GC
                                CAGATCAG  TTTG  AG
                                ||||||||  ||||  ||
                                GTCTAGTC  AGAT  TC
                                    AC   AC
GAM1433 DTNB    3' GAGTGACGTCTGGCAGCCT  37603    TCA  A
                                GA  GC TTTGGCAGCCT
                                ||  || ||||||||||
                                CT  TG AGACCGTCGGA
                                 CAC  C
GAM1433 GRIN2A  3' AGACAGATGGCATTGTAC   9102       CA    TG
                                AGACAGAT  GCATT  GC
                                ||||||||  |||||  ||
                                TCTGTCTA  CGTAA  TG
                                    C_    CA
GAM1433 ICA1    3' AGGCAGTCAGGTCTGAGGCAGC 22462    A  A   CATTT_
            CT                   AG CAG TCAG     GGCAGCCT
                                || ||| ||||     ||||||||
                                TC GTC AGTC     CCGTCGGA
                                 C  _   CAGACT
GAM1433 KIAA0857 3' AGAGGGGTCAGGGAGCAGCCT 42464    CAGA   CATTT
                                AGA   TCAG    GGCAGCCT
                                |||   ||||    ||||||||
                                TCT   AGTC    TCGTCGGA
                                  CCCC   CC___
GAM1433 LAG3    5' CAGATCAGGCAGCC       14043       GCATTT
                                CAGATCA     GGCAGCC
                                |||||||     |||||||
                                GTCTAGT     CCGTCGG
                                      ______
GAM1433 SLN     3' AGACAGATCAGGGGC      16875          CATTT
                                AGACAGATCAG    GGC
                                ||||||||||    |||
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                                TCTGTCTAGTC    CCG
                                      C____
GAM1433  TAL1    3'  GATGGATCAACATAGGC    17286    CA       TT
                                GA  GATCAGCAT  GGC
                                ||  |||||||||  |||
                                CT  CTAGTTGTA  CCG
                                 AC       T_
GAM1433  TOX     3'  CAGGTAAGCATTTGGCAG    31269    ATC
                                CAG   AGCATTTGGCAG
                                |||   ||||||||||||
                                GTC   TCGTAAACCGTC
                                  CAT
GAM1433  ZNF146  5'  AGATGGATCAACATGC     28347    CA       TTGGCA
                                AGA  GATCAGCAT     GC
                                |||  |||||||||     ||
                                TCT  CTAGTTGTA     CG
                                 AC       _______
GAM1434  CENTD1  3'  CTTTACAAGGTTTGTTCA    40141         A  A
                                CTTTACAAG TT GTTCA
                                ||||||||| || |||||
                                GAAATGTTC AA CAAGT
                                     C  A
GAM1434  GALNT7  3'  TTTACATGCACAGTTCATTGCC 38366       AGAT      CA
           A                     TTTACA   TAGTTCAT  CCA
                                ||||||   ||||||||  |||
                                AAATGT   GTCAAGTA  GGT
                                   ACGT      AC
GAM1434  HHLA1   5'  TTCACAAGGTAATGTCATCA   25054        AT   _
                                TTTACAAG  TAGT TCATCA
                                ||||||||  |||| ||||||
                                AAGTGTTC  ATTA AGTAGT
                                     C_   C
GAM1434  HMGCR   3'  CTCTACAAGAGACATCATCA   9236          TTAGT
                                CTTTACAAGA    TCATCA
                                ||||||||||    ||||||
                                GAGATGTTCT    AGTAGT
                                      CTGT_
GAM1434  HSPA4   3'  TTTACAAAGATTCAAAACATTA 44858        _   AGTT_  C
           CCA                    TTTACAA GATT    CAT ACCA
                                ||||||| ||||    ||| ||||
                                AAATGTT CTAA    GTA TGGT
                                    T   GTTTT   A
GAM1434  IL13RA1 3'  AAGATTAACTCCACCA     11436       GT  AT
                                AAGATTA  TC  CACCA
                                |||||||  ||  |||||
                                TTCTAAT  AG  GTGGT
                                    TG  __
GAM1434  KAL1    3'  TTTACAAGATTACTTCTC    6879           G   A
                                TTTACAAGATTA TTC TC
                                |||||||||||| ||| ||
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                                AAATGTTCTAAT AAG AG
                                      G  _
GAM1434  PIK3R2   5'  CCTTACAAGGGCCACTCGTCAC 22743        ATTA   A
                                CTTTACAAG   GTTC TCAC
                                |||||||||   |||| ||||
                                GGAATGTTC   TGAG AGTG
                                     CCGG   C
GAM1434  SYNGR1   3'  CTTTGAAGATCAAGAATCACCA 21757     AC      TTC
                                CTTT  AAGATTAG  ATCACCA
                                ||||  ||||||||  |||||||
                                GAAA  TTCTAGTT  TAGTGGT
                                  C_      CT_
GAM1434  ZFY      3'  CTTTACAAGCTTGTAGACACAC 18219        AT__   TT  T
                                CTTTACAAG   TAG  CA CAC
                                |||||||||   |||  || |||
                                GAAATGTTC   ATC  GT GTG
                                     GAAC   T_  _
GAM1435  BACH2    3'  AGAGGTGCACTTGCATCAGAC  34771     A  TT   GTA_
                                AGA GT  GTA   CATCAGAC
                                ||| ||  |||   ||||||||
                                TCT CA  CGT   GTAGTCTG
                                  C  __  GAAC
GAM1435  CASP7    3'  GAAGTGTGGGTCATCAGAC   10275      T  TA  A
                                GAAGT TG  GT CATCAGAC
                                ||||| ||  || ||||||||
                                CTTCA AC  CA GTAGTCTG
                                   C  C_  _
GAM1435  RAB38    3'  AGAAGTTTGTAACAGAC     41262          TACAT
                                AGAAGTTTGTAG    CAGAC
                                ||||||||||||    |||||
                                TCTTCAAACATT    GTCTG
                                          _____
GAM1435  SEMG1    3'  GAAGTTTGAAGGCGCTTCAG   16556        TA_  ACA
                                GAAGTTTG   GT   TCAG
                                ||||||||   ||   ||||
                                CTTCAAAC   CG   AGTC
                                     TTC  CGA
GAM1435  TPMT     3'  AGAAGTTTGTACATGCAGGCCA 7491          AGT   _  A
                                AGAAGTTTGT   ACAT CAG CCA
                                ||||||||||   |||| ||| |||
                                TCTTCAAACA   TGTA GTC GGT
                                     ___   C   C
GAM1436  ALPI     3'  TTGGTCAGGTGCAGGGG     11584      C  ACCA
                                TTGG CA    TGCAGGGG
                                |||| ||    ||||||||
                                AACC GT    ACGTCCCC
                                  A  CC__
GAM1436  ATP8A2   3'  TGGCCAGCCATGCAGCAG    45270       A      G
                                TGGCCA CCATGCAG GG
                                |||||| |||||||| ||
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                                ACCGGT GGTACGTC TC
                                   C       G
GAM1436  CDK2     5'  TTGGCCAACTTGAAACAATGT  12207          CA  CA   G
                                TTGGCCAAC  TG  GGG AATGT
                                |||||||||  ||  ||| |||||
                                AACCGGTTG  AC  TTT TTACA
                                     A_  __   G
GAM1436  ENAM     3'  CTGGCCAGGGGGAGGGGAATGT 36675         ACCATGC
                                TTGGCCA      AGGGGAATGT
                                |||||||      ||||||||||
                                GACCGGT      TCCCCTTACA
                                    CCCCC__
GAM1436  G6PD     3'  TTGGCAGCTGAGGAAT      7615        CAACCAT  A
                                TTGGC      GC GGGGAAT
                                |||||      || |||||||
                                AACCG      CG CTCCTTA
                                   T_______  A
GAM1436  WT1      3'  CTGGCTGACCTCGGGAATG   35959       CA   ATGCAG
                                TTGGC  ACC     GGGAATG
                                |||||  |||     |||||||
                                GACCG  TGG     CCCTTAC
                                   AC   AG____
GAM1437  BAZ1B    5'  GGACTGGCGGCTGCTGG     37089         ACA    CAC
                                GGACTGGC   TGCT   GG
                                ||||||||   ||||   ||
                                CCTGACCG   ACGA   CC
                                     CCG    ___
GAM1437  C21orf2  3'  ACAGGACTGGTGTAGACAG   22297          CACA  CTC
                                ACAGGACTGG   TG   ACGG
                                ||||||||||   ||   ||||
                                TGTCCTGACC   AC   TGTC
                                      _____ ATC
GAM1437  CARD15   5'  ACAGGACTGGTGAGCCTGG   35258          CACAT   CAC
                                ACAGGACTGG    GCT   GG
                                ||||||||||    |||   ||
                                TGTCCTGACC    CGG   CC
                                      ACT__   A__
GAM1437  DMPK     3'  ACAGGACTGGAGCTGGGCGGA  20605          CACAT   CA_
                                ACAGGACTGG    GCT   CGGA
                                ||||||||||    |||   ||||
                                TGTCCTGACC    CGA   GCCT
                                      T____   CCC
GAM1437  GAB2     3'  GAACTATGCATGCTCATGG   38679        GCA      C
                                GGACTG   CATGCTCA GG
                                ||||||   |||||||| ||
                                CTTGAT   GTACGAGT CC
                                   AC_      A
GAM1437  GPR56    3'  ACGGGACTGGCATGGTC     24995    A       CA  C
                                AC GGACTGGCA  TG TC
                                || |||||||||  || ||
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                                TG CCTGACCGT  AC AG
                                 C       __ C
GAM1437 IL5RA    3' ACAAGACTGGTGTGTCTGG   8160         CACA  C  AC
                                ACAGGACTGG   TG TC  GG
                                ||||||||||   || ||  ||
                                TGTTCTGACC   AC AG  CC
                                     AC__  _  A_
GAM1437 KEL      5' ACAGGACTGGCCTCTGGGTGGA 7677          ACA  CTCAC
                                ACAGGACTGGC  TG   GGA
                                ||||||||||  ||   |||
                                TGTCCTGACCG  AC   CCT
                                      GAG  CCA__
GAM1437 MDH2     5' ACAGGAGCTGGTGACGCGG   25410      _   CAC   TCAC
                                ACAGGA CTGG  ATGC   GG
                                ||||||  ||||  ||||   ||
                                TGTCCT GACC  TGCG   CC
                                   C   AC_  ____
GAM1437 PACSIN1  3' GGAGGGCTGGCACAGCCCGG  45154  C  A     T  T A
                                A AGG CTGGCACA GC C CGG
                                | ||| ||||||||| || | |||
                                C TCC GACCGTGT CG G GCC
                                 C  C      _ _ _
GAM1437 PDGFRB   5' CAGGACTGGTGCAGGCTCCTGA 42334        CA  T   ACG
                                CAGGACTGG  CA GCTC   GA
                                |||||||||  || ||||   ||
                                GTCCTGACC  GT CGAG   CT
                                     AC  C   GA_
GAM1437 RASAL1   3' ACAGGACTAGGCACGTCTCTGG 21652        _    ATG   AC
                                ACAGGACT GGCAC   CTC  GG
                                ||||||||| |||||   |||  ||
                                TGTCCTGA CCGTG   GAG  CC
                                    T    CA_  A_
GAM1437 REGL     3' CAGTATTGGCACAGCTTGG   27120    GAC     T   CAC
                                CAG   TGGCACA GCT   GG
                                |||   ||||||| |||   ||
                                GTC   ACCGTGT CGA   CC
                                  ATA      _   A__
GAM1437 SUFU     3' ACAGGACTGGTTACAGAGCTGG 32080         C_  T_  CAC
            A                    ACAGGACTGG  ACA  GCT   GGA
                                ||||||||||  |||  |||   |||
                                TGTCCTGACC  TGT  CGA   CCT
                                     AA   CT   ___
GAM1437 USP7     3' CAGGGCTGGTGCACGG     18448     A   CACA   TC
                                CAGG CTGG   TGC  ACGG
                                ||||  ||||   |||  ||||
                                GTCC GACC    ACG  TGCC
                                  C   _____  __
GAM1437 ZK1      3' GGACTGGACATGGCTCACGGA  25172       C    _
                                GGACTGG ACATG CTCACGGA
                                |||||||  |||||  ||||||||
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                                CCTGACC TGTAC GAGTGCCT
                                    _    C
GAM1438 BSN     3' TGCGGACCCCTGAGAA     18420     AAA   T
                                TGC   ACCC CTGAGAA
                                |||   |||| |||||||
                                ACG   TGGG GACTCTT
                                  CC_   _
GAM1438 CA12    3' GCAAAACCTAAGCAGAGAGTGC 10244        CTCT__   ATA
            ACA                   GCAAAACC     GAGA   CACA
                                |||||||||     ||||   ||||
                                CGTTTTGG     CTCT   GTGT
                                    ATTCGT    CAC
GAM1438 CASP3   3' ACAAAACTAGAATACAC     37413       CCTCTG
                                GCAAAAC     AGAATACAC
                                |||||||     |||||||||
                                TGTTTTG     TCTTATGTG
                                    A_____
GAM1438 CDK2    3' TACAAAACCCCAAGGTGCACA  12205         CT   AATA
                                TGCAAAACCCT  GAG    CACA
                                ||||||||||  |||    ||||
                                ATGTTTTGGGG  TTC    GTGT
                                      __  CAC_
GAM1438 FST     3' CAAAGCCCTCTGATACA     30176      A      GAA
                                CAAA CCCTCTGA   TACA
                                |||| ||||||||   ||||
                                GTTT GGGAGACT   ATGT
                                  C       ___
GAM1438 FZD5    3' GCAAAATAGAATACA      41047       CCCTCTG
                                GCAAAA      AGAATACA
                                ||||||      ||||||||
                                CGTTTT      TCTTATGT
                                   A_______
GAM1438 HTN3    3' ACAAATGAGAATACAC      6811       ACCCTC
                                GCAAA     TGAGAATACAC
                                |||||     ||||||||||
                                TGTTT     ACTCTTATGTG
                                    _______
GAM1438 LARGE   3' CAGGACCCTCTGGTTACA    21857    AA      AGAA
                                CA  ACCCTCTG    TACA
                                ||  ||||||||   ||||
                                GT  TGGGAGAC    ATGT
                                 CC       CA__
GAM1438 MNAT1   3' TGTCAAATCCTCTGAAAA    14603    _   AC
                                TG CAAA  CCTCTGAGAA
                                || ||||  ||||||||||
                                AC GTTT  GGAGACTTTT
                                 A   A_
GAM1438 PACSIN1 3' CAGGACCCTCTGTGCCCACA  45145    AA      AGAA
                                CA  ACCCTCTG    TACA
                                ||  ||||||||   ||||
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                                GT  TGGGAGAC   GTGT
                                 CC      ACGG
GAM1438  TIM3     3'  GCAAAACTTGGCCAATACACA  37250       CCTCTGAG
                                GCAAAAC      AATACACA
                                |||||||      ||||||||
                                CGTTTTG      TTATGTGT
                                   AACCGG__
GAM1438  ZNF236   3'  CAAAACCCTGGTTATACA    28858        CTGAGA
                                CAAAACCCT    ATACA
                                |||||||||    |||||
                                GTTTTGGGA    TATGT
                                     CCAA__
GAM1439  ASB3     3'  TAATGTACTGGTGATGAAGC  32031          TACA
                                TAATGTACTGGTG   AAGT
                                ||||||||||||   ||||
                                ATTACATGACCAC   TTCG
                                       TAC_
GAM1439  C1orf1   3'  TAATGTGTGTAAAGTGCT    10228      ACTG    CA
                                TAATGT   GTGTA  AAGTGCT
                                ||||||   |||||  |||||||
                                ATTACA   CACAT  TTCACGA
                                   ____    __
GAM1439  CYBB     3'  TAATGTTTGTAAAAGTGC    44099      ACTGG   C
                                TAATGT    TGTA AAAGTGC
                                ||||||    |||| |||||||
                                ATTACA    ACAT TTTCACG
                                   A____   _
GAM1440  CACNA2D2 3'  TCGGAGGTGAGATGTGATTTG  25725       A   A __
                                TTGGAGGT AGAT TG  TTG
                                |||||||| |||| ||  |||
                                AGCCTCCA TCTA AC  AAC
                                     C   C  TA
GAM1440  CRABP2   3'  TTGGGGCTAGGACTGCTGACTT 12431     A   A  ATA
                                TTGG GGT AG   TGTTGACTT
                                |||| ||| ||   |||||||||
                                AACC CCG TC   ACGACTGAA
                                  _  A  CTG
GAM1440  ISGF3G   3'  TTGGTGGTAAGATGCCTCTT   25884     A     TA   GA
                                TTGG GGTAAGA  TGTT  CTT
                                |||| |||||||  ||||  |||
                                AACC CCATTCT  ACGG  GAA
                                  A      __   A_
GAM1440  MTCP1    5'  GGAGGTAAGAAGGTGACTT   30582         TAT  T
                                GGAGGTAAGA   GT GACTT
                                ||||||||||   || |||||
                                CCTCCATTCT   CA CTGAA
                                      TC_  _
GAM1440  NCOA4    3'  TTGGAGGTACAGGTATGCTGTG 24137         _  A     A_
            CTT                   TTGGAGGTA AG TATGTTG  CTT
                                |||||||| || |||||||  |||
```

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                                AACCTCCAT TC ATACGAC  GAA
                                      G  C      AC
GAM1440  PSMB9    3'  GGAGGTAAGGTCAGGTGGCTTA 15829         ATATGT  A
                                GGAGGTAAG     TG CTTA
                                |||||||||     || ||||
                                CCTCCATTC     AC GAAT
                                      CAGTCC  C
GAM1441  ARF1     3'  CACATGGCTATGGAAT      43304          GAACC
                                TACATGGCTAT    GGAAT
                                ||||||||||    |||||
                                GTGTACCGATA    CCTTA
                                      _____
GAM1441  HTR4     3'  ACATGGCTGTGACGGA      9297         A   AC
                                ACATGGCT TGA  CGGA
                                |||||||| |||  ||||
                                TGTACCGA ACT  GCCT
                                      C  __
GAM1441  IL15     5'  CACATGGCCATATATTGGAATG 8222           AACC
                                TACATGGCTATG   GGAATG
                                ||||||||||||   ||||||
                                GTGTACCGGTAT   CCTTAC
                                       ATAA
GAM1441  MBL2     3'  TACATGGCAATGAAAAGGA   6963         T    CC
                                TACATGGC ATGAA  GGA
                                |||||||| |||||  |||
                                ATGTACCG TACTT  CCT
                                      T    TT
GAM1441  PIG8     3'  TAATGGCTATAAAGGGA     22189   C        CC
                                A ATGGCTATGAA  GGA
                                | ||||||||||  |||
                                A TACCGATATTT  CCT
                                 T         C_
GAM1441  TAGLN2   3'  TGATGGCTATGGGGAAGGGAAT 18685   C       AACC__
            G                    A ATGGCTATG     GGAATG
                                | |||||||||     ||||||
                                A TACCGATAC     CCTTAC
                                 C        CCCTTC
GAM1442  PCSK1    3'  TGAGTATTTTTCTATTATT   7756          TAG   G
                                TGAGTATTTTT   CTGT TATT
                                ||||||||||   |||| ||||
                                ACTCATAAAAA   GATA ATAA
                                      ___   _
GAM1443  PCSK1    3'  TGAGTATTTTTCTATTATT   7756          TAG   G
                                TGAGTATTTTT   CTGT TATT
                                ||||||||||   |||| ||||
                                ACTCATAAAAA   GATA ATAA
                                      ___   _
GAM1444  CHES1    3'  CCAGTGGCTTTCCTGGCA    23282      A  A   AACC
                                CTAGT GC TTT    CCTGGCA
                                ||||| || |||    |||||||
```

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                                GGTCA CG AAA    GGACCGT
                                  C  _  _____
GAM1444  CRYGS    3'  CTAGAAGCATTTAAGGAGAGGC 32755      T       CCCCT
              A                    CTAG AGCATTTAA     GGCA
                                   |||| |||||||||     ||||
                                   GATC TCGTAAATT     CCGT
                                     T        CCTCT
GAM1444  CXorf6   3'  CAGTGGGCATTCTTGGCA    24236      A_     AACCCC
                                   TAGT  GCATTT     TGGCA
                                   ||||  ||||||     |||||
                                   GTCA  CGTAAG     ACCGT
                                     CC     A_____
GAM1444  DSPG3    5'  CTAGTGGTATTTGCCCCTGAC  41174       AGC    AA
                                   CTAGT   ATTT  CCCCTGGC
                                   |||||   ||||  ||||||||
                                   GATCA   TAAA  GGGGACTG
                                      CCA    C_
GAM1444  EDAR     3'  CAGTGAACTCTAACCCCTGG   35301      _   A
                                   TAGT AGC TTTAACCCCTGG
                                   |||| ||| ||||||||||||
                                   GTCA TTG AGATTGGGGACC
                                     C   _
GAM1444  FBN2     3'  TAATAGCACATCCTGG      12805          TTAACC
                                   TAGTAGCAT     CCTGG
                                   |||||||||     |||||
                                   ATTATCGTG     GGACC
                                         TA_____
GAM1444  GBA      3'  CTAGGGGCCTCCAGCCCCTGGC 44068      TA  A    A
              AC                     CTAG  GC TTTA CCCCTGGCAC
                                   ||||  ||  |||| ||||||||||
                                   GATC  CG AGGT GGGGACCGTG
                                     CC  G    C
GAM1444  MAGEC1   5'  CTGGGAACCTTGACTCCTGGCA 24166    AGT   A   A  C
              C                     CT   AGC TTT AC CCTGGCAC
                                   ||   ||| ||| ||  ||||||||
                                   GA   TTG GAA TG GGACCGTG
                                    CCC   _   C  A
GAM1444  MEL      3'  CTGGTGACACCCCCCTGGC    23867    A  AG    TAA
                                   CT GT  CATT   CCCCTGGC
                                   || ||  ||||   ||||||||
                                   GA CA  GTGG   GGGGACCG
                                    C  CT    ___
GAM1444  NCOA6    3'  CTAGTAACATTTATAATGGCA  30435           ACCCC
                                   CTAGTAGCATTTA    TGGCA
                                   ||||||||||||     |||||
                                   GATCATTGTAAAT    ACCGT
                                           ATT__
GAM1444  WNT8B    3'  TGAGTAGCACCCTTGG      40589    T     ATTTA    C
                                   C AGTAGC    ACCC TGG
                                   | ||||||     |||| |||
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                                A TCATCG    TGGG ACC
                                 C     _____   A
GAM1445 ITSN1    3' CTATGGGATTTCAGCGAC    16655     CA       AACA
                                CTA  GGATTTCA    GGC
                                |||  ||||||||    |||
                                GAT  CCTAAAGT    CTG
                                  AC       CG__
GAM1445 LPHH1    3' CCACAGGATTTTAAAGCCTACG 29387          C   CAG_
                                CTACAGGATTT AAA    GCG
                                |||||||||| |||    |||
                                GGTGTCCTAAA TTT    TGC
                                       A   CGGA
GAM1445 DISC1    3' GAGTGGTTTTCCTGGGAT    33038     ATCGAC
                                GAG      TTTCCTGGGAT
                                |||      ||||||||||
                                CTC      AAAGGACCCTA
                                  ACCA__
GAM1445 MAP1A    3' GAGGTCCTCTCCTGGG      14343     A  GA
                                GAG TC  CTTTCCTGGG
                                ||| ||  ||||||||||
                                CTC AG  GAGAGGACCC
                                  C  __
GAM1445 MGAT1    5' GGAGTCGGCTTTCCGG      14437      A   A     T
                                GGAG TCG CTTTCC GG
                                |||| ||| |||||| ||
                                CCTC AGC GAAAGG CC
                                  _   C     _
GAM1445 MMP19    3' GGAAATATTTCTGGGATA    35593       CGAC    C
                                GGAGAT    TTTC TGGGATA
                                ||||||    |||| |||||||
                                CCTTTA    AAAG ACCCTAT
                                   T____    _
GAM1445 PTP4A2   3' GAAGACAAGTTTCTGGGATAAC 38630       T   C    C
                                GGAGA CGA TTTC TGGGATAAC
                                ||||| ||| |||| |||||||||
                                CTTCT GTT AAAG ACCCTATTG
                                  _   C    _
GAM1445 TEM5     3' GGAGATCAAATGATTGGGAT   37236         CTTTCC
                                GGAGATCGA      TGGGAT
                                |||||||||      ||||||
                                CCTCTAGTT      ACCCTA
                                      TACTA_
GAM1446 ATRN     3' CCCCTTCCTGTGTCCATGCG   40269     G   GAAA  A
                                CCC TTC    TG TCCATGCG
                                ||| |||    || ||||||||
                                GGG AAG    AC AGGTACGC
                                  G   GAC_  _
GAM1446 SALL2    3' CCTGTTCCAAATGATCCTATG  41895    C    G       _
                                CC GTTC AAATGATCC ATG
                                || |||| ||||||||| |||
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                                GG CAAG TTTACTAGG TAC
                                 A   G       A
GAM1447 B3GAT1   3' CATCCAGGGTGTAAGAGGT   38295       ATA   CT
                                CATCCGGG  TGAG  AGGT
                                ||||||||  ||||  ||||
                                GTAGGTCC  ATTC  TCCA
                                    CAC   __
GAM1447 CCNF     3' ATCCGGGAGGCGGAGGT     12070       TATGA  T_
                                ATCCGGGA    GC  AGGT
                                ||||||||    ||  ||||
                                TAGGCCCT    CG  TCCA
                                    C____  CC
GAM1447 DNASE1L1 3' TCCGGGACACCTGGGT     27502        GAG  A
                                TCCGGGATAT   CT GGT
                                ||||||||||   || |||
                                AGGCCCTGTG   GA CCA
                                     ___  C
GAM1447 DNMT3B   5' CCGATCGCCGAGCTAGGT   27871     GATA
                                CCGG   TGAGCTAGGT
                                ||||   ||||||||||
                                GGCT   GCTCGATCCA
                                  AGCG
GAM1447 DPYSL2   3' CACCCGGAATCAGCTGGGT   10745        ATG   A
                                CATCCGGGAT   AGCT GGT
                                ||||||||||   |||| |||
                                GTGGGCCTTA   TCGA CCA
                                     G__   C
GAM1447 EFNB2    3' CATCGGGACATTAGG       19878     C     GAGC
                                CATC GGGATAT    TAGG
                                |||| |||||||    ||||
                                GTAG CCCTGTA    ATCC
                                  _     _____
GAM1447 GATA2    3' CATCCGGGAGTGCCCGGT    13081        TATGA  A
                                CATCCGGGA    GCT GGT
                                |||||||||    ||| |||
                                GTAGGCCCT    CGG CCA
                                    CA___   G
GAM1447 PLXNA2   3' CCGGGATAATTCCAGGT     36075       TGAG
                                CCGGGATA    CTAGGT
                                ||||||||    ||||||
                                GGCCCTAT    GGTCCA
                                    TAA_
GAM1447 PTAFR    3' CATCGGGGAGAACTAGGT    9627      C   TAT
                                CATC GGGA   GAGCTAGGT
                                |||| ||||   |||||||||
                                GTAG CCCT   CTTGATCCA
                                  C   ____
GAM1448 INHBB    5' CGGGTCACTGCCGCACGGG   13554    A      GATC C
                                TG GTCACTGC    C CACGGG
                                || ||||||||    | ||||||
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                                GC CAGTGACG   G GTGCCC
                                 C       ____ C
GAM1448 LIMK1    3' TAAGTCATGGTCCCACGGG   32538       C  CGATC
                                TGAGTCA TG    CCCACGGG
                                ||||||| ||    ||||||||
                                ATTCAGT AC    GGGTGCCC
                                   _ CA___
GAM1448 SLC22A1L 5' TGAGTCACTGGGTCCCAGG   14983         CGA   CAC
                                TGAGTCACTG  TCCC  GGG
                                ||||||||||  ||||  |||
                                ACTCAGTGAC  AGGG  TCC
                                     CC_  ___
GAM1448 TBP      5' TGGGTCACTGCAAAGATCACTA 42114    A        TCCC  ___
             TGGGC                 TG GTCACTGCGA   CAC  GGGC
                                || ||||||||||   |||  ||||
                                AC CAGTGACGTT   GTG  CCCG
                                 C        TCTA  ATA
GAM1448 AF5Q31   5' CAGTGGCGGCGCCGGGCCTG  30852       T     CG
                                CAGTGGC GCGTTGG  GCCTG
                                ||||||| |||||||  |||||
                                GTCACCG CGCGGCC  CGGAC
                                   C     __
GAM1448 AIM1     3' CAGTGGCTCAGGCC       45080        G  TTGGC
                                CAGTGGCT CG    GGCC
                                |||||||| ||    ||||
                                GTCACCGA GT    CCGG
                                   _ ______
GAM1448 ALOX12   3' CAGTGACTATGCGGTCT    8687         CGTTG   C
                                CAGTGGCTG    GCGG CT
                                |||||||||    |||| ||
                                GTCACTGAT    CGCC GA
                                     A____   A
GAM1448 AVPR1A   5' CAGTGGCTGCTGTGCCT    8723         GTTGGCG
                                CAGTGGCTGC     GCCT
                                ||||||||||     ||||
                                GTCACCGACG     CGGA
                                     ACA____
GAM1448 BACH2    3' CAGTGGCTGGTTGGCCCCG   34782        C    GG
                                CAGTGGCTG GTTGGC  CCTG
                                ||||||||| ||||||  ||||
                                GTCACCGAC CAACCG  GGGC
                                   _    __
GAM1448 CACNA1A  3' GTGGCCGCCCGGCCCGGCCTG 35742        G   __
                                GTGGCTGC TTGGC  GGCCTG
                                |||||||| |||||  ||||||
                                CACCGGCG GGCCG  CCGGAC
                                   _   GG
GAM1448 CAPN10   3' CAGGGCTGCGTCTCTCCTG   35766    T       GGCGG
                                CAG GGCTGCGTT    CCTG
                                ||| |||||||||    ||||
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```
                                GTC CCGACGCAG    GGAC
                                  _       AGA__
GAM1448 CSN10    5' CAGTAGGTTGAGTTGGCCTG  23316      CTGC    C__
                                CAGTGG   GTTGG  GGCCTG
                                ||||||   |||||  ||||||
                                GTCATC   CAACT  CCGGAC
                                   ____    CAA
GAM1448 CYBB     3' GTGGCTGGCAGCTGGTGGC   44098       _ _    C
                                GTGGCTG C GTTGG GGC
                                ||||||| | ||||| |||
                                CACCGAC G CGACC CCG
                                    C T    A
GAM1448 EVPL     3' AGTGGCTGCTGTCCTGGTCTG 12765        _  GGC  C
                                AGTGGCTGC GTT   GG CTG
                                ||||||||| |||   || |||
                                TCACCGACG CAG   CC GAC
                                     A  GA_  A
GAM1448 FANCA    3' CAGTGTGGCCGGCGG      6591       GC  C
                                CAGTG  TG GTTGGCGG
                                |||||  || ||||||||
                                GTCAC  AC CGGCCGCC
                                  __ _
GAM1448 FEN1     5' TAGCGGCGGGTGGCCT     19959     T   TT  C
                                TGGC GCG  GG GGCCT
                                |||| |||  || |||||
                                ATCG CGC  CC CCGGA
                                  C   __ A
GAM1448 GAL      5' GTGGGCTCTGGCGGCCTG    45055     CT  G
                                GTGG  GC TTGGCGGCCTG
                                ||||  || ||||||||||
                                CACC  CG GACCGCCGGAC
                                  __ A
GAM1448 GFAP     3' CAGAGGCTGGGGCGGCCTG   13120    T    CGTT
                                CAG GGCTG   GGCGGCCTG
                                ||| |||||   |||||||||
                                GTC CCGAC   CCGCCGGAC
                                  T    C___
GAM1448 GLDC     5' GCGGCTGCGCCCGGCCTG    42025         GG
                                GTGGCTGCGTT  CGGCCTG
                                ||||||||||  |||||||
                                CGCCGACGCGG  GCCGGAC
                                      __
GAM1448 HSPA5    3' AATGGCTGTATTGGGC      23784        CG   CG
                                AGTGGCTG  TTGG  GC
                                ||||||||  ||||  ||
                                TTACCGAC  AACC  CG
                                    AT   __
GAM1448 MSI1     3' CAGGGGTTGGGCTGCGGCCTG 14637    T  C  C   G
                                CAG GG TG GTTG CGGCCTG
                                ||| || || |||| |||||||
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```
                                GTC CC AC CGAC GCCGGAC
                                  C A C   _
GAM1448 PDPK1    3' TGATGGCTGGCAGGTGGTCTG 15212   A     C T C C
                                C GTGGCTG GT GG GG CTG
                                | ||||||| || || || |||
                                A TACCGAC CG CC CC GAC
                                 C      _ T A A
GAM1448 PTGIS    5' TGGCGGGGCTGGCGGCCTG   9680      TGC
                                TGGC  GTTGGCGGCCTG
                                ||||  ||||||||||||
                                ACCG  CGACCGCCGGAC
                                  CCC
GAM1448 RHD      3' CAGTGGCTCAGGCC       32166        G TTGGC
                                CAGTGGCT CG    GGCC
                                |||||||| ||    ||||
                                GTCACCGA GT    CCGG
                                   _ ______
GAM1448 S100A10  5' TGGGGGTCTCGGCGGCCTG   40400    CTGCG
                                TGG    TTGGCGGCCTG
                                |||    ||||||||||||
                                ACC    AGCCGCCGGAC
                                  CCCAG
GAM1448 SFRP1    5' CAGTGGCGGCCCTCGGCCTG  16568       T G GG
                                CAGTGGC GC TT  CGGCCTG
                                ||||||| || ||  |||||||
                                GTCACCG CG GA  GCCGGAC
                                    C G __
GAM1448 SLC39A1  5' CAGTGGCTCGCGCC       30885        G  TGGCG
                                CAGTGGCT CGT    GCC
                                |||||||| |||    |||
                                GTCACCGA GCG    CGG
                                   _  ______
GAM1448 TBL1X    5' GTGGCGAATGGCGGCCTG    24897      TGCGT
                                GTGGC    TGGCGGCCTG
                                |||||    ||||||||||
                                CACCG    ACCGCCGGAC
                                   CTT__
GAM1448 TCP11    3' TGGCTGCAGGGCCT       33072        GTT  C
                                TGGCTGC   GG GGCCT
                                |||||||   || |||||
                                ACCGACG   TC CCGGA
                                   ___  _
GAM1448 UBE2H    3' GTGGCTGCAGGGCCT       17805        GTT  C
                                GTGGCTGC   GG GGCCT
                                ||||||||   || |||||
                                CACCGACG   TC CCGGA
                                   ___  _
GAM1448 USP11    5' CACTGGCTGTCCAGGCCTG   21628    G     CGTTGGC
                                CA TGGCTG      GGCCTG
                                || ||||||      ||||||
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                                GT ACCGAC      CCGGAC
                                 G     AGGT___
GAM1448  USP14    3'  GTGGCTACAGAATGGTGG    23117        T__   C
                                GTGGCTGCG   TGG GG
                                |||||||||   ||| ||
                                CACCGATGT   ACC CC
                                     CTT   A
GAM1449  PRDM4    3'  ATTAAATAATGTTATTTTGAGT 29664          CG GTA
                                ATTGAATAATGT  T   TGAGT
                                ||||||||||||  |   |||||
                                TAATTTATTACA  A   ACTCA
                                      AT AA_
GAM1450  ARSB     5'  TCCCCGGCAATTAAATTTGC   6253         TCTG   CTC
                                TCTCCGGTG   TAAA   GC
                                |||||||||   ||||   ||
                                AGGGGCCGT   ATTT   CG
                                     TA__    AAA
GAM1450  INSRR    3'  TCTCGGTGCACAAACT     42848     C    CTG
                                TCTC GGTGT   TAAACT
                                |||| |||||   ||||||
                                AGAG CCACG   GTTTGA
                                  _    T__
GAM1450  RECQL    5'  TCTCCGGTGTTTGACTGT    37275         ____
                                TCTCCGGTGT    CTGT
                                |||||||||    ||||
                                AGAGGCCACA    GACA
                                      AACT
GAM1450  TCL1B    3'  CTCCGGTGTACATTGCTTGC   22254         CT  AAA  C
                                CTCCGGTGT  GT   CT GC
                                |||||||||  ||   || ||
                                GAGGCCACA  TA   GA CG
                                     TG  AC_  A
GAM1451  ADCY6    3'  ACCTTGGTCCCTTCAGCT    34161        ATAAC   CC
                                ACTTTGGT    CCC  CAGCT
                                ||||||||    |||  |||||
                                TGGAACCA    GGG  GTCGA
                                     _____   AA
GAM1451  ASB1     3'  ACTTTAGTATAAGCCTCTCAGC 32027          C  CCC
           T                     ACTTTGGTATAA CC   CAGCT
                                ||||||||||||  ||   |||||
                                TGAAATCATATT GG   GTCGA
                                      C  AGA
GAM1451  ATP10C   3'  CTTTGGTATGTGCCATGCAGCT 35979         AAC  CCC
                                CTTTGGTAT   CC   CAGCT
                                |||||||||   ||   |||||
                                GAAACCATA   GG   GTCGA
                                     CAC  TAC
GAM1451  BTG1     5'  CTCGGACCTCCCCAGCT     11907       TATA   C
                                TTTGG    ACC CCCCAGCT
                                |||||    ||| ||||||||
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                                GAGCC    TGG GGGGTCGA
                                  _____  A
GAM1451  LASS2    3'  CTTTGCTCCTCCCCCAGCT   42674      GTATAA  _
                                CTTTG     CC CCCCCAGCT
                                |||||     || |||||||||
                                GAAAC     GG GGGGGTCGA
                                   GA____  A
GAM1451  MLLT3    3'  TTTGGTCCCCCCAG       21192       ATAAC
                                TTTGGT    CCCCCCAG
                                ||||||    ||||||||
                                AAACCA    GGGGGGTC
                                  _____
GAM1451  MMP19    5'  CTTTAAAATTCCCCCAGCTA  35584       TATAACC
                                CTTTGG      CCCCCAGCTA
                                ||||||      ||||||||||
                                GAAATT      GGGGGTCGAT
                                   TTAA___
GAM1451  CLN5     5'  TTGGAGGATATGTAGCTTGT  27090       CACATATA
                                TTGGAGGA      GGTTTGT
                                ||||||||      |||||||
                                AACCTCCT      TCGAACA
                                    ATACA___
GAM1451  DDX26    3'  TTTGGAGGAATATTTTTAGTTT 29099        CACATATA
              GT                  TTTGGAGGA      GGTTTGT
                                  |||||||||      |||||||
                                  AAACCTCCT      TCAAACA
                                      TATAAAAA
GAM1451  HOXB5    5'  TTTGGAGGGCTTGATTTG    13455       ACACATATA
                                TTTGGAGG       GGTTTG
                                ||||||||       ||||||
                                AAACCTCC       CTAAAC
                                    CGAA_____
GAM1451  MAFF     3'  TTTGGAGGGCATATTGGC    29518       ACA    A
                                TTTGGAGG   CATAT GGT
                                ||||||||   ||||| |||
                                AAACCTCC   GTATA CCG
                                    C__    A
GAM1451  POU4F1   3'  TTTGGTGGTTGGTAGGTTTGT  26401      A  ACACATA
                                TTTGG GG      TAGGTTTGT
                                ||||| ||      |||||||||
                                AAACC CC      ATCCAAACA
                                   A  AACC___
GAM1452  COL4A4   5'  CCGCAAGTTGGAGGCGGGCTGG 6395         TTTACTACA
                                TCGCAAGTT       GGCTGG
                                |||||||||       ||||||
                                GGCGTTCAA       CCGACC
                                    CCTCCGC__
GAM1452  DAAM2    3'  TCCAAGTGGCCACCTGCAGGCT 45178    G    TT    A_
              GG                  TC CAAGT  TTACT  CAGGCTGG
                                  || |||||  |||||  ||||||||
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                                AG GTTCA  GGTGG  GTCCGACC
                                 _    CC    AC
GAM1452  MN1     3'  TCCAAAGACTGCAGGCTG    14592    G   TTTTT  A
                                TC CAAG    ACT CAGGCTG
                                || ||||    ||| |||||||
                                AG GTTT    TGA GTCCGAC
                                 _   C____  C
GAM1452  AMPD3    5'  GGCCAGCCGCGTGCAGCCC   7901      T  AAA
                                GGCC GT   GCGTGCAGCCC
                                |||| ||   ||||||||||
                                CCGG CG   CGCACGTCGGG
                                  T  G__
GAM1452  AQP1     3'  GGCCTGTAGAGCTCTGCCGGTC 7548        A  G_  AG__
              C                  GGCCTGTA AGC  TGC   CC
                                |||||||| |||  |||   ||
                                CCGGACAT TCG  ACG   GG
                                    C   AG   GCCA
GAM1452  AQP6     5'  GGCCTGCAGCTGCCC      38251       AAGCGT  A
                                GGCCTGTA     GC GCCC
                                ||||||||     || ||||
                                CCGGACGT     CG CGGG
                                    _______ A
GAM1452  ARHD     3'  GGTCCTGGCAGGTGCAGCCC  31024    _   TAA  C
                                GG CCTG   AG GTGCAGCCC
                                || ||||   || |||||||||
                                CC GGAC   TC CACGTCGGG
                                 A   CG_  _
GAM1452  AVPR2    3'  GGCCTCTGCTGCAGCC     6289       GTAAA  G
                                GGCCT    GC TGCAGCC
                                |||||    || |||||||
                                CCGGA    CG ACGTCGG
                                   GA___  _
GAM1452  B4GALT7  3'  GGCCTGTAGGTACAG      28547       AA  C
                                GGCCTGT  AG GTGCAG
                                |||||||  || ||||||
                                CCGGACA  TC CATGTC
                                    __  _
GAM1452  CAPN10   3'  AGTCCGCCGCGTGCAGCC   35761    C   AAA
                                GG CTGT   GCGTGCAGCC
                                || ||||   ||||||||||
                                TC GGCG   CGCACGTCGG
                                 A   G__
GAM1452  CASP10   3'  GGCCTGTAGATTGAGTCC   37387       AAGCG  C  _
                                GGCCTGTA    TG AG CC
                                ||||||||    || || ||
                                CCGGACAT    AC TC GG
                                    CTA__  _  A
GAM1452  CDK10    3'  GGCCAGTATGCAGCC      38150     T  AAAGC
                                GGCC GT    GTGCAGCC
                                |||| ||    ||||||||
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                                CCGG CA    TACGTCGG
                                  T _____
GAM1452 CGTHBA   3' GGCCTTGAAGGATGCGGCC   28963     GTA  C   A
                                GGCCT   AAG GTGC GCC
                                |||||   ||| |||| |||
                                CCGGA   TTC TACG CGG
                                   AC_  C   C
GAM1452 CGTHBA   3' GGTCTGAGAAACGCACAGCCC 28965   C  TA   TG
                                GG CTG  AAGCG  CAGCCC
                                || |||  |||||  ||||||
                                CC GAC  TTTGC  GTCGGG
                                 A  TC    GT
GAM1452 CSNK1D   3' GGCCGCAGTGCAGCC      12467     T  AAGC
                                GGCC GTA   GTGCAGCC
                                |||| |||   ||||||||
                                CCGG CGT   CACGTCGG

                                  _  ____
GAM1452 DBY      3' GGCCTGTAGTGAGGCC     21659       AAGC  CA
                                GGCCTGTA   GTG  GCC
                                ||||||||   |||  |||
                                CCGGACAT   CAC  CGG
                                     ____  TC
GAM1452 DHCR24   5' GCCTGTAGCCCACAGCCC   31299      AA  G
                                GCCTGT  AGC TGCAGCCC
                                ||||||  ||| ||||||||
                                CGGACA  TCG GTGTCGGG
                                   __  G
GAM1452 DNASE1   5' GGCCTGCAAAGCCCACCC   23355         G GCA
                                GGCCTGTAAAGC T  GCCC
                                |||||||||||| |  ||||
                                CCGGACGTTTCG G  TGGG
                                      G ___
GAM1452 FE65L2   5' GGCCTGAGCCGCACAGCCC  39319      TAA  _ TG
                                GGCCTG  AGC G  CAGCCC
                                ||||||  ||| |  ||||||
                                CCGGAC  TCG C  GTCGGG
                                   ___  G GT
GAM1452 FES      3' GGCCTGCAGAGGCCACCAGC  12820       A  C  G__
                                GGCCTGTA AG GT  CAGC
                                |||||||| || ||  ||||
                                CCGGACGT TC CG  GTCG
                                    C  _  GTG
GAM1452 GRB10    5' GGCCTTGACCGCAGCC     23663     GTAAA  G
                                GGCCT    GC TGCAGCC
                                |||||    || |||||||
                                CCGGA    TG GCGTCGG
                                  AC___  _
GAM1452 GYS1     3' GGCCTGAGCGTGGCC      44792      TAA    CA
                                GGCCTG  AGCGTG  GCC
                                ||||||  ||||||  |||
```

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                              CCGGAC  TCGCAC  CGG
                                 ___    __
GAM1452  HDAC5    3'  GCCTTGTAGGCCCACAGCCC  40168     _  AA  G
                              GCCT GTA  GC TGCAGCCC
                              |||| |||  || ||||||||
                              CGGA CAT  CG GTGTCGGG
                                A  C_  G
GAM1452  HMGE     3'  ACCAAGCGTGCAGTCC     43743     TGTA       _
                              GCC   AAGCGTGCAG CC
                              |||   |||||||||| ||
                              TGG   TTCGCACGTC GG
                                _____       A
GAM1452  HOXC5    3'  AGCCTGTACGCCGCAGCCC   33243       AA  G
                              GGCCTGTA  GC TGCAGCCC
                              ||||||||  || ||||||||
                              TCGGACAT  CG GCGTCGGG
                                   G_  _
GAM1452  HSPB2    5'  GGTCCGAGGTGCAGCC     11365    C  TAA  C
                              GG CTG   AG GTGCAGCC
                              || |||   || ||||||||
                              CC GGC   TC CACGTCGG
                               A  ___  _
GAM1452  IL1RL1LG 5'  GGTCTGCAAAGGGGTCGCGGC  27797    C      CG__  A
                              GG CTGTAAAG   TGC GC
                              || ||||||||   ||| ||
                              CC GACGTTTC   GCG CG
                               A      CCCA  C
GAM1452  IL2RB    3'  GGCCTGTAAGTGCAGGTGCC  9388        AGC   ___
                              GGCCTGTAA  GTGCA  GCC
                              |||||||||  |||||  |||
                              CCGGACATT  CACGT  CGG
                                   ___   CCA
GAM1452  IRAK1    3'  GGTCTGTGCAGCCAGCAGCC  11474    C   AA  GT
                              GG CTGT  AGC  GCAGCC
                              || ||||  |||  ||||||
                              CC GACA  TCG  CGTCGG
                               A   CG  GT
GAM1452  ITGA3    3'  GGCCTTAGGACACAGCCC    24264     GTAA  C TG
                              GGCCT   AG G  CAGCCC
                              |||||   || |  ||||||
                              CCGGA   TC T  GTCGGG
                                 A___  C GT
GAM1452  KCNE1L   3'  GGCCTGCAACCCGTTGGC    29373       AG  GCA
                              GGCCTGTAA  CGT  GC
                              |||||||||  |||  ||
                              CCGGACGTT  GCA  CG
                                   GG  AC_
GAM1452  KCNK6    3'  GGTCTGAGCCCACAGCCC    22082    C  TAA  G
                              GG CTG   AGC TGCAGCCC
                              || |||   ||| ||||||||
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                                CC GAC   TCG GTGTCGGG
                                 A  ___  G
GAM1452  MAML1    3'  GGCCTGAGGGGCGCAGCC    31290       TAAAGC
                                GGCCTG     GTGCAGCC
                                ||||||     ||||||||
                                CCGGAC     CGCGTCGG
                                   TCCC__
GAM1452  MAPT     3'  GGTCTGCAAAGTGGCC      32585    C      GC   CA
                                GG CTGTAAA  GTG  GCC
                                || |||||||  |||  |||
                                CC GACGTTT  CAC  CGG
                                 A      __  __
GAM1452  MATK     5'  GGCCCGTGGACTCCGCAGCCC  40312       AAA  G_
                                GGCCTGT   GC  TGCAGCCC
                                |||||||   ||  ||||||||
                                CCGGGCA   TG  GCGTCGGG
                                    CC_  AG
GAM1452  MEN1     5'  GGCTGTAAAGTCTGTCC     39193     C      CG  CAG
                                GGC TGTAAAG  TG   CC
                                ||| |||||||  ||   ||
                                CCG ACATTTC  AC   GG
                                  _      AG  A__
GAM1452  MPZ      3'  GGCTGCAGTGCAGCC       8037      C    AAGC
                                GGC TGTA    GTGCAGCC
                                ||| ||||    ||||||||
                                CCG ACGT    CACGTCGG
                                  _   ____
GAM1452  MSF      3'  GGAGGGGAGCGTGCAGCCC    44735    CCTGTAA
                                GG      AGCGTGCAGCCC
                                ||      ||||||||||||
                                CC      TCGCACGTCGGG
                                 TCCCC__
GAM1452  MUC4     3'  GGCCTGTATGTAGCACAGCCC  39671        AAGC TG
                                GGCCTGTA    G  CAGCCC
                                ||||||||    |  ||||||
                                CCGGACAT    C  GTCGGG
                                     ACAT GT
GAM1452  P4HB     3'  GCTGCTGGGTGTGCAGCCC    9548     C   AAAGC
                                GC TGT     GTGCAGCCC
                                || |||     |||||||||
                                CG ACG     CACGTCGGG
                                 _  ACCCA
GAM1452  PAFAH1B1 3'  GACCTGTAAATCCAGC       7708          AGC  G
                                GGCCTGTAA   GT CAGC
                                |||||||||   || ||||
                                CTGGACATT   TA GTCG
                                      ___  G
GAM1452  PPP2R4   3'  AGCCTGTAAGAGCCAGGCCC   41324         _  GTG  _
                                GGCCTGTAA AGC   CAG CCC
                                ||||||||| |||   ||| |||
```

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                                TCGGACATT TCG   GTC GGG
                                     C   ___   C
GAM1452  PRKY     3'  GGCTTGGTGAAAATACAGCCC  15703     C  TAAAGC
                                GGC TG     GTGCAGCCC
                                ||| ||     |||||||||
                                CCG AC     TATGTCGGG
                                  A  CACTTT
GAM1452  PXF      3'  GACCTGTAGCCCCAGCCC    16010       AA   GTG
                                GGCCTGT  AGC   CAGCCC
                                |||||||  |||   ||||||
                                CTGGACA  TCG   GTCGGG
                                    __  GG_
GAM1452  RAI14    3'  GGCTGTAAACACACAG      31805     C     G  TG
                                GGC TGTAAA CG  CAG
                                ||| ||||||  ||  |||
                                CCG ACATTT GT  GTC
                                  _     _  GT
GAM1452  SIT      5'  GGCCCGTACCCCGCAGC     30900        AAGCG
                                GGCCTGTA    TGCAGC
                                ||||||||    ||||||
                                CCGGGCAT    GCGTCG
                                     GGG__
GAM1452  SLC6A9   5'  GGCCAGTCCCCATGCAGCCC  27988      T  AAAG
                                GGCC GT    CGTGCAGCCC
                                ||||  ||   ||||||||||
                                CCGG CA    GTACGTCGGG
                                  T  GGG_
GAM1452  SORCS2   3'  GGTCTGCAGCTCTTGCAGCCC 34063    C   AA   G__
                                GG CTGT  AGC   TGCAGCCC
                                ||  ||||  |||   ||||||||
                                CC GACG  TCG   ACGTCGGG
                                 A   __   AGA
GAM1452  SOST     3'  GGCCTGCAAGGCCAGTGTCC   36108        A  __   CAG
                                GGCCTGTAA GC  GTG   CC
                                |||||||||  ||  |||   ||
                                CCGGACGTT CG  CAC   GG
                                     C  GT   A__
GAM1452  SUV39H1  3'  GGTTTGTAAGTGCAACCC    17225    CC    AGC
                                GG  TGTAA   GTGCAGCCC
                                ||  |||||   |||||||||
                                CC  ACATT   CACGTTGGG
                                 AA    ___
GAM1452  TAF4     3'  CTGTAAAGTCGGCCC       17261         _  TGCA
                                CTGTAAAG CG    GCCC
                                ||||||||  ||    ||||
                                GACATTTC GC    CGGG
                                     A  _____
GAM1452  TGFA     3'  GGCTTGCATTGATGCAGCC    17443     C    AAGC
                                GGC TGTA    GTGCAGCC
                                ||| ||||    ||||||||
```

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                                CCG ACGT   TACGTCGG
                                  A   AAC_
GAM1452 THBD    5' GGCCCCCACGCGTGCAGCCC  7427      G  AA
                                GGCCT TA  GCGTGCAGCCC
                                ||||| ||  ||||||||||
                                CCGGG GT  CGCACGTCGGG
                                   G  G_
GAM1452 TP63    3' GGTTTGCAAAGCTGCATGC   19000   CC      G   _
                                GG  TGTAAAGC TGCA GC
                                ||  |||||||| |||| ||
                                CC  ACGTTTCG ACGT CG
                                 AA       _   A
GAM1452 UBE2L6  3' GGCCTGCAAGGTGACC     20123        A C   CA
                                GGCCTGTAA G GTG  GCC
                                ||||||||| | |||  |||
                                CCGGACGTT C CAC  TGG
                                      _ _  __
GAM1452 XPC     3' GGCCTGCAGAGAAATGGTCC  21550       A  C_   CAG
                                GGCCTGTA AG  GTG   CC
                                |||||||| ||  |||   ||
                                CCGGACGT TC  TAC   GG
                                    C  TT   CA_
GAM1453 AF5Q31  3' TAGCTCACGGAAACCATCTTAT 30857     C   CAT
                                TAGC CAC   GGACCATCTTAT
                                |||| |||   ||||||||||||
                                ATCG GTG   TTTGGTAGAATA
                                  A   CC_
GAM1453 RRM2B   3' TTAGCCCATCTGCAGCTT    42731       CCA  GAC  T
                                TTAGCCCA   TG   CA CTT
                                ||||||||   ||   || |||
                                AATCGGGT   AC   GT GAA
                                    AG_  ___  C
GAM1453 XK      3' TCAGTTCACCATGGCTTA    34369     CC      ACCAT
                                TTAG  CACCATGG    CTTA
                                ||||  ||||||||    ||||
                                AGTC  GTGGTACC    GAAT
                                  AA       _____
GAM1454 CETN1   3' TCTAAGGTTTCACAAAATG   45459       GTCA   C
                                TCTAAGGTT    GCA GGATG
                                |||||||||    ||| |||||
                                AGATTCCAA    TGT TTTAC
                                    AG__   _
GAM1454 FGF2    5' CCTGGGGTTCACGGATG     12836     AA   GTCAG
                                TCT  GGTT    CACGGATG
                                |||  ||||    ||||||||
                                GGA  CCAA    GTGCCTAC
                                  CC   _____
GAM1454 HRH2    5' TCTAAGGTGTTGGGAATGA   35291       T  CAGCAC
                                TCTAAGGT GT     GGATGA
                                |||||||| ||     ||||||
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                                AGATTCCA CA      CTTACT
                                     _  ACC___
GAM1454  MN1      3'  TCTGAGGTTGCCAGGACCATGA 14597     A         C  GG
                                TCT AGGTTGTCAG AC  ATGA
                                ||| |||||||||| ||  ||||
                                AGA TCCAACGGTC TG  TACT
                                  C         C  G_
GAM1454  OCLN     5'  TCCTAGGGGGCAGCACGGATG  14909     A   TT T
                                TCT AGG  G CAGCACGGATG
                                ||| |||  | ||||||||||
                                AGG TCC  C GTCGTGCCTAC
                                  A   CC _
GAM1454  RFC4     5'  TAAGATTGTGATTCTGGATGAA 16287          CAGCAC
                                TAAGGTTGT     GGATGAA
                                |||||||||     |||||||
                                ATTCTAACA     CCTACTT
                                      CTAAGA
GAM1454  HGF      3'  CATGTAAACACCTAGATTA    45318      C     G T
                                CATG AAGCA C CTAGATTA
                                |||| ||||| | ||||||||
                                GTAC TTTGT G GATCTAAT
                                  A     _ _
GAM1454  SNAP25   3'  TGCATAGCTCTAGATTA     39262      AGC
                                TGCA   AGCTCTAGATTA
                                ||||   ||||||||||||
                                ACGT   TCGAGATCTAAT
                                  A__
GAM1455  KCNJ1    5'  GAGATTGTCCCTGGTGTCTGG  6888     A  C   AG_  AA
                                GA AT GTT   GG  TGTCTGG
                                || || |||   ||  |||||||
                                CT TA CAG   CC  ACAGACC
                                 C  A   GGA  __
GAM1456  SCML1    3'  CTCAGAATTAAGCAAATTAA   27559      A       AACT
                                CTCA GAATTAAG    TTAA
                                |||| ||||||||    ||||
                                GAGT CTTAATTC    AATT
                                  _       GTTT
GAM1456  ST7      3'  TAACTCAGCTTAGAAGAACTTT 30271        AGAATT
              AA                  TAACTCA     AAGAACTTTAA
                                  |||||||     ||||||||||||
                                  ATTGAGT     TTCTTGAAATT
                                      CGAATC
GAM1457  CD59     3'  ATAAGCAAGTTTCTATTTTCCT 8304          TCC_     C
              AT                  GTGGGTAA    CTATTT CCTAT
                                  ||||||||    |||||| |||||
                                  TATTCGTT    GATAAA GGATA
                                      CAAA     A
GAM1457  ICAM1    3'  TGGGTAATCTCTGAACCT     43437          C  ATTTC
                                TGGGTAATC CT     CCT
                                ||||||||| ||     |||
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```
                                ACCCATTAG GA     GGA
                                     A  CTT__
GAM1458  ANXA4    3'  TGCAAGTACAGCTTTAAAGC   41719          T  AC__
                                TGCAAGTACA CT    AGC
                                |||||||||| ||    |||
                                ACGTTCATGT GA    TCG
                                     C  AATT
GAM1458  BAZ2A    3'  AGCACTTTTCTACAGCTGCAC  30299       A__      CA
                                AGTAC   TCTACAGC  CAC
                                |||||   ||||||||  |||
                                TCGTG   AGATGTCG  GTG
                                   AAA       AC
GAM1458  BRDT     5'  TACAAGTACATGTCCATGC    11900          CTA  _
                                TGCAAGTACAT   CA GC
                                ||||||||||   || ||
                                ATGTTCATGTA   GT CG
                                      CAG  A
GAM1458  C21orf33 3'  TGTGAGAGCAGCCCAGCCACAC 21625    CA  TA  T  A
              C                  TG  AG  CA CT CAGCCACACC
                                 ||  ||  || || ||||||||||
                                 AC  TC  GT GG GTCGGTGTGG
                                  AC  TC  C  _
GAM1458  CARP     3'  GTACATCTTCACAACAC     30795         ACA  C
                                GTACATCT   GC ACAC
                                ||||||||   || ||||
                                CATGTAGA   TG TGTG
                                     AG_  T
GAM1458  CD164    3'  TGCAAGTAAAACAAACAGCTGT 25683         CATCT_    CAC
             ACC                   TGCAAGTA     ACAGC   ACC
                                   ||||||||     |||||   |||
                                   ACGTTCAT     TGTCG   TGG
                                        TTTGTT    ACA
GAM1458  CPD      3'  TGCAAGTAGGTCTCTTCCACA  10562         CA   ACAG
                                TGCAAGTA  TCT    CCACA
                                ||||||||  |||    |||||
                                ACGTTCAT  AGA    GGTGT
                                     CC   GAA_
GAM1458  GAN      3'  TGCTGCTTCTTACAGCCA    35155     AA  ACA   _
                                TGC  GT   TCT ACAGCCA
                                |||  ||   ||| |||||||
                                ACG  CG   AGA TGTCGGT
                                  A_  A__   A
GAM1458  GAN      3'  GCCTCCAACATCTACAGCCACA 35147    AAGT_
                                GC    ACATCTACAGCCACA
                                ||    ||||||||||||||
                                CG    TGTAGATGTCGGTGT
                                 GAGGT
GAM1458  MMP8     3'  TGAAAGTGGATACAGCCACA   14548    C    ACATC
                                TG AAGT    TACAGCCACA
                                || ||||    ||||||||||
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```
                                AC TTCA     ATGTCGGTGT
                                 T    CCT__
GAM1458  MPP2     3'  AGTATACGCAGAGCCACACC   40793      C  C  C
                                AGTA AT TA AGCCACACC
                                |||| || || |||||||||
                                TCAT TG GT TCGGTGTGG
                                  A  C  C
GAM1458  MTMR6    3'  TGAAAGTACATGCCA       45283     C       CTACA
                                TG AAGTACAT     GCCA
                                || ||||||||     ||||
                                AC TTCATGTA     CGGT
                                 T       _____
GAM1458  RARG     3'  TGCAGGTGCATCACACAGC   9729       A  A   _
                                TGCA GT CATC TACAGC
                                |||| || |||| ||||||
                                ACGT CA GTAG GTGTCG
                                  C  C    T
GAM1458  SHANK2   3'  TGGAAGTACATCTGCTGAGCTC 39330    C        AC__   _  C
              ATAC                  TG AAGTACATCT    AGC CA AC
                                || ||||||||||    ||| || ||
                                AC TTCATGTAGA    TCG GT TG
                                 C         CGAC   A  A
GAM1458  SQSTM1   3'  GCAGGTTACAGCCACA      19377     A  ACATC
                                GCA GT     TACAGCCACA
                                ||| ||     ||||||||||
                                CGT CA     ATGTCGGTGT
                                  C  _____
GAM1459  PFKFB4   3'  TCACACTTCACAAAGCCAACTG 21296    G         T   G
                                TC ACACTTCACAA GCT AACTG
                                || |||||||||| ||| |||||
                                AG TGTGAAGTGTT CGG TTGAC
                                 _         T   _
GAM1460  ADD1     3'  TACACAAGGACAGAGCACA   30526         CC     A
                                TACACAAGG  CAGGG CACA
                                |||||||||  ||||| ||||
                                ATGTGTTCC  GTCTC GTGT
                                      T_    _
GAM1460  ANK1     3'  TACACAAGGCTGATTACTGTAC 33883          CCAGGG  ___
              A                  TACACAAGGC     AC   ACA
                                ||||||||||     ||   |||
                                ATGTGTTCCG     TG   TGT
                                      ACTAA_  ACA
GAM1460  AOC3     3'  CATGAGGCAGGCAGACACAA  19014    CA   CC   __
                                CA  AGGC  AGG  GACACAA
                                ||  ||||  |||  |||||||
                                GT  TCCG  TCC  CTGTGTT
                                 AC    __   GT
GAM1460  CEBPA    3'  CACAAGGCACTGCTGGGCACA 20383         CCA___   A
                                CACAAGGC     GGG CACA
                                ||||||||     ||| ||||
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                                GTGTTCCG     CCC GTGT
                                     TGACGA  _
GAM1460 CREBBP   3' TACAAAAGGTCCAAGAACA   20430     C   C
                                TACA AAGG CCAGGGACA
                                |||| |||| |||||||||
                                ATGT TTCC GGTTCTTGT
                                  T   A
GAM1460 CSK     3' ACACGGGACATGGGACACA   20455     AA  CC  _
                                ACAC  GG  CA GGGACACA
                                ||||  ||  || ||||||||
                                TGTG  CC  GT CCCTGTGT
                                  __  CT  A
GAM1460 EPHA2    3' CAAAGGCCCAGGAAAGCAA   20733   C         CA
                                CA AAGGCCCAGGGA  CAA
                                || ||||||||||||  |||
                                GT TTCCGGGTCCTT  GTT
                                 _          TC
GAM1460 EXT2     3' CACAAGCCCAGCAC       7585       G    GGA
                                CACAAG CCCAG   CAC
                                |||||| |||||   |||
                                GTGTTC GGGTC   GTG
                                   _    ____
GAM1460 FACL5    3' CATGAGGAAGGACACA     42013    CA   CCC
                                CA  AGG   AGGGACACA
                                ||  |||   |||||||||
                                GT  TCC   TTCCTGTGT
                                 AC  ____
GAM1460 GALNT2   3' CAGGGCTCAGATCACAA    21001    A   C   GA
                                CA GGC CAGG  CACAA
                                || ||| ||||  |||||
                                GT CCG GTCT  GTGTT
                                 C   A   A_
GAM1460 GARP     3' CACATAGGGGCAGACACA    24304     _  CC   G
                                CACA AGG  CAGG ACA
                                |||| |||  |||| |||
                                GTGT TCC  GTCT TGT
                                  A   CC   G
GAM1460 GARP     3' ACACAAGGCTTGGATTCAA   24302        CCAG   CA
                                ACACAAGGC    GGA  CAA
                                |||||||||    |||  |||
                                TGTGTTCCG    CCT  GTT
                                     AA__   AA
GAM1460 HGF      3' ACAATTTAGGGACACAA     45316     GGCCC
                                ACAA     AGGGACACAA
                                ||||     ||||||||||
                                TGTT     TCCCTGTGTT
                                  AAA__
GAM1460 HUNK     3' CACACACAGGGGCACA      31055      AGGCC    A
                                TACACA    CAGGG CACA
                                ||||||    ||||| ||||
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                                GTGTGT    GTCCC GTGT
                                   _____    C
GAM1460  IMPA1    3'  TACACAAGACTTTAAAGCA   24391         CC_   A
                                TACACAAGGC   AGGG CA
                                ||||||||||   |||| ||
                                ATGTGTTCTG   TTTC GT
                                     AAA   _
GAM1460  ITGA6    3'  ACACATTAGGGACACAA     6825       AGGCCC
                                ACACA     AGGGACACAA
                                |||||     ||||||||||
                                TGTGT     TCCCTGTGTT
                                  AA____
GAM1460  LY95     5'  CAAGTACCCAGGGACACAA   22097     _
                                CAAG GCCCAGGGACACAA
                                |||| ||||||||||||||
                                GTTC TGGGTCCCTGTGTT
                                  A
GAM1460  MBNL     3'  TAACAAGGCCTGATACTCA   34317   C       CA GG  A
                                A ACAAGGCC  G  AC CA
                                | ||||||||  |  || ||
                                A TGTTCCGG  C  TG GT
                                 T       A_ TA  A
GAM1460  NTSR1    3'  CACGTGAGGCCCAAAGCCAC   14877     A__         A
                                CAC   AGGCCCAGGG CAC
                                |||   |||||||||| |||
                                GTG   TCCGGGTTTC GTG
                                  CAC         G
GAM1460  PSMD9    3'  ACACAGGGCTTGCCTGGCA   15842      A  ___  AG  A
                                ACACA GGC   CC  GG CA
                                ||||| |||   ||  || ||
                                TGTGT CCG   GG  CC GT
                                   C   AAC  A_  _
GAM1460  SAA4     3'  TACCAGTTCCTGGGGACACAA  27139     A  AGG  CA
                                TAC CA   CC  GGGACACAA
                                ||| ||   ||  |||||||||
                                ATG GT   GG  CCCTGTGTT
                                  _  CAA  AC
GAM1460  SAFB     3'  CACGAGACAGGACACA      16450     A   CCA
                                CAC AGGC   GGGACACA
                                ||| ||||   ||||||||
                                GTG TCTG   TCCTGTGT
                                  C   ___
GAM1460  SHC1     3'  TACAAGAGGCCCAAATTCA   16707      CA       GA
                                TACA  AGGCCCAGG  CA
                                ||||  |||||||||  ||
                                ATGT  TCCGGGTTT  GT
                                   TC        AA
GAM1460  SIM2     3'  TAACAAGGTAGACACA      22880   C     CCCAG
                                A ACAAGG    GGACACA
                                | ||||||    |||||||
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                                A TGTTCC    TCTGTGT
                                 T    A____
GAM1460 SIX2    3' TACGGAGGGACCAGGACACA  32613    ACAA C    G
                                TAC   GG CCAGG ACACA
                                |||   || ||||| |||||
                                ATG   CC GGTCC TGTGT
                                  CCTC  T   _
GAM1460 TARBP2  3' TACATGAGCCCAGAGGCA   39536     CAA       A
                                TACA  GGCCCAGGG CA
                                ||||  ||||||||| ||
                                ATGT  TCGGGTCTC GT
                                  AC_       C
GAM1460 TIMP3   3' TACCCAGGGCCGAGTGACACA 7466     A A   C G
                                TAC CA GGCC AG GACACA
                                ||| || |||| || ||||||
                                ATG GT CCGG TC CTGTGT
                                  G C   C A
GAM1460 UBB     5' CACCCACAGGGACACAA    33250    AAGG _
                                CAC   CC CAGGGACACAA
                                |||   || ||||||||||
                                GTG   GG GTCCCTGTGTT
                                  ____ T
GAM1460 VLDLR   3' TACACAAGCTTGATCCAC   43009       G CCA  GA
                                TACACAAG C   GG  CAC
                                |||||||| |  ||  |||
                                ATGTGTTC G   CT  GTG
                                     _ AA_  AG
GAM1460 WARS    3' CACCCGTCCAGGGACACA   42620    AAGGC
                                CAC    CCAGGGACACA
                                |||    ||||||||||
                                GTG    GGTCCCTGTGT
                                  GGCA_
GAM1461 FLRT2   5' TGAAATAATTAAAGCTAA   29859          A
                                TGAAATAATTAGA CTAG
                                |||||||||||| ||||
                                ACTTTATTAATTT GATT
                                        C
GAM1461 RERE    3' TGAAAGAAAAAAAACTAGAAAC 29039      T  TT
             AT                   TGAAA AA  AGAACTAGAAACAT
                                |||||  ||  ||||||||||||||
                                ACTTT TT  TTTTGATCTTTGTA
                                   C  TT
GAM1461 GRINL1A 3' TTTCTGTAATTATTCAATT   43007      _      T
                                TTTCTG AATTATTC AATT
                                |||||| |||||||| ||||
                                AAAGAC TTAATAAG TTAA
                                   A      _
GAM1462 RTKN    3' TGCTATAGACAGCGCCGTATCC 37502   TC   A  G   AT
                                TG  ATA AC AGT  CCGTATCC
                                ||  ||| || |||  ||||||||
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                                AC  TAT TG TCG  GGCATAGG
                                 GA   C  _   C_
GAM1462  SULT1A3   3'  TGTCATAACTCACTGTATCC   17215        ___  GA
                                TGTCATAA   AC  GTATCC
                                ||||||||   ||  ||||||
                                ACAGTATT   TG  CATAGG
                                     GAG  A_
GAM1463  BTK       3'  AGGGAATCAAAGAAGAGGT    6294        A        A
                                AGGGAA TCAAAGAAGA GT
                                ||||||  |||||||||| ||
                                TCCCTT AGTTTCTTCT CA
                                   _        C
GAM1463  CA12      3'  AAGGAAATCAGAGGGAGA     10239         A  A_
                                AGGGAAATCA AG  AGA
                                ||||||||||  ||  |||
                                TTCCTTTAGT TC  TCT
                                      C  CC
GAM1463  CARPX     3'  GAAATCAAAGAATGCAGT     33569          GA_
                                GAAATCAAAGAA   AGT
                                ||||||||||||   |||
                                CTTTAGTTTCTT   TCA
                                       ACG
GAM1463  CDC27     3'  AGGGAGATTAAAGAAAAA     10366       A  C
                                AGGGA AT AAAGAAGAA
                                |||||  ||  |||||||||
                                TCCCT TA TTTCTTTTT
                                   C  A
GAM1463  CYP8B1    3'  AGGGAAATCAGGAGGAGGAGT  20503          A_  A  A
                                AGGGAAATCA  AG AG AGT
                                ||||||||||  ||  ||  |||
                                TCCCTTTAGT  TC TC TCA
                                      CC  C  C
GAM1463  DEDD      3'  AGGGAAATAAAGGGGAAG     37425        C    AA
                                AGGGAAAT AAAG  GAAG
                                ||||||||  ||||  ||||
                                TCCCTTTA TTTC  CTTC
                                     _   CC
GAM1463  ESRRG     3'  AGGGAGGTGAAAGAAGAAA    42443       AATC
                                AGGGA    AAAGAAGAAG
                                |||||    ||||||||||
                                TCCCT    TTTCTTCTTT
                                   CCAC
GAM1463  GRAF      3'  AGGGAAACAGAGAAGCCA     31434        CAA   A
                                AGGGAAAT   AGA GAAGTTA
                                ||||||||   ||| |||||||
                                TCCCTTTG   TCT CTTCGGT
                                     ___   _
GAM1463  IFNGR1    3'  AGGAAAATCAGACTTCAAAGTT 43542          AAGAA_
                                AGGGAAATCA     GAAGTT
                                ||||||||||     ||||||
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                                TCCTTTTAGT     TTTCAA
                                     CTGAAG
GAM1463 LEP      3' AGGGAAATTGACAGAGTC    6908         CAAAGA   A
                                AGGGAAAT     AGA GTT
                                ||||||||     ||| |||
                                TCCCTTTA     TCT CAG
                                    ACTG__   _
GAM1463 MYCL2    3' AGGGAGATCAAAAAGAAA    23896       A       A
                                AGGGA ATCAAAGA GAAG
                                ||||| |||||||| ||||
                                TCCCT TAGTTTTT CTTT
                                   C       _
GAM1463 MYO10    3' GGGAAATCAGGTTGGGAGGTTA 29574          AAGAA_  A
                                GGGAAATCA      GA GTTA
                                |||||||||      || ||||
                                CCCTTTAGT      CT CAAT
                                     CCAACC  C
GAM1463 PBX3     3' AGGGAAACAAAGAGTTAA    26212        T     AGAA
                                AGGGAAA CAAAGA    GTTAA
                                ||||||| ||||||    |||||
                                TCCCTTT GTTTCT    CAATT
                                   _     _____
GAM1463 PCDHA11  5' AGGGAACTCAAAGAAAAAAT  36574       A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1463 PFKFB2   3' GGGCATAGAGGGAGGAAGTTAA 26307     AAATCAAA  A
             T                   GGG       GA GAAGTTAAT
                                 |||       || |||||||||
                                 CCC       CT CTTCAATTA
                                   GTATCTCC  C
GAM1463 PIK3R3   3' AGGAAGGACAGAAGGGGTTA  41434      ATCAA    AA
                                GGGAA    AGAAG  GTTA
                                |||||    |||||  ||||
                                TCCTT    TCTTC  CAAT
                                   CCTG_    CC
GAM1463 POU3F1   3' AGGGAAATATAAGGGGAAA   40370       CA   AA
                                AGGGAAAT  AAG  GAAG
                                ||||||||  |||  ||||
                                TCCCTTTA  TTC  CTTT
                                     TA   CC
GAM1463 RARRES3  3' AGGGAAACAGAGGAAA     42842       CAA   A
                                AGGGAAAT   AGA GAAG
                                ||||||||   ||| ||||
                                TCCCTTTG   TCT CTTT
                                     ___   C
GAM1463 ADAMTS5  3' AATTCTTTTATATTAAAAACA 28172           CAT
                                AATTCTTTTGTATT   AGACA
                                ||||||||||||||   |||||
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                                TTAAGAAAATATAA  TTTGT
                                       TT_
GAM1463 BPHL    5' TGATTCTTTTGCACATTAAG  20259   A       TCAT
                                C ATTCTTTTGTAT   AG
                                | ||||||||||||   ||
                                A TAAGAAAACGTG   TC
                                 C         TAAT
GAM1463 CTSH    3' TCTTTGCGTCATAGACAC    20500     T  AT
                                TCTTT GT  TCATAGACAC
                                ||||| ||  ||||||||||
                                AGAAA CG  AGTATCTGTG
                                   _  C_
GAM1463 DMD     3' AACTTTTTTGTACAATTGCATA 19672     C      T____
           GAC                    AATT TTTTGTAT    CATAGAC
                                |||| ||||||||    |||||||
                                TTGA AAAACATG    GTATCTG
                                  A       TTAAC
GAM1463 NOS1    3' TTCTGTATAGCAAGACAC    8383        TCAT
                                TTTTGTAT   AGACAC
                                ||||||||   ||||||
                                AAGACATA   TCTGTG
                                     TCGT
GAM1463 SHANK2  3' TTCTTTGCCAATAGACAC    29477      T  ATTC
                                TTCTTT GT   ATAGACAC
                                ||||||  ||   ||||||||
                                AAGAAA CG   TATCTGTG
                                   _  GT__
GAM1464 ABCC12  3' CAGTTTTTTAATCCATTAGCTG 37715    T      AG___
           G                    CA TTTTTTAAT    GGCTGG
                                || |||||||||    ||||||
                                GT AAAAAATTA    TCGACC
                                 C       GGTAA
GAM1464 AOC3    3' AGACTTCCATAGGGCTGG    19011     A   TTTA
                                AGAC TTTT   ATAGGGCTGG
                                |||| ||||   ||||||||||
                                TCTG AAGG   TATCCCGACC
                                  _   _____
GAM1464 AVPR1A  5' GACATCTTTTTGGGTGG     8728          AATA  C
                                GACATTTTTTT   GGG TGG
                                ||||||||||   ||| |||
                                CTGTAGAAAAA   CCC ACC
                                      ____  _
GAM1464 GNAO1   3' AGATTGTTTTCTATGGGGCTGG 44937    CAT     ATA
           A                    AGA  TTTTTTA  GGGCTGGA
                                |||  |||||||  ||||||||
                                TCT  AAAAGAT  CCCGACCT
                                  AAC     AC_
GAM1464 INPP5B  3' AGACATTTTTGTGGAATATGGG 45468        TT__   _
                                AGACATTTTT   AATA GGG
                                ||||||||||   |||| |||
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                                TCTGTAAAAA   TTAT CCC
                                     CACC   A
GAM1464  JPH3    3'  ACATTTTAGGGGGCTGG    34013       TTTAATA
                                ACATTTT     GGGCTGG
                                |||||||     |||||||
                                TGTAAAA     CCCGACC
                                   TCC____
GAM1464  MMP14   3'  ACATTCAGATGGGGCTGGA   22629      TTTTAATA
                                ACATTT      GGGCTGGA
                                ||||||      ||||||||
                                TGTAAG      CCCGACCT
                                   TCTAC___
GAM1464  MOX2    3'  GACGTAAAATAGGGCTGG    42515    ATTTTTTT
                                GAC      AATAGGGCTGG
                                |||      ||||||||||
                                CTG      TTATCCCGACC
                                  CATT____
GAM1464  SCN4A   3'  AGACATCTTTGTCTGGGCTGG 7316         TTAATA
                                AGACATTTTT    GGGCTGG
                                ||||||||||    |||||||
                                TCTGTAGAAA    CCCGACC
                                     CAGA__
GAM1464  SYT4    3'  GACATTTTTTTAGTATCTTTGG 41658         A  GGGC
           A                     GACATTTTTTTA TA   TGGA
                                ||||||||||| ||   ||||
                                CTGTAAAAAAAT AT   ACCT
                                      C  AGAA
GAM1464  TRHDE   3'  AGAATTTTTTTAACTCTCTGGA 30099    C        AGGG
                                AGA ATTTTTTTAAT   CTGGA
                                ||| ||||||||||   |||||
                                TCT TAAAAAAATTG   GACCT
                                  _        AGA_
GAM1465  NCALD   3'  TTTCTCAAAACATTAACTGA  36779       T   CTAA
                                TTTCTCAAA CAT   TGA
                                ||||||||| |||   |||
                                AAAGAGTTT GTA   ACT
                                     T   ATTG
GAM1465  PLSCR1  3'  TTTCTCAAATTGACAATGA   34413        CATC
                                TTTCTCAAAT   TAATGA
                                ||||||||||   ||||||
                                AAAGAGTTTA   GTTACT
                                     ACT_
GAM1465  PPP6C   3'  TTTCTCAAGTCTTCTCAAATGA 15546       A  A  __
                                TTTCTCAA TC TCT  AATGA
                                |||||||| || |||  |||||
                                AAAGAGTT AG AGA  TTACT
                                     C  A   GT
GAM1465  TLL2    3'  CTTCTCAAAGTCAATGAAT   29750       TCA  T
                                TTTCTCAAA   TC AATGAAT
                                |||||||||   || |||||||
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                                GAAGAGTTT  AG TTACTTA
                                    C__  _
GAM1465 ZNF146   3' TTTCTCAAATTGTTCCAAGGAA 28362         CA_    T
            T                    TTTCTCAAAT  TCTAA GAAT
                                 ||||||||||  ||||| ||||
                                 AAAGAGTTTA  AGGTT CTTA
                                      ACA    C
GAM1466 CACNA2D2 3' TGGAGGACACTGGTGGCTAG  25727       _  ATCACG  A
                                 TGGAGGAC CTG     GGC AG
                                 ||||||||| |||     ||| ||
                                 ACCTCCTG GAC     CCG TC
                                     T  CA____  A
GAM1466 CR1L     3' TGGAGGATTTGGACAAA     44868       CCTGATCAC
                                 TGGAGGA       GGGCAAG
                                 |||||||       |||||||
                                 ACCTCCT       CCTGTTT
                                    AAA_______
GAM1466 CSF3     3' TGGGAGACCTGATACTCTCAAG 8904     AG      C  GGG
                                 TGG  GACCTGAT AC   CAAG
                                 |||  |||||||| ||   ||||
                                 ACC  CTGGACTA TG   GTTC
                                   CT       _ AGA
GAM1466 CSNK1G2  3' GGAGGGCCTGGGCAA      10615      A   GATCAC
                                 GGAGG CCT     GGGCAA
                                 ||||| |||     ||||||
                                 CCTCC GGA     CCCGTT
                                   C  _______
GAM1466 IL16     5' TGGAGGACTTGGTCTGTGGGC  21100       C  A  AC_
                                 TGGAGGAC TG TC   GGGC
                                 |||||||| || ||   ||||
                                 ACCTCCTG AC AG   CCCG
                                     A  C  ACA
GAM1466 NR1H2    3' TGGAAGACTCGCTGGGCA    43120       C  ATCAC
                                 TGGAGGAC TG    GGGCA
                                 |||||||| ||    |||||
                                 ACCTTCTG GC    CCCGT
                                     A  GA___
GAM1466 OAT      3' TGAAGGACTTGATTTAGAGG   7087        C   CAC_
                                 TGGAGGAC TGAT    GGG
                                 |||||||| ||||    |||
                                 ACTTCCTG ACTA    TCC
                                     A    AATC
GAM1466 PCDHA9   3' TGGAGGACTTAGGGC      36554       C  ATCAC
                                 TGGAGGAC TG    GGGC
                                 |||||||| ||    ||||
                                 ACCTCCTG AT    CCCG
                                     A  _____
GAM1466 PDGFB    5' GGAGGACCTGGGCGCAG     15184         ATCAC  _  A
                                 GGAGGACCTG    GG GCA G
                                 ||||||||||    || ||| |
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                                CCTCCTGGAC    CC CGT C
                                      _____ G   C
GAM1466 PDGFB    3' GGAGGGGTGCGGGCAAG    15186      ACC  ATCA
                                GGAGG  TG   CGGGCAAG
                                |||||  ||   ||||||||
                                CCTCC  AC   GCCCGTTC
                                  CC_ ____
GAM1466 SCNN1A   3' TGGAGCATACATAAACGGGCAA 9785      G__  C   TC
           GA                    TGGAG  AC TGA  ACGGGCAAGA
                                |||||  || |||  ||||||||||
                                ACCTC  TG ATT  TGCCCGTTCT
                                  GTA  T  __
GAM1466 TSNAX    5' TGAAGGACCTGGAGCAAG    25632          ATCAC
                                TGGAGGACCTG    GGGCAAG
                                ||||||||||    |||||||
                                ACTTCCTGGAC    CTCGTTC
                                      _____
GAM1466 TXNIP    3' TGGAGGTTCTGATCACAGG   27002       AC
                                TGGAGG  CTGATCACGGG
                                ||||||  ||||||||||
                                ACCTCC  GACTAGTGTCC
                                   AA
GAM1466 ACPT     3' CCCAGGGCCCCCTGGAGGGCC  38886         A  AA     A
                                CTCAGGGCC CC  TGGAGG CC
                                |||||||| ||  |||||| ||
                                GGGTCCCGG GG  ACCTCC GG
                                     _ G_     C
GAM1466 AKAP13   3' CCTGGGGCCGCCCAGGAGGAC  28479    CA    A  AAT
                                CCT  GGGCC CC   GGAGGAC
                                |||  ||||| ||   |||||||
                                GGA  CCCGG GG   CCTCCTG
                                  C_    C  GT_
GAM1466 BCL2L2   3' CCTCAGGGCTGTGAAG      19739         CACCAA
                                CCTCAGGGC     TGGAG
                                |||||||||     |||||
                                GGAGTCCCG     ACTTC
                                     AC_____
GAM1466 BCLG     3' CCTCAGGTTCTCAATGGAGGGC 39821        GCCAC       A
           C                     CCTCAGG    CAATGGAGG CC
                                |||||||    ||||||||| ||
                                GGAGTCC    GTTACCTCC GG
                                    AAGA_       C
GAM1466 BLTR2    5' CCTCAGGGCTCTCACCGGG   33363         ___   AAT
                                CCTCAGGGC   CACC   GG
                                |||||||||   ||||   ||
                                GGAGTCCCG   GTGG   CC
                                     AGA   C__
GAM1466 CACNG6   5' CCTCTGGGGTTCAGAGGAGG   36694     A   CCAC  AT
                                CCTC GGG    CA  GGAGG
                                ||||  |||    ||  |||||
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                                GGAG CCC   GT  CCTCC
                                  A  CAA_  CT
GAM1466 CASQ2    3' CCTCAGGGCATCAGTATGAAC 10282       CAC  A  GA
                                CCTCAGGGC  CA TG  GGAC
                                |||||||||  || ||  ||||
                                GGAGTCCCG  GT AT  CTTG
                                     TA_  C  A_
GAM1466 CD3Z     5' CCCCAGGAAGTGGAGGAC    8818        CCACCAA
                                CCTCAGGG     TGGAGGAC
                                ||||||||     ||||||||
                                GGGGTCCT     ACCTCCTG
                                    TC_____
GAM1466 CELSR2   3' CCTCAGGGCAGCCGAG     10846        CA  AATG
                                CCTCAGGGC  CC   GAG
                                |||||||||  ||   |||
                                GGAGTCCCG  GG   CTC
                                     TC  ____
GAM1466 CELSR3   3' CCTAGGGCCACGGAGGA    10835    C      CAAT
                                CCT AGGGCCAC   GGAGGA
                                ||| ||||||||   ||||||
                                GGA TCCCGGTG   CCTCCT
                                 _      ____
GAM1466 CGTHBA   3' CCTCAGGGCCAAGAGG     28960         CCAAT
                                CCTCAGGGCCA    GGAGG
                                ||||||||||    |||||
                                GGAGTCCCGGT    TCTCC
                                       _____
GAM1466 CMAR     3' CCTTGGGCCACCAGCAG    23293    CA       AT
                                CCT  GGGCCACCA  GG
                                |||  |||||||||  ||
                                GGA  CCCGGTGGT  TC
                                  A_       CG
GAM1466 CNTFR    5' CCTCGGGCCACCCGGG     12300     A      AAT
                                CCTC GGGCCACC   GG
                                ||||  ||||||||   ||
                                GGAG CCCGGTGG   CC
                                  _      GC_
GAM1466 COL6A1   3' CTCAGGGCTGAGCCCCGGAGGA 12328        CA__  AA
            CC                    CTCAGGGC   CC  TGGAGGACC
                                |||||||    ||  |||||||||
                                GAGTCCCG   GG  GCCTCCTGG
                                    ACTC  G_
GAM1466 CRY2     3' CCTCAGGGCCACCTGAG    43581          AATG
                                CCTCAGGGCCACC   GAG
                                ||||||||||||    |||
                                GGAGTCCCGGTGG   CTC
                                       A___
GAM1466 FANCC    3' CCACAGGACAGGGTGGAGGAC 43270    T     CACCAA
                                CC CAGGGC     TGGAGGAC
                                || ||||||     ||||||||
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                                GG GTCCTG     ACCTCCTG
                                 T     TCCC__
GAM1466  FAT2     3'  CCTCAGGGACTAGGTGGGGGA  11072        CCACCAA   A
                                CCTCAGGG      TGG GGA
                                ||||||||      ||| |||
                                GGAGTCCC      ACC CCT
                                    TGATCC_   C
GAM1466  FOXI1    3'  CCGTGGGGCTGGCATGGAGGAC 29151    TCA    CACCA
              C                  CC   GGGC    ATGGAGGACC
                                ||   ||||    ||||||||||
                                GG   CCCG    TACCTCCTGG
                                 CAC    ACCG_
GAM1466  G22P1    5'  TCAGGGCCGGCGGCGGC     11175        ACCAA   A  A
                                TCAGGGCC     TGG GG C
                                ||||||||     ||| || |
                                AGTCCCGG     GCC CC G
                                    CC___    G  _
GAM1466  GCN5L2   3'  CCTGGGGGCCACCACGG     40811     CA       A
                                CCT  GGGCCACCA TGG
                                |||  ||||||||| |||
                                GGA  CCCGGTGGT GCC
                                  CC        _
GAM1466  HD       3'  CTCAGAGCTGCTGACATAACC  13347        CACCAA   AG_
                                CTCAGGGC     TGG   GACC
                                ||||||||     |||   ||||
                                GAGTCTCG     ACT   TTGG
                                    ACG___   GTA
GAM1466  IL1RAP   3'  CTCAAGGCCACTAAGAC     13500          CAATGG
                                CTCAGGGCCAC     AGGAC
                                ||||||||||      |||||
                                GAGTTCCGGTG     TTCTG
                                     A_____
GAM1466  INSRR    3'  TCAGGGCCACGGGTGTGGAC   42847         CAA  GA
                                TCAGGGCCAC   TG  GGAC
                                ||||||||||   ||  ||||
                                AGTCCCGGTG   AC  CCTG
                                     CCC  A_
GAM1466  KCNH2    3'  CCTCAGGGCAGTGGGGGGACC  6947          CACCAAT  A
                                CCTCAGGGC      GG GGACC
                                |||||||||      || |||||
                                GGAGTCCCG      CC CCTGG
                                    TCACC__  _
GAM1466  KL       3'  CCTCAGGGACACAGG       22004         C   CAATGG
                                CCTCAGGG CAC     AGG
                                |||||||| |||     |||
                                GGAGTCCC GTG     TCC
                                    T  _______
GAM1466  KLK3     3'  CTGAGGGTTGTCTGGAGGAC   11611    C   CCACCAA
                                CT AGGG      TGGAGGAC
                                || ||||      ||||||||
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                                GA TCCC      ACCTCCTG
                                 C   AACAG__
GAM1466 LGR6    5' CCCAGGGCTGCTGGCTGAC   44476        CACCAA  AG
                                CTCAGGGC     TGG  GAC
                                ||||||||     |||  |||
                                GGGTCCCG     ACC  CTG
                                    ACG___   GA
GAM1466 MAN2B1  5' CCTCAGGGCACTGGTTGG    8031         C  CAA  A_
                                CCTCAGGGC AC   TGG  GG
                                ||||||||| ||   |||  ||
                                GGAGTCCCG TG   ACC  CC
                                    _ ___  AA
GAM1466 MAP1A   5' CTCGGGGTTGTGAAGGACC   14342    A  CCACCAA
                                CTC GGG      TGGAGGACC
                                ||| |||      |||||||||
                                GAG CCC      ACTTCCTGG
                                  C  AAC____
GAM1466 MGAT5   5' CTCAGGGCCACCAGGCAACC  14472          AT  AG
                                CTCAGGGCCACCA  GG  GACC
                                ||||||||||||  ||  ||||
                                GAGTCCCGGTGGT  CC  TTGG
                                    __ G_
GAM1466 NAGLU   5' CCAGGGCCGAAGGGGAC     7049        ACCAAT  A
                                TCAGGGCC     GG GGAC
                                ||||||||     || ||||
                                GGTCCCGG     CC CCTG
                                    CTT___  _
GAM1466 NESG1   5' CCTCAGGGCTGATGATTAGGGA 29580        CACCAA_  A
            C                    CCTCAGGGC      TGG GGAC
                                ||||||||||      ||| ||||
                                GGAGTCCCG      ATC CCTG
                                    ACTACTA  _
GAM1466 NF2     5' CCTCAGGGCCACCATGG     7065           A
                                CCTCAGGGCCACCA TGG
                                |||||||||||||| |||
                                GGAGTCCCGGTGGT ACC
                                                _
GAM1466 NOX5    5' CCTGGGGCCACCAGG       35993     CA       AT
                                CCT  GGGCCACCA  GG
                                |||  |||||||||  ||
                                GGA  CCCGGTGGT  CC
                                  C_       __
GAM1466 NPHS2   5' CCTCAGAGCTGCCGGGCGG   31199        CA  AAT  A
                                CCTCAGGGC  CC   GG GG
                                |||||||||  ||   || ||
                                GGAGTCTCG  GG   CC CC
                                    AC  C__  G
GAM1466 PCTK1   5' CCTCAGAGCCGCGGGG      37469         ACCAA   A
                                CCTCAGGGCC    TGG GG
                                ||||||||||    ||| ||
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                                GGAGTCTCGG    GCC CC
                                     C____  _
GAM1466  PIK3R1   3'  CCTCAGGGTGGCTGAA     42859       CCACCAA  A_
                                CCTCAGGG     TGG  GGA
                                ||||||||     |||  |||
                                GGAGTCCC     ACC  CTT
                                   ________  GA
GAM1466  PKLR     3'  CTTAGGGCCTGCTGAGCAGA  7146    C    ACCAA  A_
                                CT AGGGCC    TGG  GGA
                                || ||||||    |||  |||
                                GA TCCCGG    ACT  TCT
                                 A     ACG__  CG
GAM1466  PLXNA1   3'  CTCAGGGTCAGCAGGAAG    43620       C  C  AT
                                CTCAGGG CA CA  GGAGG
                                ||||||| || ||  |||||
                                GAGTCCC GT GT  CCTTC
                                    A  C  __
GAM1466  PSD      5'  CCTCAGGGGCACCGTGTCCAGG 15781       C   AATGG_
                                CCTCAGGG CACC     AGG
                                |||||||| ||||     |||
                                GGAGTCCC GTGG     TCC
                                    C    CACAGG
GAM1466  PTGS1    3'  CTCAGAGCTGGAGTGGAGG   38733       CACCAA
                                CTCAGGGC     TGGAGG
                                ||||||||     ||||||
                                GAGTCTCG     ACCTCC
                                     ACCTC_
GAM1466  PTPRA    5'  CCTCAGGGCCGCCGCCCGG   38910        A  AA_
                                CCTCAGGGCC CC   TGG
                                |||||||||| ||   |||
                                GGAGTCCCGG GG   GCC
                                     C  CGG
GAM1466  PTPRS    5'  CTGCAGAGACAATGGAGG    39301   _    CCAC
                                CT CAGGG    CAATGGAGG
                                || |||||    |||||||||
                                GA GTCTC    GTTACCTCC
                                 C    T___
GAM1466  RAB30    5'  CCTCAGGGGCACTGTGA     30932       C   CAA  _
                                CCTCAGGG CAC   TG GA
                                |||||||| |||   || ||
                                GGAGTCCC GTG   AC CT
                                    C   ___  A
GAM1466  RAD23A   3'  GGGCCACTCCAATGGAGGA   22797      __
                                GGGCCA  CCAATGGAGGA
                                ||||||  ||||||||||
                                CCCGGT  GGTTACCTCCT
                                   GA
GAM1466  RAD9     3'  CCTCAGGGCTGGCAGCCGGA  21371       CAC  A_
                                CCTCAGGGC   CA  TGGA
                                |||||||||   ||  ||||
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                                GGAGTCCCG  GT  GCCT
                                     ACC  CG
GAM1466 RARA    5' CCTCGGGGCATGGGG      9705      A   CACCA   A
                                CCTC GGGC    ATGG GG
                                |||| ||||    |||| ||
                                GGAG CCCG    TACC CC
                                  C  _____   _
GAM1466 SARDH   3' CCCAGGGCCATTTGGGAC    28249        CCAA  AG
                                CTCAGGGCCA   TGG  GAC
                                ||||||||||   |||  |||
                                GGGTCCCGGT   ACC  CTG
                                     AA__  __
GAM1466 SCD     5' TCGGGGTCGCCGGAGGAC    22833    A  CCA  AAT
                                TC GGG   CC   GGAGGAC
                                || |||   ||   |||||||
                                AG CCC   GG   CCTCCTG
                                 C  AGC  ___
GAM1466 SFRS7   3' CCTCAAGGTCTAGGAGGA    40466       CCACCAAT
                                CCTCAGGG      GGAGGA
                                ||||||||      ||||||
                                GGAGTTCC      CCTCCT
                                     AGAT____
GAM1466 SH3BP5  3' CCTCAAGGTCACTGAAA     22123       C   CAA
                                CCTCAGGG CAC   TGGAG
                                |||||||| |||   |||||
                                GGAGTTCC GTG   ACTTT
                                     A  ___
GAM1466 SIAT4C  5' CCTCGGGCCACCTTTGG     26577     A      AA
                                CCTC GGGCCACC  TGG
                                |||| ||||||||  |||
                                GGAG CCCGGTGG  ACC
                                  _      AA
GAM1466 SULT1C1 3' CCTCAGGGCTGGCTGCACCAGG 9838         ______    AT
                                CCTCAGGGC     CACCA  GG
                                |||||||||     |||||  ||
                                GGAGTCCCG     GTGGT  CC
                                     ACCGAC    __
GAM1466 TAL1    3' CTCAGGGCTGCAGACATGG   17284       __ CCA
                                CTCAGGGC  CA   ATGG
                                ||||||||  ||   ||||
                                GAGTCCCG  GT   TACC
                                     AC  CTG
GAM1466 TNFRSF9 5' CTCAGGGCTGCCGGAGAAC   11451       CA  AAT
                                CTCAGGGC  CC   GGAGGAC
                                ||||||||  ||   |||||||
                                GAGTCCCG  GG   CCTCTTG
                                     AC  ___
GAM1466 TRHDE   3' CTCGCTTAATGGAGGA     30106     AGG  CACC
                                CTC   GC    AATGGAGGA
                                |||   ||    |||||||||
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                              GAG  CG   TTACCTCCT
                                ___ AA__
GAM1466 UBA52    3' CCAGGGCCACGGGG       17779         CAAT  A
                              TCAGGGCCAC   GG GG
                              ||||||||||   || ||
                              GGTCCCGGTG   CC CC
                                   _____ _
GAM1466 UBE2L3   3' TCGGGGCCACCACAGAC    17832    A       ATGGA
                              TC GGGCCACCA    GGAC
                              || |||||||||    ||||
                              AG CCCGGTGGT    TCTG
                               C       G____
GAM1466 WBSCR5   3' TCAGGGCCATGGAGGGGACC  37130        CCAA   __
                              TCAGGGCCA   TGGA  GGACC
                              |||||||||   ||||  |||||
                              AGTCCCGGT   ACCT  CCTGG
                                   _____  CC
GAM1467 EPO      3' ATTGCTGGCACTGGA      9030          CCC
                              ATTGCTGGTACT  GGA
                              ||||||||||||  |||
                              TAACGACCGTGA  CCT
                                   ____
GAM1467 G6PD     3' TGTTGCTGGTGACAAGGAA   7614     A      _  TCCC
                              TG TTGCTGGT AC   GGAA
                              || ||||||| ||   ||||
                              AC AACGACCA TG   CCTT
                               _      C  TT__
GAM1467 GEMIN5   5' TGATTGCTGGGCCAATGGA   44846        TACT  C__
                              TGATTGCTGG   CC   GGA
                              ||||||||||   ||   |||
                              ACTAACGACC   GG   CCT
                                    C___  TTA
GAM1468 CDH6     3' TACAAAGGCAAACTTTCGCATG 22329      ATAC   C
             T                 TACAAA   AACT TTCGCATGT
                              ||||||   |||| |||||||||
                              ATGTTT   TTGA AAGCGTACA
                                 CCGT   _
GAM1468 PPP3CA   3' TACAAATGCAACTCTTTTCTGT 9616       ATA      CGCA
                              TACAAA  CAACTCTT   TGT
                              ||||||  ||||||||   |||
                              ATGTTT  GTTGAGAA   ACA
                                 AC_      AAG_
GAM1468 PUM1     3' CAAAATACAGTTCATCTTCTGT 31232        AC  T  GCA
                              CAAAATACA  TC TC   TGT
                              |||||||||  || ||   |||
                              GTTTTATGT  AG AG   ACA
                                    CA  T  AAG
GAM1468 RAD51C   3' TACAAAATACTACTTTCATAAT 38485        A  C   C___
             ATGT                 TACAAAATAC ACT TTCG   ATGT
                              |||||||||| ||| ||||   ||||
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                                ATGTTTTATG TGA AAGT    TACA
                                      A   _    ATTA
GAM1468  SRGAP1   3'  TACAAAATACAAATGCCCG   43603          CTC
                                TACAAAATACAA   TTCG
                                ||||||||||||   ||||
                                ATGTTTTATGTT   GGGC
                                       TAC
GAM1468  TGFBR1   3'  TACAAAATACAATTGCATG   21436          CTC  C
                                TACAAAATACAA   TT GCATG
                                ||||||||||||   || |||||
                                ATGTTTTATGTT   AA CGTAC
                                       ____  _
GAM1468  WEE1     3'  CAAAATACAGCTTTCAACTGT  18080         A  C    CA
                                CAAAATACA CT TTCG  TGT
                                ||||||||| || ||||  |||
                                GTTTTATGT GA AAGT  ACA
                                      C  _    TG
GAM1469  ATP7A    3'  CTTTGCTTCTGGTAATGG    6261     A     ACGAA
                                CT TGCTTT    GGTAATGG
                                || ||||||    ||||||||
                                GA ACGAAG    CCATTACC
                                 A     A_____
GAM1469  TBXA2R   5'  CATGCTTTACAAAATGG     9848            GGTA
                                TATGCTTTACGAA    ATGG
                                ||||||||||||    ||||
                                GTACGAAATGTTT    TACC
                                       _____
GAM1469  ADAM11   3'  TGCAAGGAGGGGCCATCCAGGC 34662          A    TTA   A
                                TGCAAGGAG GGCC   CTA GGC
                                ||||||||| ||||   ||| |||
                                ACGTTCCTC CCGG   GGT CCG
                                      C    TA_  _
GAM1469  BSN      3'  TGAAGGAGAGGTTCTGAGG   18416    C       CCTTA  A
                                TG AAGGAGAGG    CT AGG
                                || |||||||||    || |||
                                AC TTCCTCTCC    GA TCC
                                 _       AA___  C
GAM1469  CCBL1    3'  GCAGGGAGAGGCCCAGG     19765     A        TACTA
                                GCA GGAGAGGCCT    AGG
                                ||| ||||||||||    |||
                                CGT CCTCTCCGGG    TCC
                                  C         _____
GAM1469  CIT      3'  TGCAGGGAGGTGCCCAGGG   43059     A   AG   TACTAA
                                TGCA GGAG  GCCT     GG
                                |||| ||||  ||||     ||
                                ACGT CCTC  CGGG     CC
                                  C   CA   TC____
GAM1469  COPEB    3'  CAAGGAGAGGCCCTGGAGGC   44429           ACTA
                                CAAGGAGAGGCCTT    AGGC
                                ||||||||||||||   ||||
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                                GTTCCTCTCCGGGA   TCCG
                                      CC__
GAM1469 ESR2    5' TGCAAGAAGAGGCACAAAGG  11014          CTT  T
                                TGCAAGGAGAGGC  AC AAGG
                                ||||||||||||  || ||||
                                ACGTTCTTCTCCG  TG TTCC
                                     ___  T
GAM1469 FOXI1   3' TGTGAGGGTGGGCCCAAGG  29156   CA  AGA   TACT
                                TG  AGG  GGCCT   AAGG
                                ||  |||  |||||   ||||
                                AC  TCC  CCGGG   TTCC
                                 AC  CAC   ____
GAM1469 FRG1    5' TGCGCGGAGAGGCTGAGG   20991    AA      CTTACTA
                                TGC  GGAGAGGC     AGG
                                |||  ||||||||     |||
                                ACG  CCTCTCCG     TCC
                                  CG      AC_____
GAM1469 GPR56   3' TGTAAGGAGAGACCAG     25003    C        TTACTA
                                TG AAGGAGAGGCC    AG
                                || ||||||||||     ||
                                AC TTCCTCTCTGG    TC
                                 A        ______
GAM1469 H4FL    3' TGCAAGGAAAGGCCTG     18640            TACTAA
                                TGCAAGGAGAGGCCT    G
                                ||||||||||||||    |
                                ACGTTCCTTTCCGGA    C
                                      ______
GAM1469 KCNA5   3' TGAAAGGAGAGGGGTAGACTGA 40685   C       CCTT_  A
          GG                    TG AAGGAGAGG    ACT AGG
                                || |||||||||    ||| |||
                                AC TTCCTCTCC    TGA TCC
                                 T       CCATC  C
GAM1469 MAF     5' TGCAGGAGAGGGGCCAGCGGGC 23840     A   __   TTACTAA
                                TGCA GGAGA  GGCC     GGC
                                |||| |||||  ||||     |||
                                ACGT CCTCT  CCGG     CCG
                                  _    CC   TCGC___
GAM1469 MEF2D   3' TGCAGGAGAGGTGGGAAGG  25426    A     CCTTACT
                                TGCA GGAGAGG     AAGG
                                |||| |||||||     ||||
                                ACGT CCTCTCC     TTCC
                                  _      ACCC___
GAM1469 PPL     3' TGCAAGGAGTGGGCTTGG   15498        A  C  ACTAA
                                TGCAAGGAG GG CTT    GG
                                |||||||| || |||    ||
                                ACGTTCCTC CC GAA    CC
                                     A  C  _____
GAM1469 RAB36   3' CAGGGAGAGGCCTTG      22235    A       ACTAA
                                CA GGAGAGGCCTT    G
                                || ||||||||||    |
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                                GT CCTCTCCGGAA    C
                                 C        _____
GAM1469 RAMP3    3' TGCAGGCAGAGGCTTCCGG   25204     A _    C  ACTAA
                                TGCA GG AGAGGC TT    GG
                                |||| || |||||| ||    ||
                                ACGT CC TCTCCG AA    CC
                                  _ G    _ GG___
GAM1469 SERPINE1 3' CAAGGAGAGGCCAAGG     8284           TTACT
                                CAAGGAGAGGCC    AAGG
                                ||||||||||||    ||||
                                GTTCCTCTCCGG    TTCC
                                      _____
GAM1469 SLC16A2  3' TGCTGGGAGGGCCTTGAGG   27160    AA   A    ACTA
                                TGC  GGAG GGCCTT   AGG
                                |||  |||| ||||||   |||
                                ACG  CCTC CCGGAA   TCC
                                  AC   _    C___
GAM1469 SPON1    3' TGCAGGAAGAGGCTGGCTGGAG 41671     A      CTTACTA
             G                   TGCA GGAGAGGC      AGG
                                |||| ||||||||      |||
                                ACGT CTTCTCCG      TCC
                                  C       ACCGACC
GAM1469 SRC      3' TGCAGGGAGAGGCGTGCGG   24038     A      CTTACTAA
                                TGCA GGAGAGGC       GG
                                |||| ||||||||       ||
                                ACGT CCTCTCCG       CC
                                  C       CACG____
GAM1469 STC1     3' AAGAGAAGTCTATTAAGGC   17168        C  TAC
                                AGGAGAGG CT   TAAGGC
                                |||||||| ||   ||||||
                                TTCTCTTC GA   ATTCCG
                                     A  TA_
GAM1469 TCF3     3' TGCAGGGAGGGGCATGAAGGGC 43329     A   A  CTTACTAA
                                TGCA GGAG GGC       GGC
                                |||| |||| |||       |||
                                ACGT CCTC CCG       CCG
                                  C   C   TACTTC__
GAM1469 TPD52L2  3' TGCGAGAGAGGCTGCTGGGG   17641    AA      CTTA  AA
                                TGC  GGAGAGGC    CT  GG
                                |||  ||||||||    ||  ||
                                ACG  TCTCTCCG    GA  CC
                                  C_       AC__  CC
GAM1469 UNC119   3' TGCAAGAGAGGCCCAGCCAGGC 38346      G      TA  A
                                TGCAAG AGAGGCCT  CTA GGC
                                |||||| ||||||||  ||| |||
                                ACGTTC TCTCCGGG  GGT CCG
                                    _       TC  _
GAM1469 UTY      5' TGCAAGGAAAAAAGCTGAGGC  28318          CCTTA  A
                                TGCAAGGAGAGG    CT AGGC
                                ||||||||||||    || ||||
```

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                                ACGTTCCTTTTT    GA TCCG
                                      TC___  C
GAM1470 ABCA1    3'  TCAAAGCAGGATGTTAGCC   24272       T__   AC
                                TCAAAGCG  TGTT  AGCC
                                ||||||||  ||||  ||||
                                AGTTTCGT  ACAA  TCGG
                                    CCT   __
GAM1470 ACCN2    3'  CCAAAGATCCTACAGCC    33435      C  G
                                TCAAAG GTT TTACAGCC
                                |||||| ||| ||||||||
                                GGTTTC TAG GATGTCGG
                                  _  _
GAM1470 ADAM19   3'  CAAAGCACCACACGGCC    35750       TG T  A
                                CAAAGCGT  T AC GCC
                                ||||||||  | || |||
                                GTTTCGTG  G TG CGG
                                    GT _  C
GAM1470 ADAMTS1  5'  CAGAGCCGGCTACAGCC    28109    A  GTT
                                CA AGC  GTTACAGCC
                                || |||  |||||||||
                                GT TCG  CGATGTCGG
                                 C  GC_
GAM1470 ALDH3A2  3'  TCACAGCCTGCTGCAGCC    42919    A  G   A
                                TCA AGC TTGTT CAGCC
                                ||| ||| ||||| |||||
                                AGT TCG GACGA GTCGG
                                  G  _    C
GAM1470 APXL     3'  CAGAGCCCTCCACAGCC     11618    A  G  G
                                CA AGC TT TTACAGCC
                                || ||| || ||||||||
                                GT TCG GA GGTGTCGG
                                 C  G  _
GAM1470 ARHGEF6  3'  TCACAGCTCACTGCAGCC    42802    A  G TG  A
                                TCA AGC T  TT CAGCC
                                ||| ||| |  || |||||
                                AGT TCG A  GA GTCGG
                                  G  _ GT  C
GAM1470 BAG1     3'  TCAGGGCAGCACAGCC      45409    AA  TT  T
                                TCA  GCG  GT ACAGCC
                                |||  |||  || ||||||
                                AGT  CGT  CG TGTCGG
                                  CC  __  _
GAM1470 BDP1     5'  TCACGGCCGCTCACAGCC    32951    AAGC  _
                                TCA   GTTG TTACAGCC
                                |||   |||| ||||||||
                                AGT   CGGC AGTGTCGG
                                  GC__   G
GAM1470 CBFA2T2  3'  TCACAGCAACCACAGCC     22977    A   TT TT
                                TCA AGCG  G  ACAGCC
                                ||| ||||  |  ||||||
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```
                                AGT TCGT  T  TGTCGG
                                  G   __ GG
GAM1470 CEBPA    3' CCAGGGCGGTCCCACAGCC   20387    AA  TTG
                                TCA  GCG   TTACAGCC
                                |||  |||   ||||||||
                                GGT  CGC   GGTGTCGG
                                  CC   CAG
GAM1470 CMKLR1   5' CCAGAGCGCCGCAGC      19824    A     TTA
                                TCA AGCGTTG   CAGC
                                ||| |||||||   ||||
                                GGT TCGCGGC   GTCG
                                  C     ___
GAM1470 COL19A1  3' TCAAAGCATTATGC       12381          TACA
                                TCAAAGCGTTGT    GC
                                ||||||||||||    ||
                                AGTTTCGTAATA    CG
                                        _____
GAM1470 COL9A1   5' CCAAAGCGTCCAGGCC     38532         GTTA  _
                                TCAAAGCGTT    CAG CC
                                ||||||||||    ||| ||
                                GGTTTCGCAG    GTC GG
                                      _____   C
GAM1470 CROT     3' TCACAGCTCACTGCAGCC    34498    A   G TG  A
                                TCA AGC T  TT CAGCC
                                ||| ||| |  || |||||
                                AGT TCG A  GA GTCGG
                                  G   _ GT  C
GAM1470 DCT      3' CAAAGCGGAAACTACAGC    12557       TTG_
                                CAAAGCG    TTACAGC
                                |||||||    |||||||
                                GTTTCGC    GATGTCG
                                    CTTT
GAM1470 DLG5     3' CCAAAGCAAAGCAGCC      44451        TT TTA
                                TCAAAGCG  G   CAGCC
                                ||||||||  |   |||||
                                GGTTTCGT  C   GTCGG
                                     TT ___
GAM1470 DLST     3' TCAAACGTCAGCAGCC      12575      G    TTA
                                TCAAA CGTTG   CAGCC
                                ||||| |||||   |||||
                                AGTTT GCAGT   GTCGG
                                   _    C__
GAM1470 DMRT1    3' CAAATGTGTTACAGCC      34980      GC  T
                                CAAA  GT GTTACAGCC
                                ||||  || |||||||||
                                GTTT  CA CAATGTCGG
                                  A_  _
GAM1470 DUOX2    3' TCTAAGCATCACAGC       30450    A   GTT
                                TC AAGC   GTTACAGC
                                || ||||   ||||||||
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                                AG TTCG   TAGTGTCG
                                 A   ___
GAM1470  EDN1    5'  TCAAAGCGATCCTTCAGCC   12642        _  G  A
                                TCAAAGCG TT TT CAGCC
                                |||||||| || || |||||
                                AGTTTCGC AG AA GTCGG
                                     T  G  _
GAM1470  EIF3S2  3'  CAAAGCACTGGTAGCC     45464          TTAC
                                CAAAGCGTTG   AGCC
                                ||||||||||   ||||
                                GTTTCGTGAC   TCGG
                                      CA__
GAM1470  ENTPD6  3'  TCAAGCAGCACAGC       10342     A   TT  T
                                TCAA GCG  GT ACAGC
                                |||| |||  || |||||
                                AGTT CGT  CG TGTCG
                                  _   __  _
GAM1470  EPB72   3'  TCAGGTGGCAGTTACAGCC   19902     AAGC  T
                                TCA   GT GTTACAGCC
                                |||   || |||||||||
                                AGT   CG CAATGTCGG
                                  CCAC  T
GAM1470  EXTL1   5'  TCACAGCCTGGGTGCAGCC   20872     A   G   TTA_
                                TCA AGC TTG   CAGCC
                                ||| ||| |||   |||||
                                AGT TCG GAC   GTCGG
                                  G   _   CCAC
GAM1470  FRAT2   3'  TCAAGTTTCATACAGCC     28976     AGC   GT_
                                TCAA   GTT   TACAGCC
                                ||||   |||   |||||||
                                AGTT   CAA   ATGTCGG
                                   ___   AGT
GAM1470  FSTL1   3'  CCAGAGCACCATTTACAG    28214     A    TT   _
                                TCA AGCG  GTT ACAG
                                ||| ||||  ||| ||||
                                GGT TCGT  TAA TGTC
                                  C   GG   A
GAM1470  GATA2   3'  TCAAAGCAGGCACCAGC     13090        TT  TA
                                TCAAAGCG  GT  CAGC
                                ||||||||  ||  ||||
                                AGTTTCGT  CG  GTCG
                                     C_  TG
GAM1470  GPR61   3'  TCAAAGATCACAGC        44265       CGTT
                                TCAAAG   GTTACAGC
                                ||||||   ||||||||
                                AGTTTC   TAGTGTCG
                                   ____
GAM1470  HAS3    3'  TCAAACGTTGTGAGCC      39776      G     TAC
                                TCAAA CGTTGT   AGCC
                                ||||| ||||||   ||||
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                                AGTTT GCAACA  TCGG
                                  _    C__
GAM1470 HAS3    3' TCAAAACGCTGAGAACAGCC  39775        TT_
                                TCAAAGCGTTG  ACAGCC
                                ||||||||||  ||||||
                                AGTTTTGCGAC  TGTCGG
                                      TCT
GAM1470 KCNF1   5' TCACAGCGGGCAGCAGCC   13839    A   TT  TA
                                TCA AGCG  GT  CAGCC
                                ||| ||||  ||  |||||
                                AGT TCGC  CG  GTCGG
                                  G   C_  TC
GAM1470 KCNK3   3' TCAGGGCTCACTACAGCC   13913    AA  G TG
                                TCA  GC T  TTACAGCC
                                |||  || |  ||||||||
                                AGT  CG A  GATGTCGG
                                  CC  _ GT
GAM1470 KIAA0857 5' TCTGAGCGCCGCCGCAGC   42476   AA      TA
                                TC  AGCGTTGT  CAGC
                                ||  ||||||||  ||||
                                AG  TCGCGGCG  GTCG
                                 AC       GC
GAM1470 KIF3B   3' TCAGAAGTGCCACAATACAGC  22042    _  C  TG __
                                TCA AAG GT  T  TACAGC
                                ||| ||| ||  |  ||||||
                                AGT TTC CG  G  ATGTCG
                                  C   A  GT TT
GAM1470 LHX4    3' CCAAAGCACTGAGCAGCC   37850         TTA
                                TCAAAGCGTTG  CAGCC
                                ||||||||||  |||||
                                GGTTTCGTGAC  GTCGG
                                      TC_
GAM1470 LRRC2   3' CAAGGACGCTGCAGCC     35996    A_    TTA
                                CAA  GCGTTG  CAGCC
                                |||  ||||||  |||||
                                GTT  TGCGAC  GTCGG
                                  CC    ____
GAM1470 MN1     5' TCAGGACGCCGCCCGCAGCC  14591    AA      A_
                                TCA  GCGTTGTT  CAGCC
                                |||  ||||||||  |||||
                                AGT  TGCGGCGG  GTCGG
                                  CC       GC
GAM1470 MSL3L1  5' TCAGGCGAGCTACAGC     38595    AA  TT
                                TCA  GCG  GTTACAGC
                                |||  |||  ||||||||
                                AGT  CGC  CGATGTCG
                                  C_   T_
GAM1470 MYL3    3' TCACAGGTAAGCACAGCC   41906    A  C  TGT
                                TCA AG GT   TACAGCC
                                ||| || ||   |||||||
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                                AGT TC CA   GTGTCGG
                                  G  _  TTC
GAM1470  NLGN3    5'  TCCAAGCACCACAGC      33288    A    TTG
                                TC AAGCG   TTACAGC
                                || |||||   |||||||
                                AG TTCGT   GGTGTCG
                                 G    ___
GAM1470  PIGN     5'  CCAAAGGCTACAGC       29547       CGTT
                                TCAAAG    GTTACAGC
                                ||||||    ||||||||
                                GGTTTC    CGATGTCG
                                     ____
GAM1470  PMX1     5'  CAGAGCGTTGTGCACCAGCC  35504    A      TA__
                                CA AGCGTTGT    CAGCC
                                || ||||||||    |||||
                                GT TCGCAACA    GTCGG
                                 C       CGTG
GAM1470  PODXL    3'  TCAGAGCTACTACAGCC     23982     A   GTTG
                                TCA AGC    TTACAGCC
                                ||| |||    ||||||||
                                AGT TCG    GATGTCGG
                                  C   AT__
GAM1470  PTP4A2   3'  TCAGAGTAACGCTACAGCC   38641     A  CGT
                                TCA AG   TGTTACAGCC
                                ||| ||   ||||||||||
                                AGT TC   GCGATGTCGG
                                  C  ATT
GAM1470  RAB7L1   3'  TCGAAGCATCACAGCC      19437    A    GTT
                                TC AAGC   GTTACAGCC
                                || ||||   |||||||||
                                AG TTCG   TAGTGTCGG
                                 C   ___
GAM1470  RNMT     3'  TCAAGTCTCCACAGCC      19155     AGC   G
                                TCAA   GTT TTACAGCC
                                ||||   ||| ||||||||
                                AGTT   CAG GGTGTCGG
                                   ___   A
GAM1470  SIP      3'  TCATAGCTCACTGCAGCC    30845     A   G TG  A
                                TCA AGC T  TT CAGCC
                                ||| ||| |  || |||||
                                AGT TCG A  GA GTCGG
                                  A  _ GT  C
GAM1470  SLC7A5   3'  TCAGGGCTGTGCCACAGGCC  18555     AA  GT      _
                                TCA  GC  TGTTACAG CC
                                |||  ||  |||||||| ||
                                AGT  CG  ACGGTGTC GG
                                  CC  AC       C
GAM1470  THBD     5'  TCATACATGTTACAGCC     7429      AA    T
                                TCA  GCGT GTTACAGCC
                                |||  |||| |||||||||
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                                AGT  TGTA CAATGTCGG
                                  A_   _
GAM1470  TNFRSF8  3'  CCAAAGCGTGCAGAGCC     10315         T  TAC
                                TCAAAGCGT GT   AGCC
                                ||||||||| ||   ||||
                                GGTTTCGCA CG   TCGG
                                      _ TC_
GAM1470  TOP1     3'  TCAAAACAAATCATACAGC    17628        TTGT_
                                TCAAAGCG    TACAGC
                                ||||||||    ||||||
                                AGTTTTGT    ATGTCG
                                     TTAGT
GAM1470  UBE2B    3'  TCACAGCTCACTGCAGCC    17795     A   G TG  A
                                TCA AGC T  TT CAGCC
                                ||| ||| |  || |||||
                                AGT TCG A  GA GTCGG
                                  G  _ GT  C
GAM1470  WNT5A    3'  TCACAGCGGGGCCACAGCC   18137     A    TT
                                TCA AGCG  GTTACAGCC
                                ||| ||||  |||||||||
                                AGT TCGC  CGGTGTCGG
                                  G    CC
GAM1470  ZNF239   5'  TCACAGCTCCGCACAGC     24978     A  G    T
                                TCA AGC TTGT ACAGC
                                ||| ||| |||| |||||
                                AGT TCG GGCG TGTCG
                                  G   A   _
GAM1471  EYA1     3'  TTACATATAATACATTAGTG   7994           GGGG
                                TTACGTATAATATA    AGTG
                                ||||||||||||||   ||||
                                AATGTATATTATGT    TCAC
                                       AA__
GAM1471  FUS1     3'  TTACTGTAAGGGAGGGGGTG   28591     _   TAATAT    A
                                TTAC GTA     AGGGG GTG
                                |||| |||     ||||| |||
                                AATG CAT     TCCCC CAC
                                  A   TCCC__    _
GAM1471  WNT1     3'  CGTATGAACCGCGGGGAGTG   24080      _   ATA
                                CGTAT AAT   GGGGAGTG
                                ||||| |||   ||||||||
                                GCATA TTG   CCCCTCAC
                                   C   GCG
GAM1472  ACATN    3'  TGCCAACAATGTCAGACTA    21844        ___   A
                                TGTCAACA   TCA ACTA
                                ||||||||   ||| ||||
                                ACGGTTGT   AGT TGAT
                                     TAC   C
GAM1472  SH3BP4   3'  GATTTGCCAGTATCAGTCCT   30961         AC    AA_
                                GATTTGTCA  ATCA   CT
                                |||||||||  ||||   ||
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                                CTAAACGGT  TAGT   GA
                                     CA    CAG
GAM1473  C18orf1   3'  ATTATTTCTAGGGGCTTCCAA  41209          AATTA
                                ATTATTTCTA    TTCCAA
                                ||||||||||    ||||||
                                TAATAAAGAT    AAGGTT
                                     CCCCG
GAM1473  CYR61     3'  ATCATTTACAAATTATTCCA   11414        C
                                ATTATTT TAAATTATTCCA
                                ||||||| ||||||||||||
                                TAGTAAA GTTTAATAAGGT
                                    T
GAM1473  TLL2      3'  ATTATTTAAAAATTATTCCAA  29746        CT
                                ATTATTT  AAATTATTCCAA
                                |||||||  ||||||||||||
                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1473  ZNF215    3'  AATTATTTACCCTGTTATTCCA 29914         _  AAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
                                TTAATAAA GG   AATAAGGT
                                     T  GAC
GAM1473  BCAT1     3'  CCAGCTACAACATAAT      42378          TG
                                CCAGCTACGAT  ATAAT
                                ||||||||||  |||||
                                GGTCGATGTTG  TATTA
                                           __
GAM1473  KRTHA1    3'  TCCAGCCATGCAAATGAT    14016         __  T
                                TCCAGCTA  CGA TGAT
                                ||||||||  ||| ||||
                                AGGTCGGT  GTT ACTA
                                     AC   T
GAM1473  SAR1      3'  TCCAGCTATGTTTGCTAAT   33552         CGA  A
                                TCCAGCTA   TTG TAAT
                                ||||||||   ||| ||||
                                AGGTCGAT   AAC ATTA
                                     ACA   G
GAM1474  INHBB     5'  GGTGCCCGGGAGAGCCG     13565       G    TC   G
                                GGTGCC CGGGG  GAG CCG
                                |||||| |||||  ||| |||
                                CCACGG GCCCT  CTC GGC
                                          _    __   _
GAM1474  IRTA2     3'  GGTGCTGTGGCCAAAGGCTGG  36345      CGCGG    _  C
                                GGTGC    GGTCGA GGC GG
                                |||||    |||||| ||| ||
                                CCACG    CCGGTT CCG CC
                                   ACA__     T  A
GAM1474  TNFSF9    3'  TCGGGAGGTCGAGGC       19199      TGCCGC
                                TCGG     GGGGTCGAGGC
                                ||||     ||||||||||
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                                AGCC     CTCCAGCTCCG
                                   _______
GAM1475 AGTR1    3' TCAATTCTGAAAAGTAGC    28922    T      TCATG   C
                                TC ATTCTGAA    GAG AGC
                                || ||||||||    ||| |||
                                AG TAAGACTT    TTC TCG
                                 T      _____  A
GAM1475 PPP2R5E  3' TATCCTGAATCCTTTCCGGCT 26475          ATGGAGCA
                                TATTCTGAATC       GCT
                                ||||||||||        |||
                                ATAGGACTTAG       CGA
                                      GAAAGGC_
GAM1475 PRX      5' TCAGTTCTGCATGGAGCAGCT 34133    TA    AAT
                                TC  TTCTG   CATGGAGCAGCT
                                ||  |||||   ||||||||||||
                                AG  AAGAC   GTACCTCGTCGA
                                 TC    ___
GAM1475 SCN3A    3' TGCACAACTATCCCTATA    27955    A       AAAA
                                TG ACAACTATC    TATA
                                || |||||||||    ||||
                                AC TGTTGATAG    ATAT
                                 G       GG__
GAM1476 COPG2    3' TGATGCCACTAGCCTAAA    44350    T     A_
                                A ATGCCA  AGTTTAAA
                                | ||||||  ||||||||
                                A TACGGT  TCGGATTT
                                 C     GA
GAM1476 GCA      3' CATATGCCATTTCTAAA     29162         AAG
                                TATATGCCA   TTTAAA
                                |||||||||   ||||||
                                GTATACGGT   AGATTT
                                     AA_
GAM1476 PDK4     3' TATATGCCAGTTTAAA      15207         AA
                                TATATGCCA  GTTTAAA
                                |||||||||  |||||||
                                ATATACGGT  CAAATTT
                                           __
GAM1476 SMAC     5' CATACACCAAGTTTAAA     39893          A
                                TATATGCCAA GTTTAAA
                                |||||||||| |||||||
                                GTATGTGGTT CAAATTT
                                           _
GAM1476 HS3ST3A1 3' TGGTGTTGGTTATACATTAA  25810       GGTAA       C
                                TGGTGT    GTTATACA TAA
                                ||||||    |||||||| |||
                                ACCACA    CAATATGT ATT
                                   AC___       A
GAM1476 TGFBI    3' TGGTGCGGCCCATGTACATTAA 7415         AA  TA    C
             A                   TGGTGTGGT  GT  TACA TAAA
                                ||||||||| ||  |||| ||||
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                                ACCACGCCG  TA  ATGT ATTT
                                     GG  C_   A
GAM1477  BTK      3'  AGGGAATCAAAGAAGAGGT   6294        A        A
                                AGGGAA TCAAAGAAGA GT
                                |||||| |||||||||| ||
                                TCCCTT AGTTTCTTCT CA
                                   _        C
GAM1477  CA12     3'  AAGGAAATCAGAGGGAGA    10239         A  A_
                                AGGGAAATCA AG  AGA
                                |||||||||| ||  |||
                                TTCCTTTAGT TC  TCT
                                     C  CC
GAM1477  CARPX    3'  GAAATCAAAGAATGCAGT    33569           GA_
                                GAAATCAAAGAA   AGT
                                ||||||||||||   |||
                                CTTTAGTTTCTT   TCA
                                      ACG
GAM1477  CDC27    3'  AGGGAGATTAAAGAAAAA    10366       A  C
                                AGGGA AT AAAGAAGAA
                                ||||| || |||||||||
                                TCCCT TA TTTCTTTTT
                                   C  A
GAM1477  CYP8B1   3'  AGGGAAATCAGGAGGAGGAGT  20503          A_  A  A
                                AGGGAAATCA  AG AG AGT
                                ||||||||||  || || |||
                                TCCCTTTAGT  TC TC TCA
                                     CC  C  C
GAM1477  DEDD     3'  AGGGAAATAAAGGGGAAG    37425        C   AA
                                AGGGAAAT AAAG  GAAG
                                |||||||| ||||  ||||
                                TCCCTTTA TTTC  CTTC
                                   _   CC
GAM1477  ESRRG    3'  AGGGAGGTGAAAGAAGAAA   42443       AATC
                                AGGGA   AAAGAAGAAG
                                |||||   ||||||||||
                                TCCCT   TTTCTTCTTT
                                   CCAC
GAM1477  GRAF     3'  AGGGAAACAGAGAAGCCA    31434        CAA  A
                                AGGGAAAT   AGA GAAGTTA
                                ||||||||   ||| |||||||
                                TCCCTTTG   TCT CTTCGGT
                                     ___   _
GAM1477  IFNGR1   3'  AGGAAAATCAGACTTCAAAGTT 43542          AAGAA_
                                AGGGAAATCA     GAAGTT
                                ||||||||||     ||||||
                                TCCTTTTAGT     TTTCAA
                                     CTGAAG
GAM1477  LEP      3'  AGGGAAATTGACAGAGTC    6908         CAAAGA  A
                                AGGGAAAT     AGA GTT
                                ||||||||     ||| |||
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                                TCCCTTTA     TCT CAG
                                     ACTG__  _
GAM1477  MYCL2    3'  AGGGAGATCAAAAAGAAA    23896      A      A
                                AGGGA ATCAAAGA GAAG
                                ||||| |||||||| ||||
                                TCCCT TAGTTTTT CTTT
                                   C      _
GAM1477  MYO10    3'  GGGAAATCAGGTTGGGAGGTTA 29574         AAGAA_  A
                                GGGAAATCA     GA GTTA
                                |||||||||     || ||||
                                CCCTTTAGT     CT CAAT
                                      CCAACC  C
GAM1477  PBX3     3'  AGGGAAACAAAGAGTTAA    26212       T     AGAA
                                AGGGAAA CAAAGA   GTTAA
                                ||||||| ||||||   |||||
                                TCCCTTT GTTTCT   CAATT
                                   _    ____
GAM1477  PCDHA11  5'  AGGGAACTCAAAGAAAAAAT  36574      A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1477  PCDHA11  5'  AGGGAACTCAAAGAAAAAAT  36574      A
                                AGGGAA TCAAAGAAGAAGT
                                |||||| ||||||||||||
                                TCCCTT AGTTTCTTTTTTA
                                   G
GAM1477  PFKFB2   3'  GGGCATAGAGGGAGGAAGTTAA 26307    AAATCAAA  A
            T                    GGG       GA GAAGTTAAT
                                |||       || |||||||||
                                CCC       CT CTTCAATTA
                                  GTATCTCC  C
GAM1477  PIK3R3   3'  AGGAAGGACAGAAGGGGTTA  41434     ATCAA    AA
                                GGGAA    AGAAG  GTTA
                                |||||    |||||  ||||
                                TCCTT    TCTTC  CAAT
                                   CCTG_    CC
GAM1477  POU3F1   3'  AGGGAAATATAAGGGGAAA   40370      CA   AA
                                AGGGAAAT  AAG  GAAG
                                ||||||||  |||  ||||
                                TCCCTTTA  TTC  CTTT
                                     TA   CC
GAM1477  RARRES3  3'  AGGGAAACAGAGGAAA     42842      CAA   A
                                AGGGAAAT   AGA GAAG
                                ||||||||   ||| ||||
                                TCCCTTTG   TCT CTTT
                                     ___   C
GAM1477  SIRT3    3'  CACTCAGTTCACATATTC    29257       TT_
                                CACTCGGTTT   TATTC
                                ||||||||||   |||||
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                                GTGAGTCAAG  ATAAG
                                     TGT
GAM1478 ACE     3' TCTCTGGTGGGAGGCCC    8983      C  CCTC
                                TCTCT GGT   GGGGCCC
                                ||||| |||   |||||||
                                AGAGA CCA   CTCCGGG
                                  _  CC__
GAM1478 AK3     5' TCTCGGCCCCCTGGGGCC   30185        _____ GGC
                                TCTCGGTCCTC   GG  C
                                ||||||||||    ||  |
                                AGAGCCGGGGG   CC  G
                                      AIIIC CGG
GAM1478 ALAS1   5' TCTCCTGGTCCCCACATCCC 8663     TC      GGG
                                TCTC  GGTCCTCG  CCC
                                ||||  ||||||||  |||
                                AGAG  CCAGGGGT  GGG
                                  GA      GTA
GAM1478 AP1B1   3' TCTCTCGGCCCAGTCTTGGGGC 10042        TC_______ GGCC
             C                   TCTCTCGGTCC       GG  C
                                 ||||||||||        ||  |
                                 AGAGAGCCGGG       CC  G
                                       TCAGAAIII  CCGG
GAM1478 ASC     5' CCTCTGGATTGGGGCCCC   29941     C  TCCTC
                                TCTCT GG    GGGGCCCC
                                ||||| ||    ||||||||
                                GGAGA CC    CCCCGGGG
                                  _ TAA__
GAM1478 AXIN2   5' TCTCTCTGTCTCTCTGGGGCC  21640      G  _  _____ GGC
                                TCTCTC GTC CTC    GG  C
                                |||||| ||| |||    ||  |
                                AGAGAG CAG GAG    CC  G
                                   A  A  AIIIC  CGG
GAM1478 BCL11B  3' TCTCTCGGTTGGCAACGGTTCC 39756       CCT___  GG
                                TCTCTCGGT     CGG  CC
                                |||||||||     |||  ||
                                AGAGAGCCA     GCC  GG
                                     ACCGTT   AA
GAM1478 CDKN2B  5' TCTGCGGCTTGGGGCCCC   38553    _   CCTC
                                TCT CGGT    GGGGCCCC
                                ||| ||||    ||||||||
                                AGA GCCG    CCCCGGGG
                                  C    AA__
GAM1478 CFTR    5' TCTCTCGGGCGCTGGGGTCCC  7957       TC_  C   _
                                TCTCTCGG   CT GGGG CCC
                                ||||||||   || |||| |||
                                AGAGAGCC   GA CCCC GGG
                                     CGC  _   A
GAM1478 CLDN5   3' TCTTCCGGTGGGGGCCCC   17611    CT   CCTC
                                TCT  CGGT   GGGGCCCC
                                |||  ||||   ||||||||
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```
                                AGA  GCCA   CCCCGGGG
                                  AG   C___
GAM1478  CNN2     3'  TCTCACGGAGCAGGGCCCC   20406     T   TCCT
                                TCTC CGG   CGGGGCCCC
                                |||| |||   |||||||||
                                AGAG GCC   GTCCCGGGG
                                  T  TC__
GAM1478  COL4A2   5'  CCTTTCGGTCCTCGGCC     12313     C       GG
                                TCT TCGGTCCTC  GGCC
                                ||| |||||||||  ||||
                                GGA AGCCAGGAG  CCGG
                                  A       __
GAM1478  CPNE6    5'  CTCTCGGTCGGGGGCTCC    25734         CTC    _
                                CTCTCGGTC   GGGGC CC
                                |||||||||   ||||| ||
                                GAGAGCCAG   CCCCG GG
                                      C__     A
GAM1478  CYP7B1   5'  TCTCTCGGCGGCGCCC      22077        TCCT   G
                                TCTCTCGG    CGG GCCC
                                ||||||||    ||| ||||
                                AGAGAGCC    GCC CGGG
                                     _____   G
GAM1478  DNASE1   5'  TCTCTTGTCTGGGGGCCCC   23357      CG   CTC
                                TCTCT  GTC   GGGGCCCC
                                |||||  |||   ||||||||
                                AGAGA  CAG   CCCCGGGG
                                   A_   AC_
GAM1478  DVL1     3'  TCTCTCGTCTTCCGGTCCC   40417       G  C  G  G
                                TCTCTCG TC TC GG CCC
                                ||||||| || || || |||
                                AGAGAGC AG AG CC GGG
                                     _  A  G  A
GAM1478  EDG8     3'  TCTCTGGTTTTCAACC      44209      C   CC   GG
                                TCTCT GGT  TCG  GCC
                                ||||| |||  |||  |||
                                AGAGA CCA  AGT  TGG
                                   _   AA   __
GAM1478  EDN3     3'  TCTCTCTACGGGGCCC      6484        GGTCCT
                                TCTCTC     CGGGGCCC
                                ||||||     ||||||||
                                AGAGAG     GCCCCGGG
                                   AT_____
GAM1478  EPHA2    5'  CTCTCGGTCCGATCCC      20734         TCG GG
                                CTCTCGGTCC   G  CCC
                                ||||||||||   |  |||
                                GAGAGCCAGG   C  GGG
                                      ___ TA
GAM1478  EYA2     3'  TCGTCTCGGCTGTGGGGCCCC  23487    _      CCTC
                                TC TCTCGGT    GGGGCCCC
                                || |||||||    ||||||||
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                                AG AGAGCCG   CCCCGGGG
                                 C      ACA_
GAM1478  FGFR2    5'  CTGCGGCCTCGGGGCCCC    35662    _  T
                                CT CGG CCTCGGGGCCCC
                                || ||| ||||||||||||
                                GA GCC GGAGCCCCGGGG
                                 C  _
GAM1478  FSTL3    3'  CCTTGGTGAGGCAGGGCCCC  25218    C  CCT_
                                TCT GGT   CGGGGCCCC
                                ||| |||   |||||||||
                                GGA CCA   GTCCCGGGG
                                  A  CTCC
GAM1478  FUT3     3'  CTCCCGGGTGGGGCCCC     6639       TCCTC
                                CTCTCGG    GGGGCCCC
                                |||||||    ||||||||
                                GAGGGCC    CCCCGGGG
                                    CA___
GAM1478  GAB2     3'  TCTGTCGTATGGGGCCCC    38685    C  GTCCTC
                                TCT TCG     GGGGCCCC
                                ||| |||     ||||||||
                                AGA AGC     CCCCGGGG
                                  C  ATA___
GAM1478  GARP     3'  TCTTCCGGTCCTAAGC      24318    CT     CG
                                TCT  CGGTCCT  GGGC
                                |||  |||||||  ||||
                                AGA  GCCAGGA  TTCG
                                  AG     __
GAM1478  GNPAT    5'  TCTTTCGCTCAGGACGGCCC  30624    C  GTC     __
                                TCT TCG  CTCGGGGC  CCC
                                ||| |||  ||||||||  |||
                                AGA AGC  GAGTCCTG  GGG
                                  A  ___      CC
GAM1478  GPC1     5'  TCTCTCGGATCCTGGCCGGGTC 13259       _  ___  G
              C                  TCTCTCGG TCCT  CGGG CC
                                |||||||| ||||  |||| ||
                                AGAGAGCC AGGA  GCCC GG
                                    T   CCG   A
GAM1478  GPC1     3'  CCTCAGCCCTCGGGGTCC    13239          _
                                TCTCGGTCCTCGGGG CC
                                |||||||||||||| ||
                                GGAGTCGGGAGCCCC GG
                                         A
GAM1478  GRIK1    5'  CTGAGCTCTCTCGGGGCTCC  9093    C _ _     _
                                CT GG TC CTCGGGGC CC
                                || || || |||||||| ||
                                GA TC AG GAGCCCCG GG
                                 C  G  A      A
GAM1478  HDAC5    3'  TCACTCGGGGGGCCC      40173    T   TCCTC
                                TC CTCGG    GGGGCCC
                                || |||||    |||||||
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                                AG GAGCC    CCCCGGG
                                 T   _____
GAM1478 HSPG2   5' TCTCTCGCTCGCTCGCTCC  24369       G _   GGG
                                TCTCTCG TC CTCG  CC
                                ||||||| || ||||  ||
                                AGAGAGC AG GAGC  GG
                                    G  C   GA_
GAM1478 ITGBL1  3' TCTCAGTCTGAGCCC     21988       CTCG
                                TCTCGGTC   GGGCCC
                                ||||||||   ||||||
                                AGAGTCAG   CTCGGG
                                    A___
GAM1478 ITPKB   3' TCTCCGGTGGGGAGGCCCC  13657     T   CCTC
                                TCTC CGGT   GGGGCCCC
                                |||| ||||   ||||||||
                                AGAG GCCA   CTCCGGGG
                                  _   CCC_
GAM1478 JRK     3' CTCTCCGTGGGGCCC     44498      G  CCTC
                                CTCTC GT   GGGGCCC
                                ||||| ||   |||||||
                                GAGAG CA   CCCCGGG
                                  G  _____
GAM1478 LFG     5' TCTCTCGGGGAAGGGGTCCC  44151       TCCTC   _
                                TCTCTCGG    GGGG CCC
                                ||||||||    |||| |||
                                AGAGAGCC    CCCC GGG
                                    CCTT_   A
GAM1478 MADH6   5' TCTCTCGGCTCAGCTCC    24607       TC    GG
                                TCTCTCGG  CTCGG  CC
                                ||||||||  |||||  ||
                                AGAGAGCC  GAGTC  GG
                                    __    GA
GAM1478 MAP3K11  5' TCCCTCGGTTCTGGAGCAGTCC 14536        C  C    ___
                                TCTCTCGGT CT GGGGC   CC
                                ||||||||| || |||||   ||
                                AGGGAGCCA GA CCTCG   GG
                                    A  _    TCA
GAM1478 MATK    3' TCTCTCGGTCCTCTGGGGCC  40316          _____ GGC
                                TCTCTCGGTCCTC    GG   C
                                ||||||||||||    ||   |
                                AGAGAGCCAGGAG    CC   G
                                      AIIIC  CGG
GAM1478 MBD3    3' CTCTCGGCAGGGCC      19417       CCTC
                                CTCTCGGT   GGGGCC
                                ||||||||   ||||||
                                GAGAGCCG   TCCCGG
                                    _____
GAM1478 MTL5    3' TCTCCCGGGGGGCC      22273       TCCTC
                                TCTCTCGG    GGGGCC
                                ||||||||    ||||||
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                                AGAGGGCC    CCCCGG
                                        _____
GAM1478 OCLN    5' CTCTCGGTTCCTGCCGCC    14902       _  CGGG  _
                                CTCTCGGT CCT   GCC CC
                                |||||||| |||   ||| ||
                                GAGAGCCA GGA   CGG GG
                                     A  ____  C
GAM1478 P53AIP1  3' TCACCACAGCTCGGGGC    35236   _ T  TC
                                TC TC CGG  CTCGGGGC
                                || || |||  ||||||||
                                AG GG GTC  GAGCCCCG
                                 T  T  __
GAM1478 PAFAH1B2 5' TCGCTCGGTCCCGTCGGTCCC 15075   T     __   GG
                                TC CTCGGTCC  TCGG  CCC
                                || ||||||||  ||||  |||
                                AG GAGCCAGG  AGCC  GGG
                                 C       GC   A_
GAM1478 PAK1    5' TCTCTCGGCTCCTCGG     15086        _  C___
                                TCTCTCGGT CCT   GG
                                |||||||| |||   ||
                                AGAGAGCCG GGA   CC
                                     A  GIII
GAM1478 PCSK5   5' TCGCTCCTCCCGGGGCCCC   26237    G   __
                                TCG TCCTC  GGGGCCCC
                                ||| |||||  ||||||||
                                AGC AGGAG  CCCCGGGG
                                  G    GG
GAM1478 PKNOX1   3' TCTCTCGGTTCATCTTGGGGCC 21313        _ C C_____  GGCC
                                TCTCTCGGT C T    GG   C
                                |||||||| | |    ||   |
                                AGAGAGCCA G A    CC   G
                                     A T GAAIII  CCGG
GAM1478 PLXNA1   3' TCTCTGCGACCCGGGGCCCC  43629     _  T  T
                                TCTCT CGG CC CGGGGCCCC
                                ||||| ||| || |||||||||
                                AGAGA GCT GG GCCCCGGGG
                                   C  _ _
GAM1478 POLG    5' CCTCGGTCCTCACGGTGC    15443         _ _
                                TCTCGGTCCTCG GG GC
                                |||||||||||| || ||
                                GGAGCCAGGAGT CC CG
                                       G  A
GAM1478 POMC    5' TCTCTCGGTCGCGGC      9605         CTC G
                                TCTCTCGGTC   G GGC
                                ||||||||||   | |||
                                AGAGAGCCAG   C CCG
                                     ___ G
GAM1478 RANBP3   3' TCTCTCGGGAGGGCC      28767        TCCTC
                                TCTCTCGG    GGGGCC
                                ||||||||    ||||||
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                                AGAGAGCC    TCCCGG
                                    C____
GAM1478  RBM3    5'  TCTCCCGGTCCTTGAC     43259          CGG
                                TCTCTCGGTCCT   GGC
                                ||||||||||||  |||
                                AGAGGGCCAGGA  CTG
                                      A__
GAM1478  RRM2B   5'  TCCCCCGCCTCGGGGCTCC   42725       GT      _
                                TCTCTCG  CCTCGGGGC CC
                                |||||||  ||||||||| ||
                                AGGGGGC  GGAGCCCCG GG
                                   __       A
GAM1478  RRM2B   3'  TCTCAGTCCATAAGCCC     42726        TCG
                                TCTCGGTCC   GGGCCC
                                |||||||||   ||||||
                                AGAGTCAGG   TTCGGG
                                     TA_
GAM1478  SLC21A9 3'  CTCTTGGCCAGGTGGGGCCCC 28563     C   CTC_
                                CTCT GGTC    GGGGCCCC
                                |||| ||||    ||||||||
                                GAGA CCGG    CCCCGGGG
                                  A   TCCA
GAM1478  SOX4    3'  TCTCTCAGTCCCGGCGTTCC   16993         T   GG__
                                TCTCTCGGTCC CGG    CC
                                ||||||||||| |||    ||
                                AGAGAGTCAGG GCC    GG
                                      _  GCAA
GAM1478  SYN3    3'  TCTTGGCCTCAGGACCCC    39496     C  T
                                TCT GG CCTCGGGGCCCC
                                ||| || ||||||||||||
                                AGA CC GGAGTCCTGGGG
                                  A  _
GAM1478  TBX3    3'  TCTCTCGAGGGAGTCCGGGGCC 32439       _____   TC
            CC                    TCTCTCG    GTCC  GGGGCCCC
                                |||||||    ||||  ||||||||
                                AGAGAGC    CAGG  CCCCGGGG
                                    TCCCT   __
GAM1478  TEM5    3'  TCCCTCGGTTTCCATTTGGTCC 37246       __  TCGG  _
                                TCTCTCGG  TCC    GG CC
                                ||||||||  |||    || ||
                                AGGGAGCC  AGG    CC GG
                                     AA   TAAA  A
GAM1478  TEM6    3'  CCTCTCGGTCCTCACAGGC    35554          _
                                TCTCTCGGTCCTCG GGGC
                                |||||||||||||| ||||
                                GGAGAGCCAGGAGT TCCG
                                       G
GAM1478  THBD    5'  TCTCTTGGTCCTCCTGGGGC   7432       C      GG____ GCC
                                TCTCT GGTCCTC     G   C
                                ||||| |||||||     |   |
```

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                                AGAGA CCAGGAG     C   G
                                  A      GAIIIC CCG
GAM1478  TOP3B    5'  TCTCGGTCCTTCACACTCC    19467          _  GG  _
                                TCTCGGTCCT CG  GC CC
                                |||||||||| ||  || ||
                                AGAGCCAGGA GT  TG GG
                                     A  G_  A
GAM1478  TRPM2    5'  TCCCTTGGCTGGGGCCCC    17695      C   CCTC
                                TCTCT GGT    GGGGCCCC
                                ||||| |||    ||||||||
                                AGGGA CCG    CCCCGGGG
                                  A  A___
GAM1478  VANGL2   5'  CCTCTTGGGGGGCCC       43455      C  TCCTC
                                TCTCT GG     GGGGCCC
                                ||||| ||     |||||||
                                GGAGA CC     CCCCGGG
                                  A  _____
GAM1479  ABCD1    3'  CTCGGCTGCGCTGCTGTGTGGC 6196       CCCA       CACTC
                                CTCG   CGCTGCTG    GGC
                                ||||   ||||||||    |||
                                GAGC   GCGACGAC    CCG
                                  CGAC       ACA__
GAM1479  ADRBK1   5'  GCTCGCGCGGCGCTCGGC    11532    CCA   T  T  A
                                GC   CGC GC GC CTCGGC
                                ||   ||| || || ||||||
                                CG   GCG CG CG GAGCCG
                                 A__   _  C  C
GAM1479  ATP6V0A4 5'  CTCGGTCTGCAGCAGGCACTCG 39288      CCCAC  T  T_
           GC                   CTCG    GC GC  GCACTCGGC
                                ||||    || ||  |||||||||
                                GAGC    CG CG  CGTGAGCCG
                                  CAGA_  T  TC
GAM1479  CDKN2B   5'  CTTTCCCACGCTGCTCCGG    38545    CG         GCAC
                                CT  CCCACGCTGCT    TCGG
                                ||  ||||||||||    ||||
                                GA  GGGTGCGACGA    GGCC
                                 AA          ____
GAM1479  COL4A3   5'  CTCGCCTCGCCACTCG      36378       CA   TGCTG
                                CTCGCC  CGC    CACTCG
                                ||||||  |||    ||||||
                                GAGCGG  GCG    GTGAGC
                                   A_  _____
GAM1479  HOXA3    3'  TCTTCCGTGCACAGCACTCGGC 36199    GC  AC  T  T
                                TC  CC  GC GC GCACTCGGC
                                ||  ||  || || |||||||||
                                AG  GG  CG TG CGTGAGCCG
                                 AA  CA  _  T
GAM1479  MET      5'  CTCGCGCCCTCCACTCGGC   43413      CCAC   G  G
                                CTCGC    GCT CT CACTCGGC
                                |||||    ||| || ||||||||
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                                GAGCG    CGG GA GTGAGCCG
                                  _____  _ G
GAM1479  PTEN     5'  CTCGCTCTGCCGCCGCTTGGC  7209       CCAC       ACTC
                                CTCGC    GCTGCTGC    GGC
                                |||||    ||||||||    |||
                                GAGCG    CGGCGGCG    CCG
                                  AGA_       AA__
GAM1479  VLGR1    5'  GCCCGCGCTGCTGATTC     37011      A       CAC
                                GCCC CGCTGCTG   TC
                                |||| ||||||||   ||
                                CGGG GCGACGAC   AG
                                  C       TA_
GAM1479  AP1B1    5'  GCGGCTCGGAGCCCCGCGGC   10038    T         AA   C
                                GC GGCTCGGAGCC  GTG GC
                                || ||||||||||  ||| ||
                                CG CCGAGCCTCGG  CGC CG
                                 _         GG   _
GAM1479  AQP6     5'  GCTAGCTCGGGGCTGAGTCTCC 38249          A  CA   GCG
                                GCTGGCTCGG GC  AGT   CC
                                |||||||||| ||  |||   ||
                                CGATCGAGCC CG  TCA   GG
                                      C  AC   GA_
GAM1479  BCL7A    3'  TGGCTCAGAGTCAGAACAGCC  34224          CCA  T  _
                                TGGCTCGGAG   AG GC GCC
                                ||||||||||   || || |||
                                ACCGAGTCTC   TC TG CGG
                                      AG_  T  T
GAM1479  CAV1     5'  TGGCCCGGACGTGTGC      11999         G CAA
                                TGGCTCGGA C   GTGC
                                |||||||||  |   ||||
                                ACCGGGCCT G   CACG
                                      _ CA_
GAM1479  COPG2    3'  GCTGGCTCAGGGCCAAATG   44349          A
                                GCTGGCTCGG GCCAAGTG
                                |||||||||| ||||||||
                                CGACCGAGTC CGGTTTAC
                                      C
GAM1479  CPSF4    3'  GCTGCTCGGAGCTGGCTCCA   27440      G       CAAGT  G
                                GCTG CTCGGAGC    GC CCG
                                ||||  ||||||||    || |||
                                CGAC GAGCCTCG    CG GGT
                                  _       AC___  A
GAM1479  FOXI1    5'  GCTGGCCGGAGCCACCTG    29153       T       AG
                                GCTGGC CGGAGCCA  TG
                                ||||||  ||||||||  ||
                                CGACCG GCCTCGGT  AC
                                   _       GG
GAM1479  GRIN2C   3'  GCTGGCTCGGAGCCTGAGTGGC 9125             A_   C
                                GCTGGCTCGGAGCC  AGTG GC
                                ||||||||||||||  |||| ||
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                                CGACCGAGCCTCGG  TCAC CG
                                       AC   _
GAM1479 IMMP2L   5' AGCTCCGGGCCAGGTGTGCCG 37180      _ A   A  C
                                GGCTC GG GCCA GTG GCCG
                                ||||| || |||| ||| ||||
                                TCGAG CC CGGT CAC CGGC
                                   G _   C  A
GAM1479 MEST     5' GCGGCTCGGGGCTAGAGCGTCG 43081    T     A CA T  C
                                GC GGCTCGG GC  AG GCG CG
                                || ||||||| ||  || ||| ||
                                CG CCGAGCC CG  TC CGC GC
                                 _     C A_ T  A
GAM1479 NR2F2    5' TGGTTTCGGGGGGCTTTGCGCC 34242    C_   A__ CAAG
             G                   TGG  TCGG  GC   TGCGCCG
                                ||| ||||  ||   |||||||
                                ACC  AGCC  CG   ACGCGGC
                                  AA   CCC  AA__
GAM1479 PPP1R14B 5' GCTGGCTCGGGTTAGCTCGCCG 39795         AGCCA  G
                                GCTGGCTCGG    AGT CGCCG
                                ||||||||||    ||| |||||
                                CGACCGAGCC    TCG GCGGC
                                      CAA__  A
GAM1479 PPP3R1   5' GCTGGCTCGGAGAAGTG    44079          CC
                                GCTGGCTCGGAG  AAGTG
                                ||||||||||||  |||||
                                CGACCGAGCCTC  TTCAC
                                          __
GAM1479 RNPEPL1  5' GCGGGCTCGGAGCCGGGCG   32883    T       AAGT
                                GC GGCTCGGAGCC   GCG
                                || ||||||||||   |||
                                CG CCGAGCCTCGG   CGC
                                 C        CC__
GAM1480 PTPN2    3' GCAATATATAGTAGAAA     15913        T  TA
                                GCAATATGT AGT  AAA
                                ||||||||| |||  |||
                                CGTTATATA TCA  TTT
                                      _  TC
GAM1481 AVPR1A   5' AGAACGTTTCAGTATTGT    8722         C  AG_
                                AGAACGTT CAG   TGT
                                |||||||| |||   |||
                                TCTTGCAA GTC   ACA
                                    A  ATA
GAM1481 NKX2H    3' GAGAGCGTTCCAGGCGT     30758     A      A
                                GAGA CGTTCCAG GTGT
                                |||| |||||||| ||||
                                CTCT GCAAGGTC CGCA
                                  C      _
GAM1481 SRD5A2   5' TGAGAGTTTGCAATGTCTAT  40458      AC  CCAG
                                TGAGA  GTT   AGTGTCTAT
                                |||||  |||   |||||||||
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                                ACTCT  CAA    TTACAGATA
                                  __   ACG_
GAM1481  STAU     5'  GAGGGCGTTCCAGGAACAATGT 32695     AA       ____
                                GAG  CGTTCCAG    AGTGT
                                |||  ||||||||    |||||
                                CTC  GCAAGGTC    TTACA
                                  CC       CTTG
GAM1481  UTY      5'  AGAAAATGGAGTGTCT      28308      C  TCCA
                                AGAA GT    GAGTGTCT
                                ||||  ||    ||||||||
                                TCTT TA    CTCACAGA
                                  T  C___
GAM1482  ADAMTS5  3'  TAATTCTTTTATATTAAAAACA 28183             CAT
                                TAATTCTTTTGTATT   AGACA
                                ||||||||||||||   |||||
                                ATTAAGAAAATATAA   TTTGT
                                         TT_
GAM1482  BPHL     5'  ATTCTTTTGCACATTAAG    20258           TCAT
                                ATTCTTTTGTAT    AG
                                ||||||||||||    ||
                                TAAGAAAACGTG    TC
                                       TAAT
GAM1482  CTSH     3'  TCTTTGCGTCATAGACAC    20500       T  AT
                                TCTTT GT  TCATAGACAC
                                |||||  ||  ||||||||||
                                AGAAA CG  AGTATCTGTG
                                  _  C_
GAM1482  DMD      3'  TAACTTTTTTGTACAATTGCAT 19690       C       T_____
              AGAC                   TAATT TTTTGTAT     CATAGAC
                                |||||  ||||||||     |||||||
                                ATTGA AAAACATG     GTATCTG
                                   A       TTAAC
GAM1482  MTMR8    3'  TAATTTTTTGTATTTTTAGTAG 31754       C       CA___
              ACA                    TAATT TTTTGTATT     TAGACA
                                |||||  |||||||||     ||||||
                                ATTAA AAAACATAA     ATCTGT
                                  _        AAATC
GAM1482  NOS1     3'  TTCTGTATAGCAAGACAC    8383          TCAT
                                TTTTGTAT    AGACAC
                                ||||||||    ||||||
                                AAGACATA    TCTGTG
                                     TCGT
GAM1482  SHANK2   3'  TTCTTTGCCAATAGACAC    29477       T  ATTC
                                TTCTTT GT    ATAGACAC
                                ||||||  ||   ||||||||
                                AAGAAA CG    TATCTGTG
                                   _ GT__
GAM1483  GNAO1    3'  TCGGTGCAGATGGGTA      44942       A  CCGT
                                TCGGTG CG    GTGGGTA
                                ||||||  ||   |||||||
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                                AGCCAC GT    TACCCAT
                                   _ C___
GAM1483 C10orf2  3' TGGAAAAGGCTCTATAAAATGT 34827        ACC   CACC__
            CCTG                  TGGAAAGG   CTA     GTCCTG
                                  ||||||||   |||     ||||||
                                  ACCTTTTC   GAT     CAGGAC
                                     CGA   ATTTTA
GAM1483 CFTR     3' TGGAAAGAAGGGCTGTCCT    7958         CC_  ACACC
                                  TGGAAAGGA   CT    GTCCT
                                  |||||||||   ||    |||||
                                  ACCTTTCTT   GA    CAGGA
                                       CCC  _____
GAM1483 CTBP1    3' GGGAAGGATTCATTGTCCTG   42750    A    CCCTA  CC
                                  GG AAGGA    CA  GTCCTG
                                  || |||||    ||  ||||||
                                  CC TTCCT    GT  CAGGAC
                                   C    AA___  AA
GAM1483 HAX1     3' TGGAAAGGACTTGAAGGCCTCT 25936         CCTACACC  _
            G                      TGGAAAGGAC       GTC CTG
                                   ||||||||||       ||| |||
                                   ACCTTTCCTG       CGG GAC
                                        AACTTC__   A
GAM1483 KIT      3' TGGAAAGGACTCTGGCCC    6900          C  ACACC
                                  TGGAAAGGAC CT    GTCC
                                  |||||||||| ||    ||||
                                  ACCTTTCCTG GA    CGGG
                                       A  C_____
GAM1483 LY6E     5' TGGAGAGGATGGCCGTCCTG   14282     A   CCCTACA
                                  TGGA AGGA      CCGTCCTG
                                  |||| ||||      ||||||||
                                  ACCT TCCT      GGCAGGAC
                                    C   ACC_____
GAM1483 RGS16    3' TGGAAAGGGCTCACAGGCC   16329       ACC  A   C_
                                  TGGAAAGG   CT CAC  GTC
                                  ||||||||   || |||  |||
                                  ACCTTTCC   GA GTG  CGG
                                       C__  _   TC
GAM1483 RHBG     3' TGGAAAGGGGCCTCCTTCT   33823       AC   ACA  GTC
                                  TGGAAAGG  CCT   CC   CT
                                  ||||||||  |||   ||   ||
                                  ACCTTTCC  GGA   GG   GA
                                       CC   ___  AA_
GAM1484 CAT      3' TAGAAAAATAAAAATTTCTGA  11987        AAC  TT
                                  TAGAAAGA   GA  ATTTCTGA
                                  ||||||||   ||  ||||||||
                                  ATCTTTTT   TT  TAAAGACT
                                       A__  TT
GAM1484 FGA      3' TAGAAAGAAATTGGTTACTCCT 8006          CGA_
                                  TAGAAAGAAA    TTATTTCT
                                  ||||||||||    ||||||||
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                                ATCTTTCTTT   AATGAGGA
                                     AACC
GAM1484  GAS1    3'  TAAAAATAAATTATTTCTGAA  13073      GAAAC
                                TAGAAA    GATTATTTCTGAA
                                ||||||    ||||||||||||
                                ATTTTT    TTAATAAAGACTT
                                   AT___
GAM1484  ICMT    3'  TAGAAATAAGTCATATTTCTGA 29659      GAAACGAT
                                TAGAAA      TATTTCTGA
                                ||||||      |||||||||
                                ATCTTT      ATAAAGACT
                                   ATTCAGT_
GAM1484  MEL     3'  TAGAAAGAACGTCCGA     23871        A  ATTATT
                                TAGAAAGAA CG     TCTGA
                                ||||||||| ||     |||||
                                ATCTTTCTT GC     AGGCT
                                    _ _______
GAM1484  NDUFA10  3'  GAAACACTTTTATTTCTG    21232      A__
                                GAAACG   TTATTTCTG
                                ||||||   |||||||||
                                CTTTGT   AATAAAGAC
                                   GAA
GAM1484  TES     3'  GAAAGAAACTTTATTTTGA   43538        GA     C
                                GAAAGAAAC  TTATTT TGA
                                |||||||||  |||||| |||
                                CTTTCTTTG  AATAAA ACT
                                     A_     _
GAM1485  DPYSL2   3'  GTGATGGAATGACCTACT    10755        CA
                                GTGATGGGG  GCCTACT
                                |||||||||  |||||||
                                CACTACCTT  TGGATGA
                                     AC
GAM1485  IKBKB    3'  GTCACGCGGCCTGCTCC     41811    G   G   AGC  A
                                GT ATG GGC   CT CTCC
                                || ||| |||   || ||||
                                CA TGC CCG   GA GAGG
                                  G   G   ___  C
GAM1485  MME     3'  TGTGATGGTGCCCTCTC     28607        GGCA    A
                                TGTGATGG    GCCT CTC
                                ||||||||    |||| |||
                                ACACTACC    CGGG GAG
                                     A___    A
GAM1485  MSL3L1   3'  CTGTGATGGGGTGACACAATC  38585          CA  C  C
                                CTGTGATGGGG  GC TA TC
                                ||||||||||  || || ||
                                GACACTACCCC  TG GT AG
                                      AC  T  T
GAM1485  PIK3R1   3'  ACTGGGGTGGGGAAGCTTATTC 42858      TGA    C   C  C
                                ACTG   TGGGG AGC TA TC
                                ||||   ||||| ||| || ||
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                                TGAC   ACCCC TCG AT AG
                                  CCC    T   A  A
GAM1485  PML     3'  CTGTGATGGGTGGGGCCT    37726          GCA_
                                CTGTGATGGG    GCCT
                                ||||||||||    ||||
                                GACACTACCC    CGGA
                                      ACCC
GAM1485  USP6    5'  CTGTGATGGTCTATTCC     45030         GGCAGC   C
                                CTGTGATGG     CTA TCC
                                |||||||||     ||| |||
                                GACACTACC     GAT AGG
                                      A_____   A
GAM1485  ATRN    3'  TCCCCAGGCTGTGTGCAGGGAT 40282          ___     AA
            GGCAG                   TCCCCGGGTT   TGCAG  ATGGCAG
                                ||||||||||   |||||  |||||||
                                AGGGGTCCGA   ACGTC  TACCGTC
                                      CAC    CC
GAM1485  CDH13   3'  CGGGTTTGCAAACAACGG    10368           _
                                CGGGTTTGCAGA AATGG
                                |||||||||||| |||||
                                GCCCAAACGTTT TTGCC
                                       G
GAM1485  DAXX    5'  CCCCCGGAGGGAGGAAGTGG   10665        TTTGCA   A
                                TCCCCGGG     GAA TGG
                                ||||||||     ||| |||
                                GGGGGCCT     CTT ACC
                                     CCCTC_   C
GAM1485  DCN     3'  CCGAGTTGAATGGCA       39444        TGCA   A
                                CCGGGTT    GAA TGGCA
                                |||||||    ||| |||||
                                GGCTCAA    CTT ACCGT
                                     ____   _
GAM1485  HMGA2   3'  CCTAACTTGCAGAAATGG    18506    GG
                                CC  GTTTGCAGAAATGG
                                ||  ||||||||||||||
                                GG  TGAACGTCTTTACC
                                 AT
GAM1485  HMX1    5'  TCCTCGGTCCGCTGGGGATGG  33215    C   G    AGAA_
                                TCC CGG TTTGC     ATGG
                                ||| ||| |||||     ||||
                                AGG GCC AGGCG     TACC
                                  A   _    ACCCC
GAM1485  IL6R    3'  GATCTCAGAAATGGCAG     8175       G
                                GGTTT CAGAAATGGCAG
                                ||||| ||||||||||||
                                CTAGA GTCTTTACCGTC
                                      _
GAM1485  KLK10   5'  TCCCCAGCAAGGCTAGGGGTGG 15774        GTTT  _  AAA
            CAG                    TCCCCGG    GC AG   TGGCAG
                                |||||||    || ||   ||||||
```

```
                                AGGGGTC   CG TC  ACCGTC
                                    GTTC  A  CCC
GAM1485  NRXN3    3'  CCAGGCCTGCGGAAGTGG    39940         A  A
                                CCGGGTTTGC GAA TGG
                                |||||||||| ||| |||
                                GGTCCGGACG CTT ACC
                                     C  C
GAM1485  OTP      3'  CCCTGGTACGTAAAATGGC   36991     G  T  CA
                                CCC GGT TG  GAAATGGC
                                ||| ||| ||  ||||||||
                                GGG CCA GC  TTTTACCG
                                  A  T  A_
GAM1485  PREB     3'  TCTGCTCTAGAGATGGCAG   30144       ___  A
                                TTTGC   AGA ATGGCAG
                                |||||   ||| |||||||
                                AGACG   TCT TACCGTC
                                   AGA  C
GAM1485  SYNGR1   3'  CCCCAAGCGTGGGGATGG    21754        T  CA  AA
                                CCCCGGGT TG  GA  TGG
                                |||||||| ||  ||  |||
                                GGGGTTCG AC  CT  ACC
                                    C  CC  __
GAM1485  ZNF16    3'  GGTCTGGGAAGTGGCAG     28086       CA  A
                                GGTTTG  GAA TGGCAG
                                ||||||  ||| ||||||
                                CCAGAC  CTT ACCGTC
                                   C_  C
GAM1486  ABCD4    3'  TCTTACAGATCTCACACTTCCA 33749         CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                |||||||||   ||  || ||||
                                AGAATGTCT   TG  GA GGTC
                                     AGAG  T_  A
GAM1486  ABCD4    3'  TCTTACAGATCTCACACTTCCA 33749         CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                |||||||||   ||  || ||||
                                AGAATGTCT   TG  GA GGTC
                                     AGAG  T_  A
GAM1486  ABCD4    3'  TCTTACAGATCTCACACTTCCA 33749         CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                |||||||||   ||  || ||||
                                AGAATGTCT   TG  GA GGTC
                                     AGAG  T_  A
GAM1486  ABCD4    3'  TCTTACAGATCTCACACTTCCA 33753         CCA_  CT  C
           G                     TCTTACGGA   GC  CT CCAG
                                |||||||||   ||  || ||||
                                AGAATGTCT   TG  GA GGTC
                                     AGAG  T_  A
GAM1486  AP1M1    3'  TCTTGAAGACCAGCCTCT    37175     AC
                                TCTT  GGACCAGCCTCT
                                ||||  ||||||||||||
```

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                                AGAA  TCTGGTCGGAGA
                                  CT
GAM1486  CKTSF1B1  3'  CACACCAGCCTCTCCCAG    30081    G
                                CG ACCAGCCTCTCCCAG
                                || ||||||||||||||
                                GT TGGTCGGAGAGGGTC
                                 G
GAM1486  IL1R1    3'  TCTTAGGGAAAGTCTCCCAG   9370       C   CC  CC
                                TCTTA GGA  AG  TCTCCCAG
                                ||||| |||  ||  ||||||||
                                AGAAT CCT  TC  AGAGGGTC
                                  C   T_ __
GAM1486  ITPKB    3'  TCTTACAGGGCCAGGGCTGCT  13658        A_   C_ _
                                TCTTACGG  CCAG  CT CT
                                ||||||||  ||||  || ||
                                AGAATGTC  GGTC  GA GA
                                     CC    CC  C
GAM1486  LGALS3BP  5'  GACCCAGAAGCCTCTCCCAG   42930     _____
                                GACC    AGCCTCTCCCAG
                                ||||    ||||||||||||
                                CTGG    TCGGAGAGGGTC
                                  GTCT
GAM1486  NCKAP1    5'  CCTTCGCAGCAGCCTCTC    30255      A  GAC
                                TCTT CG   CAGCCTCTC
                                |||| ||   |||||||||
                                GGAA GC   GTCGGAGAG
                                  _  GTC
GAM1486  PLA2G5    3'  CTTAGGAGCCTCTCTCA     9577       C   CCA      C
                                CTTA GGA   GCCTCTC CA
                                |||| |||   ||||||| ||
                                GAAT CCT   CGGAGAG GT
                                  _  ___      A
GAM1486  RAD54L    3'  TCTTGATGATTTTCTCCCAG   18716      ACG  CCAGCC
                                TCTT   GA     TCTCCCAG
                                ||||   ||     ||||||||
                                AGAA   CT     AGAGGGTC
                                  CTA  AAA___
GAM1486  ROBO1     5'  TCTTGCGGAGCCTCCC      39488      A    CCA
                                TCTT CGGA   GCCTCTC
                                |||| ||||   |||||||
                                AGAA GCCT   CGGAGGG
                                  C   ___
GAM1486  CEACAM6   3'  TTGACATCTTGGGAAAAGC    14735           CT
                                TTGACATCTTGG  GAAGC
                                ||||||||||||  |||||
                                AACTGTAGAACC  TTTCG
                                       CT
GAM1486  CLIC3     5'  GCCTTGACAAACAGCTGGAGC  21698         TCT     A
                                GCCTTGACA   TGGCTG AGC
                                |||||||||   |||||| |||
```

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                                CGGAACTGT  GTCGAC TCG
                                     TT_    C
GAM1486  DUSP4    3'  TGCCTTGACATCTGCATGCT  38429          TG__
                                TGCCTTGACATCT   GCT
                                ||||||||||||   |||
                                ACGGAACTGTAGA   CGA
                                      CGTA
GAM1486  DUSP4    3'  TGCCTTGACATCTGCATGCT  38429          TG__
                                TGCCTTGACATCT   GCT
                                ||||||||||||   |||
                                ACGGAACTGTAGA   CGA
                                      CGTA
GAM1486  EMP1     3'  TGCCTTGGCTTTCAGCAAGAGG 10900       ACATC TG  T_  A
           CC                    TGCCTTG    T  GC  GA GCC
                                |||||||    |  ||  || |||
                                ACGGAAC    A  CG  CT CGG
                                    CGAA_ GT  TT  C
GAM1486  MEL      3'  TGCCTTGTGTCTTGGCC    23875       ACA
                                TGCCTTG  TCTTGGCT
                                |||||||  ||||||||
                                ACGGAAC  AGAACCGG
                                    AC_
GAM1486  OSR1     3'  TTGCACCAGCTGAAG      23040    A   TT
                                TTG CATC  GGCTGAAG
                                ||| ||||  ||||||||
                                AAC GTGG  TCGACTTC
                                  _   __
GAM1486  PER2     3'  TGCTTGGCACGCGCTGAAGC  35622    C   A   CTTG
                                TGC TTG CAT   GCTGAAGC
                                ||| ||| |||   ||||||||
                                ACG AAC GTG   CGACTTCG
                                  _  C  CG__
GAM1486  SMOH     3'  CTTGCCTGGCTGAAGC     24813     ACAT
                                CTTG   CTTGGCTGAAGC
                                ||||   ||||||||||||
                                GAAC   GGACCGACTTCG
                                  ____
GAM1486  SNCA     3'  TTAACATCGTAGATTGAAGCC  28661       TT_ GC
                                TTGACATC  G  TGAAGCC
                                ||||||||  |  |||||||
                                AATTGTAG  C  ACTTCGG
                                    CAT TA
GAM1486  SNCA     3'  TTAACATCGTAGATTGAAGCC  28661       TT_ GC
                                TTGACATC  G  TGAAGCC
                                ||||||||  |  |||||||
                                AATTGTAG  C  ACTTCGG
                                    CAT TA
GAM1486  ZNF267   5'  TGCCCTGGCGTCTTAGCT   18259       ACA
                                TGCCTTG  TCTTGGCT
                                |||||||  ||||||||
```

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                                ACGGGAC   AGAATCGA
                                    CGC
GAM1487 COL4A4   3' TGAACAGGTTGAACTTTTAGGA 6408      _  CTATT  AG
            GG                    TGAA AGG    AT  TTAGGAGG
                                  |||| |||    ||  ||||||||
                                  ACTT TCC    TG  AATCCTCC
                                    G   AACT_  AA
GAM1487 SCN3A    3' TGAAAGCTATTGTAGGG     27953       G    ATA  T   A
                                  TGAAAG CTATT   GT AGG G
                                  |||||| |||||   || ||| |
                                  ACTTTC GATAA   CA TCC C
                                     _    ___ _   A
GAM1487 SLC22A2  5' TGAGGACTGTAGTTAGGAGG  40529    AA   ATTA
                                  TGA  GGCT   TAGTTAGGAGG
                                  |||  ||||   ||||||||||
                                  ACT  CTGA   ATCAATCCTCC
                                    C_   C___
GAM1487 TBL2     3' TGAAAGGCTTCCACCTGGGAGG 37411        A   AGTTA
                                  TGAAAGGCT TTAT    GGAGG
                                  ||||||||| ||||    |||||
                                  ACTTTCCGA GGTG    CCTCC
                                       A   GAC__
GAM1488 GABRQ    3' AAGAAACTGAAAGGAGCACAG  32997         TA  A_
                                  AAGAAACTGAA  GA  ATAG
                                  ||||||||||  ||  ||||
                                  TTCTTTGACTT  CT  TGTC
                                        TC  CG
GAM1488 MDM1     3' AAGAAACTGAAAAGGGGCTAG  33512         T  AAA_
                                  AAGAAACTGAA AG   TAG
                                  |||||||||| ||   |||
                                  TTCTTTGACTT TC   ATC
                                        T  CCCG
GAM1488 ZFY      3' AAGAAACTGAATAGGATT    18218          AAATA
                                  AAGAAACTGAATAG    GATT
                                  ||||||||||||    ||||
                                  TTCTTTGACTTATC    CTAA
                                                _____
GAM1489 ASPH     3' CAATTATTTCTGAGCCCA    37133          ATTAT
                                  CGATTATTTCTGA    TCCA
                                  ||||||||||||    ||||
                                  GTTAATAAAGACT    GGGT
                                        C____
GAM1489 CDK10    5' ACGCTTATTTCTGGGTGTCCAA 38145    A       AATTAT
                                  ACG TTATTTCTG     TCCAA
                                  ||| |||||||||     |||||
                                  TGC AATAAAGAC     AGGTT
                                    G       CCAC__
GAM1489 KLHL3    3' TTATTTCTGGACATTCC     44653         AAT
                                  TTATTTCTG   TATTCC
                                  |||||||||   ||||||
```

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                                AATAAAGAC   GTAAGG
                                     CT_
GAM1489 NMB     3'  CGATATTTCTGGTGACCCA   43948     T     AATTAT
                                CGAT ATTTCTG     TCCA
                                |||| |||||||     ||||
                                GCTA TAAAGAC     GGGT
                                  _      CACT__
GAM1489 TLL2    3'  ATTATTTAAAAATTATTCCAA  29746       CT
                                ATTATTT  GAATTATTCCAA
                                |||||||  ||||||||||||
                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1489 ZNF215  3'  AATTATTTACCCTGTTATTCCA 29914        _ GAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
                                TTAATAAA GG   AATAAGGT
                                     T  GAC
GAM1490 ADRA1B  5'  GCCCAGCCCGCAGCACGTCTCC 8620      _       G  G_
                                GCCC GCCCGCAGCG CG  TCC
                                |||| ||||||||||  ||  |||
                                CGGG CGGGCGTCGT GC  AGG
                                  T        _ AG
GAM1490 ARRB2   5'  GCTCGCTCGCAGCCTCC    41409    C   C     GGCGG
                                GC CGC CGCAGC    TCC
                                || ||| ||||||    |||
                                CG GCG GCGTCG    AGG
                                 A  A     G____
GAM1490 ATBF1   5'  GCCCGCCCGCAGGGACCC    27846          CGGC  T
                                GCCCGCCCGCAG   GG CCC
                                ||||||||||||   || |||
                                CGGGCGGGCGTC   CC GGG
                                       _____  T
GAM1490 ATP10C  5'  GCCCGCCCGCGCCGGCC    35981         A  GG
                                GCCCGCCCGC GC  CGGTC
                                |||||||||| ||  |||||
                                CGGGCGGGCG CG  GCCGG
                                       _ __
GAM1490 ATP6V0A4 5' GCTTCCCCGCAGCGCCCC   39290   CCG      GCGGT
                                GC  CCCGCAGCG    CCCC
                                ||  |||||||||    ||||
                                CG  GGGCGTCGC    GGGG
                                 AAG       _____
GAM1490 BCR     5'  GCCCGTCTCAGCGGCGGC    34634      CCCG
                                GCCCG   CAGCGGCGGT
                                |||||   ||||||||||
                                CGGGC   GTCGCCGCCG
                                  AGA_
GAM1490 BHMT2   3'  GCCCGCCTCGGCCTCCC    32775      AG   GG
                                GCCCGC  CGGC  TCCC
                                ||||||  ||||  ||||
```

```
                                CGGGCG  GCCG  AGGG
                                   GA   G_
GAM1490 BMP4    5'  GCTCGCCAGCAGCAGCTCC   10194   C   C      GG
                                GC CGCC GCAGCGGC  TCC
                                || |||| ||||||||  |||
                                CG GCGG CGTCGTCG  AGG
                                 A   T      __
GAM1490 CAPN10  5'  GCCCGCCCCGCCCGTTCCCC  35786       GCA  GG  G
                                GCCCGCCC   GC  CG TCCCC
                                ||||||||   ||  || |||||
                                CGGGCGGG   CG  GC AGGGG
                                     G__  G_  A
GAM1490 CDX2    5'  GCCTCCGAGGCGGTCCC    10405    CGC   CAGC
                                GCC   CCG   GGCGGTCCC
                                |||   |||   |||||||||
                                CGG   GGC   CCGCCAGGG
                                  A__   T___
GAM1490 CLN5    5'  GCCCGGCCCGCGGCGGCTTCC  27084      _    A    GG
                                GCCCG CCCGC GCGGC  TCC
                                ||||| ||||| |||||  |||
                                CGGGC GGGCG CGCCG  AGG
                                   C    C    A_
GAM1490 CSK     3'  GCCCGCTCCGTGGCCTCC    20460       AG  GC   C
                                GCCCGC  CG  GGTC CC
                                ||||||  ||  |||| ||
                                CGGGCG  GC  CCGG GG
                                    AG  A_   A
GAM1490 DLG5    5'  GCTTCAGCAACCGCTGGTTCTC 44460    CC__    G  _  _ C
            C                    GC    GCAGC GC GGT C CC
                                ||   ||||| || ||| | ||
                                CG   CGTTG CG CCA G GG
                                 AAGT    G  A   A A
GAM1490 DTR     5'  GCCCGCCCGCGCGGCCGCCC  12614         A    G
                                GCCCGCCCGC GCGGC GTCC
                                |||||||||| ||||| ||||
                                CGGGCGGGCG CGCCG CGGG
                                      _    G
GAM1490 DUSP4   5'  CCGCTCTAGGGCGGTCCCC   38414     CCGC  C
                                CCGC   AG GGCGGTCCCC
                                ||||   || ||||||||||
                                GGCG   TC CCGCCAGGGG
                                  AGA_  _
GAM1490 E2F4    5'  GCCCGCCCGCCGCCTCCCC   12638         A  GGCGG
                                GCCCGCCCGC GC    TCCCC
                                |||||||||| ||    |||||
                                CGGGCGGGCG CG    AGGGG
                                      G  G_____
GAM1490 F2R     5'  CCCTCCCCGCGGTCCC     12793     G   GCAGCG
                                CCC CCC     GCGGTCCC
                                ||| |||     ||||||||
```

```
                                GGG GGG     CGCCAGGG
                                  A  G_____
GAM1490  G6PD     5'  GCCTGCCCCGGCGGCC      7605      C    GCAG
                                GCC GCCC    CGGCGGTC
                                ||| ||||    ||||||||
                                CGG CGGG    GCCGCCGG
                                  A  ____
GAM1490  GCK      5'  GCCCGCCTGTGGCAGCAACGGC 37927        C___
                                GCCCGCC    GCAGCGGCGGT
                                |||||||    ||||||||||
                                CGGGCGG    CGTCGTTGCCG
                                    ACAC
GAM1490  GNA11    5'  GCCCGCCGCGGCCCC       13163        CGCAGCG      _
                                GCCCGCC      GCGGTCC C
                                |||||||      ||||||| |
                                CGGGCGG      CGCCGGG G
                                   _______     A
GAM1490  GNE      3'  GCCCGCCTCGGCCTCCC     24214       AG    GG
                                GCCCGC  CGGC  TCCC
                                ||||||  ||||  ||||
                                CGGGCG  GCCG  AGGG
                                   GA    G_
GAM1490  GRAF     3'  GCCCGCCTCGGCCTCCC     31448       AG    GG
                                GCCCGC  CGGC  TCCC
                                ||||||  ||||  ||||
                                CGGGCG  GCCG  AGGG
                                   GA    G_
GAM1490  GYS1     3'  GCCCGTTCCGGGGATCCTCC   44788      CAG   C    _
                                GCCCG   CGG GGTCC CC
                                |||||   ||| ||||| ||
                                CGGGC   GCC CTAGG GG
                                  AAG   C     A
GAM1490  HCN4     5'  CCGCCCGTGGGGACGCGTCC   24221       CAGC   _
                                CCGCCCG    GGCG GTCC
                                |||||||    |||| ||||
                                GGCGGGC    CTGC CAGG
                                    ACCC    G
GAM1490  IMPDH1   5'  GCCTCCCTGCAGCGGTGGT    9410      CG   _      C
                                GCC  CCC GCAGCGG GGT
                                |||  ||| ||||||| |||
                                CGG  GGG CGTCGCC CCA
                                  A_   A      A
GAM1490  IQGAP2   5'  GCCCGCCCGGGGCGCGCCCCC  27369         CAGC   _
                                GCCCGCCCG    GGCG GTCCCC
                                |||||||||    |||| ||||||
                                CGGGCGGGC    CCGC CGGGGG
                                     C___    G
GAM1490  IQGAP2   5'  GCCCCCCGCGGCTACCC     27368      G    AGC   GGT
                                GCCC CCCGC   GGC   CCC
                                ||||  |||||   |||   |||
```

```
                                CGGG GGGCG  CCG  GGG
                                  _   ___  AT_
GAM1490 IRS1    5' CCGCCCGCGGGCGCGTCC   24415      AGC  _
                                CCGCCCGC  GGCG GTCC
                                ||||||||  |||| ||||
                                GGCGGGCG  CCGC CAGG
                                    C__   G
GAM1490 KCNK4   3' CGCCCGCAGCGGTGCAGACC  37828        __  T
                                CGCCCGCAGCG  GCGG CC
                                ||||||||||  |||| ||
                                GCGGGCGTCGC  CGTC GG
                                      CA   T
GAM1490 KCNN4   5' CCTGCCCAGGGTCCCCC    13923   C  GCAGC  C
                                CC GCCC    GG GGTCCCCC
                                || ||||    || ||||||||
                                GG CGGG    TC CCAGGGGG
                                 A  _____ _
GAM1490 KITLG   5' GCTTCCCGCAGCGCTTC    19645   CCG      G GG
                                GC  CCCGCAGCG C  TC
                                ||  |||||||| |  ||
                                CG  GGGCGTCGC G  AG
                                 AA_       _ A_
GAM1490 LDB1    5' GCCCGCCCCGCGGCGGCC    19338      GCA
                                GCCCGCCC  GCGGCGGTC
                                ||||||||  |||||||||
                                CGGGCGGG  CGCCGCCGG
                                    G__
GAM1490 LOXL2   5' GCTCTCCACGGTGGTCCCC   14197   CCG  CGCA   C
                                GC  CC   GCGG GGTCCCC
                                ||  ||   |||| |||||||
                                CG  GG   TGCC CCAGGGG
                                 AGA ____   A
GAM1490 LRP8    5' GCCCGCCCCGGCTCC      37794      GCAG   GG
                                GCCCGCCC   CGGC  TCC
                                ||||||||   ||||  |||
                                CGGGCGGG   GCCG  AGG
                                           ____  __
GAM1490 MAG     5' GCCCAGCTCGCAGTCCCC    14321    GC  G_
                                GCCC  AGC  GCGGTCCCC
                                ||||  |||  |||||||||
                                CGGG  TCG  CGTCAGGGG
                                  __  AG
GAM1490 MAML1   5' GCTCGCGCGCGGCGGCGGGTTT 31288   C  C  A    ____
            TCC                  GC CGC CGC GCGGCGG   TCC
                                || ||| ||| |||||||   |||
                                CG GCG GCG CGCCGCC   AGG
                                 A  C  C     CAAA
GAM1490 MAP4K5  5' CCGCCCGCAGCTCCGTTTCC  27301        GG  G_
                                CCGCCCGCAGC  CG  TCC
                                ||||||||||  ||  |||
```

```
                                GGCGGGCGTCG GC AGG
                                      AG AA
GAM1490 MN1     5' CCGCCCGCAGCCTCCC     14574         GGCGG
                                CCGCCCGCAGC   TCCC
                                ||||||||||   ||||
                                GGCGGGCGTCG   AGGG
                                      G____
GAM1490 MSI1    3' GCCTCCCCGCAGCCCTGCCC  14642    CG     GGCG
                                GCC CCCGCAGC  GTCC
                                ||| ||||||||  ||||
                                CGG GGGCGTCG  CGGG
                                  AG     GGA_
GAM1490 OPA3    3' GCCCGCCTCGGCCTCCC    36070      AG   GG
                                GCCCGC CGGC TCCC
                                |||||| |||| ||||
                                CGGGCG GCCG AGGG
                                   GA  G_
GAM1490 P2RX4   5' GCCCGCTCCCAGTCCC     14999      _ GCAGCGG
                                GCCCGC CC     CGGTCCC
                                |||||| ||     |||||||
                                CGGGCG GG     GTCAGGG
                                   A ________
GAM1490 PARK2   5' GCCTCCCACCAGCGGTCTCC  30371    CG   AG     C
                                GCC CCCGC CGGCGGTC CC
                                ||| ||||| |||||||| ||
                                CGG GGGTG GTCGCCAG GG
                                  A_   __      A
GAM1490 PDXK    5' GCCTGGCCGCGGCGGCGCGGGG 18967    CGC   A   __ TC
           CC                   GCC  CCGC GCGGC GG CC
                                |||  |||| ||||| || ||
                                CGG  GGCG CGCCG CC GG
                                  ACC  C   CG CC
GAM1490 PPP1R14B 3' GCCTGGCCGCAGGGTCCCC  39794    CGC    CGGC
                                GCC  CCGCAG   GGTCCCC
                                |||  ||||||   |||||||
                                CGG  GGCGTC   CCAGGGG
                                  ACC    ____
GAM1490 PSMB2   3' GCCCGCCTCGGCCTCCC    15820      AG   GG
                                GCCCGC CGGC TCCC
                                |||||| |||| ||||
                                CGGGCG GCCG AGGG
                                   GA  G_
GAM1490 PTPN14  5' CCTTCGCGGCGGCGGAGCC  23996   GCC  A     TC
                                CC  CGC GCGGCGG CC
                                ||  ||| ||||||| ||
                                GG  GCG CGCCGCC GG
                                 AA_  C     TC
GAM1490 PTPRJ   5' GCCCGCCCCGGGCTTCCCC  15955       GCAGC  GG
                                GCCCGCCC   GGC TCCCC
                                ||||||||   ||| |||||
```

```
                                CGGGCGGG    CCG  AGGGG
                                    GC___   A_
GAM1490  RAD51L1   5'  GCCCGCTTCGGCCTCCC     39450       AG    GG
                                GCCCGC  CGGC  TCCC
                                ||||||  ||||  ||||
                                CGGGCG  GCCG  AGGG
                                   AA   G_
GAM1490  RB1CC1    5'  GCCCGCCCGCCGCGGCCCC   31313         AGCG
                                GCCCGCCCGC   GCGGTCCC
                                ||||||||||   ||||||||
                                CGGGCGGGCG   CGCCGGGG
                                     G___
GAM1490  SHB       5'  GCCCGTCCCGGCGGCCC     16689       _   GCAGC
                                GCCCG CCC    GGCGGTCC
                                ||||| |||    ||||||||
                                CGGGC GGG    CCGCCGGG
                                  A  _____
GAM1490  SIAT1     5'  GCCTGCTTCTGGCTAATCCCCC 16722     C  AGC_  _
                                GCC GC   GGC GGTCCCCC
                                ||| ||   ||| ||||||||
                                CGG CG   CCG TTAGGGGG
                                 A  AAGA  A
GAM1490  SIRT3     5'  CCCGCCCGCGGCGCCC      29259         AGC   GT
                                CCCGCCCGC   GGCG  CCC
                                |||||||||   ||||  |||
                                GGGCGGGCG   CCGC  GGG
                                    ___    __
GAM1490  SIX2      5'  GCCCGCCCGCGCGCGCCC    32607          A   G  GT
                                GCCCGCCCGC GCG CG  CCC
                                |||||||||| ||| ||  |||
                                CGGGCGGGCG CGC GC  GGG
                                    _  _  __
GAM1490  SLC28A2   3'  GCCCGCCTCGGCCTCCC     20110       AG    GG
                                GCCCGC  CGGC  TCCC
                                ||||||  ||||  ||||
                                CGGGCG  GCCG  AGGG
                                   GA   G_
GAM1490  SMG1      3'  GCCCGCCTCGGCCTCCC     31508       AG    GG
                                GCCCGC  CGGC  TCCC
                                ||||||  ||||  ||||
                                CGGGCG  GCCG  AGGG
                                   GA   G_
GAM1490  SMTN      5'  GCCCGCTCAGCAACCGTCCCC 39523       CCG      G
                                GCCCGC   CAGCGGC GTCCCC
                                ||||||   ||||||| ||||||
                                CGGGCG   GTCGTTG CAGGGG
                                   A__      G
GAM1490  STIP1     3'  GCTCGCCGCGGTCCC       27733    C   CGCAGCG
                                GC CGCC      GCGGTCCC
                                || ||||      ||||||||
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                                CG GCGG      CGCCAGGG
                                 A  _______
GAM1490  TJP1     5'  GCCCGCCCCGCCCGGGTC    17543        _ AG   CG
                                GCCCGCCC GC  CGG  GTC
                                |||||||| ||  |||  |||
                                CGGGCGGG CG  GCC  CAG
                                     G  G_  __
GAM1490  TULP1    3'  GCCCGCCCCAGCTCC       17726        G   GGCGG
                                GCCCGCCC CAGC    TCC
                                |||||||| ||||    |||
                                CGGGCGGG GTCG    AGG
                                     _   _____
GAM1490  UQCRC1   5'  GCCCGCCGTGCAGTCCATCTCC 17890       AGCG     ____
              C                  GCCCGC   GCGGTCC   CCC
                                 ||||||   |||||||   |||
                                 CGGGCG   CGTCAGG   GGG
                                    GCA_     TAGA
GAM1490  USP11    5'  GCCGGCCCGCAGTGGACGTTC  21632     C      C  _  G
                                GCC GCCCGCAG GG CG TC
                                ||| |||||||| || || ||
                                CGG CGGGCGTC CC GC AG
                                  C       A  T  A
GAM1490  VIL2     5'  GCCCGCCCTGCCTCGTCCTCC  17999        GCA  GG  G  _
                                GCCCGCCC   GC  CG TCC CC
                                ||||||||   ||  || ||| ||
                                CGGGCGGG   CG  GC AGG GG
                                     A__  GA  _  A
GAM1490  YY1      5'  GCCCGCCCTGGCCGCGCCTCC  18172        GCA  G   GT  _
                                GCCCGCCC   GC GCG  CC CC
                                ||||||||   || |||  || ||
                                CGGGCGGG   CG CGC  GG GG
                                     AC_  G   __  A
GAM1490  ZNF76    5'  GCCCGCCCGCGCGCAGCC    18307         A   G
                                GCCCGCCCGC GCG CGGTC
                                |||||||||| ||| |||||
                                CGGGCGGGCG CGC GTCGG
                                     _  _
GAM1491  ABCD2    3'  TGCTATTATAGCCCAGTTTGA  23155     AC_       A
                                TGC   TGTGGCCCA TTTGA
                                |||   ||||||||| |||||
                                ACG   ATATCGGGT AAACT
                                  ATA        C
GAM1491  ADCY8    5'  CTGCACTGGGCTTTG       10006         T   CCAA
                                CTGCACTG GGC    TTTG
                                |||||||| |||    ||||
                                GACGTGAC CCG    AAAC
                                     _  _____
GAM1491  IMMP2L   5'  TGCCCTCGCCCAATTTG     37183     A  GTG
                                TGC CT   GCCCAATTTG
                                ||| ||   ||||||||||
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                                ACG GG   CGGGTTAAAC
                                  _ AG_
GAM1491  ITGB3    3'  TGCACTGTGGCCTCTCAGA   6841           CAA  T
                                TGCACTGTGGCC   TT GA
                                ||||||||||||   || ||
                                ACGTGACACCGG   AG CT
                                       AG_  T
GAM1491  TERT     3'  CACAGCACCTCCCCCCAATTTG 17393     T    GTGG
              AC                   CAC GCACT    CCCAATTTGAC
                                ||| |||||    ||||||||||||
                                GTG CGTGG    GGGTTAAACTG
                                  T    AGGG
GAM1491  UNC5C    3'  CTGCATCCCTGTCCAATTTGA  19008      _  G  GC
                                CTGCA CT TG  CCAATTTGA
                                ||||| || ||  |||||||||
                                GACGT GG AC  GGTTAAACT
                                   A  G  A_
GAM1492  AP2B1    3'  TGTAGAAAAAGCCAGCCAT   10497         TAA
                                TGTAGAAAA   CGGTCAT
                                |||||||||   |||||||
                                ACATCTTTT   GTCGGTA
                                      TCG
GAM1492  APP      3'  TGTAGAAAGCGATCAT      7924          ATAA
                                TGTAGAAA    CGGTCAT
                                ||||||||    |||||||
                                ACATCTTT    GCTAGTA
                                     C___
GAM1492  APPL     3'  TGCAGAAAATACAATGTATC   29014          ACG___
                                TGTAGAAAATA     GTC
                                ||||||||||      |||
                                ACGTCTTTTAT     TAG
                                       GTTACA
GAM1492  CD28     3'  GTAGAAAAATATCCATGGTCAT 26022         TAAC____
                                GTAGAAAA       GGTCAT
                                ||||||||       ||||||
                                CATCTTTT       CCAGTA
                                     TATAGGTA
GAM1492  GALNT7   3'  GTAGAAAATAGTCAT       32647          AAC
                                GTAGAAAAT   GGTCAT
                                |||||||||   ||||||
                                CATCTTTTA   TCAGTA
                                      ___
GAM1492  GAS7     3'  TGAGATCCAAACGGTCAT    25284    T   AAAT
                                TG AGA    AACGGTCAT
                                || |||    |||||||||
                                AC TCT    TTGCCAGTA
                                  _  AGGT
GAM1492  HDAC4    3'  TGCAGAAAACTCAT        25786          AACGG
                                TGTAGAAAAT    TCAT
                                ||||||||||    ||||
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                                ACGTCTTTTG    AGTA
                                      _____
GAM1492 HIP1    3' GTAGAAAGTGGAACGATC    23757       AT__
                                GTAGAAA   AACGGTC
                                |||||||   |||||||
                                CATCTTT   TTGCTAG
                                    CACC
GAM1492 JRK     3' TGGAGAAAATAACCACATC   44505   T       G T
                                TG AGAAAATAAC G CATC
                                || ||||||||||  | ||||
                                AC TCTTTTATTG T GTAG
                                 C        G _
GAM1492 NDUFA6  3' TGCAGAAAATTGGTTCATC   14742         AAC  _
                                TGTAGAAAAT  GGT CATC
                                ||||||||||  ||| ||||
                                ACGTCTTTTA  CCA GTAG
                                      A__  A
GAM1492 NOX4    3' TGTAATGTGACGGTCATC    32598     AAAATA
                                TGTAG     ACGGTCATC
                                |||||     |||||||||
                                ACATT     TGCCAGTAG
                                   ACAC__
GAM1492 NPC2    3' TGTAGAAAGAGGCCAC      26968       ATAAC
                                TGTAGAAA    GGTCAT
                                ||||||||    ||||||
                                ACATCTTT    CCGGTG
                                     CT___
GAM1492 PRPSAP2 3' TGCAGAAAATAAATACAATC  15739         ___
                                TGTAGAAAATA  ACGGTC
                                ||||||||||  ||||||
                                ACGTCTTTTAT  TGTTAG
                                      TTA
GAM1492 PTGFRN  3' TGCAGAAAATACCCAAATC   42601         AC__
                                TGTAGAAAATA   GGTC
                                ||||||||||   ||||
                                ACGTCTTTTAT   TTAG
                                      GGGT
GAM1492 SPAP1   5' TGCAGACACGGTCAT       39868      AAATA
                                TGTAGA    ACGGTCAT
                                ||||||    ||||||||
                                ACGTCT    TGCCAGTA
                                   G____
GAM1492 TP53BP2 3' TGTAGAAAACAGGATTGTC   24064         ACG__
                                TGTAGAAAATA    GTC
                                ||||||||||    |||
                                ACATCTTTTGT    CAG
                                      CCTAA
GAM1492 TSN     3' TATAGAAAATATCAAGCATC  21498         A  T
                                TGTAGAAAATA CGG CATC
                                ||||||||||| ||| ||||
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                                ATATCTTTTAT GTT GTAG
                                      A   C
GAM1493 ANGPT1   3' TCCATTGAGTTATTTATGGCAA 40245     A     CTCC
                                TCCA TGAGTT    TATGGCAA
                                |||| ||||||    ||||||||
                                AGGT ACTCAA    ATACCGTT
                                  A     TAA_
GAM1493 BMP3     3' TCAAATGAGTTCTTTGCCA    10190    C       CCTA  G
                                TC AATGAGTTCT    TG CA
                                || ||||||||||    || ||
                                AG TTACTCAAGA    AC GT
                                 T        A___  G
GAM1493 BPAG1    3' TCCTGTGAGTTCTCTGTCA    31783    AA       CTA  G
                                TCC  TGAGTTCTC   TG CA
                                |||  |||||||||   || ||
                                AGG  ACTCAAGAG   AC GT
                                  AC        ___  A
GAM1493 CACNA2D3 5' CATCGATTTCTTCTATGGCAA  32900    A  G   C
                                CA TGA TTCT CTATGGCAA
                                || ||| |||| |||||||||
                                GT GCT AAGA GATACCGTT
                                 A  A   A
GAM1493 CYFIP2   3' TCCAGTTGGATCCTATGGCA   43915     ATGA  C__
                                TCCA   GTT   TCCTATGGCA
                                ||||   |||  ||||||||||
                                AGGT   CAA   AGGATACCGT
                                   _____  CCT
GAM1493 DAG1     3' CTCCAGTTGCTATGGC      20519      ATGA  CTC
                                CTCCA   GTT   CTATGGC
                                |||||   |||  |||||||
                                GAGGT   CAA   GATACCG
                                   _____  C__
GAM1493 DLX2     3' CTCTGGCGAGTTCTCCCTGG  20588     CAA        A
                                CTC   TGAGTTCTCCT TGG
                                |||   |||||||||| |||
                                GAG   GCTCAAGAGGG ACC
                                  ACC         _
GAM1493 HEBP1    3' TCCAGTAAGTTCTTGG      31993      A      CCTA
                                TCCA TGAGTTCT    TGG
                                |||| ||||||||    |||
                                AGGT ATTCAAGA    ACC
                                  C       ____
GAM1493 PPP5C    3' CTCTGGGGGTCTTCCTATGGC 26489     CAATGA  TC
                                CTC     GT  TCCTATGGC
                                |||     ||  |||||||||
                                GAG     CA  AGGATACCG
                                  ACCCC_  GA
GAM1493 SLC25A13 3' CTCCAATGTGGTTTTCATTACA 30659        A_   C  CTATG
             A                   CTCCAATG  GTT TC     GCAA
                                ||||||||  ||| ||    ||||
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                                GAGGTTAC  CAA AG    TGTT
                                    AC   A  TAA__
GAM1493  ZNF217   3'  CTCAAATGAGTTCTCCCTTG  27192    C         A
                                CTC AATGAGTTCTCCT TG
                                ||| |||||||||||| ||
                                GAG TTACTCAAGAGGG AC
                                  T          A
GAM1493  ZNF26    3'  AATGAGTTCTCTTAAGC    43791         CTAT
                                AATGAGTTCTC   GGC
                                ||||||||||   |||
                                TTACTCAAGAG   TCG
                                      AAT_
GAM1494  ADAM19   3'  TGCTGGCCTTGAGCATCTCCAT 37781    CCA   CCC_
           C                     TGC   GCCT   CGTCTCCATC
                                |||   ||||   ||||||||||
                                ACG   CGGA   GTAGAGGTAG
                                  AC_   ACTC
GAM1494  ADRA1D   3'  TGCCCAGTTCCTCAGGGATGTC 8618       __   CCC___
                                TGCCCAG  CCTC    GTC
                                |||||||  ||||    |||
                                ACGGGTC  GGAG    CAG
                                    AA   TCCCTA
GAM1494  AMN      3'  TGCCCACCCCTTTTCCGTC   36286      G   CC__
                                TGCCCA CCT   CCGTC
                                |||||| |||   |||||
                                ACGGGT GGG   GGCAG
                                   G   AAAA
GAM1494  ANK1     3'  GCCCAGCTTCCTTGGGCCGTC  33864      C  _____
                                GCCCAGC TCC    CCGTC
                                ||||||| |||    |||||
                                CGGGTCG AGG    GGCAG
                                    A   AACCC
GAM1494  AOC3     3'  TGCCCAGCTGCTCCCCATC   19023       __
                                TGCCCAGC  CTCCCCGTC
                                ||||||||  |||||||||
                                ACGGGTCG  GAGGGGTAG
                                    AC
GAM1494  APOB48R  3'  TGCCCAGCCTCCTTGCAGTC  33093         CC___
                                TGCCCAGCCTCC    GTC
                                ||||||||||||    |||
                                ACGGGTCGGAGG    CAG
                                      AACGT
GAM1494  ATP1A2   3'  TGCCCAGCTCTCCCTGAAGGTC 8714       _   C____
                                TGCCCAGC CTCCC    GTC
                                |||||||| |||||    |||
                                ACGGGTCG GAGGG    CAG
                                    A    ACTTC
GAM1494  BACE     3'  TGCCAGCCTTTTCCTTCTCCAT 39973    C    CC_  G
           C                     TGCC AGCCT   CC TCTCCATC
                                |||| |||||   || ||||||||
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                                ACGG TCGGA   GG AGAGGTAG
                                  _    AAA  A
GAM1494  BCAT1    3'  TGCTCATCAAATCTCCAT    42385     C  GCC  CCC
                                TGC CA   TC   GTCTCCAT
                                ||| ||   ||   ||||||||
                                ACG GT   AG   TAGAGGTA
                                  A  ___  TT_
GAM1494  BCL2L2   3'  TGCTCAGCTCCCCACCCCC   19751     C    C    GT
                                TGC CAGC TCCCC  CTCC
                                ||| |||| |||||  ||||
                                ACG GTCG AGGGG  GGGG
                                  A   _    TG
GAM1494  CACNG3   5'  TGCCCCGCCTCCGTCGTC    27244      A     C_
                                TGCCC GCCTCC  CGTC
                                ||||| ||||||  ||||
                                ACGGG CGGAGG  GCAG
                                   G     CA
GAM1494  EDG8     3'  GCTTAGCTGGAATCTCCATC   44206    CC   CTCCCC
                                GC  AGC     GTCTCCATC
                                ||  |||     |||||||||
                                CG  TCG     TAGAGGTAG
                                 AA   ACCT__
GAM1494  FLRT2    3'  TGCACATGACTGTCTCCAT    29863     C  GC_  CCCC
                                TGC CA   CT    GTCTCCAT
                                ||| ||   ||    ||||||||
                                ACG GT   GA    CAGAGGTA
                                  T  ACT  _____
GAM1494  GAB2     3'  TGCCCAGCCTGTGCCTGTC    29383         C__  C
                                TGCCCAGCCT   CC GTC
                                ||||||||||   || |||
                                ACGGGTCGGA   GG CAG
                                      CAC  A
GAM1494  GSTM5    3'  TGCTCAGCCCCCTTCCCCATC  9209     C    T   CG
                                TGC CAGCC CCC  TCTCCATC
                                ||| ||||| |||  ||||||||
                                ACG GTCGG GGG  AGGGGTAG
                                  A    _  A_
GAM1494  KCNJ16   3'  TGCCTTGTTTCTGGTCTCCAT  33021     CAGCC  CCC
                                TGCC    TC   GTCTCCAT
                                ||||    ||   ||||||||
                                ACGG    AG   CAGAGGTA
                                   AACAA  AC_
GAM1494  KCNJ16   3'  CCAGCCTCCTTCCTGCCTTCAT 33015         __ _   C
                                CCAGCCTCC  CC GTCT CAT
                                |||||||||  || |||| |||
                                GGTCGGAGG  GG CGGA GTA
                                      AA A    A
GAM1494  KCNQ2    3'  TGCCCAGCCCTCCAGCCCC    41515         TC  C
                                TGCCCAGCC  CC GTCTC
                                |||||||||  || |||||
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                                ACGGGTCGG  GG CGGGG
                                     GA  T
GAM1494  LPHH1    5'  TGCCCAGCTTCATCAAGACCAT 29391        C  CC  TCT
              C                   TGCCCAGC TC  CG   CCATC
                                  |||||||| ||  ||   |||||
                                  ACGGGTCG AG  GT   GGTAG
                                       A  TA  TCT
GAM1494  LPIN2    5'  GCCCAGCACCTGTCTCCATC  31210       CT  CC
                                  GCCCAGC  CC  GTCTCCATC
                                  |||||||  ||  |||||||||
                                  CGGGTCG  GG  CAGAGGTAG
                                       T_  A_
GAM1494  MADD     3'  TGCGTAGCCCCTCTCCAT    39071     CC     CCCG
                                  TGC  AGCCTC    TCTCCAT
                                  |||  ||||||    |||||||
                                  ACG  TCGGGG    AGAGGTA
                                    CA     _____
GAM1494  MGAM     3'  CCCAGACAATGTCTCCATC    43653      CCTCCCC
                                  CCCAG      GTCTCCATC
                                  |||||      |||||||||
                                  GGGTC      CAGAGGTAG
                                     TGTTA__
GAM1494  MTA1L1   3'  ACTCTTCCCCTCCCCATC    21879    _ _   G
                                  GC CT CCCC TCTCCATC
                                  || || |||| ||||||||
                                  TG GA GGGG AGGGGTAG
                                   A  A   _
GAM1494  NRIP1    5'  CCCAGCCTCCGGCTCCGTC    40957          _____
                                  CCCAGCCTCC    CCGTC
                                  ||||||||||    |||||
                                  GGGTCGGAGG    GGCAG
                                        CCGA
GAM1494  PHYH     5'  CCCGGCCTCTGCCCCAT     26314     A    CCC   T
                                  CCC GCCTC   GTC CCAT
                                  ||| |||||   ||| ||||
                                  GGG CGGAG   CGG GGTA
                                    C    A__  _
GAM1494  PLD2     3'  TGCCTGCCTCCCCAGATC    15386      CA       TC
                                  TGCC  GCCTCCCCG  TC
                                  ||||  |||||||||  ||
                                  ACGG  CGGAGGGGT  AG
                                    A_       CT
GAM1494  PODXL    3'  CCCAGTCTTTCCCTTCCCCATC 23960      C  C_   G
                                  CCCAG CT  CCC TCTCCATC
                                  ||||| ||  ||| ||||||||
                                  GGGTC GA  GGG AGGGGTAG
                                     A  AA   A
GAM1494  PROCR    3'  TGTCCACCTCTCCTCTCCATC  26919    C   G    C  G
                                  TG CCA CCTC CC TCTCCATC
                                  || ||| |||| || ||||||||
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                                AC GGT GGAG GG AGAGGTAG
                                 A  _   A  _
GAM1494  PTN      3'  TGCTCTGCTTCCCCACCCCCAT 44392     CCA  C     GT
                                TGC   GC TCCCC  CTCCAT
                                |||   || |||||  ||||||
                                ACG   CG AGGGG  GGGGTA
                                  AGA  A     TG
GAM1494  RUNX3    3'  TGCCCAGCGTCTCATC      20330         CTCCCC    C
                                TGCCCAGC     GTCTC ATC
                                ||||||||     ||||| |||
                                ACGGGTCG     CAGAG TAG
                                     _______   _
GAM1494  SLC12A4  3'  GCTCAGCTGTCTCCAT      22898    C   CTCCCC
                                GC CAGC     GTCTCCAT
                                || ||||     ||||||||
                                CG GTCG     CAGAGGTA
                                 A   A_____
GAM1494  SLC38A3  3'  TGCCAGCCTCCCCACCCTATC  27761      C        T   C
                                TGCC AGCCTCCCCG CTC ATC
                                |||| |||||||||| ||| |||
                                ACGG TCGGAGGGGT GGG TAG
                                  _        _  A
GAM1494  SLC39A1  3'  TGCCCACTTCCCTCTC      30890       G C    CG
                                TGCCCA C TCCC  TCTC
                                |||||| | ||||  ||||
                                ACGGGT G AGGG  AGAG
                                   _ A   __
GAM1494  SLC3A2   5'  CAGACCCCGTCTCTATC     14397     CCT       C
                                CAG   CCCCGTCTC ATC
                                |||   ||||||||| |||
                                GTC   GGGGCAGAG TAG
                                  T__       A
GAM1494  TULP1    3'  GCCTGGCCCTCGTCCCCCATC  17727      __  _     _
                                GCCT  CCC CGTCTCC ATC
                                ||||  ||| ||||||| |||
                                CGGA  GGG GCAGGGG TAG
                                  CC   A      G
GAM1494  UCP3     3'  TGCCCAGCTTCTCACTTGCAT  17858        C  CC  T  C_
                                TGCCCAGC TC  CG CT  CAT
                                |||||||| ||  || ||  |||
                                ACGGGTCG AG  GT GA  GTA
                                     A  A_  _  AC
GAM1494  VTN      5'  TGCTCAACCTCCAGCCCATC   8472      C       ___
                                TGC CAGCCTCC   CCGTC
                                ||| ||||||||   |||||
                                ACG GTTGGAGG   GGTAG
                                  A       TCG
GAM1495  FTL      5'  TCCCCGGATCTGTTCCGT    6630          ACC_
                                TCCCCGGATC    CCGT
                                ||||||||||    ||||
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                                AGGGGCCTAG    GGCA
                                      ACAA
GAM1496  CD69     3'  TGATTTAGGAAAGTCACAAACC 12139        _   TAGG_
              TA                    TGATTTAG AAA     AGACCTA
                                    |||||||| |||    |||||||
                                    ACTAAATC TTT     TTTGGAT
                                       C   CAGTG
GAM1496  CDH11    3'  TGATTTAAAAAAATACCT    38036          TAGGAG
                                    TGATTTAGAAA     ACCT
                                    ||||||||||     ||||
                                    ACTAAATTTTT     TGGA
                                          TTA___
GAM1496  MME      3'  TGATTAGAAATCCTGGTCTACC 28605      T     AGGAGAC
                                    TGATT AGAAAT      CTACC
                                    ||||| ||||||      |||||
                                    ACTAA TCTTTA      GATGG
                                      _     GGACCA_
GAM1496  TNFSF4   3'  TGACTTAAAATAGGGGACCTGC 17756         A   A    A
              C                     TGATTTAGAA TAGG GACCT CC
                                    |||||||||| |||| ||||| ||
                                    ACTGAATTTT ATCC CTGGA GG
                                          _   C    C
GAM1497  SERPINB4 5'  GTGTGTCTGTGGAATGAAGG   42227       A____
                                    GTGTGT    GAATGAAGG
                                    ||||||    |||||||||
                                    CACACA    CTTACTTCC
                                       GACAC
GAM1497  AICDA    3'  AGAAGATTTGCTACTTCAGACA 34035     ACACCTA  T
              T                     AGAA      CT CTTCAGACAT
                                    ||||      || ||||||||||
                                    TCTT      GA GAAGTCTGTA
                                      CTAAAC_  T
GAM1497  ARL4     3'  AGAAAACCTACTCCACACAGA  25066      C       TT_
                                    AGAAA ACCTACTTC   CAGA
                                    ||||| |||||||||   ||||
                                    TCTTT TGGATGAGG   GTCT
                                      _       TGT
GAM1497  DDT      5'  GAAACAGCTCCTCAGA      10670       CCTAC
                                    GAAACA    TTCTTCAGA
                                    ||||||    |||||||||
                                    CTTTGT    GAGGAGTCT
                                       C____
GAM1497  FBXL11   3'  AGAGACACTTCTTTCCTCCACA 29422     A   CTAC     AG
              T                     AGA ACAC    TTCTTC  ACAT
                                    ||| ||||    ||||||  ||||
                                    TCT TGTG    AAGGAG  TGTA
                                      C   AAGA     G_
GAM1497  MSR1     3'  AGAGGCACTGATCTCAGACAT  14654     AA   CTACT   T
                                    AGA  CAC    TCT CAGACAT
                                    |||  |||    ||| |||||||
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                                TCT  GTG    AGA GTCTGTA
                                  CC   ACT__  _
GAM1497  PVR     5'  GAATACCCACTTCTTCA    27109     AC
                                GAA  ACCTACTTCTTCA
                                |||  ||||||||||||
                                CTT  TGGGTGAAGAAGT
                                  A_
GAM1497  RAD9    3'  AGCAGCACCTACTATGACA   21368    AAA      TCTTCA
                                AG   CACCTACT     GACA
                                ||   ||||||||     ||||
                                TC   GTGGATGA     CTGT
                                 GTC      TA____
GAM1497  TLL2    5'  AGAGGAACCGCAGGTTCAGACA 29744     AAC   TACTTC
             T                   AGA   ACC     TTCAGACAT
                                |||   |||     |||||||||
                                TCT   TGG     AAGTCTGTA
                                  CCT   CGTCC_
GAM1498  ASCL2   5'  CCAGGGCACGCGTCCTAGG   23184    _       C  C
                                CT GGGCACGCG CC AGG
                                || |||||||| || |||
                                GG CCCGTGCGC GG TCC
                                 T       A  A
GAM1498  CD7     3'  TGGAGCTGGGCACGGCTGGGC  26005     T        C  CCCA
                                TGG GCTGGGCACG GC    GGC
                                ||| |||||||||| ||    |||
                                ACC CGACCCGTGC CG    CCG
                                  T        _  AC__
GAM1498  CD79A   3'  TGGAGCTGGGTGCACAGCAGGC 34648     T     CAC    CC
                                TGG GCTGGG   GCGC  CAGGC
                                ||| ||||||   ||||  |||||
                                ACC CGACCC   CGTG  GTCCG
                                  T     A__    TC
GAM1498  CDH4    3'  GGTGCTGGGCAGCGGCCGGG   12180          C   C  CA
                                GGTGCTGGGCA GCG CC  GG
                                |||||||||| ||| ||  ||
                                CCACGACCCGT CGC GG  CC
                                       _   C  C_
GAM1498  GPC3    3'  GTGCTGGGCACCAG       21023          CGCGCC
                                GTGCTGGGCA     CCAG
                                ||||||||||     ||||
                                CACGACCCGT     GGTC
                                              _______
GAM1498  KCNN2   5'  TGGTGCTGGTGGTGCGCCGGG  34671         GCAC    CCA
                                TGGTGCTGG   GCGCC   GG
                                |||||||||   |||||   ||
                                ACCACGACC   CGCGG   CC
                                     ACCA    C__
GAM1498  MBD1    3'  TGGTGCTGGGGCACCAGG    31925          CACGC  C
                                TGGTGCTGGG    GC CCAGG
                                ||||||||||    || |||||
```

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                                ACCACGACCC    CG GGTCC
                                      _____  T
GAM1498  MECP2    3'  TGGTGCTGGGCCTTCCAGG   22621          ACGCGCC
                                TGGTGCTGGGC      CCAGG
                                ||||||||||       |||||
                                ACCACGACCCG      GGTCC
                                      GAA____
GAM1498  NTF5     5'  TGGGGCTGGGAGTCCCCAGGC  26139     T     CACGCG
                                TGG GCTGGG     CCCCAGGC
                                ||| ||||||     ||||||||
                                ACC CGACCC     GGGGTCCG
                                  C     TCA___
GAM1498  PDGFRB   5'  TGGTGTGGGCACAGTTCCAGGC 42345      C       CGCC
                                TGGTG TGGGCACG    CCAGGC
                                ||||| ||||||||    ||||||
                                ACCAC ACCCGTGT    GGTCCG
                                  _       CAA_
GAM1498  PPARA    5'  TGGTGCTGGTTGTGCGCC    22771         GCAC
                                TGGTGCTGG    GCGCC
                                |||||||||    |||||
                                ACCACGACC    CGCGG
                                     AACA
GAM1498  TMP21    3'  TGCTGTTGGTAGGATGCCTTAG 27750    G  C   GCACGC   CC
              GC                  TG TG TGG     GCC  AGGC
                                  || || |||     |||  ||||
                                  AC AC ACC     CGG  TCCG
                                   G  A   ATCCTA   AA
GAM1498  VIPR1    3'  TGGTGCTGGTGACCTTCCCCGG 21517         GC  GCG    A
              GC                  TGGTGCTGG  AC   CCCC GGC
                                  |||||||||  ||   |||| |||
                                  ACCACGACC  TG   GGGG CCG
                                       AC  GAA    C
GAM1499  EHHADH   3'  TGTATGATTCATAAGATTTC   12685      A    GGA
                                TGTGT ATTCA   AAGATTTC
                                ||||| |||||   ||||||||
                                ACATA TAAGT   TTCTAAAG
                                   C    A__
GAM1499  HGF      3'  TGTACAGGAAGATTTC      45324      ATT     A
                                TGTA   CAGGAA GATTTC
                                ||||   |||||| ||||||
                                ACAT   GTCCTT CTAAAG
                                     ___     _
GAM1499  TCF19    5'  TGTGTAATTCGGAGAAGA    45551          A  _
                                TGTGTAATTC GGA AAGA
                                |||||||||| ||| ||||
                                ACACATTAAG CCT TTCT
                                      _  C
GAM1499  EGFL5    5'  TCTTTGGAGTTTTAACT     44539       A       C
                                TCTTT GGAGTTTT ACT
                                ||||| |||||||| |||
```

```
                                AGAAA CCTCAAAA TGA
                                  _      T
GAM1499  MPP6    3'  TTTAAGAGTTTAATTTTCA   32398          TCAC
                                TTTAGGAGTTT   TTCA
                                ||||||||||   ||||
                                AAATTCTCAAA   AAGT
                                    TTAA
GAM1499  NUMA1   3'  TCTCTAGGGGTTTGGCTACTG  45244        A   TCA  TC
                                TCTTTAGG GTTT  CT  ACTG
                                |||||||| ||||  ||  ||||
                                AGAGATCC CAAA  GA  TGAC
                                     C   CC_ __
GAM1500  EN1     3'  GCGGCGGTTCAGTCTCGCA   10914        C  CCGG
                                GCGGCGGT CAG   CGCA
                                |||||||| |||   ||||
                                CGCCGCCA GTC   GCGT
                                     A  AGA_
GAM1500  FGF5    5'  CCGCGGGGGTCCTAAGTGCATC 37586       C   AGCC  C
                                CCGCGG GGTCC   GG GCATC
                                |||||| |||||   || |||||
                                GGCGCC CCAGG   TC CGTAG
                                   C    AT__  A
GAM1500  LBX1    3'  CCTCGGCGGTCCGGTCCGGGAG 27281   G       AG_   C__
           GC                    CC CGGCGGTCC   CCGG   GC
                                || |||||||||  ||||  ||
                                GG GCCGCCAGG   GGCC   CG
                                 A       CCA   CTC
GAM1500  PAX2    3'  GCGGCGGTCCCGGGAGAGCG  19629         AGCC__
                                GCGGCGGTCC     GGCG
                                ||||||||||     ||||
                                CGCCGCCAGG     TCGC
                                     GCCCTC
GAM1500  PTP4A2  5'  GCGGCGGCGGCGGCGC     38635        CCA  C
                                GCGGCGGT   GC GGCGC
                                ||||||||   || |||||
                                CGCCGCCG   CG CCGCG
                                     C__  _
GAM1500  TNC     5'  GCGGCGGTTCCCACGTGCGC  13467         _ AGC  _
                                GCGGCGGT CC   CG GCGC
                                |||||||| ||   || ||||
                                CGCCGCCA GG   GC CGCG
                                     A  GT_  A
GAM1500  TOP3A   5'  CCCCGGCTGCCGGCGCAT   21462   G   GGTCCA
                                CC CGGC     GCCGGCGCAT
                                || ||||     ||||||||||
                                GG GCCG     CGGCCGCGTA
                                 G   A_____
GAM1501  ARHG    5'  GGAGGCAGTGCCTCC       11685   C   TCC
                                GG GGT   GGTGCCTCC
                                || |||   |||||||||
```

```
                                CC CCG   TCACGGAGG
                                 T  ___
GAM1501  GORASP1   3'  GGCGATTCTGTTCTACTTCC   36707        CGG__   C
                                GGCGGTTC    TGC TCC
                                ||||||||    ||| |||
                                CCGCTAAG    ATG AGG
                                     ACAAG   A
GAM1501  ITGA1     5'  GCCGCGGTTCCCAGTCCTC   41844    G      _   G
                                GC GCGGTTCC GGT CCTC
                                || |||||||| ||| ||||
                                CG CGCCAAGG TCA GGAG
                                 G       G  _
GAM1501  LASS1     3'  GCGGCGGTGGCATCTTCC    34607        TCC   GC  C
                                GCGGCGGT   GGT  CT CC
                                ||||||||   |||  || ||
                                CGCCGCCA   CCG  GA GG
                                     ___   TA  A
GAM1501  LGMN      5'  CGCGGCGGCTCGCAGCCTCCC  24681          CGGT
                                CGCGGCGGTTC   GCCTCCC
                                ||||||||||    |||||||
                                GCGCCGCCGAG   CGGAGGG
                                      CGT_
GAM1501  MXI1      5'  CCGCGCGTGGTTTGTTTACCTC 39016      GC_   CCGG     _
            TCC                   CCGCG   GGTT    TGCCTC CC
                                ||||||  ||||   |||||| ||
                                GGCGC   CCAA    ATGGAG GG
                                   GCA    ACAA     A
GAM1501  NRXN2     5'  CCGCCGCGGTGCCTCC     31478     G  GGTTCC      _
                                CCGC GC     GGTGCCTC C
                                |||| ||     |||||||| |
                                GGCG CG     CCACGGAG G
                                  G  _______       A
GAM1501  PODXL     5'  GCGGCGGCTCTTCCTC      23977          CGGTG
                                GCGGCGGTTC    CCTC
                                ||||||||||    ||||
                                CGCCGCCGAG    GGAG
                                      AA___
GAM1501  PPP2R2B   5'  CCGCGACAAAATGGTGCCT   21331         TTCC
                                CCGCGGCGG   GGTGCCT
                                |||||||||   |||||||
                                GGCGCTGTT   CCACGGA
                                      TTA_
GAM1501  PTS       5'  CCGCGCGGCCGGTGCCTCC   7224       G   TT
                                CCGCG CGG  CCGGTGCCTCC
                                ||||| |||  ||||||||||
                                GGCGC GCC  GGCCACGGAGG
                                  _   __
GAM1501  RRM2B     5'  CCGCGCCGGTCCTGCTTTCTC  42717      G   T  G  GC_
                                CCGCG CGGT CC GT   CTC
                                ||||| |||| || ||   |||
```

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                                GGCGC GCCA GG CG   GAG
                                  G   _ A  AAA
GAM1501  SIAT8E   5'  CGCGGGGTTCCGGGGCCCC   40834      C      T
                                CGCGG GGTTCCGG GCCTC
                                ||||| |||||||| |||||
                                GCGCC CCAAGGCC CGGGG
                                  _      C
GAM1501  STAT1    5'  CGCGGCGGTGCAGCCTCTCC  40213        TCCGGT   _
                                CGCGGCGGT     GCCTC CC
                                |||||||||     ||||| ||
                                GCGCCGCCA     CGGAG GG
                                     CGT___    A
GAM1501  TRIM9    5'  GGTGGTGGTGCCTTCCC     31576    C   TCC     _
                                GG GGT   GGTGCCT CCC
                                || |||   ||||||| |||
                                CC CCA   CCACGGA GGG
                                 A  ___      A
GAM1501  TRPV1    5'  GGCCTCAGGTGCCTCC      38798     GG   C
                                GGC  TTC GGTGCCTCC
                                |||  ||| |||||||||
                                CCG  GAG CCACGGAGG
                                 __   T
GAM1502  ACVRL1   5'  CGGACCGGGCTGGAGC      6163      CGC   CA
                                CGG   GCT  GCTGGAGC
                                |||   |||  ||||||||
                                GCC   TGG  CGACCTCG
                                 ___   CC
GAM1502  AMPD3    5'  CGGCCGCAGGGCTGGAGC    7897       G   TCA
                                CGGC CGC   GCTGGAGC
                                |||| |||   ||||||||
                                GCCG GCG   CGACCTCG
                                  _   TCC
GAM1502  APXL     3'  GGAACGGAGCTGGAGC      11623     C   CTC
                                GG GCG   AGCTGGAGC
                                || |||   |||||||||
                                CC TGC   TCGACCTCG
                                 T   C__
GAM1502  ASCL2    5'  CGGCGCGCCGCAGGAA      23186         CA  T
                                CGGCGCGCT  GC GGAG
                                |||||||||  || ||||
                                GCCGCGCGG  CG CCTT
                                     __  T
GAM1502  ASGR2    5'  CGGGCTGGAGCTGGAGC     38951     C  GCTC
                                CGG GC    AGCTGGAGC
                                ||| ||    |||||||||
                                GCC CG    TCGACCTCG
                                  _ ACC_
GAM1502  BARX2    3'  CGTCACCCCAGCTGGGGC    18928    G   G       A
                                CG CGC CTCAGCTGG GC
                                || ||| ||||||||| ||
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                                GC GTG GGGTCGACC CG
                                 A  _       C
GAM1502 BLAME    3' GGCCACTGTGCTGGAGC     33491     G   CA
                                GGC CGCT  GCTGGAGC
                                ||| ||||  ||||||||
                                CCG GTGA  CGACCTCG
                                  _   CA
GAM1502 BMP8     5' GGGCGCTCAGCTGGGGC     11884    C         A
                                GG GCGCTCAGCTGG GC
                                || ||||||||||| ||
                                CC CGCGAGTCGACC CG
                                 _         C
GAM1502 BMP8     5' GGGGCGCTCAGCGGGC      11885    C       T  A
                                GG GCGCTCAGC GG GC
                                || |||||||| || ||
                                CC CGCGAGTCG CC CG
                                 C       _ _
GAM1502 CACNG3   5' CGGGCACCACTGGAGC      27233    C    CA
                                CGG GCGCT  GCTGGAGC
                                ||| |||||  ||||||||
                                GCC CGTGG  TGACCTCG
                                  _    __
GAM1502 CAPN5    5' CGGCGCGGGCGCTGGAGC    44929       CTCA
                                CGGCGCG    GCTGGAGC
                                |||||||    ||||||||
                                GCCGCGC    CGACCTCG
                                    CCG_
GAM1502 CBFA2T3  5' GGCTGGGCCAGCTGGGGC    23266     GC_ T     A
                                GGC   GC CAGCTGG GC
                                |||   || ||||||| ||
                                CCG   CG GTCGACC CG
                                  ACC  _     C
GAM1502 CCK      5' GGCGTTTCCAACCGGAGC    8808      CGC
                                GGCG   TCAGCTGGAGC
                                ||||   ||||||||||
                                CCGC   GGTTGGCCTCG
                                  AAA
GAM1502 CDH11    3' GGGCGCTGGCCGGAGC      38034    C    CA
                                GG GCGCT  GCTGGAGC
                                || |||||  ||||||||
                                CC CGCGA  CGGCCTCG
                                 _    C_
GAM1502 CDH12    5' CGGAGCGGCTGGAGC       19774    C  CTCA
                                CGG GCG    GCTGGAGC
                                ||| |||    ||||||||
                                GCC CGC    CGACCTCG
                                  T  _____
GAM1502 CDKN2D   5' CGGCCGCCCGCGGGGC      38610     G    A  T  A
                                CGGC CGCTC GC GG GC
                                |||| ||||| || || ||
```

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                                GCCG GCGGG CG CC CG
                                  _    _ C  _
GAM1502 CEP2     5' CGGCGCCGACTGGAGC     28434      GCT A
                                CGGCGC  C GCTGGAGC
                                ||||||  | ||||||||
                                GCCGCG  G TGACCTCG
                                   ___ C
GAM1502 CHRNB2   5' GCCTACACCGGCTGGAGC    8860    __    CA
                                GC  GCGCT  GCTGGAGC
                                ||  |||||  ||||||||
                                CG  TGTGG  CGACCTCG
                                 GA    C_
GAM1502 CHST2    5' GGCGCGCCCGGGAGC      41715        AGCT
                                GGCGCGCTC   GGAGC
                                |||||||||   |||||
                                CCGCGCGGG   CCTCG
                                     C___
GAM1502 CLDN14   5' CGGAGCCGCTCTGGAGC    40321    C  _   AGC
                                CGG GC GCTC  TGGAGC
                                ||| || ||||  ||||||
                                GCC CG CGAG  ACCTCG
                                  T  G   ___
GAM1502 CLDN3    5' CGGCGCGCGCTAACGGC    10566       TCA    A_
                                CGGCGCGC  GCTGG  GC
                                ||||||||  |||||  ||
                                GCCGCGCG  CGATT  CG
                                     ___    GC
GAM1502 CLIC3    5' GACAAACAGCTGGAGC     21697     CGCT
                                GGCG   CAGCTGGAGC
                                ||||   ||||||||||
                                CTGT   GTCGACCTCG
                                  TT__
GAM1502 CNTFR    5' CGCCGCGCCGGCTGGAGC    12301    G     CA
                                CG CGCGCT  GCTGGAGC
                                || ||||||  ||||||||
                                GC GCGCGG  CGACCTCG
                                 G     C_
GAM1502 COL18A1  5' GGCAGTGCGGCTGGAGC    39057     C_  TCA
                                GGCG  GC   GCTGGAGC
                                ||||  ||   ||||||||
                                CCGT  CG   CGACCTCG
                                  CA  C__
GAM1502 COL1A1   3' CAGCGGGCTGGGCTGGAGC   6365      C   CA
                                CGGCG GCT  GCTGGAGC
                                ||||| |||  ||||||||
                                GTCGC CGA  CGACCTCG
                                   C   CC
GAM1502 COL4A3   5' CAGCGCGCTCTGGGAGC    6392         AGCT
                                CGGCGCGCTC   GGAGC
                                ||||||||||   |||||
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                                GTCGCGCGAG   CCTCG
                                     AC__
GAM1502 COL5A1   5' GGCGCGCTCGCCCACGGGC   6419        A  ___  A
                                GGCGCGCTC GCT  GG GC
                                ||||||||| |||  || ||
                                CCGCGCGAG CGG  CC CG
                                     _  GTG  _
GAM1502 CSDA    5' GCGCGCTCGCTCTTGGGC    18895       A  ___  A
                                GCGCGCTC GCT  GG GC
                                |||||||| |||  || ||
                                CGCGCGAG CGA  CC CG
                                     _  GAA  _
GAM1502 CTNS    5' CGGCGCTCTCGCAAAG      22345       G  A  T
                                CGGCGC CTC GC GGAG
                                |||||| ||| || ||||
                                GCCGCG GAG CG TTTC
                                   A  _ _
GAM1502 CTPS    5' CGACGCGCGCGGAG        44798       TCA  T
                                CGGCGCGC  GC GGAG
                                ||||||||  || ||||
                                GCTGCGCG  CG CCTC
                                     ___  _
GAM1502 CTSB    3' GGCCACAGTCAGCTGGGGC   42108    G  __     A
                                GGC CGC  TCAGCTGG GC
                                ||| |||  |||||||| ||
                                CCG GTG  AGTCGACC CG
                                  _  TC      C
GAM1502 CXCR4   5' CGGTGGCTACTGGAGC     18442    CGC  CA
                                CGG  GCT  GCTGGAGC
                                |||  |||  ||||||||
                                GCC  CGA  TGACCTCG
                                  AC_  __
GAM1502 CYP7B1  5' CGGCGCGCGCTAGG       22074       TCA   A
                                CGGCGCGC  GCTGG G
                                ||||||||  ||||| |
                                GCCGCGCG  CGATC C
                                     ___   _
GAM1502 DAG1    5' GGCGCGCGGCCGGAGC     20524       TCA
                                GGCGCGC  GCTGGAGC
                                |||||||  ||||||||
                                CCGCGCG  CGGCCTCG
                                   C__
GAM1502 DAZL    5' GGCGCACCACTTCTGGGGC  42778       CAG_  A
                                GGCGCGCT   CTGG GC
                                ||||||||   |||| ||
                                CCGCGTGG   GACC CG
                                     TGAA   C
GAM1502 DDX16   5' GGAGCCCTCGGCTGGAGC   44958   C  G  A
                                GG GC CTC GCTGGAGC
                                || || ||| ||||||||
```

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                                CC CG GAG CGACCTCG
                                 T  G   C
GAM1502  EDARADD   5'  CGACGCGCCTGGAG       38847        TCAG
                                CGGCGCGC    CTGGAG
                                ||||||||    ||||||
                                GCTGCGCG    GACCTC
                                    ____
GAM1502  EGR1      5'  CGGCTGCGGAGGCTGGGGC    12659     _   CTCA    A
                                CGGC GCG    GCTGG GC
                                |||| |||    ||||| ||
                                GCCG CGC    CGACC CG
                                  A  CTC_    C
GAM1502  EGR1      5'  CAGCCCGGGGCTGGAGC     12655     G  CTCA
                                CGGC CG    GCTGGAGC
                                |||| ||    ||||||||
                                GTCG GC    CGACCTCG
                                  G  CC__
GAM1502  EHD2      5'  GGCGGCTGCAGCGGGC      31134     C   _   T  A
                                GGCG GCT CAGC GG GC
                                |||| ||| |||| || ||
                                CCGC CGA GTCG CC CG
                                  _   C    _ _
GAM1502  EP300     5'  CGGCGGCCAGTGCTGGAGC    10980      C   CA_
                                CGGCG GCT   GCTGGAGC
                                ||||| |||   ||||||||
                                GCCGC CGG   CGACCTCG
                                  _   TCA
GAM1502  EXTL1     5'  GGCCCCTGTGGCTGGAGC    20869     GCG   A___
                                GGC   CTC    GCTGGAGC
                                |||   |||    ||||||||
                                CCG   GGG    CGACCTCG
                                  ___   ACAC
GAM1502  FASN      5'  CGGAGAGCGAGGCTGGAGC    19934     C__   CTCA
                                CGG   GCG    GCTGGAGC
                                |||   |||    ||||||||
                                GCC   CGC    CGACCTCG
                                  TCT   TC__
GAM1502  FOSB      3'  CAGACGACAGCTGGAGC     27531     C   CT
                                CGG GCG  CAGCTGGAGC
                                ||| |||  ||||||||||
                                GTC TGC  GTCGACCTCG
                                  _   T_
GAM1502  GAN       5'  GAGCAGAAGCTGGAGC      35145    C   CTC
                                GG GCG   AGCTGGAGC
                                || |||   |||||||||
                                CT CGT   TCGACCTCG
                                  _   CT_
GAM1502  GASC1     3'  GGTGCCACCTGCTGGAGC    42031    C  _   CA
                                GG GC GCT  GCTGGAGC
                                || || |||  ||||||||
```

```
                                CC CG TGG  CGACCTCG
                                 A  G   A_
GAM1502  GBE1     5'  AGCGGGCGCTGGAGC       6686       C  TCA
                                GGCG GC   GCTGGAGC
                                |||| ||   ||||||||
                                TCGC CG   CGACCTCG
                                  C  ___
GAM1502  GCLM     5'  CGCCGCGCGGCTGGAGC     13130    G    TCA
                                CG CGCGC   GCTGGAGC
                                || |||||   ||||||||
                                GC GCGCG   CGACCTCG
                                 G    C__
GAM1502  GNG5     5'  CGGCGCGCGGCGGGGGC     23609        TCA  T  A
                                CGGCGCGC   GC GG GC
                                ||||||||   || || ||
                                GCCGCGCG   CG CC CG
                                     C__  C  C
GAM1502  GPR48    5'  CGGCCTGCGGGCTGGAGC    32984      __  CTCA
                                CGGC  GCG   GCTGGAGC
                                ||||  |||   ||||||||
                                GCCG  CGC   CGACCTCG
                                  GA  C___
GAM1502  GRB10    3'  GGCCAGCGAGCTGGGGC     23662     __  CTC     A
                                GGC  GCG   AGCTGG GC
                                |||  |||   |||||| ||
                                CCG  CGC   TCGACC CG
                                  GT  ___     C
GAM1502  GRB14    5'  CGGGCGCTCCCGCTGGGC    21031     C     A_    A
                                CGG GCGCTC  GCTGG GC
                                ||| ||||||  ||||| ||
                                GCC CGCGAG  CGACC CG
                                  _     GG    _
GAM1502  GRIK1    5'  GCGCGCTCCCCACGGAGC    9094         AGC_
                                GCGCGCTC    TGGAGC
                                ||||||||    ||||||
                                CGCGCGAG    GCCTCG
                                     GGGT
GAM1502  HOXC5    3'  GGCGCGCTCTGCGGGC      33246         A  T  A
                                GGCGCGCTC GC GG GC
                                ||||||||| || || ||
                                CCGCGCGAG CG CC CG
                                     A  _  _
GAM1502  IL13RA1  5'  CGGCCGGGCTGGAGC       11443      G  CTCA
                                CGGC CG    GCTGGAGC
                                |||| ||    ||||||||
                                GCCG GC    CGACCTCG
                                  _ C___
GAM1502  IL6R     3'  CAGCTGAACAGCTGGAGC    8168       GCGCT
                                CGGC    CAGCTGGAGC
                                ||||    ||||||||||
```

```
                                GTCG    GTCGACCTCG
                                  ACTT_
GAM1502 ILF1    5' CGCCGCGCACCGGAGC     21105    G    TCA
                                CG CGCGC   GCTGGAGC
                                || |||||   ||||||||
                                GC GCGCG   TGGCCTCG
                                 G    ___
GAM1502 IRS2    5' CGGCGCCCAGGGGTTGGGGC   40700      G T   C___   A
                                CGGCGC C CAG    TGG GC
                                |||||| | |||    ||| ||
                                GCCGCG G GTC    ACC CG
                                   _ _   CCCA   C
GAM1502 KCNQ4   5' CGGGGCGCTCAGAGACGC    21730     C       CT GA
                                CGG GCGCTCAG  G  GC
                                ||| ||||||||  |  ||
                                GCC CGCGAGTC  C  CG
                                  C       T_ TG
GAM1502 KRT15   5' GGCCAGGTAGCTGGAGC     14012     G  CTC
                                GGC CG   AGCTGGAGC
                                ||| ||   |||||||||
                                CCG GT   TCGACCTCG
                                  _  CCA
GAM1502 KRT9    3' GGGATGCTCAGCTGGGGC    44063    CGC        A
                                GG   GCTCAGCTGG GC
                                ||   |||||||||| ||
                                CC   CGAGTCGACC CG
                                 CTA         C
GAM1502 LHX1    5' CGGGGCCCCGGGCTGGAGC   24524     C  G  CA
                                CGG GC CT  GCTGGAGC
                                ||| || ||  ||||||||
                                GCC CG GG  CGACCTCG
                                  C  G  CC
GAM1502 LHX5    3' CGGCGCCCAGCCGAGGAGC   35316      G T    __
                                CGGCGC C CAGCT  GGAGC
                                |||||| | |||||  |||||
                                GCCGCG G GTCGG  CCTCG
                                   _ _    CT
GAM1502 LHX5    5' CGGCGCCTGTTCCGGGC     35317      G  CAG   A
                                CGGCGC CT   CTGG GC
                                |||||| ||   |||| ||
                                GCCGCG GA   GGCC CG
                                   _  CAA   _
GAM1502 LMO1    5' GGCGCGCTTTGGCGGGGC    14185       CA_  T  A
                                GGCGCGCT   GC GG GC
                                ||||||||   || || ||
                                CCGCGCGA   CG CC CG
                                    AAC  C  _
GAM1502 LRP5    5' CGCCGCGCTCACTCGGGC    14231    G      GC   A
                                CG CGCGCTCA  TGG GC
                                || ||||||||  ||| ||
```

```
                                GC GCGCGAGT  GCC CG
                                 G       GA  _
GAM1502  MAB21L1  5'  CGGCTGCTAGAGCTGGAGC   24587     GC  C_
                                CGGC  GCT  AGCTGGAGC
                                ||||  |||  |||||||||
                                GCCG  CGA  TCGACCTCG
                                  A_  TC
GAM1502  MADH9    5'  CGGCGCGCACGGGAAC     25375       TCA  T
                                CGGCGCGC   GC GGAGC
                                ||||||||   || |||||
                                GCCGCGCG   TG CCTTG
                                     ___  C
GAM1502  MAF      5'  CGGCGTCCGCTCGGGGC    23827      __    AGCT  A
                                CGGCG  CGCTC   GG GC
                                |||||  |||||   || ||
                                GCCGC  GCGAG   CC CG
                                   AG    C___  _
GAM1502  MAFF     5'  CGGCGCGCTCACACACGC   29514         _  TGGA
                                CGGCGCGCTCA GC   GC
                                ||||||||||| ||   ||
                                GCCGCGCGAGT TG   CG
                                      G  TG__
GAM1502  MAPK12   5'  CGGCGCGCGCCTCGGGC    16466       TCA  __  A
                                CGGCGCGC   GCT  GG GC
                                ||||||||   |||  || ||
                                GCCGCGCG   CGG  CC CG
                                     ___   AG  _
GAM1502  MAPK12   5'  CGGCGCGCACGTGACGC    16465       TCA  _  GA
                                CGGCGCGC   GC TG  GC
                                ||||||||   || ||  ||
                                GCCGCGCG   TG AC  CG
                                     ___  C  TG
GAM1502  MDM1     3'  GGCTGCAAAAGCTGGAGC   33516    GC  TC_
                                GGC  GC   AGCTGGAGC
                                |||  ||   |||||||||
                                CCG  CG   TCGACCTCG
                                  A_  TTT
GAM1502  MKI67    5'  CGCCGCGCTCACCTCCGC    14519   G      G  GGA
                                CG CGCGCTCA CT   GC
                                || ||||||| ||   ||
                                GC GCGCGAGT GA   CG
                                 G       G  GG_
GAM1502  MMP25    3'  CAGCGCGCGACCGGGGC    35376       TCA    A
                                CGGCGCGC   GCTGG GC
                                ||||||||   ||||| ||
                                GTCGCGCG   TGGCC CG
                                     C__    C
GAM1502  MYEOV    3'  GCCCCAGTCGGCTGGAGC   39876    G   ____
                                GC CTCA    GCTGGAGC
                                || ||||    ||||||||
```

```
                              CG GGGT   CGACCTCG
                               _   CAGC
GAM1502 MYLK2    3' GGCCGACAGGCTGGAGC    37527    G CT  _
                              GGC CG  CAG CTGGAGC
                              ||| ||  ||| |||||||
                              CCG GC  GTC GACCTCG
                               _ T_  C
GAM1502 NEK6     5' CGGGCGGCTGGAGC      30823    C  CTCA
                              CGG GCG   GCTGGAGC
                              ||| |||   ||||||||
                              GCC CGC   CGACCTCG
                               _  ____
GAM1502 NELL1    5' GGCGCGCCTGGCTTGGAGC  26044       CA  _
                              GGCGCGCT  GCT GGAGC
                              ||||||||  ||| |||||
                              CCGCGCGG  CGA CCTCG
                                  AC  A
GAM1502 NFKBIL2  5' CAGCGCGCTCCCGAAGC    30239       AG
                              CGGCGCGCTC  CTGGAGC
                              ||||||||||  |||||||
                              GTCGCGCGAG  GGCTTCG
                                   __
GAM1502 NLGN2    5' CGGGCGCCCAGGGG      44752    C      CT  A
                              CGG GCGCTCAG  GG G
                              ||| ||||||||  || |
                              GCC CGCGGGTC  CC C
                               _      __ _
GAM1502 NPHS2    5' CGGGCGGCTGGAGC      31200    C  CTCA
                              CGG GCG   GCTGGAGC
                              ||| |||   ||||||||
                              GCC CGC   CGACCTCG
                               _  ____
GAM1502 NT5M     5' CGCCGTGCTGCCGGAGC    33648    G  C  CA
                              CG CG GCT  GCTGGAGC
                              || || |||  ||||||||
                              GC GC CGA  CGGCCTCG
                                G  A  __
GAM1502 PCDH7    5' CGGCGCGCCAAAGAGAAGC  37115       C  CT
                              CGGCGCGCT AG  GGAGC
                              |||||||| ||  |||||
                              GCCGCGCGG TT  CTTCG
                                   T  CT
GAM1502 PHKA1    5' CGGGTGCCACCGGAGC    15275    CGC  CA
                              CGG   GCT  GCTGGAGC
                              |||   |||  ||||||||
                              GCC   CGG  TGGCCTCG
                               CA_  __
GAM1502 PPP3CB   5' CGGCGGCTACCAGAGC    34446     C  CA  TG
                              CGGCG GCT  GC  GAGC
                              ||||| |||  ||  ||||
```

```
                                GCCGC CGA  TG  CTCG
                                  _  __  GT
GAM1502  PRKY     5'  CGGAGCGCTCGGGAAGC     15696     C     AGCT
                                CGG GCGCTC    GGAGC
                                ||| ||||||    |||||
                                GCC CGCGAG    CTTCG
                                  T     CC__
GAM1502  PRSS15   3'  GGCGCGCTCCCCACAGC     21995         AG   G
                                GGCGCGCTC  CTG AGC
                                |||||||||  ||| |||
                                CCGCGCGAG  GGT TCG
                                     G_   G
GAM1502  PTBP1    3'  CAGCTCCGCAGCTGGAGC    36716      G_   TC
                                CGGC  CGC  AGCTGGAGC
                                ||||  |||  |||||||||
                                GTCG  GCG  TCGACCTCG
                                  AG   __
GAM1502  PTK7     5'  CGGAGCGCACCGGAGC      15859     C    TCA
                                CGG GCGC   GCTGGAGC
                                ||| ||||   ||||||||
                                GCC CGCG   TGGCCTCG
                                  T   ____
GAM1502  PTPRF    5'  CGGAGCCGAAGCTGGAGC    15928     C  GCTC
                                CGG GC    AGCTGGAGC
                                ||| ||    |||||||||
                                GCC CG    TCGACCTCG
                                  T  GCT_
GAM1502  PUNC     5'  GCACAAACTCAGCTGGGGC   44881      __         A
                                GCGC  GCTCAGCTGG GC
                                ||||  |||||||||| ||
                                CGTG  TGAGTCGACC CG
                                  TT         C
GAM1502  RAB30    5'  ACTTAGCTCAGCTGGAGC    30931    GC_
                                GC   GCTCAGCTGGAGC
                                ||   ||||||||||||
                                TG   CGAGTCGACCTCG
                                 AAT
GAM1502  RAD52    5'  CGGTGCACACAGGGAGC     39557     C    T   CT
                                CGG GCGC CAG  GGAGC
                                ||| |||| |||  |||||
                                GCC CGTG GTC  CCTCG
                                  A   T  __
GAM1502  RAD9     3'  GACAGCCAGCTGGGGC      21373     C  T      A
                                GGCG GC CAGCTGG GC
                                |||| || ||||||| ||
                                CTGT CG GTCGACC CG
                                  _ _      C
GAM1502  RANBP3   3'  CGAGCTGGCAGCTGGAGC    28756    C   __
                                CG GCT  CAGCTGGAGC
                                || |||  ||||||||||
```

```
                                GC CGA  GTCGACCTCG
                                 T   CC
GAM1502  RASD1    3'  GCGCGCTCCCGGCCTGGGGC   32010        AG___   A
                                GCGCGCTC    CTGG GC
                                ||||||||    |||| ||
                                CGCGCGAG    GACC CG
                                    GGCCG   C
GAM1502  REPS2    5'  CGGCGGCGGCCCGGAGC    21813      C  TCAG
                                CGGCG GC    CTGGAGC
                                ||||| ||    |||||||
                                GCCGC CG    GGCCTCG
                                  _ CCG_
GAM1502  S100B    3'  GGCCACGCTGGAGC       26572     G   TCA
                                GGC CGC   GCTGGAGC
                                ||| |||   ||||||||
                                CCG GTG   CGACCTCG
                                  _  ___
GAM1502  SCGB1A1  3'  CAGCGGCAGAGGCTGGAGC   17862      C  TCA_
                                CGGCG GC    GCTGGAGC
                                ||||| ||    ||||||||
                                GTCGC CG    CGACCTCG
                                  _ TCTC
GAM1502  SDC2     5'  CCGCGCGGCTGGAGC       42560    G    CTCA
                                C GCGCG    GCTGGAGC
                                | |||||    ||||||||
                                G CGCGC    CGACCTCG
                                 G    ____
GAM1502  SDC4     3'  CAGGCCCCAGCTGGGGC     16519     C  G       A
                                CGG GC CTCAGCTGG GC
                                ||| || |||||||| ||
                                GTC CG GGGTCGACC CG
                                  _ _       C
GAM1502  SERPINE2 5'  CGGCCGCAACCGGAGC      44003      G   TC
                                CGGC CGC  AGCTGGAGC
                                |||| |||  |||||||||
                                GCCG GCG  TTGGCCTCG
                                  _  __
GAM1502  SFN      3'  GGTGCGCTCAACAGC       43970    C       TGG
                                GG GCGCTCAGC   AGC
                                || |||||||||   |||
                                CC CGCGAGTTG   TCG
                                 A       ___
GAM1502  SFRS2IP  5'  GGCGTGATCACTGGAGC     21793      CGC   G
                                GGCG   TCA CTGGAGC
                                ||||   ||| |||||||
                                CCGC   AGT GACCTCG
                                  ACT   _
GAM1502  SH3BP2   5'  GGCAACTGAGCTGGAGC     16636      C   C
                                GGCG GCT AGCTGGAGC
                                |||| ||| |||||||||
```

```
                                CCGT TGA TCGACCTCG
                                  _  C
GAM1502 SHB     5' CGGCGCCCGCCGGAGC      16688      G  CA
                                CGGCGC CT  GCTGGAGC
                                |||||| ||  ||||||||
                                GCCGCG GG  CGGCCTCG
                                  _  __
GAM1502 SLC18A3  5' GGCGCGCCGAGGGGC      16836       C  CT  A
                                GGCGCGCT AG  GG GC
                                |||||||| ||  || ||
                                CCGCGCGG TC  CC CG
                                    C  __  _
GAM1502 SLC19A1  5' GGCGCGCTCACAGGGC      16849        G T  A
                                GGCGCGCTCA C GG GC
                                |||||||||| | || ||
                                CCGCGCGAGT G CC CG
                                     _ T  _
GAM1502 SLC20A1  5' GGCGACAGCGGCTGGAGC    40452     _ _  TCA
                                GGCG C GC   GCTGGAGC
                                |||| | ||   ||||||||
                                CCGC G CG   CGACCTCG
                                  T T  C__
GAM1502 SLC21A2  5' GGCGCCTCGGGCTGGAGC    24801      G   A_
                                GGCGC CTC  GCTGGAGC
                                ||||| |||  ||||||||
                                CCGCG GAG  CGACCTCG
                                  _  CC
GAM1502 SMARCB1  5' GGCGCCTCAGCCGGGC     42314      G       A
                                GGCGC CTCAGCTGG GC
                                ||||| |||||||| ||
                                CCGCG GAGTCGGCC CG
                                  _       _
GAM1502 SOX11    3' GGCGCGCCCAGGAGC       17026         GCT
                                GGCGCGCTCA   GGAGC
                                ||||||||||   |||||
                                CCGCGCGGGT   CCTCG
                                    ____
GAM1502 SOX12    3' CGGTGCGCTCAGGGAGGAGC  28036    C      CT_
                                CGG GCGCTCAG   GGAGC
                                ||| ||||||||   |||||
                                GCC CGCGAGTC   CCTCG
                                  A       CCT
GAM1502 SRPX     5' CAGCGCGCTTCCCGGGGGC   26709        CAG   A_
                                CGGCGCGCT   CTGG  GC
                                |||||||||   ||||  ||
                                GTCGCGCGA   GGCC  CG
                                     AG_    CC
GAM1502 STARD4   5' CGGCGCGCTACCAAGC      40124        CA  TG A
                                CGGCGCGCT  GC  G GC
                                |||||||||  ||  | ||
```

```
                                GCCGCGCGA  TG  T CG
                                     __  GT _
GAM1502  STARD5   5'  GGTGCCTGGAGGCTGGAGC   36129    C  G  CA__
                                GG GC CT    GCTGGAGC
                                || || ||    ||||||||
                                CC CG GA    CGACCTCG
                                 A  _  CCTC
GAM1502  STX8     5'  CGTGCGCGACCGGAGC      22139    _    CTCA
                                CG GCGCG    GCTGGAGC
                                || |||||    ||||||||
                                GC CGCGC    TGGCCTCG
                                 A    _____
GAM1502  SURF2    5'  CGACGCGCCCGCGGAGC     32752         A  T
                                CGGCGCGCTC GC GGAGC
                                |||||||||| || |||||
                                GCTGCGCGGG CG CCTCG

                                     _  _
GAM1502  SYNGR3   3'  CGGTGGCCAGCTGGAGC     20095    CGC  T
                                CGG   GC CAGCTGGAGC
                                |||   || ||||||||||
                                GCC   CG GTCGACCTCG
                                 AC_  _
GAM1502  TAF15    5'  CGGCGCGGCGGCCGGAGC    40184       CTCA
                                CGGCGCG    GCTGGAGC
                                |||||||    ||||||||
                                GCCGCGC    CGGCCTCG
                                    CGC_
GAM1502  TCEA1    5'  GGGCGAAGCTGGAGC       44327    C   CTC
                                GG GCG   AGCTGGAGC
                                || |||   |||||||||
                                CC CGC   TCGACCTCG
                                 _   T__
GAM1502  THRA     5'  GGCGCGCCGGACCGGGC     17521        CA    A
                                GGCGCGCT  GCTGG GC
                                ||||||||  ||||| ||
                                CCGCGCGG  TGGCC CG
                                     CC    _
GAM1502  TIMP3    5'  CGGCGCGCTGCCCTCCGAG   7448         CA  G___
                                CGGCGCGCT  GCT   GAG
                                |||||||||  |||   |||
                                GCCGCGCGA  CGG   CTC
                                     __   GAGG
GAM1502  TM6SF2   5'  CGACGCGTTCTCCAGGGC    43661        __  AGCT  A
                                CGGCGCG  CTC   GG GC
                                |||||||  |||   || ||
                                GCTGCGC  GAG   CC CG
                                    AA   GT__  _
GAM1502  TMSB4Y   5'  CGGAGGCTGCAGCTGGAGC   20088    CGC  _
                                CGG   GCT CAGCTGGAGC
                                |||   ||| ||||||||||
```

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                                GCC   CGA GTCGACCTCG
                                  TC_   C
GAM1502 TNFRSF12 3' CTTCGCCTTGGCTGGAGC    19124   GG   G  CA
                                C  CGC CT  GCTGGAGC
                                |  ||| ||  ||||||||
                                G  GCG GA  CGACCTCG
                                 AA   _  AC
GAM1502 TNFRSF12 5' CGGGCGCCCAGGGG       19123     C      CT  A
                                CGG GCGCTCAG  GG G
                                ||| ||||||||  || |
                                GCC CGCGGGTC  CC C
                                  _      __ _
GAM1502 TNNC1    3' CAGGACTCAGCTGGAG      17616     CGC
                                CGG   GCTCAGCTGGAG
                                |||   ||||||||||||
                                GTC   TGAGTCGACCTC
                                  C__
GAM1502 UGCG     5' CGGCGCGCTCGCGGGC      17871         A  T  A
                                CGGCGCGCTC GC GG GC
                                |||||||||| || || ||
                                GCCGCGCGAG CG CC CG
                                     _  _  _
GAM1502 UNC119   5' GCCTGCGCCGGCTGGAGC    38345    __    CA
                                GC  GCGCT  GCTGGAGC
                                ||  |||||  ||||||||
                                CG  CGCGG  CGACCTCG
                                 GA    C_
GAM1502 USP13    5' CGGCGCGCACCGGAGC      19480        TCA
                                CGGCGCGC   GCTGGAGC
                                ||||||||   ||||||||
                                GCCGCGCG   TGGCCTCG
                                     ___
GAM1502 VGF      5' CGGCGCGGCTCCGGGC      17988       _  AGC   A
                                CGGCGCG CTC   TGG GC
                                ||||||| |||   ||| ||
                                GCCGCGC GAG   GCC CG
                                    C  ___  _
GAM1502 WNT3A    3' CGGCGCGCCTGGAG        37542        TCAG
                                CGGCGCGC    CTGGAG
                                ||||||||    ||||||
                                GCCGCGCG    GACCTC
                                     _____
GAM1502 XT3      5' CGGCGCGCTCGGCTCCGG    33663         A  __
                                CGGCGCGCTC GCT  GG
                                |||||||||| |||  ||
                                GCCGCGCGAG CGA  CC
                                      C   GG
GAM1502 ZNF278   5' CGGCGGCGGCTGGAGC      36790      C  TCA
                                CGGCG GC   GCTGGAGC
                                |||||  ||   ||||||||
```

```
                                GCCGC CG   CGACCTCG
                                  _ C__
GAM1502 ZNFN1A3  5' CGGGCCGGGCTGGAGC     41199     CGC   CA
                                CGG   GCT  GCTGGAGC
                                |||   |||  ||||||||
                                GCC   CGG  CGACCTCG
                                 ____  CC
GAM1503 MGAT5    5' TCTCCCACTACGTACCTGCTGG 14478        GC   GG  _ C
           T                     TCTCCCAC  CGT  ACC GC GGT
                                |||||||||  |||  ||| || |||
                                AGAGGGTG  GCA  TGG CG CCA
                                    AT   __   A  A
GAM1503 RAB4A    5' CCCCACGGCAACCGCCGG    21345       CC TG A
                                TCCCACG  G  G CCGCCGG
                                |||||||  |  | |||||||
                                GGGGTGC  C  T GGCGGCC
                                   __ GT _
GAM1503 SLC13A4  5' TCTCCCACCTGGGCTCGCTGTT 29726      AC   GT  AC   C___
           GGT                    TCTCCC  GCC  GG  CGC   GGT
                                ||||||  |||  ||  |||   |||
                                AGAGGG  TGG  CC  GCG   CCA
                                   __  AC  GA   ACAA
GAM1504 BACH2    3' ATATATAATATGTACAG     34775      CAAC
                                ATATA   ATATGTACAG
                                |||||   ||||||||||
                                TATAT   TATACATGTC
                                  AT__
GAM1504 ELF3     3' TACAGATATACAGTTTACAGC  20756     _     ACATATG
                                TACA ATATACA      TACAGC
                                |||| |||||||      ||||||
                                ATGT TATATGT      ATGTCG
                                  C      CAA____
GAM1504 GPR48    3' ATATGCACAGTATGTACAG   32981      ACA  _
                                ATAT   ACA TATGTACAG
                                ||||   ||| |||||||||
                                TATA   TGT ATACATGTC
                                  CG_   C
GAM1504 IL18RAP  3' TACAATACATGGTAGACATGAC 19292         CAAC__    T
           AG                     TACAATATA     ATATG ACAG
                                |||||||||     ||||| ||||
                                ATGTTATGT     TGTAC TGTC
                                    ACCATC    _
GAM1504 KCNJ6    3' TACATAAGGCATATATATGTAC 13861     ATATA  AC_
           AG                     TACA    CA   ATATGTACAG
                                ||||    ||   ||||||||||
                                ATGT    GT   TATACATGTC
                                  ATTCC  ATA
GAM1504 PKD2     3' TACATATACATAAATATGTACA 41078     A     AC_
           G                      TACA TATACA   ATATGTACAG
                                |||| ||||||   ||||||||||
```

```
                                ATGT ATATGT   TATACATGTC
                                  _     ATT
GAM1504  PLXNA1   3'  ATATATATACATGTACAGC   43616      CAAC
                                ATATA   ATATGTACAGC
                                |||||   ||||||||||
                                TATAT   TGTACATGTCG
                                  ATA_
GAM1504  PUM1     3'  TACAATATACAACACTATATGC 31234           ___
                                TACAATATACAACAT   ATGT
                                ||||||||||||||   ||||
                                ATGTTATATGTTGTG   TACG
                                         ATA
GAM1504  RAG1     3'  TACAATATACAACAAAATG   7788            T_
                                TACAATATACAACA  ATG
                                ||||||||||||||  |||
                                ATGTTATATGTTGT  TAC
                                         TT
GAM1504  TP53BP2  3'  ACAATATACAAGGTGTGCAG  24058         CATA  A
                                ACAATATACAA   TGT CAG
                                ||||||||||    ||| |||
                                TGTTATATGTT   ACA GTC
                                      CC__  C
GAM1504  ZNF10    3'  TATACAACATTACAAGC     31743         ATG   _
                                TATACAACAT   TACA GC
                                ||||||||||   |||| ||
                                ATATGTTGTA   ATGT CG
                                     ____   T
GAM1505  ATOX1    3'  CAGCATCCTGCCCCCTTT    19722        _
                                TAGTGTCC GCCCCCTTT
                                ||||||||| |||||||||
                                GTCGTAGG CGGGGGAAA
                                    A
GAM1505  FLRT2    3'  TCAATATAATTCTTCCCTTTA 29855         G  CGCC
                                TCAATATAGT TC   CCCTTTA
                                |||||||||| ||   |||||||
                                AGTTATATTA AG   GGGAAAT
                                      _  AA__
GAM1505  WASF3    3'  CCAATGTAGTAGGCCCTTTTTA 27379      A    TCC   CC
                                TCAAT TAGTG  GCCC  TTTA
                                ||||| |||||  ||||  ||||
                                GGTTA ATCAT  CGGG  AAAT
                                   C    C__   AA
GAM1506  CACNB1   3'  TGGGCACCATCCCACGGG    8787    A T     ATTC
                                TG G CACCGT   CCCACGGG
                                || | ||||||   ||||||||
                                AC C GTGGTA   GGGTGCCC
                                 C _     _____
GAM1506  LIMK1    3'  TAAGTCATGGTCCCACGGG   14172       CC  ATTC
                                TGAGTCA  GT   CCCACGGG
                                |||||||  ||   ||||||||
```

```
                                ATTCAGT  CA   GGGTGCCC
                                   AC  ____
GAM1506  TPI1     5'  TGATTCACCGCAAGACTGTGGG 7479     G      TTCCCCAC
              C                    TGA TCACCGTA      GGGC
                                   ||| ||||||||      ||||
                                   ACT AGTGGCGT      CCCG
                                     A       TCTGACA_
GAM1506  ADAM17   3'  GGCTGCAGGCGGCCTG     17252       TT
                                   GGCTGCG  GGCGGCCTG
                                   |||||||  |||||||||
                                   CCGACGT  CCGCCGGAC
                                      __
GAM1506  ADCY8    5'  GGCTGCAGGGGGCCTG     10013       TT  C
                                   GGCTGCG  GG GGCCTG
                                   |||||||  ||  ||||||
                                   CCGACGT  CC CCGGAC
                                      C_  _
GAM1506  AF5Q31   5'  TGGCGGCGCCGGGCCTG    30862     T     CG
                                   TGGC GCGTTGG  GCCTG
                                   ||||  |||||||  |||||
                                   ACCG CGCGGCC  CGGAC
                                     C      __
GAM1506  AHR      5'  AGCTGCCTGGGCCTG      11544       G   CG
                                   GGCTGC TTGG  GCCTG
                                   ||||||  ||||  |||||
                                   TCGACG GACC  CGGAC
                                      _   __
GAM1506  ARF1     3'  TGGGTAGGGCGGCCTG     43312     CTGC  T_
                                   TGG   GT  GGCGGCCTG
                                   |||   ||  |||||||||
                                   ACC   CA  CCGCCGGAC
                                     _____  TC
GAM1506  ARHG     5'  TGGCTGCAGTGACCTG      11689       GTT  C
                                   TGGCTGC   GG GGCCTG
                                   |||||||   || ||||||
                                   ACCGACG   TC CTGGAC
                                      ___  A
GAM1506  ARHG     5'  TGGCTGCAGTGACATCTG    44116       T    GC
                                   TGGCTGCG TGGCG  CTG
                                   ||||||||  |||||  |||
                                   ACCGACGT ACTGT  GAC
                                      C     A_
GAM1506  BCL11B   3'  TGGCGGCGCTGAGTCTG     39762     T     GC  C
                                   TGGC GCGTTG  GG CTG
                                   ||||  ||||||  ||  |||
                                   ACCG CGCGAC  TC GAC
                                     C      __  A
GAM1506  BCL2     3'  GGCACTTGTGGCGGCCTG    8523      T  GT_
                                   GGC GC   TGGCGGCCTG
                                   |||  ||   ||||||||||
```

```
                                CCG TG   ACCGCCGGAC
                                  _ AAC
GAM1506 BMP1    3' TGGCTGCGGTGCCCTG     25996       TTG  GG
                                TGGCTGCG   GC  CCTG
                                ||||||||   ||  ||||
                                ACCGACGC   CG  GGAC
                                    CA_  __
GAM1506 C1orf1  5' TGACTGCAACTTGGGCCTG  10229       TTGGC
                                TGGCTGCG    GGCCTG
                                ||||||||    ||||||
                                ACTGACGT    CCGGAC
                                    TGAAC
GAM1506 CD81    5' GGCGGCGGGCGGCCTG     20345    T   TT
                                GGC GCG  GGCGGCCTG
                                ||| |||  |||||||||
                                CCG CGC  CCGCCGGAC
                                  C  __
GAM1506 COMT    5' TGGCTGCGGGAGGGGTCTG  28697       TT_  C  C
                                TGGCTGCG   GG GG CTG
                                ||||||||   || || |||
                                ACCGACGC   CC CC GAC
                                    CCT  _  A
GAM1506 CYBB    3' TGGCTGGCAGCTGGTGGC   44103      _ _    C
                                TGGCTG C GTTGG GGC
                                |||||| | ||||| |||
                                ACCGAC G CGACC CCG
                                   C T    A
GAM1506 EPHA8   3' TGGTTGCAGTGCAACCTG   33907    C   TTG
                                TGG TGCG   GCGGCCTG
                                ||| ||||   ||||||||
                                ACC ACGT   CGTTGGAC
                                  A   CA_
GAM1506 FEN1    5' TAGCGGCGGGTGGCCTG    19960     T   TT  C
                                TGGC GCG  GG GGCCTG
                                |||| |||  || ||||||
                                ATCG CGC  CC CCGGAC
                                  C   __  A
GAM1506 FLNA    3' GGCCAGGGCGGCCTG      11136      CGTT
                                GGCTG   GGCGGCCTG
                                |||||   |||||||||
                                CCGGT   CCGCCGGAC
                                  C___
GAM1506 GAL     5' GGCTCTGGCGGCCTG      45052     GCG
                                GGCT   TTGGCGGCCTG
                                ||||   ||||||||||
                                CCGA   GACCGCCGGAC
                                   ___
GAM1506 GALR1   5' GGCTGCGTGCTGCACCTG   11205       TG_  G
                                GGCTGCGT   GCG CCTG
                                ||||||||   ||| ||||
```

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                                CCGACGCA  CGT GGAC
                                    CGA  _
GAM1506  GAS1    5'  TGGCTGCGGTGGCTTCCTG   13075       T   GG
                                TGGCTGCG TGGC  CCTG
                                |||||||| ||||  ||||
                                ACCGACGC ACCG  GGAC
                                    C   AA
GAM1506  GFAP    3'  GGCTGGGGCGGCCTG      13123      CGTT
                                GGCTG   GGCGGCCTG
                                |||||   |||||||||
                                CCGAC   CCGCCGGAC
                                  C___
GAM1506  GLDC    5'  GGCTGCGCCCGGCCTG     42026       GG
                                GGCTGCGTT  CGGCCTG
                                |||||||||  |||||||
                                CCGACGCGG  GCCGGAC
                                    __
GAM1506  GPR45   5'  TGGCTGCATCTTCCTG     28521       GGCGG
                                TGGCTGCGTT   CCTG
                                ||||||||||   ||||
                                ACCGACGTAG   GGAC
                                    AA___
GAM1506  GPRC5B  3'  TGGCTGTGAGGCGGCCTG   32180      CGTT
                                TGGCTG   GGCGGCCTG
                                ||||||   |||||||||
                                ACCGAC   CCGCCGGAC
                                   ACT_
GAM1506  HNRPM   5'  GGCTGCACCGCGGTCTG    25571       TT G  C
                                GGCTGCG  G CGG CTG
                                |||||||  | ||| |||
                                CCGACGT  C GCC GAC
                                    GG _  A
GAM1506  KCNS2   5'  TGGCTGCGTGGTCCCG     42839       T  CGG
                                TGGCTGCGT GG  CCTG
                                |||||||||  ||  ||||
                                ACCGACGCA CC  GGGC
                                    _  A__
GAM1506  KIF5C   5'  GGCTGCAGACCGGCCTG    21155       TT  _
                                GGCTGCG  GGC GGCCTG
                                |||||||  ||| ||||||
                                CCGACGT  CTG CCGGAC
                                    __  G
GAM1506  LNPEP   3'  TGGCTGACAAACCAGCGGCCTG 24558      _ __ TG
                                TGGCTG CG  T  GCGGCCTG
                                ||||||  ||  |  ||||||||
                                ACCGAC GT  G  CGCCGGAC
                                   T  TT GT
GAM1506  LPIN2   5'  TGGCTGGGTACGGCCTG    31225       C  TG
                                TGGCTG GT  GCGGCCTG
                                ||||||  ||  ||||||||
```

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                                ACCGAC CA  TGCCGGAC
                                   C  __
GAM1506  MRPL49   3'  TGGTGGTGGGCGCCTG     43030     C  C  T   G
                                TGG TG GT GGCG CCTG
                                ||| || || |||| ||||
                                ACC AC CA CCGC GGAC
                                  _ _ C   _
GAM1506  MSI1     3'  GGTTGGGCTGCGGCCTG     14650    C  C   G
                                GG TG GTTG CGGCCTG
                                || || |||| |||||||
                                CC AC CGAC GCCGGAC
                                 A  C   _
GAM1506  NOVA1    3'  TGGTGTGTCAAATGGCCTG   27063     C  C  TG C_
                                TGG TG GT  G  GGCCTG
                                ||| || ||  |  ||||||
                                ACC AC CA  T  CCGGAC
                                  _  A  GT TA
GAM1506  NPR1     5'  TAGCTGCGACGGTCTG      44587       TTG   C
                                TGGCTGCG   GCGG CTG
                                ||||||||   |||| |||
                                ATCGACGC   TGCC GAC
                                     ___   A
GAM1506  PACE     3'  TGGCTGCGCCAGCCTG      15041        TGG
                                TGGCTGCGT   CGGCCTG
                                |||||||||   |||||||
                                ACCGACGCG   GTCGGAC
                                     ___
GAM1506  PC       3'  TGGCTGGCCTGGGCCTG     9555       C   GGC
                                TGGCTG GTT   GGCCTG
                                |||||| |||   ||||||
                                ACCGAC CGG   CCGGAC
                                   _   AC_
GAM1506  PDE6B    3'  TGGATGAGAAACGGCCTG    7104      C  CGTT
                                TGG TG    GGCGGCCTG
                                ||| ||    |||||||||
                                ACC AC    TTGCCGGAC
                                  T  TCT_
GAM1506  PDK4     5'  TGGCTTGTGCGCCCCGGCCTG  15208      ___    GG
                                TGGCT   GCGTT  CGGCCTG
                                |||||   |||||  |||||||
                                ACCGA   CGCGG  GCCGGAC
                                   ACA    G_
GAM1506  PDPK1    3'  TGGCTGGCAGGTGGTCTG    15213      C  T  C  C
                                TGGCTG GT GG GG CTG
                                |||||| || || || |||
                                ACCGAC CG CC CC GAC
                                   _ T  A  A
GAM1506  PPARGC1  3'  TAGCTGCATTGGCCTG      29959         GGC
                                TGGCTGCGTT   GGCCTG
                                ||||||||||   ||||||
```

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                              ATCGACGTAA  CCGGAC
                                   ___
GAM1506 PTGFRN  3' TGGCTGCAGGCAGTCTG    42602       TT   C
                              TGGCTGCG  GGCGG CTG
                              ||||||||  ||||| |||
                              ACCGACGT  CCGTC GAC
                                   __    A
GAM1506 PTGIS   5' TGGCGGGGCTGGCGGCCTG   9680     TGC
                              TGGC  GTTGGCGGCCTG
                              ||||  ||||||||||||
                              ACCG  CGACCGCCGGAC
                                CCC
GAM1506 ROR1    5' TGGCTGCAGCCTCGCCTG    22703      GTT  G__
                              TGGCTGC  GGC  GCCTG
                              |||||||  |||  |||||
                              ACCGACG  TCG  CGGAC
                                   ___  GAG
GAM1506 RUNX1   3' GGCTGCGCGGGCCTG      12026       TGGC
                              GGCTGCGT   GGCCTG
                              ||||||||   ||||||
                              CCGACGCG   CCGGAC
                                   C___
GAM1506 SFRP1   5' TGGCGGCCCTCGGCCTG    16578     T  G  GG
                              TGGC GC TT  CGGCCTG
                              |||| || ||  |||||||
                              ACCG CG GA  GCCGGAC
                                C  G  __
GAM1506 SLC2A6  3' TGGCTGCCTCCAGCCC     32773       G  GG
                              TGGCTGC TT  CGGCCT
                              ||||||| ||  ||||||
                              ACCGACG AG  GTCGGG
                                   G  __
GAM1506 STIM1   5' GGCTGCGGCGGCCTG      41132      GTT
                              GGCTGC  GGCGGCCTG
                              ||||||  |||||||||
                              CCGACG  CCGCCGGAC
                                   ___
GAM1506 SYN3    3' TAGCTGCGGAGAGCCTG    18568       TT  C
                              TGGCTGCG  GG GGCCTG
                              ||||||||  || ||||||
                              ATCGACGC  CT TCGGAC
                                   __  C
GAM1506 TBL1X   5' GGTGGCGAATGGCGGCCTG  24895   CT  T_
                              GG  GCG  TGGCGGCCTG
                              ||  |||  ||||||||||
                              CC  CGC  ACCGCCGGAC
                               AC  TT
GAM1506 TCP11   3' TGGCTGCAGGGCCT       33072       GTT  C
                              TGGCTGC  GG GGCCT
                              |||||||  || |||||
```

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                              ACCGACG   TC CCGGA
                                 ___  _
GAM1506  TEM7     3'  TGGCGGCAGATGGCCTG     33819      T   TT GC
                              TGGC GCG  G  GGCCTG
                              |||| |||  |  ||||||
                              ACCG CGT  C  CCGGAC
                                C   __ TA
GAM1506  UBE2H    3'  TGGCTGCAGGGCCT       17809        GTT  C
                              TGGCTGC   GG GGCCT
                              |||||||   || |||||
                              ACCGACG   TC CCGGA
                                 ___  _
GAM1506  VIPR2    3'  TGGCCGCAGCTGGCCTG     18030        GTT  _
                              TGGCTGC   GGC GGCCTG
                              |||||||   ||| ||||||
                              ACCGGCG   TCG CCGGAC
                                 ___   A
GAM1506  WHSC1L1  5'  GGCTGGCAGCCCGGCCTG    35713       C  TGG_
                              GGCTG GT    CGGCCTG
                              ||||| ||    |||||||
                              CCGAC CG    GCCGGAC
                                 _  TCGG
GAM1507  ABCD3    3'  CAGAGATAAAACAGTGC     16018        TT    A
                              CAGAGATA  ATGG TGC
                              ||||||||  |||| |||
                              GTCTCTAT  TGTC ACG
                                   TT   _
GAM1507  ABCF1    3'  CAGAGAAATGGATGC       9906        TATT
                              CAGAGA    ATGGATGC
                              ||||||    ||||||||
                              GTCTCT    TACCTACG
                                 T___
GAM1507  ARNT2    3'  CACCAGAGAAATTCAAGG    31353         T   AT_
                              CACCAGAGA ATT   GG
                              ||||||||| |||   ||
                              GTGGTCTCT TAA   CC
                                    T   GTT
GAM1507  D10S170  3'  ACGAGAGACATGGATG      24132     C     ATT
                              AC AGAGAT   ATGGATG
                              || ||||||   |||||||
                              TG TCTCTG   TACCTAC
                               C     ___
GAM1507  ELMO2    3'  ACCAGAGATGTTAGAGC     35220         ATTA    T
                              ACCAGAGAT    TGGA GC
                              |||||||||    |||| ||
                              TGGTCTCTA    ATCT CG
                                   CA__    _
GAM1507  FKBP10   3'  CACCAGAGATGTCTCCTCTGC  34957          A  ATGGA
                              CACCAGAGAT TT     TGC
                              |||||||||| ||     |||
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                                GTGGTCTCTA AG    ACG
                                      C  AGGAG
GAM1507 GGA3    3' CCAGAGATGTCCGATTGC   39786       ATTA  A
                                CCAGAGAT   TGG TGC
                                ||||||||   ||| |||
                                GGTCTCTA   GCT ACG
                                     CAG_  A
GAM1507 IL12A   3' CAGAGGTATCATGTGGATG   9401      A   __
                                CAGAG TATTA  TGGATG
                                ||||| |||||  ||||||
                                GTCTC ATAGT  ACCTAC
                                   C    AC
GAM1507 NESG1   3' CAGCAATTATGGATGC     29579    AGAT
                                CAG   ATTATGGATGC
                                |||   ||||||||||
                                GTC   TAATACCTACG
                                  GT__
GAM1507 NFYA    3' CACCAGAGGGATAAATGC   14767       ATATT
                                CACCAGAG    ATGGATGC
                                ||||||||    ||||||||
                                GTGGTCTC    TATTTACG
                                     CC___
GAM1507 NOTCH2  3' CCAGGCCATGGATGC      35907     AGATA
                                CCAG    TTATGGATGC
                                ||||    ||||||||||
                                GGTC    GGTACCTACG
                                  C____
GAM1507 PDK4    3' CCTAGAAAATGGATG      15203   _   TATT
                                CC AGAGA   ATGGATG
                                || |||||   |||||||
                                GG TCTTT   TACCTAC
                                 A   ____
GAM1507 PPP1R3C 3' CAGTAGAAAAGTATGGATGC 23987    _  TAT_
                                CAG AGA   TATGGATGC
                                ||| |||   |||||||||
                                GTC TCT   ATACCTACG
                                  A  TTTC
GAM1507 PRKAR1A 3' CCAGAGGAATAAATGC     15606      ATATT
                                CCAGAG    ATGGATGC
                                ||||||    ||||||||
                                GGTCTC    TATTTACG
                                   CT___
GAM1507 SNX9    3' CCAGAGACGCCGGGGTGC   32150       ATTA  A_
                                CCAGAGAT   TGG  TGC
                                ||||||||   |||  |||
                                GGTCTCTG   GCC  ACG
                                     CG__   CC
GAM1507 SYNGR1  3' CACCACAGATGGATGGATG  21752      G   ATT
                                CACCA AGAT   ATGGATG
                                ||||| ||||   |||||||
```

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                                GTGGT TCTA   TACCTAC
                                  G    CC_
GAM1507  TAT      3'  CAGGAGAATGGATGC      7400      _   TATT
                                CAG AGA    ATGGATGC
                                ||| |||    ||||||||
                                GTC TCT    TACCTACG
                                  C  ____
GAM1507  TGFBR3   3'  CCAAATTATGGATG       17489      GATA
                                CCAGA    TTATGGATG
                                |||||    |||||||||
                                GGTTT    AATACCTAC
                                   ____
GAM1507  TM7SF3   3'  CACCAGAGACTGTTGAAC    40652         ATTA
                                CACCAGAGAT    TGGAT
                                ||||||||||    |||||
                                GTGGTCTCTG    ACTTG
                                     ACA_
GAM1507  TRADD    3'  CACCAAAGATCAAGGTGC    19122         ATTAT  A
                                CACCAGAGAT     GG TGC
                                ||||||||||     || |||
                                GTGGTTTCTA     CC ACG
                                     GTT__  _
GAM1508  TNFSF9   3'  AATAAATATCAAGGTCCAACTT 19190         TA___
              GG                  AATAAATATT     CCAACTTGG
                                ||||||||||     |||||||||
                                TTATTTATAG     GGTTGAACC
                                     TTCCA
GAM1509  PPT2     3'  TACAGTTATGTTTTGCCTCCTG 39926        T     CAA_  A
              T                   TACAGTT ATGTTT    TT TGT
                                ||||||| ||||||    || |||
                                ATGTCAA TACAAA    AG ACA
                                   _     ACGG  G
GAM1510  ATP6V1E1 3'  GGAAGGAGTGGTGTGCCAC    11786      A   A  AT
                                GGAAG AGT GT  GTGTTAT
                                ||||| ||| ||  |||||||
                                CCTTC TCA CA  CACGGTG
                                  C   C  __
GAM1510  SCD      3'  TAGGAAGAAGTGAAAGTTGT   22832          ___   A
                                TAGGAAGAAGT   AGT TGT
                                ||||||||||   ||| |||
                                ATCCTTCTTCA   TCA ACA
                                     CTT   _
GAM1510  SELP     3'  CAGGAAGGGGTGGTAGGT     16548        AA  A   T
                                TAGGAAG  GT GTA GT
                                |||||||  || ||| ||
                                GTCCTTC  CA CAT CA
                                    CC  C   C
GAM1510  TPS1     3'  TAGGAAGCAGTGGTGTT      41308       AGA     AT
                                TAGGA   AGTAGT  GTGTT
                                |||||   ||||||  |||||
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                                ATCCT  TCGTCA  CACAA
                                  ___     C_
GAM1510  TPSB1    3'  TAGGAAGCAGTGGTGTT    17659      AGA     AT
                                TAGGA  AGTAGT  GTGTT
                                |||||  ||||||  |||||
                                ATCCT  TCGTCA  CACAA
                                  ___     C_
GAM1511  DGKA     3'  TGTGCGCATGGGGAACA    10647    C       AAA
                                TG TGCGCATG  GAGCG
                                || ||||||||  |||||
                                AC ACGCGTAC  CTTGT
                                 _      CC_
GAM1511  MGAT1    3'  CTGGTCAAGAGAGCGAACG   14432    CG  TGAA
                                CTG  CA   AGAGCGAACG
                                |||  ||   ||||||||||
                                GAC  GT   TCTCGCTTGC
                                  CA  TC__
GAM1511  MYOD1    3'  TGCTGCGTGGAAAAAAC    42132       CAT
                                TGCTGCG  GAAAGAGC
                                |||||||  ||||||||
                                ACGACGC  CTTTTTTG
                                    AC_
GAM1511  TNF      3'  TTCACTGTGCAGGCCACACATT 44979         _  ATTAT
                                TTCACTGTGC GGC    TACATT
                                |||||||||| |||    ||||||
                                AAGTGACACG CCG    GTGTAA
                                      T  GT___
GAM1511  XDH      3'  TCATTGTGTTTACAAATTACAT 40461    C   CG_  TT
              T                  TCA TGTG  GCA  ATTACATT
                                |||  ||||  |||  ||||||||
                                AGT ACAC  TGT  TAATGTAA
                                  A   AAA  T_
GAM1512  CTSL2    3'  TATCTTACACAATAAGCGTTTG 10638          AG    C
                                TATCTTACGCAA  AAGCG TTG
                                ||||||||||||  ||||| |||
                                ATAGAATGTGTT  TTCGC AAC
                                      A_    A
GAM1513  CENTD2   3'  TGGAAGGAAGGCTGAAGTC   31606       C  AAGTG
                                TGGAAGGA GGG    GAAGTC
                                |||||||| |||    ||||||
                                ACCTTCCT TCC    CTTCAG
                                    _  GA___
GAM1513  CLCN4    5'  GGGGGGAAGACCCTGGAAGTCC 12289    AC    ____
                                GG  GGGAAG   TGGAAGTCC
                                ||  ||||||   |||||||||
                                CC  CCCTTC   ACCTTCAGG
                                 C_    TGGG
GAM1513  ELK1     3'  GGGAGGTGGGGGAGATGTCC  23411    A  AC  AAGT  A
                                GG AGG  GGG   GGA GTCC
                                || |||  |||   ||| ||||
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                                CC TCC  CCC    TCT CAGG
                                 C   A_   CC__   A
GAM1513  JPH2     5'  TGAAAGGGTGGGGTGGAGGGGT 45380        AC   AA    A__
              CC                   TGGAAGG  GGG  GTGGA   GTCC
                                   |||||||  |||  |||||   ||||
                                   ACTTTCC  CCC  CACCT   CAGG
                                      CA   __    CCC
GAM1513  NDRG2    3'  TGGGAGACGGGAGGGCACCC   32198     AA      A T  AAG
                                   TGG  GGACGGGA G GG   TCC
                                   |||  |||||||| | ||   |||
                                   ACC  TCTGCCCT C CC   GGG
                                     C_       _ _  GT_
GAM1513  PML      3'  TGGAAGGAGGGGCTAATAGGAG 37742        C   A_    A
              TC                   TGGAAGGA GGG  AGTGG AGTC
                                   ||||||||  |||  ||||| ||||
                                   ACCTTCCT CCC  TTATC TCAG
                                      C   GA    C
GAM1513  PMM2     3'  GGCACTGGAGGTGGAAGTCC   43554    _  G   A
                                   GG AC GGA GTGGAAGTCC
                                   || || ||| ||||||||||
                                   CC TG CCT CACCTTCAGG
                                    G  A   C
GAM1513  PPP2R1A  3'  GGGAGGACGGGAGGTGGA    30599    A       A
                                   GG AGGACGGGA GTGGA
                                   || |||||||| |||||
                                   CC TCCTGCCCT CACCT
                                    C        C
GAM1513  PPP3CA   3'  TGGAAGGATGAGAATTCTGTAA 9618         C    GTGG__
              GT                   TGGAAGGA GGGAA     AAGT
                                   ||||||||  |||||     ||||
                                   ACCTTCCT CTCTT     TTCA
                                      A    AAGACA
GAM1513  RXRG     3'  GGAAAGTGCAGGGTGGGGGTCC 27943       A_   AA   AA
                                   GGAAGG  CGGG  GTGG  GTCC
                                   ||||||  ||||  ||||  ||||
                                   CCTTTC  GTCC  CACC  CAGG
                                      AC    __    CC
GAM1513  SGT      3'  TGGGAGGAGGGGAAACATGTC  16621     A   C    GT GAA
                                   TGG AGGA GGGAA  G   GTC
                                   ||| |||| |||||  |   |||
                                   ACC TCCT CCCTT  T   CAG
                                     C   C    TG A__
GAM1513  SLC6A8   3'  TGGAGGTGCGGGAAGTGCATCC 24791      A  A_       GAA
                                   TGGA GG  CGGGAAGTG   GTCC
                                   ||||  ||  |||||||||   ||||
                                   ACCT CC  GCCCTTCAC   TAGG
                                     _  AC        G__
GAM1513  SOD3     3'  TGGAAGGATGGTGGGT      16961         C  GAAG   AA
                                   TGGAAGGA GG    TGG  GT
                                   ||||||||  ||    |||  ||
```

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                                ACCTTCCT CC    ACC  CA
                                    A _____   __
GAM1513  STC1     3'  GGAGGGAGGGGAAGAGTC     17178     A   C     TGGA
                                GGA GGA GGGAAG    AGTC
                                ||| ||| ||||||    ||||
                                CCT CCT CCCTTC    TCAG
                                  C   C     _____
GAM1513  TEGT     3'  TGGAAGGAGAGGAAGTCTGG   42102        C     T_____
                                TGGAAGGA GGGAAG     GG
                                |||||||| ||||||      ||
                                ACCTTCCT TCCTTC     CC
                                    C      AGAIII
GAM1514  APLP2    3'  CAGGCTAATCTCTGTGGAAGC  44917         CA____
                                CAGGCTGG     TGGAAGC
                                ||||||||     |||||||
                                GTCCGATT     ACCTTCG
                                    AGAGAC
GAM1514  ARNTL    5'  CCCGGCACACAGGAAGC     10132    A   TG   T
                                CC GGC  GCA GGAAGC
                                || |||  ||| ||||||
                                GG CCG  TGT CCTTCG
                                 G   TG  _
GAM1514  ASB2     3'  CCAGGCTGAGAGGGAGGC    32050         CAT   A
                                CCAGGCTGG   GGA GC
                                |||||||||   ||| ||
                                GGTCCGACT   CCT CG
                                    CTC   C
GAM1514  BRCA1    3'  CCAATTGCATGGAAGC      28623      GCTG
                                CCAG    GCATGGAAGC
                                ||||    ||||||||||
                                GGTT    CGTACCTTCG
                                  AA__
GAM1514  C1QA     3'  CAGGCGGAGCATGGAAGC    31995       T _
                                CAGGC G GCATGGAAGC
                                ||||| | ||||||||||
                                GTCCG C CGTACCTTCG
                                   C T
GAM1514  CAPNS1   3'  CCTCGGGGCATGGAGGC     11978    A_  CT       A
                                CC  GG  GGCATGGA GC
                                ||  ||  |||||||| ||
                                GG  CC  CCGTACCT CG
                                 AG  __       C
GAM1514  CDK10    5'  CCAGGCCAGGCTGGGGGC    38148        _   A   AA
                                CCAGGCT GGC TGG  GC
                                ||||||| ||| |||  ||
                                GGTCCGG CCG ACC  CG
                                    T   _   CC
GAM1514  CEBPA    3'  CCAGGCTTTCAGGAGGC     20386        GG  T   A
                                CCAGGCT  CA GGA GC
                                |||||||  || ||| ||
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                                GGTCCGA  GT CCT CG
                                    AA  _  C
GAM1514 CENPC1   5' TACCAGGCCGCGGCCAAGC   12236        __  ATGG
                                TACCAGGCT  GGC   AAGC
                                |||||||||  |||   ||||
                                ATGGTCCGG  CCG   TTCG
                                    CG  G___
GAM1514 COMT     3' TACCAGGCTGGGTGAGAGAGC 28693         CAT_ GA
                                TACCAGGCTGG   G  AGC
                                ||||||||||   |  |||
                                ATGGTCCGACC   C  TCG
                                     CACT TC
GAM1514 DNASE1L1 3' TACCAGGCATGCAGAAGC    27500       TG  TG
                                TACCAGGC  GCA  GAAGC
                                ||||||||  |||  |||||
                                ATGGTCCG  CGT  CTTCG
                                    TA  __
GAM1514 DNMT3L   5' CACCAGGCTATGGGGGC     30054       GGC   AA
                                TACCAGGCT   ATGG  GC
                                |||||||||   ||||  ||
                                GTGGTCCGA   TACC  CG
                                    ___   CC
GAM1514 DTR      3' AGCTACAGGCATGGAAGC    12609     ___
                                GGCT   GGCATGGAAGC
                                ||||   ||||||||||
                                TCGA   CCGTACCTTCG
                                  TGT
GAM1514 EDG8     3' CCAGGCTGCAGTGAGC      44204       G  TG  A
                                CCAGGCTG CA  GA GC
                                |||||||| ||  || ||
                                GGTCCGAC GT  CT CG
                                    _  CA  _
GAM1514 EDN2     5' CCAGGCTGGACTGGAGC     12644        CA   A
                                CCAGGCTGG  TGGA GC
                                |||||||||  |||| ||
                                GGTCCGACC  ACCT CG
                                     TG   _
GAM1514 GLDC     3' AACTGGCACATGTGGAAGC   42023       ____
                                GGCTGGCA   TGGAAGC
                                ||||||||   |||||||
                                TTGACCGT   ACCTTCG
                                    GTAC
GAM1514 GPC6     5' ACACAGGCTGTGGGAGC     25039   _     GCA   A
                                AC CAGGCTG   TGG AGC
                                || |||||||  ||| |||
                                TG GTCCGAC   ACC TCG
                                 T      ___  C
GAM1514 GPRK6    3' ACCAGGCTGTGGGAGC      13266        GCA   A
                                ACCAGGCTG   TGG AGC
                                |||||||||   ||| |||
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                                TGGTCCGAC   ACC TCG
                                    ___   C
GAM1514  HDAC5    3'  CCAGAAGGTATGGAAGC     24191       CT  C
                                CCAGG  GG ATGGAAGC
                                |||||  || ||||||||
                                GGTCT  CC TACCTTCG
                                   T_  A
GAM1514  HOXC6    3'  CCAGGCCGGCCCTGAGGC    21073          ATG  A
                                CCAGGCTGGC   GA GC
                                ||||||||||   || ||
                                GGTCCGGCCG   CT CG
                                      GGA  C
GAM1514  IL10     3'  CAGGCTTGGAATGGAAGC    8194        _  C
                                CAGGCT GG ATGGAAGC
                                |||||| || ||||||||
                                GTCCGA CC TACCTTCG
                                    A  T
GAM1514  IL10RA   3'  TACCAGACTGGCACCTAAG   40626            GG
                                TACCAGGCTGGCAT  AAG
                                ||||||||||||||  |||
                                ATGGTCTGACCGTG  TTC
                                      GA
GAM1514  IL13     3'  CACCAGGCTGAGCCCTGG    13525          _  A_
                                TACCAGGCTG GC  TGG
                                |||||||||| ||  |||
                                GTGGTCCGAC CG  ACC
                                      T  GG
GAM1514  INHBB    3'  CCAGGCTGGGAAGAAGC     13542         CAT
                                CCAGGCTGG   GGAAGC
                                |||||||||   ||||||
                                GGTCCGACC   TCTTCG
                                     CT_
GAM1514  INPP5A   3'  TACACAGAAGAACGGCATGGGA 24407     _   C___       A
              G                  TAC CAGG    TGGCATGG AG
                                 ||| ||||    |||||||| ||
                                 ATG GTCT    GCCGTACC TC
                                   T    TCTT       C
GAM1514  ITGA3    3'  CCAGGCTGGCACAGAAAGC    13606             _
                                CCAGGCTGGCATGGAA GC
                                |||||||||||||||| ||
                                GGTCCGACCGTGTCTT CG
                                      T
GAM1514  MADH7    3'  CCAGGCTGGGGACAGAGC     25364         C_    A
                                CCAGGCTGG  ATGGA GC
                                |||||||||  ||||| ||
                                GGTCCGACC  TGTCT CG
                                     CC    _
GAM1514  MFAP2    3'  GACTGGGCAGTGGGGAGC     32707        _ _  A_
                                GGCTGG CA TGG  AGC
                                |||||| || |||  |||
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                                CTGACC GT ACC  TCG
                                   C  C   CC
GAM1514  MMP16    3'  TACTGTGCATCATGGAAGC   35439     CAG  TGG
                                TAC   GC   CATGGAAGC
                                |||   ||   |||||||||
                                ATG   CG   GTACCTTCG
                                  ACA  TA_
GAM1514  MYBPH    3'  AGCCGTCGCTATGGAAGC    22647       __ _
                                GGCTG  GC ATGGAAGC
                                |||||  || ||||||||
                                TCGGC  CG TACCTTCG
                                   AG  A
GAM1514  NEBL     5'  TACCAGGCTGGCCTCACAAG  26906           AT_ G
                                TACCAGGCTGGC   G AAG
                                ||||||||||||   | |||
                                ATGGTCCGACCG   T TTC
                                       GAG G
GAM1514  NONO     3'  TACCAGCTGGCACAGGAGC   44359       G        A
                                TACCAG CTGGCATGG AGC
                                ||||||| ||||||||| |||
                                ATGGTC GACCGTGTC TCG
                                   _        C
GAM1514  PACE     3'  CCGGGCTGGCCACGAGGGC   15032    A      _   AA
                                CC GGCTGGC ATGG  GC
                                || ||||||| ||||  ||
                                GG CCGACCG TGCT  CG
                                 C      G    CC
GAM1514  PBX1     3'  ACCAGGCTGACAGCTGGAGGC  15099           __   A
                                ACCAGGCTGGCA  TGGA GC
                                ||||||||||||  |||| ||
                                TGGTCCGACTGT  ACCT CG
                                       CG   C
GAM1514  PCTK3    3'  CCAGGCTGGCTGTCAGC     43775          A  GA
                                CCAGGCTGGC TG  AGC
                                |||||||||| ||  |||
                                GGTCCGACCG AC  TCG
                                      _ AG
GAM1514  PES1     3'  CAGGCTGGGCACAGAGGC    30712         _    A
                                CAGGCTGG CATGGA GC
                                |||||||| |||||| ||
                                GTCCGACC GTGTCT CG
                                     C     C
GAM1514  PLXNB2   3'  ACCTAGGGCATGGAGGC     29644     A  CT       A
                                ACC GG  GGCATGGA GC
                                ||| ||  |||||||| ||
                                TGG TC  CCGTACCT CG
                                  A  __       C
GAM1514  PTK2B    3'  ACCAGGCTGGCTTAGGGAGC   19912          AT_  A
                                ACCAGGCTGGC   GG AGC
                                ||||||||||   || |||
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                                TGGTCCGACCG  CC TCG
                                      AAT  C
GAM1514  RFP     3'  CCAGGCTGAGCCAAGAAGC   27130       _  AT
                                CCAGGCTG GC  GGAAGC
                                |||||||| ||  ||||||
                                GGTCCGAC CG  TCTTCG
                                     T  GT
GAM1514  SPAP1   3'  CCAGGCTGGTGAGACACAGC  39864       CAT  ___
                                CCAGGCTGG  GGA  AGC
                                |||||||||  |||  |||
                                GGTCCGACC  TCT  TCG
                                      AC_  GTG
GAM1514  TCF1    3'  CCAGGCTGGCCTCAGAGGC   8088        AT_  A
                                CCAGGCTGGC  GGA GC
                                ||||||||||  ||| ||
                                GGTCCGACCG  TCT CG
                                      GAG  C
GAM1514  TNFRSF13C 3'  CACCAAACTCCATGGGGGC   38118       GG   AA
                                TACCAGGCT  CATGG  GC
                                |||||||||  |||||  ||
                                GTGGTTTGA  GTACC  CG
                                      G_   CC
GAM1514  UBE2I   5'  CACCAGGCTTCTGAAGC    17812       GGCATG
                                TACCAGGCT    GAAGC
                                |||||||||    |||||
                                GTGGTCCGA    CTTCG
                                      AGA___
GAM1514  WBP2    3'  CCAGACTGAGGGAGC      43810       CAT  A
                                CCAGGCTGG  GG AGC
                                |||||||||  || |||
                                GGTCTGACT  CC TCG
                                      ___  C
GAM1514  WBP2    3'  CCGGGCTGGCATGGGAAGC   43811   A       _
                                CC GGCTGGCATGG AAGC
                                || |||||||||| ||||
                                GG CCGACCGTACC TTCG
                                 C         C
GAM1514  WNT1    3'  ACCAGGCTGGGACCCAGC    24076       C  GGA
                                ACCAGGCTGG AT  AGC
                                |||||||||| ||  |||
                                TGGTCCGACC TG  TCG
                                      C  GG_
GAM1514  WNT5B   5'  ACTAGGCTACATTGGGGGC   37210   C    G  _  AA
                                AC AGGCTG CAT GG  GC
                                || |||||| ||| ||  ||
                                TG TCCGAT GTA CC  CG
                                 A     _  A  CC
GAM1514  XDH     3'  CCTGCTCCATGGAAGC     40459   AG  GG
                                CC  GCT  CATGGAAGC
                                ||  |||  |||||||||
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                              GG  CGA  GTACCTTCG
                               A_   G_
GAM1514  ZNF134   3'  CCAGGTGACTTGGAGGC     18324       C   A   A
                              CCAGG TGGC TGGA GC
                              ||||| |||| |||| ||
                              GGTCC ACTG ACCT CG
                                _   A   C
GAM1514  ZNF22    3'  CACCATTCTCATGGAAG     45045       GG  GG
                              TACCA  CT  CATGGAAG
                              |||||  ||  ||||||||
                              GTGGT  GA  GTACCTTC
                                AA  __
GAM1515  CHES1    3'  TGCCTGGTGCCACAAGCTTGGG 23288        CT  C  T
            TC                  TGCCTGG  CT TA GCTTGGGTC
                              |||||||  || || |||||||||
                              ACGGACC  GG GT CGAACCCAG
                                  AC  T  T
GAM1515  GUK1     5'  TGCGCGGCTATGTTTGGGTC   9232      C    CTCT   C
                              TGC TGGCT    ATG TTGGGTC
                              ||| |||||    ||| |||||||
                              ACG GCCGA    TAC AACCCAG
                               C    _____   A
GAM1515  LRAT     3'  TGCTTGGGTTCTACTTGTTTGG 41085     C   CTC    GC__
            GT                  TGC TGG   TCTAT    TTGGGT
                              ||| |||   |||||    ||||||
                              ACG ACC   AGATG    AACCCA
                               A   CA_    AACA
GAM1515  VDR      3'  TGTCTGTTTTTCCTCCTTGGGT 7531     C   GCTC   ATG
            C                   TG CTG    TCT   CTTGGGTC
                              || |||    |||   ||||||||
                              AC GAC    AGG   GAACCCAG
                               A   AAAA   AG_
GAM1515  XK       3'  TGCCTGTGCTCTGAGACCTTGG 34374       _    CTATG
            GTC                   TGCCTG GCTCT    CTTGGGTC
                              |||||| |||||    ||||||||
                              ACGGAC CGAGA    GAACCCAG
                                 A    CTCTG
GAM1516  ACTR1B   3'  TGCCGAGGGTAGAGGGAG    43349     T_  AAATGA    AA
                              TGCC  GGG     TAGAG  AG
                              ||||  |||     |||||  ||
                              ACGG  CCC     ATCTC  TC
                                CT  _______    CC
GAM1516  ALDH3B1  3'  TGCCTGGAGAGAAGAGGGAG  45069        AAAT  T   AA
                              TGCCTGGG   GA AGAG  AG
                              ||||||||   || ||||  ||
                              ACGGACCT   CT TCTC  TC
                                  CT__  _   CC
GAM1516  ATP5J    5'  TGCCTGGGAGGCGGGAG     11772         AA  ATA
                              TGCCTGGGA  TG   GAG
                              |||||||||  ||   |||
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                                ACGGACCCT  GC   CTC
                                     CC  C__
GAM1516 B4GALT1  3'  TGCCTGGGGAGGTGCAAAG   11292        AAA_  A
                                TGCCTGGG    TG TAGAG
                                ||||||||    || |||||
                                ACGGACCC    AC GTTTC
                                     CTCC  _
GAM1516 BCL11B   3'  TGCTTGGGAAATGATGGA    39761     C         A
                                TGC TGGGAAATGAT GA
                                ||| ||||||||||| ||
                                ACG ACCCTTTACTA CT
                                  A         C
GAM1516 CBFA2T2  3'  GCCTGGGAGACAAGAGAGA   22974        A TG T
                                GCCTGGGA A  A AGAGA
                                |||||||| |  | |||||
                                CGGACCCT T  T TCTCT
                                     C GT C
GAM1516 CLN2     3'  TACTTGGGAAATATAATTGGAA 7558      C       ATAGA_  A
             GGA                    TGC TGGGAAATG     GAA GA
                                ||| |||||||||      ||| ||
                                ATG ACCCTTTAT     CTT CT
                                  A       ATTAAC   C
GAM1516 DDX26    5'  GCCCGAGGTGGTGGAGAAAGA  29094       AAA  ATA
                                GCCTGGG   TG   GAGAAAGA
                                |||||||   ||   ||||||||
                                CGGGCTC   AC   CTCTTTCT
                                     C__  CAC
GAM1516 GARP     3'  TGCCTGGGAGAGAGGAGAGA   24319        AAT  T_
                                TGCCTGGGA   GA  AGAGA
                                |||||||||   ||  |||||
                                ACGGACCCT   CT  TCTCT
                                     CT_  CC
GAM1516 GHR      3'  TGGGAAACCAAAGAAAG     6721         GA
                                TGGGAAAT  TAGAGAAAG
                                ||||||||  |||||||||
                                ACCCTTTG  GTTTCTTTC
                                     __
GAM1516 GM2A     3'  TGCTTTGGAAATGAACGAG   42691     CTG       TA
                                TGC   GGAAATGA  GAG
                                |||   ||||||||  |||
                                ACG   CCTTTACT  CTC
                                  AAA       TG
GAM1516 GNAS     5'  TGCCTGGGAGAGGACAGAG   38670         AAT
                                TGCCTGGGA   GATAGAG
                                |||||||||   |||||||
                                ACGGACCCT   CTGTCTC
                                     CTC
GAM1516 HDAC5    3'  CCTGGGAAAGAGAA       40164         ATGAT
                                CCTGGGAA    AGAGAA
                                ||||||||    ||||||
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                                GGACCCTT    TCTCTT
                                        _____
GAM1516 HDGF    3' TGCCTAGGAGAGTGGGAGAA  21067        AATGATA
                                TGCCTGGGA      GAGAA
                                |||||||||      |||||
                                ACGGATCCT      CTCTT
                                     CTCACC_
GAM1516 JAK3    5' TGCCTGGGGCACAGAGA     6864        AAATG
                                TGCCTGGG    ATAGAGA
                                ||||||||    |||||||
                                ACGGACCC    TGTCTCT
                                    CG___
GAM1516 KCNK6   3' TGCTGGGAAACAAAGGAGA   22085    C      TG TA
                                TGC TGGGAAA  A  GAGA
                                ||| |||||||  |  ||||
                                ACG ACCCTTT  T  CTCT
                                  _      GT TC
GAM1516 KRT18   5' TGTCCGGGGAGAGAGAAAG   6903    C    AAAT  T
                                TG CTGGG    GA AGAGAAAG
                                || |||||    || ||||||||
                                AC GGCCC    CT TCTCTTTC
                                 A     _____ C
GAM1516 LPIN2   3' GCCTGGGAAGGCAAAGGAG   31212        A_   TA
                                GCCTGGGAA  TGA  GAG
                                |||||||||  |||  |||
                                CGGACCCTT  GTT  CTC
                                     CC   TC
GAM1516 MAPK4   3' TGCTTGGTGACTAGGAGAAAG 15669    C   GAAA   A__
                                TGC TGG    TGAT   GAGAAAG
                                ||| |||    ||||   |||||||
                                ACG ACC    ACTG   CTCTTTC
                                  A  _____    ATC
GAM1516 MECP2   3' TGCCTGGAAGAGAA       22618        AAATGAT
                                TGCCTGGG      AGAGAA
                                ||||||||      ||||||
                                ACGGACCT      TCTCTT
                                        ________
GAM1516 NCALD   3' CCTGGGAAGGAGAAG       36762        ATGATA    A
                                CCTGGGAA     GAGAA G
                                ||||||||     ||||| |
                                GGACCCTT     CTCTT C
                                    C_____     C
GAM1516 NHLH1   3' TGCCTGGGTCAGAGAAAG    24660        AAATGA
                                TGCCTGGG     TAGAGAAAG
                                ||||||||     |||||||||
                                ACGGACCC     GTCTCTTTC
                                    A_____
GAM1516 NOLA2   3' TGCCTTGGGGAACTGGGAAGA 45399      __    A  ATA
                                TGCCT  GGGAA TG   GAGA
                                |||||  ||||| ||   ||||
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                                ACGGA  CCCTT AC   TTCT
                                  AC     G  CC_
GAM1516  NR2E1    5'  TGCTGGGAAATCTTCCGAG   17581     C       GATA_
                                TGC TGGGAAAT     GAG
                                ||| ||||||||     |||
                                ACG ACCCTTTA     CTC
                                  _       GAAGG
GAM1516  NYX      3'  TGCCTGGAAGATGAGGGGAA   35449          A    TA_
                                TGCCTGGGA ATGA   GAG
                                ||||||||| ||||   |||
                                ACGGACCTT TACT   CTT
                                     C    CCC
GAM1516  PACSIN1  3'  TGCCTGGGGAAAGGCTGGAGAG 45166          _   TGATA    A
            AGA                    TGCCTGGG AAA     GAGA AGA
                                ||||||||| |||     |||| |||
                                ACGGACCC TTT     CTCT TCT
                                     C   CCGAC    C
GAM1516  PCBD     3'  TGCTGGGAAGTTGCAAAGAAAG 7101      C      A_  A
                                TGC TGGGAA  TG TAGAGAAAG
                                ||| ||||||  || |||||||||
                                ACG ACCCTT  AC GTTTCTTTC
                                  _     CA  _
GAM1516  PDYN     3'  TGCCTGGGAATGAGAGA     35923          A   TA
                                TGCCTGGGAA TGA  GAGA
                                |||||||||| |||  ||||
                                ACGGACCCTT ACT  CTCT
                                           _  __
GAM1516  PKD2     3'  TGCTGGGGAAACAGGGAG    41080     CT       ATA
                                TGC  GGGAAATG   GAG
                                |||  ||||||||   |||
                                ACG  CCCTTTGT   CTC
                                  AC       CC_
GAM1516  PRIM2A   3'  TGCCTGGGCAACATAGGGA   9623         A   G    A
                                TGCCTGGG AAT ATAG GA
                                ||||||| ||| |||| ||
                                ACGGACCC TTG TATC CT
                                     G   _    C
GAM1516  PRKAR1A  3'  TACCTGGGAAAGGGCAGGAGAA 15611           TGATA_
                                TGCCTGGGAAA     GAGAA
                                ||||||||||     |||||
                                ATGGACCCTTT     CTCTT
                                       CCCGTC
GAM1516  PTHLH    3'  TGGGTGACGGTGGAGAAAGA   15856      AA   ATA
                                TGGG  ATG   GAGAAAGA
                                ||||  |||   ||||||||
                                ACCC  TGC   CTCTTTCT
                                  AC   CAC
GAM1516  PXN      3'  GCCTGGGAAGTAAAGAA     16027          ATGA
                                GCCTGGGAA   TAGAGAA
                                |||||||||   |||||||
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                                CGGACCCTT   ATTTCTT
                                     C___
GAM1516 RNF26   3' TGCCAGGGAGAGACAGAGA   36758     T   AAT
                                TGCC GGGA   GATAGAGA
                                |||| ||||   ||||||||
                                ACGG CCCT   CTGTCTCT
                                  T   CT_
GAM1516 SCD     3' TGCCTGGGAGGCAATAAGGGAA 22836        AA    A_
            AG                    TGCCTGGGA  TGATAG  GAAAG
                                |||||||||  ||||||  |||||
                                ACGGACCCT  GTTATT  CTTTC
                                     CC     CC
GAM1516 SF3B2   3' CCTTGGGAACTGCGGGAGA   27763    _    A  ATA
                                CCT GGGAA TG   GAGA
                                ||| ||||| ||   ||||
                                GGA CCCTT AC   CTCT
                                  A    G  GCC
GAM1516 SHMT2   3' TGCCTGAGAGAGGAGA     24012        AAT  TA
                                TGCCTGGGA   GA  GAGA
                                |||||||||   ||  ||||
                                ACGGACTCT   CT  CTCT
                                     ___ C_
GAM1516 SLC3A2  3' GCCTGGGAAGGAAAGGAGAA   14401        AT  TA
                                GCCTGGGAA  GA  GAGAA
                                |||||||||  ||  |||||
                                CGGACCCTT  TT  CTCTT
                                     CC  TC
GAM1516 SOST    3' TGTCTGGAAATGATTTTCAAAA 36110    C   G     AG__
            AGA                   TG CTGG AAATGAT    AGAAAGA
                                || |||| |||||||    |||||||
                                AC GACC TTTACTA    TTTTTCT
                                 A   _      AAAG
GAM1516 STAT1   3' TGTCTGGAAAAAGTACAGGAGA 40219    C      TG_   _  A
            GAGA                   TG CTGGGAAA   ATAG AGA AGA
                                || ||||||||   |||| ||| |||
                                AC GACCTTTT   TGTC TCT TCT
                                 A       TCA   C   C
GAM1516 STXBP1  3' TGCCTGGGGACAGAA      17212        AAAT
                                TGCCTGGG    GATAGAG
                                ||||||||    |||||||
                                ACGGACCC    CTGTCTT
                                     _____
GAM1516 SUV39H2 5' TGCCTGGGAACAGGGAA     36021        AATG   A
                                TGCCTGGGA    ATAG GAA
                                |||||||||    |||| |||
                                ACGGACCCT    TGTC CTT
                                     _____   C
GAM1516 TEGT    3' TGCCTGAGTAGAGGAA      42101        AAATGA    A
                                TGCCTGGG     TAGAG AA
                                ||||||||     ||||| ||
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                                ACGGACTC     ATCTC TT
                                       _______    C
GAM1516 VTN      5' TGCCTGAGGAAGGGAGGGA   8471        _   AT  TA
                                TGCCTG GGAA  GA  GA
                                |||||| ||||  ||  ||
                                ACGGAC CCTT  CT  CT
                                   T    CC  CC
GAM1517 SLC25A15 3' ACACATACATGGTATGGACTAT 30663         _    A
                                ACGCATACG GGTAT GACTAT
                                ||||||||| ||||| ||||||
                                TGTGTATGT CCATA CTGATA
                                      A    C
GAM1518 ACTR1B   3' CAACAGCCTGACATGGCGCTCA 43343     G   G   T __
             A                   CAA AGCT TGG CA  GCGCTCAA
                                ||| |||| ||| ||  ||||||||
                                GTT TCGG ACT GT  CGCGAGTT
                                  G   _  _  AC
GAM1518 BCLG     3' CAATAGCTGTGAGCTTGGC   39820     G     _ CA_
                                CAA AGCTGTG GT   GC
                                ||| ||||||| ||   ||
                                GTT TCGACAC CG   CG
                                  A      T  AAC
GAM1518 CD28     3' GGAGAGCTGTGGCACTATCTC  26021    A        CAGCG
                                C AGAGCTGTGGT    CTC
                                | ||||||||||    |||
                                C TCTCGACACCG    GAG
                                 C          TGATA
GAM1518 CELSR3   3' CAAGAGCTGGGGTCCTTCTC   10823        T   AGCG
                                CAAGAGCTG GGTC   CTC
                                ||||||||| ||||   |||
                                GTTCTCGAC CCAG   GAG
                                      C   GAA_
GAM1518 FOLR1    5' AAGAGCTGTGGTCAGTGGC   32500           C_
                                AAGAGCTGTGGTCAG  GC
                                |||||||||||||||  ||
                                TTCTCGACACCAGTC  CG
                                          AC
GAM1518 GAS7     3' GACACGATTCAGCGCTCAA   25268    GC  TGG
                                GA  TG   TCAGCGCTCAA
                                ||  ||   ||||||||||
                                CT  GC   AGTCGCGAGTT
                                 GT  TA_
GAM1518 GPR85    3' AAGGCTGTGGTCTCCCC     33257     A       AGCG
                                AAG GCTGTGGTC    CTC
                                ||| |||||||||    |||
                                TTC CGACACCAG    GGG
                                  _        AG__
GAM1518 INHBC    5' CAACAGCTGTGGTCTCAA    24400     G       AGCGC
                                CAA AGCTGTGGTC    TCAA
                                ||| ||||||||||    ||||
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                                GTT TCGACACCAG    AGTT
                                  G       _____
GAM1518  INSM1    3'  AAGAGCTGTCGGTTGTACA   13572        _  CA_
                                AAGAGCTGT GGT   GCG
                                ||||||||| |||   |||
                                TTCTCGACA CCA   TGT
                                     G   ACA
GAM1518  ITGB2    3'  CAAGAGCTGTGGCCAAGC    6835             C
                                CAAGAGCTGTGGTCAG GC
                                |||||||||||||||| ||
                                GTTCTCGACACCGGTT CG
                                                 _
GAM1518  KLF4     5'  AGGGGCTGTGGCCGGGGCG   20150    A_       A__
                                AG  GCTGTGGTC   GCG
                                ||  |||||||||   |||
                                TC  CGACACCGG   CGC
                                 CC        CCC
GAM1518  MCF2     3'  CAAAAGCTGTGGTTTCAAC   23861           __
                                CAAGAGCTGTGG  TCAGC
                                ||||||||||||  |||||
                                GTTTTCGACACC  AGTTG
                                      AA
GAM1518  MEIS1    3'  AAGAACTGTGGGGCT       14413          TCAGC
                                AAGAGCTGTGG    GCT
                                ||||||||||     |||
                                TTCTTGACACC    CGA
                                      C_____
GAM1518  OLIG2    3'  AAAGCCAGACAGCGCTC     25140       GT  T
                                AGAGCT  GG CAGCGCTC
                                ||||||  || ||||||||
                                TTTCGG  TC GTCGCGAG
                                   __  T
GAM1518  RANBP3   3'  AGAGCTGTGCCTGCTCAA    28747         G  AGC
                                AGAGCTGTG TC   GCTCAA
                                ||||||||| ||   ||||||
                                TCTCGACAC GG   CGAGTT
                                     _  A__
GAM1518  RNF6     5'  GAGGCTGTGGTTGGGAGGC   25575    _      C___  C
                                GAG CTGTGGT    AG GC
                                ||| |||||||    || ||
                                CTC GACACCA    TC CG
                                  C      ACCC  _
GAM1518  SPN      5'  CAAGAGCTGGGACCGGCTC   17086         T GT AGC
                                CAAGAGCTG G  C   GCTC
                                ||||||||| |  |   ||||
                                GTTCTCGAC C  G   CGAG
                                     C TG C__
GAM1518  VIPR2    5'  AGCTGGAGCGCGCTCAA     18004       TG  CA
                                AGCTG  GT  GCGCTCAA
                                |||||  ||  ||||||||
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                                TCGAC  CG  CGCGAGTT
                                  CT  __
GAM1519  ACO1     3'  TCTCTTTCTGGCACTACT    13583        CA  CAG
                                TCTCTTTC  GC   TTACT
                                ||||||||  ||   |||||
                                AGAGAAAG  CG   GATGA
                                    AC  T__
GAM1519  AOC3     3'  ATCCTTTCCAGCTCAGCTA   19012     T       _
                                ATC CTTTCCAGC CAGTTA
                                ||| ||||||||| ||||||
                                TAG GAAAGGTCG GTCGAT
                                  _       A
GAM1519  EPB42    5'  ATCTCCTGGACCAGTTACT   6514         TCCA
                                ATCTCTT   GCCAGTTACT
                                |||||||   ||||||||||
                                TAGAGGA   TGGTCAATGA
                                    CC__
GAM1519  FEZ1     3'  TCTCTTTCTAGTCCCTCCT   35423        C  _  AGTTA
                                TCTCTTTC AG CC    CT
                                |||||||| || ||    ||
                                AGAGAAAG TC GG    GA
                                    A  A  GAG__
GAM1519  GPR23    5'  ATCTCTTTCCCTTTGTTA    41314         AGCCA
                                ATCTCTTTCC    GTTA
                                ||||||||||    ||||
                                TAGAGAAAGG    CAAT
                                    GAAA_
GAM1519  IKBKAP   3'  CTCTTTCCAGTTCTCAAT    43286         C___
                                CTCTTTCCAG   CAGT
                                ||||||||||   ||||
                                GAGAAAGGTC   GTTA
                                    AAGA
GAM1519  IL27     3'  ATCTCTTCCCAGTTCATC    42104         CCA
                                ATCTCTTTCCAG  GTT
                                ||||||||||||  |||
                                TAGAGAAGGGTC  TAG
                                    AAG
GAM1519  NDRG2    3'  ATCTCTTCCAGGAGCT      32190       T   CC
                                ATCTCTT CCAG  AGTT
                                ||||||| ||||  ||||
                                TAGAGAA GGTC  TCGA
                                  _   C_
GAM1519  PLAG1    5'  CCTCTTTCCAGCAGCCA     15347          C
                                TCTCTTTCCAGC AGTTA
                                |||||||||||| |||||
                                GGAGAAAGGTCG TCGGT
                                             _
GAM1519  POLQ     3'  TCTTTCCAGGTGACT       27322        CCA  T
                                TCTTTCCAG   GT ACT
                                |||||||||   || |||
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```
                                AGAAAGGTC  CA TGA
                                     ___ C
GAM1519 RANBP9   5' ATCTCTTCCCTTAC       24246         AGCCAG
                                ATCTCTTTCC    TTAC
                                ||||||||||    ||||
                                TAGAGAAGGG    AATG
                                     _______
GAM1519 SCD      5' ATCACTTTCCAGGGGGCT    22820    T      CCA
                                ATC CTTTCCAG  GTT
                                ||| ||||||||  |||
                                TAG GAAAGGTC  CGA
                                  T       CCC
GAM1519 SVIL     5' TCTCTTTCCAATGAATACTA  34736          CCAGT
                                TCTCTTTCCAG   TACTA
                                ||||||||||    |||||
                                AGAGAAAGGTT   ATGAT
                                      ACTT_
GAM1519 TYR      5' TCTCTTTCCAGCTACT      7499           CAGT
                                TCTCTTTCCAGC  TACT
                                ||||||||||||  ||||
                                AGAGAAAGGTCG  ATGA
                                     _____
GAM1519 ZNF83    5' TCTTTCCAACATTACT      32895          CA
                                TCTTTCCAGC  GTTACT
                                ||||||||||  ||||||
                                AGAAAGGTTG  TAATGA
                                     __
GAM1520 ASPH     3' GCTGTCTCACAAAAAGA     37137    CCC   G
                                GC   TCT ACAAAAAGA
                                ||   ||| |||||||||
                                CG   AGA TGTTTTTCT
                                 AC_   G
GAM1520 CLN5     3' TAACTGCCATATCAGAAAGAA 27086        CCTC  A  A
                                TAACTGCC    TG CA AAAGAA
                                ||||||||    || || ||||||
                                ATTGACGG    AT GT TTTCTT
                                     T___  A  C
GAM1520 CNN2     3' AACTGCTCAGCTGACAAAA   20401       CCCT
                                AACTGC    CTGACAAAA
                                ||||||    |||||||||
                                TTGACG    GACTGTTTT
                                   AGTC
GAM1520 COL4A1   3' TGCTGTTAACAAAAAGA     12310     CCCTC
                                TGC     TGACAAAAAGA
                                |||     ||||||||||
                                ACG     ATTGTTTTTCT
                                  ACA__
GAM1520 DIAPH2   3' CTGCCTCCTGTAAAAAGAA   28671       C T   AC
                                CTGCC C CTG  AAAAAGAA
                                ||||| | |||  ||||||||
```

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                                GACGG G GAC  TTTTTCTT
                                  A _  A_
GAM1520  DXS1283E  3'  TAACTGCCTCTTAGTAATCAAG 43355        C  CTGACAAA
             A                    TAACTGCC CT       AAGA
                                  |||||||| ||       ||||
                                  ATTGACGG GA       TTCT
                                     A  ATCATTAG
GAM1520  EGR3      3'  AACTGCCCTGAGGCCTAAGA  40533        CTC  CAAA_
                                  AACTGCCC  TGA    AAGA
                                  ||||||||  |||    ||||
                                  TTGACGGG  ACT    TTCT
                                     ___  CCGGA
GAM1520  HHEX      3'  CAACCATATCTCTGACAAAAAG 15565       CCC
             AA                    TAACTG  CTCTGACAAAAAGAA
                                  ||||||  ||||||||||||||||
                                  GTTGGT  GAGACTGTTTTTCTT
                                     ATA
GAM1520  HYAL2     3'  CTTCCCCTCTGGCAGGGAGA  37637    G      A  AAA
                                  CT CCCCTCTG CA  AGA
                                  || |||||||| ||  |||
                                  GA GGGGAGAC GT  TCT
                                   A       C  CCC
GAM1520  ITPR3     3'  TAACTACCCACAAGGAG     13691         CTCTG   AA
                                  TAACTGCCC    ACAA  AG
                                  |||||||||    ||||  ||
                                  ATTGATGGG    TGTT  TC
                                       _____   CC
GAM1520  OSM       3'  TAACTCCCTAGCTTCACAAAGA 33915      G  CT_ G_    A
             GAA                    TAACT CCC  CT  ACAAA AGAA
                                  ||||| |||  ||  ||||| ||||
                                  ATTGA GGG  GA  TGTTT TCTT
                                     _  ATC  AG    C
GAM1520  PFKFB4    3'  TAACTCCCCTCTGTACACAGAG 21295      G      _  AAA
             A                     TAACT CCCCTCTG ACA  AGA
                                  ||||| |||||||| |||  |||
                                  ATTGA GGGGAGAC TGT  TCT
                                     _       A  GTC
GAM1520  PLAG1     3'  TAACTGGCCCTACAAAAAG   15355       C   CTG
                                  TAACTG CCCT   ACAAAAAG
                                  |||||| ||||  ||||||||
                                  ATTGAC GGGA   TGTTTTTC
                                     C   ___
GAM1520  PTP4A2    3'  TAACTGCCTTCCACAAA     38638        CC  G
                                  TAACTGCC  TCT ACAAA
                                  ||||||||  ||| |||||
                                  ATTGACGG  AGG TGTTT
                                     A_  _
GAM1520  SLC1A4    3'  CTGTCCCTTACATAAAAAAGAA 16747     C   CTGAC_
                                  CTG CCCT     AAAAAGAA
                                  ||| ||||     ||||||||
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                                GAC GGGA     TTTTTCTT
                                  A   ATGTAT
GAM1520  SORCS2   3'  CTGCCCCTCTGGGCAGA    34055          ACAAAA
                                CTGCCCCTCTG     AGA
                                ||||||||||     |||
                                GACGGGGAGAC     TCT
                                     CCG___
GAM1520  TFE3     3'  AACTGCCCCTCAAGGAAGAA  27165          TGACAAA
                                AACTGCCCCTC     AAGAA
                                ||||||||||      |||||
                                TTGACGGGGAG     TTCTT
                                     TTCC___
GAM1520  TRPM6    5'  TAACTGCCTAGAAAAG     32791        CCTCT  CAA
                                TAACTGCC    GA   AAAG
                                ||||||||    ||  ||||
                                ATTGACGG    CT   TTTC
                                   AT___  ___
GAM1520  YY1      3'  TAACTGCCCATTCTTTTAAAGA 18181        C_  GACAA
             A                   TAACTGCCC  TCT    AAAGAA
                                ||||||||| |||    ||||||
                                ATTGACGGG  AGA    TTTCTT
                                     TA   AAA__
GAM1521  ALDH2    3'  ATCTTGCTGAACTTTCCATCAA 40687     C         AG__
                                ATC TGCTGAACTTT    CAG
                                ||| ||||||||||    |||
                                TAG ACGACTTGAAA    GTT
                                  A         GGTA
GAM1521  CACNA1S  5'  CCCTGCTGAGCCAGCCAG    6302          ACT    _
                                TCCTGCTGA   TTAGC AG
                                |||||||||   ||||| ||
                                GGGACGACT   GGTCG TC
                                     C__     G
GAM1521  COL6A2   3'  TGCCCGGGCTTTAGCAGA    38450      _ AA
                                TGCT G  CTTTAGCAGA
                                |||| |  ||||||||||
                                ACGG C  GAAATCGTCT
                                  G CC
GAM1521  CXCR6    5'  CTGATGAACACCAGCAGA    27294     C    T
                                CTG TGAAC TTAGCAGA
                                ||| ||||| ||||||||
                                GAC ACTTG GGTCGTCT
                                  T    T
GAM1521  FGF5     3'  TCTTGCTGAACTGAAGGAG   37594    C       TT  C
                                TC TGCTGAACT  AG AG
                                || |||||||||  || ||
                                AG ACGACTTGA  TC TC
                                 A        CT  C
GAM1521  HOXD3    5'  CTGCTGAATCCTGAGAGA    27896        _   T  C
                                CTGCTGAA CTT AG AGA
                                |||||||| ||| || |||
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                                GACGACTT GGA TC TCT
                                     A   C  _
GAM1521  HSPCB    3'  ATCCTGCTGTCAAGAGTAGA   28875         AACTTT  C
                                ATCCTGCTG      AG AGA
                                |||||||||      || |||
                                TAGGACGAC      TC TCT
                                     AGTTC_  A
GAM1521  NCAM2    3'  TCCTGCTGTAGCCAGAA     21226         AACTT   _
                                TCCTGCTG    TAGC AGAA
                                ||||||||    |||| ||||
                                AGGACGAC    ATCG TCTT
                                     _____   G
GAM1521  PDE7A    3'  TCCTGCTGGGCTTTGCA     42289         AA   A
                                TCCTGCTG  CTTT GCA
                                ||||||||  |||| |||
                                AGGACGAC  GAAA CGT
                                     CC   _
GAM1522  ARNT2    3'  CATTCCCTGGGACTGGT     31355           CA
                                CATTCCCTGGGAC  GGT
                                ||||||||||||  |||
                                GTAAGGGACCCTG  CCA
                                       A_
GAM1522  CERD4    3'  CATTCCATGGGATATCGAGGG  28944       C    CCAG
                                CATTCC TGGGA   GTCGAGGG
                                |||||| |||||   ||||||||
                                GTAAGG ACCCT   TAGCTCCC
                                   T    A___
GAM1522  COL16A1  3'  CCTGGGACTAAACGGG      12363         C  T  A
                                CCTGGGAC AGG CG GG
                                |||||||| ||| || ||
                                GGACCCTG TTT GC CC
                                     A  _ _
GAM1522  DLEC1    3'  CATGCCCTGGGAAAAGTGAGGG 28821     T       CC   C
                                CAT CCCTGGGA  AGGT GAGGG
                                ||| ||||||||  |||| |||||
                                GTA GGGACCCT  TTCA CTCCC
                                  C       T_   _
GAM1522  EHD3     3'  TTCCCTGGGGCATCAGTGAGGG 31125         ACCA_  C
                                TTCCCTGGG    GGT GAGGG
                                |||||||||    ||| |||||
                                AAGGGACCC    TCA CTCCC
                                     CGTAG   _
GAM1522  JPH3     3'  TTCCCTGGGGTCTGGTGGGGG  34030         ACCA  CGA
                                TTCCCTGGG   GGT  GGG
                                |||||||||   |||  |||
                                AAGGGACCC   CCA  CCC
                                     CAGA   CC_
GAM1522  LDB1     3'  CTCCCTGGGGCTGTGAGGG   19335         ACCAG  C
                                TTCCCTGGG    GT GAGGG
                                |||||||||    || |||||
```

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                                GAGGGACCC    CA CTCCC
                                     CGA__  _
GAM1522  NR1D1    5'  TTCCCTGGGACAGAGG      34707          CAGGTC
                                TTCCCTGGGAC     GAGG
                                ||||||||||      ||||
                                AAGGGACCCTG     CTCC
                                      T_____
GAM1522  PCSK5    5'  TCCCTGGGGCTGCCGGG     26236        ACCAG   A
                                TCCCTGGG    GTCG GG
                                ||||||||    |||| ||
                                AGGGACCC    CGGC CC
                                     CGA__   _
GAM1523  AOC2     3'  AAACAGGGAAAAGTACA     41815        AA
                                AAACAGG  AGAAGTATA
                                |||||||  |||||||||
                                TTTGTCC  TTTTCATGT
                                    C_
GAM1523  CCRL1    3'  AAACAGGAAAAAAGATA     32423            T
                                AAACAGGAAAGAAG ATA
                                |||||||||||||| |||
                                TTTGTCCTTTTTTC TAT
                                              _
GAM1523  CHC1     3'  GGACAGGAAAGGGGCACA    10426   A       AA
                                A ACAGGAAAG  GTATA
                                | |||||||||  |||||
                                C TGTCCTTTC  CGTGT
                                 C        CC
GAM1523  DDX6     3'  AAAAAGGAAAGAAAGAGTTACT 20536    C       ___   A
           AT                     AAA AGGAAAGA   AGT TACTAT
                                  ||| ||||||||   ||| ||||||
                                  TTT TCCTTTCT   TCA ATGATA
                                    T       TTC  _
GAM1523  GAC1     3'  AAACAGGAGAAAAGAGTGAATC 26792        A    TATACT
           G                      AAACAGGA AGAAG     ATCG
                                  ||||||||| |||||     ||||
                                  TTTGTCCT TTTTC     TAGC
                                       C    TCACT_
GAM1523  MMP19    5'  AACAGGAAGGAGGTCAGAGCCC 35574        A  A  ATACTA
           G                      AACAGGAA GA GT     TCG
                                  |||||||| || ||     |||
                                  TTGTCCTT CT CA     GGC
                                       C  C  GTCTCG
GAM1523  VAMP8    3'  ACAGGAAAGGAGACCCTC    19068        A  TAT   A
                                  ACAGGAAAG AG   ACT TC
                                  ||||||||| ||   ||| ||
                                  TGTCCTTTC TC   TGG AG
                                       C  ___   G
GAM1523  ASPH     3'  CAATTATTTCTGAGCCCA    37133           ATTAT
                                  CGATTATTTCTGA    TCCA
                                  ||||||||||||     ||||
```

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                                GTTAATAAAGACT    GGGT
                                      C____
GAM1523  CDK10    5'  ACGCTTATTTCTGGGTGTCCAA 38145    A       AATTAT
                                ACG TTATTTCTG     TCCAA
                                ||| |||||||||     |||||
                                TGC AATAAAGAC     AGGTT
                                  G       CCAC__
GAM1523  KLHL3    3'  TTATTTCTGGACATTCC     44653         AAT
                                TTATTTCTG   TATTCC
                                |||||||||   ||||||
                                AATAAAGAC   GTAAGG
                                     CT_
GAM1523  NMB      3'  CGATATTTCTGGTGACCCA    43948      T      AATTAT
                                CGAT ATTTCTG     TCCA
                                |||| |||||||     ||||
                                GCTA TAAAGAC     GGGT
                                  _      CACT__
GAM1523  TLL2     3'  ATTATTTAAAAATTATTCCAA  29746        CT
                                ATTATTT  GAATTATTCCAA
                                |||||||  ||||||||||||
                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1523  ZNF215   3'  AATTATTTACCCTGTTATTCCA 29914         _ GAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
                                TTAATAAA GG   AATAAGGT
                                     T  GAC
GAM1524  ADCY6    3'  TCCCAGGACACTATCTGGGGAA 34177       A TG  T   CA
                                TTCCAG G  TT ATC  GGGAA
                                |||||| |  || |||  |||||
                                AGGGTC T  GA TAG  CCCTT
                                   C GT  _   AC
GAM1524  ALPP     3'  TCCAGATGTCTGGGGA      42871       G    ATCCA
                                TCCAGA TGTTT     GGGA
                                |||||| |||||    ||||
                                AGGTCT ACAGA     CCCT
                                   _     C_____
GAM1524  DLG5     5'  TCCTGGAGCTCCGGGGA     44466     A_   GTTTA   A
                                TCC  GAGT    TCC GGGA
                                |||  ||||    ||| ||||
                                AGG  CTCG    AGG CCCT
                                  AC    ______   C
GAM1524  FANCC    3'  CAGGCAGGTCCAGGGA      43269     A   TTTA
                                CAG GTG    TCCAGGGA
                                ||| |||    ||||||||
                                GTC CGT    AGGTCCCT
                                  _   CC__
GAM1524  HOXA3    3'  TTCCGGCAGTCCAGGGAA    36202      AGAGT  TTA
                                TTCC    GT   TCCAGGGAA
                                ||||    ||   |||||||||
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                                AAGG    CG   AGGTCCCTT
                                  C____  TC_
GAM1524  HOXD4    3'  TTCCAGAGAGTGGGGA     31184        T  TTATCCA
                                TTCCAGAG GT      GGGA
                                |||||||| ||      ||||
                                AAGGTCTC CA      CCCT
                                    T  C_______
GAM1524  LAMC1    3'  TTCCAAGGAAAAGAATTCAGGG 14098      __   TGTTT  C
             AAA                  TTCCA  GAG    AT CAGGGAAA
                                |||||  |||    || ||||||||
                                AAGGT  CTT    TA GTCCCTTT
                                  TC   TTCT_  A
GAM1524  MAP4     3'  CTCCAGGTAGATCCAGGGA   36272       A   TTT
                                TTCCAG GTG   ATCCAGGGA
                                ||||||  |||   |||||||||
                                GAGGTC CAT   TAGGTCCCT
                                   _   C__
GAM1524  MSH3     3'  TTCAAGAGTGTTTATACGTAGA 14633     C         CCAG
             AA                   TTC AGAGTGTTTAT    GGAAA
                                |||  ||||||||||    |||||
                                AAG TCTCACAAATA    TCTTT
                                  T          TGCA
GAM1524  OPCML    3'  CAGGGTGTTTATTGTGAG     14949     A       CCA
                                CAG GTGTTTAT   GGG
                                |||  ||||||||   |||
                                GTC CACAAATA   CTC
                                  C       ACA
GAM1524  RTKN     3'  TTCCAGGAAGGGTTTAGGGA   37503       __  T   ATCC
                                TTCCAG  AG GTTT    AGGGA
                                ||||||  || ||||    |||||
                                AAGGTC  TC CAAA    TCCCT
                                   CT  C   _____
GAM1524  SORBS1   3'  AGGATCCCTCCAGGGAAA    31703    TG  TA
                                AG  TT  TCCAGGGAAA
                                ||  ||  ||||||||||
                                TC  AG  AGGTCCCTTT
                                 CT  GG
GAM1524  UPK1B    3'  TCCAGAGTCACTCGGGGAA    28084        GTTTA  CA
                                TCCAGAGT    TC  GGGAA
                                ||||||||    ||  |||||
                                AGGTCTCA    AG  CCCTT
                                    GTG__  C_
GAM1524  ZNF179   3'  TCCAGGGTCATCGGGGAA    28377      A  GTT    CA
                                TCCAG GT   TATC  GGGAA
                                |||||  ||   ||||  |||||
                                AGGTC CA   GTAG  CCCTT
                                  C  ____   C_
GAM1524  SIRT3    3'  CACTCAGTTCACATATTC    29257          TT_
                                CACTCGGTTT   TATTC
                                ||||||||||   |||||
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                                GTGAGTCAAG  ATAAG
                                     TGT
GAM1525 APXL    3' GCTGTTTGTTTTCTTACTAT  11622     A   ATAAA
                                GCTG TTGT    TTTACTAT
                                |||| ||||    ||||||||
                                CGAC AACA    GAATGATA
                                  A   AAA__
GAM1526 BAK1    5' TGGAGATGGAGGTCCCGAGG  45112       AT  GG  A
                                TGGAGATG  GGT  CCC GAGG
                                ||||||||  |||  ||| ||||
                                ACCTCTAC  CCA  GGG CTCC
                                     CT  __  _
GAM1526 CAPN5   3' ATGCAGATGGTGGTGGGAACGG 44925    G    A    CCCAGA
                                ATG AGATG TGGTGG     GG
                                ||| ||||| ||||||     ||
                                TAC TCTAC ACCACC     CC
                                  G    C     CTTG__
GAM1526 CYP46   3' TGAAGGGTGGCCCAGG     27425      ATGAT       A
                                TGGAG    GGTGGCCCAG G
                                |||||    |||||||||| |
                                ACTTC    CCACCGGGTC C
                                  _____       _
GAM1526 DYRK1A  3' ATGGTGGTGGTGGTGGTGATGG 38990     AGA  A    CCCA  _
                                ATGG   TG TGGTGG   GA GG
                                ||||   || ||||||   || ||
                                TACC   AC ACCACC   CT CC
                                  ACC  C     A___  A
GAM1526 GSTT1   3' TGGGGATGGTGGCTTCGGGAGG 43864    AGAT      CCA__
                                TGG   GATGGTGGC    GAGG
                                |||   |||||||||    ||||
                                ACC   CTACCACCG    CTCC
                                  C___       AAGCC
GAM1526 HYOU1   3' TGGAGATGAATGGGGAAAACAG 40643        _  T  CC__
           AGG                    TGGAGATGA TGG GG   CAGAGG
                                |||||||| ||| ||   ||||||
                                ACCTCTACT ACC CC   GTCTCC
                                     T  _  TTTT
GAM1526 IL1RN   3' TGGAGATGGAGCTTGGAG   8217       TGA  T  CCA
                                TGGAGA  TGG GGC  GAG
                                ||||||  ||| |||  |||
                                ACCTCT  ACC TCG  CTC
                                   ___  _  AAC
GAM1526 LENG4   5' GGAGGGTGGCCCAGAG     35888     ATGAT
                                GGAG    GGTGGCCCAGAG
                                ||||    ||||||||||||
                                CCTC    CCACCGGGTCTC
                                  _____
GAM1526 LIF     3' ATGGGGACGATGGGGA     14136     A      T  CCCAG
                                ATGG GATGATGG GG    A
                                |||| |||||||| ||    |
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                                TACC CTGCTACC CC    T
                                  C      _ _____
GAM1526 MAP3K7IP1 3' GGAGGTGATGGTGGGAG    25931     A       CCCA
                                GGAG TGATGGTGG   GAG
                                |||| |||||||||   |||
                                CCTC ACTACCACC   CTC
                                  C       ____
GAM1526 MMP19   3' TGGGTGGTGGAGCCTCAGGG  35592    AGA A  T   _  A
                                TGG  TG TGG GGCC CAG GG
                                |||  || ||| |||| ||| ||
                                ACC  AC ACC TCGG GTC CC
                                  C__  C   _   A  _
GAM1526 MSN     3' TGGGGGGTGGTGGCCAGGG   41251    AGATGA      C  A
                                TGG     TGGTGGCC AG GG
                                |||     |||||||| || ||
                                ACC     ACCACCGG TC CC
                                  CCCC__      _ _
GAM1526 PKLR    3' ATGGAGATGGGGAAGGGGCC  7145        AT___  T G___
                                ATGGAGATG    GG G   CC
                                |||||||||    || |   ||
                                TACCTCTAC    CC C   GG
                                     CCCTT  _ CIII
GAM1526 PMX1    3' TGGTGGTGGTATCCCAGAGG  35528    A    ___
                                TG TGGTGG   CCCAGAGG
                                || ||||||   ||||||||
                                AC ACCACC   GGGTCTCC
                                 C     ATA
GAM1526 RORA    5' TGGAGAATGATGGGGAG    39519      TG     CCCA
                                TGGAGA  ATGGTGG   GAG
                                ||||||  |||||||   |||
                                ACCTCT  TACTACC   CTC
                                   __      C___
GAM1526 SEPN1   3' ATGGAGGGTTCTGCCCAGAGG 42422      ATGAT  G__
                                ATGGAG    GGT   GCCCAGAGG
                                ||||||    |||   |||||||||
                                TACCTC    CCA   CGGGTCTCC
                                   _____  AGA
GAM1526 SLC25A5 3' ATGGAAATGGCTTTAGAG   10099     GAT    GGCCC
                                ATGGA   GATGGT    AGAG
                                |||||   ||||||    ||||
                                TACCT   TTACCG    TCTC
                                   ___     AAA__
GAM1526 UNC13   3' ATGGAGATGGGTAGA      26859       AT   GGCCC
                                ATGGAGATG  GGT    AGA
                                |||||||||  |||    |||
                                TACCTCTAC  CCA    TCT
                                     __  _____
GAM1526 WHSC1   3' TGCAGATGATGCTGTTGGAGG 39389   G      G  GCCCA
                                TG AGATGATG TG    GAGG
                                || ||||||| ||    ||||
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                                AC TCTACTAC AC    CTCC
                                 G       G  AAC__
GAM1527  ASPH    3'  CAATTATTTCTGAGCCCA    37133           ATTAT
                                CGATTATTTCTGA    TCCA
                                |||||||||||||    ||||
                                GTTAATAAAGACT    GGGT
                                      C_____
GAM1527  ASPH    3'  CAATTATTTCTGAGCCCA    37133           ATTAT
                                CGATTATTTCTGA    TCCA
                                |||||||||||||    ||||
                                GTTAATAAAGACT    GGGT
                                      C_____
GAM1527  CDK10   5'  ACGCTTATTTCTGGGTGTCCAA 38145     A       AATTAT
                                ACG TTATTTCTG     TCCAA
                                ||| |||||||||     |||||
                                TGC AATAAAGAC     AGGTT
                                  G       CCAC__
GAM1527  KLHL3   3'  TTATTTCTGGACATTCC     44653         AAT
                                TTATTTCTG   TATTCC
                                |||||||||   ||||||
                                AATAAAGAC   GTAAGG
                                     CT_
GAM1527  NMB     3'  CGATATTTCTGGTGACCCA    43948      T      AATTAT
                                CGAT ATTTCTG     TCCA
                                |||| |||||||     ||||
                                GCTA TAAAGAC     GGGT
                                  _      CACT__
GAM1527  TLL2    3'  ATTATTTAAAAATTATTCCAA  29746       CT
                                ATTATTT  GAATTATTCCAA
                                |||||||  ||||||||||||
                                TAATAAA  TTTAATAAGGTT
                                    TT
GAM1527  ZNF215  3'  AATTATTTACCCTGTTATTCCA 29914        _  GAA
                                GATTATTT CT   TTATTCCA
                                |||||||| ||   ||||||||
                                TTAATAAA GG   AATAAGGT
                                     T  GAC
GAM1527  LARS    3'  GAAGCATACTGACACTTT    33479         ATCGT
                                GAAGTATACT    CATTTT
                                ||||||||||    ||||||
                                CTTCGTATGA    GTGAAA
                                     CT___
GAM1528  ANKRD3  3'  TGCCATGGAAAAGTATCC    33972       AAAC
                                TGTCAT    GAGTATCC
                                ||||||    ||||||||
                                ACGGTA    TTCATAGG
                                   CCTT
GAM1528  BMPR1A  3'  TATCATAAAATAAGCAGTATCC 20255         CG_____
                                TGTCATAAA     AGTATCC
                                |||||||||     |||||||
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                                ATAGTATTT     TCATAGG
                                     TATTCG
GAM1528 GOT1     3'  TGTCATGATTAAATATCC    13228       AAAC
                                TGTCAT    GAGTATCC
                                ||||||    ||||||||
                                ACAGTA    TTTATAGG
                                   CTAA
GAM1528 PHEX     3'  TGCCATAAACCAGCGTCC    7775          G  TA
                                TGTCATAAAC AG  TCC
                                |||||||||| ||  |||
                                ACGGTATTTG TC  AGG
                                      G  GC
GAM1528 SULT1A3  3'  TGTCATAACTCACTGTATCC  17215         ___  GA
                                TGTCATAA   AC  GTATCC
                                ||||||||   ||  ||||||
                                ACAGTATT   TG  CATAGG
                                     GAG  A_
GAM1529 GIPR     3'  GCGTGTGTGGAACTTGA     6725        C   CC
                                GTGTGTG GGG  CTTGA
                                ||||||| |||  |||||
                                CGCACAC CCT  GAACT
                                    A   T_
GAM1529 ZNF134   5'  AGCCGTCTGTGCGGGCAAACCT 18323       G       ___
                                AGCCGT TGTGCGGGC   CCT
                                |||||| |||||||||   |||
                                TCGGCA ACACGCCCG   GGA
                                   G        TTT
GAM1530 CUL3     3'  GTGGTAGAATACAGCATGC    18743     A       A  GG
                                GTG TAGAATACG TA  GC
                                ||| |||||||| ||  ||
                                CAC ATCTTATGT GT  CG
                                  C        C  A_
GAM1530 HLF      3'  TGTGTCAGTGATAGGGC     13399      A   AATAC
                                TGTG TAG    GATAGGGC
                                |||| |||    ||||||||
                                ACAC GTC    CTATCCCG
                                  A  A____
GAM1530 JRK      3'  TGTGGGGAGAAACAGGGCC   44507      AT_  ATAC
                                TGTG   AGA   GATAGGGCC
                                ||||   |||   |||||||||
                                ACAC   TCT   TTGTCCCGG
                                  CCC  ____
GAM1530 PRPSAP1  3'  TGGATAGTAATAGGGC      15736    T    AATAC
                                TG GATAG    GATAGGGC
                                || |||||    ||||||||
                                AC CTATC    TTATCCCG
                                 _    A____
GAM1530 SLC25A5  3'  TGTTATAGAATACAACATGCC  10100     G          GG
                                TGT ATAGAATACGATA  GCC
                                ||| ||||||||||||  |||
```

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                                ACA TATCTTATGTTGT  CGG
                                  A          A_
GAM1530  XKRY     5'  TGTGATGGAATACAAGG     21707       A      AT
                                TGTGAT GAATACG  AGG
                                |||||| |||||||  |||
                                ACACTA CTTATGT  TCC
                                   C      __
GAM1530  CCNF     3'  GCGGATCACTTGAGGTCAT    12076          AACTG
                                GCGGATTACTT    CAT
                                ||||||||||     |||
                                CGCCTAGTGAA    GTA
                                      CTCCA
GAM1531  ADAM11   3'  GGGTGTGGTCATCCTTGG    34659     C         C
                                GGG GTGGTCATCCT GG
                                ||| ||||||||||| ||
                                CCC CACCAGTAGGA CC
                                  A         A
GAM1532  HMMR     3'  AGCCAAGGTGTTTTAGCC    29807       AC    ACA
                                AGCCAAG  GTTT   AGTC
                                |||||||  ||||   ||||
                                TCGGTTC  CAAA   TCGG
                                   CA    A__
GAM1532  PIM1     5'  GCCGAGGGCGAGTCGGA     44967     A  A_  TTTACA
                                GCC AG  CG     AGTCGGA
                                ||| ||  ||     |||||||
                                CGG TC  GC     TCAGCCT
                                  C  CC  _______
GAM1532  TFAP2A   3'  GAGGCGGGTGCAGAGTCGGAG  17395    C  TTA__  _
                                GA GT     CA AGTCGGAG
                                || ||     || ||||||||
                                CT CG     GT TCAGCCTC
                                 C  CCCAC  C
GAM1532  TNS      3'  AGCCGAGCTGTTTATAATTCGA 35464      A  AC     C  G
                                AGCC AG  GTTTA AA TCGG
                                |||| ||  ||||| || ||||
                                TCGG TC  CAAAT TT AGCT
                                  C  GA    A  A
GAM1532  UFD1L    3'  AGCCAAGATGTTGCAAAT    43820         C   TA
                                AGCCAAGA GTT  CAAGT
                                |||||||| |||  |||||
                                TCGGTTCT CAA  GTTTA
                                    A   C_
GAM1532  P2RY2    3'  GCCTCCAGATGGGTCTATGATA 15015    G  G   ____
            TT                   GT TT CAGA    TCTATGATATT
                                || || ||||    ||||||||||
                                CG AG GTCT    AGATACTATAA
                                 G  _    ACCC
GAM1532  TEM8     3'  GTGTTGCAGATCTGATGTATT  38189           _  A
                                GTGTTGCAGATCT ATG TATT
                                |||||||||||| ||| ||||
```

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                                CACAACGTCTAGA TAC ATAA
                                      C  _
GAM1533 MAP3K1   5' GCGCCGCCACCGACTCGGT   42705      ATA _
                                GCGCCG  CC CCGACTCGGT
                                ||||||  || ||||||||||
                                CGCGGC  GG GGCTGAGCCA
                                   ___  T
GAM1534 ADAM23   5' TCCCGGGCGCCGCTCCGTGTGG 19207   G  AA  AT       C
                                TC CG  GT  TCGCTCCGTG GG
                                || ||  ||  |||||||||| ||
                                AG GC  CG  GGCGAGGCAC CC
                                 G  C_  C_       A
GAM1534 CACNA1A  3' GCGCCCGAGGACGCGTGTCGTA 35736         _ TT_
           CGG                   GCGCCCGAGGA GT   TCGTACGG
                                ||||||||||| ||   ||||||||
                                CGCGGGCTCCT CG   AGCATGCC
                                      G  CAC
GAM1534 CTNNA1   3' AGCCCCGAGGGGTGGGGGCGG  42322    G     A  TTTCGTA
                                AGC CCCGAGG GT      CGG
                                ||| ||||||| ||      |||
                                TCG GGGCTCC CA      GCC
                                  _     C  CCCCC__
GAM1535 DIAPH2   3' GTAATGTTAGGATGGG     28675     AC   GCGC
                                GTAG  GTTG   GGATGGG
                                ||||  ||||   |||||||
                                CATT  CAAT   CCTACCC
                                  A_   _____
GAM1536 ANKH     3' ACACGGTGGGGGTGAGAACT   38308       AA   A  TT
                                ACGCGGTG  GGT AG  GCT
                                ||||||||  ||| ||  |||
                                TGTGCCAC  CCA TC  TGA
                                     CC   C  T_
GAM1536 EPHA8    3' ACACGGTGGGGTTCCTGCTTCC 33887       AA   AAG
                                ACGCGGTG  GGT   TTGCTTCC
                                ||||||||  |||   ||||||||
                                TGTGCCAC  CCA   GACGAAGG
                                     C_   AG_
GAM1536 OLIG2    3' CGCGGTCGGGCTGTTGCTTC   25145      GAA   AA
                                CGCGGT   GGT  GTTGCTTC
                                ||||||   |||  ||||||||
                                GCGCCA   CCG  CAACGAAG
                                   GC_   A_
GAM1536 XPNPEP2  3' ACGCGGTGACAGGTTGGGTT   18150        _   AA_
                                ACGCGGTGA AGGT   GTT
                                ||||||||| ||||   |||
                                TGCGCCACT TCCA   CAA
                                     G    ACC
GAM1537 A1BG     3' TGGAAGAGCACAGATGAAAGAG 39097        G   TC  T
           G                    TGGAAGAG ACG  GT AAAGAGG
                                ||||||||  |||  ||  |||||||
```

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                                ACCTTCTC TGT  TA TTTCTCC
                                     G  C_  C
GAM1537 ABR     3'  TGGAGGAAGACTGAGGGGAGG  35020      A     GTCGTTAAA
                                TGGA GAGGAC        GAGG
                                |||| ||||||        ||||
                                ACCT CTTCTG        CTCC
                                  C     ACTCCC___
GAM1537 AMD1    3'  TGGGGGAGACACCAGGGAGAGG 11592     AA  G  GT  TTAA
                                TGG  GAG AC  CG    AGAGG
                                |||  ||| ||  ||    |||||
                                ACC  CTC TG  GT    TCTCC
                                  CC   _  TG  CCC_
GAM1537 ARHGAP6  5'  TGGAGAAGGACGAGCAAAGAGG 30231      AG     TC  T
                                TGGA  AGGACG  GT AAAGAGG
                                ||||  ||||||  || |||||||
                                ACCT  TCCTGC  CG TTTCTCC
                                  CT     T_  _
GAM1537 CIT     3'  TGGGAGGGGAAGTCGTCAA   43060     A  A   C
                                TGG AG GGA GTCGTTAA
                                ||| || ||| ||||||||
                                ACC TC CCT CAGCAGTT
                                  C  C   T
GAM1537 DEDD    3'  TGGAAAAGGGAAATAAAGGG   37431         ACGTCGT    A
                                TGGAAGAGG      TAAAG GG
                                |||||||||      ||||| ||
                                ACCTTTTCC      ATTTC CC
                                     CTTT___    _
GAM1537 DLST    3'  TGGAAGAGGTAGAAGA      12576         ACGTCG TA
                                TGGAAGAGG     T  AAGA
                                |||||||||     |  ||||
                                ACCTTCTCC     A  TTCT
                                     _______ TC
GAM1537 ELAVL2   5'  GGGGGAGGACGTCTTAAAAGGG 20744    AA       G    ___
            AGG                    GG  GAGGACGTC TTAAA   GAGG
                                ||  ||||||||| |||||   ||||
                                CC  CTCCTGCAG AATTT   CTCC
                                 CC        _    TCC
GAM1537 HDGF    3'  GGAAGAGGGTGGGAGAG     21064        ACGTC  TAA
                                GGAAGAGG    GT   AGAG
                                ||||||||    ||   ||||
                                CCTTCTCC    CA   TCTC
                                     _____  CCC
GAM1537 HRH1    3'  GAGAAAGCTGTTAAAGAGG    9252       C  C
                                GAGGA GT GTTAAAGAGG
                                ||||| || ||||||||||
                                CTCTT CG CAATTTCTCC
                                   T  A
GAM1537 LFG     3'  GGAGGAGGGCGAAGCCAAGGGA 44141     A   A  TC    A_
            GG                    GGA GAGG CG  GTTAA  GAGG
                                ||| |||| ||  |||||  ||||
```

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                                CCT CTCC GC  CGGTT  CTCC
                                  C   C TT    CC
GAM1537  MAPT    5'  GGGAGAGGACAGCGGAGGAGG  32582    A      T  TTAAA
                                GG AGAGGACG CG    GAGG
                                || |||||||| ||    ||||
                                CC TCTCCTGT GC    CTCC
                                 C      C  CTC__
GAM1537  MUC4    5'  GGAAGAGGACAAAAGAG    39670          TCGTT
                                GGAAGAGGACG    AAAGAG
                                ||||||||||    ||||||
                                CCTTCTCCTGT    TTTCTC
                                      _____
GAM1537  MYL1    5'  TGGAAGAGGATGGTGGTT    38607          C_  C
                                TGGAAGAGGA  GT GTT
                                ||||||||||  || |||
                                ACCTTCTCCT  CA CAA
                                      AC  C
GAM1537  NCOA3   3'  TGGTAGGGGGGCAGAAGAG    27220     A  A  ACGTC  TA
                                TGG AG GG    GT  AAGAG
                                ||| || ||    ||  |||||
                                ACC TC CC    CG  TTCTC
                                  A  C _____  TC
GAM1537  PAK4    3'  TGGGGGAGGGCCTGTCCCAGAG 25254     AA   AC  _  AA
           G                     TGG  GAGG  GTC GTT  AGAGG
                                ||| ||||  ||| |||  |||||
                                ACC  CTCC  CGG CAG  TCTCC
                                  CC   __  A  GG
GAM1537  PDYN    5'  TGGGAGGAGGTGCCAAAGAGG  35925     AA    C  C
                                TGG  GAGGA GT GTTAAAGAGG
                                |||  ||||| || ||||||||||
                                ACC  CTCCT CA CGGTTTCTCC
                                  __    C  _
GAM1537  PKHD1   3'  TGGAAGAAGGGTAAAGAAG   39810         ACGTC  T
                                TGGAAGAGG    GT AAAGAGG
                                |||||||||    || |||||||
                                ACCTTCTTC    CA TTTCTTC
                                     C____  _
GAM1537  PPL     3'  GGGAGAGGACGACACCAAGGAG 15497    A      T  TT  A
           G                     GG AGAGGACG CG  AA GAGG
                                || |||||||| ||  || ||||
                                CC TCTCCTGC GT  TT CTCC
                                 C      T  GG  C
GAM1537  RAB5B   3'  CGGGGAGGAACACTAGGGAGG  16091     AA    CGT    AA
                                TGG  GAGGA  CGTTA  GAGG
                                |||  |||||  |||||  ||||
                                GCC  CTCCT  GTGAT  CTCC
                                  C_    T__    CC
GAM1537  RAP1GDS1 3'  TGGATGGAGGACAGAG     34508     A_    GTCGTTAA
                                TGGA  GAGGAC      AGAG
                                ||||  ||||||      ||||
```

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                                ACCT  CTCCTG       TCTC
                                  AC     _________
GAM1537  SLC25A11  3'  TGGAAGGGAAATAAATAGAGG  18680       A   C  CGTTAA
                                TGGAAG GGA GT     AGAGG
                                |||||| ||| ||     |||||
                                ACCTTC CCT TA     TCTCC
                                   _   T  TTTA__
GAM1537  TCF2      3'  GGGAGAGGACACAGAG      27029     A       T GTTAA
                                GG AGAGGACG C     AGAG
                                || |||||||| |     ||||
                                CC TCTCCTGT G     TCTC
                                 C       _ _____
GAM1537  TNFAIP2   3'  TGGAGGGAGGCAGGAGAG    26643      A_    A  TCGTTAA
                                TGGA  GAGG CG      AGAG
                                ||||  |||| ||      ||||
                                ACCT  CTCC GT      TCTC
                                  CC    _  CC_____
GAM1538  ABCC3     3'  TCCAGGTCGATGGCAGC     33427      CAGT  G  _
                                TCCA    GG CG TGGCAGC
                                ||||    || || |||||||
                                AGGT    CC GC ACCGTCG
                                  ____  A  T
GAM1538  ACVR1     5'  CAGTGGGCTATGGTCACA     9958          _    CAGC
                                CAGTGGGC GTGG    CACA
                                |||||||| ||||    ||||
                                GTCACCCG TACC    GTGT
                                     A    A___
GAM1538  BCL11B    3'  TCTACAGCGAATAGCAGCCA   39755    C      GC
                                TC ACAGTGG  GTGGCAGCCA
                                || |||||||  ||||||||||
                                AG TGTCGCT  TATCGTCGGT
                                 A      __
GAM1538  CASP7     3'  CAGTGGACACAGCCA       10273         GTG
                                CAGTGGGC   GCAGCCA
                                ||||||||   |||||||
                                GTCACCTG   TGTCGGT
                                     ___
GAM1538  DLC1      3'  CCATGGTGGTGGAAGCGGTTGC 25900      CA___     C    CA
                                CCA    GTGGG GTGG  GC
                                |||    ||||| ||||  ||
                                GGT    CACCT CGCC  CG
                                  ACCAC    T    AA
GAM1538  GRB10     5'  TCTACAGTGGGTATCACGTGGC 23669    C       _____
                                TC ACAGTGGG    CGTGGC
                                || ||||||||    ||||||
                                AG TGTCACCC    GCACCG
                                 A       ATAGT
GAM1538  IL13      3'  TCCAAGTGCCAGCAGCCAC   13527      C   GG  G
                                TCCA AGT  GC TGGCAGCCAC
                                |||| |||  || ||||||||||
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                                AGGT TCA  CG GTCGTCGGTG
                                  _  __  _
GAM1538  ISL1     5'  TCCACAGTGAAATGGTGG    13597          C__
                                TCCACAGTGGG  GTGG
                                ||||||||||  ||||
                                AGGTGTCACTT  CACC
                                     TAC
GAM1538  ITGA5    3'  TCCACAGTGGGACGCCA     41503          CGTG  A
                                TCCACAGTGGG   GC GCCA
                                ||||||||||   || ||||
                                AGGTGTCACCC   TG CGGT
                                     _____ _
GAM1538  ITPKA    3'  CACAGTGGGGACAAAGCTGC  13635          __ T  A
                                CACAGTGGG  CG GGC GC
                                |||||||||  || ||| ||
                                GTGTCACCC  GT TCG CG
                                     CT  T   A
GAM1538  LASS1    3'  TCCACGTGGCACGGTTGC    34618       A   G    CA
                                TCCAC GTGG CGTGG  GC
                                ||||| |||| |||||  ||
                                AGGTG CACC GTGCC  CG
                                  _   _    AA
GAM1538  LZTR1    3'  GTGGCTTCATGGCAGCCACA  27640       G__
                                GTGG  CGTGGCAGCCACA
                                ||||  ||||||||||||
                                CACC  GTACCGTCGGTGT
                                  GAA
GAM1538  LZTR1    3'  CACAATGGGCAGGCGCCACA  27631          T  A
                                CACAGTGGGCG GGC GCCACA
                                |||||||||| ||| ||||||
                                GTGTTACCCGT CCG CGGTGT
                                     _  _
GAM1538  NUDT1    3'  CAGCTGTTCAGCAGCCAC    14683       GGGCG
                                CAGT   TGGCAGCCAC
                                ||||   ||||||||||
                                GTCG   GTCGTCGGTG
                                  ACAA_
GAM1538  NUMA1    5'  TCCACAGGGTCAGCCA      45243        TGGGCGT  _
                                TCCACAG      GG CAGCCA
                                |||||||      || ||||||
                                AGGTGTC      CC GTCGGT
                                   _______ A
GAM1538  PCDHB4   3'  CACTAGACATGTGGTGGTCACA 33197    G   __   CAGC
                                CA TGGGC  GTGG   CACA
                                || |||||  ||||   ||||
                                GT ATCTG  CACC   GTGT
                                 G   TA   ACCA
GAM1538  PER2     3'  CAGTGGAAACAGCCA       35616        CGT
                                CAGTGGG  GGCAGCCA
                                |||||||  ||||||||
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                                GTCACCT   TTGTCGGT
                                   ___
GAM1538  PITX3    5'  TCCCAGTAGCGGCGGCTGC   22758    A    G _   A
                                TCC CAGTGG CG TGGC GC
                                ||| |||||| || |||| ||
                                AGG GTCATC GC GCCG CG
                                  _    _ C   A
GAM1538  PRSS8    3'  TCCATGGTGGGTGAGGGGCCA  15761     CA    CGT  CA
                                TCCA  GTGGG   GG  GCCA
                                ||||  |||||   ||  ||||
                                AGGT  CACCC   CC  CGGT
                                  AC    ACT  C_
GAM1538  RAP1B    3'  CACAGTGAGAATCTACAGCTGC 31821         C  G_    CA
              A                  CACAGTGGG GT  GCAGC  CA
                                |||||||||  ||  |||||  ||
                                GTGTCACTC TA  TGTCG  GT
                                     T  GA    AC
GAM1538  SCN4A    3'  TCTGCAGGGGAGGGGCCAC   7328     CA   T   CGT  CA
                                TC  CAG GGG   GG  GCCAC
                                ||  ||| |||   ||  |||||
                                AG  GTC CCC   CC  CGGTG
                                 AC   _   T__  C_
GAM1538  SNTB1    5'  GCGGGAGTTGGCAGCTGCA   34281      C  _     CA
                                GTGGG GT GGCAGC  CA
                                ||||| || ||||||  ||
                                CGCCC CA CCGTCG  GT
                                   T  A     AC
GAM1538  HPSE     3'  AATGGATGAAAAATTACCTATT 27413        CT__  C    C
              G                  AGTGGATG    GT ACCTA TG
                                ||||||||    || ||||| ||
                                TTACCTAC    TA TGGAT AC
                                     TTTT  A    A
GAM1538  IPP      3'  GTGCATACTGCCTGCTG     25321     G     TCA   A
                                GTG ATGCTG   CCT CTG
                                ||| ||||||   ||| |||
                                CAC TATGAC   GGA GAC
                                  G     ___   C
GAM1538  TRIM14   3'  TAGCAACTGTCACCTGCTGA   37703     AT        A
                                TGG  GCTGTCACCT CTGA
                                |||  ||||||||||| ||||
                                ATC  TGACAGTGGA GACT
                                  GT         C
GAM1539  CHST2    5'  GGCTGGCTGCTGGCGCC     41716     A       ACC
                                GGC TGGCTGCTG   CC
                                ||| |||||||||   ||
                                CCG ACCGACGAC   GG
                                  _        CGC
GAM1539  GPR4     3'  AGGCATGGTGGCTCACATTTGT 40880         CT   G  CCCTA
              GG                   AGGCATGG  GCT AC     TGG
                                |||||||  ||| ||    |||
```

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                                TCCGTACC  CGA TG    ACC
                                    AC   G  TAAAC
GAM1539  PAEP     5'  AGCATGGCTGCGGCTGTG    15065          TGACCC  A
                                GGCATGGCTGC     CT TG
                                ||||||||||      || ||
                                TCGTACCGACG     GA AC
                                      CC____  C
GAM1539  PET112L  3'  GGGGTGGCTGCTGGTCGGCTGT 21282    CA       ACCC_  A
             GG                   GG  TGGCTGCTG    CT TGG
                                ||  |||||||||    || |||
                                CC  ACCGACGAC    GA ACC
                                 CC       CAGCC  C
GAM1539  SPR      3'  AGGCAGGACTGCCCCTATG   17092      T  CT    A
                                AGGCA GG  GCTG CCCCTATG
                                |||||  ||  |||| ||||||||
                                TCCGT CC  TGAC GGGGATAC
                                  _  __   _
GAM1540  AKAP13   3'  TGGCAGTGGTGTGCCCTCA   40354        CCATATACA   _
                                TGGCAGTG       GTCC CA
                                ||||||||       |||| ||
                                ACCGTCAC       CGGG GT
                                    CACA_____    A
GAM1540  CLOCK    3'  TGGCAGTGGTATGTCC     22220        CCA   ACA
                                TGGCAGTG   TAT   GTCC
                                ||||||||   |||   ||||
                                ACCGTCAC   ATA   CAGG
                                    C__   ___
GAM1540  CORO1C   3'  TGGCAGTGCCTCCC       30727          ATATACAG
                                TGGCAGTGCC       TCCC
                                ||||||||||       ||||
                                ACCGTCACGG       AGGG
                                      _________
GAM1540  DBCCR1   3'  TGGCAGTGTCAGTTGTACA   31148        C  TA__
                                TGGCAGTG CA    TACA
                                |||||||| ||    ||||
                                ACCGTCAC GT    ATGT
                                    A  CAAC
GAM1540  DLG5     5'  TGGCCGTGTCATACAGT     44472      A   CCA
                                TGGC GTG   TATACAGT
                                |||| |||   ||||||||
                                ACCG CAC   GTATGTCA
                                  G   A__
GAM1540  GYPA     3'  TGTCAGTGCCATGCCC      44627    G       ATACA
                                TG CAGTGCCAT    GTCC
                                || |||||||||    ||||
                                AC GTCACGGTA    CGGG
                                 A       _____
GAM1540  MUCDHL   3'  TGGCAGTGTGGCTGGGTTCCAC 34949         CCATATACA  C
                                TGGCAGTG       GT CCAC
                                ||||||||       || ||||
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                                ACCGTCAC       CA GGTG
                                    ACCGACC__  A
GAM1540  NKX2E    5'  TGGCAGCGCCAGTCC      20496         TATACA  C
                                TGGCAGTGCCA    GTC C
                                ||||||||||     ||| |
                                ACCGTCGCGGT    CAG G
                                       _______ A
GAM1540  RET      3'  TGTTAGTGCCATCAGC     33942   GC      ATA
                                TG  AGTGCCAT   CAGT
                                ||  ||||||||   ||||
                                AC  TCACGGTA   GTCG
                                 AA      ___
GAM1540  SLC4A7   3'  TGGCAGTGCTTTATATCAA   18828       CA   _
                                TGGCAGTGC  TATA CAG
                                |||||||||  |||| |||
                                ACCGTCACG  ATAT GTT
                                      AA   A
GAM1540  SUV39H1  3'  TAGCAGGGCATACAGTCTCA  17226      T  CAT      C
                                TGGCAG GC   ATACAGTC CA
                                |||||| ||   |||||||| ||
                                ATCGTC CG   TATGTCAG GT
                                   C ___       A
GAM1540  VCL      3'  TGACAGTGAAGTACAGT    30408       CCATA
                                TGGCAGTG    TACAGT
                                ||||||||    ||||||
                                ACTGTCAC    ATGTCA
                                     TTC__
GAM1540  BIRC7    3'  CAGCAGGCCCAGAACACA    40251          G
                                CAGCAGGCCCAGG ACACA
                                |||||||||||| |||||
                                GTCGTCCGGGTCT TGTGT
                                          _
GAM1540  CPSF4    3'  CAGCAGGTTGCAGGAGACA   27438       CC_  _
                                CAGCAGG   CAGG GACA
                                |||||||   |||| ||||
                                GTCGTCC   GTCC CTGT
                                    AAC   T
GAM1540  GALGT    3'  AGAGGCTCAGGGACAGCCA   11177   C   C      CAA
                                AG AGGC CAGGGACA   CA
                                || |||| ||||||||   ||
                                TC TCCG GTCCCTGT   GT
                                 _   A       CG_
GAM1540  GATA2    5'  ACGGGCCCAGGGACAGCA    13080   A         _
                                GC GGCCCAGGGACA CA
                                || |||||||||||| ||
                                TG CCGGGTCCCTGT GT
                                 C          C
GAM1540  GRAF     3'  CAGCAGGCTTAGCTACACA   31439       CC  GG
                                CAGCAGGC  AG  ACACA
                                ||||||||  ||  |||||
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                                GTCGTCCG  TC  TGTGT
                                    AA  GA
GAM1540  GRPR     3'  AGGGCACAGACACAACAAT   23681     CC  G
                                AGG  CA GGACACAACAAT
                                |||  || ||||||||||||
                                TCC  GT TCTGTGTTGTTA
                                  C_  G
GAM1540  LARS2    3'  CAGCAGGCCTGGGAGGCACA  31674         CA   __
                                CAGCAGGCC  GGGA  CACA
                                |||||||||  ||||  ||||
                                GTCGTCCGG  CCCT  GTGT
                                    A_   CC
GAM1540  PPEF1    5'  GCGGGCTCAGGACACAA     26411    A  CCA
                                GC GGC   GGGACACAA
                                || |||   |||||||||
                                CG CCG   TCCTGTGTT
                                 C  AG_
GAM1540  PRKCABP  3'  CAGCAGGCTCCGGGGGCA    29668        _  A  A
                                CAGCAGGC CC GGG CA
                                |||||||| || ||| ||
                                GTCGTCCG GG CCC GT
                                    A  C  C
GAM1540  PSD      5'  GGCTAGACACAACAAT      15787     CCAG
                                GGC   GGACACAACAAT
                                |||   ||||||||||||
                                CCG   TCTGTGTTGTTA
                                  A___
GAM1540  SMURF1   3'  CAGCAGCCCAGAAATTAACA  45185       G    GG CAC
                                CAGCAG CCCAG  A   AACA
                                |||||| |||||  |   ||||
                                GTCGTC GGGTC  T   TTGT
                                   _    TT AA_
GAM1540  TCF8     3'  CAGCAGGCCAGGGATGCA    36232         C    CA
                                CAGCAGGCC AGGGA  CA
                                ||||||||| |||||  ||
                                GTCGTCCGG TCCCT  GT
                                    _    AC
GAM1540  UBQLN3   5'  CAGATCTGTGGGGACACAGCA  32717     CCCA__      A
                                CAGG     GGGACACA CA
                                ||||     |||||||| ||
                                GTCT     CCCTGTGT GT
                                  AGACAC       C
GAM1541  DBY      3'  TGGTATCGTGAGCATTAC    21665       TTC  GA
                                TGGTAT   CG  AGCATTAC
                                ||||||   ||  ||||||||
                                ACCATA   GC  TCGTAATG
                                   ___  AC
GAM1541  DDX3     3'  TGATATCTTGAGCATTAC    35826       TCCG  A
                                TGGTATT    GA GCATTAC
                                |||||||    || |||||||
```

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                                ACTATAG   CT CGTAATG
                                   AA__  _
GAM1541  DMRT2    3'  TGGCATTTAGCAGGCATT    27272       C_  AA
                                TGGTATTT  CGG  GCATT
                                ||||||||  |||  |||||
                                ACCGTAAA  GTC  CGTAA
                                   TC  __
GAM1541  TEM8     3'  TGGTATTTTGGGAAGATCA   38194       CC    C
                                TGGTATTT  GGAAG ATTA
                                ||||||||  ||||| ||||
                                ACCATAAA  CCTTC TAGT
                                   AC    _
GAM1542  ARVCF    3'  CACTGGGGCACTGT       11700       GTAAGG
                                CACTGGG     GCACTGT
                                |||||||     |||||||
                                GTGACCC     CGTGACA
                                   _______
GAM1542  BACE     3'  CACTGGGGTGAGGAGATGT   39953        A   CACT
                                CACTGGGGT AGGG   GTGT
                                ||||||||| ||||   ||||
                                GTGACCCCA TCCT   TACA
                                   C   C___
GAM1542  CLASP1   3'  CTGGGGTAGGGACCTTGT    42238       A  C  G
                                CTGGGGTA GGG ACT TGT
                                |||||||| ||| ||| |||
                                GACCCCAT CCC TGG ACA
                                   _  _  A
GAM1542  FUT6     5'  ACACTGGGGGGGCCAGTG    6645        TAA   ACT
                                ACACTGGGG  GGGC  GTG
                                |||||||||  ||||  |||
                                TGTGACCCC  CCCG  CAC
                                   ___   GT_
GAM1542  KLK4     3'  CACAAGGGGGCACTGTGT    41748    T   TAAG
                                CAC GGGG   GGCACTGTGT
                                ||| ||||   ||||||||||
                                GTG TCCC   CCGTGACACA
                                  T  ____
GAM1542  MAML1    3'  CACTGGGGTAAGTGGAGCA   31277         ___
                                CACTGGGGTAAG  GGCA
                                ||||||||||||  ||||
                                GTGACCCCATTC  TCGT
                                      ACC
GAM1542  TMPRSS2  3'  CACTGAGGTAGCAATGTGT   24929        AAG   C
                                CACTGGGGT  GGCA TGTGT
                                |||||||||  |||| |||||
                                GTGACTCCA  TCGT ACACA
                                   ___   T
GAM1542  FBXL11   3'  GTGCATCCTGGGAAAGCCT   29440         CTGTAC
                                GTGCATTCTGGG    GCCT
                                ||||||||||||    ||||
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                                CACGTAGGACCC     CGGA
                                      TTT___
GAM1542 HIP12    3' GCACGGGCTGTGTGCCT     42401      TCT      AC
                                GCAT   GGGCTGT  GCCT
                                ||||   |||||||  ||||
                                CGTG   CCCGACA  CGGA
                                  ___      CA
GAM1542 S100A10  5' GCGCGGCGGGCTGTGCGCCT   40393      ATTC       A
                                GTGC    TGGGCTGT CGCCT
                                ||||    |||||||| |||||
                                CGCG    GCCCGACA GCGGA
                                  CC__       C
GAM1543 CTSK     3' TGGAAGAAATGGAAGAGCAGGA 7580      CCCCTACA   A
                T                TGG       GAA AGCAGGAT
                                |||       ||| ||||||||
                                ACC       CTT TCGTCCTA
                                  TTCTTTAC   C
GAM1543 HMG20B   3' TCGGCTGGAGGAGAGCAGGAT  26800      CCCTAC   AAA
                                TTGGC     AGA   GCAGGAT
                                |||||     |||   |||||||
                                AGCCG     TCT   CGTCCTA
                                   ACCTCC  ___
GAM1543 NGFRAP1  5' TTGGTGCTCTGACCAGCAGGAT 30777      CCC  ACA  AA
                                TTGG   CT   GA  AGCAGGAT
                                ||||   ||   ||  ||||||||
                                AACC   GA   CT  TCGTCCTA
                                  AC_  GA_  GG
GAM1543 SMOH     3' TGGCCCCTGTGGGAGCAGG   24817        ACAGAAA
                                TGGCCCCT      AGCAGG
                                ||||||||      ||||||
                                ACCGGGGA      TCGTCC
                                     CACCC__
GAM1543 SOX12    3' CTGGTCCCTACAGGGAT     28038      C       AAAAGCA
                                TTGG CCCTACAG      GGAT
                                |||| ||||||||      ||||
                                GACC GGGATGTC      CCTA
                                  A      ________
GAM1543 SUFU     3' CTGGCCCCTGCAGGAT      32086         ACAGAAAA
                                TTGGCCCCT      GCAGGAT
                                |||||||||      |||||||
                                GACCGGGGA      CGTCCTA
                                               _________
GAM1543 TGFA     3' TTGGTCTCTAAGCAGGA     17452      CCC   CAGAAA
                                TTGG   CTA     AGCAGGA
                                ||||   |||     |||||||
                                AACC   GAT     TCGTCCT
                                  AGA  _______
GAM1543 TNFRSF10B 3' CTGGCCCCTGTAGAAGTTGC  19284         AC    AA_
                                TTGGCCCCT  AGAA   GC
                                |||||||||  ||||   ||
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                                GACCGGGGA  TCTT   CG
                                     CA    CAA
GAM1543  TRIM14   3'  TTGGCCCCTGCAGCTGTGG   37712         A   AAAAGCA
                                TTGGCCCCT CAG      GG
                                ||||||||| |||      ||
                                AACCGGGGA GTC      CC
                                     C   GACA___
GAM1543  UNC119   3'  TTGGCCCCTCATGGGGAGGGAT 38347         A  GAAAAGCA
                                TTGGCCCCT CA       GGAT
                                ||||||||| ||       ||||
                                AACCGGGGA GT       CCTA
                                     _ ACCCCTC_
GAM1544  ABAT     5'  GCGCCCCGAGTTCCGGCAGC   40775    A   AG   CC
                                GC CCCC  GAG  CCGGCAGC
                                || ||||  |||  ||||||||
                                CG GGGG  CTC  GGCCGTCG
                                 C   __   AA
GAM1544  ACLY     5'  AGCACCCCAGCAGCCGGTAGC  42151         G   CC  C
                                AGCACCCCAG AGCC  GG AGC
                                |||||||||| ||||  || |||
                                TCGTGGGGTC TCGG  CC TCG
                                     G   __ A
GAM1544  ADRA2A   5'  CAGCTCTCCAGGAGCCGC    8627      ACC       CCG
                                CAGC   CCAGGAGCC   GC
                                ||||   |||||||||   ||
                                GTCG   GGTCCTCGG   CG
                                  AGA        ___
GAM1544  ALK      5'  GCACTGGAGCGGCCCCGGCGGC 43837     CCCA  ___      A
                                GCAC   GGA   GCCCCGGC GC
                                ||||   |||   |||||||| ||
                                CGTG   CCT   CGGGGCCG CG
                                  A___   CGC       C
GAM1544  ARHGAP6  5'  GCGCTCCAAGTGCCCCGGCGGC 30217    ACC    A      A
                                GC   CCAGG GCCCCGGC GC
                                ||   ||||| |||||||| ||
                                CG   GGTTC CGGGGCCG CG
                                 CGA    A       C
GAM1544  AVP      5'  GCTCCCCAGGAGCCCACGGC   7937     A         _
                                GC CCCCAGGAGCCC CGGC
                                || ||||||||||| ||||
                                CG GGGGTCCTCGGG GCCG
                                 A          T
GAM1544  B3GAT1   3'  CAGTGTCCCAGCAGCCCCTGC  38294     CAC    G     G
                                CAG   CCCAG AGCCCC GC
                                |||   ||||| |||||| ||
                                GTC   GGGTC TCGGGG CG
                                  ACA    G     A
GAM1544  B4GALT1  3'  AGCCCCCGCCCCTGGCAG    11275     A   AGGA   _
                                AGC CCCC   GCCCC GGCAG
                                ||| ||||   ||||| |||||
```

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                                TCG GGGG   CGGGG CCGTC
                                  _  ____    A
GAM1544 BACH2   5' CAGCCCCCTCCCGGCA     34780     A   AGGAGC
                                CAGC CCCC     CCCGGCA
                                |||| ||||     |||||||
                                GTCG GGGG     GGGCCGT
                                  _   A_____
GAM1544 BDP1    5' CAGCCCCGAGCCCCGGCG    32947     A  CAG       A
                                CAGC CCC   GAGCCCCGGC G
                                |||| |||   |||||||||| |
                                GTCG GGG   CTCGGGGCCG C
                                  _  ___        C
GAM1544 CACNA1C  3' GCGGCCCCGGCCCGGCGGC   8757    A_   A AGC    A
                                GC  CCCC GG   CCCGGC GC
                                ||  |||| ||   |||||| ||
                                CG  GGGG CC   GGGCCG CG
                                 CC   _ ___     C
GAM1544 CD81    3' GCTCCCAGGAGAGGCCTGGC   20343    AC      C__  C
                                GC  CCCAGGAG   CC GGC
                                ||  ||||||||   || |||
                                CG  GGGTCCTC   GG CCG
                                 A_       TCC  A
GAM1544 CDK10   3' CAGCAGTTCAGGGGCTCGG   38147      CCC   A  CC
                                CAGCA   CAGG GC  CGG
                                |||||   |||| ||  |||
                                GTCGT   GTCC CG  GCC
                                   CAA   C  A_
GAM1544 CDKN2C   5' CAGGTCCCGGGACTCCCGGCAG 38558    CAC   A   GC
            C                    CAG   CCC GGA  CCCGGCAGC
                                |||   ||| |||  |||||||||
                                GTC   GGG CCT  GGGCCGTCG
                                  CA_   C   GA
GAM1544 CHRNA4   3' AGTACCCCAGGGGCTGAAGC   8845     C      A  CCC
                                AG ACCCCAGG GC   GGC
                                || |||||||| ||   |||
                                TC TGGGGTCC CG   TCG
                                 A       C  ACT
GAM1544 CHST6   5' CAGCACCCCAAAGCTTGGCGGC 34675          G   CC__
                                CAGCACCCCAG AGC    CGGC
                                |||||||||| |||    ||||
                                GTCGTGGGGTT TCG    GCCG
                                       _  AACC
GAM1544 COMT    5' CAGTGCCTCAGAAGCAGC    8891     CA  C      CCC
                                CAG  CC CAGGAGC   GGC
                                |||  || |||||||   |||
                                GTC  GG GTCTTCG   TCG
                                  AC  A      ___
GAM1544 CORO2A   5' CAGCCTCCAGGAGCTCC     38060      ACC       C
                                CAGC   CCAGGAGC CC
                                ||||   |||||||| ||
```

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                                GTCG   GGTCCTCG GG
                                  GA_       A
GAM1544  CRYBA2   5'  CAGCGTCTCAAGAGCCCCG   38392     ACCC
                                CAGC   CAGGAGCCCCG
                                ||||   ||||||||||
                                GTCG   GTTCTCGGGGC
                                  CAGA
GAM1544  DLEC1    5'  CAGCACCCCAGAGCAGGGC   28818         G   CCC
                                CAGCACCCCAG AGC   GGC
                                |||||||||| |||   |||
                                GTCGTGGGGTC TCG   CCG
                                      _   TC_
GAM1544  DLEC1    3'  CAGCACCCCAGAGCAGGGC   28818         G   CCC
                                CAGCACCCCAG AGC   GGC
                                |||||||||| |||   |||
                                GTCGTGGGGTC TCG   CCG
                                      _   TC_
GAM1544  DVL3     3'  CAGCACCCTGCGAGCA     20673       CAGGA  CCC
                                CAGCACCC    GC   GGCA
                                ||||||||    ||   ||||
                                GTCGTGGG    CG   TCGT
                                    A_____  C__
GAM1544  ESPN     3'  GCAGTGAAAGGGTCCCGGCAGC 36444    CCCC_   AGC
                                GCA    AGG   CCCGGCAGC
                                |||    |||   |||||||||
                                CGT    TCC   GGGCCGTCG
                                  CACTT   CA_
GAM1544  ESRRA    5'  CACCTGGGGCTCCGGCAGC   20826     CCA  A  C
                                CACC   GG GC CCGGCAGC
                                ||||   || || ||||||||
                                GTGG   CC CG GGCCGTCG
                                  AC_  _  A
GAM1544  FANCA    5'  GCGCCTACAGCCCCGGCGGC   6592     A  CCAGG       A
                                GC CC    AGCCCCGGC GC
                                || ||    ||||||||| ||
                                CG GG    TCGGGGCCG CG
                                 C  ATG__       C
GAM1544  FASN     3'  CAGCACCCCACGGGTGGC    19929         _  AGCCCC
                                CAGCACCCCA GG     GGC
                                |||||||||| ||     |||
                                GTCGTGGGGT CC     CCG
                                     G  CA_____
GAM1544  FNTA     3'  CAGCACCCAAGGAGCATCAG   12993        C     CC
                                CAGCACCC AGGAGC  CGG
                                |||||||| ||||||  |||
                                GTCGTGGG TCCTCG  GTC
                                    T     TA
GAM1544  FOXG1B   5'  GCACTGAGCGCTCCGGCAGC   23505     CCCA  A  C
                                GCAC    GG GC CCGGCAGC
                                ||||    || || ||||||||
```

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                                CGTG   TC CG GGCCGTCG
                                  AC__  G  A
GAM1544  GAS7    3'  CAGCAGAGTCCTGGCAG    25266      CCCCAG  C  C
                                CAGCA    GAG CC GGCAG
                                |||||     ||| || |||||
                                GTCGT    CTC GG CCGTC
                                  _______  A  A
GAM1544  GNA11   3'  CAGCGCCACCCGCCCGGCAGC  44028     A  _  AGGAGC
                                CAGC CC CC     CCCGGCAGC
                                |||| || ||     |||||||||
                                GTCG GG GG     GGGCCGTCG
                                  C  T  GC____
GAM1544  GRB10   5'  GCCCCCAGGAGCGCGGC    23659    A        CC
                                GC CCCCAGGAGC  CGGC
                                || ||||||||||  ||||
                                CG GGGGTCCTCG  GCCG
                                 _        C_
GAM1544  GRB14   5'  GCGCTCGGGGCCCCGGCGGC  21040   ACCCCA  A      A
                                GC     GG GCCCCGGC GC
                                ||     || ||||||||  ||
                                CG     CC CGGGGCCG CG
                                 CGAG__  C       C
GAM1544  HFE     3'  CAGCACCCTGGGATTACAGGC  40001        CA   GCCCC
                                CAGCACCC  GGA    GGC
                                ||||||||  |||    |||
                                GTCGTGGG  CCT    CCG
                                     AC   AATGT
GAM1544  ILF1    3'  CAGCTCGGTGAGTCCCGGCAG  21103     ACCCCAG   C
                                CAGC      GAG CCCGGCAG
                                ||||      ||| ||||||||
                                GTCG      CTC GGGCCGTC
                                  AGCCA__   A
GAM1544  ITGB1   5'  CCCCCGCAGCTCCGGCAGC   38055     AGG   C
                                CCCC   AGC CCGGCAGC
                                ||||   ||| ||||||||
                                GGGG   TCG GGCCGTCG
                                  GCG   A
GAM1544  ITPA    3'  CAGGACCCCAGGCCTGGCGGC  37907    C       AGC  C   A
                                CAG ACCCCAGG   CC GGC GC
                                ||| ||||||||   || ||| ||
                                GTC TGGGGTCC   GG CCG CG
                                  C       ___  A   C
GAM1544  KCND3   5'  CAGCTCTTGGGCCGGCAG    22531     ACCCCA  A   CC
                                CAGC     GG GCC  GGCAG
                                ||||     || |||  |||||
                                GTCG     CC CGG  CCGTC
                                  AGAA__  _  __
GAM1544  LENG4   3'  CAGCGGCCCAGCAGGCGGCAG  35879     AC    G  CCC
                                CAGC  CCCAG AG   CGGCAG
                                ||||  ||||| ||   ||||||
```

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                                GTCG  GGGTC TC   GCCGTC
                                  CC    G  C__
GAM1544  LRP2     5'  AGCACACCGCACCGGCAG    21182      C  AGGA  C
                                AGCAC CC    GC CCGGCAG
                                ||||| ||    || |||||||
                                TCGTG GG    CG GGCCGTC
                                  T  _____  T
GAM1544  MAP3K7IP1 3'  GCAATCCTGGCCGACAGC    25928     CC  A  AGCC
                                GCA  CC GG    CCGGCAGC
                                |||  || ||    ||||||||
                                CGT  GG CC    GGCTGTCG
                                 TA  A  _____
GAM1544  MAPRE3    3'  CAGCACCCTGGGAAGTGTTGGG 29527         CA    CCCC__
              C                  CAGCACCC  GGAG     GGC
                                ||||||||  ||||     |||
                                GTCGTGGG  CCTT     CCG
                                    AC    CACAAC
GAM1544  MFGE8     3'  ACCCCAGGGCCGACG       25459         A   CC   A
                                ACCCCAGG GCC  GGC G
                                |||||||| |||  ||| |
                                TGGGGTCC CGG  CTG C
                                   _   __   _
GAM1544  MLLT1     3'  CAGCCTCCCAGGACCCCGGC   25478      AC      G
                                CAGC  CCCAGGA CCCCGGC
                                ||||  ||||||| |||||||
                                GTCG  GGGTCCT GGGGCCG
                                  GA      _
GAM1544  MYOG      3'  GCACCCCAGAGCTGGC      40423         G   CCC
                                GCACCCCAG AGC   GGC
                                ||||||||| |||   |||
                                CGTGGGGTC TCG   CCG
                                     _   A__
GAM1544  NCKAP1    5'  CAGCAGCCCGCGCCCCGGCAGC 30251       C   AGGA
                                CAGCA CCC    GCCCCGGCAGC
                                ||||| |||    ||||||||||
                                GTCGT GGG    CGGGGCCGTCG
                                  C   CG__
GAM1544  NEUROD2   3'  GCTGCCCCAGGAGAGCGGC    26061    A_       CCC
                                GC  CCCCAGGAG   CGGC
                                ||  |||||||||   ||||
                                CG  GGGGTCCTC   GCCG
                                 AC        TC_
GAM1544  NRG1      5'  GCTCCCATCGTCCGGCAGC    30342    AC    GGAGCC
                                GC  CCCA     CCGGCAGC
                                ||  ||||     ||||||||
                                CG  GGGT     GGCCGTCG
                                 A_    AGCA__
GAM1544  NRG2      5'  AGCCCTCCACCGGCA       30362     A  _   GGAGCC
                                AGC CC CCA     CCGGCA
                                ||| || |||     ||||||
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                                TCG GG GGT     GGCCGT
                                  _ A  _______
GAM1544 PKD2L1   5' ACCCCAGGTGCCCACTCTCAGC 32015        A   CGG__
                                ACCCCAGG GCCC    CAGC
                                |||||||| ||||    ||||
                                TGGGGTCC CGGG    GTCG
                                    A   TGAGA
GAM1544 PLXNA1   3' GCACCCCAGAGGCTCTCAG   43622        GA  CCCGG
                                GCACCCCAG  GC    CAG
                                |||||||||  ||    |||
                                CGTGGGGTC  CG    GTC
                                     TC  AGA__
GAM1544 PPP3CC   5' GCTCCAGGAGCCCGC      24677    ACC        CG
                                GC   CCAGGAGCCC  GC
                                ||   ||||||||||  ||
                                CG   GGTCCTCGGG  CG
                                 A__        __
GAM1544 PRX      3' GCACTTGCATTTCCGGCAGC   34120     CC_  GGAGCC
                                GCAC   CA     CCGGCAGC
                                ||||   ||     ||||||||
                                CGTG   GT     GGCCGTCG
                                  AAC  AAA___
GAM1544 PTPRH    3' CAGCACCCAGGAGTCTGGGAGC 15946        C    CCCC  C
                                CAGCACCC AGGAG    GG AGC
                                |||||||| |||||    || |||
                                GTCGTGGG TCCTC    CC TCG
                                    _     AGAC  _
GAM1544 RPS6KA2  5' GCATCCCAGGCGCGGGGC    34463     C     A  CCC
                                GCA CCCAGG GC   GGC
                                ||| |||||| ||   |||
                                CGT GGGTCC CG   CCG
                                  A     G  CC_
GAM1544 RYR3     5' GCGCCTCTGCTTCCCCCGGCAG 9772     A  CCAGGAG_
              C                  GC CC       CCCCGGCAGC
                                 || ||       ||||||||||
                                 CG GG       GGGGCCGTCG
                                  C  AGACGAAG
GAM1544 S100B    3' GCTCAGAGCCCCCGGTAG    26570    ACCCCA       _  C
                                GC     GGAGCCCC GG AG
                                ||     |||||||| || ||
                                CG     TCTCGGGG CC TC
                                 AG_____       G  A
GAM1544 SLC22A2  5' CACTCCGGGGCTCCGGCAGC   40518     C  A  A  C
                                CAC CC GG GC CCGGCAGC
                                ||| || || || ||||||||
                                GTG GG CC CG GGCCGTCG
                                  A  C  _  A
GAM1544 SMARCD2  3' GCATCCCAGGAGATGATGGCGG 16918     C       CCCC_   A
              C                  GCA CCCAGGAG     GGC GC
                                 ||| ||||||||     ||| ||
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                                CGT GGGTCCTC    CCG CG
                                  A       TACTA   C
GAM1544  SMCX     3'  GCCCCCAGGAGCTGAGG     20072    A        CCC
                                GC CCCCAGGAGC   GG
                                || ||||||||||   ||
                                CG GGGGTCCTCG   CC
                                  _        ACT
GAM1544  SNL      3'  CAGCAGGGGGGCCCCGGCGGC  16937      CCCCA  A      A
                                CAGCA    GG GCCCCGGC GC
                                |||||    || |||||||| ||
                                GTCGT    CC CGGGGCCG CG
                                   CCC__ _      C
GAM1544  TMEFF2   5'  GCGCCCCGCAGCCCGGCAGC   32103    A   AGG    C
                                GC CCCC   AGCCC GGCAGC
                                || ||||   ||||| ||||||
                                CG GGGG   TCGGG CCGTCG
                                 C   CG_    _
GAM1544  TMEPAI   5'  GCAGCCCCGGGGGGCGTCGGCAG 33609     _   A  A  CC
                                GCA CCCC GG GC  CGGCAG
                                ||| |||| || ||  ||||||
                                CGT GGGG CC CG  GCCGTC
                                  C   C  C  CA
GAM1544  TNFRSF6B 5'  CAGCACCCGGCACTGGCTGGCA 32347        CA  A  CCC__
           GC                   CAGCACCC  GG GC    GGCAGC
                                ||||||||  || ||    ||||||
                                GTCGTGGG  CC TG    CCGTCG
                                    __  G  ACCGA
GAM1544  TRIM9    5'  CAGCACCCTGGCCAGCGGCGGC 31554        CA  __   CC
                                CAGCACCC  GG  AGC  CGGC
                                ||||||||  ||  |||  ||||
                                GTCGTGGG  CC  TCG  GCCG
                                    A_  GG   CC
GAM1544  TRRAP    5'  CAGCCCCGACCTCGGCG     18588      A  CAGGA  C   A
                                CAGC CCC    GCC CGGC G
                                |||| |||    ||| |||| |
                                GTCG GGG    TGG GCCG C
                                  _  C____   A   C
GAM1544  TSSC4    3'  ACACCCCAGGAGCTTCAGC   25036          CC
                                GCACCCCAGGAGC  CGGC
                                ||||||||||||  ||||
                                TGTGGGGTCCTCG  GTCG
                                       AA
GAM1544  UBE2L3   3'  ACCTCAGGAGCCTTTCTGGC   17821     C      CC___
                                ACC CAGGAGCC    GGC
                                ||| ||||||||    |||
                                TGG GTCCTCGG    CCG
                                  A       AAAGA
GAM1544  USP7     3'  ACCCCAGGAAGGCAG       18447          CCCC
                                ACCCCAGGAG   GGCAG
                                ||||||||||   |||||
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                                TGGGGTCCTT   CCGTC
                                      ____
GAM1544 ZNF264   3' CAGCACTTTGGGGGGCCGAGGC 18268      CCCA_ A  CC
                                CAGCAC    GG GCC  GGC
                                ||||||    || |||  |||
                                GTCGTG    CC CGG  CCG
                                   AAACC  C   CT
GAM1545 MSN      3' TGTTATAGCTGGAGAGGA    41253        C  T  C
                                TGTTGTAGC GG GG GA
                                ||||||||| || || ||
                                ACAATATCG CC CT CT
                                     A  T  C
GAM1545 RLN2     3' TGTTGTAGCTGTGGTAA     39593        CG   CG
                                TGTTGTAGC  GTGG  A
                                |||||||||  ||||  |
                                ACAACATCG  CACC  T
                                     A_   AT
GAM1546 ALPI     3' GGGTGTGGAATGATCCTA    11580      C  TTGCC   C
                                GGGTG GG    TGA CCTA
                                ||||| ||    ||| ||||
                                CCCAC CC    ACT GGAT
                                   A  TT___   A
GAM1547 8D6A     3' ACAGGGCCGTTCTACCCCCTGG 32447       GATTGCCC
                                ACAGGGC       TCCCCTGG
                                |||||||       ||||||||
                                TGTCCCG       GGGGGACC
                                    GCAAGAT_
GAM1547 APAF1    5' AGGCGCCTCCCCTG       29815      ATTGC
                                GGGCG    CCTCCCCTG
                                |||||    |||||||||
                                TCCGC    GGAGGGGAC
                                     _____
GAM1547 CACNB1   3' GGGTCCTCTCCCCTGG      8785      CGATTG _
                                GGG     CC CTCCCCTGG
                                |||     || |||||||||
                                CCC     GG GAGGGGACC
                                  A_____ A
GAM1547 GALR1    5' ACAGGGCGAGAGCTCTTTTGG  11191        TT  C  CCCC
                                ACAGGGCGA  GC CT   TGG
                                |||||||||  || ||   |||
                                TGTCCCGCT  CG GA   ACC
                                     CT  A  AA__
GAM1547 LZTS1    3' CAGGGCCTTCCCCTG       34261       GATTGC C
                                CAGGGC     C TCCCCTG
                                ||||||     | |||||||
                                GTCCCG     G AGGGGAC
                                   _______ A
GAM1547 MSF      3' GGGCTGCATTCTCCCCTGG   44738      GAT   C__
                                GGGC   TGC   CTCCCCTGG
                                ||||   |||   |||||||||
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                                CCCG  ACG  GAGGGGACC
                                  ___  TAA
GAM1547 PDGFB   3' AGGGCTGCACCCTCCCTTGGA 15167     GAT      C
                                AGGGC  TGCCCTCCC TGGA
                                |||||  ||||||||| ||||
                                TCCCG  GTGGGAGGG ACCT
                                  AC_      A
GAM1547 PIGN    3' ACAGGCATATGCTCTCCTCTGG 29544     G AT  C   C
                                ACAGG CG  TGC CTCC CTGG
                                ||||| ||  ||| |||| ||||
                                TGTCC GT  ACG GAGG GACC
                                  _ AT  A   A
GAM1547 SPOCK   5' ACAGGGCGGTCTGGTAGTCCTG 41730       A GCCCTCC
            G                    ACAGGGCG TT     CCTGG
                                |||||||| ||     |||||
                                TGTCCCGC AG     GGACC
                                    C ACCATCA
GAM1547 SURF4   3' ACAGGGCGAGTGCAGCTGG   37648       T  CCTCCC
                                ACAGGGCGA TGC    CTGG
                                ||||||||| |||    ||||
                                TGTCCCGCT ACG    GACC
                                    C  TC____
GAM1547 XT3     3' ACAGGGCGGTTTTCTCC    33658       A GCC
                                ACAGGGCG TT  CTCC
                                |||||||| ||  ||||
                                TGTCCCGC AA  GAGG
                                    C AA_
GAM1548 CRIM1   3' TTTTTGATTTCAACTCAAAATG 32388       G   GGA
            T                    TTTTTGATT TAGC  AAAATGT
                                |||||||||| ||||  |||||||
                                AAAAACTAA GTTG  TTTTACA
                                    A  AG_
GAM1548 FGF2    3' TTTTTAATTGGCTTAAAAATGT 12851       TA  GG
                                TTTTTGATTG  GC  AAAAATGT
                                ||||||||||  ||  ||||||||
                                AAAAATTAAC  CG  TTTTTACA
                                    __  AA
GAM1548 SLC10A2 3' TTTCTGATTGATGGGAAA   7822        TAGC
                                TTTTTGATTG   GGAAA
                                ||||||||||   |||||
                                AAAGACTAAC   CCTTT
                                    TAC_
GAM1549 EIF2C1  3' CTTGGCTGCCCATCTTGA   29177      CA   C  C
                                TTTGGT  CCCA CT GA
                                ||||||  |||| || ||
                                GAACCG  GGGT GA CT
                                  AC   A  A
GAM1550 DPP4    3' TACAATGCTTTCCCATCACCC  12581      A  C      G
                                TACAAT CT TCCTATTAC CC
                                |||||| || ||||||||| ||
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                                ATGTTA GA AGGGTAGTG GG
                                   C  A       _
GAM1550  FOXE1    3'  TACAATCTTCTTTTTCACACCC 20948       AC   CCTA
                C                   TACAAT  TCT    TTACGCCCC
                                    ||||||  |||    |||||||||
                                    ATGTTA  AGA    AGTGTGGGG
                                       GA   AAA_
GAM1550  GM2A     3'  AATACTCTCACTTCGC      42684          _ ATTA
                                    AATACTCTC CT    CGC
                                    |||||||||  ||    |||
                                    TTATGAGAG GA    GCG
                                          T  A___
GAM1550  HOXC13   3'  TAAATACTCTTCTGCACCC   40671   C       C  ATTA
                                    A AATACTCT CT    CGCCC
                                    | ||||||||  ||    |||||
                                    A TTATGAGA GA    GTGGG
                                     T       A  C___
GAM1550  MEN1     5'  TACCATGCTCTCCTACATGGCC 39199     A  A       TAC
                                    TAC AT CTCTCCTAT   GCC
                                    |||  ||  |||||||||   |||
                                    ATG TA GAGAGGATG   CGG
                                      G  C        TAC
GAM1550  PFKFB2   5'  TACGATCTCTCCTAAGATCCC  26309     A  A      TTACG
                                    TAC AT CTCTCCTA     CCC
                                    |||  ||  ||||||||     |||
                                    ATG TA GAGAGGAT     GGG
                                      C  _       TCTA_
GAM1550  RU2      3'  TACATGCTTTCCTATTAC    32293      ATA  C
                                    TACA   CT TCCTATTAC
                                    ||||   ||  |||||||||
                                    ATGT   GA AGGATAATG
                                      AC_  A
GAM1551  DAZ      3'  TAGGGAAGAAGCCATTGA    19855     A  TATC
                                    TAG GA    AGGCCATTGA
                                    |||  ||    ||||||||||
                                    ATC CT    TTCGGTAACT
                                      C  TC__
GAM1551  FLG      3'  TGTCTAGAGCTGTCAGCC    43365         ATA   G
                                    TGTCTAGAG   TCAG CC
                                    |||||||||   ||||  ||
                                    ACAGATCTC   AGTC GG
                                         GAC   _
GAM1551  FSTL1    3'  TATCTAGAGGCAGTTATTG   28221         ATAT   GCC
                                    TGTCTAGAG    CAG   ATTG
                                    |||||||||    |||   ||||
                                    ATAGATCTC    GTC   TAAC
                                         C___    AA_
GAM1552  FMR1     3'  CTATGACGTGAAAT       12939       TCGTAC
                                    CTATG     ACGTGAAAT
                                    |||||     |||||||||
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                              GATAC     TGCACTTTA
                                 _______
GAM1552 HTR1D    3'  TATGCTAAGTAGTGAAATCT  9264       C__   CAC
                              TATGT   GTA   GTGAAATCT
                              |||||   |||   |||||||||
                              ATACG   CAT   CACTTTAGA
                                 ATT   ___
GAM1552 TAF4B    3'  TATTCCACACACGTGGAAT   44551     GT        A
                              TAT  CGTACACGTG AAT
                              |||  |||||||||| |||
                              ATA  GTGTGTGCAC TTA
                                AG         C
GAM1553 APAF1    3'  GGGAAAATGCTTTAGAAA    29824       CG  GAGGG
                              GGGAAAA  GC    TAGAAA
                              |||||||  ||    ||||||
                              CCCTTTT  CG    ATCTTT
                                  A_  AA___
GAM1553 AVPR1A   5'  GGGAGGGAGGCAGAAA      8730      AAAC  C    G
                              GGGA    GG GAGG TAGAAA
                              ||||    || |||| ||||||
                              CCCT    CC CTCC GTCTTT
                                 ____ _   _
GAM1553 BMP1     5'  GGGCGGCGGCGAGGGAAG    25987     AAAA       T
                              GGG    CGGCGAGGG AG
                              |||    |||||||||| ||
                              CCC    GCCGCTCCC TC
                                GCC_        T
GAM1553 BSN      3'  GGGAGAGGCAAGGGAG      18404      AAAC       T
                              GGGA    GGCGAGGG AG
                              ||||    |||||||| ||
                              CCCT    CCGTTCCC TC
                                CT__       _
GAM1553 GABPB1   5'  GGGAAGGCAGCAGGAGGT    23526       AA    A_
                              GGGAA  CGGCG  GGGT
                              |||||  |||||  ||||
                              CCCTT  GTCGT  TCCA
                                 CC    CC
GAM1553 GPT      5'  GGGAAGGCAGCTCAGGAG    23637       AA    GA   T
                              GGGAA  CGGC  GGG AG
                              |||||  ||||  ||| ||
                              CCCTT  GTCG  TCC TC
                                 CC    AG  _
GAM1553 HEBP1    5'  GGCGAGGCGGCGAGGCGAGA   31992    _ AAA       GT
                              GG GA   CGGCGAGG  AGA
                              || ||   ||||||||  |||
                              CC CT   GCCGCTCC  TCT
                               G  CC_       GC
GAM1553 HR       3'  AGGATGCGGTGGTAGAAACG   32907      AAACG   AG
                              GGGA    GCG  GGTAGAAACG
                              ||||    |||  ||||||||||
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                                TCCT    CGC  CCATCTTTGC
                                  A____   CA
GAM1553  HTR6     5'  GGGTGGACGGCAAGGGAG    9312      AAA        T
                                GGG   ACGGCGAGGG AG
                                |||   |||||||||| ||
                                CCC   TGCCGTTCCC TC
                                  ACC        _
GAM1553  INHBB    5'  GGGAAGGTGGCGAAAGAG    13562      AAC       T
                                GGGAA   GGCGAGGG AG
                                |||||   |||||||| ||
                                CCCTT   CCGCTTTC TC
                                   CCA      _
GAM1553  LHX1     5'  GAGAACGGCGGCGGGAACG   24525      AA     A_   TAGA
                                GGGA  ACGGCG  GGG    AACG
                                ||||  ||||||  |||    ||||
                                CTCT  TGCCGC  CCC    TTGC
                                  __     CG  _____
GAM1553  MKI67    3'  GGGAAAACAGCAGGGAG     14525          G    T
                                GGGAAAACGGC AGGG AG
                                |||||||||| |||| ||
                                CCCTTTTGTCG TCCC TC

                                      _   _
GAM1553  NPY2R    5'  GGGAAAAGGCGAGGGCAAA   9499         C
                                GGGAAAA GGCGAGGGTAGA
                                ||||||| ||||||||||||
                                CCCTTTT CCGCTCCCGTTT

                                     _
GAM1553  NPY2R    3'  GGGAAAAGGCGAGGGCAAA   9499         C
                                GGGAAAA GGCGAGGGTAGA
                                ||||||| ||||||||||||
                                CCCTTTT CCGCTCCCGTTT

                                     _
GAM1553  PCDH7    5'  GGGAGGGCAGCGATAGA     37119      AAAC   G  _
                                GGGA    GGC AG GGTAGA
                                ||||    ||| || ||||||
                                CCCT    CCG TC CTATCT
                                  C___   _  G
GAM1553  PKIA     5'  GGGAAGGCAGCCTGGAAAC   27743       AA    GAG  TAG
                                GGGAA  CGGC   GG   AAAC
                                |||||  ||||   ||   ||||
                                CCCTT  GTCG   CC   TTTG
                                   CC    GA_  ____
GAM1553  PNUTL1   3'  GGGAAGGGCAAGGGAG      15434      AAC       T
                                GGGAA   GGCGAGGG AG
                                |||||   |||||||| ||
                                CCCTT   CCGTTCCC TC
                                  C__       _
GAM1553  POLL     3'  GGGCAGTGGTGAGGTAGAA   29983     AAAAC  C    G
                                GGG     GG GAGG TAGAA
                                |||     || |||| |||||
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                                CCC    CC CTCC ATCTT
                                  GTCA_  A   _
GAM1553  SIX2     3'  GGGAGACGGCAAGTCGGC    32612      AA       __
                                GGGA  ACGGCGAG  GGT
                                ||||  ||||||||  |||
                                CCCT  TGCCGTTC  CCG
                                  C_       AG
GAM1553  SIX2     3'  GGGAAAAGGCCTCAGGAGA   32611        C   GA_   T
                                GGGAAAA GGC   GGG AGA
                                ||||||| |||   ||| |||
                                CCCTTTT CCG   TCC TCT
                                    _  GAG  _
GAM1553  SLC28A1  3'  GGGAGAACAGCCCTCAGAAGCG 20113      A     GAGGG    A
                                GGGA AACGGC    TAGAA CG
                                |||| ||||||    ||||| ||
                                CCCT TTGTCG    GTCTT GC
                                  C     GGA__    C
GAM1553  STX1A    3'  GGGAGGATGGCAAGGGCAG   21413     AAAC
                                GGGA   GGCGAGGGTAG
                                ||||   ||||||||||
                                CCCT   CCGTTCCCGTC
                                  CCTA
GAM1553  ZNF277   5'  GGGGTGGCACCAGTAGAAACG  35085     AAAAC   AG
                                GGG    GGCG  GGTAGAAACG
                                |||    ||||  ||||||||||
                                CCC    CCGT  TCATCTTTGC
                                  CA___   GG
GAM1553  BAZ1B    3'  TCGTCGTCCTTGGGCAGGAG   37096         CCTC__
                                TCGTCGTCCT     GGAG
                                ||||||||||     ||||
                                AGCAGCAGGA     CCTC
                                     ACCCGT
GAM1553  BDKRB2   5'  CGTCCCCACCCCTCCTCGGAG  8402      G  GT  _
                                CGTC TC  CC TCCTCGGAG
                                |||| ||  || |||||||||
                                GCAG GG  GG AGGAGCCTC
                                  G  TG  G
GAM1553  CACNA1A  3'  CTCGTCGTAGTCGGAGCTCCGA 35731        C  _______  CTCG
            G                   CTCGTCGT GTC      CTC   G
                                ||||||| |||      |||   |
                                GAGCAGCA CAG      GAG   C
                                    T   CCTCIII   GCTC
GAM1553  IRS1     5'  CTCCTCCTCCTCCTCCTCGGAG 24416     G  G  G
                                CTC TC TC TCCTCCTCGGAG
                                ||| || || ||||||||||||
                                GAG AG AG AGGAGGAGCCTC
                                  G  G  G
GAM1553  NXT1     5'  CTCCTCCTCCTCCTTCTTGGAG 29908     G  G  G   C  C
                                CTC TC TC TCCT CT GGAG
                                ||| || || |||| || ||||
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                                GAG AG AG AGGA GA CCTC
                                  G  G  G    A  A
GAM1553  PRG3     5'  CTCCACCGTCCTTCTTGG    25897     GT GT     C  C
                                CTC  C  CGTCCT CT GG
                                |||  |  |||||| || ||
                                GAG  G  GCAGGA GA CC
                                 __ TG     A  A
GAM1553  PRX      3'  CTCCTCCTCCTCCTCCTCGG   34116     G  G  G
                                CTC TC TC TCCTCCTCGG
                                ||| || || ||||||||||
                                GAG AG AG AGGAGGAGCC
                                  G  G  G
GAM1553  RRP22    5'  TCTCGTCGCCCCTCGGAG    27010    G     T  T
                                TC TCGTCG CC CCTCGGAG
                                || |||||| || ||||||||
                                AG AGCAGC GG GGAGCCTC
                                 _     _ _
GAM1553  TIMP3    5'  GCCGCTGGGTCCTCGGAG    7455       CGTCC
                                GTCGT    TCCTCGGAG
                                |||||    |||||||||
                                CGGCG    AGGAGCCTC
                                   ACCC_
GAM1554  A1BG     3'  GAGGCTGGGAACAGCCCAG   39091     TCC   CCCAT
                                GAG   GGG    CAGCCCAG
                                |||   |||    ||||||||
                                CTC   CCC    GTCGGGTC
                                  CGA   TT___
GAM1554  AIM1     3'  AGAGGTTCGAGATCAGCC    45075     TC_   CCC
                                AGAG   CGGG   ATCAGCC
                                ||||   ||||   |||||||
                                TCTC   GCTC   TAGTCGG
                                  CAA    ___
GAM1554  ANK1     3'  AGAGGTCATGCCGTCAGCCCAG 33846      TC  G   CA
                                AGAG  CG GCC  TCAGCCCAG
                                ||||  || |||  |||||||||
                                TCTC  GT CGG  AGTCGGGTC
                                  CA  A   C_
GAM1554  AP1S1    3'  GTCCAGGCTCCCCTCCCAG    10500         _  ATCAG
                                GTCCGGGC CC     CCCAG
                                |||||||| ||    |||||
                                CAGGTCCG GG     GGGTC
                                    A  GGA__
GAM1554  AP2B1    5'  GAGCCGGAGAGCACAGCCCAG  10484     T    CC_  T
                                GAG CCGGG   CA CAGCCCAG
                                ||| |||||   || ||||||||
                                CTC GGCCT   GT GTCGGGTC
                                  _    CTC  _
GAM1554  B4GALT5  3'  GAGTTCGAGACCAGCC      21940      C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
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                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1554  CDH1     3'  GAGTTTGAGACCAGCC      20363      CC   CCC
                                GAGT  GGG   ATCAGCC
                                ||||  |||   |||||||
                                CTCA  CTC   TGGTCGG
                                  AA  ___
GAM1554  CDH15    3'  GTCGGGCCCGGTGACCTCAG   22337     C     ATCA  _
                                GTC GGGCCC    GCC CAG
                                ||| ||||||    ||| |||
                                CAG CCCGGG    TGG GTC
                                  _     CCAC   A
GAM1554  CDKN2D   5'  GAGCCGGGCCCAACCC      38611     T       TCA
                                GAG CCGGGCCCA   GCCC
                                ||| |||||||||   ||||
                                CTC GGCCCGGGT   TGGG
                                  _       ___
GAM1554  COL5A1   3'  GAGCCCGGGCTCGGC       6416          CCA  A
                                GAGTCCGGGC   TC GC
                                ||||||||||   || ||
                                CTCGGGCCCG   AG CG
                                     ___  C
GAM1554  FCRH1    3'  GAGTTTGAGACCAGCC      38107      CC   CCC
                                GAGT  GGG   ATCAGCC
                                ||||  |||   |||||||
                                CTCA  CTC   TGGTCGG
                                  AA  ___
GAM1554  GFAP     3'  GAGTTCAAGGTCAGCC      13122      C    CCCA
                                GAGT CGGG    TCAGCC
                                |||| ||||    ||||||
                                CTCA GTTC    AGTCGG
                                  A   C___
GAM1554  GPR4     3'  GAGTTCAAGATCAGCC      40885      C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
                                CTCA GTTC   TAGTCGG
                                  A   ___
GAM1554  GRAF     3'  GAGTTCGAGATCAGCCC     31447      C    CCC
                                GAGT CGGG   ATCAGCCC
                                |||| ||||   ||||||||
                                CTCA GCTC   TAGTCGGG
                                  A   ___
GAM1554  GRM1     3'  AAGATGAGGAGTCTGTCAGCCC 9130       GTCC   CCCA
            AG                    AAGA    GGG    TCAGCCCAG
                                ||||    |||    |||||||||
                                TTCT    CTC    AGTCGGGTC
                                  ACTC   AGAC
GAM1554  GRM7     5'  AGGTCCGGGCCCTTCAG      9182      A        A
                                AG GTCCGGGCCC TCAG
                                || ||||||||| ||||
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                                TC CAGGCCCGGG AGTC
                                 _        A
GAM1554  IFRD2    3'  AAGTGTCCGGGCCCCCAG    27626     A        A
                                AAG GTCCGGGCCC TCAG
                                ||| |||||||||| ||||
                                TTC CAGGCCCGGG GGTC
                                  A        _
GAM1554  KAL1     3'  AGAGTCCGGGCCTCTGAGC   6866            CATC
                                AGAGTCCGGGCC   AGC
                                ||||||||||||   |||
                                TCTCAGGCCCGG   TCG
                                       AGAC
GAM1554  LHX1     5'  GAGTCCGGGGCCCCGGGC    24526          _  ATCA
                                GAGTCCGGG CCC   GC
                                ||||||||| |||   ||
                                CTCAGGCCC GGG   CG
                                     C  GCC_
GAM1554  MHC2TA   3'  AAGAGTTCGAGACCAGCCC   6977        C   CCC
                                AAGAGT CGGG  ATCAGCCC
                                |||||| ||||  ||||||||
                                TTCTCA GCTC  TGGTCGGG
                                   A  ___
GAM1554  PCDHB16  3'  GAGTTCAAGATCAGCC      34141      C   CCC
                                GAGT CGGG  ATCAGCC
                                |||| ||||  |||||||
                                CTCA GTTC  TAGTCGG
                                  A  ___
GAM1554  PIK3CD   3'  GAGTTCGAGACCAGCCCAG   22729      C   CCC
                                GAGT CGGG  ATCAGCCCAG
                                |||| ||||  ||||||||||
                                CTCA GCTC  TGGTCGGGTC
                                  A  ___
GAM1554  PIM2     3'  AAGAGTCCCGGGGCTCAG    41018         __  CCA
                                AAGAGTCC  GGGC  TCAG
                                ||||||||  ||||  ||||
                                TTCTCAGG  CCCG  AGTC
                                     GC  ___
GAM1554  PRSS8    3'  GAGTCAGGGCTCGGGGGCGCTC 15759      C   CCATCA__  C
            AG                   GAGTC GGGC       GC CAG
                                ||||| ||||       || |||
                                CTCAG CCCG       CG GTC
                                   T   AGCCCCCG  A
GAM1554  RBL2     5'  AGGGCCCGGGCCCGCAG     24703    A       AT
                                AG GTCCGGGCCC  CAG
                                || ||||||||||  |||
                                TC CGGGCCCGGG  GTC
                                 C        C_
GAM1554  SEDL     3'  GAGTTTGAAACCAGCCC     31007     CC  CCC
                                GAGT  GGG  ATCAGCCC
                                ||||  |||  ||||||||
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                                CTCA  CTT   TGGTCGGG
                                  AA  ___
GAM1554  SFTPA2   3'  AAGAGTCAGGGCCCATCAG   27960       C
                                AAGAGTC GGGCCCATCAG
                                ||||||| ||||||||||
                                TTCTCAG CCCGGGTAGTC
                                   T
GAM1554  SLC7A6   3'  AGAGTTGGGCCCACAG     19587     CC     T
                                AGAGT  GGGCCCA CAG
                                |||||  ||||||| |||
                                TCTCA  CCCGGGT GTC
                                  A_     _
GAM1554  SMOH     5'  AGAATCCGGGCCCGGGCCC   24806          ATCA
                                AGAGTCCGGGCCC   GCCC
                                ||||||||||||   ||||
                                TCTTAGGCCCGGG   CGGG
                                       CC__
GAM1554  SMOH     3'  GGGCACCCATCAGCCCAG    24814     __
                                GGGC  CCATCAGCCCAG
                                ||||  ||||||||||||
                                CCCG  GGTAGTCGGGTC
                                  TG
GAM1554  SNX6     5'  GGAAGTCCGGGCCGTCGTCCAG 34564   A        CA  AGC
                                A GAGTCCGGGCC  TC   CCAG
                                | ||||||||||  ||   ||||
                                C TTCAGGCCCGG  AG   GGTC
                                 C         C_  CA_
GAM1554  TAF7L    3'  GAGTCTGAATTCAGCC     36058      C   CCCA
                                GAGTC GGG   TCAGCC
                                ||||| |||   ||||||
                                CTCAG CTT   AGTCGG
                                  A  A___
GAM1554  TBX3     3'  GAGTCCGGGGCCCCTTCCCAG  32436        _   ATCAG
                                GAGTCCGGG CCC    CCCAG
                                ||||||||| |||    |||||
                                CTCAGGCCC GGG    GGGTC
                                     C   GAA__
GAM1554  TP53     3'  GAGTTTGAGACCAGCC      8095      CC   CCC
                                GAGT  GGG   ATCAGCC
                                ||||  |||   |||||||
                                CTCA  CTC   TGGTCGG
                                  AA  ___
GAM1554  XRCC3    3'  GTCTGAGGCCCCAGCCCAG   24106    C _    AT
                                GTC G GGCCC  CAGCCCAG
                                ||| | |||||  ||||||||
                                CAG C CCGGG  GTCGGGTC
                                 A T    __
GAM1554  ZFX      5'  GAGTTCGAGACCAGCC      18215     C    CCC
                                GAGT CGGG   ATCAGCC
                                |||| ||||   |||||||
```

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                                CTCA GCTC   TGGTCGG
                                  A   ___
GAM1554  CEBPA    3'  CGTGGAGGAGCGGCTG      20392       _  TGTACC   A
                                CGTGG GGA     GCG CTG
                                ||||| |||     ||| |||
                                GCACC CCT     CGC GAC
                                  T  _______  C
GAM1554  PXN      3'  CGTGGGGACGTACATGGGCTG  16025           CGCGA
                                CGTGGGGATGTAC    CTG
                                ||||||||||||    |||
                                GCACCCCTGCATG    GAC
                                       TACCC
GAM1554  TBL2     3'  GTGAGGATGTGCTGCCACAA   29728          A___
                                GTGGGGATGT   CCGCGA
                                ||||||||||   ||||||
                                CACTCCTACA   GGTGTT
                                      CGAC
GAM1554  VAMP1    5'  CGAGGGACGCTGCGGCTGAA   32573    T      ACC   A
                                CG GGGGATGT   GCG CTGAA
                                || ||||||||   ||| |||||
                                GC TCCCTGCG   CGC GACTT
                                 _       A__   C
GAM1554  WNT1     3'  CGCGGGGAGTGTGACTG      24079        _  ACCGC
                                CGTGGGGA TGT    GACTG
                                |||||||| |||    |||||
                                GCGCCCCT ACA    CTGAC
                                    C  ______
GAM1554  ZNF22    3'  CATGGGGATGTATCGACATGAA 45047           CCG   _
                                CGTGGGGATGTA   CGAC TGAA
                                ||||||||||||   |||| ||||
                                GTACCCCTACAT   GCTG ACTT
                                       A__    T
GAM1555  BTEB1    3'  AAGAGAATATCAAATGTGA    10209          ATGTT
                                AAGAGAATAT    ATGTGA
                                ||||||||||    ||||||
                                TTCTCTTATA    TACACT
                                      GTT__
GAM1555  DDT      3'  GAAGAGGATTATGTGA       10671       AATATAT
                                GAAGAG      GTTATGTGA
                                ||||||      |||||||||
                                CTTCTC      TAATACACT
                                   C_______
GAM1555  P23      3'  TTAAACATTTTTCACTCA     27349            T
                                TTAGACATTTTTC TTTA
                                |||||||||||| ||||
                                AATTTGTAAAAAG GAGT
                                       T
GAM1556  CDH8     5'  TTGTGGGGCCCTGCGCTGGC   12198          CGG  CGG
                                TTGTGGGGCCC   GC   GGC
                                ||||||||||   ||   |||
```

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                                AACACCCCGGG  CG  CCG
                                     A__  CGA
GAM1556 COL11A2  3' GTTGTGGGATTCCAGGTGGGC 38779       CC   CCG
                                GTTGTGGGG CCGGG  GGGC
                                ||||||||| |||||  ||||
                                CAACACCCT GGTCC  CCCG
                                     AA   A__
GAM1556 CYP17    3' GTTGTGGGGCCACATAGGG  6440         C GGCC
                                GTTGTGGGGCC CG   GGG
                                |||||||||| ||   |||
                                CAACACCCCGG GT   CCC
                                      T AT__
GAM1556 DAZ      5' CGCTGTGGGGCTTCGAGTGG 44365        CC  CC
                                CGTTGTGGGGC CGGG GG
                                |||||||||| |||| ||
                                GCGACACCCCG GCTC CC
                                      AA  A_
GAM1556 KCNJ5    5' GTTGTGGGGTCCTGTGGGC  9440        _ CC_
                                GTTGTGGGG CC  GGGC
                                ||||||||| ||  ||||
                                CAACACCCC GG  CCCG
                                     A ACA
GAM1556 LTA      3' CGTGTGGGGCTCTGGTCGG  8239    T    CCCG C
                                CGT GTGGGGC   GG CGG
                                ||| |||||||   || |||
                                GCA CACCCCG   CC GCC
                                  _     AGA_ A
GAM1556 MAD2L2   3' CTGAGCGGCCCCGGGCTGGGGC 26803    T _      C
                                TTG GG GGCCCCGGGC GGGGC
                                ||| || |||||||||| |||||
                                GAC TC CCGGGGCCCG CCCCG
                                  _ G       A
GAM1556 RECQL5   3' GTTGTTGGGTCCTGGATAAGGG 20169     G  C C  CC
                                GTTGT GGG CC GGG  GGGG
                                ||||| ||| || |||  ||||
                                CAACA CCC GG CCT  TCCC
                                   A  A A  AT
GAM1556 ROR2     5' AGAGCTTCGGGCCGGGGC   21256     CC
                                GGGGC CGGGCCGGGGC
                                ||||| ||||||||||
                                TCTCG GCCCGGCCCCG
                                   AA
GAM1556 SLC2A6   3' TGTGGGCTGCCTGGGCTGGGGC 32774      __  CC  C
                                TGTGGG GCC GGGC GGGGC
                                |||||| ||| |||| |||||
                                ACACCC CGG CCCG CCCCG
                                   GA  A_  A
GAM1556 SORCS2   3' CGTGTGTGGGGTCTGGGGGGC 34053    _    CCCCG CC
                                CGT TGTGGGG   GG GGGGC
                                ||| |||||||   || |||||
```

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                                GCA ACACCCC    CC  CCCCG
                                  C      AGA__  __
GAM1556  TXNRD2   5'  CGTCGTGGGGCTTCTGGGG   26975          CCCGGGCC
                                CGTTGTGGGGC       GGGG
                                ||||||||||        ||||
                                GCAGCACCCCG       CCCC
                                      AAGA____
GAM1556  ACVRL1   5'  GCCCCGGACCGGGCTGGAGCCG 6165            C___   AC
            GGG                   GCCCCGGGCCGGGC   GCC  GGGG
                                ||||||||||||||   |||  ||||
                                CGGGGCCTGGCCCG   CGG  CCCC
                                      ACCT  __
GAM1556  ANK1     5'  CCCCGGCCCACCACGGG     33882       G  GGGCC
                                CCCCGG CC    GCCACGGG
                                |||||| ||    ||||||||
                                GGGGCC GG    TGGTGCCC
                                   G  _____
GAM1556  ARHGAP6  3'  CGGGCAGGGCATCGGGG     30212      C    CGCCA
                                CGGGC GGGC    CGGGG
                                ||||| ||||    |||||
                                GCCCG CCCG    GCCCC
                                   T   TA___
GAM1556  ARHGDIA  3'  GCTCCTGGCTGGGCCCAGGTGG 20209    C  G   C    GCCAC
            G                    GC CC GGC GGGCC    GGG
                                || || ||| |||||    |||
                                CG GG CCG CCCGG    CCC
                                 A  A   A    GTCCA
GAM1556  CACNA1A  3'  GCTCCGGGCCGGGCCTGGG   35737    C         GCCAC
                                GC CCGGGCCGGGCC    GGG
                                || ||||||||||||    |||
                                CG GGCCCGGCCCGG    CCC
                                 A          A____
GAM1556  CASP7    5'  GCCCTGGGTAGGGCCGGGCGGG 37848     C   CC     CCA
            G                    GCCC GGG  GGGCCG   CGGGG
                                |||| |||  ||||||   |||||
                                CGGG CCC  CCCGGC   GCCCC
                                  A   AT     CC_
GAM1556  CENPB    3'  GCCCCGGGCCCGGCCGAGG   43012         G    CCAC
                                GCCCCGGGCC GGCCG    GGG
                                |||||||||| |||||    |||
                                CGGGGCCCGG CCGGC    TCC
                                     G    _____
GAM1556  CHAD     5'  GCCTGGGGCCGGGGCTGGG   10414     CC      CC  CAC
                                GCC  GGGCCGGG  GC   GGG
                                |||  ||||||||  ||   |||
                                CGG  CCCGGCCC  CG   CCC
                                  AC       __  A__
GAM1556  CYP46    3'  GCCCTGGGTGGGCACAGG    27423     C   CC    CGCC
                                GCCC GGG  GGGC    ACGGG
                                |||| |||  ||||    |||||
```

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                                CGGG CCC  CCCG   TGTCC
                                  A  A_   ____
GAM1556  DBN1    5'  GCTTCGGGCCGGACCGG    38935   CC       GCCAC
                                GC  CGGGCCGGGCC   GG
                                ||  ||||||||||    ||
                                CG  GCCCGGCCTGG   CC
                                 AA       _____
GAM1556  DMPK    5'  CCCCGGGCCGGGGGCTCGGGG  20607         CC  CA
                                CCCCGGGCCGGG  GC  CGGGG
                                ||||||||||||  ||  |||||
                                GGGGCCCGGCCC  CG  GCCCC
                                      C_  A_
GAM1556  DNASE1L1  3'  GCCCCAGGGCTGGATGGACGGG 27498     _   C   CCGCC
            G                    GCCCC GGGC GGG    ACGGGG
                                |||||  |||| |||    ||||||
                                CGGGG CCCG CCT    TGCCCC
                                   T   A  ACC__
GAM1556  EPHA1   5'  GCTCCGGGCCGGGACCTGGG  23434   C       CC  AC
                                GC CCGGGCCGGG  GCC  GGG
                                ||  ||||||||||  |||  |||
                                CG GGCCCGGCCC  TGG  CCC
                                 A        __   A_
GAM1556  EPIM    5'  GCCTCCGGCCGGGCCGCGGG   12741    _   G       CAC
                                GCC CCGG CCGGGCCGC   GGG
                                |||  ||||  |||||||||   |||
                                CGG GGCC GGCCCGGCG   CCC
                                  A   _       ___
GAM1556  FZD4    5'  CCCGGGCCGAGGCCGAGGG   29157         _    CCAC
                                CCCGGGCCG GGCCG    GGGG
                                |||||||||  |||||    ||||
                                GGGCCCGGC CCGGC    TCCC
                                     T    _____
GAM1556  GAL     5'  GCGTCGGGCCGGGTCGG     45051    CC       CCGCCA
                                GC  CGGGCCGGG     CGG
                                ||  |||||||||     |||
                                CG  GCCCGGCCC     GCC
                                 CA       A_____
GAM1556  GHRHR   3'  GCCCCGGGCTGGGTAACAGCTG 9067          C   CC  CAC_
            GGG                   GCCCCGGGC GGG  GC   GGGG
                                |||||||||  |||  ||   ||||
                                CGGGGCCCG CCC  TG   CCCC
                                     A   AT  TCGA
GAM1556  GPR48   5'  GCCTGCGGGCTGGAGCGGG   32987    C_    C   CCGCCA
                                GCC  CGGGC GGG     CGGG
                                |||  |||||  |||     ||||
                                CGG  GCCCG CCT     GCCC
                                  AC    A  C_____
GAM1556  HDGF    5'  GCTCCGCGCCGGGCCGG     21063    C   G      GCCAC
                                GC CCG GCCGGGCC    GG
                                ||  ||| ||||||||    ||
```

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                                CG GGC CGGCCCGG    CC
                                 A  G      _____
GAM1556 IL2RB   5' GCCCTGGCTGAGACATGGG   9383      CG  C  CCGC  C
                                GCCC  GGC GGG   CA GGG
                                ||||  ||| |||   || |||
                                CGGG  CCG CTC   GT CCC
                                  A_  A  T___  A
GAM1556 ISG20   5' GCTCCGGGCCGAGTCAGG    13591    C       CCGCCA
                                GC CCGGGCCGGG     CGGG
                                || ||||||||||     ||||
                                CG GGCCCGGCTC     GTCC
                                 A        A_____
GAM1556 LZTR1   5' CCCGGCACACAGCCACGGGG  27635      GC  G  C
                                CCCGG  CG GC GCCACGGGG
                                |||||  || || |||||||||
                                GGGCC  GT TG CGGTGCCCC
                                  __  G  T
GAM1556 MAD2L2  3' GCCCCGGGCTGGGGCGG    26806        C  CCGCCA
                                GCCCCGGGC GGG     CGG
                                ||||||||| |||     |||
                                CGGGGCCCG CCC     GCC
                                    A  C_____
GAM1556 MAML1   5' GCCCGGGGCCGGGCCTCTCGGG 31284     C       GCCA
            G                    GCCC GGGCCGGGCC   CGGGG
                                ||||  ||||||||||   |||||
                                CGGG CCCGGCCCGG   GCCCC
                                  C        AGA_
GAM1556 MNT     3' GCCCAGGGCTGGGGACTGGGG  33715     C   C  CC  CAC
                                GCCC GGGC GGG  GC  GGGG
                                |||| |||| |||  ||  ||||
                                CGGG CCCG CCC  TG  CCCC
                                  T   A  C_  A__
GAM1556 MUCDHL  3' GCCAGCTCGGGCCGCTGCGGGG 34936    CCG  _     CA
                                GCC  GGC CGGGCCGC  CGGGG
                                |||  ||| ||||||||  |||||
                                CGG  TCG GCCCGGCG  GCCCC
                                  ___  A      AC
GAM1556 MYO1D   3' GCTCCGGGCCAGGCCTCCGCGG 43498   C        G  A
            GG                   GC CCGGGCCGGGCC CC CGGGG
                                || ||||||||||| || |||||
                                CG GGCCCGGTCCGG GG GCCCC
                                 A         A  C
GAM1556 NF1     5' GCCCTGGGCCGGGAAGAGGGCG 7056      C      CCGCCA_
            GGG                  GCCC GGGCCGGG     CGGGG
                                ||||  ||||||||     |||||
                                CGGG CCCGGCCC     GCCCC
                                  A      TTCTCCC
GAM1556 NLGN2   3' CCCTTGGGCCGGGCTCGGG   44749    C_      CGCCA
                                CCC  GGGCCGGGC    CGGG
                                |||  |||||||||    ||||
```

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                                GGG  CCCGGCCCG    GCCC
                                  AA        A____
GAM1556  PEX14    3'  CCAGGGCCGGGCCCAGG     41870    C        GCCA
                                CC GGGCCGGGCC   CGGG
                                || ||||||||||   ||||
                                GG CCCGGCCCGG   GTCC
                                 T        _____
GAM1556  PGLS     3'  GCCCCGGGTAGGGCTGCTGG  28984         CC   C  CAC
                                GCCCCGGG  GGGC GC   GG
                                ||||||||  |||| ||   ||
                                CGGGGCCC  CCCG CG   CC
                                     AT    A  A__
GAM1556  PLCG2    5'  GCCCCGGGTTTGGGCTCCGGGG 43674        CC_   CGCCA
                                GCCCCGGG   GGGC    CGGGG
                                ||||||||   ||||    |||||
                                CGGGGCCC   CCCG    GCCCC
                                     AAA    AG___
GAM1556  PTEN     5'  GCTCCGGGCCGCGGCCGCC    7218     C      _
                                GC CCGGGCCG GGCCGCC
                                || |||||||| |||||||
                                CG GGCCCGGC CCGGCGG
                                 A       G
GAM1556  PVRL2    5'  CCCGCGGGCCACTCTGTGGGG  15999      GGC       CAC__
                                CCCG   CGGGCCGC    GGGG
                                ||||   ||||||||    ||||
                                GGGC   GCCCGGTG    CCCC
                                  ___       AGACA
GAM1556  RCN1     5'  GCTCCGAGTCGGGCCGCACCAC 16202    C    C       __
            G                    GC CCGGG CGGGCCGC  CACG
                                || |||||  ||||||||  ||||
                                CG GGCTC GCCCGGCG  GTGC
                                 A    A       TG
GAM1556  RENT1    3'  CCCTCAGGCCGCCGCGGGG    16249     GGGC       A
                                CCC    CGGGCCGCC CGGGG
                                |||    |||||||||| |||||
                                GGG    GTCCGGCGG GCCCC
                                  A___        C
GAM1556  ROR2     5'  GCTTCGGGCCGGGGCGCGGGG  21262    CC       C   CAC
                                GC  CGGGCCGGG CGC   GGGG
                                ||  |||||||||  |||   ||||
                                CG  GCCCGGCCC GCG   CCCC
                                 AA        C   ___
GAM1556  RPS6KA1  5'  GCTCCGGCTGGGCCGTCC    40382    C    G C     _
                                GC CCGG C GGGCCG CC
                                || |||| | |||||| ||
                                CG GGCC G CCCGGC GG
                                 A   _ A     A
GAM1556  RUNX3    3'  CCCGGGCCGGGGTGGG      20318          CCGCCAC
                                CCCGGGCCGGG      GGG
                                ||||||||||       |||
```

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                                GGGCCCGGCCC      CCC
                                      CA_____
GAM1556 SCA1     5' GCTCTGGCTGTTGCTCCACGGG 7282     CCCG  CGG_ CG
              G                    GC   GGC   GC CCACGGGG
                                   ||   |||   || ||||||||
                                   CG   CCG   CG GGTGCCCC
                                    AGA_  ACAA  A_
GAM1556 SEPN1    3' GCCCCGGGTGGGGTGAGGG   42426       CC  CCGCCAC
                                   GCCCCGGG  GGG     GGG
                                   ||||||||  |||     |||
                                   CGGGGCCC  CCC     CCC
                                       A_  CACT___
GAM1556 SIAT7D   5' CCCCGGGCCGGGCCGACTGGG  30829           CC  _
                                   CCCCGGGCCGGGCCG  AC GGG
                                   ||||||||||||||  || |||
                                   GGGGCCCGGCCCGGC  TG CCC
                                         __ A
GAM1556 SLC8A2   3' GCCCCGGGCGGGCGGTGGG   42415       C   CGCCAC
                                   GCCCCGGGC GGGC    GGG
                                   ||||||||| ||||    |||
                                   CGGGGCCCG CCCG    CCC
                                      _   CCA___
GAM1556 TAZ      5' GCCCCGGGCCGGCCTGTGGGG  31767         G  GCCAC
                                   GCCCCGGGCCGG CC    GGGG
                                   |||||||||||| ||    ||||
                                   CGGGGCCCGGCC GG    CCCC
                                         _ ACA__
GAM1556 TEAD3    5' GCTCCGGCCGGGCCGCTCCG  17376   C   G      CA
                                   GC CCGG CCGGGCCGC  CG
                                   || |||| |||||||||  ||
                                   CG GGCC GGCCCGGCG  GC
                                    A   _       AG
GAM1556 TERF2    5' CCCGGGCCGGAAGCGGG    24906         CCGCCA
                                   CCCGGGCCGGG    CGGG
                                   ||||||||||     ||||
                                   GGGCCCGGCCT    GCCC
                                         TC_____
GAM1556 TJP1     5' CCCGGGTCTTCTCCACGGGG  17536      CCGGGCCG
                                   CCCGGG      CCACGGGG
                                   ||||||      ||||||||
                                   GGGCCC      GGTGCCCC
                                      AGAAGA__
GAM1556 TM7SF3   5' GCCTGGGCCGGGCTGG     40656    CC       CGCCAC
                                   GCC  GGGCCGGGC     GG
                                   |||  |||||||||     ||
                                   CGG  CCCGGCCCG     CC
                                    A_       A_____
GAM1557 AGTR1    5' GCCGCCTCGGCGTCCCGGCTG  28914     _      C C
                                   GCC CCTTGGC G CCCGGCTG
                                   ||| ||||||| | ||||||||
```

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                                CGG GGAGCCG C GGGCCGAC
                                  C      _ A
GAM1557 BCLG     5'  CCCTGGCCACGGAATGGCTG  39829         CCC__
                                CCTTGGCCGC     GGCTG
                                ||||||||||     |||||
                                GGGACCGGTG     CCGAC
                                     CCTTA
GAM1557 CDH16    5'  GCTCCCTTGGTCCAGCTG    19787    _     CCGCC
                                GC CCCTTGG     CCGGCTG
                                || |||||||     |||||||
                                CG GGGAACC     GGTCGAC
                                 A      A____
GAM1557 CLECSF5  3'  GCTCCCTTGGCTGCCTGG    29927    _      C   CC
                                GC CCCTTGGC GCC  GG
                                || |||||||| |||  ||
                                CG GGGAACCG CGG  CC
                                 A       A  A_
GAM1557 CRHR1    3'  GCCCCCCAAAGCCCTGCCCTGG 20442        __   __   C
             CTG                   GCCCCTT  GGCC  GCCC GGCTG
                                |||||||  ||||  |||| |||||
                                CGGGGGG  TCGG  CGGG CCGAC
                                    TT    GA    A
GAM1557 CRHR2    3'  CCCCTTGGCTGCCGC       12440         C   CCG
                                CCCCTTGGC GCC   GC
                                |||||||| |||   ||
                                GGGGAACCG CGG   CG
                                     A  ____
GAM1557 CRMP1    5'  ACGCGCGGCTGCCCCGGCTGC  10590      CCCT    C
                                ACGC    TGGC GCCCCGGCTGC
                                ||||    |||| ||||||||||
                                TGCG    GCCG CGGGGCCGACG
                                  C___    A
GAM1557 CRMP1    5'  CGCCCGCCGCCGCTCCGGCTGC 10595      _ TG     C
                                CGCCC CT  GCCGC CCGGCTGC
                                ||||| ||  ||||| ||||||||
                                GCGGG GG  CGGCG GGCCGACG
                                   C  __     A
GAM1557 CTNS     3'  GCCCTTGGCTCACCCGGCTGC  22346      C    _    C
                                GCCC TTGGC CGCCC GGCTGC
                                |||| ||||| ||||| ||||||
                                CGGG AACCG GTGGG CCGACG
                                  _     A    _
GAM1557 DBN1     5'  GCCCTTGGCCGCCCCGTGC    38932      C         _
                                GCCC TTGGCCGCCCCG GC
                                |||| |||||||||||| ||
                                CGGG AACCGGCGGGGC CG
                                  _          A
GAM1557 ICA1     5'  CGTCCCCGACCGTCCCGGCTGC 22465    _    TT     C
                                CG CCCC  GGCCG CCCGGCTGC
                                || ||||  ||||| |||||||||
```

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                                GC GGGG  CTGGC GGGCCGACG
                                 A   __    A
GAM1557 IDH2    5' CGCCGCTCCTCCCGGCTG    13476     C  TGG  GC
                                CGCC CT   CC  CCCGGCTG
                                |||| ||   ||  ||||||||
                                GCGG GA   GG  GGGCCGAC
                                  C  ___  A_
GAM1557 IRS2    5' GCCCCCCTCCCCGGCT     40705      TTGG  G
                                GCCCC    CC CCCCGGCT
                                |||||    || ||||||||
                                CGGGG    GG GGGGCCGA
                                   ____  A
GAM1557 KNS2    5' CCCCTTGGCCGCCGAGC    24470           CC
                                CCCCTTGGCCGCC  GGC
                                ||||||||||||  |||
                                GGGGAACCGGCGG  TCG
                                       C_
GAM1557 KNS2    3' GCCTCCCTGCCGCCCTGGCTG 24472    _    G     C
                                GCC CCTTG CCGCCC GGCTG
                                ||| ||||| |||||| |||||
                                CGG GGGAC GGCGGG CCGAC
                                  A    _     A
GAM1557 MDFI    3' CCCCAGCCCTGGCTGC     24612     TTGGCC   C
                                CCCC     GCCC GGCTGC
                                ||||     |||| ||||||
                                GGGG     CGGG CCGACG
                                  T_____   A
GAM1557 MS4A1   3' GCCTTCTGGATCCTTGGCTG  6600     CC   CCG  CC
                                GCC  TTGG   CC  GGCTG
                                |||  ||||   ||  |||||
                                CGG  GACC   GG  CCGAC
                                  AA   TA_  AA
GAM1557 PPP2R5A 5' ACGCTTGGCAGCTCCGGCTGC 26429     CCC    C  C
                                ACGC   TTGGC GC CCGGCTGC
                                ||||   ||||| || ||||||||
                                TGCG   AACCG CG GGCCGACG
                                   ___    T  A
GAM1557 PPT2    3' ACAGCTCAGCCACCTGTTCTGG 39913   CC  TG    CC____
            CTGC                  GC  CT  GCCGCC    GGCTGC
                                ||  ||  ||||||    ||||||
                                TG  GA  CGGTGG    CCGACG
                                 TC  GT    ACAAGA
GAM1557 RPL4    5' ACGCTCCTCTCAGCCCGGCTGC 9732     _ _  TG   GCCC
                                ACGC CC CT  GCC   CGGCTGC
                                |||| || ||  |||   |||||||
                                TGCG GG GA  CGG   GCCGACG
                                  A  A  GT  ____
GAM1557 TLX1    5' GCTTCCCCGCTCCGGCTGC   24340   C_ TTGG   C
                                GC  CC   CCGC CCGGCTGC
                                ||  ||   |||| ||||||||
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                                CG  GG    GGCG GGCCGACG
                                 AA  ____    A
GAM1557  FBXL7    3'  GGCCTTGGGGGGGGGGCGT   29409     G   A     A  A
                                GGC CTT GGGGG GG TGT
                                ||| ||| ||||| || |||
                                CCG GAA CCCCC CC GCA
                                  _  C    C  C
GAM1558  EN1      5'  TGGGCGCGCGCGGGACTTTGCG 10925    A       CC    C
              G                  TG GTGCGCGCG  GGCT TGCGG
                                || |||||||||  |||| |||||
                                AC CGCGCGCGC  CTGA ACGCC
                                 C        C_    A
GAM1558  GPC6     5'  GCGCGCGCCGGCTCCCCCGG  25044            _ G
                                GCGCGCGCCGGCTC T CGG
                                |||||||||||||| | |||
                                CGCGCGCGGCCGAG G GCC
                                         G G
GAM1558  PIG3     5'  GAGTGGTTCTGGCTCTGCGG  22195      CGCGCGCC
                                GAGTG       GGCTCTGCGG
                                |||||       ||||||||||
                                CTCAC       CCGAGACGCC
                                   CAAGA___
GAM1558  RAB33A   5'  GTGCGTGCGCCGGCACCG    22000      C       T
                                GTGCG GCGCCGGC CTG
                                ||||| |||||||| |||
                                CACGC CGCGGCCG GGC
                                   A       T
GAM1558  ADCY1    3'  GCCTGCTCGGTGGT       45222     G       CTC
                                GCC TGTTCGGT   GGT
                                ||| ||||||||   |||
                                CGG ACGAGCCA   CCA
                                  _      ___
GAM1558  GFI1     3'  TGCCTGGTACTTGGTAGCC   23559     TC  _  C
                                TGT  GGT CT GGTAGCC
                                |||  ||| || |||||||
                                ACG  CCA GA CCATCGG
                                  GA   T  A
GAM1559  ADH5     5'  GGCGGGGCGTGGGGGGG     8580         GTTC
                                GGCGGGGCG    GGGGGGG
                                |||||||||    |||||||
                                CCGCCCCGC    CCCCCCC
                                     A___
GAM1559  ALDH3A2  5'  GCGGCGGGGTGTAGGG      42916         CG  TC
                                GCGGCGGGG  GT  GGGG
                                |||||||||  ||  ||||
                                CGCCGCCCC  CA  TCCC
                                     A_  __
GAM1559  ANK1     3'  AGCGGCGGGGCGGACGGGG   33847           TT
                                AGCGGCGGGGCGG  CGGGG
                                ||||||||||||  |||||
```

```
                                TCGCCGCCCCGCC  GCCCC
                                      T_
GAM1559 AQP5     5'  GCGCGGGGCCGGCGCGGGGGGG 11631     G     _   T
                                GCG CGGGGC GGT CGGGGGGG
                                ||| |||||| ||| ||||||||
                                CGC GCCCCG CCG GCCCCCCC
                                  _     G   C
GAM1559 AR       5'  GGCGGGGGGGGCGGGTGGG    6236         C  TT   _
                                GGCGGGG GG  CGGG GGG
                                ||||||| ||  |||| |||
                                CCGCCCC CC  GCCC CCC
                                    _ C_   A
GAM1559 ATP6V0C  3'  GGTGGGGCGCCGGGGG      44559    C     GT
                                GG GGGGCG  TCGGGGG
                                || ||||||  |||||||
                                CC CCCCGC  GGCCCCC
                                 A     __
GAM1559 AXIN1    3'  AGGTGCCGGGGGATGGGGGGG  41369    CG  G   C  TTC
                                AG  GC GGG GG   GGGGGGG
                                ||  || ||| ||   |||||||
                                TC  CG CCC CC   CCCCCCC
                                 CA  G   _  TA_
GAM1559 BMP2     5'  AGTGGAGGGGCGGTGGGG    10184    C  C       TC
                                AG GG GGGGCGGT  GGGG
                                || || ||||||||  ||||
                                TC CC CCCCGCCA  CCCC
                                 A  T       __
GAM1559 BMP8     5'  GCGGCGGGCGGCGGGG      11881         G   TT
                                GCGGCGGG CGG  CGGGG
                                |||||||| |||  |||||
                                CGCCGCCC GCC  GCCCC

                                    _   __
GAM1559 CACNA2D2 5'  CGGCGGCGGGGTTGGGGGG   25712        _ C    C
                                CGGCGG GG GGTT GGGGGG
                                |||||| || |||| ||||||
                                GCCGCC CC CCAA CCCCCC
                                   G  _   _
GAM1559 CAPG     3'  GGTGGGGGGCAGGGG       11963    C   C   TC
                                GG GGGG GGT  GGGGG
                                || |||| |||  |||||
                                CC CCCC CCG  TCCCC
                                 A   _  __
GAM1559 CD5L     3'  GCAGGCGGGGCCAGGGGGG   25317    _       GGTT
                                GC GGCGGGGC    CGGGGGGG
                                || ||||||||    ||||||||
                                CG CCGCCCCG    GTCCCCCC
                                 T       _____
GAM1559 CDK2AP1  5'  AGCCGGCGGGGCGGCCGGGG  21593     _         T
                                AGC GGCGGGGCGGT CGGGG
                                ||| |||||||||| |||||
```

```
                                TCG CCGCCCCGCCG GCCCC
                                  G        _
GAM1559  CKB     5'  GCGGCCGGGCGGGGGCGGGGG  12253      G     TT_
                                GCGGC GGGCGG   CGGGGG
                                ||||| ||||||   ||||||
                                CGCCG CCCGCC   GCCCCC
                                   G     CCC
GAM1559  DBH     3'  AGCAGCGGGGCGGGGGCGGGGG 8964           TT_
                                AGCGGCGGGGCGG   CGGGGG
                                ||||||||||||   ||||||
                                TCGTCGCCCCGCC   GCCCCC
                                       CCC
GAM1559  DECR1    5'  GCGGTTGGGCGCAGGGGG    10680     CG    GTT
                                GCGG  GGGCG   CGGGGGG
                                ||||  |||||   |||||||
                                CGCC  CCCGC   GTCCCCC
                                  AA    ___
GAM1559  DIA1     3'  GGCGTGGGGTGCGCGGGGG    28790     _  CG  T
                                GGCG GGG  GT CGGGGG
                                |||| |||  || ||||||
                                CCGC CCC  CG GCCCCC
                                  A   CA  C
GAM1559  FAAH     5'  GCGGCGGGGGGCGGAGCGGGGG 11056       __      TT
                                GCGGC  GGGGCGG  CGGGGG
                                |||||  |||||||  ||||||
                                CGCCG  CCCCGCC  GCCCCC
                                   CC      TC
GAM1559  FMNL     5'  GGTGGTGGCGGTGGCGGGGG   25311    C _     T_
                                GG GG GGCGGT  CGGGGG
                                || || ||||||  ||||||
                                CC CC CCGCCA  GCCCCC
                                 A  A     CC
GAM1559  FOXD1    5'  GCGGCGGGGCGGCGCATGGGGG 20929           T _
                                GCGGCGGGGCGGT CG GGGGG
                                |||||||||||| || |||||
                                CGCCGCCCCGCCG GT CCCCC
                                       C  A
GAM1559  GALR1    5'  AGCGGCGGGGCGCGCGGGG    11193          GTT  G
                                AGCGGCGGGGCG   CG GGGG
                                ||||||||||||   || ||||
                                TCGCCGCCCCGC   GC CCCC
                                       ___  G
GAM1559  GNA15    5'  AGGGCGGGGCGGTGGCGGG    40899    C        TC  G
                                AG GGCGGGGCGGT  GG GGG
                                || ||||||||||  || |||
                                TC CCGCCCCGCCA  CC CCC
                                 _         __ G
GAM1559  GNB1     3'  GGGGGGCGGGGCGGGGG     13207    C      TT
                                GG GGGGCGG  CGGGGG
                                || |||||||  ||||||
```

```
                                CC CCCCGCC  GCCCCC
                                 _      CC
GAM1559  GNB3     5'  CGGCGGGGGGTTGGGGGGG   13217        C   C
                                CGGCGGGG GGTT GGGGGGG
                                ||||||| |||| |||||||
                                GCCGCCCC CCAA CCCCCCC
                                    _   _
GAM1559  GTF2IRD1 5'  AGGGCGGGGCGGCGCGGGG   32251    C        T
                                AG GGCGGGGCGGT CGGGG
                                || |||||||||| |||||
                                TC CCGCCCCGCCG GCCCC
                                 _        C
GAM1559  HCN2     3'  GCGCGGGGCGATGAGGGGGG   10168    G       TC
                                GCG CGGGGCGGT  GGGGGG
                                ||| |||||||||  ||||||
                                CGC GCCCCGCTA  CCCCCC
                                 _       CT
GAM1559  HHIP     5'  GGCGCGGGAGGATGGGGGGG   35413     _  C  TTC
                                GGCG GGG GG   GGGGGGG
                                |||| ||| ||   |||||||
                                CCGC CCC CC   CCCCCCC
                                  G   T  TA_
GAM1559  HIP2     3'  GGCGGGGGTGGGGG       23768        CG  TC
                                GGCGGGG  GT  GGGGG
                                |||||||  ||  |||||
                                CCGCCCC  CA  CCCCC
                                    __  __
GAM1559  IL6R     5'  GGCAGGGGCGGGGCGGGG    8180     _      TT
                                GGC GGGGCGG  CGGGG
                                ||| |||||||  |||||
                                CCG CCCCGCC  GCCCC
                                  T      CC
GAM1559  IL6R     5'  GCGGCAGGGGTGGCAGGGG    8176      _   C   TC
                                GCGGC GGGG GGT  GGGGG
                                ||||| |||| |||  |||||
                                CGCCG CCCC CCG  TCCCC
                                   T   A   __
GAM1559  KCNC3    5'  GGGGGGCGGGGCGGGAGG    22516    C      TT
                                GG GGGGCGG  CGGGGGG
                                || |||||||  |||||||
                                CC CCCCGCC  GCCCTCC
                                 _      CC
GAM1559  LMO6     3'  AGGGGCGGGGCGTGGGGG    26039    C       GTTC
                                AG GGCGGGGCG    GGGGG
                                || |||||||||    |||||
                                TC CCGCCCCGC    CCCCC
                                 C       A___
GAM1559  MGMT     5'  GCGGCGGGGGGGGCGGGGGGG  14488         C  TT
                                GCGGCGGGG GG  CGGGGGGG
                                |||||||| ||  ||||||||
```

```
                                CGCCGCCCC CC  GCCCCCCC
                                      _ CC
GAM1559  MKPX     5'  AGCGGCGGGGCGGGCGGGG   33631          TT
                                AGCGGCGGGGCGG  CGGGG
                                |||||||||||||  |||||
                                TCGCCGCCCCGCC  GCCCC
                                     C_
GAM1559  MSX2     3'  GCGGTGGGGGGCGGGGG    42295     C   C  TT
                                GCGG GGGG GG  CGGGGG
                                |||| |||| ||  ||||||
                                CGCC CCCC CC  GCCCCC
                                  A   _ __
GAM1559  MSX2     3'  GGTGGGGCGGTGGGGGG    42297    C      TC
                                GG GGGGCGGT  GGGGGG
                                || ||||||||  ||||||
                                CC CCCCGCCA  CCCCCC
                                 A      __
GAM1559  NPY2R    5'  AGCGGCTGGGCGGTTGG     9487       G      C
                                AGCGGC GGGCGGTT GG
                                ||||||| |||||||| ||
                                TCGCCG CCCGCCAA CC
                                   A      _
GAM1559  NRG2     3'  GGCGGGCGGGGCGGAGGG    30367      G   TT
                                GGCGGG CGG  CGGGGGG
                                |||||| |||  |||||||
                                CCGCCC GCC  GCCTCCC
                                    _  CC
GAM1559  OPTN     5'  GGCGGCGGCGGTGGCGGAGGGG 35069      _    T_
                                GGCGG GGCGGT  CGGGGGGG
                                ||||| ||||||  ||||||||
                                CCGCC CCGCCA  GCCTCCCC
                                   G    CC
GAM1559  OTP      3'  GCGGCGGGCGAGGGGGG     36995       G   TTC
                                GCGGCGGG CGG   GGGGGG
                                |||||||| |||   ||||||
                                CGCCGCCC GCT   CCCCCC
                                     _  ___
GAM1559  PCBP1    5'  AGCGGCGGGCGGCGTTCGGGGG 26218        G   __
                                AGCGGCGGG CGGT  TCGGGGG
                                ||||||||| ||||  |||||||
                                TCGCCGCCC GCCG  AGCCCCC
                                     _   CA
GAM1559  PDE4A    3'  GGCGGGGGGGCGGGGG      26262       C  TT
                                GGCGGGG GG  CGGGGG
                                ||||||| ||  ||||||
                                CCGCCCC CC  GCCCCC
                                     _ __
GAM1559  PLCD1    5'  GCGGCGCGGCGGGAGGGG    26344      G    TTC
                                GCGGCG GGCGG   GGGGGG
                                |||||| |||||   ||||||
```

```
                                CGCCGC CCGCC  CTCCCC
                                   G   ___
GAM1559  PTMS    5'  GCGCGCGGGGTGGGGCGGGGG  15887    _    C  TT
                                GCG GCGGGG GG  CGGGGG
                                ||| |||||| ||  ||||||
                                CGC CGCCCC CC  GCCCCC
                                  G    A  CC
GAM1559  PTPN1   3'  GGTGGGGGGGCGGGGG      15903    C   C  TT
                                GG GGGG GG  CGGGGG
                                || |||| ||  ||||||
                                CC CCCC CC  GCCCCC
                                 A   _ __
GAM1559  PTPRS   3'  GCGGCCGGGGCCGGTGGGGGGG 39303      _   _  TC
                                GCGGC GGGGC GGT  GGGGGGG
                                ||||| ||||| |||  |||||||
                                CGCCG CCCCG CCA  CCCCCCC
                                   G    G  __
GAM1559  PYGO2   3'  AGCAGCGGGGTGGGGGTGGGGG 41944         C  TTCG
            G                    AGCGGCGGGG GG   GGGGGG
                                |||||||||| ||   ||||||
                                TCGTCGCCCC CC   CCCCCC
                                     A  CCCA
GAM1559  RAB3A   3'  GGCGGGGGGGGGGGG       16071       C  TTC
                                GGCGGGG GG  GGGGG
                                ||||||| ||  |||||
                                CCGCCCC CC  CCCCC
                                   _ ___
GAM1559  RAD23B  5'  GGCGGTGGGGGTGGGGG    16139     _  C  TC
                                GGCGG GG GGT  GGGGG
                                ||||| || |||  |||||
                                CCGCC CC CCA  CCCCC
                                   A  C  __
GAM1559  RFX1    3'  GGCGGGTGGGGCGGGGGG    16292      GC  TT
                                GGCGGG  GG  CGGGGGG
                                ||||||  ||  |||||||
                                CCGCCC  CC  GCCCCCC
                                   A_  CC
GAM1559  RUNX3   3'  GGTGGTGGGGGTGGGGG    20324    C  _  C  TC
                                GG GG GG GGT  GGGGG
                                || || || |||  |||||
                                CC CC CC CCA  CCCCC
                                 A  A  C  __
GAM1559  SALL1   3'  AAGGGGCGGGGCGGGGTGGGGG 16452    C       TTC
            G                    AAG GGCGGGGCGG   GGGGGG
                                ||| ||||||||||   ||||||
                                TTC CCGCCCCGCC   CCCCCC
                                  C        CCA
GAM1559  SDC1    3'  AGTGGCAGGGCGGAGGGGG   16498    C       TTC
                                AG GGCGGGGCGG   GGGGGG
                                || ||||||||||   ||||||
```

```
                                TC CCGTCCCGCC   TCCCCC
                                 A       ___
GAM1559  SPTBN4   3'  GCGGCGGAGTGCAGGGGG    36087        CGGTT
                                GCGGCGGGG    CGGGGGG
                                |||||||||    |||||||
                                CGCCGCCTC    GTCCCCC
                                     AC___
GAM1559  SRD5A1   5'  GGCGGCGGCGCGGGGG     9828      _   GTT
                                GGCGG GGCG   CGGGGG
                                ||||| ||||   ||||||
                                CCGCC CCGC   GCCCCC
                                   G   ___
GAM1559  TGFB1    3'  GGCGGGGCGGGGTGGGG     8543         TTC  _
                                GGCGGGGCGG   GG GGGG
                                ||||||||||   || ||||
                                CCGCCCCGCC   CC CCCC
                                     ___  A
GAM1559  TPT1     5'  AGCGGCGCTCGGGGG      17661       GGGGCG
                                AGCGGC     GTTCGGGGG
                                ||||||     |||||||||
                                TCGCCG     CGAGCCCCC
                                     _______
GAM1559  VIPR1    3'  AGGGTGGGGTGGCAAGGGG   21504    C  C    C   TC
                                AG GG GGGG GGT  GGGGG
                                || || |||| |||  |||||
                                TC CC CCCC CCG  TCCCC
                                 _ A   A  T_
GAM1559  ZNF278   5'  GCGGCGGGGCGCGCACGGGGG  36798          _  T
                                GCGGCGGGGCG GT CGGGGG
                                |||||||||||  || ||||||
                                CGCCGCCCCGC CG GCCCCC
                                      G  T
GAM1559  ABCA2    5'  CCCGCTCCTCTGCGCGCCCC   45521      _  A  C  _
                                CCCGC CC TC GCG GCCCC
                                ||||| || || ||| |||||
                                GGGCG GG AG CGC CGGGG
                                   A  _  A   G
GAM1559  ACTN4    3'  GCCCAGGCCCCTCC        22275       TCCGC
                                GCCCA    GGCCCCTCC
                                |||||    |||||||||
                                CGGGT    CCGGGGAGG
                                     _____
GAM1559  ADD2     3'  GCTCCTCCTCCCTCCC      32729    _  A   GCGGC
                                GC CC TCC    CCCTCCC
                                || || |||    |||||||
                                CG GG AGG    GGGAGGG
                                 A  _   A____
GAM1559  AES      3'  CGTCCCTCGTGCCCCCCC    10054    _   A  CGCG
                                CG CCC TC   GCCCCTCC
                                || ||| ||   ||||||||
```

```
                                GC GGG AG    CGGGGGGG
                                 A   _  CA__
GAM1559 ARHGEF5  3'  CCATCCACAGAAGGCCTCTC   24126         ____    C
                                CCATCCGC    GGCC CTC
                                ||||||||    |||| |||
                                GGTAGGTG    CCGG GAG
                                     TCTT    A
GAM1559 ARL2     3'  CCCGCCCAGCCCTCTC      11691         TCCGCG   _
                                CCCGCCCA     GCCC CTC
                                ||||||||     |||| |||
                                GGGCGGGT     CGGG GAG
                                     _______   A
GAM1559 DGKG     5'  CCCGCCTGCGCAGCCCTCTC   10650       CATC      _
                                CCCGCC    CGCGGCCC CTC
                                ||||||    |||||||| |||
                                GGGCGG    GCGTCGGG GAG
                                    AC__       A
GAM1559 DIPA     3'  CCATGCCAGCGGCCCCTCC    27785     _ _
                                CCAT CC GCGGCCCCTCC
                                |||| || ||||||||||
                                GGTA GG CGCCGGGGAGG
                                  C  T
GAM1559 DUX4     5'  CCGTCCGTCCCCGGCTCCCTCC 43756     C  A   G   _
             CG                   CCG CC TCC CGGC CCCTCCCG
                                ||| || ||| |||| ||||||||
                                GGC GG AGG GCCG GGGAGGGC
                                  A  C   G    A
GAM1559 ECEL1    3'  CCCTGCTCCAGGCCCCTCC    22092     _ CCA    C
                                CCC GC   TCCG GGCCCCTCC
                                ||| ||   |||| |||||||||
                                GGG CG   AGGT CCGGGGAGG
                                  A  ___   _
GAM1559 EP300    5'  CCTGCCCAGCCGAGGTCTCTCG 10977    C     T   C  CCC   C
                                CC GCCCA CCG GG   CTC CG
                                || ||||| ||| ||   ||| ||
                                GG CGGGT GGC CC   GAG GC
                                 A    C   T  A__   A
GAM1559 GPC1     5'  CCCGCCCGCGCCTCTCC     13238        ATCC   G  C   C
                                CCCGCCC    GCG CC CTC C
                                |||||||    ||| || ||| |
                                GGGCGGG    CGC GG GAG G
                                     ____   _ A   A
GAM1559 H1F0     3'  CCCGCCCACTCCCCCTCCCCCT 23699         _   GCGG_
             CCCG                   CCCGCCCA TCC    CCCCTCCCG
                                ||||||||| |||    |||||||||
                                GGGCGGGT AGG    GGGGAGGGC
                                     G   GGGAG
GAM1559 HDAC6    3'  CCTGCCAGTTAACTCCCCTCCC 25816    C   CATCC  GG
             G                    CC GCC    GC  CCCCTCCCG
                                || |||    ||  |||||||||
```

```
                              GG CGG    TG  GGGGAGGGC
                               A  TCAAT  A_
GAM1559 ID3     3' CCTGCCGTCCGGCTTCC    44272   C  CA  GC  CCC
                              CC GCC  TCC  GGC  TCC
                              || |||  |||  |||  |||
                              GG CGG  AGG  CCG  AGG
                               A  C_  __  A__
GAM1559 IMPA2   5' CCCAGAAGCCGCGGCCTCT  45456    T___     C
                              CCCA   CCGCGGCC CT
                              ||||   |||||||| ||
                              GGGT   GGCGCCGG GA
                                CTTC      A
GAM1559 KIFC3   5' CCCGCTCGCGCCCCTCCC   24456     CCATC   G
                              CCCGC    CGCG CCCCTCCC
                              |||||    |||| ||||||||
                              GGGCG    GCGC GGGGAGGG
                                 A____   _
GAM1559 KRTHA5  5' CCCCCACTGGCCCCTCC    14021    AT   _
                              CCC  CCGC GGCCCCTCC
                              |||  |||| |||||||||
                              GGG  GGTG CCGGGGAGG
                                __   A
GAM1559 MADH6   3' CCTCCCACCCGCCCCTCCC  24595   G     GCG
                              CC CCCATCC   GCCCCTCCC
                              || |||||||   |||||||||
                              GG GGGTGGG   CGGGGAGGG
                               A     ___
GAM1559 MAP3K1  5' CCGCCCGCTCGCGGCCCCC  42701      ATC
                              CCGCCC   CGCGGCCCCT
                              ||||||   ||||||||||
                              GGCGGG   GCGCCGGGGG
                                 CGA
GAM1559 NDRG1   3' CCCATCCGTACTCAGCCTCTC 40575       ____   C
                              CCCATCCG   CGGCC CTC
                              ||||||||   ||||| |||
                              GGGTAGGC   GTCGG GAG
                                   ATGA    A
GAM1559 NFRKB   5' CCCTTCCGCGCCCCTCCC   26093    A    G
                              CCC TCCGCG CCCCTCCC
                              ||| |||||| ||||||||
                              GGG AGGCGC GGGGAGGG
                                A    _
GAM1559 NMB     5' CCCGCCGTCCCCACCCTCCCG 43947      CA  G  GC
                              CCCGCC  TCC CG  CCCTCCCG
                              ||||||  ||| ||  ||||||||
                              GGGCGG  AGG GT  GGGAGGGC
                                 C_  G  __
GAM1559 PTGFRN  3' CCCTCTGTCACTCCCCTCCCG 42587    A ___  GG
                              CCC TC   CGC  CCCCTCCCG
                              ||| ||   |||  |||||||||
```

```
                              GGG AG  GTG  GGGGAGGGC
                                _ ACA  A_
GAM1559 PYGB    3' CCTGACCCCCATGGCCCCTCC 16047   C_  AT  C
                              CC  GCCC  CCG GGCCCCTCC
                              ||  ||||  ||| |||||||||
                              GG  TGGG  GGT CCGGGGAGG
                               AC   __  A
GAM1559 RB1CC1  5' CCCGCCCGCCGCGGCCCC   31309      AT
                              CCCGCCC  CCGCGGCCCC
                              |||||||  ||||||||||
                              GGGCGGG  GGCGCCGGGG
                                  C_
GAM1559 RFC2    3' CGCCTGCCACAGCCTCCCG  16280    CAT     CC
                              CGCC  CCGCGGCC  TCCCG
                              ||||  ||||||||  |||||
                              GCGG  GGTGTCGG  AGGGC
                                AC_     __
GAM1559 RFXANK  5' CCCGTTCCACAACAAGGTCCC 39589    CCCA     CCC_
                              CCCG  TCCGCGGC  TCCC
                              ||||  ||||||||  ||||
                              GGGC  AGGTGTTG  AGGG
                                A___     TTCC
GAM1559 RPL10   3' GCCCACAAGCCCCTC     25670      CCGC
                              GCCCAT  GGCCCCTC
                              ||||||  ||||||||
                              CGGGTG  TCGGGGAG
                                 T___
GAM1559 SERPINH2 3' GCCCAGAAGCCCCTCC    10297     TCCGC
                              GCCCA   GGCCCCTCC
                              |||||   |||||||||
                              CGGGT   TCGGGGAGG
                                CT___
GAM1559 SLC4A1  3' CCCGCTCACCCACCTCC    7353      C    CGGCC
                              CCCGC CATCCG   CCTCC
                              ||||| ||||||   |||||
                              GGGCG GTGGGT   GGAGG
                                A    _____
GAM1559 SLC9A5  5' CCTGCCCAGCCGCCCTCCC  21385   C   T  GGCC
                              CC GCCCA CCGC  CCTCCC
                              || ||||| ||||  ||||||
                              GG CGGGT GGCG  GGAGGG
                               A   C  ____
GAM1559 SMAC    5' CCAGCTCCCCCGGCCCCT   39895   C  CCA  G
                              CC GC  TCC CGGCCCCT
                              || ||  ||| ||||||||
                              GG CG  GGG GCCGGGGA
                               T  A__  G
GAM1559 ZNF134  5' GCCTGTCCAAGCCCCTCC   18327    CA   C
                              GCC  TCCG GGCCCCTCC
                              |||  |||| |||||||||
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```
                                CGG  AGGT TCGGGGAGG
                                  AC   _
GAM1560  ACTR1B   3'  TGCAGTGACACACCAG      43348         CT   G
                                TGCAGTGGC  ACG CAG
                                |||||||||  ||| |||
                                ACGTCACTG  TGT GTC
                                     __   G
GAM1560  ADD2     5'  TGCAGCGGCTCCGCGGCGGC   32733          _ TA    A
                                TGCAGTGGC C  CGGC GC
                                |||||||||  |  |||| ||
                                ACGTCGCCG G  GCCG CG
                                     A GC    C
GAM1560  AKT1     3'  TGCAGCGGCAGCGGCAG     23142         CTA
                                TGCAGTGGC   CGGCAG
                                |||||||||   ||||||
                                ACGTCGCCG   GCCGTC
                                     TC_
GAM1560  ALPP     3'  TGCAGTGGCATGACCTCGG    42873          _____  A
                                TGCAGTGGC    CT CGG
                                |||||||||    || |||
                                ACGTCACCG    GG GCC
                                     TACT  A
GAM1560  AP1M1    5'  GCGGTGGCGGCGGCAGC     37172    A    CTA
                                GC GTGGC   CGGCAGC
                                || |||||   |||||||
                                CG CACCG   GCCGTCG
                                  C    CC_
GAM1560  ATP2B4   5'  TGCATGTTACCATGGCAGCAA  43203     _  G   TAC
                                TGCA GT GCC   GGCAGCAA
                                |||| || |||   ||||||||
                                ACGT CA TGG   CCGTCGTT
                                   A  A   TA_
GAM1560  BHMT2    3'  TGCAATGGCCTGATCTCGG    32777          A_____
                                TGCAGTGGCCT    CGG
                                ||||||||||     |||
                                ACGTTACCGGA    GCC
                                      CTAGA
GAM1560  BNIP3L   5'  GCAGGACTGCGGCAGCA     20257     T   CTA
                                GCAG GGC   CGGCAGCA
                                |||| |||   ||||||||
                                CGTC CTG   GCCGTCGT
                                   _   AC_
GAM1560  BSCL2    5'  TGCAGTCGTACAGCAG      37220       GGCC
                                TGCAGT    TACGGCAG
                                ||||||    ||||||||
                                ACGTCA    ATGTCGTC
                                   GC__
GAM1560  C14orf1  5'  GCAGTGGCAGCAGCA       28413         CTAC
                                GCAGTGGC    GGCAGCA
                                ||||||||    |||||||
```

```
                                CGTCACCG   TCGTCGT
                                    ____
GAM1560 CACNA2D2 5' GCAGTGGCGGCGGCGGC    25717       CTA   A
                                GCAGTGGC  CGGC GC
                                ||||||||  |||| ||
                                CGTCACCG  GCCG CG
                                    CC_   C
GAM1560 CCNT2    3' GCAGTGGCAGCAACAGCA    38493       CTA
                                GCAGTGGC  CGGCAGCA
                                ||||||||  ||||||||
                                CGTCACCG  GTTGTCGT
                                    TC_
GAM1560 CHGA     5' TGCAGTGGCAGGAGCGGTGGCA 10472       CTA__  CA
                                TGCAGTGGC   CGG  GCA
                                |||||||||   |||  |||
                                ACGTCACCG   GCC  CGT
                                     TCCTC  AC
GAM1560 CIS4     3' TGAAATAGTTATGGCAGCAA  20132   C   CC  C
                                TG AGTGG  TA GGCAGCAA
                                || |||||  || ||||||||
                                AC TTATC  AT CCGTCGTT
                                 T    A_  A
GAM1560 CTNS     3' TGCAGCGGTGGCAGCAA     22352       CCTAC
                                TGCAGTGG    GGCAGCAA
                                ||||||||    ||||||||
                                ACGTCGCC    CCGTCGTT
                                    A____
GAM1560 CXorf6   3' GCAGCGGTGGCAGCA      24239       CCTAC
                                GCAGTGG    GGCAGCA
                                |||||||    |||||||
                                CGTCGCC    CCGTCGT
                                   A____
GAM1560 CXorf6   3' GCGGTGGCAGCAGCA      24240    A   CTAC
                                GC GTGGC   GGCAGCA
                                || |||||   |||||||
                                CG CACCG   TCGTCGT
                                 C    ____
GAM1560 D1S155E  3' TGCAGTGATCTAAGCAGCA  28391       GC  C
                                TGCAGTG  CTA GGCAGCA
                                |||||||  ||| |||||||
                                ACGTCAC  GAT TCGTCGT
                                   TA  _
GAM1560 DBN1     5' GCGGTCGCCATGTGGCAGCAA 38934    A G  TAC_
                                GC GT GCC   GGCAGCAA
                                || || |||   ||||||||
                                CG CA CGG   CCGTCGTT
                                 C G  TACA
GAM1560 DDX6     3' ACAGTGTGGCAGCAA       20541       GCCTAC
                                GCAGTG     GGCAGCAA
                                ||||||     ||||||||
```

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                                TGTCAC     CCGTCGTT
                                  A_____
GAM1560  DLX4     5'  TGCATGCCGTCGGCAGCAA   39623     GTG   TA
                                TGCA   GCC  CGGCAGCAA
                                ||||   |||  |||||||||
                                ACGT   CGG  GCCGTCGTT
                                  A__   CA
GAM1560  EGR3     3'  TGCGTGCGGCGGGCAGCAA   40562     A_    CTAC
                                TGC  GTGGC    GGCAGCAA
                                |||  |||||    ||||||||
                                ACG  CGCCG    CCGTCGTT
                                  CA    C___
GAM1560  EHD3     3'  CAGTGGCCATGAAGCAA     31109        TAC  C
                                CAGTGGCC   GG AGCAA
                                ||||||||   || |||||
                                GTCACCGG   CT TCGTT
                                     TA_  _
GAM1560  EPHB1    3'  TGCAGTGGTCAGCAA       20779        CCTA
                                TGCAGTGG    CGGCAG
                                ||||||||    ||||||
                                ACGTCACC    GTCGTT
                                     A___
GAM1560  EPHB2    3'  TGCAGTGGCTGGCACCA     32681         CTAC    G
                                TGCAGTGGC    GGCA CA
                                |||||||||    |||| ||
                                ACGTCACCG    CCGT GT
                                     A___    G
GAM1560  FGFR1    3'  TGAAGTGGCTGGCAGCAA    31957    C     CTAC
                                TG AGTGGC    GGCAGCAA
                                || ||||||    ||||||||
                                AC TCACCG    CCGTCGTT
                                 T     A___
GAM1560  GCK      5'  GCCCGCCTGTGGCAGCAA    37926    AGTG    AC
                                GC    GCCT  GGCAGCAA
                                ||    ||||  ||||||||
                                CG    CGGA  CCGTCGTT
                                  GG__    CA
GAM1560  GCNT3    5'  GCGGTGTTCCGTGGCAGCAA  21907    A   GC  AC
                                GC GTG  CT  GGCAGCAA
                                || |||  ||  ||||||||
                                CG CAC  GG  CCGTCGTT
                                 C   AA  CA
GAM1560  GGCX     3'  TGCAGTGGCTCGATCTCGG   9064          _____  A
                                TGCAGTGGC     CT CGG
                                |||||||||     || |||
                                ACGTCACCG     GA GCC
                                     AGCTA  _
GAM1560  GMPR     5'  TGCAGCGGCTCCTGGCTGCGGC 44955          _______ A    A
              GGC                    TGCAGTGGC     CT CGGC GC
                                |||||||||      || |||| ||
```

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                              ACGTCGCCG     GA GCCG CG
                                   AGGACC  C    C
GAM1560  GRM1     3'  GCAGTAGCGGCAGCA       9135         CTAC
                              GCAGTGGC    GGCAGCA
                              ||||||||    |||||||
                              CGTCATCG    CCGTCGT
                                   _____
GAM1560  GUCY1A2  5'  TGCAGCGGCCGAGGCGGTGGC  9225          TA__   CA
                              TGCAGTGGCC    CGG  GC
                              ||||||||||    |||  ||
                              ACGTCGCCGG    GCC  CG
                                   CTCC   AC
GAM1560  HIC1     5'  GCAGCGGCGGCAGC        44566         CTAC
                              GCAGTGGC    GGCAGC
                              ||||||||    ||||||
                              CGTCGCCG    CCGTCG
                                   _____
GAM1560  HOXA7    3'  TGCAGTGCCCTTAGCAG     27891        G   AC
                              TGCAGTG CCT  GGCAG
                              ||||||| |||  |||||
                              ACGTCAC GGA  TCGTC
                                  G   A_
GAM1560  IFNAR1   3'  TGCAGTAGCCAGCAG       8433          TAC
                              TGCAGTGGCC   GGCAG
                              ||||||||||   |||||
                              ACGTCATCGG   TCGTC
                                   ____
GAM1560  IFNAR1   3'  TGCAGTGGCGTGATCTCGG   8434          _____  A
                              TGCAGTGGC    CT CGG
                              |||||||||    || |||
                              ACGTCACCG    GA GCC
                                   CACTA  _
GAM1560  IFRD1    5'  GCGGTGGCGGCAGCA       41108    A    CTAC
                              GC GTGGC    GGCAGCA
                              || |||||    |||||||
                              CG CACCG    CCGTCGT
                               C    _____
GAM1560  IL1R1    3'  TGCAGTGGCCCAAACTCGG   9372           _____
                              TGCAGTGGCCTA    CGG
                              ||||||||||||    |||
                              ACGTCACCGGGT    GCC
                                     TTGA
GAM1560  ITPR3    3'  TGCACTGGCTACAGCAG     13693      G    C
                              TGCA TGGC TACGGCAG
                              |||| |||| ||||||||
                              ACGT ACCG ATGTCGTC
                                G    _
GAM1560  JUN      5'  TGCAGTGGCCGGCCGGCGGC   13752          TA_    A
                              TGCAGTGGCC   CGGC GC
                              ||||||||||   |||| ||
```

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                                ACGTCACCGG   GCCG CG
                                     CCG    C
GAM1560  LENG4    3'  TGCAGGGCCCAGCAG      35892      T    TA
                                TGCAG GGCC  CGGCAG
                                ||||| ||||  ||||||
                                ACGTC CCGG  GTCGTC
                                  _    __
GAM1560  MAP3K7IP2 3'  TGGCACTATGCGGCAGCAA   31525     _   __
                                TGGC CTA  CGGCAGCAA
                                |||| |||  |||||||||
                                ACCG GAT  GCCGTCGTT
                                  T   AC
GAM1560  MAPK7    3'  GGTCTACTGTGGCAGCAA    40045    C    ___
                                GG CTAC   GGCAGCAA
                                || ||||   ||||||||
                                CC GATG   CCGTCGTT
                                 A    ACA
GAM1560  MECP2    3'  TGCAGTGACTTGGAAAGTGGCA 22616          CTAC_____
              A                  TGCAGTGGC        GGCAG
                                |||||||||        |||||
                                ACGTCACTG        CCGTT
                                     AACCTTTCA
GAM1560  MHC2TA   3'  TGCAGTGGCGTGATCTCGG    6991          _____  A
                                TGCAGTGGC    CT CGG
                                |||||||||    || |||
                                ACGTCACCG    GA GCC
                                     CACTA  _
GAM1560  MUC4     3'  GCAGTGGCCTTGATTGTAGCAG 39668          AC_____
                                GCAGTGGCCT      GGCAG
                                ||||||||||      |||||
                                CGTCACCGGA      TCGTC
                                     ACTAACA
GAM1560  MYD88    3'  TGTCGTGGTCACAGCAG     14723    CA   CC
                                TG  GTGG  TACGGCAG
                                ||  ||||  ||||||||
                                AC  CACC  GTGTCGTC
                                 AG   A_
GAM1560  MYO1B    3'  TGCAGTGGCGTGACCTCGG    29226         ____  A
                                TGCAGTGGC    CT CGG
                                |||||||||    || |||
                                ACGTCACCG    GG GCC
                                     CACT  A
GAM1560  MYO1D    3'  TGCAGGGTCAGCAGCA      43507      T  CCTA
                                TGCAG GG    CGGCAGCA
                                ||||| ||    ||||||||
                                ACGTC CC    GTCGTCGT
                                  _  A___
GAM1560  NEU3     3'  TGCAGTAGCTAAGGCAA     27410         C  C
                                TGCAGTGGC TA GGCAG
                                ||||||||| || |||||
```

```
                                ACGTCATCG AT CCGTT
                                      _ T
GAM1560  P53AIP1   3'  TGCAGTGGCGTGATCTCGG   35241        _____ A
                                TGCAGTGGC    CT CGG
                                |||||||||    || |||
                                ACGTCACCG    GA GCC
                                     CACTA _
GAM1560  PCOLCE    5'  GCGGTGGCGGCAGCA      45238    A    CTAC
                                GC GTGGC    GGCAGCA
                                || |||||    |||||||
                                CG CACCG    CCGTCGT
                                 C    ____
GAM1560  PDHA1     5'  GCAGTGGCGGCAGC       7106         CTAC
                                GCAGTGGC    GGCAGC
                                ||||||||    ||||||
                                CGTCACCG    CCGTCG
                                     ____
GAM1560  PNOC      3'  TGCAGTGGCCGGTACAG    26352         TACG
                                TGCAGTGGCC    GCAG
                                ||||||||||    ||||
                                ACGTCACCGG    TGTC
                                     CCA_
GAM1560  PPP2R2B   5'  TGCAGTGGCGAGATGGCAG   21340        CTAC_
                                TGCAGTGGC    GGCAG
                                |||||||||    |||||
                                ACGTCACCG    CCGTC
                                     CTCTA
GAM1560  PRKAR2A   3'  GCAGTGGCGGCAACGGCAG   20007        CT__
                                GCAGTGGC    ACGGCAG
                                ||||||||    |||||||
                                CGTCACCG    TGCCGTC
                                    CCGT
GAM1560  PRM2      5'  TGCAGTGGGCCCTGGAG     15719        _   AC  C
                                TGCAGTGG CCT  GG AG
                                |||||||| |||  || ||
                                ACGTCACC GGG  CC TC
                                     C   A_ _
GAM1560  PSMB2     3'  TGCAGTGGCATGATCTCGG   15823        _____ A
                                TGCAGTGGC    CT CGG
                                |||||||||    || |||
                                ACGTCACCG    GA GCC
                                     TACTA _
GAM1560  PTEN      5'  GCAGCGGCGGCAGC       7211         CTAC
                                GCAGTGGC    GGCAGC
                                ||||||||    ||||||
                                CGTCGCCG    CCGTCG
                                     ____
GAM1560  PTK2B     3'  GCAGTGGCCAGGCAGCA     19919         TAC
                                GCAGTGGCC   GGCAGCA
                                |||||||||   |||||||
```

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                                CGTCACCGG  CCGTCGT
                                     T__
GAM1560  RAB23    5'  TGAGTGGCTCAGCAG      32223    C     CTA
                                TG AGTGGC  CGGCAG
                                || ||||||  ||||||
                                AC TCACCG  GTCGTC
                                 _     A__
GAM1560  SBF1     5'  TGCAGTGGCTCTGGCAA     42282         _  AC
                                TGCAGTGGC CT  GGCAG
                                ||||||||| ||  |||||
                                ACGTCACCG GA  CCGTT
                                     A  __
GAM1560  SET7     5'  CAGCTGCTGCGGCAGCA     36153      G  CTA
                                CAGT GC   CGGCAGCA
                                |||| ||   ||||||||
                                GTCG CG   GCCGTCGT
                                  A  AC_
GAM1560  SFRP4    3'  TGCAGTGAGTTGTTAGGGCAA  16587        CC___  C
                                TGCAGTGG    TA GGCAG
                                ||||||||    || |||||
                                ACGTCACT    AT CCGTT
                                     CAACA  C
GAM1560  SLC25A11 3'  GCAGTGGCTATAGGCGCAGCA  18677        CTACG__
                                GCAGTGGC      GCAGCA
                                ||||||||      ||||||
                                CGTCACCG      CGTCGT
                                     ATATCCG
GAM1560  SLC5A2   3'  TGCAGTGGGCCCCAGGCAG    16779        _  AC
                                TGCAGTGG CCT  GGCAG
                                |||||||| |||  |||||
                                ACGTCACC GGG  CCGTC
                                     C   GT
GAM1560  SLC6A8   3'  TGCAGTGGCTTTTTAGCACA   24789        CTAC_   G
                                TGCAGTGGC    GGCA CA
                                |||||||||    |||| ||
                                ACGTCACCG    TCGT GT
                                     AAAAA   _
GAM1560  SLC7A8   3'  TGCAGGGCCCACAGCAA     29297      T
                                TGCAG GGCCTACGGCAG
                                ||||| ||||||||||||
                                ACGTC CCGGGTGTCGTT
                                   _
GAM1560  SNX9     3'  TGCCGTGGCCACAGCAG     32161     A     T
                                TGC GTGGCC ACGGCAG
                                ||| |||||| |||||||
                                ACG CACCGG TGTCGTC
                                  G     _
GAM1560  SPF30    5'  GCGGTGGCAGCAGCA       25236    A    CTAC
                                GC GTGGC    GGCAGCA
                                || |||||    |||||||
```

```
                                CG CACCG   TCGTCGT
                                 C   ____
GAM1560 SRRM1   3' TGCAGGGGTCACAGCAG    25193     T  CC
                                TGCAG GG  TACGGCAG
                                ||||| ||  ||||||||
                                ACGTC CC  GTGTCGTC
                                  _  CA
GAM1560 STAT6   3' GCTGGCACGGCAGCA     17155    AG   CT
                                GC  TGGC  ACGGCAGCA
                                ||  ||||  |||||||||
                                CG  ACCG  TGCCGTCGT
                                 __   __
GAM1560 SUPT6H  3' GCGGTGGCAGCAGCA     41287    A    CTAC
                                GC GTGGC   GGCAGCA
                                || |||||   |||||||
                                CG CACCG   TCGTCGT
                                 C   ____
GAM1560 TARBP2  3' TGAGGACACGGCAGCA     39538    C  T   CT
                                TG AG GGC  ACGGCAGCA
                                || || |||  |||||||||
                                AC TC CTG  TGCCGTCGT
                                 _ _  __
GAM1560 TGFB1   5' GCAGTGGCGGGGGCGGCGGC  8541        CTA__   A
                                GCAGTGGC   CGGC GC
                                ||||||||   |||| ||
                                CGTCACCG   GCCG CG
                                     CCCCC   C
GAM1560 TNFRSF1B 3' TGCAGTGGCGTGATCTCGG   9879        _____ A
                                TGCAGTGGC   CT CGG
                                |||||||||   || |||
                                ACGTCACCG   GA GCC
                                     CACTA _
GAM1560 TNFRSF7  5' GCAGTGGCTGCTTCAGGTGGCA 10304       __ A  CA_
            A                    GCAGTGGC  CT CGG  GCAA
                                |||||||  || |||  ||||
                                CGTCACCG  GA GTC  CGTT
                                     AC  A  CAC
GAM1560 UBE2V1  3' AGTGGTCCTGAACAGCAA   35342     _  AC
                                AGTGG CCT  GGCAGCAA
                                ||||| |||  ||||||||
                                TCACC GGA  TTGTCGTT
                                  A  C_
GAM1560 UBE4A   3' TGCAATGGCTGCTTAGCAA  21979       CTACG __
                                TGCAGTGGC   GC  AGCAA
                                |||||||||   ||  |||||
                                ACGTTACCG   CG  TCGTT
                                     A____  AA
GAM1560 UGT1A1  3' TGCAGTAGGGGCAGC      7868        CCTAC
                                TGCAGTGG   GGCAGC
                                ||||||||   ||||||
```

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                                ACGTCATC    CCGTCG
                                    C____
GAM1560  UGT1A4   3'  TGCAGTAGGGGCAGC      28297       CCTAC
                                TGCAGTGG    GGCAGC
                                ||||||||    ||||||
                                ACGTCATC    CCGTCG
                                    C____
GAM1560  UGT1A9   3'  TGCAGTAGGGGCAGC      34291       CCTAC
                                TGCAGTGG    GGCAGC
                                ||||||||    ||||||
                                ACGTCATC    CCGTCG
                                    C____
GAM1560  WHSC1    5'  TGCAGTGGCTCACACCTGCAA  39390        C   GCA
                                TGCAGTGGC TACG   GCAA
                                ||||||||| ||||   ||||
                                ACGTCACCG GTGT   CGTT
                                     A   GGA
GAM1560  XPC      3'  TGTAGTGGGGCAGCA      21552    C    CCTAC
                                TG AGTGG    GGCAGCA
                                || |||||    |||||||
                                AC TCACC    CCGTCGT
                                 A   _____
GAM1560  YWHAB    5'  TGCAGTGGCTGCAGC      18189        CTACG
                                TGCAGTGGC    GCAGC
                                |||||||||    |||||
                                ACGTCACCG    CGTCG
                                    A____
GAM1560  ZNF91    3'  TGCAGTGGCGTGATCTCGG   18317        _____ A
                                TGCAGTGGC    CT CGG
                                |||||||||    || |||
                                ACGTCACCG    GA GCC
                                     CACTA  _
GAM1561  ANKH     3'  TAGATGGTTTCGAACTCCGTGG 38325       C  A ___  _
                                TAGATGGT TC GA   CCG GG
                                |||||||| || ||   ||| ||
                                ATCTACCA AG CT   GGC CC
                                    A  _  TGA   A
GAM1561  MBP      3'  GATGGTCTGGAGCTCG      44888       CAGACC   A_
                                GATGGTCT     GGG  TCG
                                ||||||||     |||  |||
                                CTACCAGA     CCT  AGC
                                     _______  CG
GAM1561  NXF5     3'  TAGAGTGGTCTTAGGCTGG    37620     _     C  ACCG
                                TAGA TGGTCT AG    GG
                                |||| |||||| ||    ||
                                ATCT ACCAGA TC    CC
                                  C     A  CGA_
GAM1561  TACR1    3'  TAGATGGTCTTGTGGCCCCTGG 31859         CAGA__  G_
                                TAGATGGTCT     CC  GG
                                ||||||||||     ||  ||
```

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                                ATCTACCAGA     GG  CC
                                     ACACCG  GA
GAM1562 BCLG     3'  TTCCCATCCACCGTG      39826     G   CGA
                                TTC CCA   TCGCCGTG
                                ||| |||   ||||||||
                                AAG GGT   GGTGGCAC
                                  _   A__
GAM1562 BCS1L    5'  TCCGCCGTGACCCTCGTG    20251       AC    GC
                                TTCGCC  GATC  CGTG
                                ||||||  ||||  ||||
                                AGGCGG  CTGG  GCAC
                                   CA    GA
GAM1562 CALU     3'  TTCCCACCACAGCTGTG     10268     G   G  C  C
                                TTC CCAC AT GC GTG
                                ||| |||| || || |||
                                AAG GGTG TG CG CAC
                                  _   G  T  A
GAM1562 GUCY1A2  5'  CTCGGCGCATCGCCGTG     9217      CCA  _
                                TTCG   CG ATCGCCGTG
                                ||||   || |||||||||
                                GAGC   GC TAGCGGCAC
                                  C__  G
GAM1562 IL1RL2   5'  TTCCCCGCCACCGTG       40479     G  A  A
                                TTC CC CG TCGCCGTG
                                ||| || || ||||||||
                                AAG GG GC GGTGGCAC
                                  _  _  _
GAM1562 MADH6    5'  TCCGCCGCGGACCGCCGTG   24606       A  _
                                TTCGCC CG ATCGCCGTG
                                |||||| || |||||||||
                                AGGCGG GC TGGCGGCAC
                                   C  C
GAM1562 MTMR3    3'  TTCACCACGTTCAAACTGTG  34402         A  __  C
                                TTCGCCACG TC  GC GTG
                                ||||||||| ||  || |||
                                AAGTGGTGC AG  TG CAC
                                     A  TT  A
GAM1562 POLR2E   3'  TTCACCACAGGCTGTG      40928         ATC  C
                                TTCGCCACG   GC GTG
                                |||||||||   || |||
                                AAGTGGTGT   CG CAC
                                     C__  A
GAM1562 TMPRSS2  3'  TTCGCCGCCACCATG       24938       ACGA
                                TTCGCC    TCGCCGTG
                                ||||||    ||||||||
                                AAGCGG    GGTGGTAC
                                   C___
GAM1562 XYLB     5'  TCCGCCACGCGGCGTG      23026         AT  C
                                TTCGCCACG  CG CGTG
                                |||||||||  || ||||
```

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                                AGGCGGTGC  GC GCAC
                                     __  C
GAM1563  IRS1     3'  GAGAACCATCTATGGCACTAT  24421    A      _____
                                GA AACCATCT    ACTAT
                                || ||||||||    |||||
                                CT TTGGTAGA    TGATA
                                 C       TACCG
GAM1563  PKP2     3'  CAGGAAGCCATCTACCATA   21316    A  A
                                TAG AA CCATCTACTATA
                                ||| || ||||||||||||
                                GTC TT GGTAGATGGTAT
                                  C  C
GAM1563  TR2      3'  TAGAAAACCACTACTTTAT   43635         T    A
                                TAGAAAACCA CTACT TAT
                                |||||||||| ||||| |||
                                ATCTTTTGGT GATGA ATA
                                     _    A
GAM1564  GPR18    5'  TAACGCTTGGCGTCGGAGT   23624      GAGAAA
                                TAACGC     GGCGTCGGAGT
                                ||||||     ||||||||||
                                ATTGCG     CCGCAGCCTCA
                                   AA____
GAM1564  GRM6     5'  CGCGGGGAGGGACACCGGGGTC 9169      A_  AA   GT   A
                                CGCG  GA  GGC  CGG GTC
                                ||||  ||  |||  ||| |||
                                GCGC  CT  CTG  GCC CAG
                                  CC  CC   TG   C
GAM1564  TBXA2R   3'  CGCGGGAGGGGCGCTCTGTC   9849      A  AA    CGGA
                                CGCG GA  GGCGT    GTC
                                |||| ||  |||||    |||
                                GCGC CT  CCGCG    CAG
                                  C  CC    AGA_
GAM1564  FGFR1    5'  TCCGCCGTGGCTTGTGCGAG   31954       AAA  ____
                                TCCGCCGT   CT    CGGG
                                ||||||||   ||    ||||
                                AGGCGGCA   GA    GCTC
                                     CC_  ACAC
GAM1564  XRCC4    5'  TCCGCCGGCCTGCGGGACGT   35426       TAAA  _
                                TCCGCCG    CT CGGGACGT
                                |||||||    || ||||||||
                                AGGCGGC    GA GCCCTGCA
                                    CG__  C
GAM1565  DMRT2    3'  TGAGGACAAGGGATACTGTCT  27269     AAT   __      A
                                TGA   GGGC  GGGATACT TCT
                                |||   ||||  |||||||| |||
                                ACT   CCTG  CCCTATGA AGA
                                  ___    TT       C
GAM1565  ETV3     3'  TATGAATGGAGTTTGGTACTAT 23478       A   CG__  A
            CT                    TATGAA TGGG    GG TACTATCT
                                ||||||  ||||    ||  ||||||||
```

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                                ATACTT ACCT    CC ATGATAGA
                                   _    CAAA  _
GAM1565  SCA1     3'  TGAAACGAAGAAAGTACTAT   7293          C GG _
                                TGAAATGGG G  A TACTAT
                                |||||||||  |  | ||||||
                                ACTTTGCTT C  T ATGATA
                                     _ TT C
GAM1565  SHOX     3'  TGAAACGGGATATTGTC     27831      ATGG       CTA
                                TGAA   GCGGGATA   TC
                                ||||   ||||||||  ||
                                ACTT   TGCCCTAT   AG
                                  ____       AAC
GAM1565  APXL     3'  TGGGAACTGACAGCATGACAG  11626    AA    A  C
                                TG  AACT AC GCATGATGG
                                ||  |||| || |||||||||
                                AC  TTGA TG CGTACTGTC
                                 CC    C  T
GAM1565  CFTR     3'  AAAACTAATTCATGATTGGTGC 7947         CCG     _  C
                                AAAACTAA   CATGAT GG GC
                                ||||||||   |||||| || ||
                                TTTTGATT   GTACTA CC CG
                                     AA_     A  A
GAM1565  EMX2     3'  TGAAAACTTGCCGCCGTGC    44698        AA    ATGATG
                                TGAAAACT  CCGC     GC
                                ||||||||  ||||     ||
                                ACTTTTGA  GGCG     CG
                                     AC    GCA___
GAM1565  FMR2     3'  TGAAAACTGGTCCACTGTCTGG 12985        AA_    A  A_
                                TGAAAACT   CCGC TG  TGG
                                ||||||||   |||| ||  |||
                                ACTTTTGA   GGTG AC  ACC
                                     CCA    _  AG
GAM1565  RP2      3'  TGAAAGCTGATTTCATAATAGC 27937       A  AACCG
                                TGAAA CT     CATGATGGC
                                ||||| ||     |||||||||
                                ACTTT GA     GTATTATCG
                                   C  CTAAA
GAM1565  VPS41    3'  TGAAAACTAGCAGTGTAGC    38763         ACC   _  A
                                TGAAAACTA   GCA TG TGGC
                                |||||||||   ||| || ||||
                                ACTTTTGAT   CGT AC ATCG
                                     ___   C  _
GAM1566  BCL11B   3'  CATTCCCTCCCCCCTTTT    39745       A  G
                                TATTCC CT TCCCCTTTT
                                ||||||  || |||||||||
                                GTAAGG GA GGGGGAAAA
                                   _  G
GAM1566  CEACAM5  5'  TCTGCTGTCCTTCCTCCCTCT  20378    CA     C_   TT
                                TC  CTGTCC  CTT  CTCT
                                ||  ||||||  |||  ||||
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                                AG  GACAGG  GGA  GAGA
                                 AC     AA   GG
GAM1566  FGD1    3'  TCCATTGTCCTCCCCCCT    20912      C    C   TT
                                TCCA TGTCC CTT  CT
                                |||| ||||| |||  ||
                                AGGT ACAGG GGG  GA
                                  A    A   GG
GAM1566  GATA2   3'  CCGTCCCCTCCTTTTCTCTA  13084          ___
                                CTGTCCCCTT   TTCTCTA
                                ||||||||||   |||||||
                                GGCAGGGGAG   AAGAGAT
                                      GAA
GAM1566  GRIA1   5'  CTGCCTGTTCTTTTCCTCC   9088       CC__     _
                                CTGTC    CTTTTC TCT
                                |||||    |||||| |||
                                GACGG    GAAAAG AGG
                                   ACAA     G
GAM1566  KMO     3'  TATTCCACTTTATTTTTTCTCT 18958         GTCCCC
                                TATTCCACT     TTTTCTCT
                                |||||||||     ||||||||
                                ATAAGGTGA     AAAAGAGA
                                     AATAA_
GAM1566  Nrap    3'  TTCCACTGTCTCCACCCT    40201          C  TTTT
                                TTCCACTGTC CC    CTCT
                                |||||||||| ||    ||||
                                AAGGTGACAG GG    GGGA
                                      A  T___
GAM1566  OAS3    3'  TTCCTGTTCCTTCCTCT     26187      AC   CCC
                                TTCC  TGT   CTTTTCTCT
                                ||||  |||   |||||||||
                                AAGG  ACA   GGAAGGAGA
                                  __   A__
GAM1566  OCA2    3'  TATTCCACTGTGTCTC      41192          CCCCTTT
                                TATTCCACTGT      TCTC
                                ||||||||||      ||||
                                ATAAGGTGACA      AGAG
                                      C_______
GAM1566  PAG     3'  TATTCCATTTATTTCTCT    32958        CTGTCCCCT
                                TATTCCA        TTTCTCT
                                |||||||        |||||||
                                ATAAGGT        AAAGAGA
                                    AAAT______
GAM1566  PITX2   3'  ATTCAGTGGTTTCCTTTTCTCT 7250       CACT  CC
            A                    ATTC    GT  CCTTTTCTCTA
                                ||||    ||  ||||||||||
                                TAAG    CA  GGAAAAGAGAT
                                  TCAC  AA
GAM1566  SCA7    5'  TTCCGCTCCTTTTCT       7311       A  GTCC
                                TTCC CT    CCTTTTCT
                                |||| ||    ||||||||
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                                AAGG GA    GGAAAAGA
                                  C _____
GAM1566 SCTR     3' TTCCCTGTCCCTTTCT      16489      A      CT
                                TTCC CTGTCCC  TTTCT
                                |||| |||||||  |||||
                                AAGG GACAGGG  AAAGA
                                  _      __
GAM1566 SLC1A4   3' CATTCCCTCTCCTTTTTTCT   16743       A  G   CC
                                TATTCC CT TCC  TTTTCT
                                |||||| || |||  ||||||
                                GTAAGG GA AGG  AAAAGA
                                   _ G   AA
GAM1566 SNCA     3' TTCCATTTTCTCTACCTCTTCT 7368       CTG  C___
                                TTCCA   TC    CCTTTTCT
                                |||||   ||    ||||||||
                                AAGGT   AG    GGAGAAGA
                                   AAA  AGAT
GAM1566 UBE2G2   3' TATTCCATCGTCCCCTGGAAGT 42127        C       TTTC_
             CT                   TATTCCA TGTCCCCT     TCT
                                |||||||  ||||||||     |||
                                ATAAGGT GCAGGGGA     AGA
                                    A       CCTTC
GAM1566 XYLB     3' TATGCCACTGTCTTATCTTTT  23025     T       CC__
                                TAT CCACTGTC    CTTTT
                                |||  ||||||||    |||||
                                ATA GGTGACAG    GAAAA
                                  C       AATA
GAM1566 ATP2B2   5' CAGTGGTGGTGAGCTCCAAGA  11755      A  A
                                CAGTG TG TGAGCTTCGAGA
                                |||||  || ||||||||||||
                                GTCAC AC ACTCGAGGTTCT
                                   C  C
GAM1566 PBX1     3' TCAGTGATATGAGAGAG      15100         A    CTTC
                                TCAGTGATG TGAG    GAG
                                |||||||||  ||||    |||
                                AGTCACTAT ACTC    CTC
                                     _    T___
GAM1566 TRIM9    5' GTGATTGATGTTTCGAGACG   31577       _    AGC
                                GTGAT GATG   TTCGAGACG
                                |||||  ||||   |||||||||
                                CACTA CTAC   AAGCTCTGC
                                   A    A__
GAM1567 CACNG3   3' TCTGACATCTTTGATTTCTGG  27241          CTCCCTACC
                                TCTGACGTCT        CTGG
                                ||||||||||        ||||
                                AGACTGTAGA        GACC
                                      AACTAAA__
GAM1567 FBXL11   3' TGGCGTCTCTCTTCTCAGTGGC 29444     A       C_  ACCC
                                TG CGTCTCTC  CT    TGGC
                                || ||||||||  ||    ||||
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                                AC GCAGAGAG  GA    ACCG
                                 C       AA  GTC_
GAM1567  LFG      3'  TCTGACGCCTCTCCTG      44152            CTACCC
                                TCTGACGTCTCTCC     TG
                                ||||||||||||||     ||
                                AGACTGCGGAGAGG     AC
                                          _______
GAM1567  NEBL     5'  CTGACGTCTCTGGTGCTCTGGC 26901           CCCTACC
                                CTGACGTCTCT      CTGGC
                                ||||||||||       |||||
                                GACTGCAGAGA      GACCG
                                      CCACGA_
GAM1567  STK24    5'  TCTGCTGGCTCTCTGCCTTGGC 18706      ACGT    CCTA  C
                                TCTG    CTCTC    CC TGGC
                                ||||    |||||    || ||||
                                AGAC    GAGAG    GG ACCG
                                  GACC     AC__  A
GAM1567  DRD3     5'  GAAATCACCCATTTTTGCCT   38014      AC       ____
                                GAAA  CACCCATTT   CCT
                                ||||  |||||||||   |||
                                CTTT  GTGGGTAAA   GGA
                                  A_        AAC
GAM1567  FZD8     3'  GAAAATGTCCATTTTCCCCAT  36612       CCAC     _
                                GAAAA    CCATTT CCTCAT
                                |||||    |||||| ||||||
                                CTTTT    GGTAAA GGGGTA
                                   ACA_     A
GAM1567  LANGERIN 3'  GAAAGAGGCATTTCCTCATGTT 31844      ACCACC
                                GAAA     CATTTCCTCATGTT
                                ||||     ||||||||||||||
                                CTTT     GTAAAGGAGTACAA
                                  CTCC__
GAM1567  PCTP     3'  GAAATCATCCATTTCCT     34533      AC  C
                                GAAA  CA CCATTTCCT
                                ||||  ||  |||||||||
                                CTTT  GT GGTAAAGGA
                                  A_  A
GAM1567  TLL1     3'  GAAGACTCCCATTTCACAT    29737     A  CA       CT
                                GAA AC  CCCATTTC  CAT
                                |||  ||  ||||||||  |||
                                CTT TG  GGGTAAAG  GTA
                                  C  A_       T_
GAM1567  TSG      3'  GAAAACCACATCAGACTTTATG 34004          CCATTTCCTC
              TT                  GAAAACCAC         ATGTT
                                  |||||||||         |||||
                                  CTTTTGGTG         TACAA
                                       TAGTCTGAAA
GAM1568  COL19A1  3'  TTTATAAGCCAAATATCAAAT  12391        TTAA
                                TTTATA    GAATATCAAAT
                                ||||||    ||||||||||
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                                AAATAT    TTTATAGTTTA
                                   TCGG
GAM1568  GRAF     3'  TAACTTAAAGAATATCAAA   31452       TATT
                                TAATTTA    AAGAATATCAAA
                                |||||||    ||||||||||||
                                ATTGAAT    TTCTTATAGTTT
                                    ____
GAM1568  FGF2     3'  ATTTCCCCATAATTATTTTT   12830      G
                                GTTTTT TATAATTATTTTT
                                |||||| ||||||||||||
                                TAAAGG GTATTAATAAAAA
                                   G
GAM1569  BIN3     3'  TGTGGACGTTTCATTGAA    33088     _     CG_
                                TGTG ACGTTTC   GAA
                                |||| |||||||   |||
                                ACAC TGCAAAG   CTT
                                  C      TAA
GAM1569  HDAC4    3'  TATGTGACGTGTGAGAA     25783        TTCC
                                TATGTGACGT    GGAA
                                ||||||||||    ||||
                                ATACACTGCA    TCTT
                                      CAC_
GAM1569  TMSB4Y   5'  GTGGAATGTTCCGGAATAAA   20090     AC  _
                                GTG  GT TTCCGGAATAAA
                                |||  || ||||||||||||
                                CAC  TA AAGGCCTTATTT
                                  CT  C
GAM1569  ATP2B2   5'  ACGAAGTTCAGCTCGTC     11749     T_  CTC
                                ACG  GT   CAGCTCGTC
                                |||  ||   |||||||||
                                TGC  CA   GTCGAGCAG
                                  TT  A__
GAM1569  SLC9A6   3'  TCAAATGCCATCAGCTCGT    26831     ATAC    TC
                                TCGA   GTGTC  CAGCTCGT
                                ||||   |||||  ||||||||
                                AGTT   TACGG  GTCGAGCA
                                  ____    TA
GAM1570  BCAT2    3'  TATCCTTGACCGCACGAC     10163      C_  ACG
                                TATCT  GAC   CGCACGAC
                                |||||  |||   ||||||||
                                ATAGG  CTG   GCGTGCTG
                                   AA   ___
GAM1571  CRHR1    3'  GCTAGTGGTCCTGCCCCA     20444     A  C  AAA
                                GCTA TG GT   CCTGCCCCA
                                |||| || ||   |||||||||
                                CGAT AC CA   GGACGGGGT
                                  C  _  ___
GAM1571  DDEF2    3'  TGCTAATGTGTAAATTTCC    19329       C    CCTG
                                TGCTAATG GTAAA    CC
                                |||||||| |||||    ||
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                                ACGATTAC CATTT   GG
                                    A    AAA_
GAM1571  HK1     5'  TCGCTGGCAGATCTGCCCC   37921     AAT   TAAAC
                                TTGCT   GCG    CTGCCCC
                                |||||   |||    |||||||
                                AGCGA   CGT    GACGGGG
                                  C__   CTA__
GAM1571  PLCB4   3'  TTGCTAATGCACTG       9587          TAAAC
                                TTGCTAATGCG    CTG
                                ||||||||||    |||
                                AACGATTACGT    GAC
                                      _____
GAM1571  POLS    3'  TGAGCCCAACCTGCCTCA    28128    C  A_      C
                                TG GT  AACCTGCC CA
                                || ||  |||||||| ||
                                AC CG  TTGGACGG GT
                                 T  GG       A
GAM1571  RFP     3'  TTGCTTGAAGTGATCTGCCCCA 27137      AA  CGTAAAC
                                TTGCT  TG      CTGCCCCA
                                |||||  ||      ||||||||
                                AACGA  AC      GACGGGGT
                                   __  TTCACTA
GAM1571  SIAT8E  3'  GGGGGCACCAAGACCGCA    40838         AAATTT
                                GGGGGCACTAA     TTGCG
                                ||||||||||     |||||
                                CCCCCGTGGTT     GGCGT
                                      CT_____
GAM1572  ITGA6   3'  GATGGACGTCTGCGCAGC    6830         CG   _
                                GATGGACG  TTGT CAGC
                                ||||||||  |||| ||||
                                CTACCTGC  GACG GTCG
                                    A_    C
GAM1572  MSX2    3'  TCGTGTGGCCCTGTCAGC    42302     A  GAC  G
                                TCG TG   GC TTGTCAGC
                                ||| ||   || ||||||||
                                AGC AC   CG GACAGTCG
                                  _  AC_  G
GAM1572  CABC1   5'  GCCACGCGCTCCGGATC     33684         C   AAC
                                GCCACGTGC CCG   ATC
                                ||||||||| |||   |||
                                CGGTGCGCG GGC   TAG
                                    A   C__
GAM1573  ADD2    5'  CAGCGGCTCCGCGGCG      32724         T    TT
                                CAGCGGCT CTGT  GCG
                                |||||||| ||||  |||
                                GTCGCCGA GGCG  CGC
                                    _    C_
GAM1573  APLP2   3'  CAGCGGCTGCTGCTTGGCA   44916         T      C
                                CAGCGGCT CTGTTTG GCA
                                |||||||| ||||||| |||
```

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                                GTCGCCGA GACGAAC CGT
                                    C     _
GAM1573  CAPN10   3'  CAGCGGCTCCTGCAGCA    35765          TT
                                CAGCGGCTTCTGT  GCG
                                |||||||||||||  |||
                                GTCGCCGAGGACG  CGT
                                     T_
GAM1573  CDX2     5'  GCGGCTTCCGTGATTAACG   10408         TT___
                                GCGGCTTCTGT    GCG
                                ||||||||||     |||
                                CGCCGAAGGCA    TGC
                                     CTAAT
GAM1573  FACL3    5'  CAGCAGCTTCTGAGGGTGGCAA 20880          TT__  C
                                CAGCGGCTTCTG   TG GCAA
                                ||||||||||||   || ||||
                                GTCGTCGAAGAC   AC CGTT
                                     TCCC  _
GAM1573  GGA3     3'  CAGTGGCTTCAGTGAATGCCA  39784    C    __ TT   G
                                CAG GGCTTC  TG  TGC CA
                                ||| ||||||  ||  ||| ||
                                GTC CCGAAG  AC  ACG GT
                                  A     TC  TT  _
GAM1573  GLI2     3'  AGCGGCCATTGCGCAACA    36114       TCTGT
                                AGCGGCT    TTGCGCAACA
                                |||||||    ||||||||||
                                TCGCCGG    AACGCGTTGT
                                    T_____
GAM1573  GMPR     5'  CAGCGGCTCCTGGCTGCGGC   44953          T    _
                                CAGCGGCTTCTG TTGCG C
                                |||||||||||| ||||| |
                                GTCGCCGAGGAC GACGC G
                                     C    C
GAM1573  MYO1D    3'  CAGTGGCTTTGGCTGGCG    43487    C    CT   T
                                CAG GGCTT  GTT GCG
                                ||| |||||  ||| |||
                                GTC CCGAA  CGA CGC
                                  A    AC   C
GAM1573  NEUROD2  5'  CAGCGGCTCCTCAAGGCGGC  26056          GTTT  _
                                CAGCGGCTTCT    GCG C
                                ||||||||||    ||| |
                                GTCGCCGAGGA    CGC G
                                     GTTC   C
GAM1573  PRKY     3'  CAGTGATTTCCATTGCGCAACA 15688    C GC      T
              A                  CAG G  TTCTGTT GCGCAACAA
                                 ||| |  ||||||| |||||||||
                                 GTC C  AAGGTAA CGCGTTGTT
                                   A TA      _
GAM1573  RFX2     5'  CAGCGGCTCCCGCGGCG     8447           TT
                                CAGCGGCTTCTGT  GCG
                                ||||||||||||  |||
```

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                                GTCGCCGAGGGCG CGC
                                      C_
GAM1573 SERPINB5 3' GCGGCTTCCTGATCCAGCAA 15282        __ TT C
                                GCGGCTTCT GT G GCAA
                                ||||||||| || | ||||
                                CGCCGAAGG TA T CGTT
                                    AC GG _
GAM1573 SLC25A11 3' CAGTGGCTATAGGCGCAGCA 18675   C  TCT TT   A
                                CAG GGCT GT GCGCA CA
                                ||| |||| || ||||| ||
                                GTC CCGA TA CGCGT GT
                                  A ___ TC   C
GAM1573 TCF7   3' CAGAGGCTTCTGGCTGGCAA 17319   C     T C
                                CAG GGCTTCTG TTG GCAA
                                ||| |||||||| ||| ||||
                                GTC CCGAAGAC GAC CGTT
                                  T     C _
GAM1573 TNS    3' GGCTCTGTTTGGTTTGACAA 35477    T    CGCA_
                                GGCT CTGTTTG   ACAA
                                |||| |||||||   ||||
                                CCGA GACAAAC   TGTT
                                  _     CAAAC
GAM1573 VTN    5' CAGCGGCTGCTGCAGCA   8468       T  TT
                                CAGCGGCT CTGT GCG
                                |||||||| |||| |||
                                GTCGCCGA GACG CGT
                                    C  T_
GAM1573 PTGIS   3' TTCATTCTTGCCACTGAGCTTA 9682       C_ ATAGC
           AA                   TTCATTC GC   GAGCTTAAA
                                ||||||| ||   |||||||||
                                AAGTAAG CG   CTCGAATTT
                                   AA GTGA_
GAM1573 SMN1   3' TCATTCCTAAATGCTTAA   35644      GCAT CGA
                                TCATTCC  AG  GCTTAA
                                |||||||  ||  ||||||
                                AGTAAGG  TT  CGAATT
                                    AT__ A__
GAM1574 ABCD1   3' GGGGTGGTGCCCGGCCCGAGG 6203   A  G  GA
                                GG GTGG GTC CGGCCCGAGG
                                || |||| ||| ||||||||||
                                CC CACC CGG GCCGGGCTCC
                                 C  A __
GAM1574 ACP1   5' GGGTGGGGTCACCTGGAGG  28243   A    GACG C_
                                GG GTGGGGTC  GCC GAGG
                                || ||||||||  ||| ||||
                                CC CACCCCAG  TGG CTCC
                                 _     _____ AC
GAM1574 ATRN   3' GGAGTGGGGTTAGTGTTGGGGA 40275       CGAC___ CCCGA
                                GGAGTGGGGT    GG   GGA
                                ||||||||||    ||   |||
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                                CCTCACCCCA      CC     CCT
                                     ATCACAA  _____
GAM1574 BSN      3'  GGGTGGGGTGGGGAG      18410    A     CGAC  CCC
                                GG GTGGGGT    GG   GAG
                                || |||||||    ||   |||
                                CC CACCCCA    CC   CTC
                                 _      _____  C__
GAM1574 CELL     3'  GGAGTGGGGTGGCAAAGG    12228         CGAC   CC
                                GGAGTGGGGT    GGC  GAGG
                                ||||||||||    |||  ||||
                                CCTCACCCCA    CCG  TTCC
                                     _____  T_
GAM1574 CHST1    3'  GGAGTGGGGTGAGCTGGGG   18910         C  CG  CCGA
                                GGAGTGGGGT GA  GC    GG
                                |||||||||| ||  ||    ||
                                CCTCACCCCA CT  CG    CC
                                     _  __  ACC_
GAM1574 CHST1    5'  GGAGTAGGGTCGCCGGGG    18909          ACGGC   A
                                GGAGTGGGGTCG    CCG GG
                                ||||||||||||    ||| ||
                                CCTCATCCCAGC    GGC CC
                                     ______  C
GAM1574 CXCL16   5'  GAGGACGACGGCCCGAGGA   35198      T
                                GGGG CGACGGCCCGAGGA
                                |||| ||||||||||||||
                                CTCC GCTGCCGGGCTCCT
                                  T
GAM1574 DNMT3L   5'  GGAGTGGGGTTCAGGG      30060         CGA   CCCGA
                                GGAGTGGGGT   CGG    G
                                ||||||||||   |||    |
                                CCTCACCCCA   GTC    C
                                     A__   C_____
GAM1574 DNMT3L   5'  GGAGTGAGGGGTGGGGTTTGGG 30059         TCGAC  CCCGA
           GA                    GGAGTGGGG    GG    GGA
                                |||||||||    ||    |||
                                CCTCACTCC    CC    CCT
                                     CCACC  AAACC
GAM1574 ENIGMA   3'  GGAGTGGGGTGGGAG       41636         CGAC  CCC
                                GGAGTGGGGT   GG   GAG
                                ||||||||||   ||   |||
                                CCTCACCCCA   CC   CTC
                                     _____  ___
GAM1574 EPHA8    3'  GGGTGGGGTGGGGAG       33899    A     CGAC  CCC
                                GG GTGGGGT   GG   GAG
                                || |||||||   ||   |||
                                CC CACCCCA   CC   CTC
                                 _      _____  C__
GAM1574 GRN      3'  GAGTGGGGTCCCGAG       13293         CGACGG
                                GAGTGGGGT    CCCGAG
                                |||||||||    ||||||
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                                CTCACCCCA     GGGCTC
                                          _______
GAM1574  HYOU1    3'  GGAGTGGGGCTGGGGAGG    40634          CGAC  CCC
                                GGAGTGGGGT    GG   GAGG
                                ||||||||||    ||   ||||
                                CCTCACCCCG    CC   CTCC
                                      A___   C__
GAM1574  KCNC3    3'  GGGTGGGGTCTGCAAGG     22524    A      GACGGCC
                                GG GTGGGGTC      CGAGG
                                || ||||||||      |||||
                                CC CACCCCAG      GTTCC
                                 _       AC_____
GAM1574  LASS1    3'  GGGTGGGGCCGGGTCCACGGGG 34614    A       AC  _  _  A
                                GG GTGGGGTCG  GG CC CG GG
                                || |||||||||  || || || ||
                                CC CACCCCGGC  CC GG GC CC
                                 _       __  A  T  C
GAM1574  MADH7    5'  GCGGCGGCGGCCCGAG      25365      _  TCGA
                                GTGG GG    CGGCCCGAG
                                ||||  ||    |||||||||
                                CGCC CC    GCCGGGCTC
                                  G  _____
GAM1574  MAP3K11  3'  GGGTGGGGTCCCTGGG      14535    A     CGACGG   GA
                                GG GTGGGGT     CCC  GG
                                || |||||||     |||  ||
                                CC CACCCCA     GGG  CC
                                 _      _______  AC
GAM1574  MEIS2    3'  GGTGTGGGGTCATCTGGGGA   33544    A       AC_  CCCGA
                                GG GTGGGGTCG   GG    GGA
                                || |||||||||   ||    |||
                                CC CACCCCAGT   CC    CCT
                                 A        AGA  ______
GAM1574  MFI2     5'  GGGCTGGGTCCGGGTCCGAGGA 25469    A  G    GA   C_
                                GG GT GGGTC  CGG  CCGAGGA
                                || || |||||  |||  |||||||
                                CC CG CCCAG  GCC  GGCTCCT
                                 _ A     __   CA
GAM1574  MSF      3'  GGGTGGTGGGAGGGCCTGGGG  44739    A   _  TC  C    CGA
                                GG GTGG GG  GA GGCC   GG
                                || |||| ||  || ||||   ||
                                CC CACC CC  CT CCGG   CC
                                 _   A  __  C    ACC
GAM1574  NESH     5'  GGGATGGGGTCGGAGACTGGGG 32340    AG       AC   CCGA
             A                   GG  TGGGGTCG  GGC    GGA
                                ||  ||||||||  |||    |||
                                CC  ACCCCAGC  CTG    CCT
                                 CT       CT   ACC_
GAM1574  NORE1    3'  GTGGGGCACAGCCTGGGG    36431        CG     CGA
                                GTGGGGT  ACGGCC   GG
                                |||||||  ||||||   ||
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                                CACCCCG TGTCGG  CC
                                   __    ACC
GAM1574 NUCB1   3' GGAGTGGGGTCAGCTCTGGGA 26156       GAC  CCGA
                                GGAGTGGGGTC GGC  GGA
                                |||||||||||  |||  |||
                                CCTCACCCCAG TCG  CCT
                                    ___  AGAC
GAM1574 OPHN1   3' GTGGGGTCGGGGGAGG    14968      AC CCC
                                GTGGGGTCG GG  GAGG
                                |||||||||  ||  ||||
                                CACCCCAGC CC  CTCC
                                     C_ ___
GAM1574 PAX2    3' GGGTGGGGTCAGACGGGG   19638   A    _   CCCGA
                                GG GTGGGGTC GACGG   GG
                                || |||||||| |||||   ||
                                CC CACCCCAG CTGCC   CC
                                 _     T   _____
GAM1574 PCDHGA1  3' GGAGTGGGGTGGGGAG    36731      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
                                CCTCACCCCA  CC  CTC
                                    _____ C__
GAM1574 PCDHGA10 3' GGAGTGGGGTGGGGAG    36873      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
                                CCTCACCCCA  CC  CTC
                                    _____ C__
GAM1574 PCDHGA11 3' GGAGTGGGGTGGGGAG    36884      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
                                CCTCACCCCA  CC  CTC
                                    _____ C__
GAM1574 PCDHGA12 3' GGAGTGGGGTGGGGAG    36892      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
                                CCTCACCCCA  CC  CTC
                                    _____ C__
GAM1574 PCDHGA2  3' GGAGTGGGGTGGGGAG    36738      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
                                CCTCACCCCA  CC  CTC
                                    _____ C__
GAM1574 PCDHGA3  3' GGAGTGGGGTGGGGAG    33161      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
                                CCTCACCCCA  CC  CTC
                                    _____ C__
GAM1574 PCDHGA4  3' GGAGTGGGGTGGGGAG    36822      CGAC CCC
                                GGAGTGGGGT  GG  GAG
                                ||||||||||  ||  |||
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                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGA5  3' GGAGTGGGGTGGGGAG    36831       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGA6  3' GGAGTGGGGTGGGGAG    36838       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGA7  3' GGAGTGGGGTGGGGAG    36847       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGA8  3' GGAGTGGGGTGGGGAG    30416       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGA9  3' GGAGTGGGGTGGGGAG    36864       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGB1  3' GGAGTGGGGTGGGGAG    36900       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGB2  3' GGAGTGGGGTGGGGAG    36909       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGB3  3' GGAGTGGGGTGGGGAG    36918       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGB4  3' GGAGTGGGGTGGGGAG    36927       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
                                CCTCACCCCA   CC  CTC
                                     _____ C__
GAM1574 PCDHGB5  3' GGAGTGGGGTGGGGAG    36936       CGAC CCC
                                GGAGTGGGGT   GG  GAG
                                ||||||||||   ||  |||
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                              CCTCACCCCA   CC  CTC
                                   _____ C__
GAM1574 PCDHGB6  3' GGAGTGGGGTGGGGAG     36942        CGAC  CCC
                              GGAGTGGGGT   GG  GAG
                              ||||||||||   ||  |||
                              CCTCACCCCA   CC  CTC
                                   _____ C__
GAM1574 PCDHGB7  3' GGAGTGGGGTGGGGAG     36950        CGAC  CCC
                              GGAGTGGGGT   GG  GAG
                              ||||||||||   ||  |||
                              CCTCACCCCA   CC  CTC
                                   _____ C__
GAM1574 PCDHGC3  3' GGAGTGGGGTGGGGAG     37050        CGAC  CCC
                              GGAGTGGGGT   GG  GAG
                              ||||||||||   ||  |||
                              CCTCACCCCA   CC  CTC
                                   _____ C__
GAM1574 PCDHGC4  3' GGAGTGGGGTGGGGAG     37072        CGAC  CCC
                              GGAGTGGGGT   GG  GAG
                              ||||||||||   ||  |||
                              CCTCACCCCA   CC  CTC
                                   _____ C__
GAM1574 PCDHGC5  3' GGAGTGGGGTGGGGAG     37080        CGAC  CCC
                              GGAGTGGGGT   GG  GAG
                              ||||||||||   ||  |||
                              CCTCACCCCA   CC  CTC
                                   _____ C__
GAM1574 PEX14    3' GAGTGGGGTTGGGGCTGGGGA 41871        CGAC   CCGA
                              GAGTGGGGT   GGC   GGA
                              |||||||||   |||   |||
                              CTCACCCCA   CCG   CCT
                                   ACC_  ACC_
GAM1574 PLAT     5' GGGTGGGGTCGGTGGCCCCGG 37449    A      AC    GA
                              GG GTGGGGTCG  GGCCC  GG
                              || |||||||||  |||||  ||
                              CC CACCCCAGC  CCGGG  CC
                               _       CA    G_
GAM1574 RAD54L   5' GGAGTGGGGATGATGGTCCCA 18714        TC  C  _
                              GGAGTGGGG  GA GG CCCG
                              |||||||||  || || ||||
                              CCTCACCCC  CT CC GGGT
                                   TA  A  A
GAM1574 SHANK2   3' GGAGTGGGGTTGATGCTCA   29461        C  CG  C
                              GGAGTGGGGT GA  GC CG
                              |||||||||| ||  || ||
                              CCTCACCCCA CT  CG GT
                                   A  A_  A
GAM1574 SMT3H1   3' GGAGTGGGGTGGGAG      40999        CGAC  CCC
                              GGAGTGGGGT   GG  GAG
                              |||||||||   ||  |||
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                              CCTCACCCCA   CC  CTC
                                    ____  ___
GAM1574 SOX10   3' GGAGTGGGGCTGACTGAGCAGG 28006        C  __  CCG
                              GGAGTGGGGT GAC  GGC  AGG
                              |||||||||| |||  |||  |||
                              CCTCACCCCG CTG  TCG  TCC
                                   A  AC  ___
GAM1574 STAC    3' GGAGTGGGATCCTGGG     17136         GAC  CCCGA
                              GGAGTGGGGTC  GG   G
                              ||||||||||  ||   |
                              CCTCACCCTAG  CC   C
                                   GA_ _____
GAM1574 TGFB1   5' GGAATGGGGGCGCCTGAGG   8542        T GACG  C
                              GGAGTGGGG C   GCC GAGG
                              ||||||||| |   ||| ||||
                              CCTTACCCC G   CGG CTCC
                                   C ____  A
GAM1574 ZAP70   3' GGGTGGGGCTGAGGGTGGGGA 43340   A    C  C  CCCGA
                              GG GTGGGGT GA GG   GGA
                              || ||||||| || ||   |||
                              CC CACCCCG CT CC   CCT
                               _     A  C  ACC__
GAM1574 ATP1A1  5' CGCTGTTGCTGCCGCCGCCCGG 8693    C  C  C   _
                              CGC GT GC GCCGC GCTCGG
                              ||| || || ||||| ||||||
                              GCG CA CG CGGCG CGGGCC
                                A  A  A   G
GAM1574 BCL7A   5' GCGCCGCCGCCGCCGCCGGA  34212           GCT
                              GCGCCGTCGCCGCCGC  CGGA
                              ||||||||||||||||  ||||
                              CGCGGCGGCGGCGGCG  GCCT
                                        ___
GAM1574 CCNF    5' CGTCGCTGCCGCCGG      12073      C   GCT
                              CGTCGC GCCGC  CGG
                              |||||| |||||  |||
                              GCAGCG CGGCG  GCC
                                 A   ___
GAM1574 CDC2L1  5' GCCGCCGCCGCCGCCGCCGG  37912          _ T
                              GCCGTCGCCGCCGC GC CGG
                              |||||||||||||| || |||
                              CGGCGGCGGCGGCG CG GCC
                                      G _
GAM1574 CDC34   5' GCGCCGCCGCCGCCGCCCGG  20354           G T
                              GCGCCGTCGCCGCCGC C CGG
                              |||||||||||||||| | |||
                              CGCGGCGGCGGCGGCG G GCC
                                        _ _
GAM1574 CEBPA   5' GCGTCGCGCCGCCCACCCGGA 20395    C  T     G
                              GCG CG CGCCGCC CGCTCGGA
                              ||| || ||||||| ||||||||
```

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                                CGC GC GCGGCGG GTGGGCCT
                                  A _     _
GAM1574 CRAT    5' GCGCCGCCGCCGCCGCGGCTGG 8893              _ C
                G                  GCGCCGTCGCCGCCGCG CT GG
                                   |||||||||||||||| || ||
                                   CGCGGCGGCGGCGGCGC GA CC
                                             C  C
GAM1574 CSNK1D  5' GCGCCGCCGCCGCTGCTCCGG 40067          C  GC
                                   GCGCCGTCGCCGC GC  TCGG
                                   |||||||||||| ||  ||||
                                   CGCGGCGGCGGCG CG  GGCC
                                           A  A_
GAM1574 DNMT3B  5' CCGTCGGGGGGCGCTCGGA  27873      CCGCC
                                   CCGTCG    GCGCTCGGA
                                   ||||||    |||||||||
                                   GGCAGC    CGCGAGCCT
                                      CCCC_
GAM1574 DYRK2   5' GCCGTCGCCGCCGCCGG    27038          GCT
                                   GCCGTCGCCGCCGC   CGG
                                   ||||||||||||||   |||
                                   CGGCAGCGGCGGCG   GCC
                                                ___
GAM1574 EFNB1   5' GCCGCGCTGCGCTCGGA    20719     T   CGCC
                                   GCCG CGC    GCGCTCGGA
                                   |||| |||    |||||||||
                                   CGGC GCG    CGCGAGCCT
                                     _   A___
GAM1574 EZH2    5' GCGCCGCCGCCGCCGCCGCCGG 20877             _ T
                                   GCGCCGTCGCCGCCGC GC CGG
                                   |||||||||||||||| || |||
                                   CGCGGCGGCGGCGGCG CG GCC
                                             G  _
GAM1574 GRB14   5' GCCTCGCCGCCTGCGCTCGG  21038    G      _
                                   GCC TCGCCGCC GCGCTCGG
                                   ||| |||||||| ||||||||
                                   CGG AGCGGCGG CGCGAGCC
                                     _       A
GAM1574 IFNAR2  5' CCGCGGGCTGCGCTCGG    9316     T  CC  C
                                   CCG CG  GC GCGCTCGG
                                   ||| ||  || ||||||||
                                   GGC GC  CG CGCGAGCC
                                     _  C_  A
GAM1574 JAG1    5' GCGCTGGTGCTGCCGCCGG   6859      C_  C  C    GCT
                                   GCGC  GT GC GCCGC   CGG
                                   ||||  || || |||||   |||
                                   CGCG  CA CG CGGCG   GCC
                                     AC  _  A    ___
GAM1574 LASS2   5' GCGCCGCCGCCGCCGCCCGCCG 42676             __ T
                A                  GCGCCGTCGCCGCCGC  GC CGG
                                   ||||||||||||||||  || |||
```

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                                CGCGGCGGCGGCGGCG  CG GCT
                                        GG  _
GAM1574  LRP8     5'  GCGCCGCCGCCGCCGCGTCTCA 37797              _
              G                  GCGCCGTCGCCGCCGCG CTCGG
                                 |||||||||||||||| |||||
                                 CGCGGCGGCGGCGGCGC GAGTC
                                        A
GAM1574  MAP3K5   5'  GCGCCCTCGCCGCCGCGCCG  25441      G         T
                                 GCGCC TCGCCGCCGCGC CG
                                 ||||| |||||||||||| ||
                                 CGCGG AGCGGCGGCGCG GC
                                    G         _
GAM1574  MATK     5'  GCGCCGCCGCCGCCGCCGG   40320             GCT
                                 GCGCCGTCGCCGCCGC   CGG
                                 ||||||||||||||||   |||
                                 CGCGGCGGCGGCGGCG   GCC
                                          ___
GAM1574  NCKAP1   5'  GCCGCCGCCGCCGCCGG     30257           GCT
                                 GCCGTCGCCGCCGC   CGG
                                 ||||||||||||||   |||
                                 CGGCGGCGGCGGCG   GCC
                                          ___
GAM1574  OSBP     5'  CGCCGTCGCCGCCCGGA     14987           GCGCT
                                 CGCCGTCGCCGCC    CGGA
                                 ||||||||||||     ||||
                                 GCGGCAGCGGCGG    GCCT
                                          _____
GAM1574  PFKL     5'  CGTCGCCGCCGCTGGTCAG   15232           GC_
                                 CGTCGCCGCCGC   TCGG
                                 ||||||||||||   ||||
                                 GCAGCGGCGGCG   AGTC
                                        ACC
GAM1574  PKNOX1   3'  GCCGTTGTCACCGCACACTGG  21308    ___      C    C
                                 GCC   GTCGCCGC GCGCT GG
                                 |||   |||||||| ||||| ||
                                 CGG   CAGTGGCG TGTGA CC
                                   CAA       _    _
GAM1574  PREB     5'  GCCCCGTCGCCGCCGGG     30142    G        CGCTC
                                 GC CCGTCGCCGCCG    GG
                                 || ||||||||||||    ||
                                 CG GGCAGCGGCGGC    CC
                                   G          _____
GAM1574  RAD51L3  5'  GCGCCGCGCTGCCGCTTCCGG 39472       T  C    GC
                                 GCGCCG CGC GCCGC  TCGG
                                 |||||| ||| |||||  ||||
                                 CGCGGC GCG CGGCG  GGCC
                                    _  A    AA
GAM1574  SLC1A1   5'  CGCCGTTGCCGCCGCCACCCGG 20032       C      _
                                 CGCCGT GCCGCCGC GCTCGG
                                 |||||| |||||||| ||||||
```

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                                GCGGCA CGGCGGCG TGGGCC
                                   A      G
GAM1574 SORCS2   5' GCGCCGTCCTCGCCGGG    34056       GC    CGCTC
                                GCGCCGTC CGCCG    GG
                                |||||||| |||||    ||
                                CGCGGCAG GCGGC    CC
                                    GA    _____
GAM1574 SREBF2   5' GCCGTCGCCACCGCCCATGA  21403          G CG
                                GCCGTCGCCGCCGC CT  GA
                                |||||||||||||| ||  ||
                                CGGCAGCGGTGGCG GG  CT
                                       _ TA
GAM1574 TACC3    5' GCGCCGCCGCCGCCAGGA    26810          CGCTC
                                GCGCCGTCGCCGCCG    GGA
                                |||||||||||||||    |||
                                CGCGGCGGCGGCGGT    CCT
                                                   _____
GAM1574 TSN      5' GCGCCGTCCGCTGCGTTCGGAA 21494       CG   C  C
                                GCGCCGT  CCGC GCG TCGGAA
                                |||||||  |||| ||| ||||||
                                CGCGGCA  GGCG CGC AGCCTT
                                   __   A  A
GAM1574 WHSC1L1  5' GCGCCGCCGCTGCTGCCAGA  32819        C CGC T
                                GCGCCGTCGC GC   GC CGGA
                                |||||||||| ||   || ||||
                                CGCGGCGGCG CG   CG GTCT
                                     A  A__  _
GAM1574 ZNF216   5' GCCGCCGCCGCGGGCCGGGA  25654        C C   C
                                GCCGTCGCCGC G GCT GGA
                                |||||||||| | ||| |||
                                CGGCGGCGGCG C CGG CCT
                                      _ C   C
GAM1574 ZNF216   5' GCGCCGCCGCCGCCGCGGGG  25655           CTC
                                GCGCCGTCGCCGCCGCG   GG
                                |||||||||||||||||   ||
                                CGCGGCGGCGGCGGCGC   CC
                                      C__
GAM1575 AFP      5' AGTTATTTTGTTATTGGC    10065       AC    A
                                AGTTATTTT  TATTG GC
                                |||||||||  ||||| ||
                                TCAATAAAA  ATAAC CG
                                    CA    _
GAM1575 ARF4L    5' GTTATCTCTCGTGAGCC     43072       ACTAT
                                GTTATTTT    TGAGCC
                                ||||||||    ||||||
                                CAATAGAG    ACTCGG
                                    AGC__
GAM1575 COX6A1   3' TAAGTTATTTATTTAAGCCA  20415        TACTA
                                TAAGTTATTT    TTGAGCCA
                                ||||||||||    ||||||||
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                                ATTCAATAAA    AATTCGGT
                                    TA___
GAM1575 GPR34    3' AATTATTTTGCTGTTAGAGCCA 23626        A  A  _
                                AGTTATTTT CT TT GAGCCA
                                ||||||||| || || ||||||
                                TTAATAAAA GA AA CTCGGT
                                    C  C  T
GAM1575 IL18R1   3' TAAGTTATTTTACTCTTTTTAG 19295          ATTG__  C
             TCA                  TAAGTTATTTTACT     AG CA
                                ||||||||||||||     || ||
                                ATTCAATAAAATGA     TC GT
                                      GAAAAA  A
GAM1575 SLC10A2  3' AGTTATTTTCCCCTGGCAGCC  7813        A  A  __
                                AGTTATTTT CT TTG  AGCC
                                ||||||||| || |||  ||||
                                TCAATAAAA GG GAC  TCGG
                                    _ G   CG
GAM1575 ADSS     3' TATTACTAAACATTGAAAA   43479      AAAAA
                                TGTTAC    AAACATTGAAAA
                                ||||||    ||||||||||||
                                ATAATG    TTTGTAACTTTT
                                   A____
GAM1575 ATP11B   3' TTACAGGAAAAACACCAA    44312      AA      TG
                                TTACA  AAAAACAT  A
                                ||||| ||||||||  |
                                AATGT  TTTTTGTG  T
                                   CC       GT
GAM1575 B3GALT2  3' TTACAAATTGCACATTGAAAAA 19116       AAAA
                                TTACAAA   ACATTGAAAAA
                                |||||||   ||||||||||
                                AATGTTT   TGTAACTTTTT
                                    AACG
GAM1575 DNMT3B   3' GTTACAAAAAAAATTTTAATGA 27880          CAT___
             AAA                  GTTACAAAAAAAA     TGAAAA
                                ||||||||||||     ||||||
                                CAATGTTTTTTTT     ACTTTT
                                      AAAATT
GAM1575 GUCY1B2  3' TGTTACAACAAAACACAGAAA  19967        AA      T
                                TGTTACAA  AAAACAT GAAA
                                ||||||||  ||||||| ||||
                                ACAATGTT  TTTTGTG CTTT
                                    G_      T
GAM1575 NFIA     3' TGTTACAGAAAAACATTG    43225       AA
                                TGTTACA  AAAAACATTG
                                |||||||  ||||||||||
                                ACAATGT  TTTTTGTAAC
                                    C_
GAM1575 NKX3A    3' TGTTGCAAAAAACACATAGAAA 26118      A      A   T
                                TGTT CAAAAAA ACAT GAAA
                                |||| ||||||| |||| ||||
```

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                                ACAA GTTTTTT TGTA CTTT
                                  C      G    T
GAM1575  PPAT     3'  TGTTACAAGAAAAAACTTCAAA 15489         _      A TG
                AA                  TGTTACAA AAAAAAC T  AAAA
                                    |||||||| ||||||| |  ||||
                                    ACAATGTT TTTTTTG A  TTTT
                                       C       A GT
GAM1575  RNASE4   3'  TATTACAAGGAAAACATAAAAA 16346         AA      T
                                    TGTTACAA  AAAACAT GAAA
                                    ||||||||  ||||||| ||||
                                    ATAATGTT  TTTTGTA TTTT
                                       CC      T
GAM1575  SLC7A8   3'  TTACAAAAAAAATAATTGAA   29298          AC
                                    TTACAAAAAAA  ATTGAA
                                    ||||||||||  ||||||
                                    AATGTTTTTTT  TAACTT
                                          AT
GAM1575  TMPRSS3  3'  TGCTACAAAGAAATCATGAAAA 37066         A   A   T
                                    TGTTACAAA AAA CAT GAAAA
                                    ||||||||| ||| ||| |||||
                                    ACGATGTTT TTT GTA CTTTT
                                       C   A   _
GAM1575  ZFP36L1  3'  GTTACAAAAAATGTCGTTGAA  22293          AACA_
                                    GTTACAAAAAA    TTGAA
                                    ||||||||||    |||||
                                    CAATGTTTTTT    AACTT
                                          ACAGC
GAM1576  PTGFRN   3'  TGTCAATGCAGAATCTAATGTT 42605        A  AC   _
                                    TGTCAAT CA  AGTC AATGTT
                                    ||||||| ||  |||| ||||||
                                    ACAGTTA GT  TTAG TTACAA
                                       C  C_   A
GAM1576  TNFAIP1  3'  CATGTCAGTGAGTTCAATGTT  34476        ATACAACAG
                                    TATGTCA       TCAATGTT
                                    |||||||       ||||||||
                                    GTACAGT       AGTTACAA
                                       CACTCA___
GAM1576  VDAC2    3'  TCAATGGTAACAGTCAATGTT  17935       AC_
                                    TCAAT   AACAGTCAATGTT
                                    |||||   ||||||||||||
                                    AGTTA   TTGTCAGTTACAA
                                      CCA
GAM1576  ATP8A2   3'  AGAAAAAAAAATAAATGAAG   45249           T
                                    AGAAAAAGAAATA GATGAAG
                                    |||||||||||| |||||||
                                    TCTTTTTTTTTAT TTACTTC
                                                  _
GAM1576  CD2AP    3'  AGAAGGAGAAACATGAAGA   29068      AA        T
                                    AGAA  AGAAATATGA GA
                                    ||||  |||||||||| ||
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                                TCTT  TCTTTGTACT CT
                                  CC         T
GAM1576  EGF      5'  GAAAGAAGAAATATGGAGA   12651      _        AT
                                GAAA AAGAAATATG  GA
                                |||| ||||||||||  ||
                                CTTT TTCTTTATAC  CT
                                  C         CT
GAM1576  ENAM     3'  TAAGAAAAAGAAATGATAAAG  36676           AT
                                TAAGAAAAAGAA  ATGATGAAG
                                ||||||||||||  |||||||||
                                ATTCTTTTTCTT  TACTATTTC
                                              __
GAM1576  GALNT3   3'  TAAGAAAAAAAAATACTAGAAGA 21016           A   GAT
                                TAAGAAAAAGAA TAT   GAAGA
                                |||||||||||| |||   |||||
                                ATTCTTTTTTTT ATG   CTTCT
                                       _  AT_
GAM1576  GCH1     3'  TAAAAAAAAGAAGAAGAAG    6705           ATAT  T
                                TAAGAAAAAGAA    GA GAAG
                                ||||||||||||    || ||||
                                ATTTTTTTTCTT    CT CTTC
                                       _____  T
GAM1576  HAP1     3'  GAGAAGAAAGGATGAAG     19499     AA     TAT
                                GA  AAGAAA   GATGAAG
                                ||  ||||||   |||||||
                                CT  TTCTTT   CTACTTC
                                 C_     C__
GAM1576  HMG20A   3'  AGAAACAGAAATATGAGGA   32862       A         T
                                AGAAA AGAAATATGA GA
                                ||||| ||||||||||  ||
                                TCTTT TCTTTATACT CT
                                   G         C
GAM1576  IF       3'  AGAAAAAGAATAGAATGAAGA  6815           A  T
                                AGAAAAAGAA TA GATGAAGA
                                |||||||||| ||  ||||||||
                                TCTTTTTCTT AT TTACTTCT
                                       _  C
GAM1576  LZTS1    3'  AAGAAAAAGAAAGAA       34258           TATGAT
                                AAGAAAAAGAAA      GAA
                                ||||||||||||      |||
                                TTCTTTTTCTTT      CTT
                                              _______
GAM1576  PCDHB13  3'  AAAAAAAGAGAATCAAATGAAG 33184          _   AT
              A                  AGAAAAAGA AAT  GATGAAGA
                                 |||||||||  |||  ||||||||
                                 TTTTTTTCT TTA  TTACTTCT
                                       C   GT
GAM1576  PMX1     3'  AAGAAAAAGAAATGGAAG    35491           ATGAT
                                AAGAAAAAGAAAT     GAAG
                                ||||||||||||      ||||
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                                TTCTTTTTCTTTA    CTTC
                                      C____
GAM1576  PPEF2    3'  TAAGAAAAAGTAAATAATGAAG 26404         AAAT
              A                  TAAGAAAAAG   ATGATGAAGA
                                 ||||||||||   ||||||||||
                                 ATTCTTTTTC   TATTACTTCT
                                      ATT_
GAM1576  PPP1CB   3'  TAAAAAAAAGAAATAGGA    15505           T
                                 TAAGAAAAAGAAATA GA
                                 |||||||||||||| ||
                                 ATTTTTTTTCTTTAT CT
                                       C
GAM1576  PROX1    3'  GAGAGAAACGTGATGAGGA   15721   AAA   TA    A
                                 GA  AGAAA  TGATGA GA
                                 ||  |||||  |||||| ||
                                 CT  TCTTT  ACTACT CT
                                  C__    GC     C
GAM1576  RBP3     3'  TAAGAAAAAGAGCAAAGTATGA 16187         AATATG_
              AGA                  TAAGAAAAAGA     ATGAAGA
                                   ||||||||||      |||||||
                                   ATTCTTTTTCT     TACTTCT
                                        CGTTTCA
GAM1576  RENT1    3'  AGAAAAAGAAATAAAAG     16245          TGAT
                                 AGAAAAAGAAATA   GAAG
                                 ||||||||||||    ||||
                                 TCTTTTTCTTTAT   TTTC
                                       ____
GAM1576  SELL     3'  GAAAAAGAGAGGTGGCTGAAGA 8511        AATA  A_
                                 GAAAAAGA   TG  TGAAGA
                                 ||||||||   ||  ||||||
                                 CTTTTTCT   AC  ACTTCT
                                      CTCC  CG
GAM1576  SOX13    3'  AAAAAAAGAAACAGCCTGGAGA 25004          TGA  A
                                 AGAAAAAGAAATA   TG AGA
                                 ||||||||||||   || |||
                                 TTTTTTTCTTTGT   AC TCT
                                       CGG  C
GAM1576  STK24    3'  AAAAAAGGAGGAGGATGAAGA  18702       AAATAT
                                 GAAAAAG     GATGAAGA
                                 |||||||     ||||||||
                                 TTTTTTC     CTACTTCT
                                     CTCCTC
GAM1576  TBL1X    3'  AGACAAAGAAATTATGAAGA   24869     A      ATG
                                 AGA AAAGAAAT   ATGAAGA
                                 ||| ||||||||   |||||||
                                 TCT TTTCTTTA   TACTTCT
                                   G       A__
GAM1576  UBE4A    3'  AAGAAAAAGAAAAGAAG     21966          TATGAT
                                 AAGAAAAAGAAA     GAAG
                                 ||||||||||||     ||||
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                                TTCTTTTTCTTT     CTTC
                                      T_____
GAM1576 UFD1L    3' AGGAAAAGAAAGGATAAATGAA 43821    A      TAT__
             GA                  AG AAAAGAAA    GATGAAGA
                                 || ||||||||    ||||||||
                                 TC TTTTCTTT    TTACTTCT
                                  C       CCTAT
GAM1576 ZNF26    3' GAAAAAGAAATCAAAAGA    43799          ATGAT
                                 GAAAAAGAAAT    GAAGA
                                 ||||||||||    |||||
                                 CTTTTTCTTTA    TTTCT
                                       GT___
GAM1577 ASB2     3' GTGAGTTTTCCAGAACAAG   32053    C   ATATAA
                                 GTG GTT     CCAGAACAAG
                                 ||| |||     ||||||||||
                                 CAC CAA     GGTCTTGTTC
                                   T   AA____
GAM1577 DGCR6    3' GCGGCTGAGACCAGAACAAGC  24983    C   ATATA
                                 GTG GTT    ACCAGAACAAGC
                                 ||| |||    ||||||||||||
                                 CGC CGA    TGGTCTTGTTCG
                                  _   CTC__
GAM1577 MYLK     5' GTGCGTTAATGTGACTAAACAA 38166        TATAACCA
             G                   GTGCGTTA       GAACAAG
                                 ||||||||       |||||||
                                 CACGCAAT       TTTGTTC
                                      TACACTGA
GAM1578 CCR2     3' GAAAGTTCTGCTCTGTCCCCAC 8496         CACCACA_
             TT                   GAAAGTTCT       CCCACTT
                                  |||||||||       |||||||
                                  CTTTCAAGA       GGGTGAA
                                       CGAGACAG
GAM1578 PDE4A    3' GAAGGAGGCCCCACACCTGCTT 26254    AGTTC  A      CA
                                 GAA    TC CCACACC  CTT
                                 |||    || |||||||  |||
                                 CTT    GG GGTGTGG  GAA
                                   CCTCC  _      AC
GAM1578 TRPC5    3' CGAAAGTTCCTCATTTCTCTTA 29767         _   CCACACCC
             CTT                  CGAAAGTTC TCA       ACTT
                                  ||||||||| |||       ||||
                                  GCTTTCAAG AGT       TGAA
                                       G   AAAGAGAA
GAM1578 USP6     3' GAAAGTTCTCTATCAGACAGCT 45031         ACCA  CC  _
             T                    GAAAGTTCTC    CA  CA CTT
                                  ||||||||||    ||  || |||
                                  CTTTCAAGAG    GT  GT GAA
                                       ATA_  CT  C
GAM1578 ZNF200   5' GCAACCACACACCACACTC   18372    TC    C    _
                                 GT  TCAC ACACC CACTT
                                 ||  |||| ||||| |||||
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                              CG  GGTG TGTGG GTGAG
                               TT   _    T
GAM1578 ADRA2B   3' CCCAGCTCCCCACCACA    8647     GAA     _
                              CCC   AGTTCTC ACCACA
                              |||   ||||||| ||||||
                              GGG   TCGAGGG TGGTGT
                                ___      G
GAM1578 CALCB    5' ACCCGGGATGAACACCACACC  44710      AAAGTTCT
                              ACCCG       CACCACACC
                              |||||       |||||||||
                              TGGGC       GTGGTGTGG
                                 CCTACTT_
GAM1578 ESRRB    5' CCTCAAAGTTCTGGACACC   42629    CG      ___
                              CC  AAAGTTCT   CACC
                              ||  ||||||||   ||||
                              GG  TTTCAAGA   GTGG
                               AG       CCT
GAM1578 GYS1     3' ACCTGAAAGCACCATC     44782     C    TTCT    CA
                              ACC GAAAG    CACCA  C
                              ||| |||||    |||||  |
                              TGG CTTTC    GTGGT  G
                               A    _____     AC
GAM1578 KCNAB1   3' CCTGAAGGTAGTACCACACC   41400    C   A  TCTC
                              CC GAA GT    ACCACACC
                              || ||| ||    ||||||||
                              GG CTT CA    TGGTGTGG
                               A   C  TCA_
GAM1578 MUC4     3' TAACTTAGGGCCATCACCACA  32905     CCGAAA  TC
                              TAAC     GT  TCACCACA
                              ||||     ||  ||||||||
                              ATTG     CG  AGTGGTGT
                                AATCC_  GT
GAM1578 TEM8     3' GAGTTTCTTACCACACC     38182    AAG    C
                              GA   TTCT ACCACACC
                              ||   |||| ||||||||
                              CT   AAGA TGGTGTGG
                               CA_    A
GAM1578 TPD52L2  3' CAACCTGCCTTCTCACCACACC 17633      CGAAAG
                              TAACC     TTCTCACCACACC
                              |||||     ||||||||||||
                              GTTGG     AAGAGTGGTGTGG
                                 ACGG__
GAM1578 ZFP93    3' TAACTGAAGGCTGAACCACACC 20146     CC   A   CTC
                              TAAC  GAA GTT   ACCACACC
                              ||||  ||| |||   ||||||||
                              ATTG  CTT CGA   TGGTGTGG
                                A_   C   CT_
GAM1579 FLRT2    3' TGATTTGTGTGAAATGAC    29862     CCG       C
                              TGA   TGTGTGAAA GAC
                              |||   ||||||||| |||
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                                ACT   ACACACTTT CTG
                                  AA_        A
GAM1579  ZNF236   3'  GCAATGGAACGGCCGCT     28861     T   A    A
                                GTG GTG AACG CCGCT
                                ||| ||| |||| |||||
                                CGT TAC TTGC GGCGA
                                  _   C    C
GAM1580  CDC23    3'  TCTGTATAATCACCAATGTTA  21669         ACTG   __
                                TCTGTATAA    CACC  TGTTA
                                |||||||||    ||||  |||||
                                AGACATATT    GTGG  ACAAT
                                     A___    TT
GAM1580  CUL3     3'  TCTGTATCATTACCTGTTA    18747        AAACTGC
                                TCTGTAT      ACCTGTTA
                                |||||||      ||||||||
                                AGACATA      TGGACAAT
                                    GTAA___
GAM1580  FLT4     3'  TCTGGGAAGGCACCTGTTA    12919      TATAAACT
                                TCTG       GCACCTGTTA
                                ||||       ||||||||||
                                AGAC       CGTGGACAAT
                                  CCTTC___
GAM1580  PTGS1    3'  CTGTGTCCCCACACCTGTTA   38735      ATAAA TG
                                CTGT    C  CACCTGTTA
                                ||||    |  |||||||||
                                GACA    G  GTGGACAAT
                                  CAGG_ GT
GAM1580  SLC7A6   3'  TATCTGTAAGAGCTGCATCTA  19595         TAAA    C
                                TATCTGTA    CTGCA CTG
                                ||||||||    ||||| |||
                                ATAGACAT    GACGT GAT
                                     TCTC    A
GAM1580  BASP1    3'  GGAGTGCATGTGGCGGCAGTTT 44013    A        AAAT  A  _
                                A AGTGCATGT    CG GT GTTT
                                | |||||||||    || || ||||
                                C TCACGTACA    GC CG CAAA
                                 C        CC__  _  T
GAM1580  DISC1    3'  AAAGTGATGTAAATCAGAGT   33022        C        _
                                AAAGTG ATGTAAATC GAGT
                                |||||| ||||||||| ||||
                                TTTCAC TACATTTAG CTCA
                                   _         T
GAM1580  DNCI1    3'  GGAGTGCATGTAAGCACAAAT  44990    A         AT_
                                A AGTGCATGTAA   CGAGT
                                | ||||||||||   |||||
                                C TCACGTACATT   GTTTA
                                 C          CGT
GAM1580  ETF1     3'  AAGTGCTTGTAAGTCCCACATT 21828        A     A  GA TG
           T                     AAGTGC TGTAA TC  G  TTT
                                ||||||  ||||| ||  |  |||
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                                TTCACG ACATT AG  T  AAA
                                   A    C  GG GT
GAM1580  SLC6A12   3'  GGAGGCATGCCGAGTGTT    16801   A  T    AAAT
                                A AG GCATGT   CGAGTGTT
                                | || ||||||   ||||||||
                                C TC CGTACG   GCTCACAA
                                 C  _    _____
GAM1581  BLAME     3'  TGTGGAGGGAGAGCTGCAGG  33502       TA    CC
                                TGTGGAGG  AGAGCT  CGGG
                                ||||||||  ||||||  ||||
                                ACACCTCC  TCTCGA  GTCC
                                     C_    C_
GAM1581  CBFA2T2   3'  TGTGGAGGGGGAGGAGGGG   22982       TAA   CTCCC
                                TGTGGAGG   GAG    GGGG
                                ||||||||   |||    ||||
                                ACACCTCC   CTC    CCCC
                                     CC_   CT___
GAM1581  CENTD2    5'  TGGAGGTATCTCCGGGG    31607       AGAGC  _
                                TGGAGGTA    TC CCGGGG
                                ||||||||    || ||||||
                                ACCTCCAT    AG GGCCCC
                                     _____  A
GAM1581  FGD1      3'  TGTGGGGTGGGGGCTCCCAG  20915      A   AAGA
                                TGTGG GGT   GCTCCCGG
                                ||||| |||   ||||||||
                                ACACC CCA   CGAGGGTC
                                   _  CCCC
GAM1581  FKBP10    3'  TGTGGAGGGGAGGTATGGTGGG 34961       TA  AGCTCCC
            GG                   TGTGGAGG  AG     GGGGG
                                ||||||||  ||      |||||
                                ACACCTCC  TC      CCCCC
                                     CC  CATACCA
GAM1581  GAS11     3'  TGTGGAGGTGAGAGCCCCAG   11225        A    T
                                TGTGGAGGT AGAGC CCCGG
                                ||||||||| ||||| |||||
                                ACACCTCCA TCTCG GGGTC
                                     C    _
GAM1581  GDI1      3'  GTGGGGGTAAGAGCGGTGGGGG 41017      A       TCCC
                                GTGG GGTAAGAGC   GGGGG
                                |||| |||||||||   |||||
                                CACC CCATTCTCG   CCCCC
                                   C       CCA_
GAM1581  IHPK1     3'  TGTGGAGGAAGGGCATGGGG   45499       T  A  TCCC
                                TGTGGAGG AAG GC   GGGG
                                |||||||| ||| ||   ||||
                                ACACCTCC TTC CG   CCCC
                                     _  C  TA__
GAM1581  OBP2A     3'  TGGAGGTGCAGACCCGGGGG   31043       A_  GCT
                                TGGAGGT  AGA  CCCGGGGG
                                |||||||  |||  ||||||||
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                                ACCTCCA  TCT   GGGCCCCC
                                   CG  ___
GAM1581  OBP2B    3'  TGGAGGTGCAGACCCGGGGG  31038       A_  GCT
                                TGGAGGT  AGA   CCCGGGGG
                                |||||||  |||   ||||||||
                                ACCTCCA  TCT   GGGCCCCC
                                   CG  ___
GAM1581  SLC38A3  3'  TGGGGTCTTTGGCTCCCGGGGG 27762     A  AAGA_
                                TGG GGT    GCTCCCGGGGG
                                ||| |||    ||||||||||
                                ACC CCA    CGAGGGCCCCC
                                  _  GAAAC
GAM1581  ATRX     3'  TCATACTTGAATGCTTTTCT  39611        ATC   CTC
                                TCATACTT   TGCT   TTCT
                                ||||||||   ||||   ||||
                                AGTATGAA   ACGA   AAGA
                                     CTT   A__
GAM1581  FEN1     3'  TTATCTCCCTCTCTCTTCT   19961       G___
                                TTATCT   CTCTCTTCT
                                ||||||   |||||||||
                                AATAGA   GAGAGAAGA
                                   GGGA
GAM1581  HLA-G    3'  CTTCATACTTACTTGCAGCCT  13400         TC  TC
                                CTTCATACTTA  TGC  TCT
                                ||||||||||  |||  |||
                                GAAGTATGAAT  ACG  GGA
                                      GA   TC
GAM1581  MAF      5'  CTTCATGCTTCTCGCCTCCTCT 23829       A  A  T  T
                                CTTCAT CTT TC GC CTCTTCT
                                |||||| ||| || || |||||||
                                GAAGTA GAA AG CG GAGGAGA
                                   C  G  _  _
GAM1581  PRKAR2B  3'  CTTCATGTAGAGAGCTCTCTT  15619       ACTTATCT
                                CTTCAT      GCTCTCTT
                                ||||||      ||||||||
                                GAAGTA      CGAGAGAA
                                   CATCTCT_
GAM1581  RAB5B    3'  CTCCATACTTGTTTGCTGCT   16092         AT___
                                CTTCATACTT    CTGCT
                                ||||||||||    |||||
                                GAGGTATGAA    GACGA
                                      CAAAC
GAM1581  SLC1A3   3'  CTTCATACTGATTCATCTTCT  20042         T  CTGC  _
                                CTTCATACT AT   TC TCTTCT
                                ||||||||| ||   || ||||||
                                GAAGTATGA TA   AG AGAAGA
                                      C  ____  T
GAM1581  UGDH     3'  CTTTATATTTGTCTCCCTCTTC 17882     C  C  A  G
            T                    CTT ATA TT TCT CTCTCTTCT
                                ||| ||| || ||| |||||||||
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                                GAA TAT AA AGA GGGAGAAGA
                                  A  A C  _
GAM1582 INPPL1   3' GTCCCGGGCTGAGACCTGCGAG 11466      AAACCC AT
                                GTTCC    GA CCTGCGAG
                                |||||    ||  ||||||||
                                CAGGG    CT GGACGCTC
                                   CCCGA_ CT
GAM1583 IRS2     5' CTCGGCGGCGCCGCGCCC   40703     ACA A      G
                                TTCG  GC GCGCCGCGC CC
                                ||||  || |||||||| ||
                                GAGC  CG CGCGGCGCG GG
                                  ___ C      _
GAM1583 SLC30A4  5' CTCGAGGGCAGTGCCGCGCGTC 30015      CA  C      _
            CC                    TTCGA GCAG GCCGCGCG CCC
                                |||||  |||| |||||||| |||
                                GAGCT CGTC CGGCGCGC GGG
                                   CC  A      A
GAM1583 TERF2    5' TCCGATCGCCGCGCGCCC   24915     CAGCAG
                                TTCGA    CGCCGCGCGCCC
                                |||||    ||||||||||||
                                AGGCT    GCGGCGCGCGGG
                                   A_____
GAM1583 JUNB     5' GCTGCAGCGAGCGGCGAGCTCT 13756    C  TC T  CAA_
                                GCT GC  G CGA   CGAGCTCT
                                ||| ||  | |||   ||||||||
                                CGA CG  C GCT   GCTCGAGA
                                  _ T_ _  CGCC
GAM1583 RAB33A   5' CGCTCGAGGCGAGCGAGCTCT 21998      T__  CAA
                                CGCTCG  CGA  CGAGCTCT
                                ||||||  |||  ||||||||
                                GCGAGC  GCT  GCTCGAGA
                                   TCC  C__
GAM1583 SURF4    5' GCTCGCTCGCTCGCTGGCTCT 37654       _  ACAACGA
                                GCTCGCTCG TCG     GCTCT
                                ||||||||| |||     |||||
                                CGAGCGAGC AGC     CGAGA
                                     G  GAC____
GAM1584 ARCN1    3' ATCATGCCATTGCATTCCAGC 11648       CA A_
                                ATCATGCCAT CG TCAGC
                                ||||||||||  ||  |||||
                                TAGTACGGTA GT GGTCG
                                      AC AA
GAM1584 DMXL1    5' TCATGCCACGGGTCAGCGGC  24291       CACGA   A
                                TCATGCCAT   TCAGC GC
                                |||||||||   ||||| ||
                                AGTACGGTG   AGTCG CG
                                     CCC__   C
GAM1584 ESR1     3' CATCATGCATCACCACAG   6527        C   G T
                                CATCATGC ATCAC A CAG
                                |||||||| ||||| | |||
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                                GTAGTACG TAGTG T GTC
                                   _    G _
GAM1584  GNAI3    3'  ATCATACTACATCAGCAG    27097        CATC  G
                                ATCATGC    AC ATCAGCAG
                                |||||||    || ||||||||
                                TAGTATG    TG TAGTCGTC
                                   A____  _
GAM1584  LGR6     5'  GCCAGCGAACACGGTCAGCAGC 44480      T_____    A
                                GCCA     CACG TCAGCAGC
                                ||||     |||| ||||||||
                                CGGT     GTGC AGTCGTCG
                                  CGCTT    C
GAM1584  RUNX1    3'  CATGTGTCAAAATCAGCAG   12014      CCA   C
                                CATG   TCA GATCAGCAG
                                ||||   ||| |||||||||
                                GTAC   AGT TTAGTCGTC
                                  AC_   T
GAM1584  SAS      3'  ATCATGCCATTGCACTCCAGC  25585          __   GA
                                ATCATGCCAT  CAC  TCAGC
                                ||||||||||  |||  |||||
                                TAGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1584  ZFP161   3'  CATCATCCTGGGTGTCAGCAGC 40840        G  ATCACGA
                                CATCAT CC      TCAGCAGC
                                |||||| ||      ||||||||
                                GTAGTA GG      AGTCGTCG
                                   _ ACCCAC_
GAM1584  ZNF157   3'  TCATGCCATTGCACTCCAGC   18354          __   GA
                                TCATGCCAT  CAC  TCAGC
                                |||||||||  |||  |||||
                                AGTACGGTA  GTG  GGTCG
                                     AC   A_
GAM1584  ZNF36    3'  CATCATACTGTTCAGCAG    45290         CATCACGA
                                CATCATGC       TCAGCAG
                                ||||||||       |||||||
                                GTAGTATG       AGTCGTC
                                     ACA_____
GAM1584  KDR      3'  GTCAGCTCCCCAGGTACTGCTA 13942      A    ATTCCG
              C                  GTCA TTCC      ACTGCTAC
                                 |||| ||||     ||||||||
                                 CAGT GAGG     TGACGATG
                                   C    GGTCCA
GAM1584  M6PR     3'  GTTGATTCCATCCCTCT     14306    CA        GA
                                GT  ATTCCATTCC  CT
                                ||  ||||||||||  ||
                                CA  TAAGGTAGGG  GA
                                 AC         A_
GAM1584  NR5A2    3'  CGTCAATTTTGTTTCCAACTAC 19236         CCA_
                                CGTCAATT    TTCCGACTGC
                                ||||||||    ||||||||||
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                                GCAGTTAA   AAGGTTGATG
                                    AACA
GAM1584 PCDHA9   5' CGTCAGTCCCATTCTGCT   36543     A      CGAC
                                CGTCA TTCCATTC   TGCT
                                ||||| ||||||||   ||||
                                GCAGT AGGGTAAG   ACGA
                                   C      ____
GAM1584 PPP1R12A 3' GCAATTCCATTACTTGCTGC  14727   T       CCGA_
                                G CAATTCCATT    CTGC
                                | ||||||||||    ||||
                                C GTTAAGGTAA    GACG
                                _       TGAAC
GAM1584 SIAT8E   3' TCAATTCCATTCTCTG     40839          CGA
                                TCAATTCCATTC   CTG
                                ||||||||||||   |||
                                AGTTAAGGTAAG   GAC
                                      A__
GAM1585 COG7     3' CACGATGTGCTGGA       42656       ATACTA
                                TACGAT     GTGTTGGA
                                ||||||     ||||||||
                                GTGCTA     CACGACCT
                                  _______
GAM1585 ATP11B   3' CCCTGGCCCATACTTTGC    44307         G___
                                CCCTGGCCCA   TTGT
                                ||||||||||   ||||
                                GGGACCGGGT   AACG
                                     ATGA
GAM1585 ATP8B2   5' CCTGGCCCAGCTCCTCG     42205         TGTA
                                CCTGGCCCAGT   TTCG
                                ||||||||||   ||||
                                GGACCGGGTCG   GAGC
                                      AG__
GAM1585 BUB1B    5' CCTGGCTCAGGTCCTCG     10227       C  TT  A
                                CCTGGC CAG  GT TTCG
                                |||||| |||  || ||||
                                GGACCG GTC  CA GAGC
                                   A  __ G
GAM1585 CYBB     3' CTGGCCCAGTTACCCTGC    44094         TA  C
                                CTGGCCCAGTTG  TT GC
                                ||||||||||||  || ||
                                GACCGGGTCAAT  GA CG
                                      GG  _
GAM1585 E2F3     3' CACCCTGGCATTGTTTTGC   12628        CCA    A  C
                                CACCCTGGC   GTTGT TT GC
                                |||||||||   ||||| || ||
                                GTGGGACCG   TAACA AA CG
                                     ___    A  _
GAM1585 EGLN2    5' CCTGGCCCAGGGCCGTTTGC  38820         TT  ATTC_
                                CCTGGCCCAG  GT    GC
                                ||||||||||  ||    ||
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                                GGACCGGGTC  CG    CG
                                     C_  GCAAA
GAM1585  GALNT7   5'  CCTGGTCCTGACATTTGCC   38356      C  AGT  _   C
                                CCTGG CC   TG TATT GCC
                                ||||| ||   || |||| |||
                                GGACC GG   AC GTAA CGG
                                   A  ___  T   A
GAM1585  GPR56    3'  CCCTGGGCCCCATTCGC     24997       _  AGTTG
                                CCCTGG CCC    TATTCGC
                                |||||| |||    |||||||
                                GGGACC GGG    GTAAGCG
                                   C  _____
GAM1585  HNRPD    5'  CCCTGGCCTGCCCCCTTCGCC  36389        CA   GTA
                                CCCTGGCC  GTT   TTCGCC
                                ||||||||  |||   ||||||
                                GGGACCGG  CGG   AAGCGG
                                     A_   GGG
GAM1585  IL17R    3'  CCCGGCCCATCCTGTTCG    30739        G_   AT
                                CCTGGCCCA  TTGT  TCG
                                |||||||||  ||||  |||
                                GGGCCGGGT  GACA  AGC
                                     AG   __
GAM1585  LASS1    3'  CCCTGGCCCGCTTGCGC     34595        A  GTATT
                                CCCTGGCCC GTT    CGC
                                |||||||||  |||    |||
                                GGGACCGGG CGA    GCG
                                     _  AC___
GAM1585  PPT2     5'  CAGCCTGGCCCAGTTTCTCCTG 23121    C         GTA  _
            CC                    CA CCTGGCCCAGTT   TTC GCC
                                || ||||||||||||   ||| |||
                                GT GGACCGGGTCAA   AGG CGG
                                 C          AG_  A
GAM1585  ZNF22    5'  CACTCTGGCTCGCTGGGCGCC  45046    C    CCA    TATT
                                CAC CTGGC   GTTG    CGCC
                                ||| |||||   ||||    ||||
                                GTG GACCG   CGAC    GCGG
                                  A    AG_    CC__
GAM1586  TFAP2C   3'  ATTGTTGATCTGTTGATC    17402      GG   C    C
                                GTTG  TGA TCTGT GATC
                                ||||  ||| ||||| ||||
                                TAAC  ACT AGACA CTAG
                                  A_  _    A
GAM1586  AUP1     3'  ACCACCCACCCATCCAGCC    29041     G      TCCC   A
                                ACC ACCCACCT    CCA CC
                                ||| ||||||||    ||| ||
                                TGG TGGGTGGG    GGT GG
                                  _       TA__   C
GAM1586  CD3Z     3'  CCGCCCACCTTCCCATGCCCC  8819      A         CCAA
                                CCG CCCACCTTCCC    CCC
                                ||| ||||||||||    |||
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                                GGC GGGTGGAAGGG   GGG
                                  _        TACG
GAM1586 CKMT2    5' CCTGGTTCCTCCCCAACCC   12265   GACCCA  TC
                                CC     CCT  CCCCAACCC
                                ||     |||  |||||||||
                                GG     GGA  GGGGTTGGG
                                 ACCAA_  __
GAM1586 CLK2     5' CCACCCCCCCAACCCG      41276      TT
                                CCACC  CCCCCAACCCG
                                |||||  ||||||||||
                                GGTGG  GGGGGTTGGGC
                                   __
GAM1586 DHCR7    5' CGCCCACCTTCCCCTGGCC   10685   A         CAA
                                CG CCCACCTTCCCC   CC
                                || ||||||||||||   ||
                                GC GGGTGGAAGGGG   GG
                                 _         ACC
GAM1586 DIRC1    3' ACCAGGCCCCTCCTCCAA    38124     ACCCA    C
                                ACCG    CCTTCC CCAA
                                ||||    |||||| ||||
                                TGGT    GGGAGG GGTT
                                  CCG__     A
GAM1586 E2F2     5' CCGGACCCTCCCCTCCTGGCCC 19870    _   A_    CCCAA
           G                     CCG ACCC  CCTTCC    CCCG
                                ||| ||||  ||||||    ||||
                                GGC TGGG  GGGAGG    GGGC
                                  C   AG     ACC__
GAM1586 HIS1     5' CCGACTTTCCCTCCCAACC   26991      CCACC   _
                                CCGAC    TTCC CCCAACC
                                |||||    |||| |||||||
                                GGCTG    AGGG GGGTTGG
                                   AA___    A
GAM1586 M17S2    3' CCGCTCCACCTTCTACCC    36588    AC      CCCCA
                                CCG  CCACCTTC    ACCC
                                |||  ||||||||    ||||
                                GGC  GGTGGAAG    TGGG
                                  GA       A____
GAM1586 NTRK2    5' ACCGGCCGCTTTCCCCCACCCG 26140     A  CACC      A
                                ACCG CC    TTCCCCCA CCCG
                                |||| ||    |||||||| ||||
                                TGGC GG    AAGGGGGT GGGC
                                  C  CGA_       _
GAM1586 PRX      3' CGGCCCCCTCCTTGGCCCG   34115    A  A    CCCCAA
                                CG CCC CCTTC     CCCG
                                || ||| |||||     ||||
                                GC GGG GGAGG     GGGC
                                 C   _    AACC__
GAM1586 ROM1     3' CGATCCCCCCCAACC       7261      CCCACC
                                CGA     TTCCCCCAACC
                                |||     ||||||||||
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                                GCT     AGGGGGGTTGG
                                  _______
GAM1586  SDHC     3'  ACCAACCCACCCCCCAACCCG  42973          TTC
                                ACCGACCCACC   CCCCAACCCG
                                ||||||||||   ||||||||||
                                TGGTTGGGTGG   GGGGTTGGGC
                                     ___
GAM1586  TGM3     3'  GACCCAGCCCCAACC       17504       CCTTC
                                GACCCA    CCCCAACC
                                ||||||    ||||||||
                                CTGGGT    GGGGTTGG
                                   C_____
GAM1586  ZIC1     5'  CGACCCACCTCGCGAAGTCCTA 18234          ________  C__
              GCC                  CGACCCACCT      TCC   CC
                                ||||||||||      |||   ||
                                GCTGGGTGGA      AGG   GG
                                      GCGCTTC   ATC
GAM1587  BAK1     3'  TCTACACCCCTGGATTACACTG 45110         A  AAT
                                TCTGCACC CC   GATTACACTG
                                ||||||||  ||   ||||||||||
                                AGATGTGG GG   CTAATGTGAC
                                     _  AC_
GAM1587  MTR      3'  TCTGCACCATGACAC       7019          CCAA   TTA
                                TCTGCACCA    TGA   CAC
                                |||||||||    |||   |||
                                AGACGTGGT    ACT   GTG
                                     _____  ___
GAM1587  NBS1     3'  TCTGCACCACTGAAGCCA    42988         CAA   TTA
                                TCTGCACCAC   TGA   CA
                                ||||||||||   |||   ||
                                AGACGTGGTG   ACT   GT
                                     ____   TCG
GAM1587  TNFSF8   3'  TCTGCCCACCACACTACA    10331       A     ATG
                                TCTGC CCACCA   ATTACA
                                |||||  ||||||   ||||||
                                AGACG GGTGGT   TGATGT
                                   _     G__
GAM1587  APXL     3'  GCCTGCTTGGTGCGTGACTG   11621     C       ___
                                GTC GCTTGGTGC   ACTG
                                |||  |||||||||   ||||
                                CGG CGAACCACG   TGAC
                                  A        CAC
GAM1587  HK1      3'  GTCTGCTGGTGATAATACATTT 37919     C   T    CACTGA
                                GTC GCT GGTG     ACATTT
                                |||  |||  ||||     ||||||
                                CAG CGA CCAC     TGTAAA
                                  A  _    TATTA_
GAM1587  ROBO1    3'  CTGATTGCACTGAACATTT    39483       _
                                TTGGT GCACTGAACATTT
                                |||||  ||||||||||||
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                                GACTA CGTGACTTGTAAA
                                   A
GAM1588 DACH    3' GTTGTTGTCAACATCCA    38877   CA      C
                                GT  TTGTCGGCA TCCA
                                ||  ||||||||| ||||
                                CA  AACAGTTGT AGGT
                                 AC       _
GAM1588 FLRT2   3' GCCATTTCTTGTTTTACCCAT  29850      G  GGCACTCC
                                GTCATT TC       ACCCAT
                                |||||| ||       ||||||
                                CGGTAA AG       TGGGTA
                                   _ AACAAAA_
GAM1588 P4HA1   3' GTCATTGTTGTCACAACAC   9539        CGG   TC
                                GTCATTGT   CAC  CAC
                                ||||||||   |||  |||
                                CAGTAACA   GTG  GTG
                                     ACA   TT
GAM1588 ROCK2   3' AATCATTGTTGGTTCAACC   42348        C  CAC  C
                                AGTCATTGT GG   TC ACC
                                ||||||||| ||   || |||
                                TTAGTAACA CC   AG TGG
                                     A  A__  T
GAM1588 TLR1    3' AGTCATTGTTGGAACTTCC   17557        C  C  _
                                AGTCATTGT GG ACT CC
                                ||||||||| || ||| ||
                                TCAGTAACA CC TGA GG
                                     A  T   A
GAM1588 B4GALT4 5' CCTGCCTCTTCCTTC      19098       A  AAAGACC
                                CCTGCC TC      TCCTTC
                                |||||| ||      ||||||
                                GGACGG AG      AGGAAG
                                   _ A_______
GAM1588 COL9A3  3' CCTGCCACACCCCCGCTCCTTC 12344        CAAAGAC
             AT                   CCTGCCAT      CTCCTTCAT
                                |||||||      |||||||||
                                GGACGGTG      GAGGAAGTA
                                     TGGGGGC
GAM1588 EDAR    3' CCTGCCATCAGGGAGTTC    35303         AA  CC
                                CCTGCCATCA  GA  TC
                                ||||||||||  ||  ||
                                GGACGGTAGT  CT  AG
                                      CC  CA
GAM1588 GALNS   3' CCTGTTGTCAGGACCTCCT   8009      CCA   AA
                                CCTG   TCA  GACCTCCT
                                ||||   |||  ||||||||
                                GGAC   AGT  CTGGAGGA
                                  AAC   C_
GAM1588 HKE4    3' CCTTCCAGCCTTCTTC      28093     G   TCAAA A   C
                                CCT CCA     G CCT CTTC
                                ||| |||     | ||| ||||
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                                GGA GGT    C GGA GAAG
                                  A  _____ _  A
GAM1588 IREB2    3' CCTGCCATGGTCCATCTTCAT 42453       CAAAGA TC
                                CCTGCCAT    CC CTTCAT
                                ||||||||    || ||||||
                                GGACGGTA    GG GAAGTA
                                    CCA___ TA
GAM1588 MFAP4    3' TGCCATCAAAATGAGGCCT  42911         ACCT_
                                TGCCATCAAAG    CCT
                                ||||||||||    |||
                                ACGGTAGTTTT    GGA
                                      ACTCC
GAM1588 OAS2     3' CCTGCCATCTGGAGGCACC  32549       AA_ __
                                CCTGCCATC  AG ACC
                                |||||||||  ||  |||
                                GGACGGTAG  TC TGG
                                     ACC CG
GAM1588 SFTPA2   3' CCTGCCACAGAGACCTC    27963       T A
                                CCTGCCA CA AGACCTC
                                ||||||| || |||||||
                                GGACGGT GT TCTGGAG
                                   _ C
GAM1588 SLIT3    3' CCAGCTTCATTTCCTTCAT  16865   T CA  AAGACC
                                CC GC  TCA    TCCTTCAT
                                || ||  |||    ||||||||
                                GG CG  AGT    AGGAAGTA
                                 T A_  AA____
GAM1588 TAF11    3' CCTGCCATTACCGCATCCTTCA 24864       CAAAG ___
            T                    CCTGCCAT   ACC  TCCTTCAT
                                ||||||||   |||  ||||||||
                                GGACGGTA   TGG  AGGAAGTA
                                    A____  CGT
GAM1588 TEC      5' CCTGCCACTGAAGATCCC   17385       CA  CC
                                CCTGCCAT AAGA TCCT
                                |||||||| |||| ||||
                                GGACGGTG TTCT AGGG
                                    AC  __
GAM1589 JJAZ1    3' ATATATGAAATAATTTCTAGA 31685      AA
                                GTATAT GGATAGTTTCTAGA
                                |||||| ||||||||||||||
                                TATATA TTTATTAAAGATCT
                                   C_
GAM1589 PCM1     3' AGTATGTAAGGACAGAGTTAGA 26224     A      TTTC
                                AGTAT TAAGGATAG   TAGA
                                ||||| |||||||||   ||||
                                TCATA ATTCCTGTC   ATCT
                                  C       TCA_
GAM1589 TGFBR2   5' TAGTATACAAGTATAATTT  17476         G
                                TAGTATATAAG ATAGTTT
                                |||||||||| |||||||
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                                ATCATATGTTC TATTAAA
                                      A
GAM1589 UBL3    3' ATATATAAGTATTTCTAG    28264        GATA
                                GTATATAAG   GTTTCTAG
                                |||||||||   ||||||||
                                TATATATTC   TAAAGATC
                                     A___
GAM1590 FLRT2   3' AGGGAGATTAAAACATATAAGT 29837       CATCT  TG
                                AGGGAGA    AG  ATATAAGT
                                |||||||    ||  ||||||||
                                TCCCTCT    TT  TATATTCA
                                    AAT__  TG
GAM1591 MCP     3' TATGGCTGTCAGAGTCC     14386       GC    AT
                                TATGGC  GTCG  GGTCC
                                ||||||  ||||  |||||
                                ATACCG  CAGT  TCAGG
                                   A_   C_
GAM1591 SOX12   3' CACTGGCCAAGTCGATGGTCTC 28030     AT   GC_       C
             T                   CACT  GGC   GTCGATGGTC CT
                                 ||||  |||   |||||||||| ||
                                 GTGA  CCG   CAGCTACCAG GA
                                   __  GTT        A
GAM1591 XYLB    3' CACTTGGGAGATGGTCCC    23020     A   CGCGTC
                                CACT TGG     GATGGTCCC
                                |||| |||     |||||||||
                                GTGA ACC     CTACCAGGG
                                  _  CT_____
GAM1591 MYBPH   3' TCGCTATGGAAGCGGGGGTC  22650       AC_   TCGA
                                TCGCTATG   GCG    GGGTC
                                ||||||||   |||    |||||
                                AGCGATAC   CGC    CCCAG
                                     CTT   C___
GAM1592 DRG2    3' GAAGGGCCCCCAACCCAA    10785     AA    G
                                GAAG  CCTC TGACCCAA
                                ||||  |||| ||||||||
                                CTTC  GGGG GTTGGGTT
                                  CC   _
GAM1592 LPIN1   3' GAAATGTGTGGTCCAAATAC  42637    CCTC   AC
                                GAA    GTG  CCAAATAC
                                |||    |||  ||||||||
                                CTT    CAC  GGTTTATG
                                  TACA   CA
GAM1592 MAPK14  3' GAAACACCTTGGCCCAAATAC 40012     A    CG  A
                                GAAG ACCT  TG CCCAAATAC
                                |||| ||||  || |||||||||
                                CTTT TGGA  AC GGGTTTATG
                                  G    __ C
GAM1592 NSF     3' AGACCTTTAACCAAATAC    41781     A  CG    C
                                AGA CCT  TGACC AAATAC
                                ||| |||  ||||| ||||||
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                                TCT GGA  ATTGG TTTATG
                                  _  A_    _
GAM1592 RET     3' TGAAGAACCAAAACTTCAA   33940        TCGT  C_
                                TGAAGAACC   GAC  CAA
                                |||||||||   |||  |||
                                ACTTCTTGG   TTG  GTT
                                     TT__   AA
GAM1592 SLC10A2  3' TGAAGAGCTCTTTGCCAAATAC 7820       AC  GTGAC
                                TGAAGA  CTC    CCAAATAC
                                ||||||  |||    ||||||||
                                ACTTCT  GAG    GGTTTATG
                                   C_   AAAC_
GAM1592 ZNF266   3' TGAAAACCCTATGTCCAAATAC 44780      A  CG  AC
                                TGAAGA CCT  TG  CCAAATAC
                                |||||| |||  ||  ||||||||
                                ACTTTT GGG  AC  GGTTTATG
                                   _   AT  A_
GAM1593 DAP     3' TGGCATTGCTGTTCCCTGCC  43692     CGA     ATA
                                TGGCA  CTGTTCCT  TGCT
                                |||||  ||||||||  ||||
                                ACCGT  GACAAGGG  ACGG
                                   AAC      ___
GAM1593 KIAA0442 3' TGTTACGGCTGTTCCCAGACT  31793   GC  A      TAT
                                TG  ACG CTGTTCCTA  GCT
                                ||  ||| |||||||||  |||
                                AC  TGC GACAAGGGT  TGA
                                 AA  C       C__
GAM1593 RPS6KA6  3' TGGTGGACACCAATTATATGCT 30940    CAC  TGTTCC
                                TGG  GAC    TATATGCT
                                |||  |||    ||||||||
                                ACC  CTG    ATATACGA
                                  AC_  TGGTTA
GAM1593 SIX1    5' GGCGCGGCTGTTCCTAACCTC  25596    A  A      TATG
                                GGC CG CTGTTCCTA   CTC
                                ||| || |||||||||   |||
                                CCG GC GACAAGGAT   GAG
                                  C  C       TG__
GAM1593 CHC1    3' TGGTGTCTCTTTGCGATT    10429    CA     TACA
                                TGG  TCTCTTT   GTGGTT
                                |||  |||||||   ||||||
                                ACC  AGAGAAA   CGCTAA
                                  AC     _____
GAM1593 GCH1    3' TGGTTATCTGGCAGTGGTT   6708     C_   CTTTTA
                                TGG  ATCT    CAGTGGTT
                                |||  ||||    ||||||||
                                ACC  TAGA    GTCACCAA
                                  AA   CC____
GAM1593 GPR62   3' AGTGTCTCTCCAGTGGTTCT  44870   CA    TTA
                                GG  TCTCTT   CAGTGGTTCT
                                ||  ||||||   ||||||||||
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                                TC  AGAGAG   GTCACCAAGA
                                 AC     ___
GAM1593  HYAL1    3'  TGGTGTCTGCTGTGGTTC    37646     CA  _  TTTACA
                                TGG  TCT CT     GTGGTTC
                                |||  ||| ||     |||||||
                                ACC  AGA GA     CACCAAG
                                  AC   C  _______
GAM1593  IL11     3'  TGGGATCACAGCATGCAGTGGT 8482      C   TCTTTTA_
              T                  TGG ATC       CAGTGGTT
                                 |||  |||       ||||||||
                                 ACC TAG       GTCACCAA
                                   C   TGTCGTAC
GAM1593  LIG4     5'  TGACATCTTTGTGGTT      14166         CTTTTACA
                                 TGGCATCT       GTGGTT
                                 ||||||||       ||||||
                                 ACTGTAGA       CACCAA
                                      AA_______
GAM1593  OLFM1    3'  TGGTATCTTTTTGGCAGCAGTT 26786     C    C   TA   TG
                                 TGG ATCT TTT  CAG  GTT
                                 |||  |||| |||  |||  |||
                                 ACC TAGA AAA  GTC  CAA
                                   A    A   CC   GT
GAM1593  OTOA     5'  TGGCATCTCTCTTGTAGTT    40344            ACA
                                 TGGCATCTCTTTT   GTGGTT
                                 ||||||||||||   ||||||
                                 ACCGTAGAGAGAA   CATCAA
                                                ___
GAM1593  PAK4     3'  TGGTTCTTCAGGCAGTGGTTCT 25255     CATC     TA_
                                 TGG    TCTTT   CAGTGGTTCT
                                 |||    |||||   ||||||||||
                                 ACC    AGAAG   GTCACCAAGA
                                   A___     TCC
GAM1593  RGS16    3'  GGCATCTCTTTTTGCCTGTTCT 16324           ACA  G_
                                 GGCATCTCTTTT   GT  GTTCT
                                 ||||||||||||   ||  |||||
                                 CCGTAGAGAAAA   CG  CAAGA
                                        A__  GA
GAM1593  SLC10A2  5'  TGGTGTCTCTTTTGAAAGC   7821      CA       AC_
                                 TGG  TCTCTTTT   AGT
                                 |||  ||||||||   |||
                                 ACC  AGAGAAAA   TCG
                                   AC       CTT
GAM1594  AQP6     3'  AAGCAGAGTGGCTGTCTG    38234       A       AAT
                                 AAGCA GAGTGGCT   GTCTG
                                 |||||  ||||||||   |||||
                                 TTCGT CTCACCGA   CAGAC
                                    _      ___
GAM1594  ARF4L    3'  TGAGTGAGAGTGGCGGCTG   43073    A  CA       TAAT T
                                 C AG  AGAGTGGC    G CTG
                                 | ||  ||||||||    | |||
```

```
                                A TC  TCTCACCG    C GAC
                                 C  AC       C___ _
GAM1594  CALM1    5'  GGAGCGAGGGTGGCTGCACCAG 27860    A   A  A     AA GT T
                C                 C AGC AG GTGGCT  T  C GC
                                | ||| || ||||||  |  | ||
                                C TCG TC CACCGA  G  G CG
                                 C   C  C     C_ TG T
GAM1594  CALU     3'  TGAGAAAGAGTAAAGAGCTAAT 10265    A  C     ____        C
                GTTTG                   C AG AAGAGT    GGCTAATGT TG
                                | || ||||||    |||||||||  ||
                                A TC TTCTCA    TCGATTACA AC
                                 C  T     TTTC        A
GAM1594  CDC23    3'  GCAAGATAATGTCTG       21667        GTGGC
                                GCAAGA     TAATGTCTG
                                ||||||     |||||||||
                                CGTTCT     ATTACAGAC
                                   _____
GAM1594  CDKN2B   3'  AGAGTGGCAGGGTCTGC     38538         TAAT
                                AGAGTGGC    GTCTGC
                                ||||||||    ||||||
                                TCTCACCG    CAGACG
                                     TCC_
GAM1594  DNMT3B   3'  AGCTAAGAGTGGCCCCTG    27867     _        AATG
                                AGC AAGAGTGGCT    TCTG
                                ||| ||||||||||    ||||
                                TCG TTCTCACCGG    GGAC
                                  A         ____
GAM1594  EXTL1    3'  CAGGCACGCAGTTAATGTCTGC 20864    A   AGA TG C
                                CA GCA   G  G TAATGTCTGC
                                || |||   |  | ||||||||||
                                GT CGT   C  C ATTACAGACG
                                 C   G__ GT A
GAM1594  GPLD1    3'  GAGTAAGCAGAATGTCTG    45114      _  T_
                                GAGTG GC  AATGTCTG
                                ||||| ||  ||||||||
                                CTCAT CG  TTACAGAC
                                   T  TC
GAM1594  PML      3'  CAAGCAGAGGTGTCT       37723        A   TGGCTAA
                                CAAGCA GAG       TGTCT
                                |||||| |||       |||||
                                GTTCGT CTC       ACAGA
                                   _   C_______
GAM1594  RFXAP    3'  CAAACAAGAAATGTCT      8051          GTGGCT
                                CAAGCAAGA     AATGTCT
                                |||||||||     |||||||
                                GTTTGTTCT     TTACAGA
                                     _______
GAM1594  RPL10    3'  CAAGGAGGGTGGTTAATCTGC  25668      CA  A    CTAAT
                                CAAG  AG GTGG    GTCTGC
                                ||||  || ||||    ||||||
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                                GTTC  TC CACC    TAGACG
                                  C_  C   AAT__
GAM1594  SECTM1   3'  CAAGCAAGCCGGTGTCTG    16535       AG   CTAA
                                CAAGCAAG  TGG   TGTCTG
                                ||||||||  |||   ||||||
                                GTTCGTTC  GCC   ACAGAC
                                    G_  _____
GAM1594  SOX12    3'  AGGTGAAGTGGCTCTCTG    28028    CAA      AATG
                                AG   GAGTGGCT   TCTG
                                ||   ||||||||   ||||
                                TC   TTCACCGA   AGAC
                                 CAC       G___
GAM1594  SPAG8    3'  GCAATGGCCACCATGTCTGC   29693    AGA      __
                                GCA   GTGGCTA  ATGTCTGC
                                |||   |||||||  ||||||||
                                CGT   TACCGGT  TACAGACG
                                 ___      GG
GAM1594  SPG4     3'  AACAATTGTTTAATGTCTG   31395      GAG  GC
                                AGCAA   TG  TAATGTCTG
                                |||||   ||  |||||||||
                                TTGTT   AC  ATTACAGAC
                                  A__  AA
GAM1594  TMEM2    3'  AAGTAAGAGTGACTCATTCCTG 30148     C        AATG
           C                     AAG AAGAGTGGCT    TCTGC
                                ||| ||||||||||    |||||
                                TTC TTCTCACTGA    GGACG
                                  A         GTAA
GAM1594  CELSR2   3'  TTAACCCTTTGCAGGAATTGC  10862           C   _
                                TTAACCCTTTGCG GAAT GC
                                |||||||||||||| |||| ||
                                AATTGGGAAACGT CTTA CG
                                       C    A
GAM1594  COL15A1  3'  CTCTTAACCTATGTTGGGATGC 12353         CTT  CGCGA
                                CTCTTAACC   TG    ATGC
                                |||||||||   ||    ||||
                                GAGAATTGG   AC    TACG
                                     AT_  AACCC
GAM1594  VAPB     3'  CTTCTAACCCTTTGCAGC    21874    CT        _
                                CT  TAACCCTTTGC GC
                                ||  ||||||||||| ||
                                GA  ATTGGGAAACG CG
                                 AG         T
GAM1594  WHSC1    3'  TCTTAACCGGCGAT       39405        CTTT C    A
                                TCTTAACC    G GCGA T
                                ||||||||    | |||| |
                                AGAATTGG    C CGCT A
                                     _____ _    C
GAM1595  HMGCS2   3'  AAGAGGTCTTCTCTCCATTGC  24325          A  GCA   C
                                AAGAGGTCTTC TC   CAT GC
                                |||||||||| ||   ||| ||
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                                TTCTCCAGAAG AG   GTA CG
                                      _ AG_   A
GAM1595  KCNE2    3'  AAAGAGGTCTTCAGCACA    23082          TC
                                AAAGAGGTCTTCA  GCACA
                                |||||||||||||  |||||
                                TTTCTCCAGAAGT  CGTGT
                                      __
GAM1595  MYH11    3'  AAAGAGGTCTCGTTTCCTCGC  35623          CA____
                                AAAGAGGTCTT     TCGC
                                ||||||||||     ||||
                                TTTCTCCAGAG     AGCG
                                      CAAAGG
GAM1595  TACSTD1  3'  AAAGATGTCTTCGTCCCAC   14296      G     A  G
                                AAAGA GTCTTC TC CAC
                                ||||| |||||| || |||
                                TTTCT CAGAAG AG GTG
                                   A     C  G
GAM1595  UBE4A    3'  AAAGAGTCTTCATTTTGC    21965       G      C__
                                AAAGAG TCTTCAT   GC
                                ||||||| |||||||   ||
                                TTTCTC AGAAGTA   CG
                                   _      AAA
GAM1595  HYAL3    5'  GATGCTGGCCTCTGGGATG   18645     AACAT
                                GAT    CCTCTGGGATG
                                |||    ||||||||||
                                CTA    GGAGACCCTAC
                                  CGACC
GAM1595  SEZ6L    5'  GCGGTGACAGGGCTGGGATG  34423     ATA   TCCT
                                GCG   ACA   CTGGGATG
                                |||   |||   ||||||||
                                CGC   TGT   GACCCTAC
                                  CAC   CCC_
GAM1595  VIPR2    3'  TGTGATGGATCCTCTGCGG   18031    C   AAC      _
                                TG GAT   ATCCTCTG GG
                                || |||   |||||||| ||
                                AC CTA   TAGGAGAC CC
                                 A   CC_       G
GAM1596  NFIA     3'  GGCGTAATCCATTATAGTG   43218     AA    AT_
                                GGC  TGAT   TTATAGTG
                                |||  ||||   ||||||||
                                CCG  ATTA   AATATCAC
                                  C_    GGT
GAM1596  EGR1     5'  CAGGGGACACCGTTGCG     12656     AA    AGAA
                                CAGG  ACAT    GTTGCG
                                ||||  ||||    ||||||
                                GTCC  TGTG    CAACGC
                                   CC    G___
GAM1596  ELK1     3'  ACAGAAAACAGAGAAGTTGTGG 23404          T       C
                                ACAGGAAACA AGAAGTTG GG
                                |||||||||| |||||||| ||
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                                TGTCTTTTGT TCTTCAAC CC
                                      C       A
GAM1596  MEN1     3'  CAGGAAACACAGCAAACTG   39163          _  GT
                                CAGGAAACATAG AA  TG
                                |||||||||||| ||  ||
                                GTCCTTTGTGTC TT  AC
                                      G  TG
GAM1596  MSF      3'  TAACAGGAAGCAGGAAG     44741         A  TA
                                TAACAGGAA CA  GAAG
                                ||||||||| ||  ||||
                                ATTGTCCTT GT  CTTC
                                      C  C_
GAM1596  TAF4B    5'  CAGGAAACTGGATTGTCGTGG  44550        ATAGAA   C
                                CAGGAAAC     GTTG GG
                                ||||||||     |||| ||
                                GTCCTTTG     CAGC CC
                                     ACCTAA    A
GAM1597  TRHDE    3'  TGAGAATATCATTTCTGTTTT  30113     A       AAA
                                TGA AATATCATT   TTGTTTT
                                ||| |||||||||   |||||||
                                ACT TTATAGTAA   GACAAAA
                                  C       A__
GAM1597  ADSS     3'  TTTAAACAGAATTCATAGCA   43481       _     TT
                                TTTAAA AGAATTT  GTAGCA
                                |||||| |||||||  ||||||
                                AAATTT TCTTAAG  TATCGT
                                   G     __
GAM1597  CAPON    3'  TTCAAGGCTCCCTTTGTAGCA  41938      AAGAA
                                TTTAA    TTTTTGTAGCA
                                |||||    ||||||||||
                                AAGTT    GGAAACATCGT
                                   CCGAG
GAM1597  MLLT2    3'  TTTAAAAGTTTTTTTGTAG    25518        AA
                                TTTAAAAG  TTTTTGTAG
                                ||||||||  |||||||||
                                AAATTTTC  AAAAACATC
                                     AA
GAM1597  SCAMP1   3'  TTTAAAAGAAATTCTTGCA    38069         _
                                TTTAAAAGAA TTTTTGTA
                                |||||||||| ||||||||
                                AAATTTTCTT AAGAACGT
                                      T
GAM1598  ACCN1    3'  TGGGCAGCTTGGGGAAA     9917     AG   TATAT
                                TGG  AGCT    TGGGGGAA
                                |||  ||||    ||||||||
                                ACC  TCGA    ACCCCTTT
                                  CG   _____
GAM1598  ACHE     3'  GGAGGGGGAGGTTGGGGGAAAA 8565      AGCTTATA
                                GGAG       TTGGGGGAAAA
                                ||||       ||||||||||
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                                CCTC       AACCCCCTTTT
                                  CCCCTCC_
GAM1598 ACVR1B   3' GAGGGGCTCTGGGGGA     33758     A_   ATAT
                                GAG  GCTT    TGGGGGA
                                |||  ||||    |||||||
                                CTC  CGAG    ACCCCCT
                                  CC   _____
GAM1598 ARG1     3' TGTAGAGTTTATACTAATTGGA 6248     G   C       GG_
           AAA                    TG AGAG TTATATTG   GGAAAA
                                || |||| ||||||||   ||||||
                                AC TCTC AATATGAT   CCTTTT
                                 A   A       TAA
GAM1598 CACNG2   5' TGGAGAGTTATAAAAAAAGGGA 25880        C    TT__
                                TGGAGAG TTATA    GGGGGA
                                ||||||| |||||    ||||||
                                ACCTCTC AATAT    TTCCCT
                                    _    TTTT
GAM1598 CENTD2   5' GGAGGCCCCTGGGGGA      31598     A   ATA
                                GGAG GCTT   TTGGGGGA
                                |||| ||||   ||||||||
                                CCTC CGGG   GACCCCCT
                                  _   ____
GAM1598 CHRNB4   3' TGGGAAGCCCTGGGGGAA    8872     AG   TATA
                                TGG  AGCT    TTGGGGGAA
                                |||  ||||    |||||||||
                                ACC  TCGG    GACCCCCTT
                                  CT   _____
GAM1598 CLOCK    3' GGAGAGGGGTTGGGGGA     22217      CTTATA
                                GGAGAG     TTGGGGGA
                                ||||||     ||||||||
                                CCTCTC     AACCCCCT
                                   CCC____
GAM1598 CNN1     3' TGGGGGCTTTGCTGGGGGA   10542     AGA   ATA
                                TGG   GCTT   TTGGGGGA
                                |||   ||||   ||||||||
                                ACC   CGAA   GACCCCCT
                                  CC_   AC_
GAM1598 CPLX2    3' GGAGAGCTGAGGGGGA      27398       TATATT
                                GGAGAGCT     GGGGGA
                                ||||||||     ||||||
                                CCTCTCGA     CCCCCT
                                    CT_____
GAM1598 DPYSL3   3' TGGGAAGCTTGTGGCAAGGAA 10782     AG    ATAT  __
                                TGG  AGCTT   TGG  GGGAA
                                |||  |||||   |||  |||||
                                ACC  TCGAA   ACC  TCCTT
                                  CT    C___  GT
GAM1598 EGR1     5' TGGAGAGCTGGTGTCGGGG   12672        TATA
                                TGGAGAGCT   TTGGGG
                                |||||||||   ||||||
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                                ACCTCTCGA   AGCCCC
                                     CCAC
GAM1598 FNTB    3' TGGAGAGCTGGTGAGGAGG  13009       TATATT
                                TGGAGAGCT    GGGGG
                                |||||||||    |||||
                                ACCTCTCGA    CCTCC
                                     CCACT_
GAM1598 GRM1    5' TGGAGGCGTTTGTAAGGGAA  9145      A  TTATAT
                                TGGAG GC    TGGGGGAA
                                ||||| ||    ||||||||
                                ACCTC CG    ATTCCCTT
                                   _ CAAAC_
GAM1598 GSS     3' TGGAAAGCTGGGGGAA     6760        TATATT
                                TGGAGAGCT    GGGGGAA
                                |||||||||    |||||||
                                ACCTTTCGA    CCCCCTT
                                     _______
GAM1598 HAL     3' TGGAGAGCTTGTTGAAG    13334        ATA
                                TGGAGAGCTT  TTGGGG
                                ||||||||||  ||||||
                                ACCTCTCGAA  AACTTC
                                     C__
GAM1598 KCNJ4   3' TGAAGAGTCAGTGGGGGAA  22542      C  TAT
                                TGGAGAG TTA  TGGGGGAA
                                ||||||| |||  ||||||||
                                ACTTCTC AGT  ACCCCCTT
                                   _  C__
GAM1598 L1CAM   3' TGGGGAGTGGCTGGGGGA   35807    A  CTTATA
                                TGG GAG    TTGGGGGA
                                ||| |||    ||||||||
                                ACC CTC    GACCCCCT
                                  C  ACC___
GAM1598 LOXL2   3' TGGAGGGTTTCATTGGAAGA  14200     AGC  A
                                TGGAG  TT TATTGGGGGA
                                |||||  || ||||||||||
                                ACCTC  AA GTAACCTTCT
                                   CC_  A
GAM1598 MAFF    3' TGGACAGTGTTGGGGGA    29517     G  CTTATA
                                TGGA AG    TTGGGGGA
                                |||| ||    ||||||||
                                ACCT TC    AACCCCCT
                                  G  AC____
GAM1598 MAPK4   3' TGGGAGTGTTGGGGGAA    15670    A  CTTATA
                                TGG GAG    TTGGGGGAA
                                ||| |||    |||||||||
                                ACC CTC    AACCCCCTT
                                  _  AC____
GAM1598 MASP1   3' TGGAGGGCTTATATCTTGGA  40113     A       GGG
                                TGGAG GCTTATATT  GGA
                                ||||| |||||||||  |||
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                                ACCTC CGAATATAG   CCT
                                   C       AA_
GAM1598 MGST2    5' TGGGGACCGGGTGGGGGGGAAA 14498    A  G  TATATT
                                TGG GA CT     GGGGGGAAA
                                ||| || ||     ||||||||
                                ACC CT GG     CCCCCTTT
                                  C  _  CCCAC_
GAM1598 NFE2L1   3' GAGAGCTTGTGTGTTTGGGGA 17331        ATA___
                                GAGAGCTT     TTGGGGG
                                ||||||||     |||||||
                                CTCTCGAA     AACCCCT
                                     CACACA
GAM1598 NID      3' TGGGGGGCTAGTATTGGGAAAA 14799     AGA   TA     GG
                                TGG   GCT  TATTGGG  AA
                                |||   |||  |||||||  ||
                                ACC   CGA  ATAACCC  TT
                                  CCC   TC      TT
GAM1598 NOTCH3   3' TGGGGGGTTCACAGGGGGA   7743     AGAGC    TT
                                TGG    TTATA  GGGGGA
                                |||    |||||  ||||||
                                ACC    AGTGT  CCCCCT
                                  CCCCA    __
GAM1598 NRXN2    3' TGGAGGGCTTGGGAAGA     31494      A    ATATT
                                TGGAG GCTT    GGGGGA
                                ||||| ||||    ||||||
                                ACCTC CGAA    CCTTCT
                                   C    C____
GAM1598 NSD1     3' TGGAAAAGTTGGGGGAAA    35362       CTTATA
                                TGGAGAG     TTGGGGGAAA
                                |||||||     ||||||||||
                                ACCTTTT     AACCCCCTTT
                                     C_____
GAM1598 PACE4    3' GGAGAGTTTTGGGGAAA     15052       C  ATA
                                GGAGAG TT   TTGGGGGAA
                                ||||||  ||  |||||||||
                                CCTCTC AA   AACCCCTTT
                                     _  ____
GAM1598 PAWR     5' TGGAGGAGCTTGTAGGGGA   15098      _    ATAT
                                TGGAG AGCTT    TGGGGGA
                                ||||| |||||    |||||||
                                ACCTC TCGAA    ATCCCCT
                                   C    C___
GAM1598 PAX9     3' TGGGAATTGGGGGGA       26209     A  GCTTAT
                                TGG GA     ATTGGGGGA
                                ||| ||     |||||||||
                                ACC CT     TAACCCCCT
                                  _  _______
GAM1598 PCDHA9   3' GAGAGCTTGTACTCTGAGA   36547        A    GG
                                GAGAGCTT TATT  GGGA
                                |||||||| ||||  ||||
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                                CTCTCGAA ATGA  CTCT
                                    C   GA
GAM1598 PKM2     3'  TGGATGGGCTGGGGGAA    15339     GA_  TATATT
                                TGGA  GCT    GGGGGAA
                                ||||  |||    |||||||
                                ACCT  CGA    CCCCCTT
                                  ACC  _______
GAM1598 PPP6C    3'  TGGGGATGGGATGGGGGAAAA  15545    A  GCTTATAT
                                TGG GA      TGGGGGAAAA
                                ||| ||      ||||||||||
                                ACC CT      ACCCCCTTTT
                                  C  ACCCT___
GAM1598 PRKACA   3'  TGGGGGGCTGTGGGGAAA    15591    AGA  TATAT
                                TGG  GCT    TGGGGGAA
                                |||  |||    ||||||||
                                ACC  CGA    ACCCCTTT
                                  CCC  C____
GAM1598 RUNX1    3'  GGAGATATTGGGGG       12025     GCTTA
                                GGAGA    TATTGGGGG
                                |||||    |||||||||
                                CCTCT    ATAACCCCC
                                   _____
GAM1598 SLC22A12 3'  TGGAGGGGCAGCCCTGGGGGA  40337     A_  TTATA
                                TGGAG  GC    TTGGGGGA
                                |||||  ||    ||||||||
                                ACCTC  CG    GACCCCCT
                                   CC  TCGG_
GAM1598 SLC4A4   3'  TGGAGAGCTCTATAAGTGAGAA 19066        A  T  _
                                TGGAGAGCTT TAT GG GGGAA
                                |||||||||| ||| || |||||
                                ACCTCTCGAG ATA TC CTCTT
                                      _  T  A
GAM1598 SURF5    3'  GAGGGACTGTTGGGGGA    39504    A_  TATA
                                GAG  GCT   TTGGGGGA
                                |||  |||   ||||||||
                                CTC  TGA   AACCCCCT
                                  CC  C___
GAM1598 TFRC     3'  TGGAGGCTTATGGGGGAA    17437     A    TAT
                                TGGAG GCTTA  TGGGGGAA
                                ||||| |||||  ||||||||
                                ACCTC CGAAT  ACCCCCTT
                                   _    ____
GAM1598 TMC1     5'  TGGAGGGCTTGTGAAAGAAA  39799     A   ATAT  GG
                                TGGAG GCTT   TG  GGAAA
                                ||||| ||||   ||  |||||
                                ACCTC CGAA   AC  TCTTT
                                   C   C___  TT
GAM1598 TNFRSF4  3'  TGGAAGAGTAGTGGGGGGAAA  17764     _  CTTATATT
                                TGGA GAG      GGGGGAAA
                                |||| |||      ||||||||
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                                ACCT CTC       CCCCCTTT
                                  T  ATCAC___
GAM1598  ZNF195   3'  TGGAGACTTATATTTCATGAAA 28383       G       GGGG
                                TGGAGA CTTATATT    GAAA
                                |||||| ||||||||    ||||
                                ACCTCT GAATATAA    CTTT
                                   _       AGTA
GAM1599  ABCB11   3'  AGGAAAATGACTGTAAAAG   19041          GAAGAT
                                AGGAAAATGAC     GAAG
                                ||||||||||      ||||
                                TCCTTTTACTG     TTTC
                                      ACAT__
GAM1599  ABCD3    3'  CACAGGAAAATGAAACTGAAG  16017           CGAAGA
                                TACAGGAAAATGA     TGAAG
                                ||||||||||||      |||||
                                GTGTCCTTTTACT     ACTTC
                                      TTG___
GAM1599  BPAG1    3'  ACAGGAAAATGTCATGA     31780          A GAAG
                                ACAGGAAAATG C    ATGA
                                |||||||||| |    ||||
                                TGTCCTTTTAC G    TACT
                                      A _____
GAM1599  CD28     3'  ACAGGAAAATGATGGAAG    26013          C_
                                ACAGGAAAATGA  GAAG
                                ||||||||||||  ||||
                                TGTCCTTTTACT  CTTC
                                      AC
GAM1599  CHST1    3'  CAGGAAGGACACGAAGATGA  18903       AATG
                                CAGGAA    ACGAAGATGA
                                ||||||    ||||||||||
                                GTCCTT    TGCTTCTACT
                                   CCTG
GAM1599  EGFL5    5'  CAGGAATGGAGATGAA      44519      AA   ACGA
                                CAGGA  ATG    AGATGAA
                                |||||  |||    |||||||
                                GTCCT  TAC    TCTACTT
                                   __   C___
GAM1599  ENAM     3'  TACAGAGAGAAAAAGATGA   36677       AAAAT  C
                                TACAGG     GA GAAGATGA
                                ||||||     || ||||||||
                                ATGTCT     CT TTTCTACT
                                   CT___  T
GAM1599  FHIT     3'  TACAGGATGGTGAGATGAA   12877       AAA  AC  A
                                TACAGGA   TG  GA GATGAA
                                |||||||   ||  || ||||||
                                ATGTCCT   AC  CT CTACTT
                                    ___ CA  _
GAM1599  FY       5'  GGAAGGGAGAAAAGATGA    13035      AAT_  C
                                GGAA    GA GAAGATGA
                                ||||    || ||||||||
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                                CCTT    CT TTTCTACT
                                  CCCT  _
GAM1599  GCN1L1   3'  CACAGGAAAAGGTGAGAGATG  43067          __   C  A
                                TACAGGAAAA  TGA GA GATG
                                ||||||||||  ||| || ||||
                                GTGTCCTTTT  ACT CT CTAC
                                     CC   _ _
GAM1599  GDF8     3'  AGGAAAATGCCCCTGAAG    23541         ACGAAGA
                                AGGAAAATG      TGAAG
                                |||||||||      |||||
                                TCCTTTTAC      ACTTC
                                     GGGG___
GAM1599  GJA5     3'  CAGGAAGATTCCGTAGATGAAG 23579        A  GA  A
                                CAGGAA AT  CG AGATGAAG
                                |||||| ||  || ||||||||
                                GTCCTT TA  GC TCTACTTC
                                   C  AG  A
GAM1599  HNRPDL   3'  TACAGGGAGAAGATGAA     24178       AAAAT  C
                                TACAGG    GA GAAGATGAA
                                ||||||    || |||||||||
                                ATGTCC    CT CTTCTACTT
                                  ______  _
GAM1599  PIK3CD   3'  TACAGTAGAGAAAGATGA    22731       GAAAAT  C
                                TACAG     GA GAAGATGA
                                |||||     || ||||||||
                                ATGTC     CT TTTCTACT
                                  AT_____  C
GAM1599  PPP2R5C  3'  GGAGAACATGAAGATGAAG   15523     A   GAC
                                GGA AAT   GAAGATGAAG
                                ||| |||   ||||||||||
                                CCT TTG   CTTCTACTTC
                                  C   TA_
GAM1599  PRG2     5'  CAGACAGAGATGAAGATGAAG  15560      AAAAT  C
                                CAGG    GA GAAGATGAAG
                                ||||    || ||||||||||
                                GTCT    CT CTTCTACTTC
                                  GTCT_  A
GAM1599  PRKY     3'  CAGAAGGAGACAGATGAAG   15687      AAAT   GA
                                CAGGA   GAC  AGATGAAG
                                |||||   |||  ||||||||
                                GTCTT   CTG  TCTACTTC
                                  CCT_   __
GAM1599  RRAS2    3'  TGAGGAGAGAAAGAGAAGATGA 29311   C    AAAT__  C
                                A AGGA     GA GAAGATGA
                                | ||||     || ||||||||
                                A TCCT     CT CTTCTACT
                                 C   CTCTTT  _
GAM1599  SHC1     3'  CACAGGAAAGGCCCAGGTGA   16696         ATGACGA  A
                                TACAGGAAA      AG TGA
                                |||||||||      || |||
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                                GTGTCCTTT      TC ACT
                                     CCGGG__  C
GAM1599  TIMM17A   3'  CAGGAAAATGACCTGTTCTGAA 26789           GAAGA_
              G                   CAGGAAAATGAC     TGAAG
                                  ||||||||||||     |||||
                                  GTCCTTTTACTG     ACTTC
                                       GACAAG
GAM1599  TMOD4     3'  TACAGGAAAGGAGGACAGATGA 30041         AT  C  _
                                  TACAGGAAA  GA GA AGATGA
                                  |||||||||  || || ||||||
                                  ATGTCCTTT  CT CT TCTACT
                                       C_  C  G
GAM1599  YY1       3'  TACAGGAAAATACTTTTGAAG  18182           A GAAGA
                                  TACAGGAAAATG C     TGAAG
                                  ||||||||||||| |    |||||
                                  ATGTCCTTTTAT G     ACTTC
                                        _ AAA__
GAM1599  CAV1      3'  GCATAACAGACGGTTGCAAGTG 11993         TTAAACC
                                  GCATAACG      GCAAGTG
                                  ||||||||      |||||||
                                  CGTATTGT      CGTTCAC
                                       CTGCCAA
GAM1600  ASGR2     3'  TTGCTCAGCTCTTCCCCAT   38958      A    CC
                                  TTGT CAGC  CTTCCCCAT
                                  |||| ||||  |||||||||
                                  AACG GTCG  GAAGGGGTA
                                    A   A_
GAM1600  CCND2     3'  TTGTACTCCTTCCCCAT     12057       AGCC
                                  TTGTAC    CCTTCCCCAT
                                  ||||||    ||||||||||
                                  AACATG    GGAAGGGGTA
                                     A___
GAM1600  CDH13     3'  TACCTGTACACCTCTT      10370       T    G  C
                                  TACCT GTACA CC CTT
                                  ||||| ||||| || |||
                                  ATGGA CATGT GG GAA
                                     _    _  A
GAM1600  CIT       3'  CCCGACGGGCCTCTTCCCCAT  43044      T  A_   C
                                  CTTG AC  GCC CTTCCCCAT
                                  |||| ||  ||| |||||||||
                                  GGGC TG  CGG GAAGGGGTA
                                    _  CC   A
GAM1600  CX3CR1    3'  CTTATATATCCCTTCCCCAT   43294       CAGC
                                  CTTGTA    CCCTTCCCCAT
                                  ||||||    ||||||||||||
                                  GAATAT    GGGAAGGGGTA
                                     ATA_
GAM1600  DLG4      5'  CTTAAGCCCCTTCCTCAT     10705      TAC        C
                                  CTTG   AGCCCCTTCC CAT
                                  ||||   |||||||||| |||
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                                GAAT   TCGGGGAAGG GTA
                                  ___        A
GAM1600  DNAI2    5'  ACCCCACCGGCCCCTTCCC   35745      TG ACA
                                ACCT  T   GCCCCTTCCC
                                ||||  |   ||||||||||
                                TGGG  G   CGGGGAAGGG
                                  GT GC_
GAM1600  DNMT3B   3'  GCACAGTTTTTTCCCCAT    27875       CCCC
                                GTACAG    TTCCCCAT
                                ||||||    ||||||||
                                CGTGTC    AAGGGGTA
                                   AAAA
GAM1600  MATN2    3'  TACCTTGCATAGCTTATTC    14372         C   CCC
                                TACCTTGTA AGC   TTC
                                ||||||||| |||   |||
                                ATGGAACGT TCG   AAG
                                     A   AAT
GAM1600  NEO1     3'  TACTCTGTACAATTCCTT    14757     C       CC
                                TAC TTGTACAG  CCTT
                                ||| ||||||||  ||||
                                ATG GACATGTT  GGAA
                                  A       AA
GAM1600  SLC6A12  5'  CTGTACAGCTCGCCACCAT    16797         CCCTT  _
                                TTGTACAGC     CC CCAT
                                |||||||||     || ||||
                                GACATGTCG     GG GGTA
                                     AGC__  T
GAM1600  TNS      3'  CCCCACAAGCCCCTTCCCCAT  35471     TG  C
                                CCT  TA AGCCCCTTCCCCAT
                                |||  || ||||||||||||||
                                GGG  GT TCGGGGAAGGGGTA
                                  GT  _
GAM1601  BDKRB2   3'  CACCTGTTTTCTTCCTCCA    8398        C___
                                CACCTG    CTTCTTTCA
                                ||||||    |||||||||
                                GTGGAC    GAAGGAGGT
                                   AAAA
GAM1601  FALZ     3'  CCTTTTCTTCTCTTTCAAT    20889     GC_    __
                                CCT   CTTCTT  TCAAT
                                |||   ||||||  |||||
                                GGA   GAAGAG  AGTTA
                                  AAA     AA
GAM1601  HSPB3    5'  TCCACTGCCTTCAGTCA     26712       C      TT
                                TCCAC TGCCTTC  TCA
                                ||||| |||||||  |||
                                AGGTG ACGGAAG  AGT
                                   _      TC
GAM1601  KLHL1    3'  CTGCCTTCTTTCTAGCAA    34079           AAT
                                CTGCCTTCTTTC   CAA
                                ||||||||||||   |||
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                                GACGGAAGAAAG  GTT
                                      ATC
GAM1601  MGA     3'  TCCACCGTTTTCAATC     41728       TGCCTTC
                                TCCACC     TTTCAATC
                                ||||||     ||||||||
                                AGGTGG     AAAGTTAG
                                   CA_____
GAM1601  NCOA6IP  5'  TCCGCTTGGCTTCTTTCA    36054     ACC  C
                                TCC   TG CTTCTTTCA
                                |||   || |||||||||
                                AGG   AC GAAGAAAGT
                                  CGA  C
GAM1601  SURF6    3'  CACCTGTTTTCTTTCAACC   27588       CC
                                CACCTG  TTCTTTCAATC
                                ||||||  ||||||||||
                                GTGGAC  AAGAAAGTTGG
                                   AA
GAM1601  ZNF146   3'  CTGCTCTGCTCAATCAAT    28352      CT  _
                                CTGC  TCT TTCAATCAAT
                                ||||  ||| ||||||||||
                                GACG  AGA GAGTTAGTTA
                                  __  C
GAM1601  DNASE1L1  3'  CCCCTTTCCGGGACACCT    27490      A_  AAAT
                                CCCCT  CCG   GGATGCCT
                                |||||  |||   ||||||||
                                GGGGA  GGC   CCTGTGGA
                                  AA  _____
GAM1601  E2F2     5'  CCCCCTACCCAAAAGGGC    19868        G  T  AT
                                CCCCCTACC AAA GG  GC
                                ||||||||| ||| ||  ||
                                GGGGGATGG TTT CC  CG
                                     G  T  __
GAM1601  JAG2     3'  CCCACCGAGGGCCC       13705        AAT  AT
                                CCTACCGA  GG  GCCT
                                ||||||||  ||  ||||
                                GGGTGGCT  CC  CGGG
                                     ___  __
GAM1601  LILRB4   3'  CCTGTATGGAAATGGATGCCTG 27775     ACC__
                                CCT    GAAATGGATGCCTG
                                |||    ||||||||||||||
                                GGA    CTTTACCTACGGAC
                                  CATAC
GAM1601  NCOA3    3'  CCTTTCTTCCAAGATGGATGCC 27214    CC_  A   A
            TG                    CC   CT CCGA ATGGATGCCTG
                                ||   || |||| ||||||||||
                                GG   GA GGTT TACCTACGGAC
                                 AAA  A   C
GAM1601  PIG3     5'  CCTCCACCGGAATGGACGGCTG 22192    C     A      C
                                CC CTACCG AATGGATG CTG
                                || |||||| |||||||| |||
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                                GG GGTGGC TTACCTGC GAC
                                 A     C       C
GAM1601  PODXL    3'  CCTTTACTGAAATGGAGC    23966    CC   C      T
                                CC  TAC GAAATGGA GC
                                ||  ||| |||||||| ||
                                GG  ATG CTTTACCT CG
                                 AA   A      _
GAM1601  PRDM2    3'  CCCCCACCGAAGCAGCAGATGC 31968          A___
           CTG                    CCCCTACCGAA    TGGATGCCTG
                                ||||||||||    ||||||||||
                                GGGGGTGGCTT    GTCTACGGAC
                                      CGTC
GAM1601  TCF2     3'  CCTCTTACGGGGAATGCCC    27023    C  AC  AAAT
                                CC CT  CG    GGATGCCT
                                || ||  ||    ||||||||
                                GG GA  GC    CTTACGGG
                                 A  AT  CC__
GAM1601  WWOX     3'  CCCCTACTGGGAACCC      39118       CGAAA   AT
                                CCCCTAC     TGG  GCCT
                                |||||||     |||  ||||
                                GGGGATG     ACC  TGGG
                                    ______  CT
GAM1602  CUGBP1   3'  TCAAAGGTGAGAGTTCAAGCAT 27278         A     ATGAC
                                TTAAAGGT AGAGTT     GCAT
                                |||||||| ||||||     ||||
                                AGTTTCCA TCTCAA     CGTA
                                     C      GTT__
GAM1602  PCK1     3'  TAAAGGTAAGGAACAATG    40945          _  TT
                                TAAAGGTAAG AG  ATG
                                |||||||||| ||  |||
                                ATTTCCATTC TT  TAC
                                      C  GT
GAM1602  AIPL1    3'  AAACTGATTTAAACAGATTACT 40815     G   CTCCTC
                                AAA TGA      CAGATTACT
                                ||| |||      |||||||||
                                TTT ACT      GTCTAATGA
                                  G   AAATTT
GAM1602  BAZ2A    3'  GTGACTCCCCACCTCCCT    30311        T   GA TA
                                GTGACTCC CCA  T  CT
                                |||||||| |||  |  ||
                                CACTGAGG GGT  A  GA
                                     _  GG GG
GAM1602  GFI1     3'  AAATGATTCCTCCAAGATT    23548       C      _
                                AAGTGA TCCTCCA GATT
                                |||||| ||||||| ||||
                                TTTACT AGGAGGT CTAA
                                   A      T
GAM1602  HDAC4    3'  AAAGTGGCCCTCCAGAACC    25736       A T       TT
                                AAAGTG C CCTCCAGA  ACT
                                |||||| | ||||||||  |||
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                                TTTCAC G GGAGGTCT  TGG
                                   C _      __
GAM1602  KCNA5    3'  AAGTATTCCTCCAATATCA   40680      AC      _
                                AAGTG  TCCTCCAG ATTA
                                |||||  |||||||| ||||
                                TTCAT  AGGAGGTT TAGT
                                   A_       A
GAM1602  KCNJ16   3'  AAAGTGACTCTTTACT      33012         CTCCAGA
                                AAAGTGACTC      TTACT
                                ||||||||||      |||||
                                TTTCACTGAG      AATGA
                                     A_______
GAM1602  KIAA0857 3'  GTGACTCCCCCTCTCTCA    42475          AGA  A
                                GTGACTCCTCC   TT CTCA
                                ||||||||||   || ||||
                                CACTGAGGGGG   AG GAGT
                                     ___  A
GAM1602  MTMR8    3'  AAATGGTTTTAAAGATTACTCA 31746      ACTCCTCC
                                AAGTG       AGATTACTCA
                                |||||       ||||||||||
                                TTTAC       TCTAATGAGT
                                   CAAAATT_
GAM1602  OCM      3'  AAGTGACTCTCTCGTGACCTC  26188        _  CA   TA
                                AAGTGACTC CTC  GAT  CTC
                                |||||||| |||  |||  |||
                                TTCACTGAG GAG  CTG  GAG
                                     A  CA  __
GAM1602  PDGFRB   3'  AGGGATTCCTCCAAAGCCTCA  42331    T  C       TTA
                                AG GA TCCTCCAGA   CTCA
                                || || |||||||||   ||||
                                TC CT AGGAGGTTT   GAGT
                                 C  A        CG_
GAM1602  SSA1     3'  AAGTGACTTCCCTGCTAAAGCT 17119        _  CCAGATTA
            C                    AAGTGACT CCT       CTC
                                |||||||| |||       |||
                                TTCACTGA GGG       GAG
                                     A   ACGATTTC
GAM1602  STAT3    3'  AAAGTGCCCAGATTGCTC    40229       ACTCC       A
                                AAAGTG    TCCAGATT CTC
                                ||||||    |||||||| |||
                                TTTCAC    GGGTCTAA GAG
                                   _____       C
GAM1602  STAT3    3'  AAAGTGCCCAGATTGCTC    40229       ACTCC       A
                                AAAGTG    TCCAGATT CTC
                                ||||||    |||||||| |||
                                TTTCAC    GGGTCTAA GAG
                                   _____       C
GAM1602  TGFBR2   5'  AAAGTGACTTCTCAATGTAAAC 17466         C  CAGATT_
            T                    AAAGTGACT CTC       ACT
                                |||||||| |||       |||
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                                TTTCACTGA GAG      TGA
                                     A   TTACATT
GAM1603  CASP8    3'  AAAGATTTCAAACAAATTTT  37864          GAT
                                AAAGATTTCAAA   GTTTT
                                ||||||||||||   |||||
                                TTTCTAAAGTTT   TAAAA
                                      GTT
GAM1603  GRM1     3'  TAAAGATTCTAAGATGATTTT  9139         CA     _
                                TAAAGATTT  AAGATG TTTT
                                |||||||||  |||||| ||||
                                ATTTCTAAG  TTCTAC AAAA
                                     A_     T
GAM1603  NDN      3'  ACTCCACGAGGGTGTTTTCTG  14737      A_  A_
                                ATTTCA  AG  TGTTTTCTG
                                ||||||  ||  |||||||||
                                TGAGGT  TC  ACAAAAGAC
                                   GC  CC
GAM1603  PCDHA1   3'  AGAATTTCAAAGCATTCT    36403    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1603  PCDHA10  3'  AGAATTTCAAAGCATTCT    36563    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1603  PCDHA11  3'  AGAATTTCAAAGCATTCT    36573    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1603  PCDHA12  3'  AGAATTTCAAAGCATTCT    36594    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1603  PCDHA13  3'  AGAATTTCAAAGCATTCT    36602    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1603  PCDHA2   3'  AGAATTTCAAAGCATTCT    36465    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T       GT___
GAM1603  PCDHA3   3'  AGAATTTCAAAGCATTCT    33141    _      ATGTT
                                AGA TTTCAAAG    TTCT
                                |||  ||||||||    ||||
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                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHA4   3'  AGAATTTCAAAGCATTCT   36487    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHA5   3'  AGAATTTCAAAGCATTCT   36496    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHA6   3'  AGAATTTCAAAGCATTCT   36509    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHA7   3'  AGAATTTCAAAGCATTCT   36517    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHA8   3'  AGAATTTCAAAGCATTCT   36527    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHA9   3'  AGAATTTCAAAGCATTCT   36537    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHAC1  3'  AGAATTTCAAAGCATTCT   36617    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  PCDHAC2  3'  AGAATTTCAAAGCATTCT   36628    _     ATGTT
                                AGA TTTCAAAG    TTCT
                                ||| ||||||||    ||||
                                TCT AAAGTTTC    AAGA
                                  T      GT___
GAM1603  APPL     3'  CATTCCATAGCAGTATCTTTAC 29006    _  _  T  A
                                CAT CCA AG CA TATCTTTAC
                                ||| ||| || || |||||||||
                                GTA GGT TC GT ATAGAAATG
                                  A   A  _  C
GAM1603  PREB     3'  TACTACCCAAGTCTTCCTT   30143    C      AATA
                                TAC ATCCAAGTC   TCTTT
                                ||| |||||||||   |||||
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                                ATG TGGGTTCAG   AGGAA
                                  A       A___
GAM1603  PTPN7    3'  CATCCAAGAAGTCTTTA    38711       TCAATA
                                CATCCAAG    TCTTTA
                                ||||||||    ||||||
                                GTAGGTTC    AGAAAT
                                    TTC___
GAM1603  RANBP2   3'  ATCCAAGTTGTGGTCCCTTTA  26536       CAATA__
                                ATCCAAGT    TCTTTA
                                ||||||||    ||||||
                                TAGGTTCA    GGAAAT
                                    ACACCAG
GAM1604  DUOX1    3'  TGATTTATTTGGAAGGGA    32657    G_     TTT
                                TGA  TATTTGGA  GGA
                                |||  ||||||||  |||
                                ACT  ATAAACCT  CCT
                                  AA      TC_
GAM1604  FCMD     5'  TTTGGATTTGGAAAGGAA    27530          A
                                TTTGGATTTGGAAA GAA
                                |||||||||||||| |||
                                AAACCTAAACCTTT CTT
                                        C
GAM1604  GORASP1  3'  AGTGTTTGGGACTTGAAA    36702    A   _
                                AGT TTTGG ATTTGGAA
                                ||| ||||| ||||||||
                                TCA AAACC TGAACTTT
                                  C   C
GAM1604  HUNK     3'  TGAGTACTTGGGAGGAA     31085         ATTT
                                TGAGTATTTGG   GGAA
                                ||||||||||   ||||
                                ACTCATGAACC   CCTT
                                      CT__
GAM1604  KCNA6    3'  GAGTATTTGGCTCTGAGAA   13812         A   _
                                GAGTATTTGG TTTG GAA
                                |||||||||| |||| |||
                                CTCATAAACC AGAC CTT
                                      G   T
GAM1604  LENG4    3'  GTATTTAGCTGGGGAAGA    35889       AT   AA
                                GTATTTGG  TTGG  AAGA
                                ||||||||  ||||  ||||
                                CATAAATC  GACC  TTCT
                                    __   CC
GAM1604  SLC13A3  3'  TGAGTGCTCACTTGGAAAGGA  41301      A  GG      A
                                TGAGT TTT  ATTTGGAAA GA
                                ||||| |||  |||||||| ||
                                ACTCA GAG  TGAACCTTT CT
                                  C  __       C
GAM1604  SNX9     3'  GAAATAGGATTTGGGGAAGAA  32154     TATTT      AA
                                GAG    GGATTTGG  AAGAA
                                |||    ||||||||  |||||
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                                CTT    CCTAAACC  TTCTT
                                  TAT__       CC
GAM1604  TRPS1    3'  TGAGTATTTGAACATCTAAAGG 30471           TT_____
              A                    TGAGTATTTGGAT      GGA
                                   ||||||||||||      |||
                                   ACTCATAAACTTG      CCT
                                         TAGATTT
GAM1604  XK       3'  TGAGGTAGGTTGGAAAAG    34373     TATTT  AT
                                   TGAG    GG  TTGGAAAAG
                                   ||||    ||  |||||||||
                                   ACTC    CC  AACCTTTTC
                                     CAT__ __
GAM1604  MSL3L1   3'  ATATCTCAATCAAGCTGTTTTA 38577          T_   C
              A                    GTATCTCAATTG  CTGT TTAA
                                   ||||||||||||  ||||  ||||
                                   TATAGAGTTAGT  GACA AATT
                                         TC    A
GAM1605  RB1CC1   3'  TTGTTATTTAAATGACCTCTA  31321          ATAA
                                   TTGTTATTTAAA    TTCTA
                                   ||||||||||||    |||||
                                   AACAATAAATTT    GAGAT
                                         ACTG
GAM1605  TRHDE    3'  CTACTAATTTAAAATAATTCTA 30105       TT
                                   TTATTG  ATTTAAAATAATTCTA
                                   ||||||  ||||||||||||||||
                                   GATGAT  TAAATTTTATTAAGAT
                                     __
GAM1605  BTG3     3'  TTAATAAAATTTCTCAAACTAT 27717         ATAAT__
              ATCA                   TTAATAAAAT      ACTATATCA
                                     ||||||||||      |||||||||
                                     AATTATTTTA      TGATATAGT
                                         AAGAGTT
GAM1605  EYA1     3'  TTAATAAAATATATCTACTAT  7993           A_
                                   TTAATAAAATATA  TACTAT
                                   ||||||||||||  ||||||
                                   AATTATTTTATAT  ATGATA
                                         AG
GAM1606  S100A8   3'  TTGAGGTATTGATGACTTTATT 16448     AT    AT
              A                    TTGA  GTATT  TGATTTTATTA
                                   ||||  |||||  ||||||||||||
                                   AACT  CATAA  ACTGAAATAAT
                                     C_    CT
GAM1606  XRCC4    3'  TTCAATGTATCAAAAATTTTAT 35428    G       TT
              TA                     TT AATGTATTA  GATTTTATTA
                                     ||  |||||||||  ||||||||||
                                     AA TTACATAGT  TTAAAATAAT
                                      G       TT
GAM1606  BACH1    3'  TTTAAAAAATCATCAAACA    10154           T
                                   TTTAAAAAATCATTA ATA
                                   ||||||||||||||| |||
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                                AAATTTTTTAGTAGT TGT
                                         T
GAM1606  PCSK2    3'  TTTAAAAAATCATATTATTACA 15140          TATA
                                TTTAAAAAATCAT   TATTACA
                                |||||||||||||   |||||||
                                AAATTTTTTAGTA   ATAATGT
                                      TA__
GAM1606  SUFU     3'  TTTAAAAAACATTATATAC   32099        T
                                TTTAAAAAA CATTATATAT
                                ||||||||| ||||||||||
                                AAATTTTTT GTAATATATG
                                        _
GAM1607  ANXA4    3'  TCCATTTAAAAAATTTTTCA  41718
                                TCCGTTTAAAAAATTTTTTA
                                ||||||||||||||||||||
                                AGGTAAATTTTTTAAAAAGT

GAM1607  ITPR1    3'  TCCCTTTAAAAAATTCATTA  13668    G         T
                                TCC TTTAAAAAATTT TTA
                                ||| |||||||||||| |||
                                AGG AAATTTTTTAAG AAT
                                  G         T
GAM1607  NDUFB9   3'  TCCATTTCACTGATTTTTTATT 22672       AAAAA
           A                     TCCGTTT    ATTTTTTATTA
                                 |||||||    ||||||||||
                                 AGGTAAA    TAAAAAATAAT
                                     GTGAC
GAM1607  RENT1    3'  TCCGTTTATTTTTATTTTTTAT 16259       AAAA_
           TA                    TCCGTTTA    ATTTTTTATTA
                                 ||||||||    ||||||||||
                                 AGGCAAAT    TAAAAAATAAT
                                     AAAAA
GAM1608  TREM1    3'  TACAGATTTAATTCATGTT   32999         ATT
                                TATAGATTTAAT   TGTT
                                ||||||||||||  ||||
                                ATGTCTAAATTA   ACAA
                                       AGT
GAM1609  SIAT1    5'  ATATTTACTGGTTTATCATC  16718        AA
                                ATATTTACT  TTTATCATC
                                |||||||||  |||||||||
                                TATAAATGA  AAATAGTAG
                                     CC
GAM1610  STK18    3'  TATATCCACTATATTTA    30685      AT
                                TATATC  TACTATATTTA
                                ||||||  ||||||||||
                                ATATAG  GTGATATAAAT
                                       __
GAM1611  IGF1     3'  TATTAGATATTATTTTAAT   8350          A
                                TATTAGATATTAT TTAAT
                                |||||||||||| |||||
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```
                                ATAATCTATAATA AATTA
                                       A
GAM1611  BPAG1    3'  TTTTCATTTTTTGAAGCAATCT 31785           T____
              AA                  TTTTCATTTTTTGA    TCTAA
                                  ||||||||||||||    |||||
                                  AAAAGTAAAAAACT    AGATT
                                        TCGTT
GAM1611  DAF      3'  TTTTCATTTTTTATTTCC    8209           A
                                  TTTTCATTTTTTG TTCT
                                  |||||||||||| ||||
                                  AAAAGTAAAAAAT AAGG
                                        A
GAM1611  NBEA     3'  TTTTCTTTTTTTGATTTCCAA  45435      A       _
                                  TTTTC TTTTTTGATT CTAA
                                  ||||| |||||||||| ||||
                                  AAAAG AAAAAACTAA GGTT
                                     A        A
GAM1611  PPP3CC   3'  TTTTCATTTTCCAATAATAA  24679         TG  TC
                                  TTTTCATTTTT  AT  TAA
                                  ||||||||||  ||  |||
                                  AAAAGTAAAAG  TA  ATT
                                        GT  TT
GAM1611  STC1     3'  TTTTTTGAAACCAATAAA    17188        TT
                                  TTTTTTGA  CTAATAAA
                                  ||||||||  ||||||||
                                  AAAAAACT  GGTTATTT
                                       TT
GAM1612  ABH      3'  AGAGATAGTTGTGATTAATTT  40737     T    A    T
                                  AGA GATAG TGTG ATTAATTT
                                  ||| ||||| |||| ||||||||
                                  TCT CTATC ACAC TAATTAAA
                                    _     A   _
GAM1612  PTHR2    3'  AAGATATAGATGCAGCAT    22782       A     _
                                  AAGATG TAGATGT GTAT
                                  |||||| ||||||| ||||
                                  TTCTAT ATCTACG CGTA
                                     _      T
GAM1612  GLS      3'  TCTATTTTTTCCCAAAGA    31379          A   T
                                  TCTATTTTTTC TCAA AGA
                                  |||||||||| |||| |||
                                  AGATAAAAAAG GGTT TCT
                                        _   _
GAM1612  ID4      3'  ATCATCTATTTTAAACAATAGA 11375          TTCAT
                                  ATCATCTATTTT    CAATAGA
                                  ||||||||||||    |||||||
                                  TAGTAGATAAAA    GTTATCT
                                        TTT__
GAM1613  ITPR2    3'  TCATGTATTAATCTCAATATAT 13679        A     T_
              TT                    TCATGTAT TAATTTT  TATATTT
                                  ||||||||  |||||||  |||||||
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                                AGTACATA ATTAGAG  ATATAAA
                                    _      TT
GAM1613  MEF2C    3'  ATGTACATATTTTTATATTT   14407         AT
                                ATGTATATA  TTTTTATATTT
                                |||||||||  ||||||||||
                                TACATGTAT  AAAAATATAAA
                                    __
GAM1613  PSMB9    3'  TCATGTATAGGGCTCTTTATAT 15830         TAA
              TT                  TCATGTATA   TTTTTTATATTT
                                |||||||||   ||||||||||||
                                AGTACATAT   GAGAAATATAAA
                                     CCC
GAM1613  TNS      3'  TCATGTATATATTATATAATAT 35478          ATTTTTT
              TT                  TCATGTATATA      ATATTT
                                ||||||||||       ||||||
                                AGTACATATAT      TATAAA
                                      AATATAT
GAM1613  DAZ      3'  TTAAACTATATATTAAAC    19857           C
                                TTAAACTATATAT AAAT
                                |||||||||||| ||||
                                AATTTGATATATA TTTG
                                       A
GAM1614  ERBB4    3'  AACATTGTGGTTCCTC      23452         C  C  AAAAA
                                AACATTGT GG TC     CTC
                                |||||||| || ||     |||
                                TTGTAACA CC AG     GAG
                                    _  A  _____
GAM1614  HMG20A   3'  CACTGTCAGCAAGAAGCTCC   32866          TCAAAAA
                                CATTGTCGGC      CTCC
                                ||||||||||      ||||
                                GTGACAGTCG      GAGG
                                      TTCTTC_
GAM1614  MFAP3    5'  TTGGAGAACTCAAAAACT    25456     TC  _
                                TTG  GG CTCAAAAACT
                                |||  || ||||||||||
                                AAC  CT GAGTTTTTGA
                                  CT  T
GAM1614  P23      3'  CTATCAACTCAGGAATTCTC   27341          AAAA__
                                TTGTCGGCTCA     CTC
                                ||||||||||      |||
                                GATAGTTGAGT     GAG
                                      CCTTAA
GAM1614  POU2AF1  5'  TGATGAGCCCAAAAGCTCC    26378    TC_       A
                                TG   GGCTCAAAA CTCC
                                ||   ||||||||| ||||
                                AC   TCGGGTTTT GAGG
                                  TAC        C
GAM1614  PSD      3'  AACATTATCACAAAAAGGGGCT 15776          __________
              C                   AACATTGTC        GGCTC
                                |||||||||        |||||
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                                TTGTAATAG       CCGAG
                                     TGTTTTTCC
GAM1614  PTX3    3'  AACATTATCCTCAAAAGCT   15989        GG      A
                                AACATTGTC  CTCAAAA CT
                                |||||||||  ||||||| ||
                                TTGTAATAG  GAGTTTT GA
                                     __      C
GAM1614  RP42    3'  ACATTTTCTAAATAAAAGCTCC 33978      G  GGCTC    A
              C                   ACATT TC     AAAA CTCCC
                                |||||  ||     |||| |||||
                                TGTAA AG     TTTT GAGGG
                                   A  ATTTA    C
GAM1614  SIGLEC5  3'  AACATTGCCACAAGGGCTC   19257         _____
                                AACATTGTC    GGCTC
                                |||||||||    |||||
                                TTGTAACGG    CCGAG
                                     TGTTC
GAM1614  TCTA    3'  ACATCTTTGGAAACTCC     35276      GTC  CTCAA
                                ACATT   GG    AAACTCC
                                |||||   ||    |||||||
                                TGTAG   CC    TTTGAGG
                                   AAA  _____
GAM1614  VASP    3'  CTATAGCATTTAAAAACTCCC  17916     C   TC__
                                TTGT GGC    AAAAACTCCC
                                |||| |||    ||||||||||
                                GATA TCG    TTTTTGAGGG
                                   _   TAAA
GAM1615  FRAT2   3'  TGAGAAAGCTCCTGGCAT    28978     A        TTTAT
                                TGA AAAGCTTCTG    GCAT
                                ||| ||||||||||    ||||
                                ACT TTTCGAGGAC    CGTA
                                  C       _____
GAM1615  GAN     3'  TGAAAAAGTTTCTGATCCCTAT 35150        C    ___
              G                   TGAAAAAG TTCTG   TTTATG
                                |||||||| |||||   ||||||
                                ACTTTTTC AAGAC   GGATAC
                                     A    TAG
GAM1615  NFRKB   5'  CGGAAAAGCTTCTGGGCA    26094    A        TTTAT
                                TG AAAAGCTTCTG    GCA
                                || ||||||||||    |||
                                GC TTTTCGAAGAC    CGT
                                  C         C____
GAM1615  SIM2    3'  TGAAAGGATTTCTGTTTAC   22882      AAGC
                                TGAAA   TTCTGTTTAT
                                |||||   ||||||||||
                                ACTTT   AAGACAAATG
                                   CCTA
GAM1616  ADD1    3'  TGAGAACAGTCCCCTGAAGC  30528        A_  ACAATAA
                                TGAGAACA  CC      GAGC
                                ||||||||  ||      ||||
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                                ACTCTTGT  GG      TTCG
                                    CA  GGAC___
GAM1616 ATP6V0D1 3' TAAGAACAGTCTCTAAGAG   21728        ACCACAA
                                TGAGAACA      TAAGAG
                                ||||||||      ||||||
                                ATTCTTGT      ATTCTC
                                    CAGAG__
GAM1616 B4GALT7  3' TGGCAACAACCAGCTAGAGC  28550    AG      CAATA
                                TG  AACAACCA    AGAGC
                                ||  ||||||||    |||||
                                AC  TTGTTGGT    TCTCG
                                 CG      CGA__
GAM1616 ETS2     3' TGAGAACAATTATAAGA     23474        CCACA
                                TGAGAACAA    ATAAGA
                                |||||||||    ||||||
                                ACTCTTGTT    TATTCT
                                     AA___
GAM1616 GPR48    3' TGAGAACATTACATGAAGC   32992        ACC   ATAA
                                TGAGAACA   ACA   GAGC
                                ||||||||   |||   ||||
                                ACTCTTGT   TGT   TTCG
                                    AA_   AC__
GAM1616 HAL      3' TGAGGAAGGTTACAATAAGAA 13333      AACAACC
                                TGAG      ACAATAAGAG
                                ||||      ||||||||||
                                ACTC      TGTTATTCTT
                                  CTTCCAA
GAM1616 IKBKB    3' GAGGACAACCACCAAAG     41805     A      AAT
                                GAG ACAACCAC   AAG
                                ||| ||||||||   |||
                                CTC TGTTGGTG   TTC
                                  C       GT_
GAM1616 LGI1     5' TAAGAACAGGTCACATAGGAG 22999        AC_   A  A
                                TGAGAACA   CACA TA GAG
                                ||||||||   |||| || |||
                                ATTCTTGT   GTGT AT CTC
                                    CCA   _  C
GAM1616 NPC2     3' TGAGAACCAGCCACCCGGAGC 26967       AA_   AATAA
                                TGAGAAC   CCAC    GAGC
                                |||||||   ||||    ||||
                                ACTCTTG   GGTG    CTCG
                                    GTC   GGC__
GAM1616 SLC24A1  3' AGAAACACAACAATAAGAG   21814     CA  C
                                AGAA  AC ACAATAAGAG
                                ||||  ||  ||||||||||
                                TCTT  TG TGTTATTCTC
                                  TG  T
GAM1616 SORCS1   3' TGAGAACAACTGGCCAAG    38104         CACAA
                                TGAGAACAAC    TAAG
                                ||||||||||    ||||
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                                ACTCTTGTTG    GTTC
                                      ACCG_
GAM1616 SULT1C1  3' AGAACTTAGGCCAATAAGAG  9835      AACCA_
                                AGAAC     CAATAAGAG
                                |||||     |||||||||
                                TCTTG     GTTATTCTC
                                   AATCCG
GAM1617 DACH     3' TAAAATGGGCACATTTTACTT 38878       GA   C_
                                TAGAATGGG  ACAT  TACTT
                                |||||||||  ||||  |||||
                                ATTTTACCC  TGTA  ATGAA
                                      G_   AA
GAM1617 GAS7     3' AGGGTGGGGGGCATCCACT   25262    AA    AA
                                AG  TGGGG  CATCTACT
                                ||  |||||  ||||||||
                                TC  ACCCC  GTAGGTGA
                                 CC    CC
GAM1617 SLC17A4  5' TAGGGACTGGCATTTACTTACT 24257      A___   C
                                TGGGGA    CAT TACTTACT
                                ||||||    ||| ||||||||
                                ATCCCT    GTA ATGAATGA
                                   GACC   A
GAM1618 YES1     3' CTGATCTGGTCATATTTT    24119      C  GGTA
                                TTGATC GG    TTATATTTT
                                |||||| ||    |||||||||
                                GACTAG CC    AGTATAAAA
                                   A _____
GAM1619 COL17A1  5' GAGTGATCTTTCAAAAAT    39080    AC       T
                                GA  GATCTTTCGA GAT
                                ||  |||||||||| |||
                                CT  CTAGAAAGTT TTA
                                 CA        T
GAM1620 AK2      3' TTTGTCCTAGGTCCCCTG    30193       T  A    G
                                TTTGTCCT AG GTTTT TG
                                |||||||| || ||||| ||
                                AAACAGGA TC CAGGG AC
                                   _ _    G
GAM1620 APOA2    5' TCTGTCCTTGGTGTCTGTG   11606       AGA  _
                                TTTGTCCTT   GT TTTGTG
                                |||||||||   || ||||||
                                AGACAGGAA   CA AGACAC
                                     C__  C
GAM1620 BGN      3' TGTCCCTGGGGTTTTGTG    11823       AGA
                                TGTCCTT   GTTTTGTG
                                |||||||   ||||||||
                                ACAGGGA   CAAAACAC
                                    CCC
GAM1620 CDH11    3' TTGTCCTTTCTAATTTTGTG  38039       AG_
                                TTGTCCTT   AGTTTTGTG
                                ||||||||   |||||||||
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                                AACAGGAA  TTAAAACAC
                                    AGA
GAM1620 CHN2    3' TTTATCCTTAGCTGT      19815         AGTT
                                TTTGTCCTTAG   TTGT
                                ||||||||||   ||||
                                AAATAGGAATC   GACA
                                     ____
GAM1620 GABRB2  3' TTTGTCCTGGATTGATGTG  34871       TA GTTT
                                TTTGTCCT GA   TGTG
                                |||||||| ||   ||||
                                AAACAGGA CT   ACAC
                                    C_ AACT
GAM1620 LMO2    3' TCTGTCCTTCCCTTGTG    24551        AGAGT
                                TTTGTCCTT   TTTGTG
                                |||||||||   ||||||
                                AGACAGGAA   GAACAC
                                    GG___
GAM1620 MYOD1   3' TGTCCTTGCCCTGTG      42135       AGA
                                TGTCCTT  GTTTTGTG
                                |||||||  ||||||||
                                ACAGGAA  CGGGACAC
                                    ___
GAM1620 PBX2    3' TTTGTCCTCTGGAAGCCT   15112        A__
                                TTTGTCCTT  GAGTTT
                                |||||||||  ||||||
                                AAACAGGAG  TTCGGA
                                    ACC
GAM1620 PLCB4   3' TTGTGTTCAGAAGTTTTGTG 9588     CC   _
                                TTGT TTAGA GTTTTGTG
                                ||||  ||||| ||||||||
                                AACA  AGTCT CAAAACAC
                                  CA   T
GAM1620 PRKACA  3' TTTGCCCTTAGCAAGTG    15592        AGTTTT
                                TTTGTCCTTAG    GTG
                                ||||||||||    |||
                                AAACGGGAATC    CAC
                                    GTT___
GAM1620 SUFU    3' CTTGTCCTTTTATTTGTG   32087        AGAGT
                                TTTGTCCTT   TTTGTG
                                |||||||||   ||||||
                                GAACAGGAA   AAACAC
                                    AAT__
GAM1620 TMOD2   3' TTTGTCCTTGAGATAACATG 30972       A  TTT_
                                TTTGTCCTT GAG   TGTG
                                ||||||||| |||   ||||
                                AAACAGGAA CTC   GTAC
                                    _  TATT
GAM1620 TTN     3' TTTGTCATGATAATTTTGTG  39424      CTTAG
                                TTTGTC   AGTTTTGTG
                                ||||||   |||||||||
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                                AAACAG    TTAAAACAC
                                   TACTA
GAM1620 XK      3' TCTGTCCTTATAAATGTG    34372         GAGTTT
                                TTTGTCCTTA    TGTG
                                ||||||||||    ||||
                                AGACAGGAAT    ACAC
                                     ATTT__
GAM1621 LIFR    5' TGATAATGGTCTTGCAAGTGCA 14160      TACAAAG      C
                                TGATA     TTTGCAAG GCA
                                |||||     |||||||| |||
                                ACTAT     GAACGTTC CGT
                                   TACCA__      A
GAM1622 MASP1   3' AGTATTCAGCCTGGGGCT    40095        AGTATA
                                AGTATTCGG     GGGCT
                                |||||||||     |||||
                                TCATAAGTC     CCCGA
                                     GGAC__
GAM1622 SLC2A1  3' GTCTCGACAGGGCT       27143    A   GAGT
                                GT TTCG    ATAGGGCT
                                || ||||    ||||||||
                                CA GAGC    TGTCCCGA
                                 _   _____
GAM1622 TEM7    3' AATATTCGGGGTGTGCT     33796        A  ATAGG
                                AGTATTCGG GT    GCT
                                ||||||||| ||    |||
                                TTATAAGCC CA    CGA
                                     C  CA___
GAM1622 ZNF141  5' AAGTATTCGGGAGTCTTAG   18344         _  A_
                                AAGTATTCGG AGT  TAG
                                |||||||||| |||  |||
                                TTCATAAGCC TCA  ATC
                                     C   GA
GAM1623 ADAM10  5' TCGCTCCACTTCAGGGGCC   9972         CC   ACC
                                TCGCTCCGC  CAG   GCC
                                |||||||||  |||   |||
                                AGCGAGGTG  GTC   CGG
                                     AA   CC_
GAM1623 BCL7A   3' TCGCTCCACCCTGCCTGCTCCG 34220          CAGA  _  _
           A                     TCGCTCCGCCC    CC GC CCGA
                                ||||||||||    || || ||||
                                AGCGAGGTGGG    GG CG GGCT
                                      AC__  A  A
GAM1623 CEBPD   3' CGCTCCGCTCCGGGCCGTCG   45516        C  AGA   CC
                                CGCTCCGC CC   CCG  CG
                                |||||||| ||   |||  ||
                                GCGAGGCG GG   GGC  GC
                                     A  CCC   A_
GAM1623 DSCAM   5' CGCTCCGCCCGGCCCG      10800         CAGACC
                                CGCTCCGCCC     GCCCG
                                ||||||||||     |||||
```

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                                GCGAGGCGGG     CGGGC
                                      C_____
GAM1623  EMS1     3'  CACACCGCCCCAGGCTGCCCG  39737     T       ACC
                                CGC CCGCCCCAG   GCCCG
                                ||| |||||||||   |||||
                                GTG GGCGGGGTC   CGGGC
                                  T       CGA
GAM1623  FOXD2    5'  TCCTCCGCCCCCTGCCCGA   20974    G       AGACC
                                TC CTCCGCCCC    GCCCGA
                                || |||||||||    ||||||
                                AG GAGGCGGGG    CGGGCT
                                 _       GA___
GAM1623  GPR48    5'  TCGCTCCGCTGCCCTCCGA   32991        CCCAGA  GC
                                TCGCTCCGC     CC  CCGA
                                |||||||||     ||  ||||
                                AGCGAGGCG     GG  GGCT
                                      ACG___  A_
GAM1623  HIF1A    5'  TCGCTCCGGCCTAAGCGC    11354        _ CC  AC
                                TCGCTCCG CC  AG  CGC
                                |||||||| ||  ||  |||
                                AGCGAGGC GG  TC  GCG
                                     C  AT  __
GAM1623  MAN1A1   5'  TCCTGCGTAGCCAGGCCGCCCG 45099     _ C___    A
              AC                  TCC GC    CCAG CCGCCCGAC
                                ||| ||    |||| |||||||||
                                AGG CG    GGTC GGCGGGCTG
                                  A  CATC    C
GAM1623  MAOB     5'  TCGCCCCGTTCCAGGCCTCCC  41031        CC    A  G
                                TCGCTCCG  CCAG CC CCC
                                ||||||||  |||| || |||
                                AGCGGGGC  GGTC GG GGG
                                     AA    C  A
GAM1623  MAP7     5'  CCGCTCCGCCCTTTCCTCG    19572          CAGACCG  _
                                TCGCTCCGCCC      CC CG
                                ||||||||||       || ||
                                GGCGAGGCGGG      GG GC
                                      AAA____  A
GAM1623  MTNR1A   5'  TCGTCCGCCCGCCCG      25551     C      CAGACC
                                TCG TCCGCCC     GCCCG
                                ||| |||||||     |||||
                                AGC AGGCGGG     CGGGC
                                 _      _______
GAM1623  S100A10  5'  TCGCCCGCCCCAGACAGAGC   40399      T        C__
                                TCGC CCGCCCCAGAC   GC
                                |||| ||||||||||   ||
                                AGCG GGCGGGGTCTG   CG
                                  _         TCT
GAM1623  TIA1     5'  ACTCCGCCTCCTCCTCCG    35285         _ AGA  GC
                                GCTCCGCC CC   CC  CCG
                                |||||||| ||   ||  |||
```

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                                TGAGGCGG GG   GG  GGC
                                    A  A__  A_
GAM1623  TR2      5'  TCGCTCTCGCTCCTGGCCCG   43636       _   C  AGACC
                                TCGCTC CGC CC    GCCCG
                                |||||| ||| ||    |||||
                                AGCGAG GCG GG    CGGGC
                                   A   A  AC___
GAM1624  AGRN     3'  CAGCGGGCGCGGGGCTCTGGTG 44248      AT  AT       CGAC
              C                  CAGC  GT  CGGGGCTC   GC
                                ||||  ||  ||||||||   ||
                                GTCG  CG  GCCCCGAG   CG
                                  CC  C_      ACCA
GAM1624  ANK1     3'  GCGGCCAGGGGGCTCTGACG   33868    AT  ATC      C
                                GC  GT   GGGGCTC GACG
                                ||  ||   ||||||| ||||
                                CG  CG   CCCCGAG CTGC
                                 C_  GTC      A
GAM1624  EDNRA    5'  TGTCCCGGGCTCCGGCGC    42007     A  G       A
                                TGT TC GGGCTCCG CGC
                                ||| || |||||||| |||
                                ACA GG CCCGAGGC GCG
                                  _  G       C
GAM1624  SORCS2   3'  CACCATCCAGGGCTCTGGCG   34045    G   GTA       CGA
                                CA CAT   TCGGGGCTC   CG
                                || |||   |||||||||   ||
                                GT GTA   GGTCCCGAG   GC
                                 G   ___        ACC
GAM1624  UBE2H    3'  ACATGGCTGGCTCCGAG     17801       TATCGG       C
                                GCATG     GGCTCCGA G
                                |||||     |||||||| |
                                TGTAC     CCGAGGCT C
                                   CGA___       A
GAM1625  AOAH     5'  GAGGGATGCTGGAGCTGAG   45020    AAA     T TCT
                                GA   ATGCT G   GGCTGAG
                                ||   ||||| |   |||||||
                                CT   TACGA C   TCGACTC
                                 CCC    _ C__
GAM1625  ASTN     3'  GAGGAATGCTTGAGGGTG    42947    AA       TCT  C
                                GA  AATGCTTG   GG TG
                                ||  ||||||||   || ||
                                CT  TTACGAAC   CC AC
                                 CC       TC_  _
GAM1625  EHD2     3'  GAGGGTGTTGCCTGGCTG    31132    AAAA  C
                                GA    TG TTGTCTGGCTG
                                ||    || ||||||||||
                                CT    AC AACGGACCGAC
                                 CCC_  _
GAM1625  EIF4A1   3'  CCAGAGATTGAGCCCTGGCTG  10866    _  AAAAT_   TGT
                                CC GA     GCT   CTGGCTG
                                || ||     |||   |||||||
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                                GG CT     CGG   GACCGAC
                                 T  CTAACT   ___
GAM1625  HS3ST2    5'  CCGAGGGGGCACCGGCGGCTGA 25812      AAAAT  _   TC
              G                   CCGA    GC TTG  TGGCTGAG
                                  ||||    || |||  ||||||||
                                  GGCT    CG GGC  GCCGACTC
                                    CCCC_  T   C_
GAM1625  IL2RB     5'  CCGAGGAAGGAAGCCCTGGCTG 9380       AAAAT___   TGT
              AG                  CCGA      GCT   CTGGCTGAG
                                  ||||      |||   |||||||||
                                  GGCT      CGG   GACCGACTC
                                    CCTTCCTT   ___
GAM1625  IMPDH1    3'  GAAGTGCCACATGGCTGAG   9407      AAA    TGTC
                                  GAA   TGCT    TGGCTGAG
                                  |||   ||||    ||||||||
                                  CTT   ACGG    ACCGACTC
                                    C__    TGT_
GAM1625  IREB2     3'  AAAAAATGCATAGGGTTGAG   42451         TTGTCT  C
                                  GAAAAATGC     GG TGAG
                                  |||||||||     || ||||
                                  TTTTTTACG     CC ACTC
                                       TATC__  A
GAM1625  ITK       3'  GAAAGCTGTCAGGTTGA     24443      AAT   T   T  C
                                  GAAA   GCT GTC GG TGA
                                  ||||   ||| ||| || |||
                                  CTTT   CGA CAG CC ACT
                                    ___   _   T  A
GAM1625  MAP2K2    5'  CCGAGGGGCGCTGGGGCTGAG  36206      AAAA    T TCT
                                  CCGA    TGCT G   GGCTGAG
                                  ||||    |||| |   |||||||
                                  GGCT    GCGA C   CCGACTC
                                    CCCC    _ C__
GAM1625  MUCDHL    3'  CCGAGAAGCGCTTGTCCTCCGA 36319      A  A       GG
              G                   CCGA AA TGCTTGTCT  CTGAG
                                  |||| || |||||||||  |||||
                                  GGCT TT GCGAACAGG  GGCTC
                                    C  C        A_
GAM1625  TAF12     3'  CCAAGGATGAGATGGCTGAG   24866      AAA   CTTGTC
                                  CCGA   ATG     TGGCTGAG
                                  ||||   |||     ||||||||
                                  GGTT   TAC     ACCGACTC
                                    CC_   TCT___
GAM1625  TOP2B     3'  GAAAAATGTTTGTGCT      9885          C    CTG
                                  GAAAAATG TTGT   GCT
                                  |||||||| ||||   |||
                                  CTTTTTAC AACA   CGA
                                       A   ___
GAM1625  TRIM9     3'  GAAAGATCTTGCCCATGAG   31567      A  G       GC
                                  GAAA AT CTTGTCTG  TGAG
                                  |||| || ||||||||  ||||
```

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                                CTTT TA GAACGGGT  ACTC
                                  C _      __
GAM1626 CNTNAP2  3' TTTCCATTTTATTCAGCCGGG 30502       GC___ C
                                TTTCCATT    CA CCGGG
                                ||||||||    || |||||
                                AAAGGTAA    GT GGCCC
                                    AATAA  C
GAM1626 ELK3     5' TTTCTAGGAGGACCCGGGCGAA 23422     CATTGCC
              A                  TTTC      ACCCGGGCGAAA
                                ||||      ||||||||||||
                                AAAG      TGGGCCCGCTTT
                                  ATCCTCC
GAM1626 FLRT2    3' TTTCCATTTGTTACACAAGGAA 29870       GCC_ C   C
              A                  TTTCCATT   AC CGGG GAAA
                                ||||||||   || |||| ||||
                                AAAGGTAA   TG GTTC CTTT
                                    ACAA  T   _
GAM1626 GNPI     3' TTTCCATTGCACTTGTTAC   24188        C  CCGG_
                                TTTCCATTGC AC    GC
                                ||||||||||  ||    ||
                                AAAGGTAACG TG    TG
                                    _  AACAA
GAM1626 HLCS     3' TTCCCATTGTCATTTCCATGTA 7651        C  C__  GGC
              AAA                  TTTCCATTG CA   CCG   GAAA
                                ||||||||| ||   |||   ||||
                                AAGGGTAAC GT   GGT   TTTT
                                    A  AAA   ACA
GAM1626 HMGCR    3' CACTGCCACTTCCATGAAAA  9234        __  GGC
                                CATTGCCAC  CCG   GAAAA
                                |||||||||  |||   |||||
                                GTGACGGTG  GGT   CTTTT
                                    AA   A__
GAM1626 INSR     3' TTTCCATCTGCTGGGGGCG   43382       _  CACCC
                                TTTCCAT TGC    GGGCG
                                |||||||  |||    |||||
                                AAAGGTA ACG    CCCGC
                                    G   ACC__
GAM1626 KLF7     3' TTTCCATTGGCAACAGCGGG  18986        _ C  C_
                                TTTCCATTG C AC  CGGG
                                |||||||||  | ||  ||||
                                AAAGGTAAC G TG  GCCC
                                    C T  TC
GAM1626 LCT      3' TTTCCATTTTACTCAGCAA   14112       GCC  C   G
                                TTTCCATT   AC CGG CGA
                                ||||||||   || ||| |||
                                AAAGGTAA   TG GTC GTT
                                    AA_  A   _
GAM1626 MLPH     3' TTTCCATTCCATTCATGAAA  35870       G   CC  GGC
                                TTTCCATT CCA  CG   GAAA
                                ||||||||  |||  ||   ||||
```

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                                AAAGGTAA GGT  GT   CTTT
                                    _   AA  A__
GAM1626  NAPB     3'  CATTGCCACCCCCAGTAGTGGG 43171          _________  C
                GA                  CATTGCCACCC       GGG GA
                                    ||||||||||        ||| ||
                                    GTAACGGTGGG       CCC CT
                                        GGTCATCA  _
GAM1626  SCD      3'  TTTCCATTCCATCTAGCAAAA  22839        G   CCCG
                                    TTTCCATT CCA    GGCGAAA
                                    |||||||| |||    |||||||
                                    AAAGGTAA GGT    TCGTTTT
                                        _   AGA_
GAM1626  ZNF146   3'  TTTCTGTTCCCACTTTTAGTGA 28363      CA  G    CCG_  C
                AAA                   TTTC  TT CCAC    GG GAAAA
                                    ||||  || ||||    || |||||
                                    AAAG  AA GGTG    TC CTTTT
                                      AC  G    AAAA  A
GAM1627  BCL11B   3'  TGTTTTGCTTTTCATTCAA   39764        T    GA
                                    TGTTTT GCTT  CGTTCAA
                                    |||||| ||||  |||||||
                                    ACAAAA CGAA  GTAAGTT
                                        _   AA
GAM1627  CDH18    5'  TCTGTTCTTGCTCCTCTTCA  22342           GACG
                                    TCTGTTTTTGCTT    TTCA
                                    ||||||||||||    ||||
                                    AGACAAGAACGAG    AAGT
                                          GAG_
GAM1627  CPSF6    3'  CCTCTGTTTTTTTTGAC     28131          GC
                                    CCTCTGTTTTT  TTGAC
                                    ||||||||||  |||||
                                    GGAGACAAAAA  AACTG
                                        A_
GAM1627  D12S2489E 3'  CCTGTTTTTGTTTGTTTCC   28884          C   ACG
                                    TCTGTTTTTG TTG   TTC
                                    |||||||||| |||   |||
                                    GGACAAAAAC AAC   AGG
                                        A   AA_
GAM1627  DSCR3    3'  CCTCTGTTTTCTGCTACTCAGT 25823          _    TGAC_
                T                    CCTCTGTTT TTGCT     GTT
                                    |||||||| |||||     |||
                                    GGAGACAAA GACGA     CAA
                                        A     TGAGT
GAM1627  EDAR     3'  TCTGTTTTTATTCCCATT    35310          C  GA
                                    TCTGTTTTTG TT  CGTT
                                    |||||||||| ||  ||||
                                    AGACAAAAAT AA  GTAA
                                        _ GG
GAM1627  FANCD2   3'  TCTATTTTTGTATGTTTCAA  37514          CT  ACG
                                    TCTGTTTTTG  TG   TTCAA
                                    |||||||||  ||   |||||
```

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                                AGATAAAAAC  AC   AAGTT
                                      AT  A__
GAM1627  HLF      5'  CCTCGTTTTGCAAAATGTTCAA 13388      T    T  TT  C
                                CCTC GTTTT GC  GA GTTCAA
                                |||| ||||| ||  || ||||||
                                GGAG CAAAA CG  TT CAAGTT
                                  _    _ TT  A
GAM1627  IL2RA    3'  CCTCTGTTTTTTAGAAATTCAA 7670          GCTT  C
                                CCTCTGTTTTT    GA GTTCAA
                                ||||||||||    || ||||||
                                GGAGACAAAAA    CT TAAGTT
                                      AT__  T
GAM1627  MYO9A    3'  TGTTTTTGCTTTCCCCA     27906          GACG
                                TGTTTTTGCTT    TTCA
                                ||||||||||    ||||
                                ACAAAAACGAA    GGGT
                                      AG__
GAM1627  PSAP     3'  CCTTTGTTTTGCTGCTTTGTTC 42966     C     __     GAC
              AA                  CCT TGTTTT  TGCTT   GTTCAA
                                ||| ||||||  |||||   ||||||
                                GGA ACAAAA  ACGAA   CAAGTT
                                  A     CG    A__
GAM1627  SLC9A5   3'  CTCTGTTTGGGGAATGTTCA   21386        TTGCTT  C
                                CTCTGTTT     GA GTTCA
                                ||||||||     || |||||
                                GAGACAAA     TT CAAGT
                                     CCCC__  A
GAM1627  ZNF24    3'  TTTTTAGCCTGACGTTCAA    28091      _
                                TTTTT GCTTGACGTTCAA
                                ||||| ||||||||||||
                                AAAAA CGGACTGCAAGTT
                                   T
GAM1628  AXL      3'  GAATTGCAGATTCTAGAGCTTT 34884     G        CC_
                                GAA TGCAGATTTT   GCTTT
                                ||| ||||||||||   |||||
                                CTT ACGTCTAAGA   CGAAA
                                  A         TCT
GAM1628  RYR2     3'  AAGTGCAAACTGCTT       9765           TTCC
                                AAGTGCAGATT    GCTT
                                ||||||||||    ||||
                                TTCACGTTTGA    CGAA
                                      ____
GAM1628  TTN      3'  GAGGTGCAGATAGCTTGCTTT  39421    A      TTTCC
                                GA GTGCAGAT    GCTTT
                                || ||||||||    |||||
                                CT CACGTCTA    CGAAA
                                 C       TCGAA
GAM1629  PCDH11Y  3'  TAGTACGCTCTGTCATGA    37351        GC   C  G
                                TAGTACGC  CTG CG GA
                                ||||||||  ||| || ||
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                                ATCATGCG  GAC GT CT
                                    A_   A  A
GAM1629  SLC1A2   5'  GTGCGCGCCTGGGGAG     41602    A      CC
                                GT CGCGCCTG  GGGAG
                                || ||||||||  |||||
                                CA GCGCGGAC  CCCTC
                                 C      __
GAM1629  STAR     3'  GCAGCGGCCGGGAG       7389     C   CCT
                                GTA GCG   GCCGGGAG
                                ||| |||   ||||||||
                                CGT CGC   CGGCCCTC
                                  _  ___
GAM1630  ATRN     3'  CACCATAAATGGGG       40267         CCAC
                                CACCGTGAAT   GGGG
                                ||||||||||   ||||
                                GTGGTATTTA   CCCC
                                     _____
GAM1630  ATRN     3'  GTCAAATTCTCCACGGGGA   40278    G  _____
                                GT AA   TCCACGGGGA
                                || ||   ||||||||||
                                CA TT   AGGTGCCCCT
                                 G  TAAG
GAM1630  CARKL    3'  ACACCGTGGATAAGGGG     29984        A  CCAC
                                ACACCGTG AT   GGGG
                                |||||||| ||   ||||
                                TGTGGCAC TA   CCCC
                                    C  TT__
GAM1630  CD79B    3'  ACACCGTTTATTCCACGGGG  8419        GAA_
                                ACACCGT   TCCACGGGG
                                |||||||   |||||||||
                                TGTGGCA   AGGTGCCCC
                                   AATA
GAM1630  EDARADD  5'  ACCGTGGGACCACGGGGA   38844       AAT
                                ACCGTG   CCACGGGGA
                                ||||||   |||||||||
                                TGGCAC   GGTGCCCCT
                                   CCT
GAM1630  ENG      5'  CGTGGGCTCGCACGGGGA   6494      AA_  _
                                CGTG   TC CACGGGGA
                                ||||   || ||||||||
                                GCAC   AG GTGCCCCT
                                  CCG  C
GAM1630  GPC1     3'  CACCGTGAACAGGG       13236        ATCC
                                CACCGTGA   ACGGGG
                                ||||||||   ||||||
                                GTGGCACT   TGTCCC
                                     _____
GAM1630  GRIN2A   5'  CATCGCCCCCACGGGG     9106     C   GAA
                                CA CGT   TCCACGGGG
                                || |||   |||||||||
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                                GT GCG   GGGTGCCCC
                                 A   G__
GAM1630  LZTR1    5'  ACACAGCCACGGGGA       27629      C TGAAT
                                ACAC G     CCACGGGGA
                                |||| |     |||||||||
                                TGTG C     GGTGCCCCT
                                  T _____
GAM1630  MAP1A    3'  AACACAGCAGCACGGGGA    14336      C   AATC
                                AACAC GTG    CACGGGGA
                                ||||| |||    ||||||||
                                TTGTG CGT    GTGCCCCT
                                   T   C___
GAM1630  MEF2D    3'  CACCGTGAATTGCAGGG     25417         CCA
                                CACCGTGAAT   CGGGG
                                ||||||||||   |||||
                                GTGGCACTTA   GTCCC
                                      AC_
GAM1630  MEN1     5'  AACACACACCACGGGG      39139      _ TGAAT
                                AACAC CG     CCACGGGG
                                ||||| ||     ||||||||
                                TTGTG GT     GGTGCCCC
                                   T _____
GAM1630  PTPRA    5'  AACACCGTGAACACCAGG    38904         TC   G
                                AACACCGTGAA  CAC GGG
                                ||||||||||  ||| |||
                                TTGTGGCACTT  GTG TCC
                                      __   G
GAM1630  SIAT7D   3'  CCATGAATTACTCAGGGA    30828        CCA_
                                CCGTGAAT    CGGGGA
                                ||||||||    ||||||
                                GGTACTTA    GTCCCT
                                     ATGA
GAM1630  SLC6A3   3'  ACTGTGAGCACGGGGA      9805     C    ATC
                                AC GTGA   CACGGGGA
                                || ||||   ||||||||
                                TG CACT   GTGCCCCT
                                 A    C__
GAM1630  SMARCA1  3'  ACCATGAATACACTGGA     16892         C   GG
                                ACCGTGAAT CAC  GGA
                                ||||||||| |||  |||
                                TGGTACTTA GTG  CCT
                                      T   A_
GAM1630  TBL1X    5'  ACAGTGACCTCCACGGGGA   24868    C    A_
                                AC GTGA  TCCACGGGGA
                                || ||||  ||||||||||
                                TG CACT  AGGTGCCCCT
                                 T    GG
GAM1630  TNFRSF6B 3'  ACACGTGCCCACGGGG      32346     C   AA
                                ACAC GTG  TCCACGGGG
                                |||| |||  |||||||||
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                                TGTG CAC  GGGTGCCCC
                                  _  __
GAM1630  UCP3     3'  ACCAGATTTCACGGGGA     17849      T  ATC
                                ACCG GA   CACGGGGA
                                |||| ||   ||||||||
                                TGGT CT   GTGCCCCT
                                  _  AAA
GAM1631  MAP4K5   5'  CGGGTTTGCCGTCGCCGC    27304    A  CC  G
                                CG GT  GC GTCGCCGC
                                || ||  || ||||||||
                                GC CA  CG CAGCGGCG
                                 C  AA  G
GAM1631  TNS      3'  CGAGCTCAACAGCTGCCTGTTC 35473      _ C    CGCC
                                CGAG TC GCGGT    GCCTGTTC
                                |||| || |||||    ||||||||
                                GCTC AG TGTCG    CGGACAAG
                                  G  T    A___
GAM1632  OAS2     3'  TGGATATATCAGGTATATCTTG 14898          TATGC  C
              GT                  TGGATGTATC    TA CTTGGT
                                ||||||||||    || ||||||
                                ACCTATATAG    AT GAACCA
                                     TCCAT  A
GAM1633  LFG      3'  TAGCAGGAGCCCGCTGGCAGTG 44147         A    AATTGT
              A                   TAGTAGGA CCCGC     GTGA
                                |||||||| |||||     ||||
                                ATCGTCCT GGGCG     CACT
                                    C    ACCGT_
GAM1633  PMX1     5'  TAATAGGAGCCTGTAATTACGT 35516         A  CGC
              G                   TAGTAGGA CC   AATTGTGTG
                                |||||||| ||   |||||||||
                                ATTATCCT GG   TTAATGCAC
                                    C  ACA
GAM1633  RERE     3'  GTAGGAATTCACAATTAGTGA  29032        CC       T
                                GTAGGAA  CGCAATTG GTGA
                                |||||||  |||||||| ||||
                                CATCCTT  GTGTTAAT CACT
                                   AA       _
GAM1633  SCAP2    3'  TAATAGGAATTAAATGTGTGA  19443         CCCGCAAT
                                TAGTAGGAA       TGTGTGA
                                |||||||||       |||||||
                                ATTATCCTT       ACACACT
                                     AATTT___
GAM1634  ADAMTS13 5'  GCCAGCCCGAGGAGTGGAGC   40035      T  __    AAACAA
                                GCCA GTT  GGGAG     AGC
                                |||| |||  |||||     |||
                                CGGT CGG  TCCTC     TCG
                                  _  GC    ACC___
GAM1634  ARNT2    3'  ATGTTGGAGAGTAGAGCA    31352        _  AAACAA
                                ATGTTGG GAG     AGCA
                                ||||||| |||     ||||
```

```
                                TACAACC CTC     TCGT
                                   T  ATC___
GAM1634 BCL11B   3' TGCCTGTTTCTTAAACAGAGCA 39760     A   GGGAG    A
                                TGCC TGTT    AAACA AGCA
                                |||| ||||    ||||| ||||
                                ACGG ACAA    TTTGT TCGT
                                  _   AGAA_    C
GAM1634 CKTSF1B1 3' ACCTGAGGGACAAAGCA    30078    A  TT   GAAA
                                GCC TG  GGGA   CAAAGCA
                                ||| ||  ||||   |||||||
                                TGG AC  CCCT   GTTTCGT
                                  _ T_   ____
GAM1634 CYP2B6   3' CCAGCCTGGGAGACAGAGCA  8921     TG      AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __ C
GAM1634 DDB2     5' GCCTCTGGGGAGAAACAAGGC  6462     A_  TT        A
                                GCC  TG  GGGAGAAACAA GC
                                |||  ||  ||||||||||| ||
                                CGG  AC  CCCTCTTTGTT CG
                                  AG  __         C
GAM1634 DLC1     5' TGTCCTGGCTGGGAGCGAAGC  25906    _ AT      AAACA
                                TG CC  GTTGGGAG    AAGC
                                || ||  ||||||||    ||||
                                AC GG  CGACCCTC    TTCG
                                 A  AC       GC___
GAM1634 ENG      3' TGCCATGCTGCTGGTGGAG   6508          _____
                                TGCCATGTTG    GGAG
                                ||||||||||    ||||
                                ACGGTACGAC    CCTC
                                      GACCA
GAM1634 ESPN     5' TGCGGGCCGGGAGGCGGAGC  36449     CAT      AAACAA
                                TGC   GTTGGGAG     AGC
                                |||   ||||||||     |||
                                ACG   CGGCCCTC     TCG
                                  CC_       CGCC__
GAM1634 ESR1     3' TGCAGTTGGAAACAGAGC    6539     CAT     GAA   A
                                TGC   GTTGGGA   ACA AGC
                                |||   |||||||   ||| |||
                                ACG   CAACCTT   TGT TCG
                                  T__       ___   C
GAM1634 FGF2     3' TGCCACGTGAGAGCAGAGC   12846        T    AAA  A
                                TGCCATGT GGGAG   CA AGC
                                |||||||| |||||   || |||
                                ACGGTGCA CTCTC   GT TCG
                                      _    ___ C
GAM1634 FLRT2    3' TGCCATGTTGTACACAA     29864          GGAGAA
                                TGCCATGTTG     ACAA
                                ||||||||||     ||||
```

```
                                ACGGTACAAC     TGTT
                                     ATG___
GAM1634  GPC4     3'  TGCTTGTAAGAAACAAGGC   11088    CATG   GG      A
                                TGC   TTG  AGAAACAA GC
                                |||   |||  |||||||| ||
                                ACG   AAC  TCTTTGTT CG
                                 _____  AT       C
GAM1634  GUCY1A2  3'  TGCTTGTTCTCAACAAAGC   9226     CA   GGGAGA
                                TGC  TGTT     AACAAAGC
                                |||  ||||     ||||||||
                                ACG  ACAA     TTGTTTCG
                                 A_   GAG___
GAM1634  HDAC5    3'  CCATATCCAGGGAGACAAAGCA 40162        __     AA
                                CCATGTT  GGGAGA  CAAAGCA
                                |||||||  ||||||  |||||||
                                GGTATAG  CCCTCT  GTTTCGT
                                    GT    __
GAM1634  ITPR1    5'  GCCGGTTTGGGGGAGCAGGGC  13666    ATG    A  AA  AA
                                GCC   TTGGG GA  CA  GC
                                |||   |||||  ||  ||  ||
                                CGG   AACCC CT  GT  CG
                                 CCA    C  C_  CC
GAM1634  MADH4    3'  TGCTAGGAGCAAGGC      23820         AAA   A
                                TGTTGGGAG   CAA GC
                                |||||||||   ||| ||
                                ACGATCCTC   GTT CG
                                     ___   C
GAM1634  MEOX1    3'  GCTGGTGTTGGGAGACAGAGC  30399    CA_       AA  A
                                GC   TGTTGGGAGA  CA AGC
                                ||   ||||||||||  || |||
                                CG   ACAACCCTCT  GT TCG
                                 ACC         __  C
GAM1634  MYCL1    3'  TGCCTGGTTGGGATGGAGC   23892     AT     GAAACAA
                                TGCC  GTTGGGA      AGC
                                ||||  |||||||      |||
                                ACGG  CAACCCT      TCG
                                  AC      ACC____
GAM1634  NPAS2    5'  GCCGCCGCTGGGAGACGAGGC  14819     A_       AACAAA
                                GCC  TGTTGGGAGA     GC
                                |||  ||||||||||     ||
                                CGG  GCGACCCTCT     CG
                                 CG        GCTC__
GAM1634  NR1D1    5'  TGATGGGGAGAAACGGGGCA   34705    TT_      AAA
                                TG   GGGAGAAAC   GCA
                                ||   |||||||||   |||
                                AC   CCCTCTTTG   CGT
                                 TAC       CCC
GAM1634  RBBP9    3'  CCAGCCTGGGAGACAGAGCA   43136     TG      AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
```

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                                GGT  GACCCTCT  GT TCGT
                                  CG       __  C
GAM1634  SLC16A2   3'  TGCCATGTGTATACAAGAA   27158        ___  G
                                TGCCATGT   TG GAGAA
                                ||||||||   || |||||
                                ACGGTACA   AT TTCTT
                                     CAT  G
GAM1634  SRGAP2    3'  TGCCATGAGGGGTGGAGCA   43987       TT   AGAAACAA
                                TGCCATG  GGG       AGCA
                                |||||||  |||       ||||
                                ACGGTAC  CCC       TCGT
                                    TC   ACC_____
GAM1634  TCF12     3'  TATTATTAGAAATAAAGCA   17345      GG    C
                                TGTTG  AGAAA AAAGCA
                                |||||  ||||| ||||||
                                ATAAT  TCTTT TTTCGT
                                   AA    A
GAM1634  XRCC2     3'  CCAGCCTGGGAGACAGAGCA   24091     TG       AA  A
                                CCA  TTGGGAGA  CA AGCA
                                |||  ||||||||  || ||||
                                GGT  GACCCTCT  GT TCGT
                                  CG       __  C
GAM1634  XRCC5     3'  TGCTTGTTGGGAGGAAGC    34495     CA       AAACA
                                TGC  TGTTGGGAG    AAGC
                                |||  |||||||||    ||||
                                ACG  ACAACCCTC    TTCG
                                  A_       C____
GAM1635  ABCC1     5'  GGCGGCGGGCACCGGGCGGCGG 33406         _  T  A_  A
                                GGCGGCGGG GC CG  CG CGG
                                ||||||||| || ||  || |||
                                CCGCCGCCC TG GC  GC GCC
                                     G  _  CC  C
GAM1635  ABCC4     5'  AGGCGGCGGTGGCCGCGGG   25195         _   T  A  AC
                                AGGCGGCGG GGC CG CG  GG
                                ||||||||| ||| || ||  ||
                                TCCGCCGCC CCG GC GC  CC
                                     A  _  _  __
GAM1635  ACTN2     5'  GGCGGCGGGCGGCGG       9948          GCTCGA  A
                                GGCGGCGGG     CG CGG
                                |||||||||     || |||
                                CCGCCGCCC     GC GCC
                                      _______  C
GAM1635  ACTN2     5'  AGGCGGCGGGCGGCGG       9939          GCTCGA  A
                                AGGCGGCGGG     CG CGG
                                ||||||||||     || |||
                                TCCGCCGCCC     GC GCC
                                      _______  C
GAM1635  ALDH3B1   3'  AGGCGGCGCGGCGATTGCGGCG 45059         G   TCGA_  A
            G                    AGGCGGCG GGC     CG CGG
                                ||||||| |||     || |||
```

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                                TCCGCCGC CCG    GC GCC
                                    G  CTAAC  C
GAM1635  ANKH    5'  GGCGACGGGGGCGACGG    38319         CTCGA
                                GGCGGCGGGG    CGACGG
                                ||||||||||    ||||||
                                CCGCTGCCCC    GCTGCC
                                    C____
GAM1635  AQP3    5'  AGGCGGCGGCGCTGTCGGGCGG 40581        G  CGA  A_
                                AGGCGGCGG GCT  CG  CGG
                                ||||||||| |||  ||  |||
                                TCCGCCGCC CGA  GC  GCC
                                    G  CA_  CC
GAM1635  AQP5    5'  AGGCGGCGGAGGAGGTGGA   11627         CTC  CGAC
                                AGGCGGCGGGG  GA   GGA
                                ||||||||||  ||   |||
                                TCCGCCGCCTC  CT   CCT
                                   ___  CCA_
GAM1635  AQP6    5'  GGCAGCGGGGCTCATGGGA   38250          ACGAC
                                GGCGGCGGGGCTCG    GGA
                                ||||||||||||||    |||
                                CCGTCGCCCCGAGT    CCT
                                    AC___
GAM1635  ARD1    5'  GGCGGCGGGGCTCGCGGG    18573          A  AC
                                GGCGGCGGGGCTCG CG  GG
                                |||||||||||||| ||  ||
                                CCGCCGCCCCGAGC GC  CC
                                    _  __
GAM1635  BAPX1   3'  AGGCAGCGGCACTGCGGTGG   10157        G  CGA  AC
                                AGGCGGCGG GCT  CG  GG
                                ||||||||| |||  ||  ||
                                TCCGTCGCC TGA  GC  CC
                                    G  C__  CA
GAM1635  BCL11A  5'  GGCGGCGGCGGCGGCGGCGGCG 39715        _  T_  A  A
          G                      GGCGGCGG GGC  CG CG CGG
                                ||||||||| |||  || || |||
                                CCGCCGCC CCG  GC GC GCC
                                    G  CC  C  C
GAM1635  BMP2    5'  GGCGGTGGGGCTCGGAGA    10186       C       AC
                                GGCGG GGGGCTCG  GA
                                ||||| ||||||||  ||
                                CCGCC CCCCGAGC  CT
                                   A       CT
GAM1635  BTG1    5'  GGCGCTGGGGCTCGGCGGCG   11909      GC       A  A
                                GGCG  GGGGCTCG CG CG
                                ||||  |||||||| || ||
                                CCGC  CCCCGAGC GC GC
                                  GA       C  C
GAM1635  C1orf6  5'  GGCGGTGGGCCGGCGG      33531       CG    T  ACGA
                                GGCGG  GGGC CG    CGG
                                |||||  |||| ||    |||
```

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                                CCGCC  CCCG GC   GCC
                                  A_   _ C___
GAM1635  CACNA1A  5'  GGCGGCGGCGGCTCGGCGCCTC 35739       _    A  A__
              GG                  GGCGGCGG GGCTCG CG   CGG
                                  |||||||| |||||| ||   |||
                                  CCGCCGCC CCGAGC GC   GCC
                                     G     C  GGA
GAM1635  DNCI1    5'  AGGTGGCGGGGCCGGCGCGG   44987    C      T  A  A
                                  AGG GGCGGGGC CG CG CGG
                                  ||| |||||||| || || |||
                                  TCC CCGCCCCG GC GC GCC
                                    A       _ C  _
GAM1635  DNMT3B   5'  GGCGGCGGAGCCGCGG      27877          TCGA  A
                                  GGCGGCGGGGGC   CG CGG
                                  ||||||||||    || |||
                                  CCGCCGCCTCG   GC GCC
                                        _____  _
GAM1635  E2F1     5'  AGGCGGCGGCGGCGGCGCGG   44483         _  TCGA  A
                                  AGGCGGCGG GGC   CG CGG
                                  |||||||| |||   || |||
                                  TCCGCCGCC CCG   GC GCC
                                       G   CC__  _
GAM1635  FKBP1A   5'  GGCGGGCGGCGCGACGG     38281      _  G  TCGAC
                                  GGCGG CGG GC    GACGG
                                  ||||| ||| ||    |||||
                                  CCGCC GCC CG    CTGCC
                                    C   G  _____
GAM1635  FMR2     5'  AGGCGGCGGCGGCGGGCGG   12949         _  TCGACGA
                                  AGGCGGCGG GGC      CGG
                                  |||||||| |||      |||
                                  TCCGCCGCC CCG      GCC
                                       G   CCC_____
GAM1635  FOXD1    5'  GGTGGCGGGGCCCGGGCGG   20931    C        ACGA
                                  GG GGCGGGGCTCG    CGG
                                  || ||||||||||    |||
                                  CC CCGCCCCGGGC    GCC
                                   A          CC__
GAM1635  FOXG1B   5'  GGCGCGGGGGGGCGGCGG    23508     G    CTCGA  A
                                  GGCG CGGGG     CG CGG
                                  |||| |||||     || |||
                                  CCGC GCCCC     GC GCC
                                    _    CCC__  C
GAM1635  FOXG1B   5'  GGCGGCGCGGCGACCGG     23509       G  TC  GA
                                  GGCGGCG GGC  GAC  CGG
                                  ||||||| |||  |||  |||
                                  CCGCCGC CCG  CTG  GCC
                                     G   __   __
GAM1635  FXYD1    3'  GGCGGCGGAGGGGGCGGTGG  34863         CTCGA  AC
                                  GGCGGCGGGG    CG  GG
                                  ||||||||||    ||  ||
```

```
                                CCGCCGCCTC    GC  CC
                                     CCCC_  CA
GAM1635  G6PT1    5'  GGCGGCGAAGAGGCGGCGG   11165        CTCGA  A
                                GGCGGCGGGG    CG CGG
                                ||||||||||    || |||
                                CCGCCGCTTC    GC GCC
                                     TCC__  C
GAM1635  GAA      5'  GGCGGGGCCGCGGTGG      6666        T  A  AC
                                GGCGGGGC CG CG  GG
                                ||||||||  || ||  ||
                                CCGCCCCG GC GC  CC
                                    _ _  CA
GAM1635  GAS1     5'  AGGCGCGGGGAGCGGCGGA   13064      G    CTCGA  A
                                AGGCG CGGGG    CG CGGA
                                |||||  |||||    || ||||
                                TCCGC GCCCC    GC GCCT
                                  _    TC___  C
GAM1635  GATA2    5'  GGCTGGCGGGGCTTACAGG   13087     _       CG   AC
                                GGC GGCGGGGCT  ACG  GG
                                |||  |||||||||  |||  ||
                                CCG CCGCCCCGA  TGT  CC
                                  A       A_  __
GAM1635  HCN2     3'  GGCAGCGGGAAGCCGGCGG   10171        CTCGA  A
                                GGCGGCGGGG    CG CGG
                                ||||||||||    || |||
                                CCGTCGCCCT    GC GCC
                                     TCG__  C
GAM1635  HIC1     5'  AGGCGGCGGGGCCGGCG     44561          T  A
                                AGGCGGCGGGGC CG CG
                                ||||||||||||  || ||
                                TCCGCCGCCCCG GC GC
                                      _  C
GAM1635  IL6R     5'  AGGGGCGGGGCGGGGCGGTGG  8165     C      TCGA  AC
                                AGG GGCGGGGC   CG  GG
                                |||  ||||||||   ||  ||
                                TCC CCGCCCCG   GC  CC
                                  _      CCCC  CA
GAM1635  LAMA5    5'  GCGGCGGGAGCCCGGCGG    24499        _    ACGA
                                GCGGCGGG GCTCG   CGG
                                ||||||||  |||||   |||
                                CGCCGCCC CGGGC   GCC
                                     T    C___
GAM1635  LATS2    5'  GGCGGCGGTGGCGTGGAC    31022        _  TC_
                                GGCGGCGG GGC   GAC
                                ||||||||  |||   |||
                                CCGCCGCC CCG   CTG
                                     A   CAC
GAM1635  MEN1     3'  AGGCGGCAGGGGAGGCGG    39148          CTC  CGA
                                AGGCGGCGGGG   GA   CGG
                                ||||||||||   ||   |||
```

```
                                TCCGCCGTCCC  CT  GCC
                                    ___  CC_
GAM1635  MYO6    5'  GGCGGCGGGGCTACCTGTACGG 22665          CGACG_
                                GGCGGCGGGGCT    ACGG
                                ||||||||||||    ||||
                                CCGCCGCCCCGA    TGCC
                                    TGGACA
GAM1635  NFATC1  5'  GGCGGCGGGGAGTGGAGCGGCG 26079         CTC_ _ A
           G                    GGCGGCGGGG   GA CG CGG
                                ||||||||||   || || |||
                                CCGCCGCCCC   CT GC GCC
                                    TCAC  C  C
GAM1635  NR2F2   5'  GGCGGCGGCGGCTCCCCGGG  34236        _   GA  AC
                                GGCGGCGG GGCTC  CG  GG
                                ||||||||| |||||  ||  ||
                                CCGCCGCC CCGAG  GC  CC
                                    G    GG  __
GAM1635  PDGFB   5'  GGCGGCGGGCCCGGGCGGCGG  15187        G   A_  A
                                GGCGGCGGG CTCG  CG CGG
                                ||||||||| ||||  || |||
                                CCGCCGCCC GGGC  GC GCC
                                    _   CC  C
GAM1635  PFKP    3'  AGCTGGTGGGGCAGATGG    15240    _ C    TCGAC  C
                                GGC GG GGGGC    GA GG
                                ||| || |||||    || ||
                                TCG CC CCCCG    CT CC
                                  A  A    T____  A
GAM1635  PRSS11  5'  GGCGGCGGCGGCGGTGGCGGCG 15766        _  TCGA_  A
           GAC                    GGCGGCGG GGC    CG CGGAC
                                  ||||||||| |||    || |||||
                                  CCGCCGCC CCG    GC GCCTG
                                      G  CCACC  C
GAM1635  PYGL    5'  GGCGGCGGGCTGCGCGGCGG  16056        G  _  A  A
                                GGCGGCGGG CT CG CG CGG
                                ||||||||| || || || |||
                                CCGCCGCCC GA GC GC GCC
                                    _  C  _  C
GAM1635  RAB23   5'  GGTGGTGGGGCGCGGGA    32219    C  C    T  ACGAC
                                GG GG GGGGC CG    GGA
                                || || ||||| ||    |||
                                CC CC CCCCG GC    CCT
                                 A  A    C  _____
GAM1635  RAD52   3'  GGCGGCGGCGAGGACGG    39560        GGCT   C
                                GGCGGCGG   CGA GACGG
                                ||||||||   ||| |||||
                                CCGCCGCC   GCT CTGCC
                                    ____  C
GAM1635  RET     5'  GCGGCGGACGCGACGGAC    33937        GCT  A
                                GCGGCGGG  CG CGACGGAC
                                ||||||||  || ||||||||
```

```
                                CGCCGCCT  GC GCTGCCTG
                                    ___  _
GAM1635 RXRA    5' AGGCAGCGGGCGGCGG     16410        GCTCGA  A
                                AGGCGGCGGG    CG CGG
                                ||||||||||    || |||
                                TCCGTCGCCC    GC GCC
                                     _______ C
GAM1635 SFRP1   5' AGGCGCGGGGCGGCGG     16567     G    TCGAC A
                                AGGCG CGGGGC   G CGG
                                ||||| ||||||   | |||
                                TCCGC GCCCCG   C GCC
                                  _    ______ C
GAM1635 SMARCA5 5' GGTGGGCGGGGCCAGACGG  18780   C_      CGAC
                                GG  GGCGGGGCT   GACGG
                                ||  |||||||||   |||||
                                CC  CCGCCCCGG   CTGCC
                                 AC       T___
GAM1635 ST14    5' AGGCGGCGGGATTCCGG    35057        GC  GACGA
                                AGGCGGCGGG  TC    CGG
                                ||||||||||  ||    |||
                                TCCGCCGCCC  AG    GCC
                                     TA _____
GAM1635 TM4SF2  5' GGCGGCGGCGGCAGGCGGCGG 21448       _  TCGA  A
                                GGCGGCGG GGC   CG CGG
                                |||||||| |||   || |||
                                CCGCCGCC CCG   GC GCC
                                    G  TCC_  C
GAM1635 VIM     5' GGCGGCGGTGGCGCGGAC   45225       _  T  AC
                                GGCGGCGG GGC CG  GAC
                                |||||||| ||| ||  |||
                                CCGCCGCC CCG GC  CTG
                                    A  C __
GAM1635 ZNF219  5' GGCGGCGGCGGCGGGCGGCGG 32332       _  TCGA  A
                                GGCGGCGG GGC   CG CGG
                                |||||||| |||   || |||
                                CCGCCGCC CCG   GC GCC
                                    G  CCC_  C
GAM1635 ZNF219  5' GGCGGCGGCGGCGGCGGCGGCG 32331       _  T_  A  A
            G                    GGCGGCGG GGC  CG CG CGG
                                |||||||| |||  || || |||
                                CCGCCGCC CCG  GC GC GCC
                                    G  CC  C  C
GAM1635 ZNF7    5' GGTGGCTGGGCTCGACCAC  18262   C  G      G
                                GG GGC GGGCTCGAC AC
                                || ||| |||||||| ||
                                CC CCG CCCGAGCTG TG
                                 A  A       G
GAM1636 CRHR1   3' TAGTGCTGTGGCCGCAAG   20448    _   CA
                                TGG GTTG  GCCGCAAG
                                ||| ||||  ||||||||
```

```
                                ATC CGAC  CGGCGTTC
                                  A   AC
GAM1636  TBL1X    3'  GCTTGCGGCCGCAGGC     24887    G  _      CC
                                GC TTG GGTTGCAG  GC
                                || ||| ||||||||  ||
                                CG AAC CCGGCGTC  CG
                                 _  G      __
GAM1637  ABCD1    5'  TCTCGGGCAGAGGGGGCG    6208     GC         AA
                                TC  CGGGCGGGGGGG  GCG
                                ||  ||||||||||||  |||
                                AG  GCCCGTCTCCCC  CGC
                                 A_          __
GAM1637  AQP5     5'  GCCGGCGGGGGGGCGCC      11629      G     GGAA
                                GCCGG CGGGGG   GCGCC
                                ||||| ||||||   |||||
                                CGGCC GCCCCC   CGCGG

                                  _    _____
GAM1637  CACNG1   5'  TCGCCGAGGCGTGGGTGCC   8805       _   GG   GAAGC
                                TCGCCG GGCG  GGG    GCC
                                |||||| ||||  |||    |||
                                AGCGGC CCGC  CCC    CGG
                                   T   A_  A_____
GAM1637  DLX4     3'  TCGCTGGGTGGGTGGGAGC   39621     C   C   G    A
                                TCGC GGG GGG GGGA GC
                                |||| ||| ||| |||| ||
                                AGCG CCC CCC CCCT CG
                                  A  A  A   _
GAM1637  FUS1     3'  GCCGGGGCAGGGGGTGC     28588       _     GAA
                                GCCGGG CGGGGGG   GC
                                |||||| |||||||   ||
                                CGGCCC GTCCCCC   CG
                                   C      A__
GAM1637  G6PT1    5'  TCGTGGGCGGGAAGGTGCC   11168     CC         AAGC
                                TCG  GGGCGGGGGGG   GCC
                                |||  ||||||||||   |||
                                AGC  CCCGCCCTTCC   CGG
                                  A_         A___
GAM1637  HOXB9    5'  GCAGGGGGAAGGGAAGCGC   35842    C   C
                                GC GGG GGGGGGGAAGCGC
                                || ||| ||||||||||||
                                CG CCC CCTTCCCTTCGCG
                                 T  _
GAM1637  LMO2     5'  GCCGGGCGGCGGGGGCGC    24542         G    AA
                                GCCGGGCGG GGGG  GCGC
                                ||||||||| ||||  ||||
                                CGGCCCGCC CCCC  CGCG
                                     G   __
GAM1637  MEF2D    5'  TCGCTGGGTGGTGGGTCTGG  25423      C   C  _  _______
                                TCGC GGG GG GGG     GG
                                |||| ||| || |||     ||
```

```
                                AGCG CCC CC CCC     CC
                                  A  A A  AGAIII
GAM1637 MTCP1    5' CGCCGGTACTCGGGAGGCGCC 30575      _ GG    AA
                                CGCCGG GC  GGGGG  GCGCC
                                |||||| ||  |||||  |||||
                                GCGGCC TG  CCCTC  CGCGG
                                   A  AG    __
GAM1637 SERPIND1 3' TCACCGGAGCGGGAGGTGC   6775        _      GAA
                                TCGCCGG GCGGGGGGG   GC
                                ||||||| ||||||||   ||
                                AGTGGCC CGCCCTCC   CG
                                    T       A__
GAM1637 SORBS1   5' TCGCCGGGCGGGCGGGCTGCGC 31714          G   AA
                                TCGCCGGGCGGG GGG  GCGC
                                |||||||||||| |||  ||||
                                AGCGGCCCGCCC CCC  CGCG
                                       G   GA
GAM1637 ZRF1     5' TCCCGGGCGGAGGGCGC     45350    G        GGAA
                                TC CCGGGCGGGGG    GCGC
                                || ||||||||||    ||||
                                AG GGCCCGCCTCC    CGCG
                                 _        _____
GAM1638 AKT1     3' AGAACTGTGACACAG       23135       AACTT
                                AGAACT    GTGACACAG
                                ||||||    |||||||||
                                TCTTGA    CACTGTGTC
                                   ______
GAM1638 ARHGDIA  3' ATAGAACCTGGGGGGCACAGAA 20199        AACTTGTGA
                                ATAGAACT       CACAGAA
                                ||||||||       |||||||
                                TATCTTGG       GTGTCTT
                                     ACCCCCC__
GAM1638 MUC4     3' CAGGACTGGTTCTGACACAG   39665     A   AAC  G
                                TAG ACT   TT TGACACAG
                                ||| |||   || ||||||||
                                GTC TGA   AA ACTGTGTC
                                  C   CC_  G
GAM1638 PAK4     3' TAAAACTAACTCGAGGCAG    25251           TGACA
                                TAGAACTAACTTG     CAG
                                ||||||||||||     |||
                                ATTTTGATTGAGC     GTC
                                       TCC__
GAM1638 PLA2G4C  3' ACAGAGCTAACTTGTGCAGA   43856      A        ACA
                                ATAGA CTAACTTGTG   CAGA
                                ||||| ||||||||||   ||||
                                TGTCT GATTGAACAC   GTCT
                                   C        ____
GAM1638 TAGLN2   3' GAATGAACGGAGGACACAGA   18683     CT   TTGT
                                GAA  AAC    GACACAGA
                                |||  |||    ||||||||
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                                CTT  TTG   CTGTGTCT
                                  AC   CCTC
GAM1638  TMEM1    3'  GAGCTAAAAGACAACACAGA   17593    A   CTT TG
                                GA CTAA   G  ACACAGA
                                || ||||   |  |||||||
                                CT GATT   T  TGTGTCT
                                 C    TTC GT
GAM1638  VAPB     3'  ACAGAACTGAAGACACGGA   21871       AACTTGT    A
                                ATAGAACT      GACAC GA
                                ||||||||      ||||| ||
                                TGTCTTGA      CTGTG CT
                                     CTT____     C
GAM1639  ELMO3    5'  TAACGCTCAGAGTGCGTCA   36023         ATATC
                                TAGCGCTCAGA     TCA
                                ||||||||||     |||
                                ATTGCGAGTCT     AGT
                                      CACGC
GAM1640  BYSL     3'  CACTGCCCTGATCTGGG     19754         A  AA  CCA
                                TACTGCCCT GG  TG   GG
                                ||||||||| ||  ||   ||
                                GTGACGGGA CT  AC   CC
                                     _  AG  ___
GAM1640  C21orf2  3'  TCTAGCTGCTTCCTGTGCCAGG 22305     _   __   AGGAA
              C                  TCTA CTGC  CCT     TGCCAGGC
                                |||| ||||  |||    ||||||||
                                AGAT GACG  GGA     ACGGTCCG
                                  C    AA   C____
GAM1640  COL1A1   3'  CCAGGGCCTGGGGGTGCTGGGC 6368     CT   CTA  AA   CA
                                CTA  GCC   GG  TGC  GGC
                                |||  |||   ||  |||  |||
                                GGT  CGG   CC  ACG  CCG
                                  CC   AC_  CC   AC
GAM1640  FBP1     3'  CTGCTCTCTAGGAATGTAAGG  8002      C__       CC
                                CTGC   CTAGGAATG  AGG
                                ||||   |||||||||  |||
                                GACG   GATCCTTAC  TCC
                                  AGA        AT
GAM1640  IRF1     3'  CTGTTCCCCTAGGAGCCAG    42041     ___       AT
                                CTG   CCCTAGGA  GCCAG
                                |||   ||||||||  |||||
                                GAC   GGGATCCT  CGGTC
                                  AAG       __
GAM1640  LAMC2    3'  TCTACTGCCTTAGAGCAGG    33122         C    AAT  C
                                TCTACTGCC TAGG   GC AGG
                                ||||||||| ||||   || |||
                                AGATGACGG ATCT   CG TCC
                                     A   ___  _
GAM1640  MASP1    3'  TGCCCCAGGGATGCCAGGC    40111         A
                                TGCCCTAGG ATGCCAGGC
                                ||||||||| |||||||||
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                                ACGGGGTCC TACGGTCCG
                                     C
GAM1640  POLG    3'  TCCACTGCCTTGGAGCAGG   15451        CTA   AT  C
                                TCTACTGCC   GGA  GC AGG
                                |||||||||   |||  || |||
                                AGGTGACGG   CCT  CG TCC
                                     AA_  __  _
GAM1640  SHMT2   3'  TCCACTGCCCTGAGCTGGG   24009          A  AAT  CA
                                TCTACTGCCCT GG   GC  GG
                                |||||||||||  ||   ||  ||
                                AGGTGACGGGA CT   CG  CC
                                      _ ____ AC
GAM1640  TXNRD1  3'  TCTGCTGCCTAAATGCCAGGC  17773     A    CTAG
                                TCT CTGCC    GAATGCCAGGC
                                |||  |||||    ||||||||||
                                AGA GACGG    TTTACGGTCCG
                                  C    A___
GAM1641  BCAT1   3'  TAGAATGTTGCTCGGGGTACAC 42383      _  CAATGAAGA
            AG                    TAGA TGT        GTACACAG
                                |||| |||         ||||||||
                                ATCT ACA         CATGTGTC
                                  T   ACGAGCCC_
GAM1641  DSCR3   3'  GATGTCAACTGGCCACA     25827         GAAGA  A
                                GATGTCAAT     GT CACA
                                |||||||||     || ||||
                                CTACAGTTG     CG GTGT
                                     AC___  _
GAM1641  NPR2L   3'  AGATGTCAGTGAGAGCA     27250         A   A
                                AGATGTCA TGA GAGTA
                                |||||||| ||| |||||
                                TCTACAGT ACT CTCGT
                                     C   _
GAM1641  TLL2    3'  GATGTCAAGGAGTCCA      29752         TGAA    A
                                GATGTCAA    GAGT CA
                                ||||||||    |||| ||
                                CTACAGTT    CTCA GT
                                     C___    G
GAM1641  TRAP240 3'  TAGAGTCAATGAAAAATA    23057      T
                                TAGA GTCAATGAAGAGTA
                                |||| ||||||||||||||
                                ATCT CAGTTACTTTTTAT
                                  _
GAM1641  XK      3'  GATTACATGAAGAGTGCA    34362     GTCA        A
                                GAT    ATGAAGAGT CA
                                |||    ||||||||| ||
                                CTA    TACTTCTCA GT
                                  ATG_        C
GAM1642  FGF7    3'  GTTTTTACATATTTGTATTG   12861      GTCA        C
                                GTTT    GCATATTTG ATTG
                                ||||    ||||||||| ||||
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                                CAAA    TGTATAAAC TAAC
                                  AA__        A
GAM1642 NR1I2    3' TGATTGTCAGCGTAGCCTTG  35110    T      ATATTT  A
                                TG TTGTCAGC     GC TTG
                                || ||||||||     || |||
                                AC AACAGTCG     CG AAC
                                 T       CAT___  G
GAM1642 STATH    3' TGTTTTTCATTTGCATTG    17166      G   GCATA
                                TGTTT TCA    TTTGCATTG
                                ||||| |||    |||||||||
                                ACAAA AGT    AAACGTAAC
                                  A  _____
GAM1643 APXL     3' ATTGAGCTTGCCAGTTTGG   11617     T   AATAG
                                ATT AGCT    CAGTTTGG
                                ||| ||||    ||||||||
                                TAA TCGA    GTCAAACC
                                  C   ACG__
GAM1643 CKTSF1B1 3' TTTAGCTAACTTGCTTGG    30098         AGCA
                                TTTAGCTAAT   GTTTGG
                                ||||||||||   ||||||
                                AAATCGATTG   CGAACC
                                      AA__
GAM1643 FMO4     3' ATTTGGCTAATAGCAGTT    12923     A
                                ATTT GCTAATAGCAGTT
                                |||| ||||||||||||
                                TAAA CGATTATCGTCAA
                                  C
GAM1643 FRAT2    3' TTTAGCTACCTTAAAGTTTGG 28979        ATAGC_
                                TTTAGCTA     AGTTTGG
                                ||||||||     |||||||
                                AAATCGAT     TCAAACC
                                     GGAATT
GAM1643 PGK1     3' TTTAGCTAATGCCAAGTGG   7115          A  AGTT
                                TTTAGCTAAT GC    TGG
                                |||||||||| ||    |||
                                AAATCGATTA CG    ACC
                                      _ GTTC
GAM1643 RECQL5   3' TTAGAGACAGCAGTTTGG    20174     CTA
                                TTAG   ATAGCAGTTTGG
                                ||||   ||||||||||||
                                AATC   TGTCGTCAAACC
                                  TC_
GAM1644 ADARB1   3' TCTGAGCTTGGTGGAGGTGGTC 31885    CC   CC      CA
                                TC  GGT  GGTGGAGG  GTC
                                ||  |||  ||||||||  |||
                                AG  TCG  CCACCTCC  CAG
                                 AC   AA       AC
GAM1645 BAT4     5' GGTTAGGAAAGGCCCTCAG   37690         TC_
                                GGTTAGGAG   CCCTCAG
                                |||||||||   |||||||
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                                CCAATCCTT  GGGAGTC
                                     TCC
GAM1645 PPP2R5A  5' GCCATCGCGGGTCCCCTC   26437   G  A_ A
                                GC GTT  GG GTCCCCTC
                                || |||  || ||||||||
                                CG TAG  CC CAGGGGAG
                                 G  CG  _
GAM1645 TAL1     5' TACGCGGTTGCCTCCTCA   17289       AGGA  C
                                TACGCGGTT   GTC CCTCA
                                |||||||||   ||| |||||
                                ATGCGCCAA   CGG GGAGT
                                     ____  A
GAM1646 GLI2     5' CACGGGGTTGATGGGGTGGGG 36115    T     TAT  AC
                                CAC GGGTTGA  TGG  TGGGG
                                ||| |||||||  |||  |||||
                                GTG CCCAACT  ACC  ACCCC
                                  C     ___  CC
GAM1646 KCNE1L   3' CACTGGGATGAAAACTGGG  29371      T  TATT
                                CACTGGG TGA   GGACTGGG
                                ||||||| |||   ||||||||
                                GTGACCC ACT   TTTGACCC
                                    T  ____
GAM1646 MEF2B    5' CTGGGTTGGCGGAGGCTGGGG 25411       ATATT  A
                                CTGGGTTG    GG CTGGGG
                                ||||||||    || ||||||
                                GACCCAAC    CC GACCCC
                                     CGCCT  _
GAM1646 SLC39A4  3' ACTGGAGTTGGGACTGGG   39293     _   ATATT
                                ACTGG GTTG    GGACTGGG
                                ||||| ||||    ||||||||
                                TGACC CAAC    CCTGACCC
                                   T  _____
GAM1646 TIMP3    5' CTGGGTTGGACATGACTGGGG 7452       _   TG
                                CTGGGTTG ATAT  GACTGGGG
                                |||||||| ||||  ||||||||
                                GACCCAAC TGTA  CTGACCCC
                                     C  __
GAM1646 TNFRSF10B 3' CACTGGGTGATGTTGGATGGG 19283       T  A   C
                                CACTGGGT GAT TTGGA TGGG
                                |||||||| ||| ||||| ||||
                                GTGACCCA CTA AACCT ACCC
                                     _  C   _
GAM1647 ABCE1    3' TAAGTGCACAGAAAAAAGCA  40504      AAA  TT
                                TAAGTGCA  AAA  AGCA
                                ||||||||  |||  ||||
                                ATTCACGT  TTT  TCGT
                                     GTC  TT
GAM1647 ATP6V0E  3' AAGTGCAAAAAAGGCAAA   19484         ATTA
                                AAGTGCAAAAAA   GCAAA
                                ||||||||||||   |||||
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                                TTCACGTTTTTT   CGTTT
                                      C___
GAM1647 COL4A4   3' TAAGTGCACGGAAACAAA    6404        AAAAAATT
                                TAAGTGCA      AGCAAA
                                ||||||||      ||||||
                                ATTCACGT      TTGTTT
                                    GCCT____
GAM1647 COX11    3' TAAGTGAAAAAAATTAG     20418       C
                                TAAGTG AAAAAAATTAG
                                |||||| ||||||||||
                                ATTCAC TTTTTTTAATC
                                  _
GAM1647 EMX2     3' AAGTGCAAAAAACAAAAA    44676         AATTA
                                AAGTGCAAAAA    GCAAAAG
                                ||||||||||    |||||||
                                TTCACGTTTTT    TGTTTTT
                                      _____
GAM1648 KCNJ1    5' TGGCATTTACTGAAGGTGTTTT 6892       GC   AG  A
             TT                   TGGCAT  GCT  AG TGTTTTTT
                                ||||||  |||  || ||||||||
                                ACCGTA  TGA  TC ACAAAAAA
                                   AA   CT  C
GAM1648 PEA15    3' GCATGTGAATTTAATGTTTTTT 19078      CGCTAGA
                                GCATG      GATGTTTTTT
                                |||||      ||||||||||
                                CGTAC      TTACAAAAAA
                                  ACTTAAA
GAM1649 ADAMTS5  3' GAATGTGTTGGACATGA     28179         AAAAA
                                GAATGTGTTG    ATGA
                                ||||||||||    ||||
                                CTTACACAAC    TACT
                                     CTG__
GAM1649 CDKN2A   3' AGAATATATAAAAAATGA    38465        TG
                                AGAATGTGT  AAAAAATGA
                                |||||||||  |||||||||
                                TCTTATATA  TTTTTTACT
                                     __
GAM1649 COL10A1  3' GAAAAGCCTTGAAAGAATG   7963      T_  G     A
                                GAA  GT TTGAAA AATG
                                |||  || |||||| ||||
                                CTT  CG AACTTT TTAC
                                  TT  G     C
GAM1649 ESRRBL1  3' GAATGCTATGAAAAATGA    32840       GT      A
                                GAATGT  TGAAAAA TGA
                                ||||||  ||||||| |||
                                CTTACG  ACTTTTT ACT
                                   AT      _
GAM1649 IDH1     3' TAGAACATGAGAAAAAGTGA  41522         TT     A
                                TAGAATGTG  GAAAAA TGA
                                |||||||||  |||||| |||
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                                ATCTTGTAC  CTTTTT ACT
                                     T_     C
GAM1649  KCNAB1   3'  TAAAATGTAGTAAAAAATGA   41403        TTG
                                TAGAATGTG   AAAAAATGA
                                |||||||||   |||||||||
                                ATTTTACAT   TTTTTTACT
                                     CA_
GAM1649  MAGP2    5'  TAGAATGTGTGTTACAATGA   18499        TGAAAA
                                TAGAATGTGT     AATGA
                                ||||||||||     |||||
                                ATCTTACACA     TTACT
                                      CAATG_
GAM1649  MEN1     3'  GAATGTATACTTAAAAATGA   39179        TGA_
                                GAATGTGT    AAAAATGA
                                ||||||||    ||||||||
                                CTTACATA    TTTTTACT
                                     TGAA
GAM1649  PIK3R3   3'  AGAATGAAAAAAAAAATGA    41432       TGTT
                                AGAATG    GAAAAAATGA
                                ||||||    ||||||||||
                                TCTTAC    TTTTTTTACT
                                   TTT_
GAM1649  POLH     3'  AGAATGTGAAGAAAATGA     27100        TT   AA
                                AGAATGTG  GAAA  ATGA
                                ||||||||  ||||  ||||
                                TCTTACAC  CTTT  TACT
                                     TT   __
GAM1649  RARA     3'  AAATGTGCTTAAAATGA      9699         GAA
                                GAATGTGTT   AAAATGA
                                |||||||||   |||||||
                                TTTACACGA   TTTTACT
                                     A__
GAM1649  RNF17    3'  CAGAAACATTGAAAAAATGA   36733       T TG
                                TAGAA G  TTGAAAAAATGA
                                |||||  |  ||||||||||||
                                GTCTT T  AACTTTTTTACT
                                   _ GT
GAM1649  RRM2B    3'  CAGACATTTGAAAAAATGA    42712      ATGTG
                                TAGA    TTGAAAAAATGA
                                ||||    ||||||||||||
                                GTCT    AACTTTTTTACT
                                  GTA__
GAM1649  SPOCK    3'  TAGAATGTCTCTGAAAATG    41741        G  GAA
                                TAGAATGT TT   AAAATG
                                ||||||||  ||   ||||||
                                ATCTTACA AG   TTTTAC
                                     G  AC_
GAM1649  SYT1     3'  GAATGCATGGCTGGAAAAATGA 24853        ___    A
                                GAATGT   GTTG AAAAATGA
                                ||||||   ||||  ||||||||
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                                CTTACG   CGAC TTTTTACT
                                   TAC    C
GAM1649  TLL1     3'  TGTGTTTTGAAAAAATGA    29742       __
                                TGTGT  TGAAAAAATGA
                                |||||  ||||||||||
                                ACACA  ACTTTTTTACT
                                   AA
GAM1649  TRIM37   3'  AAATGTGTTGACACTGA     31622           AAAAA
                                GAATGTGTTGA    TGA
                                ||||||||||     |||
                                TTTACACAACT    ACT
                                      GTG__
GAM1649  UBL1     3'  AATGTCCTGAAAAAGGTGA   17838       G       A_
                                AATGT TTGAAAAA  TGA
                                |||||  ||||||||  |||
                                TTACA GACTTTTT  ACT
                                   G       CC
GAM1649  VANGL2   3'  GAATGGGAAGAAAAAATGA   43457       TGTT
                                GAATG    GAAAAAATGA
                                |||||    ||||||||||
                                CTTAC    CTTTTTTACT
                                   CCTT
GAM1649  VNN2     3'  CAGAGTAGCCAAAAAAATG   21682      A  T  TG
                                TAGA TG GT  AAAAAATG
                                ||||  ||  ||  ||||||||
                                GTCT AT CG  TTTTTTAC
                                  C  _  GT
GAM1650  ENAM     3'  AAGACACTGTGCTAGGT     36671     T    T     A
                                AAG TACT GTGCTA GT
                                |||  ||||  ||||||  ||
                                TTC GTGA CACGAT CA
                                  T    _     C
GAM1650  PRKY     3'  TCTTAAAAGTTATTTGTG    15711     C       C
                                TCT AAAAGTTA TTGTG
                                |||  ||||||||  |||||
                                AGA TTTTCAAT AACAC
                                  A       A
GAM1650  TIMM17A  3'  TCTCAGAAGTCACTTCAAG   26791       A       GTGC
                                TCTCA AAGTTACTT    TAAG
                                |||||  |||||||||    ||||
                                AGAGT TTCAGTGAA    GTTC
                                   C        ____
GAM1650  TMOD     3'  TCAAAAGTATTTGGCC      17602        TAC   T
                                TCAAAAGT   TTG GCT
                                ||||||||   |||  |||
                                AGTTTTCA   AAC CGG
                                     TA_   _
GAM1650  TNC      3'  TCAAAAGTACTTGTGCT     13471         T
                                TCAAAAGT ACTTGTGCT
                                ||||||||  |||||||||
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                                AGTTTTCA TGAACACGA
                                      _
GAM1651  EP300    5'  GCTCCGACGGCACCCGA     10988    C       CAC
                                GC CCGACGGC   CCCGA
                                || ||||||||   |||||
                                CG GGCTGCCG   GGGCT
                                 A       T__
GAM1651  F2RL1    5'  GCCCCGACGCCGGGCGCG    40508         G  ACCC  A
                                GCCCCGACG CC    CG CG
                                ||||||||| ||    || ||
                                CGGGGCTGC GG    GC GC
                                      _ CCC_  _
GAM1651  FTH1     5'  ACCCCGACGACTCTCGGCGAAG 42784           CACCC  A
                                GCCCCGACGGC     CG CGAAG
                                ||||||||||     || |||||
                                TGGGGCTGCTG     GC GCTTC
                                       AGA__  C
GAM1651  HAGH     5'  GCCCCGACTGCCACGGGCCG   23711         G    C__
                                GCCCCGAC GCCAC   CCG
                                |||||||| |||||   |||
                                CGGGGCTG CGGTG   GGC
                                     A    CCC
GAM1651  LEF1     5'  GCCCCGGCGGCCACCCCG     32209        A
                                GCCCCG CGGCCACCCCG
                                |||||| ||||||||||
                                CGGGGC GCCGGTGGGGC
                                   C
GAM1651  MOCS1    3'  GCCTCCATCTCCACCCCG     45123     _  ACGG
                                GCC CCG    CCACCCCG
                                ||| |||    ||||||||
                                CGG GGT    GGTGGGGC
                                  A  AGA_
GAM1651  POLG     3'  GCCTGCACCACCCCGATGAAG  15447     CCGACG        C
                                GCC     GCCACCCCGA GAAG
                                |||     |||||||||| ||||
                                CGG     TGGTGGGGCT CTTC
                                  ACG___         A
GAM1651  RARA     3'  GCCCCAACCCCTGGTGAA     9710        ACGGCC    GAC_
                                GCCCCG     ACCCC    GAA
                                ||||||     |||||    |||
                                CGGGGT     TGGGG    CTT
                                   _______    ACCA
GAM1651  TBL3     5'  CCCGGCAGCCACCGCCGCG    26985      A       _  A
                                CCCG CGGCCACC CCG CG
                                |||| |||||||| ||| ||
                                GGGC GTCGGTGG GGC GC
                                  C       C  _
GAM1652  BCL7A    5'  CGCCGGAGTGCGGCTCCG     34206          _  GA
                                CGCCGGAGTG GGC  CG
                                |||||||||| |||  ||
```

```
                                GCGGCCTCAC CCG  GC
                                      G   AG
GAM1652  CDH15    5'  GCCGGAGTGCACCCGCGACCCG 22336         G  GA_
                                GCCGGAGTG GC   CGACCCG
                                ||||||||| ||   |||||||
                                CGGCCTCAC TG   GCTGGGC
                                      G  GGC
GAM1652  DUSP7    5'  CGATGTGCGACGACTCG     42269    GA  G      C
                                CG  GTG GCGACGAC CG
                                ||  ||| |||||||| ||
                                GC  TAC CGCTGCTG GC
                                 __  A       A
GAM1652  EGLN3    5'  GCGGAGCTCCACGACCCG    35208    C    GGG G
                                GC GGAGT   C ACGACCCG
                                || |||||   | ||||||||
                                CG CCTCG   G TGCTGGGC
                                 _    AG_ _
GAM1652  ELF3     5'  ACCGGAGTGGCGGAGTCCG   20748         G  ACGAC
                                GCCGGAGTGG CG    CCG
                                |||||||||| ||    |||
                                TGGCCTCACC GC    GGC
                                      _  CTCA_
GAM1652  GLUL     5'  CAGCTGGAGCGCGACCC     13154     AG  _  A
                                CGG  TGG GCG CGACCC
                                |||  ||| ||| ||||||
                                GTC  ACC CGC GCTGGG
                                  G_   T  _
GAM1652  GPC6     5'  CGCCGGAGTGTGCGGCAA    25042         G  A
                                CGCCGGAGTG GCG CGA
                                |||||||||| ||| |||
                                GCGGCCTCAC CGC GTT
                                      A   C
GAM1652  HPS4     3'  CGTGGGAGTGGAGTCGGCC   35215    CC      CGA  A
                                CG  GGAGTGGG   CG CC
                                ||  ||||||||   || ||
                                GC  CCTCACCT   GC GG
                                 AC       CA_  C
GAM1652  IGFBP4   5'  GCCGGAGGGGAGCAAGCC    11401       T  CGA  C
                                GCCGGAG GGG   CGA CC
                                ||||||| |||   ||| ||
                                CGGCCTC CCC   GTT GG
                                    _  TC_   C
GAM1652  NDUFA10  3'  GCTGGAGCAGAAGGCGGCCCG  21233    C   ___    ACGA
                                GC GGAGT   GGGCG   CCCG
                                || |||||   |||||   ||||
                                CG CCTCG   TCCGC    GGGC
                                 A    TCT    C___
GAM1652  P3       5'  CGCCCGAGTGGGCGATCG    33377     G       _
                                CGCC GAGTGGGCGA CG
                                |||| |||||||||| ||
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```
                                GCGG CTCACCCGCT GC
                                  G        A
GAM1652 PDLIM1   5' GCTGTGGCGGGCGACGACCCG 34193    CGGA
                                GC   GTGGGCGACGACCCG
                                ||   ||||||||||||||
                                CG   CGCCCGCTGCTGGGC
                                 ACAC
GAM1652 PPP2R2C  5' CGCTGGAAGATGACGACCCG  41544    C   T  GC
                                CGC GGAG GG  GACGACCCG
                                ||| |||| ||  |||||||||
                                GCG CCTT CT  CTGCTGGGC
                                  A   _ A_
GAM1652 SPAG6    5' GATCGTGGCGACGACTCG    29702    G _      C
                                GA TG GGCGACGAC CG
                                || || ||||||||| ||
                                CT GC CCGCTGCTG GC
                                 A A       A
GAM1653 APBA2    3' TGGGGAGCCAGCGTCCGTGG  24283    A      AGCC _  _
                                TG GGAGCCAG   CG CCG GG
                                || ||||||||   || ||| ||
                                AC CCTCGGTC   GC GGC CC
                                 C      _____ A  A
GAM1653 ARHC     5' TGGGGCGCTGGAGCCGGG    23178    A  A  CA   CGCCG
                                TG GG GC  GAGCC    GGG
                                || || ||  |||||    |||
                                AC CC CG  CTCGG    CCC
                                 C  G  AC   ______
GAM1653 B4GALT3  3' TGAGGAGCTGAGGGTGGGG   19107       CA  CCCGCC
                                TGAGGAGC  GAG     GGGG
                                ||||||||  |||     ||||
                                ACTCCTCG  CTC     CCCC
                                     A_   CCA___
GAM1653 B4GALT6  5' TGGGAGGCCAGAGAGTCGGGG 40855    A  _     CCCGC
                                TG GGAG CCAGAG    CGGGG
                                || |||| ||||||    |||||
                                AC CCTC GGTCTC    GCCCC
                                 _   C     TCA__
GAM1653 BAK1     3' TGAGGAGCATGGAGGGTGGGG 45111       CA_  CCCGCC
                                TGAGGAGC   GAG     GGGG
                                ||||||||   |||     ||||
                                ACTCCTCG   CTC     CCCC
                                     TAC   CCA___
GAM1653 CARD10   3' TGAGAGGCCAGAGCCAAGGG  30974     GA       CGCC
                                TGAG  GCCAGAGCC   GGGG
                                ||||  |||||||||   ||||
                                ACTC  CGGTCTCGG   TCCC
                                  TC       T___
GAM1653 CDO1     5' TGAGCGAGCCAAGGAGCTGGGG 12216     _    __   CCGCC
                                TGAG GAGCCA  GAGC    GGGG
                                |||| ||||||  ||||    ||||
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                                ACTC CTCGGT  CTCG    CCCC
                                  G     TC    A____
GAM1653  COL6A2   3'  TGAGAGCCAGCCTGTCGGGG  38449     G    GA   CGC
                                TGAG AGCCA  GCC   CGGGG
                                |||| |||||  |||   |||||
                                ACTC TCGGT  CGG   GCCCC
                                  _    __   ACA
GAM1653  EPHB6    5'  TGGGGCGCCGGGAGAATCCTGG 20806    A  A   A_   CCCG  _
            GG                    TG GG GCC  GAG    CC GGGG
                                || || |||  |||    || ||||
                                AC CC CGG  CTC    GG CCCC
                                 C  G   CC   TTA_  A
GAM1653  FKBP10   3'  AGGAGCCAGTCAGGATTGGGGA 34955         AGCCCGCC
                                AGGAGCCAG       GGGGA
                                |||||||||       |||||
                                TCCTCGGTC       CCCCT
                                      AGTCCTAA
GAM1653  FXR2     5'  GAGGAGCCGGAGGGG       22160         A   CCCGCC
                                GAGGAGCC GAG     GGG
                                |||||||| |||     |||
                                CTCCTCGG CTC     CCC
                                     C   _______
GAM1653  GAA      3'  TGGGGGCCAGAGCCCCGG    6668     A  A        GC
                                TG GG GCCAGAGCCC  CGG
                                || || ||||||||||  |||
                                AC CC CGGTCTCGGG  GCC
                                 _  C         __
GAM1653  IPF1     5'  CGGGAGCTGGAGCCGGGG    6823     A    CA    CGCC
                                TG GGAGC  GAGCC   GGGG
                                || |||||  |||||   ||||
                                GC CCTCG  CTCGG   CCCC
                                 _    AC    _____
GAM1653  KIF5C    5'  TGGGGGGCCGGGGCCGGGA   21165    A  A   AGAGCCC
                                TG GG GCC      GCCGGGG
                                || || |||      |||||||
                                AC CC CGG      CGGCCCT
                                 C  C   CCC_____
GAM1653  LTB4R    5'  TGAGGAGCAGGAGTGAGGG   8890         CA   CCCGCC
                                TGAGGAGC  GAG     GGGG
                                ||||||||  |||     ||||
                                ACTCCTCG  CTC     TCCC
                                     TC   AC_____
GAM1653  MADH7    5'  GGGGCGCCCGCCGGGG      25372    A  CAGA
                                GG GC    GCCCGCCGGGG
                                || ||    ||||||||||
                                CC CG    CGGGCGGCCCC
                                 C  _____
GAM1653  MSF      3'  CGGGGAGCCAGGCCTGGGG   44725    A      A   CGCC
                                TG GGAGCCAG GCC    GGGG
                                || |||||||| |||    ||||
```

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                                GC CCTCGGTC CGG    CCCC
                                 C       _  A___
GAM1653  MSI1     3'  GGAGCCAGACGCTGTTGGGG   14645          _  CCGCC
                                GGAGCCAGA GC     GGGG
                                ||||||||| ||     ||||
                                CCTCGGTCT CG     CCCC
                                     G  ACAA_
GAM1653  NFE2     3'  TGAGGAGCCGAGTCAGGG    26084          A   CCCGC
                                TGAGGAGCC GAG    CGGGG
                                ||||||||| |||    |||||
                                ACTCCTCGG CTC    GTCCC
                                     _  A____
GAM1653  PES1     3'  TGAGGGGTCAGGGCTGGCTGGA 30714       AGC   A  CC  C
                                TGAGG   CAG GC  GC GGG
                                |||||   ||| ||  || |||
                                ACTCC   GTC CG  CG CCT
                                   CCA   C  AC  A
GAM1653  PIM2     5'  TGGGGAGCCAGGGCTGGGG   41029    A       A  CCGCC
                                TG GGAGCCAG GC    GGGG
                                || ||||||| ||    ||||
                                AC CCTCGGTC CG    CCCC
                                 C       C  A____
GAM1653  PLAT     3'  TGAGAGCCAGGGAGTGGGG   37450      G     AGCCCGCC
                                TGAG AGCCAG       GGGG
                                |||| ||||||       ||||
                                ACTC TCGGTC       CCCC
                                  _     CCTCA___
GAM1653  PSCD4    3'  TGAGGACCAGAGAGGG      30135       G     CCCGCC
                                TGAGGA CCAGAG     GGG
                                |||||| ||||||     |||
                                ACTCCT GGTCTC     CCC
                                   _     T_____
GAM1653  RAD50    5'  GGGGCTGCCCGCCGGGG     39439    A  CAGA
                                GG GC    GCCCGCCGGGG
                                || ||    ||||||||||
                                CC CG    CGGGCGGCCCC
                                 C  A___
GAM1653  RPL10    3'  TGGGAGCCACAGGCTGGGG   25676    A      G  CCC  C
                                TG GGAGCCA AG   GC GGGG
                                || ||||||| ||   || ||||
                                AC CCTCGGT TC   CG CCCC
                                 _      G  ___  A
GAM1653  TNP1     3'  AGGGCAGAGCCCGCTGGGG   40474     A  C       C
                                AGG GC AGAGCCCGC GGGG
                                ||| || ||||||||| ||||
                                TCC CG TCTCGGGCG CCCC
                                  _ _       A
GAM1653  VEGF     3'  TGGGGAGCCAGGGGATCGGGGA 17975    A       AGCCCGC
                                TG GGAGCCAG      CGGGGA
                                || ||||||||      ||||||
```

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                                AC CCTCGGTC      GCCCCT
                                 C       CCCTA__
GAM1653  WNT3A    3'  TGAGGGGCCAGGAAGGGG    37552      A    AGCCCGCC
                                TGAGG GCCAG       GGGG
                                ||||| |||||       ||||
                                ACTCC CGGTC       CCCC
                                   C     CTT_____
GAM1654  BACH1    3'  TATTCATGTAGCCAGACTTTCT 10150      TA_     A T
              A                  TATTC   TAGCCA G ATTTTCTA
                                |||||   |||||| | ||||||||
                                ATAAG   ATCGGT C TGAAAGAT
                                   TAC     _ _
GAM1654  CHC1     3'  TTCTGAGCCAAATATTT     10431      AT
                                TTCT  AGCCAAGTATTT
                                ||||  ||||||||||||
                                AAGA  TCGGTTTATAAA
                                  C_
GAM1654  CLOCK    3'  TATTCTAATAATGTATTTTCTA 22219        TAGCCAA
                                TATTCTA      GTATTTTCTA
                                |||||||      ||||||||||
                                ATAAGAT      CATAAAAGAT
                                     TATTA__
GAM1654  H3F3B    3'  TATTCTATAGCTGCCAGGT    23705         ___    A
                                TATTCTATA   GCCA GT
                                |||||||||   |||| ||
                                ATAAGATAT   CGGT CA
                                      CGA    C
GAM1654  RAD18    3'  TTCTATAGCCATTTCT      33559          AGTAT
                                TTCTATAGCCA     TTTCT
                                ||||||||||     |||||
                                AAGATATCGGT     AAAGA
                                                _____
GAM1654  SF3A1    3'  TATTCTATTAGCCAAGTGCCAC 25247         _       A TT
              CT                  TATTCTAT AGCCAAGT T  TCT
                                |||||||| |||||||| |  |||
                                ATAAGATA TCGGTTCA G  GGA
                                     A       C GT
GAM1654  TRAM     3'  TTCATAGTAAATATTTTCT    30706     T    CC
                                TTC ATAG  AAGTATTTTCT
                                ||| ||||  ||||||||||
                                AAG TATC  TTTATAAAAGA
                                  _    A_
GAM1655  ACADL    3'  ACATGTTTAGTGTTTCCTCGC  11494     G     CGCT
                                ACA GTTTAG    TTTTCTCGC
                                ||| ||||||    |||||||||
                                TGT CAAATC    AAAGGAGCG
                                  A      AC__
GAM1655  BDKRB2   3'  ACATGTTTACATGATTTTCTCG 8393      G    G  CT_
                                ACA GTTTA CG   TTTTCTCG
                                ||| ||||| ||   ||||||||
```

```
                                TGT CAAAT GT   AAAAGAGC
                                  A    _ ACT
GAM1655  CLCA3    3'  TAGCTGTGTTTTTTCTTGCC  22265      GC___      C
                                TAGC    TTTTTCT GCC
                                ||||    ||||||| |||
                                ATCG    AAAAAGA CGG
                                  ACACA      A
GAM1655  PCDHGC3  5'  GGGTTAGCGCTTGGGCGC    37057    T       TTTCT
                                GG TTAGCGCTT    CGC
                                || |||||||||    |||
                                CC AATCGCGAA    GCG
                                 C       CCC__
GAM1655  RAD17    5'  AGATTTCCTCTTTTTCTCGC  39408       AGCG
                                AGGTTT   CTTTTTCTCGC
                                ||||||   ||||||||||
                                TCTAAA   GAAAAAGAGCG
                                   GGA_
GAM1655  TBX6     5'  AGTTTGGCGCTTCCGGC     38853      A    TTT   C
                                GGTTT GCGCT   TCT GC
                                ||||| |||||   ||| ||
                                TCAAA CGCGA   AGG CG
                                  C     ___   C
GAM1656  ALPL     3'  GTTCAGAGCCCAGGAGTG    7892          TGTACC
                                GTTCAGAGTCC     GTG
                                ||||||||||     |||
                                CAAGTCTCGGG     CAC
                                      TCCT__
GAM1657  EHD4     3'  CTGTATAAAGGCTTTTATCC  40207     C   TCC T
                                CTG ATA   G CTTTTATCC
                                ||| |||   | |||||||||
                                GAC TAT   C GAAAATAGG
                                  A   TTC _
GAM1657  MYH3     3'  TGCATATCTTCTGTC       14725       ATCC      A
                                TGCAT    GTCTTTT TC
                                |||||    ||||||| ||
                                ACGTA    TAGAAGA AG
                                  _____      C
GAM1657  PTPRO    3'  CTACTGCTGTCTTTTGTC    36223        ATATCC      A
                                TTACTGC     GTCTTTT TC
                                |||||||     ||||||| ||
                                GATGACG     CAGAAAA AG
                                   A_____      C
GAM1657  ATP10C   3'  AACTGGACACACTGTCTTTGCA 35974     G      A  GA
            A                    AAC GGACACA TG  CTTTGCAA
                                ||| ||||||| ||  ||||||||
                                TTG CCTGTGT AC  GAAACGTT
                                  A      G  A_
GAM1657  CACNA1C  3'  GGGCTACAGGACTTTG      8758      AC   AT
                                GGG  ACA  GGACTTTG
                                |||  |||  ||||||||
```

```
                                CCC  TGT  CCTGAAAC
                                  GA  __
GAM1657  CLOCK    3'  CGGGATAGCTTTGCA      22215      CACAA  A
                                CGGGA    TGG CTTTGCA
                                |||||    ||| |||||||
                                GCCCT    ATC GAAACGT
                                  ______  _
GAM1657  GDI1     3'  GGGACACATTCACTTTGCAA  41014       A GG
                                GGGACACA T  ACTTTGCAA
                                |||||||| |  |||||||||
                                CCCTGTGT A  TGAAACGTT
                                    _ AG
GAM1657  GNAL     3'  ACAGGACACATTTTGCA     13170         ATGGAC
                                ACGGGACACA     TTTGCA
                                ||||||||||     ||||||
                                TGTCCTGTGT     AAACGT
                                    A_____
GAM1657  MAPRE1   3'  GAGACACATTTTGCA      29521        ATGGAC
                                GGGACACA     TTTGCA
                                ||||||||     ||||||
                                CTCTGTGT     AAACGT
                                    A_____
GAM1657  SPON2    3'  ACGGGACACGGGGGCCCCTA  29710        AAT  A
                                ACGGGACAC   GG CTTTG
                                |||||||||   || |||||
                                TGCCCTGTG   CC GGGAT
                                    CCC  G
GAM1658  COX6C    3'  TTTCAAAGTATTTGTTAATTGT 20416        C_    TTC
                                TTTCAAAGTA  TGTTG   GT
                                ||||||||||  |||||   ||
                                AAAGTTTCAT  ACAAT   CA
                                    AA    TAA
GAM1658  MS4A4A   3'  TTTCAAGTGCTGTTGCCTCAT  35853      A  A     _
                                TTTCAA GT CTGTTGT TCGT
                                |||||| || ||||||| ||||
                                AAAGTT CA GACAACG AGTA
                                   _ C      G
GAM1658  SURF6    3'  TTTCAGATACTGTTGTGTC   27591      AA       _
                                TTTCA  GTACTGTTGT TC
                                |||||  |||||||||| ||
                                AAAGT  TATGACAACA AG
                                  C_        C
GAM1658  TLL2     3'  TTTCAAGGTGCTATTGTT    29760      A  A
                                TTTCAA GT CTGTTGTT
                                |||||| || ||||||||
                                AAAGTT CA GATAACAA
                                   C  C
GAM1658  RANBP3   3'  GAGCCAGTGTGTGAGGGT    28778        AC_  C
                                GAGCCAGTGT   AG GT
                                ||||||||||   || ||
```

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                                CTCGGTCACA   TC CA
                                     CAC  C
GAM1659  CHI3L1   3'  TGTCTTGTAGGATGTTTGGCT  10476     A    TCGTT
                                TGTC TGTA    GTGTTTGGCT
                                |||| ||||    ||||||||||
                                ACAG ACAT    TACAAACCGA
                                  A   CC___
GAM1659  FRG1     3'  TCAGAAAAAAACACAGAAAGA  20990     A        TATT
                                TCA AAAAAAACACA    AGA
                                ||| ||||||||||    |||
                                AGT TTTTTTTGTGT    TCT
                                  C         CTT_
GAM1659  GTF2E2   3'  AAAAACACAGCAAAGACA    13315        TATT
                                AAAAACACA    AGACA
                                |||||||||    |||||
                                TTTTTGTGT    TCTGT
                                     CGTT
GAM1659  LMO7     3'  TCAAAAAAGGCCACATACT    31915        AAA
                                TCAAAAAA   CACATATT
                                ||||||||   ||||||||
                                AGTTTTTT   GTGTATGA
                                     CCG
GAM1659  SDC4     3'  TCAAAAAAAATCAGTAACAGAC 16529         A  CATAT
           A                     TCAAAAAAAA CA     TAGACA
                                ||||||||||  ||    ||||||
                                AGTTTTTTTT GT     GTCTGT
                                      A  CATT_
GAM1659  SLC6A6   3'  TCAAAACAAAACACACAC    16793       A
                                TCAAAA AAAACACATAT
                                |||||| ||||||||||
                                AGTTTT TTTTGTGTGTG
                                   G
GAM1659  TIMP4    3'  CAAAGGAAAACACATATT    17529      AA
                                CAAA  AAAACACATATT
                                ||||  ||||||||||||
                                GTTT  TTTTGTGTATAA
                                  CC
GAM1659  TNFSF4   3'  TCAAAGACAAACACACAC    17752      AAA
                                TCAAA   AAACACATAT
                                |||||   ||||||||||
                                AGTTT   TTTGTGTGTG
                                   CTG
GAM1660  ACVRL1   5'  CGGCGCGGCCCCGGACCGG   6164     AC  TA
                                CGG  CG  CCCGGACCGG
                                |||  ||  ||||||||||
                                GCC  GC  GGGCCTGGCC
                                  GC  CG
GAM1660  C7orf2   5'  CAGCCGCGCCGGGGACCGG   35366      GA   TACCC
                                CAGCCG  CCG    GGACCGG
                                ||||||  |||    |||||||
```

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                                GTCGGC  GGC    CCTGGCC
                                   GC   C____
GAM1660  DGCR2    5'  GCCGGACCGGGCCG       23094        TACCC  A
                                GCCGGACCG    GG CCG
                                |||||||||    || |||
                                CGGCCTGGC    CC GGC
                                      _____  _
GAM1660  HCN4     5'  GCCGGGGTCGGACCGG     24225      ACC  ACC
                                GCCGG   GT   CGGACCGG
                                |||||   ||   ||||||||
                                CGGCC   CA   GCCTGGCC
                                  C__  ___
GAM1660  NPEPPS   5'  CAGCCGGAGCGCTAGGGGCTGG 41787        C   ACCC  ACC
                                CAGCCGGA CGT    GG   GG
                                |||||||| |||    ||   ||
                                GTCGGCCT GCG    CC   CC
                                     C   ATCC  GA_
GAM1661  ETS1     5'  GCGGCGAAGTGAGCGCGCTCG  23462     A   CCCG
                                GCG TGG    GAGCGCGCTCG
                                ||| |||    ||||||||||
                                CGC GCT    CTCGCGCGAGC
                                  C   TCA_
GAM1661  HDGF     5'  GCGCGGTGGGTGCGCGCTC    21062     A   CCC  A
                                GCG TGG   GG GCGCGCTC
                                ||| |||   || ||||||||
                                CGC GCC   CC CGCGCGAG
                                  _   AC_  A
GAM1661  ADD2     3'  AGCCTGTGAGAGCTCACGGCCC 32722     GCGC   C   _
            A                    AGC    GGG AGC CACGGCCCA
                                |||    ||| ||| |||||||||
                                TCG    CTC TCG GTGCCGGGT
                                  GACA   _   A
GAM1661  ADRBK1   3'  GCGCCGGGCAGCGGC       11530      G       CAC
                                GCGC CGGGCAGC   GGC
                                |||| ||||||||   |||
                                CGCG GCCCGTCG   CCG
                                   _      ____
GAM1661  ARHGEF7  5'  AGCGACGCCCACGGCCC     19357      _   GGGCAG
                                AGCG CGC     CCACGGCCC
                                |||| |||     |||||||||
                                TCGC GCG     GGTGCCGGG
                                  T  _______
GAM1661  BRF1     5'  CGCGCGGGCAGCGCCC      11331           CACG
                                CGCGCGGGCAGC    GCCC
                                ||||||||||||    ||||
                                GCGCGCCCGTCG    CGGG
                                      _____
GAM1661  CACNA1C  3'  GCGCGCGGGAAGCCGGGG    8756          C    AC
                                GCGCGCGGG AGCC  GG
                                ||||||||| ||||  ||
```

```
                                CGCGCGCCC TCGG  CC
                                     T    CC
GAM1661  CDS2     5'  GCGCGCGGCTCTGAGCGGCTCA 19215        GCAGCCA    C
                                GCGCGCGG      CGGC CA
                                ||||||||      |||| ||
                                CGCGCGCC      GCCG GT
                                     GAGACTC    A
GAM1661  COL15A1  5'  GCGCGCGGCTAGTCGAGC    12355        GC  CCA  _
                                GCGCGCGG  AG   CG GC
                                ||||||||  ||   || ||
                                CGCGCGCC  TC   GC CG
                                     GA  A__  T
GAM1661  COL5A1   5'  GCGCGGGTCACGGCCC      6417         CAGC
                                GCGCGGG    CACGGCCC
                                |||||||    ||||||||
                                CGCGCCC    GTGCCGGG
                                     A___
GAM1661  CRAT     5'  GCTGCGGGCAGGCACCC     19663     GC       C ACG
                                GC  GCGGGCAG C   GCCC
                                ||  |||||||| |   ||||
                                CG  CGCCCGTC G   TGGG
                                 A_       C ___
GAM1661  CRLF1    5'  GCGCGGCGGGCTGCGGC     21900       _    A  CAC
                                GCGCG CGGGC GC   GGC
                                ||||| ||||| ||   |||
                                CGCGC GCCCG CG   CCG
                                   C     A ___
GAM1661  CUTL1    3'  GCTGCGGGCAGAGCCC      12534     GC       CCAC
                                GC  GCGGGCAG    GGCCC
                                ||  ||||||||    |||||
                                CG  CGCCCGTC    TCGGG
                                 A_       _____
GAM1661  DAG1     5'  GCGCGCGGCCGGAGCC      20523        GGCA   AC
                                GCGCGCG    GCC  GGCC
                                |||||||    |||  ||||
                                CGCGCGC    CGG  TCGG
                                     _____  CC
GAM1661  DDX16    5'  AAGCGTCGGGCAGCCGCG    44957       CG        A
                                AAGCG  CGGGCAGCC CG
                                |||||  ||||||||| ||
                                TTCGC  GCCCGTCGG GC
                                   A_       C
GAM1661  DIO3     3'  GCGCGCGGGCGTGGCC      10692          AGCCAC
                                GCGCGCGGGC     GGCC
                                ||||||||||     ||||
                                CGCGCGCCCG     CCGG
                                     CA_____
GAM1661  DSCAM    5'  GCGGGCGGGCAGGCC       10806     C      GCCAC   C
                                GCG GCGGGCA    GGC C
                                ||| |||||||    ||| |
```

```
                                CGC CGCCCGT    CCG G
                                  C      _____  A
GAM1661  DVL3     5'  GCGCGCGGCGCGGCCC      20683        _  AGCCAC
                                GCGCGCGG GC     GGCCC
                                |||||||| ||     |||||
                                CGCGCGCC CG     CCGGG
                                    G _______
GAM1661  EN1      3'  GCGCGGGCGCGGCCCCGGCC   10913        A__   A
                                GCGCGGGC   GCC CGGCC
                                |||||||   ||| |||||
                                CGCGCCCG   CGG GCCGG
                                    CGC   G
GAM1661  FGD1     5'  AGGCGCGGGCGGAGGAGGCCC  20898    C       AGCCAC
                                AG GCGCGGGC     GGCCC
                                || ||||||||     |||||
                                TC CGCGCCCG     CCGGG
                                 _       CCTCCT
GAM1661  FGFR2    5'  GCGCGGGCATGACGCCC     35664        GCC   G
                                GCGCGGGCA   ACG CCC
                                |||||||||   ||| |||
                                CGCGCCCGT   TGC GGG
                                    AC_   _
GAM1661  FHL2     5'  AGGGCGCGGGCGGCTGG     11104    C       A  CAC
                                AG GCGCGGGC GC   GG
                                || |||||||| ||   ||
                                TC CGCGCCCG CG   CC
                                 C       C  A__
GAM1661  GPC1     5'  GCGCGCGCGGCTCGCGGTCCA  13246        _   A_  CAC  C
                                GCGCGCG GGC  GC   GG CCA
                                ||||||| |||  ||   || |||
                                CGCGCGC CCG  CG   CC GGT
                                    G   AG  ___  A
GAM1661  GPC1     5'  GCGCGCGGGGTGCGAGGTCC   13247        CA  CAC  C
                                GCGCGCGGG  GC   GG CC
                                |||||||||  ||   || ||
                                CGCGCGCCC  CG   CC GG
                                    CA  CT_  A
GAM1661  GRB14    5'  GCGCGCGGGCGGCGAGGC    21039        A  CAC
                                GCGCGCGGGC GC   GGC
                                |||||||||| ||   |||
                                CGCGCGCCCG CG   CCG
                                    C  CT_
GAM1661  HDAC4    5'  GCGGCGGACAATGGCCC     25771     C       CCAC
                                GCG GCGGGCAG    GGCCC
                                ||| ||||||||    |||||
                                CGC CGCCTGTT    CCGGG
                                  _       A___
GAM1661  HMGN2    5'  GCGCGCGGGCTTTGGTCGGTCC 24323          AGCCA_   C
                                GCGCGCGGGC     CGG CC
                                ||||||||||     ||| ||
```

```
                                CGCGCGCCCG     GCC GG
                                     AAACCA   A
GAM1661  HUNK     5'  GCGCGCGGGGTGGGGCGCGGTC 31071         CA___  CA   C
              C                   GCGCGCGGG    GC  CGG CC
                                  |||||||||    ||  ||| ||
                                  CGCGCGCCC    CG  GCC GG
                                       CACCC  C_   A
GAM1661  INSR     5'  AACGCGCGGGCTTGGCCC    43376          AGCCAC
                                  AGCGCGCGGGC     GGCCC
                                  ||||||||||      |||||
                                  TTGCGCGCCCG     CCGGG
                                       AA____
GAM1661  KCNJ8    5'  GCCGCGGGCAGGTCCC      22543    G       CCACGG
                                  GC CGCGGGCAG     CCC
                                  || |||||||||     |||
                                  CG GCGCCCGTC     GGG
                                   _       CA____
GAM1661  MAFK     5'  GCGCGCGGCGGCTCC       14319        GCAGCCA   _
                                  GCGCGCGG      CGGC CC
                                  ||||||||      |||| ||
                                  CGCGCGCC      GCCG GG
                                       ________   A
GAM1661  MAP2K2   5'  AGCCCGGGGCTGCGGCCGCGGC 36203     G  C    A___   A
              CCA                   AGC CG GGGC    GCC CGGCCCA
                                  ||| || ||||    ||| |||||||
                                  TCG GC CCCG    CGG GCCGGGT
                                    G  _    ACGC   C
GAM1661  MTMR3    3'  AAGTGCACGGGCCTCTCGG   34388     C       AGCCA
                                  AAG GCGCGGGC     CGG
                                  ||| ||||||||     |||
                                  TTC CGTGCCCG     GCC
                                    A       GAGA_
GAM1661  PAX2     5'  AGCGCGCGGCCAGGCCC     19616         GGCA    C
                                  AGCGCGCG    GCCA GGCCC
                                  ||||||||    |||| |||||
                                  TCGCGCGC    CGGT CCGGG
                                       _____   _
GAM1661  POU3F1   3'  GCGGCGGGCAGGATGCCC    40372     C       CCACG
                                  GCG GCGGGCAG     GCCC
                                  ||| ||||||||     ||||
                                  CGC CGCCCGTC     CGGG
                                   _       CTA__
GAM1661  PPOX     5'  GCGGCGGGCAGTACGCC     7181      C       CC   G
                                  GCG GCGGGCAG  ACG CC
                                  ||| ||||||||  ||| ||
                                  CGC CGCCCGTC  TGC GG
                                   _       A_  _
GAM1661  RB1CC1   5'  GCCGCGGACACCGCCGCGGC   31314    G       __   A
                                  GC CGCGGGCA  GCC CGGC
                                  || ||||||||  ||| ||||
```

```
                                CG GCGCCTGT  CGG GCCG
                                 _      GG   C
GAM1661  RBM6     5'  GCGGCGAAGCCTCCACGGCCC  25104     C   _ AG
                                GCG GCGG GC  CCACGGCCC
                                ||| |||| ||  |||||||||
                                CGC CGCT CG  GGTGCCGGG
                                  _   T  GA
GAM1661  SCG3     5'  GCGCGCGGGAGTCAAGTCTCCA 29890         C  C  CGGC_
                                GCGCGCGGG AG CA    CCA
                                |||||||| || ||    |||
                                CGCGCGCCC TC GT    GGT
                                      _ A  TCAGA
GAM1661  SLC1A5   3'  GCAGGCAGACCCCCA       24747         _ ACGG
                                GCGGGCAG CC    CCCA
                                |||||||| ||    ||||
                                CGTCCGTC GG    GGGT
                                     T  ____
GAM1661  SLC38A3  3'  AGGGCGCAGACCGTGGCC    27757    C       AGCCAC
                                AG GCGCGGGC     GGCC
                                || ||||||||     ||||
                                TC CGCGTCTG     CCGG
                                 C       GCA___
GAM1661  SLC6A8   5'  GCGCGCGGGCGGCGTCGGGGCC 24770          A  CAC__
            C                    GCGCGCGGGC GC    GGCCC
                                ||||||||||  ||    |||||
                                CGCGCGCCCG CG    CCGGG
                                      C  CAGCC
GAM1661  SLIT3    5'  GCGCGCGGGGAGCGCGGGCGGC 16869         C   CA___
            C                    GCGCGCGGG AGC    CGGCC
                                ||||||||| |||    |||||
                                CGCGCGCCC TCG    GCCGG
                                     C   CGCCC
GAM1661  TAZ      5'  AGCGCGCGGCGGCCGCC     31764         G A   ACG
                                AGCGCGCGG C GCC   GCC
                                ||||||||| | |||   |||
                                TCGCGCGCC G CGG   CGG
                                     _ C   ___
GAM1661  TNA      5'  AACGCAGTGAGCAGCCACGGCC 17612       C_
            CA                    AGCGCG  GGGCAGCCACGGCCCA
                                ||||||  ||||||||||||||||
                                TTGCGT  CTCGTCGGTGCCGGGT
                                   CA
GAM1661  WNT1     5'  GCGGCGGACAGCATGGC     24083     C       CAC
                                GCG GCGGGCAGC   GGC
                                ||| |||||||||   |||
                                CGC CGCCTGTCG   CCG
                                  _       TA_
GAM1662  ABCD4    3'  CGCCACAGTGTGGTTCTCC    33745     G TCT   C  C
                                CGT G   GTG GG TCTCC
                                ||| |   ||| || |||||
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                                GCG T   CAC CC AGAGG
                                  G GT_   A  A
GAM1662  ABCD4    3'  CGCCACAGTGTGGCTCTCC   33744     G TCT   C
                                CGT G   GTG GGCTCTCC
                                ||| |   ||| ||||||||
                                GCG T   CAC CCGAGAGG
                                  G GT_   A
GAM1662  ARF1     3'  CGTGGCCGGCTCTCC       43307       CTGTG
                                CGTGGT    CGGCTCTCC
                                ||||||    |||||||||
                                GCACCG    GCCGAGAGG

                                      _____
GAM1662  ATP8A2   3'  TGGTCTGTTAACACCTTTC   45272         __   G  C
                                TGGTCTGT  GCG CT TC
                                ||||||||  ||| || ||
                                ACCAGACA  TGT GA AG
                                     AT   G  A
GAM1662  B4GALT4  5'  CGTGGCCTGCCTCTTCC     19101          GCGG   _
                                CGTGGTCTGT   CTCT CC
                                ||||||||||   |||| ||
                                GCACCGGACG   GAGA GG
                                     ____   A
GAM1662  C10orf2  3'  CACGTGGCTCTCTC        34826        T  GTGCGG
                                CACGTGG CT     CTCTC
                                ||||||| ||     |||||
                                GTGCACC GA     GAGAG

                                    _ _______
GAM1662  CDH17    3'  GTGGGTCTGTGTCATTTCC   19790      _     _ GCTC
                                GTGG TCTGTG CG    TCC
                                |||| |||||| ||    |||
                                CACC AGACAC GT    AGG
                                  C     A  AA__
GAM1662  EGR3     3'  CGTGGCTGGCTTTCC       40545       T  GTGC    C
                                CGTGG CT    GGCT TCC
                                ||||| ||    |||| |||
                                GCACC GA    CCGA AGG
                                  _ ____    A
GAM1662  FSTL1    3'  CACTGGTCTGTGCCTCC     28212     G        GGCT
                                CAC TGGTCTGTGC    CTCC
                                ||| ||||||||||    ||||
                                GTG ACCAGACACG    GAGG

                                  _       ____
GAM1662  GARP     3'  CACGTGGCTCTGCAGCACTC   24305        T  G     T
                                CACGTGG CT TGCGGC CTC
                                ||||||| || |||||| |||
                                GTGCACC GA ACGTCG GAG
                                    _ G     T
GAM1662  GDF5     3'  GTGGCACCTGTGGCTCTCC    8145       __   GC
                                GTGGT  CTGT  GGCTCTCC
                                |||||  ||||  ||||||||
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                                CACCG  GACA  CCGAGAGG
                                  TG   __
GAM1662  GRB10    5'  CACGTGGCTGTGTC       23648        T    CGGCTC
                                CACGTGG CTGTG     TC
                                ||||||| |||||     ||
                                GTGCACC GACAC     AG
                                  _    ______
GAM1662  HCS      3'  CATGATCTGTGGTTTTCT    33226          CGGC
                                CGTGGTCTGTG    TCT
                                ||||||||||    |||
                                GTACTAGACAC    AGA
                                     CAAA
GAM1662  HPCA     3'  CGTGGGTCTGTGTGTATCC    13424       _     CGGCTC
                                CGTGG TCTGTG     TCC
                                ||||| ||||||     |||
                                GCACC AGACAC     AGG
                                  C     ACAT__
GAM1662  ITGAM    3'  GTGGTCTGGGCAGAGTCC    43515        T    CTC
                                GTGGTCTG GCGG   TCC
                                |||||||| ||||   |||
                                CACCAGAC CGTC   AGG
                                     C    TC_
GAM1662  LETM1    3'  CACGTGGTCCTCATTCTCT   29495         GTGCGG
                                CACGTGGTCT     CTCT
                                ||||||||||     ||||
                                GTGCACCAGG     GAGA
                                     AGTAA_
GAM1662  MAPT     3'  CACGTGGCTTCCTCTCC     32577        T  GTGCGG
                                CACGTGG CT     CTCTCC
                                ||||||| ||     ||||||
                                GTGCACC GA     GAGAGG
                                  _  AG____
GAM1662  MEIS2    3'  CATGATCTCCAGTGTGGTTCT  33539         ___   C  C
                                CGTGGTCT   GTG GG TCT
                                ||||||||   ||| || |||
                                GTACTAGA   CAC CC AGA
                                     GGT   A  A
GAM1662  MLN      5'  CACGTGGTCTGAGTGGGTCT   14529          TGC  C
                                CACGTGGTCTG   GG TCT
                                ||||||||||   || |||
                                GTGCACCAGAC   CC AGA
                                     TCA  C
GAM1662  MOCS1    3'  GTGGTCTGGCAGGAGTCC    45124        T    CTC
                                GTGGTCTG GCGG   TCC
                                |||||||| ||||   |||
                                CACCAGAC CGTC   AGG
                                  _    CTC
GAM1662  MXI1     5'  CGTGGTTTGTTTACCTCTCCC  39019       C   GCGG
                                CGTGGT TGT    CTCTCCC
                                |||||| |||    |||||||
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                                GCACCA ACA    GAGAGGG
                                   A   AATG
GAM1662  MYO1E    3'  CACCTGGTCTGTGCCTGGAGCT 22652     G        ____
                CC                  CAC TGGTCTGTGC    GGCTCT
                                    ||| ||||||||||    ||||||
                                    GTG ACCAGACACG    TCGAGG
                                      G         GACC
GAM1662  NFKB1    5'  CGCGGGTGGGCTCTC       19651       TCT   C
                                    CGTGG   GTG GGCTCTC
                                    |||||   ||| |||||||
                                    GCGCC   CAC CCGAGAG
                                      ____  _
GAM1662  PCDH12   5'  TGACCGTGTGGCTCTCC     32453     T    C
                                    TGG CTGTG GGCTCTCC
                                    ||| ||||| ||||||||
                                    ACT GGCAC CCGAGAGG
                                      _    A
GAM1662  PDGFRB   3'  GTGATCTGGAATCTCCC     42340        TGC GC
                                    GTGGTCTG   G  TCTCCC
                                    ||||||||   |  ||||||
                                    CACTAGAC   C  AGAGGG
                                         ___ TT
GAM1662  PODXL    5'  CGCGCTGCGGCGGCTCTTCC   23967      GT    _     _
                                    CGTG  CTGTG CGGCTCT CC
                                    ||||  ||||| ||||||| ||
                                    GCGC  GACGC GCCGAGA GG
                                      __    C      A
GAM1662  REGL     3'  ATGGTCTACAGAAGGCTCT    27119        TGC__
                                    GTGGTCTG    GGCTCT
                                    ||||||||    ||||||
                                    TACCAGAT    CCGAGA
                                        GTCTT
GAM1662  RXRA     3'  CGCTGGTGTGCGGCTCTC     16422    _   CT
                                    CG TGGT  GTGCGGCTCTC
                                    || ||||  ||||||||||
                                    GC ACCA  CACGCCGAGAG
                                     G   __
GAM1662  S100A11  5'  CGGGTCTGGAGCCTCTCC     24731    T     T_  GG
                                    CG GGTCTG  GC  CTCTCC
                                    || ||||||  ||  ||||||
                                    GC CCAGAC  CG  GAGAGG
                                      _     CT  __
GAM1662  SLC4A1AP 3'  CACATGGTCCACAAGGTTTTCT 32860         TG  C  C__
                                    CACGTGGTC  TG GG   TCT
                                    |||||||||  || ||   |||
                                    GTGTACCAG  GT CC   AGA
                                         GT  T  AAA
GAM1662  SOX15    3'  GTATGTTGTGCGGCTCTCCC   28020     GTC
                                    GTG   TGTGCGGCTCTCCC
                                    |||   ||||||||||||||
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                                CAT   ACACGCCGAGAGGG
                                  ACA
GAM1662  GYPB     3'  GGTGCAGCCAGTTTGCATAAAG 13322    C       GTTTT
                A                  GG GCAGCCAGT     TAAAGA
                                   || |||||||||     ||||||
                                   CC CGTCGGTCA     ATTTCT
                                    A        AACGT
GAM1662  ILVBL    3'  CGGCACAGTTGGGTCCGTGAAG 27768        CCAGT    TTA
                A                  CGGCGCAG    GTTT   AAGA
                                   ||||||||    ||||  ||||
                                   GCCGTGTC    CAGG   TTCT
                                       AACC_    CAC
GAM1662  MHC2TA   3'  CAGCGTGGTTAGTGTCCTCAGA 6980       CAGCC        A
                GA                   CGGCG    AGTGTTTTTA AGA
                                   |||||    |||||||||| |||
                                   GTCGC    TCACAGGAGT TCT
                                      ACCAA        C
GAM1662  NEO1     3'  GGCGTTTTTGTTTTTGAAG   14756     CAGCCAG      A
                                   GGCG      TGTTTTT AAG
                                   ||||      ||||||| |||
                                   CCGC      ACAAAAA TTC
                                     AAAA___      C
GAM1662  SLC1A4   3'  GGCTTAGCTGGTTTAAAG    16751    GC   CA  GTTT
                                   GGC  AGC  GT    TTAAAG
                                   |||  |||  ||   ||||||
                                   CCG  TCG  CA    AATTTC
                                     AA   AC  _____
GAM1662  TERF2    3'  GGCTAAAGAGTTTTTAAAG   24912    GCAGCC  T
                                   GGC     AG GTTTTTAAAG
                                   |||     || ||||||||||
                                   CCG     TC CAAAAATTTC
                                     ATT___  T
GAM1663  GPR23    5'  GGCACCAATTTTATCTA     41316        ATTAAC
                                   GGCACTAAT     TTATCTA
                                   |||||||||     |||||||
                                   CCGTGGTTA     AATAGAT
                                        A_____
GAM1663  ACE2     3'  TTTACATACAACAAAATC    34764          CCC
                                   TTTACATATAGCG   AAATC
                                   ||||||||||||   |||||
                                   AAATGTATGTTGT   TTTAG
                                                ___
GAM1663  CNR1     3'  TTTACATACATTCAGCCCAAAT 32006         GC__
                C                   TTTACATATA    GCCCAAATC
                                   ||||||||||    |||||||||
                                   AAATGTATGT    CGGGTTTAG
                                         AAGT
GAM1663  ODC1     3'  TTACATGGTCCCCCCAAATC   14925       ATAGCG
                                   TTACAT     CCCAAATC
                                   ||||||     ||||||||
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                                AATGTA     GGGTTTAG
                                   CCAGGG
GAM1663  PTGS2    3'  TTCGCATACACAACCCAAAT  9698     TA     GC
                                TT  CATATA  GCCCAAAT
                                ||  ||||||  ||||||||
                                AA  GTATGT  TGGGTTTA
                                  GC     GT
GAM1663  SHC1     3'  TACAAGAGGCCCAAAT      16706      TAT  C
                                TACA   AG GCCCAAAT
                                ||||   || ||||||||
                                ATGT   TC CGGGTTTA
                                  TC_  _
GAM1663  TMEM2    3'  TTTACATATCTTCTCCAAATC  30157         AGCGC
                                TTTACATAT    CCAAATC
                                |||||||||    |||||||
                                AAATGTATA    GGTTTAG
                                     GAAGA
GAM1664  MTL5     3'  TAGAGATTTCTAGACTAAGACA 22270         A  _  T  CC
                                TAGAGATT TC AG AT  AAGACA
                                |||||||| || || ||  ||||||
                                ATCTCTAA AG TC TG  TTCTGT
                                     _  A  _  A_
GAM1664  PTGS2    3'  TACAGATTTAAATCCAAGACA  9692     G     ATCAGT
                                TA AGATT     ATCCAAGACA
                                || |||||     ||||||||||
                                AT TCTAA     TAGGTTCTGT
                                 G    ATT___
GAM1664  TEC      3'  TAGGTATTTATTTATCCAAGA  17388     AG   ATCAG
                                TAG  ATT    TATCCAAGA
                                |||  |||    |||||||||
                                ATC  TAA    ATAGGTTCT
                                  CA   ATAA_
GAM1664  AAT1     3'  TTGTGAACACCACTACTATA   44330      ATA_
                                TTGT    ACTATTACTATA
                                ||||    ||||||||||||
                                AACA    TGGTGATGATAT
                                  CTTG
GAM1665  NPHS2    3'  TTTTGCATTCACTCTGAAACAT 31201      T     _    A
              TT                  TTTT CATTC TTCT GAAACATTT
                                ||||  |||||  ||||  |||||||||
                                AAAA GTAAG GAGA CTTTGTAAA
                                  C     T    _
GAM1665  SLC39A1  3'  TTTTTTTTTTTTCTAGAAACAT 30892       CA  C
                                TTTTT  TT TTCTAGAAACAT
                                |||||  ||  ||||||||||||
                                AAAAA  AA AAGATCTTTGTA
                                  AA  A
GAM1665  TKT      3'  TTTTTCATTTTTCTCAAAACAT 9866          C    A
                                TTTTTCATT TTCT GAAACAT
                                |||||||||  ||||  |||||||
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                                AAAAAGTAA AAGA TTTTGTA
                                     A   G
GAM1665 ANKTM1   3' GATGATGGAGAAAATCAGA   28803    CA       GT_
                                GA  ATGGAGAAAA   GA
                                ||  ||||||||||   ||
                                CT  TACCTCTTTT   CT
                                 AC        AGT
GAM1665 CYP3A4   3' GACAATGAGAGAGCTCAATG   32713       _   AA__
                                GACAATG GAGA    AGTG
                                ||||||| ||||    ||||
                                CTGTTAC CTCT    TTAC
                                    T   CGAG
GAM1665 NBS1     3' GACAATGGTGGAAGGGTGA   42987       A_  AA
                                GACAATGG  GAA  GTGA
                                ||||||||  |||  ||||
                                CTGTTACC  CTT  CACT
                                     AC   CC
GAM1665 PMX1     3' GACAATGAGAAAGGGAAT    35509       G    A T
                                GACAATG AGAAA G GAAT
                                ||||||| ||||| | ||||
                                CTGTTAC TCTTT C CTTA
                                   _    _ C
GAM1665 RUNX1    3' CAAAAATGAAAGTGAATATA   12007    T   GA
                                CAA GGA  AAAGTGAATATA
                                ||| |||  ||||||||||||
                                GTT TTT  TTTCACTTATAT
                                  _  AC
GAM1665 TNFRSF9  3' GAGGATGGAGAAGACCATAGGA 11453    CA      AA__  A_
           TATAC                  GA  ATGGAGAA   GTG  ATATAC
                                ||  ||||||||   |||  ||||||
                                CT  TACCTCTT   TAT  TATATG
                                 CC       CTGG   CC
GAM1666 WRB      3' TTTAGTAGCGGTATTAA     21547      A      C
                                TTTAG TAGCGGTA TGA
                                ||||| ||||||| |||
                                AAATC ATCGCCAT ATT
                                  _       A
GAM1667 ADRA1A   5' CCGAAGCTGGGTGCG       37806         AGCC
                                TCGAAGCTGG   GTGTG
                                ||||||||||   |||||
                                GGCTTCGACC   CACGC
                                          ____
GAM1667 ARHGEF7  5' GAAGTCCGAGTGTGCAAA    19362     _   AGCC
                                GAAG CTGG   GTGTGCAAA
                                |||| ||||   |||||||||
                                CTTC GGCT   CACACGTTT
                                  A  _____
GAM1667 B3GNT3   3' GAAGCTGGGGGCTGCA      30679       A_  CGTG
                                GAAGCTGG  GC   TGCA
                                ||||||||  ||   ||||
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                                CTTCGACC  CG    ACGT
                                     CC  ____
GAM1667  BMP1     3'  TCGAGGCTGGAGCAGGGGTG  25993      A       CGT_
                                TCGA GCTGGAGC    GTG
                                |||| ||||||||    |||
                                AGCT CGACCTCG    CAC
                                  C       TCCC
GAM1667  CRTL1    5'  GAAGCTGGAGATCAAGTG    12449          C_  T
                                GAAGCTGGAG  CG GTG
                                ||||||||||  || |||
                                CTTCGACCTC  GT CAC
                                      TA  T
GAM1667  DIO1     3'  TCAAAGACCGTGTGCA      9002        CTGGA
                                TCGAAG    GCCGTGTGCA
                                ||||||    ||||||||||
                                AGTTTC    TGGCACACGT
                                  ______
GAM1667  DPYSL3   3'  TCAAGCTGGAGTTTTCCA    10778    G       _____
                                TC AAGCTGGAG    CCG
                                || |||||||||    |||
                                AG TTCGACCTC    GGT
                                 _       AAAA
GAM1667  EGR1     5'  CCGGGGCTGGAGCTGCA     12657     AA       CGTG
                                TCG  GCTGGAGC    TGCA
                                |||  ||||||||    ||||
                                GGC  CGACCTCG    ACGT
                                  CC       _____
GAM1667  FAAH     5'  CGAAGCTGGAGAGGTCGTA   11051           C___
                                CGAAGCTGGAG    CGTG
                                ||||||||||    ||||
                                GCTTCGACCTC    GCAT
                                      TCCA
GAM1667  FASN     5'  CGAGGCTGGAGCGCGGC     19932     A       C   T
                                CGA GCTGGAGC GTG GC
                                ||| |||||||| ||| ||
                                GCT CGACCTCG CGC CG
                                  C       _  _
GAM1667  FY       5'  GCTGGAGGAGCAGTGCAA    13034        CC  _
                                GCTGGAG  GT GTGCAA
                                |||||||  || ||||||
                                CGACCTC  CG CACGTT
                                    CT  T
GAM1667  HDAC7A   3'  GAGCCTGGGGCTGTGTGCAAA  32470    AG    A  C
                                GA  CTGG GC GTGTGCAAA
                                ||  |||| || |||||||||
                                CT  GACC CG CACACGTTT
                                 CG    C  A
GAM1667  MBD1     3'  TCGAAGCTGGAGGTGGTG    31924           CC_
                                TCGAAGCTGGAG   GTG
                                ||||||||||||   |||
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                                AGCTTCGACCTC  CAC
                                      CAC
GAM1667 RTKN    3' TCAAAGCTGGTTAGTGCA   37501        AGCCGT
                                TCGAAGCTGG    GTGCA
                                ||||||||||    |||||
                                AGTTTCGACC    CACGT
                                     AAT___
GAM1667 TNFRSF6B 3' TCTGAGCTGGAGCTGCTGGC  37284   GA      C  GT
                                TC  AGCTGGAGC GT  GC
                                ||  ||||||||| ||  ||
                                AG  TCGACCTCG CG  CG
                                 AC       A  AC
GAM1667 ACP2    3' ATGTGGCTGGCTGGCTGTTG  11504    A  A  AGC  ACC
                                ATGT GCT GGC  GG  GTTG
                                |||| ||| |||  ||  ||||
                                TACA CGA CCG  CC  CAAC
                                  C  _  A__  GA_
GAM1667 RGS14   3' ATGCAGCTGTCCTGGACTGTTG 27015       AGGCAGC   C
                                ATGTAGCT     GGAC GTTG
                                ||||||||     |||| ||||
                                TACGTCGA     CCTG CAAC
                                     CAGGA__   A
GAM1667 TNFAIP2  3' ATGTAGCTGGGCGTGGGGGA  26634       A  AGC__
                                ATGTAGCT GGC    GGA
                                |||||||| |||    |||
                                TACATCGA CCG    CCT
                                     C  CACCC
GAM1668 ARVCF   3' CCGAAGGTCAGTCCCGGAGG  11701     ATCT  AC
                                TCGAA   TCA  CCCGGAGG
                                |||||   |||  ||||||||
                                GGCTT   AGT  GGGCCTCC
                                   CC__   CA
GAM1668 HTR1D   3' GAAATCTTCAGTCCTGCG   9262        AC _____
                                GAAATCTTCA  CC    CG
                                ||||||||||  ||    ||
                                CTTTAGAAGT  GG    GC
                                     CA  ACIII
GAM1668 KLHL1   5' CCGAAGCTCCGGAGG      34077      AT  TCAACC
                                TCGAA  CT    CCGGAGG
                                |||||  ||    |||||||
                                GGCTT  GA    GGCCTCC
                                   C_  _______
GAM1668 LHX5    3' TCGAAATCTCTTGACCCTCCG  35325       CAA__  _
                                TCGAAATCTT    CC CCG
                                ||||||||||    || |||
                                AGCTTTAGAG    GG GGC
                                     AACTG  A
GAM1668 OLIG2   3' GAATCTTTTCCCGGAGG    25146    A   CAAC
                                GAA TCTT   CCCGGAGG
                                ||| ||||   ||||||||
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                                CTT AGAA   GGGCCTCC
                                  _   AA__
GAM1668 BFSP2   3' GAAGGAGGACAAGGGAGA   18700        A   A_
                                GAAGGAGGA CAAG  AGA
                                ||||||||| ||||  |||
                                CTTCCTCCT GTTC  TCT
                                     _   CC
GAM1668 CSNK2A1 3' GGTGGGAATGGGAAGAAGTC  12479   A_   CAA
                                GG  GGAA   GAAGAAGTC
                                ||  ||||   |||||||||
                                CC  CCTT   CTTCTTCAG
                                 AC    ACC
GAM1668 GTF2H1  3' AGGAGGAATACTTAAGGTC   23686        CAAG_   AA
                                AGGAGGAA    AAG  GTC
                                ||||||||    |||  |||
                                TCCTCCTT    TTC  CAG
                                    ATGAA  __
GAM1668 ITGAM   3' TCGCGGGGGAGAAGAAGT    43518    AA  A   ACAA
                                TCG  GG GGA    GAAGAAGT
                                |||  || |||    ||||||||
                                AGC  CC CCT    CTTCTTCA
                                  GC  _  ____
GAM1668 KCNS2   3' GGAGGAGGAAACAGTC      42833       ACAA    A
                                GGAGGA    GAAG AGTC
                                ||||||    |||| ||||
                                CCTCCT    CTTT TCAG
                                   C___    G
GAM1668 KNSL1   3' AAAGGAGGGATACAACTAG   21174        A__    GA
                                GAAGGAGG   ACAA  AG
                                ||||||||   ||||  ||
                                TTTCCTCC   TGTT  TC
                                    CTA    GA
GAM1668 MYO1D   3' GAAGGAGAGAGGAAGT      43496        GAACA   A
                                GAAGGAG    AGA GAAGT
                                |||||||    ||| |||||
                                CTTCCTC    TCT CTTCA
                                   _____  C
GAM1668 PML     3' GAAGGAGGGGCTAATAGGAGTC 37727         AACAAGA  A
                                GAAGGAGG      AG AGTC
                                ||||||||      || ||||
                                CTTCCTCC      TC TCAG
                                    CCGATTA  C
GAM1668 RARG    3' GGAGGAAGAAAGGAGGGGTC  9725        C_   A  AA
                                GGAGGAA  AAG AG  GTC
                                |||||||  ||| ||  |||
                                CCTCCTT  TTC TC  CAG
                                    CT   C  CC
GAM1668 RBP5    3' AGAAGGAAAAGAAGAGGTC   36459        C      A
                                AGGAGGAA AAGAAGA GTC
                                |||||||| ||||||| |||
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                                TCTTCCTT TTCTTCT CAG
                                    _      C
GAM1668  SLC2A3   3'  GAGACTACTACAAGAAGGAGT  27978      A____       A
                                GAGG    ACAAGAAG AGT
                                ||||    |||||||| |||
                                CTCT    TGTTCTTC TCA
                                  GATGA       C
GAM1668  SLC7A8   3'  GAAGGAGGGGAGGAAGT     29287        AACAA  A
                                GAAGGAGG    GA GAAGT
                                ||||||||    || |||||
                                CTTCCTCC    CT CTTCA
                                    C____  C
GAM1669  JAG2     5'  CGGGGTCGAGCGCAGCGC    13718     CA         TTC
                                CGG  GTCGAGCGCGGC   GC
                                |||  ||||||||||||   ||
                                GCC  CAGCTCGCGTCG   CG
                                 C_          ___
GAM1669  LASS1    3'  CGTGGTTGAGCGCCGGCGGCC  34604    GCA  C     _  TTC
                                CG   GT GAGCGC GGC   GCC
                                ||   || |||||| |||   |||
                                GC   CA CTCGCG CCG   CGG
                                 AC_  A     G   C__
GAM1669  NDUFB10  5'  CGGCGGCGGGCGCGGACT    21236      A T  A     _
                                CGGC G CG GCGCGG CT
                                |||| | || |||||| ||
                                GCCG C GC CGCGCC GA
                                  C _  C      T
GAM1669  NLGN2    5'  ACGGTAGTTGAGCGTGGCT   44744      C   C     C
                                ACGG AGT GAGCG GGCT
                                |||| ||| ||||| ||||
                                TGCC TCA CTCGC CCGA
                                  A   A     A
GAM1669  PABPC4   5'  CGGCGGCGGGCGCGGGGCAGGC 19223      A T  A     CTTC_
            C                    CGGC G CG GCGCGG     GCC
                                |||| | || ||||||     |||
                                GCCG C GC CGCGCC     CGG
                                  C _  C      CCGTC
GAM1669  PDGFB    5'  ACGGCAGTCGATGGTTCG    15166          GCGC  C
                                ACGGCAGTCGA    GG TTCG
                                ||||||||||    || ||||
                                TGCCGTCAGCT    CC AAGC
                                      A___  _
GAM1669  RAC3     5'  CGGCGGCGGGCGCGGCC     22787      A T  A
                                CGGC G CG GCGCGGCT
                                |||| | || ||||||||
                                GCCG C GC CGCGCCGG
                                  C _  C
GAM1669  RHEB2    5'  CGGCGGCGGGCGCGGCTGCC  24716      A T  A       TC
                                CGGC G CG GCGCGGCT  GCC
                                |||| | || ||||||||  |||
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                                GCCG C GC CGCGCCGA  CGG
                                  C _  C       __
GAM1669  SNX13    5'  CGGCGGTTTTACTCGGCTTCGC 31534      A  CGA  G
                                CGGC GT   GC CGGCTTCGC
                                |||| ||   || |||||||||
                                GCCG CA   TG GCCGAAGCG
                                  C  AAA  A
GAM1669  GATA3    5'  GCCTCGGCTGTCGTCGCGCC   13097       A   C    T
                                GCCTCG CTG CGTCG CGTC
                                |||||| ||| ||||| ||||
                                CGGAGC GAC GCAGC GCGG
                                   C   A    _
GAM1670  ALDH8A1  3'  TGATGAAAGAAACACTATGAAA 35453     G         GC
              A                  TGA TGAAAGAGATA  ATGAAAA
                                 ||| ||||||||||  |||||||
                                 ACT ACTTTCTTTGT  TACTTTT
                                  _         GA
GAM1670  ALOX15   3'  TGGGTGCAGAGACCATGAAAA  10077    A   AA     AG
                                 TG GTG  AGAGAT  CATGAAAA
                                 || |||  ||||||  ||||||||
                                 AC CAC  TCTCTG  GTACTTTT
                                  C   G_     __
GAM1670  CCR2     3'  TGAGTGAAGAAATTATGAA    8503          A    AGC
                                 TGAGTGAA GAGAT   ATGAA
                                 |||||||| |||||   |||||
                                 ACTCACTT CTTTA   TACTT
                                     _     A__
GAM1670  COLQ     3'  TGGTGGAAGCAGCATGAAA    38698    A   AAA   A
                                 TG GTG   GAG TAGCATGAAA
                                 || |||   ||| ||||||||||
                                 AC CAC   TTC GTCGTACTTT
                                  _   C__   _
GAM1670  DISC1    3'  TGAGTGAAACAGGTTCCACG   33052         G  ATAG
                                 TGAGTGAAA AG    CATG
                                 ||||||||| ||    ||||
                                 ACTCACTTT TC    GTGC
                                       G  CAAG
GAM1670  FBXL5    3'  TGAGTAAAGTGCATGAAA     37948         AGAGATA
                                 TGAGTGAA      GCATGAAA
                                 ||||||||      ||||||||
                                 ACTCATTT      CGTACTTT
                                     CA_____
GAM1670  FXYD6    3'  GAGTGAAAGGAGTCCATGAA   35116         A  TAG
                                 GAGTGAAAG GA   CATGAA
                                 ||||||||| ||   ||||||
                                 CTCACTTTC CT   GTACTT
                                       _ CAG
GAM1670  HNF3A    3'  GAAAGGTTGTGCATGAAAA   40727       AGATA
                                 GAAAG    GCATGAAAA
                                 |||||    |||||||||
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                                CTTTC    CGTACTTTT
                                   CAACA
GAM1670 IGFBP4   3' TGAGTGAAGGAATGAGTGA   11409       A  AT  CA
                                TGAGTGAA GAG  AG  TGA
                                |||||||| |||  ||  |||
                                ACTCACTT CTT  TC  ACT
                                     C   AC  __
GAM1670 IL1F5    3' TGAGGGAAGAGATAGGAAA   29360     T  A     CAT
                                TGAG GAA GAGATAG   GAAA
                                |||| ||| |||||||   ||||
                                ACTC CTT CTCTATC   CTTT
                                  C  _     ____
GAM1670 MFGE8    3' GTGAAAAGCCAGCATGA     25462      A  A
                                GTGAA GAG TAGCATGA
                                ||||| ||| ||||||||
                                CACTT TTC GTCGTACT
                                   _  G
GAM1670 PARK2    3' AGTGAAAGGGATCCAGGA    30369       A  AG  T
                                AGTGAAAG GAT  CA GA
                                |||||||| |||  || ||
                                TCACTTTC CTA  GT CT
                                     C  G_  C
GAM1670 PHLDA3   3' TGAGGTGGTGGGTAGCATGAA  29614     _ AAAGAGA
                                TGAG TG      TAGCATGAA
                                |||| ||      |||||||||
                                ACTC AC      ATCGTACTT
                                  C  CACCC__
GAM1670 POU3F4   3' GAGTGAGAGAGAAAGGAAA   7170       A    T  CAT
                                GAGTGA AGAGA AG   GAAA
                                |||||| ||||| ||   ||||
                                CTCACT TCTCT TC   CTTT
                                   C    T  ____
GAM1670 PPT2     5' TGAGGAAAGAGAACGCA     39929      T      TA
                                TGAG GAAAGAGA  GCA
                                |||| ||||||||  |||
                                ACTC CTTTCTCT  CGT
                                  _       TG
GAM1670 PSD      5' AGTGGAAGAGATAGATG     15777     A       C
                                AGTG AAGAGATAG ATG
                                |||| ||||||||| |||
                                TCAC TTCTCTATC TAC
                                  C       _
GAM1670 RAB11A   3' AGTGAAGCCATAGCATGAAAA  21678       A AG
                                AGTGAA G  ATAGCATGAAAA
                                |||||| |  ||||||||||||
                                TCACTT C  TATCGTACTTTT
                                   _ GG
GAM1670 SCD      3' TGAGTGAAGGGGCACAACAC   22835       AGAG_
                                TGAGTGAA    ATAGCAT
                                ||||||||    |||||||
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                                ACTCACTT    TGTTGTG
                                    CCCCG
GAM1670 SLC16A1  3' TAAGTGAAAGGGGTCACAAAA 16815        AGATAG TG
                                TGAGTGAAAG     CA AAA
                                ||||||||||     || |||
                                ATTCACTTTC     GT TTT
                                    CCCA__  GT
GAM1670 SORD     3' TGAGTGGCAGATTTTCATGAAA 16969      AA  GATAG
           A                     TGAGTG AGA    CATGAAAA
                                ||||||  |||    ||||||||
                                ACTCAC TCT    GTACTTTT
                                   CG  AAAA_
GAM1670 WAS      3' TGAGTGAAGAGAACTGA     7536        A   TA A
                                TGAGTGAA GAGA  GC TGA
                                |||||||| ||||  || |||
                                ACTCACTT CTCT  TG ACT
                                    _   __ _
GAM1670 CCRL1    3' GTACATTTATTATCTTGTT   32430     AT
                                GTA  TTTATTATCTTGTT
                                |||  ||||||||||||||
                                CAT  AAATAATAGAACAA
                                  GT
GAM1671 BCL11A   3' CTTAGCTTCGTTACTTCTG   39711        A TA A
                                CTTAGCTTC TT  AC TTTG
                                ||||||||| ||  || ||||
                                GAATCGAAG AA  TG AGAC
                                    C  __  A
GAM1672 AFM      5' TTATGGAATTTAGACTCTT   10064     AT   C
                                TTGT  GATT AGACTCTT
                                ||||  |||| ||||||||
                                AATA  TTAA TCTGAGAA
                                  CC   A
GAM1672 GPR18    5' TTGTATTTTGTTTTAGACTCTT 23625      GATTC___
           T                     TTGTAT       AGACTCTTT
                                ||||||       |||||||||
                                AACATA       TCTGAGAAA
                                   AAACAAAA
GAM1672 KLHL3    3' AAAGGTTAGAGACAAGATG   44635     A    __
                                GAAG TTAGAG  GAGATG
                                |||| ||||||  ||||||
                                TTTC AATCTC  TTCTAC
                                  C     TG
GAM1672 NOS1     3' TCAGGATTAGAAGGGGTGAGTG 8378     AA       AGA  A
                                TCG  GATTAGAGG   TGA TG
                                |||  |||||||||  ||| ||
                                AGT  CTAATCTTC   ACT AC
                                  C_       CCC   C
GAM1673 C7orf2   3' AAAAATCCAAGTTACAAG    35364         AA
                                AAAAATCCAAG  ACAAG
                                ||||||||||  |||||
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                                TTTTTAGGTTC  TGTTC
                                      AA
GAM1673  CLECSF11  5'  AAAAATCCAAAAAATTAG    39040           CA
                                AAAAATCCAAGAAA  AG
                                |||||||||||||  ||
                                TTTTTAGGTTTTTT  TC
                                      AA
GAM1673  CYP4F3    3'  AAAATCCAACAATAAGAAG   9446         G  AC
                                AAAATCCAA AA  AAGAAG
                                |||||||||  ||  ||||||
                                TTTTAGGTT TT  TTCTTC
                                     G  A_
GAM1673  GJA1      3'  AAAACCCAAGAATACCAG    6727           _  A
                                AAAATCCAAGAA AC AG
                                ||||||||||||  || ||
                                TTTTGGGTTCTT TG TC
                                      A  G
GAM1673  GOCAP1    3'  AAAACCCTCCTACAAGAAG   35544        AAGAA
                                AAAATCC    ACAAGAAG
                                |||||||    ||||||||
                                TTTTGGG    TGTTCTTC
                                    AGGA_
GAM1673  IDH3G     3'  AATCCAAGGAGCAAACCAAGAA 19978        ____   _     III
              GC                  AATCCAAG    AAAC AAGAAG   C
                                |||||||    |||| ||||||   |
                                TTAGGTTC    TTTG TTCTTC   G
                                    CTCG    G     III
GAM1673  IGF1      3'  AAAAATCCAAAAAATTAG    8332            CA
                                AAAAATCCAAGAAA  AG
                                ||||||||||||||  ||
                                TTTTTAGGTTTTTT  TC
                                      AA
GAM1673  JAM3      3'  AAAAACCCAAGACACTGGAAG  37256          A  AA
                                AAAAATCCAAGA AC  GAAG
                                ||||||||||| ||  ||||
                                TTTTTGGGTTCT TG  CTTC
                                      G  AC
GAM1673  LAMC2     3'  AAAATCCAAGGAAATACAGAAG 33112          _  CA_
                                AAAATCCAAG AAA   AGAAG
                                |||||||||| |||   |||||
                                TTTTAGGTTC TTT   TCTTC
                                      C   ATG
GAM1673  MX2       3'  AATCAGGGAAACAAGAAG    14693      CAA
                                AATC   GAAACAAGAAG
                                ||||   ||||||||||
                                TTAG   CTTTGTTCTTC
                                  TCC
GAM1673  NFATC3    3'  GGAAACCCAAGGTCCAAG    21253    A       AAA
                                A AAATCCAAG   CAAG
                                | |||||||||   ||||
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                                C TTTGGGTTC   GTTC
                                 C        CAG
GAM1673  NHP2L1   3'  AAAAATCCAGAAACCAG     22675          A    A
                                AAAAATCCA GAAAC AG
                                ||||||||| ||||| ||
                                TTTTTAGGT CTTTG TC
                                      _    G
GAM1673  NSF      3'  AAAACCCAAAACAAAGAAG   41779           AAC
                                AAAATCCAAGA   AAGAAG
                                ||||||||||   ||||||
                                TTTTGGGTTTT   TTCTTC
                                      GT_
GAM1673  PIWIL1   3'  ATCTATGAGAAACAAGAAG   43750     CA__
                                ATC   AGAAACAAGAAG
                                |||   ||||||||||||
                                TAG   TCTTTGTTCTTC
                                  ATAC
GAM1673  RECQL5   3'  ACACAGAGAAACAAGAAG    20163   TC  _
                                A  CA AGAAACAAGAAG
                                |  || ||||||||||||
                                T  GT TCTTTGTTCTTC
                                 GT  C
GAM1673  SDHC     3'  GGAAATCCAAGAAAAAG     42979   A         C
                                A AAATCCAAGAAA AAG
                                | ||||||||||| |||
                                C TTTAGGTTCTTT TTC
                                 C         _
GAM1673  SLC21A9  3'  AAAACCTGGGAAACAAGA    28554       CAA
                                AAAATC   GAAACAAGA
                                ||||||   |||||||||
                                TTTTGG   CTTTGTTCT
                                    ACC
GAM1673  TIF1     3'  AAAAATCCAAGAAGTGGGAAG  41271           ACAA
                                AAAAATCCAAGAA    GAAG
                                ||||||||||||    ||||
                                TTTTTAGGTTCTT    CTTC
                                       CACC
GAM1673  TNFRSF1B 3'  AAAAACCCAAGGGCTCCAGAAG 9871           AAACA_
                                AAAAATCCAAG     AGAAG
                                ||||||||||     |||||
                                TTTTTGGGTTC     TCTTC
                                      CCGAGG
GAM1673  USH3A    3'  AAAACTCCAAGAAGACAGAGA  38155      A      _  _
                                AAAA TCCAAGAA ACA AGA
                                |||| |||||||| ||| |||
                                TTTT AGGTTCTT TGT TCT
                                  G       C  C
GAM1673  RAD18    3'  TTGGATTCAGTGTTACAGA   33560         ATATTA  G
                                TTGGATTCA     TTG AGA
                                |||||||||     ||| |||
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                                AACCTAAGT     AAT TCT
                                     CAC___   G
GAM1673  WIF1     3'  ATTGGATTCAGGTGGA      41163          ATATTAT
                                ATTGGATTCA      TGGA
                                ||||||||||      ||||
                                TAACCTAAGT      ACCT
                                     CC_____
GAM1674  COL10A1  3'  TCTGCAATCATAGAAAAGTT   7965           TAGT
                                TTTGCAATCATA    GAGTT
                                ||||||||||||    |||||
                                AGACGTTAGTAT    TTCAA
                                      CTT_
GAM1674  PLXNA2   3'  TTTGCAATTTGTGCAAAGTTCT 36081         CATATAGT
                                TTTGCAAT       GAGTTCT
                                ||||||||       |||||||
                                AAACGTTA       TTCAAGA
                                     AACACGT_
GAM1674  DEFA4    3'  GGCGTTCCCAGCATGACATTC  12562    A  A_   CT    C   C
                                G GC  TCCC  GGCAT GACA TC
                                | ||  ||||  ||||| |||| ||
                                C CG  AGGG  TCGTA CTGT AG
                                 _ CA   __    _   A
GAM1674  FCMD     3'  GAGTTCTTGCCCCATCGACATT 27520     CATC__   TGG      C
           C                     GAG     CCC   CATCGACA TC
                                |||     |||   |||||||| ||
                                CTC     GGG   GTAGCTGT AG
                                  AAGAAC  ___       A
GAM1674  NCOA6    5'  AAGCATCTCCTGCAACACTC   30431       C   GCAT
                                GAGCATC CCTG    CGACACTC
                                ||||||| ||||    ||||||||
                                TTCGTAG GGAC    GTTGTGAG
                                    A   ____
GAM1674  PFKFB4   3'  GCACCCCTGGCCACCAGCTC   21290     T      ATCGA  _
                                GCA CCCCTGGC     CA CTC
                                ||| ||||||||     || |||
                                CGT GGGGACCG     GT GAG
                                  _       GTG__  C
GAM1675  ATP8A2   3'  CCAGGGCATCAGTTGGTTTG   45255          TACACCA
                                CCAGGGTATT      GTTTG
                                ||||||||||      |||||
                                GGTCCCGTAG      CAAAC
                                     TCAAC__
GAM1675  DDEF2    3'  CCTAGGTATTTATGTACCAGT  19316    A       C__
                                CC GGGTATTTA   ACCAGT
                                || |||||||||   ||||||
                                GG TCCATAAAT   TGGTCA
                                 A        ACA
GAM1675  IRTA2    3'  GGATTTTATGCCAGTTTG    36343      A   CA
                                GGGT TTTA  CCAGTTTG
                                ||||  ||||  ||||||||
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                                CCTA AAAT  GGTCAAAC
                                  _   AC
GAM1675 MAFF    3'  CCCAGGGTCATTCGGTCCCAGT 29513       _   ACA_
            TTG                  CCCAGGGT ATTT   CCAGTTTG
                                 |||||||| ||||   ||||||||
                                 GGGTCCCA TAAG   GGTCAAAC
                                    G   CCAG
GAM1675 MB      3'  GGGGTTACAGCCAGTTTG   23860    TAT   _
                                 GGG  TTACA CCAGTTTG
                                 |||  ||||| ||||||||
                                 CCC  AATGT GGTCAAAC
                                   C__   C
GAM1675 MMP9    3'  CCAGAACAGAATACCAGTTTG  22627     GG  TTTAC
                                 CCAG  TA   ACCAGTTTG
                                 ||||  ||   |||||||||
                                 GGTC  GT   TGGTCAAAC
                                   TT  CTTA_
GAM1675 SP4     3'  CCAGTACATCAGTTT      17048     GGTATT   C
                                 CCAG     TACA CAGTTT
                                 ||||     |||| ||||||
                                 GGTC     ATGT GTCAAA
                                   _______   A
GAM1675 TAC3    3'  AGGGTATTCTACAGTC     29919        ACAC
                                 AGGGTATTT   CAGTT
                                 |||||||||   |||||
                                 TCCCATAAG   GTCAG
                                     AT__
GAM1675 TNFSF11  3'  CCCCAGGGAATTTACAAAGT  37453       T     CC
                                 CCCCAGGG ATTTACA  AGT
                                 |||||||| |||||||  |||
                                 GGGGTCCC TAAATGT  TCA
                                    T     T_
GAM1675 VAMP1   3'  CCCAGGGTTTTGTTGCACATTT 32572       ATTTA__  CA
            G                    CCCAGGGT     CAC  GTTTG
                                 ||||||||     |||  |||||
                                 GGGTCCCA     GTG  TAAAC
                                    AAACAAC  __
GAM1676 SLC24A1  3'  TAGCTCGTGCGCCTAT     21823     ATCA   GATA
                                 TAGC   TCG   CGCCTAT
                                 ||||   |||   |||||||
                                 ATCG   AGC   GCGGATA
                                   ____  AC__
GAM1676 ANKRD3   3'  GCTGGCTGCTACCATTCGT   33968     A
                                 GCTG CTGTTACCATTTGT
                                 |||| ||||||||||||||
                                 CGAC GACGATGGTAAGCA
                                   C
GAM1676 MYOZ1    3'  TGACTGTTACTGGTG      34557        CATT  T  A
                                 TGACTGTTAC   TG GT G
                                 ||||||||||   || || |
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                                ACTGACAATG    AC CA C
                                      _____  _  C
GAM1676  PCSK1    3'  GCTAACTGTTGCCATGAGC    7752          A    TT
                                GCTGACTGTT CCAT  GT
                                |||||||||| ||||  ||
                                CGATTGACAA GGTA  CG
                                      C    CT
GAM1676  PMX1     3'  TGACTGTTGGCACCTGGT    35527         AC     T
                                TGACTGTT  CATTTG GT
                                ||||||||  |||||| ||
                                ACTGACAA  GTGGAC CA
                                     CC     _
GAM1676  SYN2     3'  GCTGACTGTTGTTGGTGAATGT 39461          ACCATTT_
                                GCTGACTGTT       GTGT
                                ||||||||||       ||||
                                CGACTGACAA       TACA
                                      CAACCACT
GAM1676  ZNF236   3'  GCTGACTGTGGCGTGTG     28863         TACCATT    A
                                GCTGACTGT      TGTGT G
                                |||||||||      ||||| |
                                CGACTGACA      GCACA C
                                     CC_____    C
GAM1677  RAD23A   3'  TAAATAAACATGAATATATAT  22799    T    TT
                                A GATG  TGTGAATATATAT
                                | ||||  ||||||||||||
                                A TTAT  GTACTTATATATA
                                 T    TT
GAM1677  RECK     3'  ATGAATACCGATGAATATATAT 34414      TGT   _
                                ATGA   TTG TGAATATATAT
                                ||||   ||| ||||||||||
                                TACT   GGC ACTTATATATA
                                   TAT   T
GAM1677  SVIL     3'  ATGGTGTTTATATAAATATATA 34724     A    __
                T                ATG TGTT  TGTGAATATATAT
                                ||| ||||  ||||||||||||
                                TAC ACAA  ATATTTATATATA
                                  C    AT
GAM1677  BTEB1    3'  CATTGTGGTATTTTCCCT    10212        A
                                TATTGT GTATTTTTTTT
                                ||||||  ||||||||||
                                GTAACA CATAAAAGGGA
                                    C
GAM1678  DLEU2    3'  CTACCATATAGTTATAATTATA 25692     TT     A
                                CTG  GTATA TTATAATTATA
                                |||  ||||| ||||||||||
                                GAT  TATAT AATATTAATAT
                                  GG    C
GAM1678  PTPRG    3'  CTGTTGTATAAGATTATA    15935          __
                                CTGTTGTATA  ATTATA
                                ||||||||||  ||||||
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                                GACAACATAT  TAATAT
                                      TC
GAM1679  PBX2     3'  TATTTAACATATTTGGCAATAA 15110      A       TTT_
             CTC                   TATT AACATATTT    ATAACTC
                                |||| |||||||||   |||||||
                                ATAA TTGTATAAA    TATTGAG
                                  A       CCGT
GAM1679  BCL11A   3'  TTTGCGTAAAATGCAATAG   39724      CAGACAAT
                                TTTGT       AATGCAATAG
                                |||||       ||||||||||
                                AAACG       TTACGTTATC
                                   CATT____
GAM1679  PROML1   3'  TTTGTCAGATGGAGTTACGCA  25689         CAATA__
                                TTTGTCAGA      ATGCA
                                |||||||||      |||||
                                AAACAGTCT      TGCGT
                                      ACCTCAA
GAM1679  RDX      3'  TTTGTCAGACGTGATAAT    16239         A__
                                TTTGTCAGAC   ATAAT
                                ||||||||||   |||||
                                AAACAGTCTG   TATTA
                                      CAC
GAM1679  SH3GL3   5'  TTTGTCAGAAACGGATAG    16685         CAAT    CA
                                TTTGTCAGA   AATG  ATAG
                                |||||||||   ||||  ||||
                                AAACAGTCT   TTGC  TATC
                                     ____   C_
GAM1680  IAPP     3'  TAATAGAAGCTCACT       7664          TCCGG
                                TAATAGAAGT    TCACT
                                ||||||||||    |||||
                                ATTATCTTCG    AGTGA
                                     _____
GAM1681  CCNF     3'  TTCTTTCTTACATTTGCAG   12082         CTTG
                                TTCTTTCT    GTTTGCAG
                                ||||||||    ||||||||
                                AAGAAAGA    TAAACGTC
                                     ATG_
GAM1681  DMD      5'  TGGATCCTTTTTCTTTTGGCAG 19697    A      C    GGTTT
                                TG ATTCTTT TCTT     GCAG
                                || ||||||| ||||     ||||
                                AC TAGGAAA AGAA     CGTC
                                 C      A    AAC__
GAM1681  EPHB1    3'  TTCTTTTTCCTTTTTGCAG   20781       C    GG
                                TTCTTT TCTT  TTTGCAG
                                |||||| ||||  |||||||
                                AAGAAA AGGA  AAACGTC
                                   A    A_
GAM1681  FSHR     5'  TGATTTCTTTCTGCATTTGCAG 6627      A       CTTG
                                TGA TTCTTTCT    GTTTGCAG
                                ||| ||||||||    ||||||||
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```
                                ACT AAGAAAGA    TAAACGTC
                                  A       CG__
GAM1681  HEPH     3'  TGAGTTTTTCTCTTGGTC    31346     A  C
                                TGA TT TTTCTCTTGGTT
                                ||| || ||||||||||||
                                ACT AA AAAGAGAACCAG
                                  C  _
GAM1681  IGF1     3'  TAAATTCTTTCTTTATCAGT   8348            C__ TG
                                TGAATTCTTTCT   T  GT
                                ||||||||||||   |  ||
                                ATTTAAGAAAGA   A  CA
                                       AAT GT
GAM1681  BLAME    3'  AGCGGATGGAGATGGTGAGGAT 33484    G          CATC_
              GT                  AG GGATGGAGATGG    GTGT
                                || ||||||||||||     ||||
                                TC CCTACCTCTACC     TACA
                                 G           ACTCC
GAM1681  LLGL1    3'  AGGGGGGGAGGTGGCAC     42500       AT    A
                                AGGGG  GGAG TGGCAT
                                |||||  |||| ||||||
                                TCCCC  CCTC ACCGTG
                                   C_    C
GAM1681  STAT6    3'  GGGGATGGAGTGAGAGTGT    17157          A   CATC
                                GGGGATGGAG TGG    GTGT
                                |||||||||| |||    ||||
                                CCCCTACCTC ACT    CACA
                                      _   CT__
GAM1682  TFRC     3'  TCATATTGTGTTATACGATGA  17435     _    GTAGAT
                                TCA ATTG     TTATACGATGA
                                ||| ||||     ||||||||||||
                                AGT TAAC     AATATGCTACT
                                  A    AC_____
GAM1683  CARPX    3'  AGGCTTGGGGGAAAGAA     33565       CGA   TT
                                AGGCT   GGG  GGAAAGAA
                                |||||   |||  ||||||||
                                TCCGA   CCC  CCTTTCTT
                                   A__   __
GAM1683  CHRM1    5'  GGCTGGGGTTGGAGAG      45425      CGA       A
                                GGCT   GGGTTGGA AG
                                ||||   |||||||| ||
                                CCGA   CCCAACCT TC
                                   C__       C
GAM1683  COL4A4   3'  ATAAAGCTTTTTGGGAAGGA   6394         CGA_   TT
                                ATAAGGCT    GGG  GGA
                                ||||||||    |||  |||
                                TATTTCGA    CCC  CCT
                                     AAAA   TT
GAM1683  DVL3     3'  AGGGTTAGGGGTCTGAAGGAA  20672     CTCGA    G   A
                                AGG     GGGTT GAA GAA
                                |||     ||||| ||| |||
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                                TCC    CCCAG CTT CTT
                                  CAATC    A  C
GAM1683  ENO2     3'  AGGGAACCTAGGGTTGGGGAGA 12707    C__  G      AA
                                AGG  TC AGGGTTGG  AGA
                                |||  || ||||||||  |||
                                TCC  GG TCCCAACC  TCT
                                  CTT  A       CC
GAM1683  EPHA2    3'  GGCCCGAGGGTCTAAAGAA   20741          GG
                                GGCTCGAGGGTT  AAAGAA
                                ||||||||||||  ||||||
                                CCGGGCTCCCAG  TTTCTT
                                       A_
GAM1683  FACL4    3'  AAGGCAAGTTGGGAAGA     35674      TCGA      A
                                AAGGC    GGGTTGG AAGA
                                |||||    ||||||| ||||
                                TTCCG    TTCAACC TTCT
                                  _____      C
GAM1683  INPP1    5'  AGGACGAGGGTTGGGGAG    13570     CT        AA
                                AGG  CGAGGGTTGG  AG
                                |||  ||||||||||  ||
                                TCC  GCTCCCAACC  TC
                                  T_         CC
GAM1683  LALBA    3'  AAGCTTTGGGGGAACAGAA   14057      CGA   TT   _
                                AGGCT   GGG  GGAA AGAA
                                |||||   |||  |||| ||||
                                TTCGA   CCC  CCTT TCTT
                                   AA_   __    G
GAM1683  MCC      3'  ATAAGGCTCCACTGAGAGGG   14379         _______
                                ATAAGGCTC     GAGGG
                                |||||||||     |||||
                                TATTCCGAG     CTCCC
                                      GTGACT
GAM1683  MME      3'  TAAGGCTGAGAGAAAGAA    28612        C     TT
                                TAAGGCT GAGGG  GGAA
                                ||||||| |||||  ||||
                                ATTCCGA CTCTC  TCTT
                                   _    TT
GAM1683  MN1      3'  TAAGGTTGAGGGGGAAGGAA   14589      CTC    TT   A
                                TAAGG   GAGGG  GGAA GAA
                                |||||   |||||  |||| |||
                                ATTCC   CTCCC  CCTT CTT
                                   AA_     __    C
GAM1683  NOS2A    3'  ATAAGACTTGAGGCTGG     8416         C   G
                                ATAAGGCT GAGG TTGG
                                |||||||| |||| ||||
                                TATTCTGA CTCC GACC
                                      A   _
GAM1683  NOTCH3   3'  ATAAGGCTGGGCCAGA      7733         CGA   TG
                                ATAAGGCT   GGGT  GA
                                ||||||||   ||||  ||
```

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                                TATTCCGA  CCCG  CT
                                    ___   GT
GAM1683  NRXN2    3'  GGATTGGAGGGCTTGGGAAGA  31484    CTC_     _  A
                                GG   GAGGGTT GG AAGA
                                ||   ||||||| || ||||
                                CC   CTCCCGA CC TTCT
                                 TAAC      A  C
GAM1683  POU2AF1  3'  AAGGAAGGAAGGGGTTGGAAAG 26361     CTC  __
                                AAGG  GA  GGGTTGGAAAG
                                ||||  ||  ||||||||||
                                TTCC  CT  CCCAACCTTTC
                                  TTC  TC
GAM1683  POU2AF1  3'  AAGGAAGGAAGGGGTTGGAAAG 26361     CTC  __
                                AAGG  GA  GGGTTGGAAAG
                                ||||  ||  ||||||||||
                                TTCC  CT  CCCAACCTTTC
                                  TTC  TC
GAM1683  PPEF1    3'  AGGGGTGTTGGAAAG      26408    CTCGA  _
                                AGG   GG GTTGGAAAG
                                |||   || |||||||||
                                TCC   CC CAACCTTTC
                                 _____  A
GAM1683  PPT1     3'  ATAAGGCTTAAGAGAGAG    41549       CG   TT
                                ATAAGGCT  AGGG  GG
                                ||||||||  ||||  ||
                                TATTCCGA  TCTC  TC
                                    AT    TC
GAM1683  RPH3AL   3'  ATAAGGTCGGGGGCTGA    28098      C   A
                                ATAAGG TCG GGGTTGG
                                ||||||| ||| |||||||
                                TATTCC AGC CCCGACT
                                   _  C
GAM1683  RTN2     3'  AAGGCTCGGGCCGAGGAG    24722       GA     AA
                                AAGGCTC  GGGTTGG  AG
                                |||||||  |||||||  ||
                                TTCCGAG  CCCGGCT  TC
                                   __      CC
GAM1683  SUV39H1  3'  AGGGTTGAGGGGTGTACAAGA  17221    CTC    T  GA_
                                AGG   GAGGG TG   AAGA
                                |||   |||||  ||   ||||
                                TCC   CTCCC AC   TTCT
                                  CAA    C  ATG
GAM1683  TEM5     3'  TAAGGCTGAGACTAGGGA    37242       C    GTT_
                                TAAGGCT GAGG   GGA
                                ||||||| ||||   |||
                                ATTCCGA CTCT   CCT
                                   _   GATC
GAM1683  TEM8     3'  GGCAGGGTTGGGGAGA     38184     TCG      AA
                                GGC   AGGGTTGG  AGA
                                |||   ||||||||  |||
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                                CCG   TCCCAACC  TCT
                                  ___       CC
GAM1683  TPTE     3'  GGCAGGGTTGGAAAGAA     30022     TCG
                                GGC   AGGGTTGGAAAGAA
                                |||   ||||||||||||||
                                CCG   TCCCAACCTTTCTT
                                  ___
GAM1683  ZNF10    5'  AAGGTTCGATGGGAGAA     31731     C   _   TT
                                AAGG TCGA GGG  GGAA
                                |||| |||| |||  ||||
                                TTCC AGCT CCC  TCTT
                                  A   A  __
GAM1683  ZNF144   3'  AGGCTTGGCTGGAAGA      28337      CGAG       A
                                AGGCT    GGTTGGAA GA
                                |||||    |||||||| ||
                                TCCGA    CCGACCTT CT
                                  A___       _
GAM1683  CASP8    3'  GCTTACTTCATAGTTCACT    37874    CCC  GG  _
                                GC   TA  TC TAGTTCACT
                                ||   ||  || |||||||||
                                CG   AT  AG ATCAAGTGA
                                 A__  GA  T
GAM1683  IL1R1    3'  GCCCTTTCTTCTAGTTCGCT   9361      CTAGG       A
                                GCCC     TCTAGTTC CT
                                ||||     |||||||| ||
                                CGGG     AGATCAAG GA
                                  AAAGA       C
GAM1683  NMBR     5'  TCGCCCCTGCAAGTTTACT    14803        AG  CT    C
                                TCGCCCCT  GT  AGTT ACT
                                ||||||||  ||  |||| |||
                                AGCGGGGA  CG  TCAA TGA
                                    __  T_   A
GAM1684  FBLN2    3'  TAATGTACATGTACTACT     12802        T   _
                                TAATGTAC TGT TTACT
                                |||||||| ||| |||||
                                ATTACATG ACA GATGA
                                     T   T
GAM1684  PLN      3'  ATGTGTTAATTTACTGTTTAT  15403      ACTT
                                ATGT    GTTTACTGTTTAT
                                ||||    ||||||||||||||
                                TACA    TAAATGACAAATA
                                  CAAT
GAM1685  ADRB3    3'  TGGCTAAAGTGAGAGAGGCC   6181     A       _  A__
                                TG CTAAAGTG GA   GCC
                                || ||||||||  ||   |||
                                AC GATTTCAC CT   CGG
                                 C       T  CTC
GAM1685  MCCC2    5'  TGGCTGGGGCGGAAGCTGAGC  35254    A  AAA       C   C
                                TG CT   GTGGAAGC TGA GC
                                || ||   |||||||| ||| ||
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                                AC GA   CGCCTTCG ACT CG
                                 C  CCC      _  _
GAM1685  MOCS1    3'  TGATTAAAGGAACCTGACG   45125    C    T  AA
                                TGA TAAAG GG  GCCTGACG
                                ||| ||||| ||  ||||||||
                                ACT ATTTC CT  TGGACTGC
                                  A    _ __
GAM1685  RFNG     3'  TGCTGGGGTGGAAGCCTG    44777    A  AAA
                                TG CT   GTGGAAGCCTG
                                || ||   ||||||||||
                                AC GA   CACCTTCGGAC
                                 _ CCC
GAM1685  ABCB11   5'  AGGAAATAATGGACTCCACTGT 19042       CAAAATA  GT
              G                  AGGAAA      GC  CACTGTG
                                ||||||      ||  |||||||
                                TCCTTT      TG  GTGACAC
                                   ATTACC_  AG
GAM1685  AHR      3'  AGGAAACACAAATAATATTTGT 11545         _     CG CAC
              G                  AGGAAACA AAATAG  T   TGTG
                                |||||||| ||||||  |   ||||
                                TCCTTTGT TTTATT  A   ACAC
                                    G     AT A__
GAM1685  CBL      3'  AGGGCAAGACTTCACTGTG   23278     AAA   AATA  G
                                AGG   CAA    GC TCACTGTG
                                |||   |||    || ||||||||
                                TCC   GTT    TG AGTGACAC
                                  C__   C___  A
GAM1685  GRLF1    3'  GGAAACAAGAGGAACCCTGTG  44228        AAT  CGTCA
                                GGAAACAA   AG    CTGTG
                                ||||||||   ||    |||||
                                CCTTTGTT   TC    GACAC
                                    C__  CTTGG
GAM1685  HDAC4    3'  AGAGACAGGCAGTTCACTGTG  25745     A   AAA   CG
                                GGA ACA   TAG  TCACTGTG
                                ||| |||   |||  ||||||||
                                TCT TGT   GTC  AGTGACAC
                                  C   CC_   A_
GAM1685  IGFBP5   5'  GGAAGCAGGGCAGCGCCAGGTG 8272       A  AAA       CT
                                GGAA CA   TAGCGTCA  GTG
                                |||| ||   ||||||||  |||
                                CCTT GT   GTCGCGGT  CAC
                                  C  CCC       C_
GAM1685  INSL5    3'  GGAGAAAATAGAGATCACTGTG 24234     AAC      C_
                                GGA   AAAATAG  GTCACTGTG
                                |||   |||||||  |||||||||
                                CCT   TTTTATC  TAGTGACAC
                                  C__      TC
GAM1685  KCNS2    3'  AGGAAACAAGGAGGCTTGACTG 42819         AATA  GTC
              TG                   AGGAAACAA   GC   ACTGTG
                                |||||||||   ||   ||||||
```

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                                TCCTTTGTT   CG  TGACAC
                                     CCTC  AAC
GAM1685  MAT1A    3'  AGCAAACAAAATAGCCCTGTG  44898    G        GT A
                                AG AAACAAAATAGC  C CTGTG
                                || ||||||||||||  | |||||
                                TC TTTGTTTTATCG  G GACAC
                                 G          __ _
GAM1685  MCSP     3'  GGAAATGGTAGTCACTGTG   36210     CAAAATAGC
                                GGAAA       GTCACTGTG
                                |||||       |||||||||
                                CCTTT       CAGTGACAC
                                   ACCAT____
GAM1685  MLC1     3'  AAGAAACAAAACCATTGT    40146          AGCGT  C
                                AGGAAACAAAAT    CA TGT
                                ||||||||||||    || |||
                                TTCTTTGTTTTG    GT ACA
                                      _____  A
GAM1685  MRPL49   3'  AGGAAACAAAGTGCCCAGT   43021        AAT  C   ACT
                                AGGAAACAA   AG GTC   GT
                                |||||||||   || |||   ||
                                TCCTTTGTT   TC CGG   CA
                                     ___  A   GT_
GAM1685  NRAS     3'  AGGAAAAAGGCACTTCACTGTG 14847      CAAAATA  G
                                AGGAAA      GC TCACTGTG
                                ||||||      || ||||||||
                                TCCTTT      TG AGTGACAC
                                    TTCCG__  A
GAM1685  RAB3B    3'  AGGAAACAAGCACGTTGT    16078        AATA   CAC
                                AGGAAACAA   GCGT   TGT
                                |||||||||   ||||  |||
                                TCCTTTGTT   TGCA   ACA
                                     CG__   ___
GAM1685  RALBP1   3'  GGAAACAAAACACTG      27701         TAGCGT
                                GGAAACAAAA     CACTG
                                ||||||||||     |||||
                                CCTTTGTTTT     GTGAC
                                      _______
GAM1685  RNF4     3'  AGGAAACAGGGGAGTGCCCTG  16350       AAAT  C   A
                                AGGAAACA    AG GTC CTG
                                ||||||||    || ||| |||
                                TCCTTTGT    TC CGG GAC
                                     CCCC  A   _
GAM1685  TMC2     3'  GGAGGCAAGGTCGACCACTGTG 38851     AA   AATAG  _
                                GGA  CAA     CG TCACTGTG
                                |||  |||     || ||||||||
                                CCT  GTT     GC GGTGACAC
                                  CC   CCA__  T
GAM1685  TPMT     3'  AGAAGCAAGAATCACTGTG   7490      A  AAAT  C
                                GGAA CA    AG GTCACTGTG
                                ||||  ||    || |||||||||
```

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                                TCTT GT    TC TAGTGACAC
                                  C _____  T
GAM1685  VIPR2    3'  GGAGGCAAAACAGCCCTGTG   18020     AA        GT A
                                GGA  CAAAATAGC  C CTGTG
                                |||  |||||||||  | |||||
                                CCT  GTTTTGTCG  G GACAC
                                  CC        __ _
GAM1685  ZNF36    3'  AAGAAACAGAAAAGTCACTGTG 45285         A  TAGC
                                AGGAAACA AA    GTCACTGTG
                                |||||||| ||    |||||||||
                                TTCTTTGT TT    CAGTGACAC
                                     C  TT__
GAM1686  AHR      3'  TTTTTGGAGACGGAGCTCGG   11555         _  AAGTT
                                TTTTTGG GA     GGGCTCGG
                                ||||||| ||     ||||||||
                                AAAAACC CT     CTCGAGCC
                                     T  GC___
GAM1686  BAZ1B    3'  TTTTTGGGGGGGGTGGGAGGAGC 37098         AAA  T   CTC
                                TTTTTGGG   GT GGG   GGC
                                ||||||||   || |||   |||
                                AAAAACCC   CA CCC   TCG
                                     CCC  _   TCC
GAM1686  EHD2     3'  TTTTTGGGAAGAAGCCTTGGC  31142         A TT  G  C
                                TTTTTGGGAA G  GG CT GGC
                                |||||||||| |  || || |||
                                AAAAACCCTT C  TC GA CCG
                                      _ T_  G  A
GAM1686  ELAVL4   5'  TTTTTGGGGGGGTGGGC     34984         AAA  T
                                TTTTTGGG   GT GGGC
                                ||||||||   || ||||
                                AAAAACCC   CA CCCG
                                     CCC  _
GAM1686  GPC1     3'  TTTTTGGCAAAGTCAGTCCTTG 13265         G     TG G_  C
              GCC                  TTTTTGG AAAGT  G  CT GGCC
                                |||||||  |||||  |  || ||||
                                AAAAACC TTTCA  C  GA CCGG
                                     G    GT AG  A
GAM1686  NFKB2    5'  TCCGGAGTTGGGCTTGGC     14765       GAA        C
                                TTTGG   AGTTGGGCT GGC
                                |||||   ||||||||| |||
                                AGGCC   TCAACCCGA CCG
                                   ___         A
GAM1686  SHMT1    3'  TCTTTGGGAAGGTGACATTTGG 20026          A  TG   TC__
              C                   TTTTTGGGAA GT  GGC    GGC
                                |||||||||| ||  |||    |||
                                AGAAACCCTT CA  CTG    CCG
                                      C  __   TAAA
GAM1686  WNT3A    3'  TCTTTGGGAGGGCCTCGG    37551          AAGTT   _
                                TTTTTGGGA    GGGC TCGG
                                |||||||||    |||| ||||
```

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                                AGAAACCCT    CCCG AGCC
                                     _____   G
GAM1686 AXIN1    3' CCCCACCCAGACCTGGGTAC  41371   AA  AA     A  C
                                C  CGC  CAGACCT GG AC
                                |  |||  ||||||| || ||
                                G  GTG  GTCTGGA CC TG
                                 GG   G_     C  A
GAM1686 B4GALT1  3' CAGCACAACAGGTCTCTGGGAC 11280    A      AC  A_  C
             A                   CA CGCAACAG  CT  GG ACA
                                 || ||||||||  ||  || |||
                                 GT GTGTTGTC  GA  CC TGT
                                  C       CA  GA  C
GAM1686 CARD10   3' CAGCGGGACAGACCTGAGC   30973    A  CA      AG
                                CA CG  ACAGACCT  GC
                                || ||  ||||||||  ||
                                GT GC  TGTCTGGA  CG
                                 C  CC       CT
GAM1686 EGR4     5' CAGCGCACAGACCTAGGC    12673    A   A
                                CA CGCA CAGACCTAGGC
                                || |||| ||||||||||
                                GT GCGT GTCTGGATCCG
                                 C   _
GAM1686 ITGA4    5' CAACGCAACACACCTGAAC   9419          G   AG
                                CAACGCAACA ACCT  GC
                                |||||||||| ||||  ||
                                GTTGCGTTGT TGGA  TG
                                      G   CT
GAM1686 MNT      3' GCAGCAGCAGCACACG      33714     A   ACCTA
                                GCA CAG    GGCACACG
                                ||| |||    ||||||||
                                CGT GTC    TCGTGTGC
                                  C  G____
GAM1686 NET1     5' ACGCTATGCAGAGGCACACG   25226     AA__   CCTA
                                ACGC   CAGA   GGCACACG
                                ||||   ||||   ||||||||
                                TGCG   GTCT   CCGTGTGC
                                  ATAC   ____
GAM1686 PACE4    3' GCTGCGACTATAGGCACACG   15051    AACA   C_
                                GC   GAC  TAGGCACACG
                                ||   |||  ||||||||||
                                CG   CTG  ATCCGTGTGC
                                 ACG_  AT
GAM1686 SOLH     5' CACCTCAGGGCCTGGGCACACG 24824     AA   A_   A
                                CGC  CAG  CCT GGCACACG
                                |||  |||  ||| ||||||||
                                GTG  GTC  GGA CCGTGTGC
                                  GA   CC   C
GAM1687 HEM1     5' TGTGGCGAACCAGCCAG     23745    C   AAC
                                TG GGC   ACCAGCCAG
                                || |||   |||||||||
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                                AC CCG   TGGTCGGTC
                                 A   CT_
GAM1687 HSPG2    3' TGTGGGGCACCAGCCCACAA  24371    C  CAA      A
                                TG GG   CACCAGCC GCAA
                                || ||   |||||||| ||||
                                AC CC   GTGGTCGG TGTT
                                 A  CC_      G
GAM1687 INPP5D   3' TGGGCAGGAGGAGCCAGCA   44426    C   ACACC
                                TG GGCA    AGCCAGCA
                                || ||||    ||||||||
                                AC CCGT    TCGGTCGT
                                 _   CCTCC
GAM1687 LIFR     3' TGTAGCAACACTAGCAG     14161    CG     C  C
                                TG  GCAACAC AGC AG
                                ||  ||||||| ||| ||
                                AC  CGTTGTG TCG TC
                                 AT      A  _
GAM1687 MBD3     3' TGTGGCACCACCAGCCGCA   19426    C   A      A
                                TG GGCA CACCAGCC GCA
                                || |||| |||||||| |||
                                AC CCGT GTGGTCGG CGT
                                 A   G      _
GAM1687 RFNG     3' CGGCAACAGCAAAGCA      44768        C  CC
                                CGGCAACA CAG  AGCA
                                |||||||| |||  ||||
                                GCCGTTGT GTT  TCGT
                                     C  __
GAM1687 SLC2A3   3' TGCGGCAATATCAGAACCCAA 27983        CAC  ___
                                TGCGGCAA   CAG   CCAG
                                ||||||||   |||   ||||
                                ACGCCGTT   GTC   GGTT
                                     ATA   TTG
GAM1687 THY1     3' GCTCAGGCACCAGCCAGCA   26625    GG  A_
                                GC  CA  CACCAGCCAGCA
                                ||  ||  ||||||||||||
                                CG  GT  GTGGTCGGTCGT
                                 A_  CC
GAM1687 UNG      5' TGTGGAACAGGTCCCAGCAAAA 38948    C  C   CCAG
              G                  TG GG AACA    CCAGCAAAAG
                                || || ||||    ||||||||||
                                AC CC TTGT    GGTCGTTTTC
                                 A  _    CCAG
GAM1687 VIPR1    3' TGGGCAGAAGAGCCAGCA    21516    C   ACACC
                                TG GGCA    AGCCAGCA
                                || ||||    ||||||||
                                AC CCGT    TCGGTCGT
                                 _   CTTC_
GAM1687 CDH7     5' GCGTCAGACGCCAGGGA     38002          A  CT
                                GCGTCAGACGC CG  GGA
                                |||||||||| ||  |||
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```
                                CGCAGTCTGCG GT  CCT
                                       _ C_
GAM1687  DAAM1    5'  CAGCCCCTGCATGCTGGAAA  31430     G  AGAC   C
                                CAGC TC    GCA GCTGGAAA
                                |||| ||    ||| ||||||||
                                GTCG GG    CGT CGACCTTT
                                  G A___   A
GAM1687  EDG6     3'  GCGTCAGAAGCCCCGAGA    19095       C  A_  CT
                                GCGTCAGA GC  CG  GGA
                                |||||||| ||  ||  |||
                                CGCAGTCT CG  GC  TCT
                                     T  GG  __
GAM1687  EGFL4    3'  CAGCGTCAGGCGGA       41561         ACGCAC  T
                                CAGCGTCAG     GC GGA
                                |||||||||     || |||
                                GTCGCAGTC     CG CCT
                                       _______ _
GAM1687  GLTSCR1  3'  GCGGGCACAGCACGCTGG    31838     TCAG  _
                                GCG    AC GCACGCTGG
                                |||    || |||||||||
                                CGC    TG CGTGCGACC
                                  CCG_  T
GAM1687  GNA11    3'  CAGCGCAGGCTCCGTGGAA   44027      T   AC  A_  C
                                CAGCG CAG  GC  CG TGGAA
                                ||||| |||  ||  || |||||
                                GTCGC GTC  CG  GC ACCTT
                                   _  __  AG  _
GAM1687  IGFBP2   3'  GTCAGAACTGGAAA       8262        CGCAC
                                GTCAGA    GCTGGAAA
                                ||||||    ||||||||
                                CAGTCT    TGACCTTT
                                       _____
GAM1687  KCNC4    5'  CAGCGTCAGACGGGGGA     22526           CACGCT
                                CAGCGTCAGACG     GGA
                                ||||||||||||     |||
                                GTCGCAGTCTGC     CCT
                                       CC____
GAM1687  NUCB1    3'  CAGTGTCAGATGAGGCCAGAA  26153     C     CGCAC  TG
                                CAG GTCAGA    GC  GAA
                                ||| ||||||    ||  |||
                                GTC CAGTCT    CG  CTT
                                  A     ACTC_  GT
GAM1687  PAFAH1B1 3'  CAGTGTCAGACAGCAGTGCAGG 7701      C      _  C_  T
            AAA                   CAG GTCAGAC GCA  GC GGAAA
                                ||| ||||||| |||  || |||||
                                GTC CAGTCTG CGT  CG CCTTT
                                  A      T   CA  T
GAM1687  PPARA    3'  CAGCTTCAGAACTCCTGGAAAA 22766     G    CGC  G_
                                CAGC TCAGA   AC  CTGGAAAA
                                |||| |||||   ||  ||||||||
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                                GTCG AGTCT   TG  GACCTTTT
                                  A    ___  AG
GAM1687  SCA1     3'  GCGGCAGACGCACGGGG     7281      T        CT
                                GCG CAGACGCACG  GG
                                ||| ||||||||||  ||
                                CGC GTCTGCGTGC  CC
                                  C         C_
GAM1687  SLC7A5   3'  CAGCTCAGACGCCCAGAA    18542      G       ACG TG
                                CAGC TCAGACGC   C  GAA
                                |||| ||||||||   |  |||
                                GTCG AGTCTGCG   G  CTT
                                  _       ___ GT
GAM1687  SNRPA    3'  CAGCGCCAGGTGCAATGTCTGG 21399         AC   CG__
                                CAGCGTCAG  GCA    CTGG
                                |||||||||  |||    ||||
                                GTCGCGGTC  CGT    GACC
                                     CA   TACA
GAM1687  TCF3     3'  CAGGGTCGGACGCACAGCCCAA 43318     C   A      _   G
                                CAG GTC GACGCAC GCT GA
                                ||| ||| ||||||| ||| ||
                                GTC CAG CTGCGTG CGG TT
                                  C  C      T   G
GAM1687  ZNF42    5'  CAGCGTCAGACGCTGG      18289          GCAC
                                CAGCGTCAGAC    GCTGG
                                ||||||||||    |||||
                                GTCGCAGTCTG    CGACC
                                      ____
GAM1688  AGPAT2   3'  TGCCGTGGGCGCGAGTCCC   26930           C  CG
                                TGCCGTGGGCGCG GG  CCC
                                |||||||||||| ||  |||
                                ACGGCACCCGCGC TC  GGG
                                       _  A_
GAM1688  CRLF1    5'  TGCCGGGGGCGCGCGGCG    21901      T
                                TGCCG GGGCGCGCGGCG
                                ||||| ||||||||||||
                                ACGGC CCCGCGCGCCGC
                                   C
GAM1688  DLC1     5'  CCGTGAGCCGGCGCTCC     25901        GCG     C
                                CCGTGGGC   CGGCGC CC
                                ||||||||   |||||| ||
                                GGCACTCG   GCCGCG GG
                                     ___      A
GAM1688  GPRC5B   3'  TGCCGTGGTGCCTGCCTTCCA  32179        GC  GCGGC   C_
                                TGCCGTGG  GC    GCC  CCA
                                ||||||||  ||    |||  |||
                                ACGGCACC  CG    CGG  GGT
                                     A_  GA___   AA
GAM1688  JUNB     3'  GTGGTTTGCGGCGCCCC     13765      GCGC
                                GTGG   GCGGCGCCCC
                                ||||   ||||||||||
```

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                                CACC   CGCCGCGGGG
                                  AAA_
GAM1688 LETM1    3' TGCTGTGGGCGCACTGGAC   29506    C       _ C
                                TGC GTGGGCGCGC GG GC
                                ||| |||||||||| || ||
                                ACG CACCCGCGTG CC TG
                                  A        A  _
GAM1688 LMO2     3' TGCCATGGAGACGGCG     24552        CGC
                                TGCCGTGGG  GCGGCG
                                |||||||||  ||||||
                                ACGGTACCT  TGCCGC
                                     C__
GAM1688 MASP1    3' TGCCATGGGTGAGCC      40110        CGCGC  C
                                TGCCGTGGG    GG GCC
                                |||||||||    || |||
                                ACGGTACCC    CT CGG
                                     A_____  _
GAM1688 RANBP3   5' TGCTGCGGGCACTGCCCCC   28771    C      GCGGC
                                TGC GTGGGCGC    GCCCCC
                                ||| ||||||||    ||||||
                                ACG CGCCCGTG    CGGGGG
                                  A       A_____
GAM1688 RPA3     5' TGCTGTGGGTGCTGCGTACC  16385    C    C _  GC
                                TGC GTGGG GC GCG  GCC
                                ||| ||||| || |||  |||
                                ACG CACCC CG CGC  TGG
                                  A    A A  A_
GAM1688 TGFBI    3' TGCCGTGGTGCATTCCTCC   7414        GC  CGGCG  C
                                TGCCGTGG  GCG    CC CC
                                ||||||||  |||    || ||
                                ACGGCACC  CGT    GG GG
                                     A_  AA___  A
GAM1688 THBD     5' TGCCGTGCGCGCAGCCCC    7433       GG       G
                                TGCCGT  GCGCGCGGC CCC
                                ||||||  ||||||||| |||
                                ACGGCA  CGCGCGTCG GGG
                                     __       _
GAM1688 TIA1     5' TGCTGTCGCGGCGGCGCCTCCA 35287    C  GG  C      C
                                TGC GT  GCG GCGGCGCC CCA
                                ||| ||  ||| |||||||| |||
                                ACG CA  CGC CGCCGCGG GGT
                                  A  G_  _      A
GAM1688 VCP      3' GCTGTGGGCGCACCCC     44010    C      GCGGC
                                GC GTGGGCGC    GCCCC
                                || ||||||||    |||||
                                CG CACCCGCG    TGGGG
                                 A      ______
GAM1688 ADAM10   5' GCGCGGGGGACGGTTCCCG   9971        C  CAC  A
                                GCGCGGGG ACG   TTC CG
                                |||||||| |||   ||| ||
```

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                                CGCGCCCC TGC   AAG GC
                                    C   C__   G
GAM1688 APP     5'  GCGCGGGGCACCGAGTGCGC   7918          GCACTTCA
                                GCGCGGGGCAC       CGC
                                ||||||||||        |||
                                CGCGCCCCGTG       GCG
                                     GCTCAC__
GAM1688 ATP11A   3'  GCGCGGGGCGGGCGTGAGGGCC 44176         AC  ACTTCAC
           G                     GCGCGGGGC  GC      GCCG
                                |||||||||  ||      ||||
                                CGCGCCCCG  CG      CGGC
                                     CC  CACTCC_
GAM1688 CCND3    5'  GCGCGGGGCGCGGGTCTGGCGC 12061         A  CACTTCA
                                GCGCGGGGC CG      CGC
                                |||||||||  ||      |||
                                CGCGCCCCG GC      GCG
                                     C  CCAGACC
GAM1688 CEBPA    5'  GCGCGGGGCGTCGCGC      20393         ACGCACT  A
                                GCGCGGGGC      TC CGC
                                |||||||||       || |||
                                CGCGCCCCG      AG GCG
                                     C_______  C
GAM1688 FHIT     5'  GCGCGGGGCCGGAGCGCC    12870         A  CACTTCA
                                GCGCGGGGC CG      CGCC
                                |||||||||  ||      ||||
                                CGCGCCCCG GC      GCGG
                                     _  CTC_____
GAM1688 GAD2     5'  GCGCGGGGACGCGCGGGGCCG  9056         C   ACTTCAC
                                GCGCGGGG ACGC      GCCG
                                ||||||||  ||||      ||||
                                CGCGCCCC TGCG      CGGC
                                     _   CGCCC__
GAM1688 HYAL2    5'  GCGCGGGGCGCCACCGGGACCG 19092         ACG   TCAC
                                GCGCGGGGC   CACT   GCCG
                                |||||||||   ||||   ||||
                                CGCGCCCCG   GTGG   TGGC
                                     CG_   CCC_
GAM1688 KCNMB4   5'  GCGCGGGGAGCGCACGGACCG  30945         CA    TTCAC
                                GCGCGGGG  CGCAC    GCCG
                                ||||||||  |||||    ||||
                                CGCGCCCC  GCGTG    TGGC
                                     TC    CC___
GAM1688 KIF1B    5'  GCGCGGGGGCGCGGGGGGCCG  31465         CA   ACTTCAC
                                GCGCGGGG  CGC      GCCG
                                ||||||||  |||      ||||
                                CGCGCCCC  GCG      CGGC
                                     C_   CCCCC__
GAM1688 MUC5B    3'  GCGCGGGGTGCCACACACAGGC 42497         CA_    TT  C
           CG                      GCGCGGGG   CGCAC  CA GCCG
                                |||||||||   |||||  ||  ||||
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                                CGCGCCCC  GTGTG  GT CGGC
                                    ACG    T_  C
GAM1688 PFN1    5' GCTCGGGGCACGCGCTGCC  22716   G       A  TCAC
                                GC CGGGGCACGC CT   GCC
                                || |||||||||| ||   |||
                                CG GCCCCGTGCG GA   CGG
                                 A       C ____
GAM1688 PPP2R5A 5' GCGCGGGGTGCTCGCGCC   26439       CAC  ACT  A
                                GCGCGGGG  GC  TC CGCC
                                ||||||||  ||  || ||||
                                CGCGCCCC  CG  AG GCGG
                                    A__ ___ C
GAM1688 PRKY    5' CGCGGGGCGTGCACCGAGTGC 15695       AC    TCAC
                                CGCGGGGC GCACT   GC
                                |||||||| |||||   ||
                                GCGCCCCG CGTGG   CG
                                    CA    CTCA
GAM1688 SLC22A5 5' GCGCGGGGCACCCGC      16859         GCACTT A
                                GCGCGGGGCAC    C CGC
                                ||||||||||     | |||
                                CGCGCCCCGTG    G GCG
                                       _______ _
GAM1688 TACSTD1 5' GCCTGGGGCACGCGGGTCCGC 14300   GC       ACT  A
                                GC  GGGGCACGC  TC CGC
                                ||  |||||||||  || |||
                                CG  CCCCGTGCG  AG GCG
                                 GA       CCC  _
GAM1688 TNFRSF6B 3' GCCCGGGGCAATCACGCC   32355   G     CGCACT
                                GC CGGGGCA     TCACGCC
                                || |||||||     |||||||
                                CG GCCCCGT     AGTGCGG
                                 G      T_____
GAM1689 A1BG    3' AGACCAGCCTGGGCAACATAG 39085     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG   GTTGTATC
                                  _____    ACCC
GAM1689 APAF1   3' AGACCAGCCTAGACAACATAG 29814     AAACA    ___
                                AGAC    CAGTT   ACAACATAG
                                ||||    |||||   |||||||||
                                TCTG    GTCGG   TGTTGTATC
                                  _____    ATC
GAM1689 CASP10  3' AGACCAGCTTAGGCAACATAG 37368     AAACA    A___
                                AGAC    CAGTT   CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGA   GTTGTATC
                                  _____    ATCC
GAM1689 CASP8   3' AAACACAGTTATTCACAG    37863         CAA
                                AAACACAGTTA   CATAG
                                ||||||||||   |||||
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                                TTTGTGTCAAT   GTGTC
                                      AA_
GAM1689  CDH1     3'  AGACCAGCTTGGGCAACATAGC 20359      AAACA     A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGA    GTTGTATCG
                                  _____    ACCC
GAM1689  DDEF2    3'  AACAAATGCAGTTAACAG    19313       CA     CAAC
                                GACAAA  CAGTTA    ATAG
                                ||||||  ||||||    ||||
                                TTGTTT  GTCAAT    TGTC
                                   AC    _____
GAM1689  EIF4G2   3'  CAAATGCAGTTACATCATAGC  10873      CA       A
                                CAAA  CAGTTACA CATAGC
                                ||||  |||||||| ||||||
                                GTTT  GTCAATGT GTATCG
                                  AC       A
GAM1689  FGFR2    3'  AGGCAGACACAGTCATTCAT   35657     A  A       CAA
                                AG CA ACACAGTTA   CAT
                                || || |||||||||   |||
                                TC GT TGTGTCAGT   GTA
                                 C  C       AA_
GAM1689  GRM6     3'  AGACCAGCCTGGGCAACATAG  9166       AAACA     A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG    GTTGTATC
                                  _____    ACCC
GAM1689  IQGAP1   3'  AAACAAACACCAAAGCTTACAA 42897          ___   _   C
            TATAG                   AGACAAACAC   AGTT ACAA ATAG
                                ||||||||||   |||| |||| ||||
                                TTTGTTTGTG   TCGA TGTT TATC
                                      GTT    A    A
GAM1689  KLRD1    3'  AGACCAGCCTGGGCAACATAGC 13965      AAACA     A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM1689  PCOLN3   3'  AGACAAACAGCACAGCACA    15745       AC     T   A
                                AGACAA  ACAGT ACA CATA
                                ||||||  ||||| ||| ||||
                                TCTGTT  TGTCG TGT GTGT
                                   __    _   C
GAM1689  RPP30    3'  AGACCAGCCTCAGCAACATAG  26932      AAACA     A___
                                AGAC    CAGTT    CAACATAG
                                ||||    |||||   ||||||||
                                TCTG    GTCGG    GTTGTATC
                                  _____    AGTC
GAM1689  SLC4A4   3'  AGACAAACAGGTTACAATGTAG 19060          CA      CA
                                AGACAAACA  GTTACAA  TAG
                                |||||||||  |||||||  |||
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                                TCTGTTTGT  CAATGTT  ATC
                                     C_      AC
GAM1689  SULT1C1   3'  AGACCAGCCTGGGCAACATAGC 9836      AAACA    A___
                                AGAC    CAGTT    CAACATAGC
                                ||||    |||||   |||||||||
                                TCTG    GTCGG    GTTGTATCG
                                  _____    ACCC
GAM1689  TAF1A     3'  AAACAGACATAGTTACAAAGAG 40303      A  C      CAT
              C                  AGACA ACA AGTTACAA   AGC
                                |||||| ||| ||||||||   |||
                                TTTGT TGT TCAATGTT   TCG
                                   C  A       TC_
GAM1689  TNFRSF9   3'  AGACCAGCCTGTACAACAT   11450     AAACA   ___
                                AGAC    CAGT   TACAACAT
                                ||||    ||||  ||||||||
                                TCTG    GTCG   ATGTTGTA
                                  _____   GAC
GAM1689  GNAI1     3'  GGAGAAATTTGAATTATCTA   13165     CTGTC      C
                                GGA    AATTTGAA TATCTA
                                |||    |||||||| ||||||
                                CCT    TTAAACTT ATAGAT
                                  CT___       A
GAM1689  NR3C1     3'  AGGACTGTTAATTTGCACAACC 6752        C     A  T
              TA                   AGGACTGT AATTTG AC ATCTA
                                |||||||| |||||| || |||||
                                TCCTGACA TTAAAC TG TGGAT
                                     A     G  T
GAM1689  PART1     3'  AGGACTGCACTCAGCTAT    32457       CA   GAA
                                AGGACTGT  ATTT   CTAT
                                ||||||||  ||||  ||||
                                TCCTGACG  TGAG   GATA
                                     __   TC_
GAM1690  ACP1      3'  AAATGCTGATGAAGA      28230       TACTG
                                AAATGT    TGATGAAGA
                                ||||||    |||||||||
                                TTTACG    ACTACTTCT
                                          _____
GAM1690  BRCA1     3'  TAAAATGTCACTCTGAGA    28638          G  T
                                TAAAATGTTACT TGA GA
                                |||||||||||| ||| ||
                                ATTTTACAGTGA ACT CT
                                       G  _
GAM1690  C18orf1   3'  ATGTTACTGTGTGCAAAG    41208          AT_
                                ATGTTACTGTG   GAAG
                                ||||||||||   ||||
                                TACAATGACAC   TTTC
                                       ACG
GAM1690  CLASP2    3'  TAAAATGCTACTGAGAAGA   42079           TGAT
                                TAAAATGTTACTG    GAAGA
                                ||||||||||||    |||||
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                                ATTTTACGATGAC   CTTCT
                                       T___
GAM1690  FBN1    3'  TGCACATGCTGTGATGAAG   42056    TA___
                                TGT    CTGTGATGAAG
                                |||    ||||||||||
                                ACG    GACACTACTTC
                                  TGTAC
GAM1690  ITPR1   3'  ATGTTGGTTCAGATGAAGAA  13664     ACTGT_
                                ATGTT    GATGAAGAA
                                |||||    |||||||||
                                TACAA    CTACTTCTT
                                   CCAAGT
GAM1690  MFAP3   3'  AAAATGTTACTTCTTCTAAGAA 25451         GTGATG
                                AAAATGTTACT    AAGAA
                                ||||||||||    |||||
                                TTTTACAATGA    TTCTT
                                       AGAAGA
GAM1690  PCDHGA7  3'  TAAAGTGTCACCACTGAAG   36848     A    TG GA
                                TAAA TGTTAC  T  TGAAG
                                |||| ||||||  |  |||||
                                ATTT ACAGTG  G  ACTTC
                                  C     GT __
GAM1690  PPP1CB   3'  AAATGCTACTGCACAATAGA  15499          ATGA
                                AAATGTTACTGTG   AGA
                                ||||||||||||   |||
                                TTTACGATGACGT   TCT
                                       GTTA
GAM1690  SIP     3'  TAAAACTGTTCTAATGAAGAA  30844   TT   ___
                                TG  ACTGT   GATGAAGAA
                                ||  |||||   |||||||||
                                AT  TGACA   TTACTTCTT
                                 TT    AGA
GAM1690  STAU2   3'  ATGTATACAGATGAAGAA   30799    _  TGT
                                ATGT TAC   GATGAAGAA
                                |||| |||   |||||||||
                                TACA ATG   CTACTTCTT
                                  T   T__
GAM1690  TCF20   5'  TAAAACGCTGTGGTGAAG   42539      TTA   A
                                TAAAATG   CTGTG TGAAG
                                |||||||   ||||| |||||
                                ATTTTGC   GACAC ACTTC
                                    ___    C
GAM1690  TTC3    5'  TGTTTGCTGAATGAAGAA   17721     A_  T
                                TGTT  CTG GATGAAGAA
                                ||||  ||| |||||||||
                                ACAA  GAC TTACTTCTT
                                  AC  _
GAM1690  PRNP    3'  ACAATATTTACTCTTGTTGA  7184        _ CG
                                ACAATATT AC  CTTGTTGA
                                ||||||||  ||  ||||||||
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                                TGTTATAA TG  GAACAACT
                                    A  A_
GAM1690  TRAP240   3'  CAAAACAATATTTGTT      23055          ACCGCT
                                TAAAACAATATT     TGTT
                                ||||||||||||     ||||
                                GTTTTGTTATAA     ACAA
                                          _______
GAM1690  WASF3     3'  AAACAATATCACTTACTGGTTG 27374          C_   T
                                AAACAATATTAC  GCT GTTG
                                ||||||||||||  ||| ||||
                                TTTGTTATAGTG  TGA CAAC
                                      AA   C
GAM1691  MAP3K14   3'  TGTGTTGCAACAACCTGAAAA  19549           G  A
                                TGTGTTGCAACAGC CT AAAA
                                |||||||||||||| || ||||
                                ACACAACGTTGTTG GA TTTT
                                      _  C
GAM1691  CASP3     3'  TTTATATAATAGCTCTTCA   37419     C         G
                                TTTA ATAATAGCTTTT CA
                                |||| ||||||||||| ||
                                AAAT TATTATCGAGAA GT
                                  A          _
GAM1691  DAPP1     3'  TTTATATCATAGCTTTGCA   30819     C  A      T
                                TTTA AT ATAGCTTT GCA
                                |||| || |||||||| |||
                                AAAT TA TATCGAAA CGT
                                  A  G       _
GAM1691  STX7      3'  TTTATACAATAGCTTTAAAATA 18698     C         TGC
              A                  TTTA ATAATAGCTTT   AATAA
                                ||||| ||||||||||   |||||
                                AAAT TGTTATCGAAA   TTATT
                                  A          TT_
GAM1692  LILRB4    3'  TTGTCTGACTTCTGTTT     27784     _    GGTCTATA
                                TTG CTGAC       TTCTGTTT
                                ||| |||||       ||||||||
                                AAC GACTG       AAGACAAA
                                  A    _________
GAM1692  ADAMTS5   3'  CAATAGGCACATTTGGCA    28175       AGA       A
                                CAATAG   CACGTTTG CA
                                ||||||   |||||||| ||
                                GTTATC   GTGTAAAC GT
                                    C__       C
GAM1692  HAP1      3'  TAACCAATGGGGACACATC    19504        AGA
                                TAACCAAT   GACACGTT
                                ||||||||   ||||||||
                                ATTGGTTA   CTGTGTAG
                                     CCC
GAM1692  HNF3G     3'  TAACCAATGGGACAAGT     43648        AGA    C
                                TAACCAAT   GACA GT
                                ||||||||   |||| ||
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                                ATTGGTTA  CTGT CA
                                   CC_   T
GAM1692 RNASE1   5' TAACCAGTGGACACGCT    16342      ATAGA
                                TAACCA    GACACGTT
                                ||||||    ||||||||
                                ATTGGT    CTGTGCGA
                                   CAC__
GAM1692 TGFBR3   3' TAACCAACTGGAGACCGAC   17493       A_    ACGTT
                                TAACCAAT  GAGAC    TGAC
                                ||||||||  |||||    ||||
                                ATTGGTTG  CTCTG    GCTG
                                   AC    _____
GAM1693 HTRA3    3' TGTTCACAGGGGCAGAGGC   44838       AA_    A
                                TGTTTACG   GCAGA GC
                                ||||||||   ||||| ||
                                ACAAGTGT   CGTCT CG
                                   CCC    C
GAM1693 MAB21L1  3' AGATTGTTTGCACTGCGGA   24584        A  AA  A
                                AGATTGTTT CG  GC GA
                                ||||||||| ||  || ||
                                TCTAACAAA GT  CG CT
                                   C  GA  C
GAM1693 PSG11    3' TGAAGTTATCAGGAACT     15814      C      TT
                                TGAAG TTATCAG  ATT
                                ||||| |||||||  |||
                                ACTTC AATAGTC  TGA
                                   _      CT
GAM1693 PSG3     3' TGAAGTTATCAGGAACT     34255      C      TT
                                TGAAG TTATCAG  ATT
                                ||||| |||||||  |||
                                ACTTC AATAGTC  TGA
                                   _      CT
GAM1693 PSG5     3' TGAAGTTATCAGGAACT     15804      C      TT
                                TGAAG TTATCAG  ATT
                                ||||| |||||||  |||
                                ACTTC AATAGTC  TGA
                                   _      CT
GAM1694 POLI     3' TGACCATGATATTCTTTTTATT 28445    TAA  T         C
             GA                   TG   GT GTATTCTTTTTAT GA
                                ||   || |||||||||||||| ||
                                AC   TA TATAAGAAAAATA CT
                                  TGG  C           A
GAM1694 CAPZA1   3' TTAGTTATGAGATGCAATAAAT 43724        G  A  A  __
             GAT                   TTAGTTA GA GA GT  TAAATGAT
                                |||||||  ||  ||  ||  ||||||||
                                AATCAAT CT CT CG  ATTTACTA
                                   A  _  A  TT
GAM1694 XK       3' TTAATTAGGAAGAAACAAAAAA 34376             TT__
             TGAT                  TTAGTTAGGAAGAAG    AAATGAT
                                ||||||||||||||||   |||||||
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                                AATTAATCCTTCTTT   TTTACTA
                                      GTTT
GAM1695 GAB2    3' AGTGGGCAGAGGAGGTGCCTT 38673   C CCT  TT  AC
                                AG GG  CGG GAG GCCTT
                                || ||  ||| ||| |||||
                                TC CC  GTC CTC CGGAA
                                 A C__  TC  CA
GAM1695 HCFC1   3' AGGGCCAAGAGGGACGCCTT 43384   C   TC TTGA
                                AG GGCC GG   GACGCCTT
                                || |||| ||   ||||||||
                                TC CCGG TC   CTGCGGAA
                                 _   T_ TCC_
GAM1695 IRTA2   3' AAGCGGCCTCGGTGGGA    36335          T A
                                AAGCGGCCTCGGT G GA
                                |||||||||||| | ||
                                TTCGCCGGAGCCA C CT
                                      _ C
GAM1695 LHX5    5' GCGGCTTCGGCCGCCT     35318     C    TGAGA
                                GCGGC TCGGT    CGCCT
                                ||||| |||||    |||||
                                CGCCG AGCCG    GCGGA
                                   A   _____
GAM1696 ADCY3   5' GCCTCCTCTCAGGGCT     19718          TCGA
                                GTCTCCTCTCAGG   GCT
                                ||||||||||||   |||
                                CGGAGGAGAGTCC   CGA
                                      ____
GAM1696 CIT     5' ATCTCCTCTTCAGCT      43039         CAGG  G
                                GTCTCCTCT   TC AGCT
                                |||||||||   || ||||
                                TAGAGGAGA   AG TCGA
                                     ____ _
GAM1696 DEDD    5' GTCTCTTCTCTCGGCT     37429     C   AGG  A
                                GTCTC TCTC  TCG GCT
                                ||||| ||||  ||| |||
                                CAGAG AGAG  AGC CGA
                                   A  ___  _
GAM1696 IL1F5   3' TAAGTCTCTTTATAGGCCTGCT 29356       CTCTC   GA
            C                    TAAGTCTC   AGGTC GCTC
                                ||||||||   |||||  ||||
                                ATTCAGAG   TCCGG  CGAG
                                     AAATA   A_
GAM1696 RGS16   3' AGCCTCCTTTCAGGGCT    16316       C    TCGA
                                AGTCTCCT TCAGG   GCT
                                |||||||| |||||   |||
                                TCGGAGGA AGTCC   CGA
                                     A   ____
GAM1697 ACP2    3' GCACTGAGAGGCAAGACCGTG 11509       AAAA     C
                                GCGCTGA   CAAGGCT TG
                                |||||||   ||||||| ||
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                                CGTGACT   GTTCTGG AC
                                    CTCC      C
GAM1697 ASL      5'  CTGGAAGACAAGACCGGACTGA 43531     A  A       ___
              CG                    CTG AA ACAAGGCT   CTGACG
                                    ||| || ||||||||   ||||||
                                    GAC TT TGTTCTGG   GACTGC
                                      C  C       CCT
GAM1697 CERD4    3'  GCTGAAAACCTCTCTGA     28951         A AAGG
                                    GCTGAAAA C    CTCTGA
                                    |||||||| |    ||||||
                                    CGACTTTT G    GAGACT
                                        _ GA__
GAM1697 FE65L2   3'  GCACTGGAAGCTCTGA      39318       AAAAACA
                                    GCGCTG      AGGCTCTGA
                                    ||||||      |||||||||
                                    CGTGAC      TTCGAGACT
                                       C_______
GAM1697 GPC3     5'  GCCCTGAGGAGCAAGAGAC   21021    G   AAAA    CTCT
                                    GC CTGA    CAAGG    GAC
                                    || ||||    |||||    |||
                                    CG GACT    GTTCT    CTG
                                     G    CCTC    _____
GAM1697 IHPK1    3'  GCTGAAAAGAGGGGCCCTG    45491        ACAA
                                    GCTGAAAA    GGCTCTG
                                    ||||||||    |||||||
                                    CGACTTTT    CCGGGAC
                                         CTCC
GAM1697 RNF4     3'  GCTGAAAAGTAGGTAAC     16355        ACA   CTC
                                    GCTGAAAA   AGG   TGAC
                                    ||||||||   |||   ||||
                                    CGACTTTT   TCC   ATTG
                                         CA_   ____
GAM1697 SCAP2    5'  GCGCTGAAAAGGTGACCGACG  19442         AACA   CT_
                                    GCGCTGAAA    AGG   CTGACG
                                    |||||||||    |||   ||||||
                                    CGCGACTTT    TCC   GGCTGC
                                          _____   ACT
GAM1698 MCL1     3'  GTAGTTGGTCCTAACCCTT    34999      CCAA
                                    GTAG    TCCTAACTCTT
                                    ||||    ||||||||||||
                                    CATC    AGGATTGGGAA
                                      AACC
GAM1699 ARR3     3'  TGATTTATTAGAGTGTTACAGT 20218          A  AA_
                                    TGATTTATTA AG   TATAGT
                                    |||||||||| ||   ||||||
                                    ACTAAATAAT TC   ATGTCA
                                          C  ACA
GAM1699 PPM1D    3'  TGATTTATTAGATGAATATA   18841          AA_
                                    TGATTTATTA   GAATATA
                                    |||||||||   |||||||
```

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                                ACTAAATAAT   CTTATAT
                                     CTA
GAM1699  CTLA4    3'  TAAGCCATTGTCTTCAAGACA  23331         A   G  _
                                TAAGTCATT TTTT AA ACA
                                |||||||||  |||| || |||
                                ATTCGGTAA AGAA TT TGT
                                     C   G  C
GAM1699  ETF1     3'  TAAGTCCCACATTTGAAACA  21834       ATTAT
                                TAAGTC    TTTGAAACA
                                ||||||    |||||||||
                                ATTCAG    AAACTTTGT
                                   GGTGT
GAM1699  FGF5     3'  AGTCACACTGAAACAA      37579       TATT
                                AGTCAT    TTGAAACAA
                                ||||||    |||||||||
                                TCAGTG    GACTTTGTT
                                   T___
GAM1699  FGF5     3'  AGTCACATTGAAACAA      37580       TATT
                                AGTCAT    TTGAAACAA
                                ||||||    |||||||||
                                TCAGTG    AACTTTGTT
                                   T___
GAM1699  GRIA2    3'  TAAGTCATTATGAATCAA    9084          TTT   A
                                TAAGTCATTA   TGAA CAA
                                ||||||||||   |||| |||
                                ATTCAGTAAT   ACTT GTT
                                     ___   A
GAM1699  HTR4     3'  GTCGTTCCTTTGAAACAA    9301      A  A
                                GTC TT TTTTGAAACAA
                                ||| || ||||||||||
                                CAG AA GAAACTTTGTT
                                  C  G
GAM1699  MYC      3'  TGATCATGCATTTGAAACAA  14713   A    TAT
                                A GTCAT   TTTGAAACAA
                                | |||||   ||||||||||
                                A TAGTA   AAACTTTGTT
                                 C    CGT
GAM1699  PPP3R1   3'  CAAGTCTTTTGAAACA      44074       ATTA
                                TAAGTC    TTTTGAAACA
                                ||||||    ||||||||||
                                GTTCAG    AAAACTTTGT
                                     ____
GAM1699  RDX      3'  AGTCAGAGATTGAAACAA    16233       TTATT
                                AGTCA     TTGAAACAA
                                |||||     |||||||||
                                TCAGT     AACTTTGTT
                                   CTCT_
GAM1700  HAL      3'  AGTCAACTGGTGGAGAGC    13331           __
                                AGTCAATTGGT  AGAGT
                                ||||||||||  |||||
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```
                                TCAGTTGACCA  TCTCG
                                      CC
GAM1700  JAM2     3'  CAAAGCAGAGTTTTATAA    34540     TT
                                CAA  GGTAGAGTTTTATAA
                                |||  ||||||||||||||
                                GTT  TCGTCTCAAAATATT
                                  __
GAM1700  A1BG     3'  TGAGACCCTGTCTACAAAAAAT 39096        CGC    TCCT
              AA                  TGAGACCT   CTAT    GATAA
                                |||||||||  ||||    |||||
                                ACTCTGGG   GATG    TTATT
                                    ACA    TTTT
GAM1700  G6PT1    3'  TGGGACCTCACTAGCCACTGAT 11171    A       C  TT _
              AA                  TG GACCTCGC TA  C CTGATAA
                                || ||||||||  ||  | |||||||
                                AC CTGGAGTG AT  G GACTATT
                                 C       _  CG T
GAM1700  GCDH     3'  TGAGAGTTTCGGGCCCCTGAT  6689       CC_   CCTA
                                TGAGA   TCG    TTCCTGAT
                                |||||   |||    ||||||||
                                ACTCT   AGC    GGGGACTA
                                  CAA   CC__
GAM1700  GUCY1A3  5'  TGCGATCTCCTCCTGAT     41839    A  C   GCCTA
                                TG GA CTC     TTCCTGAT
                                || || |||     ||||||||
                                AC CT GAG     GAGGACTA
                                 G  A  _____
GAM1700  MAP1B    3'  GAGGTATCATTATTCCTG    25394     ACC   CC
                                GAG   TCG  TATTCCTG
                                |||   |||  ||||||||
                                CTC   AGT  ATAAGGAC
                                  CAT   A_
GAM1700  MEL      3'  TGGGACCTCGCTTCCGTG    23876    A       CTA   _
                                TG GACCTCGC   TTCC TG
                                || ||||||||   |||| ||
                                AC CTGGAGCG   AAGG AC
                                 C       ___    C
GAM1700  MHC2TA   3'  TGAGACCCTGTCTAAAAATAA  6988         CGC   TTCCT
                                TGAGACCT   CTA    GATAA
                                |||||||   |||    |||||
                                ACTCTGGG   GAT    TTATT
                                    ACA   TT___
GAM1700  PHKA2    3'  TGGGACATGCTTTCCTGATA   7119    A   CTC  CTA
                                TG GAC   GC   TTCCTGATA
                                || |||   ||   |||||||||
                                AC CTG   CG   AAGGACTAT
                                 C  TA_  A__
GAM1701  ATRX     3'  AATTATTTCAGCACATATAACT 39599      C   T   G
                                AGTTA TTC GCA CATATAACT
                                ||||| ||| ||| |||||||||
```

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                                TTAAT AAG CGT GTATATTGA
                                  A  T  _
GAM1701  IL22RA2  3'  AGTACTTGCATATAAC     38133     T   CTGCA
                                AGT ACTT    GCATATAAC
                                ||| ||||    |||||||||
                                TCA TGAA    CGTATATTG
                                 _   _____
GAM1701  RECK     3'  GTTGCTTACAACATATAA    34417     A  TC
                                GTT CT  TGCAGCATATAA
                                ||| ||  ||||||||||||
                                CAA GA  ATGTTGTATATT
                                  C  __
GAM1701  SELL     5'  AGTTCTTCTGCAGCCCAT    8509      A        A
                                AGTT CTTCTGCAGC TAT
                                |||| |||||||||| |||
                                TCAA GAAGACGTCG GTA
                                  _        G
GAM1701  SMS      3'  GCTATTTGCAGCACAT      21397     CTTC
                                GTTA   TGCAGCATAT
                                ||||   ||||||||||
                                CGAT   ACGTCGTGTA
                                  AA__
GAM1701  SWAP70   3'  GTTGCTTCTCAATTATAACTA  43423     A    G   CA
                                GTT CTTCT CAG  TATAACTA
                                ||| ||||| |||  ||||||||
                                CAA GAAGA GTT  ATATTGAT
                                  C    _  A_
GAM1701  TAF1A    3'  AGCTACTTACTGTGTAGC    24994        _  C__
                                AGTTACTT CTG   AGC
                                |||||||| |||   |||
                                TCGATGAA GAC   TCG
                                     T   ACA
GAM1701  COX4I1   3'  CTGTTTGGCATAACAGGTTTC  12402        G  A    A
                                TTGTTTGG TA AACAG TTTC
                                |||||||| || ||||| ||||
                                GACAAACC GT TTGTC AAAG
                                     _ A    C
GAM1701  EGFL5    3'  TTATTTAAAAATAAACAGATTT 44545        TA_
              C                  TTGTTTGGG   AAACAGATTTC
                                 |||||||||   ||||||||||
                                 AATAAATTT   TTTGTCTAAAG
                                      TTA
GAM1701  FN1      3'  TGTTTGGGTGACTT       38342         AAAACA
                                TGTTTGGGT     GATTT
                                |||||||||     |||||
                                ACAAACCCA     CTGAA
                                              _____
GAM1701  GNE      3'  TTGTCTGATGTACAGAGCAGAT 24216        _  AAA__
              TTC                  TTGTTTGG GTA    CAGATTTC
                                   |||||||| |||    ||||||||
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                                AACAGACT CAT    GTCTAAAG
                                    A  GTCTC
GAM1701  MMP11    3'  TCTGGAGAACAGATTT     25541      TAA
                                TTTGGG  AACAGATTT
                                ||||||  |||||||||
                                AGACCT  TTGTCTAAA
                                   C__
GAM1701  MYOC     3'  TTTGGGTAAGAAAATTT     7033        AAC
                                TTTGGGTAA  AGATTT
                                |||||||||  ||||||
                                AAACCCATT  TTTAAA
                                     CT_
GAM1701  NCALD    3'  TTATTTGGGACAGAACAG    36778        _  A
                                TTGTTTGGG TA AACAG
                                ||||||||| || |||||
                                AATAAACCC GT TTGTC
                                     T  C
GAM1701  NIF3L1   3'  TGTTAAGTAAACAGATTT    41428     T     A
                                TGTT GGGTAAA CAGATTT
                                |||| ||||||| |||||||
                                ACAA TTCATTT GTCTAAA
                                  _     _
GAM1701  NPC1     3'  TTGCTTTTTTCAAACAGATTT  7080       GGGTA
                                TTGTTT    AAACAGATTT
                                ||||||    ||||||||||
                                AACGAA    TTTGTCTAAA
                                   AAAAG
GAM1701  PCDHA9   3'  TTTAAAAAAACAGATTTC    36561      T
                                TTTGGG AAAACAGATTTC
                                |||||| ||||||||||||
                                AAATTT TTTTGTCTAAAG
                                  _
GAM1701  PPP1CC   3'  TCTGTTGAAACAGATTT     43919     GGTA
                                TTTG   AAACAGATTT
                                ||||   ||||||||||
                                AGAC   TTTGTCTAAA
                                  AAC_
GAM1701  RPA3     5'  TGTCTATGGGGCAGATTTC   16386     __   TAAAA
                                TGTT  TGGG    CAGATTTC
                                ||||  ||||    ||||||||
                                ACAG  ACCC    GTCTAAAG
                                  AT   C_____
GAM1701  RUNX3    3'  TTGTAGGGCAGATTTC      20331     TT   TAAAA
                                TTGT  GGG    CAGATTTC
                                ||||  |||    ||||||||
                                AACA  CCC    GTCTAAAG
                                  T_  ______
GAM1701  TRPC6    3'  TTGTTTGGGGTTTTGATTT   21487        TAAAACA
                                TTGTTTGGG     GATTT
                                |||||||||     |||||
```

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                                AACAAACCC      CTAAA
                                     CAAAA__
GAM1701  WSX1     3'  CTGTTACAGCGGAACAGATTT  22117       TG   AA
                                TTGTT  GGT  AACAGATTT
                                |||||  |||  |||||||||
                                GACAA  TCG  TTGTCTAAA
                                   TG   CC
GAM1702  MAT1A    3'  TCGAGTGTGAGCCAAGTTAGA  44906      ATATAC
                                TCGA     GGGCCAAGTTAGA
                                ||||     ||||||||||||||
                                AGCT     CTCGGTTCAATCT
                                  CACA__
GAM1702  MEF2C    3'  GAATATGGGCAAGTTAG     14408       AC    C
                                GAATAT  GGGC AAGTTAG
                                ||||||  |||| |||||||
                                CTTATA  CCCG TTCAATC
                                     __   _
GAM1702  CAPZA1   3'  TCTTCCATTTAGCTAGAGAC  43722    A   GC_
                                TC TCCA   AGCTAGAGAC
                                || ||||   ||||||||||
                                AG AGGT   TCGATCTCTG
                                 A   AAA
GAM1702  HIP1     3'  TCACTCAGCAGCTCCG      23759     TC       AGAGA
                                TCA  CAGCAGCT    CCG
                                |||  ||||||||    |||
                                AGT  GTCGTCGA    GGC
                                  GA      _____
GAM1702  IL8RA    3'  TCTCCAGCAGACACG       8443     A      GCTA  G  C
                                TC TCCAGCA    GA AC G
                                || |||||||    || || |
                                AG AGGTCGT    CT TG C
                                 _     ____  G  A
GAM1702  MUC4     3'  ATCCAGCAGGACACG       39663         CTAGA  _
                                ATCCAGCAG     GAC CG
                                |||||||||     ||| ||
                                TAGGTCGTC     CTG GC
                                     _____  T
GAM1702  NGFB     5'  CCATCCAGCCCCTTGGACTGC  14770         AG  AGA   C
                                TCATCCAGC  CT   GAC GC
                                |||||||||  ||   ||| ||
                                GGTAGGTCG  GA   CTG CG
                                     GG  AC_   A
GAM1702  OAS3     3'  TCATCCAGTAGGACC       26183         CAGC   A
                                TCATCCAG    TAG GACC
                                ||||||||    ||| ||||
                                AGTAGGTC    ATC CTGG
                                     ____   _
GAM1703  AGRN     3'  TGGGATGGGGGTGGGGAAGGG  44260           T    T
                                TGGGATGGGGGTG GGGA GGGG
                                |||||||||||| |||| ||||
```

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                                ACCCTACCCCCAC CCCT TCCC
                                        _   _
GAM1703 AK1      3' TGAGGTGGGGGTGAGGGGG   7879      A      T  AT
                                TGGG TGGGGGTG GGG  GG
                                |||| |||||||| |||  ||
                                ACTC ACCCCCAC CCC  CC
                                  C       T  __
GAM1703 ARVCF    3' TAGGATGGGGGGAGTGGGGTGG 11710          T_    A
           GGG                    TGGGATGGGGG  GTGGG TGGGGG
                                |||||||||||  ||||| ||||||
                                ATCCTACCCCC  CACCC ACCCCC
                                      CT    C
GAM1703 BAT1     3' TGGGGTGGGGGGCTGTCAGGGG  21591     A     G  GGAT
                                TGGG TGGGGGT TG    GGGG
                                |||| ||||||| ||    ||||
                                ACCC ACCCCCG AC    CCCC
                                  C      _ AGT_
GAM1703 BSN      3' TGGGGTGGGGAGGGGTGGGGG  18423     A     TGT   A
                                TGGG TGGGGG   GGG TGGGGG
                                |||| ||||||   ||| ||||||
                                ACCC ACCCCT   CCC ACCCCC
                                  C     ___   C
GAM1703 C1QG     3' TGGGGAGGGGGGTGCAGTGGGGG 41692      AT      TG GA
                                TGGG  GGGGGTG  G  TGGGGG
                                ||||  |||||||  |  ||||||
                                ACCC  CCCCCAC  C  ACCCCC
                                  CT      GT __
GAM1703 C5R1     3' TGGGGGGGGGGTGGGGGG     11929      AT    T    AT
                                TGGG  GGGGG GTGGG  GGG
                                ||||  ||||| |||||  |||
                                ACCC  CCCCC CACCC  CCC
                                        __    _    __
GAM1703 DCTN1    5' GGGGTGGGGGGCAGTGATGGGGG 35701     A       TGG
                                GGG TGGGGGTG   GATGGGGG
                                ||| ||||||||   ||||||||
                                CCC ACCCCCGT   CTACCCCC
                                  C       CA_
GAM1703 EMX2     5' TGGGGTGGGGGTGGGGGTGGGG 44705     A      T  A
           G                     TGGG TGGGGGTG GGG TGGGGG
                                |||| |||||||| ||| ||||||
                                ACCC ACCCCCAC CCC ACCCCC
                                  C       _  C
GAM1703 EMX2     5' TGGGGGTGGGGGTGGGG     44703        T  A
                                TGGGGGTG GGG TGGGG
                                |||||||| ||| |||||
                                ACCCCCAC CCC ACCCC
                                      _  C
GAM1703 FGD1     3' TGGGCAACTAGAGTGTGGGGTG 20914      ATG__        A
           GGGG                    TGGG    GGGGTGTGGG TGGGGG
                                ||||    |||||||||| ||||||
```

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                                ACCC    TCTCACACCC ACCCCC
                                  GTTGA        C
GAM1703  FMNL    5'  GGCGGTGGCGGGGGTGGGGG  25303    A  G   T  A
                                GG TGG GGTG GGG TGGGGG
                                || ||| |||| ||| ||||||
                                CC GCC CCGC CCC ACCCCC
                                 _  A   _  C
GAM1703  GCGR    3'  GGGGTGGGGGGGTAGGTGGGGG  6696     A    T   A
                                GGG TGGGGG GTGGG TGGGGG
                                ||| |||||| ||||| ||||||
                                CCC ACCCCC CATCC ACCCCC
                                  C    _    _
GAM1703  HLCS    3'  TGGGGTGGGGGGTGGGGACAGG  7650      A      T
                                TGGG TGGGGGTG GGGATGGG
                                |||| |||||||| ||||||||
                                ACCC ACCCCCAC CCCTGTCC
                                  C      _
GAM1703  HNF3B   3'  TGGGGGTGTTGGGGTGGGG   34744        _  A
                                TGGGGGTGT GGG TGGGG
                                ||||||||| ||| |||||
                                ACCCCCACA CCC ACCCC
                                     A  C
GAM1703  HOXB5   5'  TGGGGGGGGGGGTTGGGGGGGGTG 13454     AT    GT__  A
           GGGG                  TGGG  GGGGGT   GGG TGGGGG
                                ||||  ||||||   ||| ||||||
                                ACCC  CCCCCA   CCC ACCCCC
                                  CC    ACCC  C
GAM1703  HOXC4   3'  TGGGGGCATGGGGTGGGG   31162          A
                                TGGGGGTGTGGG TGGGG
                                |||||||||||| |||||
                                ACCCCCGTACCC ACCCC
                                       C
GAM1703  KPNB1   5'  GGGATGGGGGTTGGGG     13974          GTGGGA
                                GGGATGGGGGT    TGGGG
                                ||||||||||     |||||
                                CCCTACCCCCA    ACCCC

                                _______
GAM1703  LIF     3'  TGGGTGGGAGTGGGATGGGGG  14157    A     GT
                                TGGG TGGGGGT  GGGATGGGGG
                                |||| |||||||  ||||||||||
                                ACCC ACCCTCA  CCCTACCCCC

                                  _     __
GAM1703  MECP2   3'  TGGGAGTGGGGGGAGGTGGGGG  22620      _    TGT  A
                                TGGGA TGGGGG   GGG TGGGGG
                                ||||| ||||||   ||| ||||||
                                ACCCT ACCCCC   TCC ACCCCC
                                  C    ___  _
GAM1703  MNT     3'  TGGGGGTGGGACCCGGGATGGG 33729     ATG   TG
           GG                    TGGG   GGGG  TGGGATGGGGG
                                ||||   ||||  ||||||||||
```

```
                                ACCC  CCCT  GCCCTACCCCC
                                  CCA   GG
GAM1703  MOCS2    3'  TGAGGTGGGGTTGGTGGGG   21208     A    GTGTG  A
                                TGGG TGGGG    GG TGGGG
                                |||| |||||    || ||||||
                                ACTC ACCCC    CC ACCCC
                                  C    AA___  _
GAM1703  MSN      3'  GGGGTGGGGGTGTGGAAGGG  41245     A          T
                                GGG TGGGGGTGTGGGA GGG
                                ||| ||||||||||||| |||
                                CCC ACCCCCACACCTT CCC
                                  C          _
GAM1703  MSX2     3'  TGGTGGGGCGGTGGGG      42304     _  T   GA
                                TGG GGG GTGG  TGGGG
                                ||| ||| ||||  |||||
                                ACC CCC CGCC  ACCCC
                                  A  _   __
GAM1703  PAK4     3'  TGGGGCGGGGGTGACCCGGGGG 25253      A       TGGGA
                                TGGG TGGGGGTG    TGGGGG
                                |||| ||||||||    ||||||
                                ACCC GCCCCCAC    GCCCCC
                                  C       TGG__
GAM1703  PGM1     5'  TGGGGTGAGGGCACGGCGGGTG 15261      A      ___    A
            GGGG                  TGGG TGGGGGT   GTGGG TGGGGG
                                |||| |||||||   ||||| ||||||
                                ACCC ACTCCCG   CGCCC ACCCCC
                                  C      TGC    _
GAM1703  PIK3R3   3'  TGGGTGTGGGGCATGATGGGGG 41451      A _      GG
                                TGGG TG GGGGTGT  GATGGGGG
                                |||| || |||||||  ||||||||
                                ACCC AC CCCCGTA  CTACCCCC
                                  _ A      __
GAM1703  PRKACA   3'  TGGGATGGGGGGTGTGGGTGGGG 15590              A
            G                    TGGGATGGGGGGTGTGGG TGGGGG
                                |||||||||||||||| ||||||
                                ACCCTACCCCCACACCC ACCCCC
                                                  _
GAM1703  RING1    3'  TGGGCTGGGGGGTACTGGGG    16337      A       TGGGA
                                TGGG TGGGGGTG    TGGGG
                                |||| ||||||||    |||||
                                ACCC ACCCCCAT    ACCCC
                                  G       G____
GAM1703  SLC2A4   3'  TGGGGAGGAAAGGGGATGGGGG 9803       AT    TGT
                                TGGG  GGGGG   GGGATGGGGG
                                ||||  |||||   ||||||||||
                                ACCC  CTCCT   CCCTACCCCC
                                  __    TTC
GAM1703  SOD3     3'  TGGGTGGGGAGGGGTGGGG    16963      A     TGT   A
                                TGGG TGGGGG   GGG TGGGG
                                |||| ||||||   ||| |||||
```

```
                                ACCC ACCCCT   CCC ACCCC
                                  _     ___   C
GAM1703  SPTBN4   3'  TGGGGTGGGGGTGGTGAGTGGG 36094      A       _    A
                                TGGG TGGGGGTG TGGG TGGG
                                |||| |||||||| |||| ||||
                                ACCC ACCCCCAC ACTC ACCC
                                  C       C   _
GAM1703  ZFP36L1  3'  GGGGTGGGGGGGGGTGGGG    22290     A     TGT   A
                                GGG TGGGGG   GGG TGGGG
                                ||| ||||||   ||| |||||
                                CCC ACCCCC   CCC ACCCC
                                  C     ___   _
GAM1703  IRTA2    3'  CTCCTGGCCTTGACTT      36338       ACTTGT
                                TTCCTG     GTCTTGACTT
                                ||||||     ||||||||||
                                GAGGAC     CGGAACTGAA

                                  _______
GAM1704  ACOX1    5'  GAAGGCATAGGCAGTG      44573     TGA      GACAA
                                GAA   CATAGGC    AGTG
                                |||   |||||||    ||||
                                CTT   GTATCCG    TCAC
                                  CC_     ______
GAM1704  ATP12A   3'  TGAGAGACATAGGAAGGGAGGT 11727     AT       CGACAAA
           G                     TGA  GACATAGG      GTG
                                |||  ||||||||      |||
                                ACT  CTGTATCC      CAC
                                  CT       TTCCCTC
GAM1704  COG5     3'  TGAATGGGTTAGCACAAAGTG  26814       ACATA   G
                                TGAATG     GGC ACAAAGTG
                                ||||||     ||| ||||||||
                                ACTTAC     TCG TGTTTCAC
                                   CCAA_   _
GAM1704  FBXL5    3'  TGATGACATAGGGACAGTG   37949     A       C    AA
                                TGA TGACATAGG GACA  GTG
                                ||| ||||||||| ||||  |||
                                ACT ACTGTATCC CTGT  CAC
                                  _       _   ___
GAM1704  HGF      3'  AATGACACAAAATAAAGTG   45315          CGAC
                                AATGACATAGG    AAAGTG
                                ||||||||||    ||||||
                                TTACTGTGTTT    TTTCAC
                                      TA__
GAM1704  NARS     3'  TGAATAACTTGGATAAAGTGA 21220        ATA  CGAC
                                TGAATGAC   GG    AAAGTGA
                                ||||||||   ||    |||||||
                                ACTTATTG   CC    TTTCACT
                                    AA_  TA__
GAM1704  NFE2L1   3'  TGAATGACATGCGTGATGTTG  17336         AG   ACAAAG
                                TGAATGACAT  GCG     TG
                                ||||||||||  |||     ||
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                                ACTTACTGTA CGC     AC
                                     __  ACTACA
GAM1704 TIE     3' TGAATGACAGGCCGGGAGTG  24052        TA  GACAA
                                TGAATGACA GGC    AGTG
                                ||||||||| |||    ||||
                                ACTTACTGT CCG    TCAC
                                     __  GCCC_
GAM1704 TLR4    3' GAATGACATCGAGTGACAAAGT 17563        A_ C
             GA                   GAATGACAT GG GACAAAGTGA
                                ||||||||| || ||||||||||
                                CTTACTGTA TC CTGTTTCACT
                                     GC A
GAM1704 FCMD    3' GAAGTACTGTAGTCGTGTAAG 27519      TTCAA
                                GAAGT    AGTCGTGTAAG
                                |||||    ||||||||||
                                CTTCA    TCAGCACATTC
                                   TGACA
GAM1704 PAX5    3' TCAGAAGTTCTGGCTGTA    32521         CAAA C
                                TCAGAAGTTT   GT GTG
                                ||||||||||   || |||
                                AGTCTTCAAG   CG CAT
                                     AC__ A
GAM1704 RASA1   3' TCAGAAGTTCAAAGATGGATAA 35487        T    TCGT
             G                   TCAGAAGTT CAAAG   GTAAG
                                ||||||||| |||||   |||||
                                AGTCTTCAA GTTTC   TATTC
                                     _    TACC
GAM1704 RASGRP1 3' CCAAACTAAAGTCGTGT     25074      AGTTTC
                                TCAGA     AAAGTCGTGT
                                |||||     ||||||||||
                                GGTTT     TTTCAGCACA
                                   GA____
GAM1704 SLC4A7  3' TCAGAAGTTATAAATGGTAT  18826        TCA   C
                                TCAGAAGTT  AAGT GTGT
                                |||||||||  |||| ||||
                                AGTCTTCAA  TTTA CATA
                                     TA_   C
GAM1704 VDR     3' CAGAAGTTTCACAATGTAAG  7514          AAGTC
                                CAGAAGTTTCA    GTGTAAG
                                ||||||||||    |||||||
                                GTCTTCAAAGT    TACATTC
                                     GT___
GAM1705 CKTSF1B1 3' TAGTGTTGAGGAAATTCT   30088         T
                                TAGTGTTGAGG AATTCT
                                |||||||||| ||||||
                                ATCACAACTCC TTAAGA
                                     T
GAM1705 MME     3' GTGACTTATAATTCTAGAA   28601     TTGAG
                                GTG    GTAATTCTAGAA
                                |||    ||||||||||||
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                                CAC    TATTAAGATCTT
                                  TGAA_
GAM1705  TAC3     3'  TGTTGAGGAATAGAGA      29922        T   TCT
                                TGTTGAGG AAT   AGA
                                |||||||| |||   |||
                                ACAACTCC TTA   TCT
                                     _   TC_
GAM1706  ADAMTS5  3'  TGACAAGGGGGAGACA      28185       T    TAAAT
                                TGACAA GGGGG    GACA
                                |||||| |||||    ||||
                                ACTGTT CCCCC    CTGT
                                   _    T____
GAM1706  ARF3     3'  CAATGGGGCAAGACAA      11666        G   AT
                                CAATGGGG TAA  GACAA
                                |||||||| |||  |||||
                                GTTACCCC GTT  CTGTT
                                     _  __
GAM1706  COL19A1  3'  GATGATGAGGGTTTGAC     12376    CA      AAA
                                GA  ATGGGGGT   TGAC
                                ||  ||||||||   ||||
                                CT  TACTCCCA   ACTG
                                 AC       A__
GAM1706  ISL1     3'  AATGACATGAAAAGTGGCAA   13592       AT__  _
                                AATGACA    GGG GGTAA
                                |||||||    ||| |||||
                                TTACTGT    TTC CCGTT
                                     ACTT   A
GAM1706  MAP1A    3'  GATGATGGGGAGGGACAA    14344    CA      TAAAT
                                GA  ATGGGGG    GACAA
                                ||  |||||||    |||||
                                CT  TACCCCT    CTGTT
                                 AC      CC___
GAM1706  MOG      3'  AATGAAGAGAAAAGGTAGATGA 14606      CAAT_     A
              CA                   AATGA    GGGGGTA ATGACA
                                |||||    ||||||| ||||||
                                TTACT    TTTCCAT TACTGT
                                   TCTCT      C
GAM1706  NCOR2    3'  AACGACGTGTGTAAATGACA   26724       AAT GGG
                                AATGAC   G   GTAAATGACA
                                ||||||   |   ||||||||||
                                TTGCTG   C   CATTTACTGT
                                   ___ ACA
GAM1706  NFRKB    5'  TGGAACTCATAAATGACA    26104      ___
                                TGGGG   GTAAATGACA
                                |||||   ||||||||||
                                ACCTT   TATTTACTGT
                                   GAG
GAM1706  PCDHB9   3'  AATGAACAAGGATGGCAA    33317      _   T   _
                                AATGA CAA GGG GGTAA
                                ||||| ||| ||| |||||
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                                TTACT GTT CCT CCGTT
                                   T  _  A
GAM1706 PCSK2    3' ATGCAATGGGAATTGATGA   15124    A       AA
                                ATG CAATGGGGGT  ATGA
                                ||| ||||||||||  ||||
                                TAC GTTACCCTTA  TACT
                                  _       AC
GAM1706 PKHD1    3' AATGCATGAATTTTAAATGACA 39800     A  A   GG_
                                AATG CA TGGG   TAAATGACA
                                |||| || ||||   |||||||||
                                TTAC GT ACTT   ATTTACTGT
                                  _ _   AAA
GAM1706 SLC25A17 3' ATGACAATTAAGGTGACA    26823       GG   AAAT
                                ATGACAAT  GGGT   GACA
                                ||||||||  ||||   ||||
                                TACTGTTA  TCCA   CTGT
                                    AT   ____
GAM1706 SSX2     3' ATGGCAATGGGAAAAGCAGATG 45530    A     ___   A  A
             GCA                   ATG CAATGGG   GGTA ATG CA
                                ||| |||||||   |||| ||| ||
                                TAC GTTACCC   TCGT TAC GT
                                  C      TTT   C  C
GAM1706 TRPS1    3' AATGAATACAGAGGTGAGTGA  30454      CA      AAA
                                AATGA  ATGGGGGT   TGA
                                |||||  ||||||||   |||
                                TTACT  TGTCTCCA   ACT
                                   TA       CTC
GAM1706 WHN      3' ATGAAGATGGGGGAATAA    18753     CA     TA
                                ATGA  ATGGGGG  AATGA
                                ||||  |||||||  |||||
                                TACT  TACCCCC  TTATT
                                  TC     __
GAM1706 MAP3K7IP2 5' GCCGTCTCCACCGTCGCCT   31520    ____
                                GCC   CCACCGTCGCCT
                                |||   ||||||||||||
                                CGG   GGTGGCAGCGGA
                                  CAGA
GAM1706 NCALD    3' GACACACTTGCCCATGTC    36763          CACC
                                GACACATTTGCCC   GTC
                                ||||||||||||   |||
                                CTGTGTGAACGGG   CAG
                                       TA__
GAM1706 PRKAR1A  3' GGACATTTGCTCCATC     15608   C      CCCA
                                A ACATTTGC   CCGTC
                                | ||||||||   |||||
                                C TGTAAACG   GGTAG
                                 C       A___
GAM1707 MAT1A    3' TCGAGTGTGAGCCAAGTTAGA  44906     ATATAC
                                TCGA     GGGCCAAGTTAGA
                                ||||     ||||||||||||
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                                AGCT     CTCGGTTCAATCT
                                  CACA__
GAM1707  MEF2C    3'  GAATATGGGCAAGTTAG     14408       AC    C
                                GAATAT  GGGC AAGTTAG
                                ||||||  |||| |||||||
                                CTTATA  CCCG TTCAATC
                                  __    _
GAM1708  AICDA    3'  TATAAATTTATGAAGCTTTGA  34041          AT   A
                                TATAAATTTA  AAG CTTTGA
                                ||||||||||  ||| ||||||
                                ATATTTAAAT  TTC GAAACT
                                      AC  _
GAM1708  ASTN     3'  GATGGTCATATTATATTCTTTC 42948     TA TG C
                TT                GAT  T  T TTATATTCTTTCTT
                                |||  |  | ||||||||||||||
                                CTA  A  A AATATAAGAAAGAA
                                  CC GT T
GAM1708  SCN7A    3'  GATTATTATCTCTACTTTTCTT 16482           A    C
                                GATTATTGTCTT TATT TTTCTT
                                ||||||||||| |||| ||||||
                                CTAATAATAGAG ATGA AAAGAA
                                      _    _
GAM1709  B3GALT2  5'  AGCTGCAATGTAAAGCA     19108        AATAG    A
                                AGCTGCAA    GTGAA CA
                                ||||||||    ||||| ||
                                TCGACGTT    CATTT GT
                                    A____    C
GAM1709  BCL2     3'  GCTGCAAAAGACACCACA    8522         AT  GT AA
                                GCTGCAAA  AG  G  ACA
                                ||||||||  ||  |  |||
                                CGACGTTT  TC  T  TGT
                                    __  TG GG
GAM1709  CFTR     3'  GCTTGCAAAACACAAGTG    7954      _      __
                                GCT GCAAAATA  GGTG
                                ||| ||||||||  ||||
                                CGA CGTTTTGT  TCAC
                                  A       GT
GAM1709  CREBL2   3'  AGCTGCAAGGGGAAA       10573       AAAT   T
                                AGCTGCA    AGG GAAA
                                |||||||    ||| ||||
                                TCGACGT    TCC CTTT
                                    ____  C
GAM1709  EPO      3'  AGGTGCGAAAACAGGTAA    9029     C  _
                                AG TGC AAAATAGGTGA
                                || ||| ||||||||||
                                TC ACG TTTTGTCCATT
                                 C  C
GAM1709  GAGED2   3'  AAGCTGCAAAACTTTATTGA  39415          AGG__
                                AAGCTGCAAAAT    TGA
                                ||||||||||||    |||
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                                TTCGACGTTTTG    ACT
                                      AAATA
GAM1709  HDAC4    3'  TAAGCTACAAGATGA      25779        AAAT
                                TAAGCTGCA   AGGTGA
                                |||||||||   ||||||
                                ATTCGATGT   TCTACT
                                     ____
GAM1709  IRS2     3'  TAAGCTGCAGTATGAACA    40713        AAATAG    A
                                TAAGCTGCA    GTGAA CA
                                |||||||||    ||||| ||
                                ATTCGACGT    TACTT GT
                                     CA____   _
GAM1709  LANCL1   3'  AGCTGTGAAATAGGCACA    25847      CA      GAA
                                AGCTG  AAATAGGT   ACA
                                |||||  ||||||||   |||
                                TCGAC  TTTATCCG   TGT
                                   AC      ___
GAM1709  MAP3K5   3'  TAAGTTACAAAATAGAGTCAA  25443     C       _  G
                                TAAG TGCAAAATAG GT AA
                                |||| ||||||||| || ||
                                ATTC ATGTTTTATC CA TT
                                  A        T  G
GAM1709  MYO1C    3'  GCTGCAAAAGATGCAGATG    41470        ____
                                GCTGCAAAA    TAGGTG
                                |||||||||   ||||||
                                CGACGTTTT    GTCTAC
                                     CTAC
GAM1709  NOV      3'  AGTGCAATGTGAAACA      14806    C    AATAG
                                AG TGCAA    GTGAAACA
                                || |||||    ||||||||
                                TC ACGTT    CACTTTGT
                                 _    A____
GAM1709  PCDH7    3'  TAATTTGCAAAATACAGTG    37120     GC       _
                                TAA  TGCAAAATA GGTG
                                |||  ||||||||| ||||
                                ATT  ACGTTTTAT TCAC
                                  AA        G
GAM1709  PFKFB3   3'  TAAGCTGCAGAAATGGAAA    44438        _   A  T
                                TAAGCTGCA AAAT GG GA
                                ||||||||| |||| || ||
                                ATTCGACGT TTTA CC TT
                                     C   _  T
GAM1709  PIGK     3'  AAGCTGCAGGATTCCATGAGTG 42489       AA_____  AG
            A                    AAGCTGCA      AT  GTGA
                                ||||||||      ||  ||||
                                TTCGACGT      TA  CACT
                                    CCTAAGG  CT
GAM1709  PPP2CB   3'  TAAGCGCAAAAGGAGATGA    20002      T     T_
                                TAAGC GCAAAA  AGGTGA
                                ||||| ||||||  ||||||
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                                ATTCG CGTTTT  TCTACT
                                   _     CC
GAM1709  PPP3R1   3'  AGCTGCAAGTCTTTTGAAACAA 44071        AATAGG
                                AGCTGCAA     TGAAACAA
                                ||||||||     ||||||||
                                TCGACGTT     ACTTTGTT
                                     CAGAAA
GAM1709  RAB7L1   3'  TAAGCTCAGAAGTAGGTGA   19435       G  A  _
                                TAAGCT CA AA TAGGTGA
                                |||||| || || |||||||
                                ATTCGA GT TT ATCCACT
                                   _ C  C
GAM1709  RANBP2   3'  CAAGCTGCAGTTTCTGAGGTA  26537        AAAT___
                                TAAGCTGCA      AGGTG
                                |||||||||      |||||
                                GTTCGACGT      TCCAT
                                     CAAAGAC
GAM1709  SEL1L    3'  CAAGCAAATTACAGAGTAGGTG 22844       ____   AAA
                                TAAGC   TGCA   TAGGTG
                                |||||   ||||   ||||||
                                GTTCG   ATGT   ATCCAC
                                   TTTA   CTC
GAM1709  SHANK2   3'  CTGCAAAAGGTTTTGGAACA   29455       AT   GA___
                                CTGCAAA  AGGT    AACA
                                |||||||  ||||    ||||
                                GACGTTT  TCCA    TTGT
                                    __   AAACC
GAM1709  SLC10A1  3'  TAAGTTGGGGATAGGTGA    16809     C  CAAA
                                TAAG TG    ATAGGTGA
                                ||||  ||    ||||||||
                                ATTC AC    TATCCACT
                                  A  CCC_
GAM1709  SLC30A4  3'  TGACTGCAGGATAAATAA    30019    A     AA
                                A GCTGCA  ATAGGTGA
                                | ||||||  ||||||||
                                A TGACGT  TATTTATT
                                 C     CC
GAM1709  STE      5'  TAAGCTGCAAAAAAAGATGA   24050          T_
                                TAAGCTGCAAAA  AGGTGA
                                ||||||||||||  ||||||
                                ATTCGACGTTTT  TCTACT
                                      TT
GAM1709  TEM7     3'  AGGTGCAGGAATAGGTAA    33799    C    A_
                                AG TGCA  AATAGGTGA
                                || ||||  |||||||||
                                TC ACGT  TTATCCATT
                                 C    CC
GAM1709  TRPM6    3'  AGCTGCAAAGTGCCCTGGACA  32783        AATA    AA____
                                AGCTGCAA    GGTG     ACA
                                ||||||||    ||||     |||
```

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                              TCGACGTT   TCAC    TGT
                                  ____   GGGACC
GAM1709 UBE4A   3' TAAGCTGCACAATTGAGTA  21974       A  A_
                              TAAGCTGCA AAT  GGTG
                              ||||||||| |||  ||||
                              ATTCGACGT TTA  TCAT
                                   G   AC
GAM1710 AK2     3' TGGCATAACCAACTTCCTTTT 30191     TACA  __
                              TGGC   AACT  TTTCCTTTT
                              ||||   ||||  |||||||||
                              ACCG   TTGG  GAAGGAAAA
                                TA__   TT
GAM1710 ATP8A2  3' TGGCTCAATGCCCTTTT    45271      A  ACTTT
                              TGGCT CAA    TCCTTTT
                              ||||| |||    |||||||
                              ACCGA GTT    GGGAAAA
                                _  AC___
GAM1710 C1orf1  3' TGTCTACTTTCCTTTT     10230    G   AAACT
                              TG CTAC    TTTCCTTTT
                              || ||||    |||||||||
                              AC GATG    AAAGGAAAA
                               A  _____
GAM1710 CARP    3' TGGCTTCACTGTCCTTTTC   30796     ACAA  TT
                              TGGCT   ACT  TCCTTTTC
                              |||||   |||  ||||||||
                              ACCGA   TGA  AGGAAAAG
                                 AG__  C_
GAM1710 CRTAP   3' TGGCTTTCTTCCTTTT     26842     ACAAAC
                              TGGCT    TTTTCCTTTT
                              |||||    ||||||||||
                              ACCGA    AGAAGGAAAA
                                 A_____
GAM1710 ENC1    3' GCAACTTCTTTTCCTTTT    18863    T  AAA
                              GC AC   CTTTTCCTTTT
                              || ||   ||||||||||
                              CG TG   GAAAAGGAAAA
                               T  AA_
GAM1710 FLRT2   3' TGACTATGCCTCTTCCTTTTC 29860      CAAA
                              TGGCTA   CTTTTCCTTTTC
                              ||||||   ||||||||||||
                              ACTGAT   GAGAAGGAAAAG
                                 ACG_
GAM1710 FOXD1   3' TAACCATTTTTCCTTTTC    20932      CAAAC
                              TGGCTA    TTTTCCTTTTC
                              ||||||    ||||||||||
                              ATTGGT    AAAAGGAAAAG
                                 A____
GAM1710 FZD3    3' TGGCTACAAATTAAAATTTTTC 32635         CTTTTCC
                              TGGCTACAAA      TTTTC
                              |||||||||      |||||
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                                ACCGATGTTT      AAAAG
                                      AATTTTA
GAM1710  GNAS     3'  TGGCCTTTTTTCCTTTT     38666       ACAAAC
                                TGGCT     TTTTCCTTTT
                                |||||     ||||||||||
                                ACCGG     AAAAGGAAAA
                                   AA____
GAM1710  HAS3     3'  TGGCAAACTTTCCTTTT     39778       TAC      T
                                TGGC   AAACTTT CCTTTT
                                ||||   ||||||| ||||||
                                ACCG   TTTGAAA GGAAAA
                                   ___     _
GAM1710  HMGA2    3'  TGGCCACAAGCTTTTTTTTTC  18533          A     CC
                                TGGCTACAA CTTTT  TTTTC
                                |||||||||| |||||  |||||
                                ACCGGTGTT GAAAA  AAAAG
                                      C    A_
GAM1710  HOXC9    3'  GCTCTTTCCTTTTCTTTTTC   41481     ACAAA     C
                                GCT    CTTTTC TTTTC
                                |||    |||||| |||||
                                CGA    GAAAAG AAAAG
                                  GAAAG     A
GAM1710  IFNAR2   3'  GCTACTATTTTCCTTTTC     9319        AAAC
                                GCTAC    TTTTCCTTTTC
                                |||||    ||||||||||||
                                CGATG    AAAAGGAAAAG
                                   AT__
GAM1710  IGF2R    3'  TGGCTGTTTTTTTTTCCTTTT  9345        ACAAAC
                                TGGCT     TTTTCCTTTT
                                |||||     ||||||||||
                                ACCGA     AAAAGGAAAA
                                   CAAAAA
GAM1710  LEP      3'  CGGCCAAACTTTTTTTTTT    6913       TA       CC
                                TGGC  CAAACTTTT  TTTT
                                ||||  |||||||||  ||||
                                GCCG  GTTTGAAAA  AAAA
                                   __        AA
GAM1710  MTMR2    3'  TGGGTACAAACTGAACATTTTC 32069     C       TTTCC
                                TGG TACAAACT     TTTTC
                                ||| ||||||||     |||||
                                ACC ATGTTTGA     AAAAG
                                  C       CTTGT
GAM1710  NR1D1    3'  TGGTTTGCTTTTCCTTTTC    34706     CTACAAA
                                TGG      CTTTTCCTTTTC
                                |||      ||||||||||||
                                ACC      GAAAAGGAAAAG
                                  AAAC___
GAM1710  NRXN2    3'  AGCACGGGGTTTTTCCTTTTC  39830     TACAAAC
                                GGC      TTTTCCTTTTC
                                |||      ||||||||||
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                              TCG      AAAAGGAAAAG
                                TGCCCCA
GAM1710  PBX3     3'  GGCTACAAAAACGCTTTCCTTT 26214        __ _
              TC                  GGCTACAA  AC TTTTCCTTTTC
                                  ||||||||  || ||||||||||
                                  CCGATGTT  TG GAAAGGAAAAG
                                      TT  C
GAM1710  POU5F1   3'  TGGCACAAACTCCAGGTTTTC  15478      T       TCC
                                  TGGC ACAAACTTT   TTTTC
                                  |||| |||||||||   |||||
                                  ACCG TGTTTGAGG   AAAAG
                                    _       TCC
GAM1710  PPP2R2C  3'  TGGCGGTGAACGCTTCCTTTCC 41546      TACA   T
                                  TGGC    AAC TTTCCTTTTC
                                  ||||    ||| ||||||||||
                                  ACCG    TTG GAAGGAAAGG
                                    CCAC   C
GAM1710  RAD54B   3'  AGCTACATTCCTTTT       29675        AACTT
                                  GGCTACA    TTCCTTTT
                                  |||||||    ||||||||
                                  TCGATGT    AAGGAAAA
                                       _____
GAM1710  TLR3     5'  GCTAGCCTTTCCTTTT      17559      CAAA
                                  GCTA    CTTTTCCTTTT
                                  ||||    ||||||||||
                                  CGAT    GGAAAGGAAAA
                                    C___
GAM1710  TRPM6    3'  TGGTTTTCCACCTTCCTTTTC  32804     CTACAA    T
                                  TGG      ACTTT CCTTTTC
                                  |||      ||||| |||||||
                                  ACC      TGGAA GGAAAAG
                                    AAAAGG    _
GAM1710  GNG5     3'  AAGTTTGTATATTATGGCACAT 23606         C    A_   A
              GT                  GAGTTTGTA ATTA  GCA CATGT
                                  |||||||||  ||||  |||  |||||
                                  TTCAAACAT TAAT  CGT GTACA
                                       A    AC  _
GAM1710  SH3GL2   3'  GAGTTTATACATTAAGCA    16682
                                  GAGTTTGTACATTAAGCA
                                  ||||||||||||||||||
                                  CTCAAATATGTAATTCGT

GAM1711  PCDHA1   3'  TTGTATTCATATTTCTCTTT   36402          TCAATG
                                  TTGTATTCAT     TCTCTTT
                                  ||||||||||     |||||||
                                  AACATAAGTA     AGAGAAA
                                       TAA___
GAM1711  PCDHA10  3'  TTGTATTCATATTTCTCTTT   36570          TCAATG
                                  TTGTATTCAT     TCTCTTT
                                  ||||||||||     |||||||
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                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA11 3' TTGTATTCATATTTCTCTTT 36585       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA12 3' TTGTATTCATATTTCTCTTT 36600       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA13 3' TTGTATTCATATTTCTCTTT 36609       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA2  3' TTGTATTCATATTTCTCTTT 36472       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA3  3' TTGTATTCATATTTCTCTTT 36479       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA4  3' TTGTATTCATATTTCTCTTT 36494       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA5  3' TTGTATTCATATTTCTCTTT 36503       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA6  3' TTGTATTCATATTTCTCTTT 36515       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA7  3' TTGTATTCATATTTCTCTTT 36525       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
                              AACATAAGTA    AGAGAAA
                                   TAA___
GAM1711 PCDHA8  3' TTGTATTCATATTTCTCTTT 36533       TCAATG
                              TTGTATTCAT    TCTCTTT
                              ||||||||||    |||||||
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                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM1711  PCDHA9   3'  TTGTATTCATATTTCTCTTT  36560         TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM1711  PCDHAC1  3'  TTGTATTCATATTTCTCTTT  36626         TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM1711  PCDHAC2  3'  TTGTATTCATATTTCTCTTT  36636         TCAATG
                                TTGTATTCAT     TCTCTTT
                                ||||||||||     |||||||
                                AACATAAGTA     AGAGAAA
                                     TAA___
GAM1711  LAMC1    3'  TTAATTTAGAGAATGGAGATGC 14097          TC__ _ A
            TGCAA                   TTAGTTTAGAG    GA AT CTGCAA
                                ||||||||||    || || ||||||
                                AATTAAATCTC    CT TA GACGTT
                                      TTAC  C  C
GAM1711  SCA1     3'  GTTTAGAGTTGAGCA       7284          C  ATACT
                                GTTTAGAGT GA    GCA
                                |||||||| ||    |||
                                CAAATCTCA CT    CGT
                                     A _____
GAM1711  SLC31A1  3'  TTAGTTCAGAGACTG       12401          TCGAAT
                                TTAGTTTAGAG     ACTG
                                ||||||||||     ||||
                                AATCAAGTCTC     TGAC
                                          _______
GAM1711  TDE1     3'  TTTAAAGGATACTGCAA     27721        TCGA
                                TTTAGAG   ATACTGCAA
                                |||||||   |||||||||
                                AAATTTC   TATGACGTT
                                    C___
GAM1712  AK2      3'  TGGCATAACCAACTTCCTTTTT 30192      TACA   __       C
            CA                    TGGC   AACT  TTTCCTTTT CA
                                ||||   ||||  |||||||| ||
                                ACCG   TTGG  GAAGGAAAA GT
                                  TA__   TT       A
GAM1712  CRTAP    3'  TGGCTTTCTTCCTTTTCC    26843      ACAAAC
                                TGGCT     TTTTCCTTTTCC
                                |||||     ||||||||||||
                                ACCGA     AGAAGGAAAAGG
                                  A_____
GAM1712  CXorf6   5'  TGATTACAAGCCGACTTTTCCA 24244    GC    A  TTTC
                                TG  TACAA CT    CTTTTCCA
                                ||  ||||| ||    ||||||||
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```
                                AC  ATGTT GG   GAAAAGGT
                                 TA    C  CT__
GAM1712  EPHB2    3'  TGGCACCAGTTTTTCTTTTCCA 32682     T  AAAC    C
                                TGGC AC    TTTTC TTTTCCA
                                |||| ||    ||||| |||||||
                                ACCG TG    AAAAG AAAAGGT
                                  _  GTCA    _
GAM1712  FZD3     3'  TGGCTACAAATTAAAATTTTTC 32636         CTTTTCC
              CA                   TGGCTACAAA      TTTTCCA
                                |||||||||||      |||||||
                                ACCGATGTTT      AAAAGGT
                                      AATTTTA
GAM1712  HMGA2    3'  TGGCCACAAGCTTTTTTTTTC  18533        A    CC
                                TGGCTACAA CTTTT  TTTTC
                                |||||||||| |||||  |||||
                                ACCGGTGTT GAAAA  AAAAG
                                      C    A_
GAM1712  SLC2A4   3'  GGCTGCAGGGATTCTTTTCCA  9799      A  AACTT   C
                                GGCT CA    TTC TTTTCCA
                                |||| ||    ||| |||||||
                                CCGA GT    AAG AAAAGGT
                                  C  CCCT_  _
GAM1712  CDK9     3'  AGAGTTTGTGCCAGCCCCA    10387        ACATTA   AA
                                AGAGTTTGT     AGC  CA
                                |||||||||     |||  ||
                                TCTCAAACA     TCG  GT
                                      CGG___   GG
GAM1712  MORF     5'  CAGACTGTATTAAGCAACA    29566     GT    CA
                                TAGA  TTGTA  TTAAGCAACA
                                ||||  |||||  ||||||||||
                                GTCT  GACAT  AATTCGTTGT
                                  __    __
GAM1712  RORB     3'  TAGAGTTTGTATATAGAGGCCA 27923          C  TAA_  A
              CAC                    TAGAGTTTGTA AT    GC ACAT
                                |||||||||| ||    || ||||
                                ATCTCAAACAT TA    CG TGTG
                                      A  TCTC  G
GAM1713  HAL      3'  TTTATATTCATTCCTTATCTCC 13336           AA
              TT                   TTTGTATTCATTC  TGTCTCCTT
                                ||||||||||||  |||||||||
                                AAATATAAGTAAG  ATAGAGGAA
                                       GA
GAM1713  KCNJ16   3'  TATTTATTCCAGCCTCCTT    33017     C    AAT
                                TATT ATTC   GTCTCCTT
                                |||| ||||   ||||||||
                                ATAA TAAG   CGGAGGAA
                                  A   GT_
GAM1713  NEBL     3'  TTGTAAAACATTCAATGT     26916      TT_
                                TTGTA   CATTCAATGT
                                |||||   ||||||||||
```

```
                                AACAT  GTAAGTTACA
                                  TTT
GAM1713  PCDHA1   3' TTGTATTCATATTTCTC    36404       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA10  3' TTGTATTCATATTTCTC    36569       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA11  3' TTGTATTCATATTTCTC    36584       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA12  3' TTGTATTCATATTTCTC    36599       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA13  3' TTGTATTCATATTTCTC    36608       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA2   3' TTGTATTCATATTTCTC    36471       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA3   3' TTGTATTCATATTTCTC    33143       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA4   3' TTGTATTCATATTTCTC    36493       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA5   3' TTGTATTCATATTTCTC    36502       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
                                AACATAAGTA    AGAG
                                    TAA___
GAM1713  PCDHA6   3' TTGTATTCATATTTCTC    36514       TCAATG
                                TTGTATTCAT    TCTC
                                ||||||||||    ||||
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                                AACATAAGTA     AGAG
                                      TAA___
GAM1713  PCDHA7   3'  TTGTATTCATATTTCTC     36524          TCAATG
                                TTGTATTCAT     TCTC
                                ||||||||||     ||||
                                AACATAAGTA     AGAG
                                      TAA___
GAM1713  PCDHA8   3'  TTGTATTCATATTTCTC     36532          TCAATG
                                TTGTATTCAT     TCTC
                                ||||||||||     ||||
                                AACATAAGTA     AGAG
                                      TAA___
GAM1713  PCDHA9   3'  TTGTATTCATATTTCTC     36559          TCAATG
                                TTGTATTCAT     TCTC
                                ||||||||||     ||||
                                AACATAAGTA     AGAG
                                      TAA___
GAM1713  PCDHAC1  3'  TTGTATTCATATTTCTC     36625          TCAATG
                                TTGTATTCAT     TCTC
                                ||||||||||     ||||
                                AACATAAGTA     AGAG
                                      TAA___
GAM1713  PCDHAC2  3'  TTGTATTCATATTTCTC     36635          TCAATG
                                TTGTATTCAT     TCTC
                                ||||||||||     ||||
                                AACATAAGTA     AGAG
                                      TAA___
GAM1713  PKHD1    5'  TCTGTTTCTGTCTCCT      39807       A   ATTCAA
                                TTTGT TTC      TGTCTCCT
                                ||||| |||      ||||||||
                                AGACA AAG      ACAGAGGA
                                  _  _______
GAM1713  LAMC1    3'  TTAATTTAGAGAATGGAGATGC 14097           TC__  _  A
            TGCAA                   TTAGTTTAGAG    GA AT CTGCAA
                                ||||||||||    || || ||||||
                                AATTAAATCTC    CT TA GACGTT
                                      TTAC  C  C
GAM1713  SCA1     3'  GTTTAGAGTTGAGCA       7284           C  ATACT
                                GTTTAGAGT GA     GCA
                                |||||||| ||     |||
                                CAAATCTCA CT     CGT
                                     A  _____
GAM1713  SLC31A1  3'  TTAGTTCAGAGACTG       12401          TCGAAT
                                TTAGTTTAGAG      ACTG
                                ||||||||||      ||||
                                AATCAAGTCTC      TGAC
                                        _______
GAM1713  TDE1     3'  TTTAAAGGATACTGCAA      27721        TCGA
                                TTTAGAG    ATACTGCAA
                                |||||||    |||||||||
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                                AAATTTC   TATGACGTT
                                   C___
GAM1714 AK2     3' TGGCATAACCAACTTCCTTTTT 30192     TACA  __      C
            CA                   TGGC   AACT  TTTCCTTTT CA
                                 ||||   ||||  ||||||||| ||
                                 ACCG   TTGG  GAAGGAAAA GT
                                   TA__   TT       A
GAM1714 CRTAP   3' TGGCTTTCTTCCTTTTCC   26843      ACAAAC
                                 TGGCT    TTTTCCTTTTCC
                                 ||||||    ||||||||||||
                                 ACCGA    AGAAGGAAAAGG
                                   A_____
GAM1714 CXorf6  5' TGATTACAAGCCGACTTTTCCA 24244   GC    A  TTTC
                                 TG  TACAA CT   CTTTTCCA
                                 ||  ||||| ||   ||||||||
                                 AC  ATGTT GG   GAAAAGGT
                                   TA    C  CT__
GAM1714 EPHB2   3' TGGCACCAGTTTTTCTTTTCCA 32682     T  AAAC    C
                                 TGGC AC   TTTTC TTTTCCA
                                 |||| ||   ||||| |||||||
                                 ACCG TG   AAAAG AAAAGGT
                                   _ GTCA    _
GAM1714 FZD3    3' TGGCTACAAATTAAAATTTTTC 32636        CTTTTCC
            CA                   TGGCTACAAA      TTTTCCA
                                 ||||||||||      |||||||
                                 ACCGATGTTT      AAAAGGT
                                      AATTTTA
GAM1714 HMGA2   3' TGGCCACAAGCTTTTTTTTTC  18533       A    CC
                                 TGGCTACAA CTTTT  TTTTC
                                 ||||||||| |||||  |||||
                                 ACCGGTGTT GAAAA  AAAAG
                                      C    A_
GAM1714 SLC2A4  3' GGCTGCAGGGATTCTTTTCCA  9799      A  AACTT   C
                                 GGCT CA    TTC TTTTCCA
                                 |||| ||    ||| |||||||
                                 CCGA GT    AAG AAAAGGT
                                   C  CCCT_  _
GAM1714 CDK9    3' AGAGTTTGTGCCAGCCCCA   10387       ACATTA   AA
                                 AGAGTTTGT     AGC  CA
                                 |||||||||     |||  ||
                                 TCTCAAACA     TCG  GT
                                      CGG___   GG
GAM1714 MORF    5' CAGACTGTATTAAGCAACA   29566     GT    CA
                                 TAGA  TTGTA  TTAAGCAACA
                                 ||||  |||||  ||||||||||
                                 GTCT  GACAT  AATTCGTTGT
                                   __    __
GAM1714 RORB    3' TAGAGTTTGTATATAGAGGCCA 27923         C  TAA_  A
            CAC                   TAGAGTTTGTA AT    GC ACAT
                                 |||||||||| ||    || ||||
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                                ATCTCAAACAT TA   CG TGTG
                                      A  TCTC  G
GAM1715  COL4A3   3'  TAACAATATCATTTTAAAAC  36384           TG
                                TAACAATATCATTTT  GAT
                                ||||||||||||||  |||
                                ATTGTTATAGTAAAA  TTG
                                     TT
GAM1715  MLLT2    3'  CAATATCACTTGCAGTGTT   25494         T   A
                                CAATATCATTT TGG TGTT
                                |||||||||| ||| ||||
                                GTTATAGTGAA GTC ACAA
                                      C  _
GAM1715  CREBL2   3'  ATACTTTATTTGGAAGC    10576          TTTTA
                                ATACTTTATTTG    AAGC
                                ||||||||||||    ||||
                                TATGAAATAAAC    TTCG
                                      C____
GAM1715  GCG      3'  CACTTTCATATTTTAAAGCT  13117       ATT
                                TACTTT  TGTTTTAAAGCT
                                ||||||  ||||||||||||
                                GTGAAA  ATAAAATTTCGA
                                   GT_
GAM1715  SNAI2    3'  ACTTTATTTGTCATTTGGCT  16879          TTAAA
                                ACTTTATTTGTT    GCT
                                ||||||||||||    |||
                                TGAAATAAACAG    CGA
                                      TAAAC
GAM1716  CAPZA1   3'  TATTTTATCACAGTTACACTTG 43719          ATTG  TC
            A                    TATTTTATCACG   ATA  TGA
                                ||||||||||||   |||  |||
                                ATAAAATAGTGT   TGT  ACT
                                      CAA_  GA
GAM1717  BTEB1    5'  TGGTTGATGTCACT      10222    C       TTATT
                                TG GTTGATGTCG    CT
                                || ||||||||||    ||
                                AC CAACTACAGT    GA
                                 _       _____
GAM1717  SVIL     3'  GTTGTGTTTATTCTG      34731     A   CG
                                GTTG TGT  TTATTCTG
                                |||| |||  ||||||||
                                CAAC ACA  AATAAGAC
                                  _  __
GAM1717  LYPLA1   3'  GAGTATTAAATAGAAATAA   26759      AAATTT
                                GAGTAT     TAGAAATAA
                                ||||||     |||||||||
                                CTCATA     ATCTTTATT
                                   ATTT__
GAM1717  RNGTT    3'  GTATAACAGAAATAACAT    19164      ATTT
                                GTATAA   TAGAAATAACAT
                                ||||||   ||||||||||||
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                                CATATT   GTCTTTATTGTA
                                      ____
GAM1718 AR      5' TGCGGGAAGCTCCAGAG    6247    A     CT  C
                                TG CGGGAAGC  TA GAG
                                || ||||||||  || |||
                                AC GCCCTTCG  GT CTC
                                  _      AG  _
GAM1718 CKAP1   5' GACGGGACTTACGAG      43882       AGC
                                GACGGGA  CTTACGAG
                                |||||||  ||||||||
                                CTGCCCT  GAATGCTC
                                      ___
GAM1718 GPC1    3' TGACAGGAGGTCACCAG    13260       AGCC   G
                                TGACGGGA   TTAC AG
                                ||||||||   |||| ||
                                ACTGTCCT   AGTG TC
                                     CC__   G
GAM1718 GRP     5' GACGGGAAGCCCTTGGAG   13299          AC
                                GACGGGAAGCCTT  GAG
                                ||||||||||||  |||
                                CTGCCCTTCGGGA  CTC
                                       AC
GAM1718 HDAC4   3' CGGCGGGAAGCCGCGAG    25759   A       TTA
                                TG CGGGAAGCC   CGAG
                                || |||||||||   ||||
                                GC GCCCTTCGG   GCTC
                                 C       C__
GAM1718 HUS1    3' TGGGAGGATGCCTTGAG    45005   AC   A    AC
                                TG  GGGA GCCTT  GAG
                                ||  |||| |||||  |||
                                AC  TCCT CGGAA  CTC
                                 CC   A    __
GAM1718 POLR2E  5' CAGCCCGAGCCTTACGAG   40914    GA__
                                CGG   AGCCTTACGAG
                                |||   ||||||||||
                                GTC   TCGGAATGCTC
                                  GGGC
GAM1718 ROBO1   3' TGACAGGAGGCATCTTGAG  16363       A  C  AC
                                TGACGGGA GC TT  GAG
                                |||||||| || ||  |||
                                ACTGTCCT CG AG  CTC
                                     C  T  AA
GAM1718 SPAP1   3' TGACAGGAGGTGCCTCCTGAG 39866       A__    AC
                                TGACGGGA   GCCTT  GAG
                                ||||||||   |||||  |||
                                ACTGTCCT   CGGAG  CTC
                                     CCA    GA
GAM1718 ADD2    3' AGGAGACCTGAATTCGAGT   32723    TCT   TA
                                AGGA   CCT  AATTCGAGT
                                ||||   |||  |||||||||
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                                TCCT   GGA  TTAAGCTCA
                                  CT_   C_
GAM1718  ADRB1    3'  ACGAGGATTGTGGGCTTCGAGT 8655         CTCCTTAAA
                                ACGAGGAT        TTCGAGT
                                ||||||||        |||||||
                                TGCTCCTA        AAGCTCA
                                    ACACCCG__
GAM1718  FLT1     3'  ACAAGGATAAATTTGA      12901        TCTCCT     C
                                ACGAGGA     TAAATT GA
                                |||||||     |||||| ||
                                TGTTCCT     ATTTAA CT
                                    _______     A
GAM1719  BAZ1B    3'  TATGATGCTGGTGAATACACAA 37095         AATA_
                                TATGATGC    AATACACGA
                                ||||||||    |||||||||
                                ATACTACG    TTATGTGTT
                                    ACCAC
GAM1719  LAMC2    3'  TATGGTGCAATAAGAC      33121      A       ATACAC
                                TATG TGCAATAA     GAC
                                |||| ||||||||     |||
                                ATAC ACGTTATT     CTG
                                  C      _______
GAM1719  PCDHB7   3'  TATGATGCATTAAAAGCA    33204          A    TA
                                TATGATGCA TAAA  CA
                                ||||||||| ||||  ||
                                ATACTACGT ATTT  GT
                                     A    TC
GAM1719  SHOC2    3'  TATGATATAATAAATACA    28896        C
                                TATGATG AATAAATACA
                                ||||||| ||||||||||
                                ATACTAT TTATTTATGT
                                    A
GAM1719  TP63     3'  ATGCTCAAATACATGAC     18993      AA       C
                                ATGC  TAAATACA GAC
                                ||||  |||||||| |||
                                TACG  GTTTATGT CTG
                                  A_       A
GAM1720  CALU     3'  GGTGGCATTATTAAATTA    10259       AGA
                                GGTGG   ATTATTAAATTA
                                |||||   ||||||||||||
                                CCACC   TAATAATTTAAT
                                  G__
GAM1720  FGF23    3'  TATACTATTATACATAGTTTT  33958          ___
                                TATACTGTT   CATAGTTTT
                                |||||||||   |||||||||
                                ATATGATAA   GTATCAAAA
                                     TAT
GAM1720  LCP1     3'  CATACTGTTCTGGTTTT     14103          ATA
                                TATACTGTTC   GTTTT
                                ||||||||||   |||||
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                                GTATGACAAG   CAAAA
                                     AC_
GAM1720  ZNF140   3'  CATACATTCATAGTTTT     18341       T
                                TATAC GTTCATAGTTTT
                                |||||| ||||||||||||
                                GTATG TAAGTATCAAAA

                                  _
GAM1721  AMD1     3'  TTTTTGCGTTTTTTCTTCATTT 11594      _    __
           TTC                    TTTTT CGTTT  TTTTCGTTTTTT
                                |||||| |||||  ||||||||||||
                                AAAAA GCAAA  AGAAGTAAAAAG
                                   C     AA
GAM1721  BCL6     3'  TTTTTTGTTCTTTTTGTTTTTT 39912       C       C
           T                     TTTTT GTTTTTTT GTTTTTTT
                                |||||| |||||||| ||||||||
                                AAAAA CAAGAAAA CAAAAAAA
                                   A       A
GAM1721  CASP1    3'  TTTTTTTTTTTTTTCATTTTTC 37788       CG
                                TTTTT  TTTTTTTCGTTTTTT
                                ||||||  ||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM1721  DDX3     5'  TTTTTCGTTTTTTTTGTTTTT  35832            C
                                TTTTTCGTTTTTTT GTTTTT
                                |||||||||||||| ||||||
                                AAAAAGCAAAAAAA CAAAAA
                                      A
GAM1721  DDX3     5'  TTTCGTTTTTCGTTTTTTT    35831          TT
                                TTTCGTTTT  TCGTTTTTTT
                                |||||||||  ||||||||||
                                AAAGCAAAA  AGCAAAAAAA

                                   __
GAM1721  DDX6     3'  TTTTTTGCTTTTTTCCCCCCCT 20572       C       G
           T                     TTTTT GTTTTTTTC TTTTTTT
                                |||||| |||||||| |||||||
                                AAAAA CGAAAAAAG GGGGGAA
                                   A       G
GAM1721  EBF      3'  TTTTTCCTTTTTTTCTTTTTTT 42371       G       G
                                TTTTTC TTTTTTTC TTTTTTT
                                |||||| |||||||| |||||||
                                AAAAAG AAAAAAAG AAAAAAA
                                   G      _
GAM1721  ETV5     3'  TTTTTCGTTTTTTTGCTTT    20860            C
                                TTTTTCGTTTTTTT GTTTT
                                |||||||||||||| |||||
                                AAAAAGCAAAAAAA CGAAA

                                     _
GAM1721  LMO4     3'  TTTTTCTTTTTTTCATTCTTTT 27666       G
                                TTTTTC TTTTTTTCGTTTTTTT
                                |||||| ||||||||||||||||
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                                AAAAAG AAAAAAAGTAAGAAAA
                                     _
GAM1721  MECP2    3'  TCGTTTTTTTTTCTTTTTT   22614          CG
                                TCGTTTTTTT  TTTTTTT
                                ||||||||||  |||||||
                                AGCAAAAAAA  GAAAAAA
                                      AA
GAM1721  NFIB     3'  TTTTTCTTTTTTTCCTTTTTTT 24643       G      G
                                TTTTTC TTTTTTTC TTTTTTT
                                |||||| |||||||| |||||||
                                AAAAAG AAAAAAAG AAAAAAA
                                   _      G
GAM1721  NFIB     3'  TTTTTCCTTTTTTCTTTTTTTC 24642       G      G
                                TTTTTC TTTTTTTC TTTTTTTC
                                |||||| |||||||| ||||||||
                                AAAAAG GAAAAAAG AAAAAAAG
                                   _      _
GAM1721  NFIB     3'  TTTTCCTTTTTTTTTCATTTTT 24641       G_
              TC                  TTTTTC  TTTTTTTCGTTTTTTT
                                  ||||||  ||||||||||||||||
                                  AAAAGG  AAAAAAAGTAAAAAAG
                                     AA
GAM1721  PPP4C    3'  TTTTTTTTTTTTTTCATTTTTC 15540       CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  ||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM1721  PRDM2    3'  TTTTTCATTTCCCAATTTGTTT 31977            TC___
              TTTTC                 TTTTTCGTTTTTT    GTTTTTTTC
                                    ||||||||||||    |||||||||
                                    AAAAAGTAAAGGG    CAAAAAAAG
                                          TTAAA
GAM1721  RPP30    3'  TTTTTCGCTTTTAATGTTTTTT 26944           TTC
              T                    TTTTTCGTTTTT   GTTTTTTT
                                   ||||||||||||   ||||||||
                                   AAAAAGCGAAAA   CAAAAAAA
                                         TTA
GAM1721  RPP30    3'  TTTTTTTTTTTTTTCGCTTTT  26945      CG
                                TTTTT  TTTTTTTCGTTTTT
                                |||||  |||||||||||||
                                AAAAA  AAAAAAAGCGAAAA
                                   AA
GAM1721  TKT      3'  TTTTTTTTTTTTTTCATTTTTC 9867       CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  |||||||||||||||
                                AAAAA  AAAAAAAGTAAAAAG
                                   AA
GAM1721  UBQLN2   3'  TTTTTTTTTTTTTTCATTTTTT 30284      CG
                                TTTTT  TTTTTTTCGTTTTTT
                                |||||  |||||||||||||||
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                                AAAAA  AAAAAAAGTAAAAAA
                                  AA
GAM1722  GPRC5B   3'  TACACGAAATCCCCT      32177        TAGGA
                                TACGCGGA    ATCCCCT
                                ||||||||    |||||||
                                ATGTGCTT    TAGGGGA
                                          _____
GAM1722  NRG1     5'  TACGCGGACGGCTCTC      30346        A  AATCCC
                                TACGCGGAT GG     CTC
                                ||||||||| ||     |||
                                ATGCGCCTG CC     GAG
                                     _ GA____
GAM1722  PAK1     5'  GCGGGGCTCCCCTCA       15082      ATA  AA
                                GCGG   GG  TCCCCTCA
                                ||||   ||  ||||||||
                                CGCC   CC  AGGGGAGT
                                  ___  G_
GAM1722  RAMP3    3'  GCGGATAGCCTGAGCCTCAG   25200        GAATCC
                                GCGGATAG     CCTCAG
                                ||||||||     ||||||
                                CGCCTATC     GGAGTC
                                     GGACTC
GAM1722  SYNGR3   3'  CACGCGGGTCCACCCCCTC    20093        ATAGGA
                                TACGCGG     ATCCCCTC
                                |||||||     ||||||||
                                GTGCGCC     TGGGGGAG
                                    CAGG__
GAM1722  WISP2    3'  TGTGTGTGTAGGCAGGGAGTGG 19312    A    A     TCA  C
            G                    TG TGTGT TAGGCG   AG GGG
                                || ||||| ||||||   || |||
                                AC ACACA ATCCGT   TC CCC
                                 _    C     CCC  A
GAM1723  CBFB     3'  TAAGGCAGGAGGATCGCT    35634        CAA  CA
                                TAAGGCAGG   GA  GCT
                                |||||||||   ||  |||
                                ATTCCGTCC   CT  CGA
                                     TC_  AG
GAM1723  GPC1     3'  AAGGCAGGCGAGGCCAGGCC   13229        A  A_  _
                                AAGGCAGGC AG  CAG CT
                                ||||||||| ||  ||| ||
                                TTCCGTCCG TC  GTC GG
                                     C  CG   C
GAM1723  ICMT     3'  AGGGTGGGCAAGCCCAACT   29651     CA_     A_
                                AGG   GGCAAG  CAGCT
                                |||   ||||||  |||||
                                TCC   CCGTTC  GTTGA
                                  CAC     GG
GAM1723  MATN2    3'  TAAGGCAGGATGAGGCAG    14371         CA_  A
                                TAAGGCAGG   AG CAG
                                |||||||||   || |||
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                                ATTCCGTCC  TC GTC
                                     TAC  C
GAM1723  MME     3'  TAAGTTAGAGACAGCT     28613     GC  GCA
                                TAAG  AG   AGACAGCT
                                ||||  ||   ||||||||
                                ATTC  TC   TCTGTCGA
                                  AA  ___
GAM1723  SLC3A2  5'  TAAGGCAGGAGGATCACT    14402        CAA  CA
                                TAAGGCAGG   GA  GCT
                                |||||||||   ||  |||
                                ATTCCGTCC   CT  TGA
                                     TC_  AG
GAM1723  SURF5   3'  CAAGGCAGGCAGGCT      39501          AGACA
                                TAAGGCAGGCA    GCT
                                ||||||||||     |||
                                GTTCCGTCCGT    CGA
                                      C____
GAM1723  TEK     3'  TGAGTAGGCAAGACATTTATT  7851    A  C       GC
                                A GG AGGCAAGACA  TATT
                                | || ||||||||||  ||||
                                A TC TCCGTTCTGT  ATAA
                                 C  A        AA
GAM1723  BTG3    3'  TTTTGCCTCAAACTATT     27718       C
                                TTTTGCC TTAGACTATT
                                ||||||| ||||||||||
                                AAAACGG AGTTTGATAA
                                        _
GAM1723  FZD10   3'  CTGTCTTGCAGAGAGACTATT  28452        CCTT
                                CTGTTTTGC    AGACTATT
                                |||||||||    ||||||||
                                GACAGAACG    TCTGATAA
                                     TCTC
GAM1723  USP7    3'  TCTCTGTTTTGCCTTAACAGA  18457    C       CT__
                                TC CTGTTTTGCC    TAGA
                                || ||||||||||    ||||
                                AG GACAAAACGG    GTCT
                                 A         AATT
GAM1724  KLHL1   3'  TTAATTGTAATTAAAATTTACA 34086       GAATT
                                TTAATTG    TTGGAATTTACA
                                |||||||    ||||||||||||
                                AATTAAC    AATTTTAAATGT
                                    ATT__
GAM1724  FGF5    3'  CATAACCATAACCAAATAATTT 37585        __  TG  A
           TA                    CATAACTA  AT  AA TAATTTTA
                                 ||||||||  ||  || ||||||||
                                 GTATTGGT  TG  TT ATTAAAAT
                                     AT  GT  _
GAM1724  ITGA6   3'  CTAATCATGAAATAATTTTAC  6828       __
                                 CTAAT  TGAAATAATTTTAC
                                 |||||  ||||||||||||||
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                                GATTA  ACTTTATTAAAATG
                                   GT
GAM1725  PRKG2    3'  TAATGGTCTTCCAAAGATAT   26521      AA      _
                                TAAT  TTTTCCAA GATGT
                                ||||  |||||||| |||||
                                ATTA  AGAAGGTT CTATA
                                  CC       T
GAM1725  UBQLN2   3'  TAATATTTTTAGATGTACA   30283      A    CCA
                                TAATA TTTT   AGATGTACA
                                ||||| ||||   |||||||||
                                ATTAT AAAA   TCTACATGT
                                  A   ___
GAM1725  CDH1     3'  TTGGAATTTTGAATATTC    20373           _
                                TTGGAATTTTGGA ATTT
                                |||||||||||| ||||
                                AACCTTAAAACTT TAAG
                                       A
GAM1726  AIPL1    3'  AGCTCTAAGTGTCCT       40816        A  TAAATA
                                AGCTTTAA GT     TCCT
                                |||||||| ||     ||||
                                TCGAGATT CA     AGGA
                                    _ C_____
GAM1726  DLD      3'  AGCTGTGAGAATATCCTG    6465       TTAA  TTA
                                AGCT   AG   AATATCCTG
                                ||||   ||   |||||||||
                                TCGA   TC   TTATAGGAC
                                  CAC_ ___
GAM1726  DNMT3B   3'  AGCTTTGCAGTTTTCCCTG   27868       AA   AAATA
                                AGCTTT  AGTT    TCCTG
                                ||||||  ||||    |||||
                                TCGAAA  TCAA    GGGAC
                                   CG   AA___
GAM1726  GALNT3   3'  AGCTTTAAATGAGTCAAGTATT 21014        ___     A   C
            CTGC                  AGCTTTAA   AGTTAA TAT CTGC
                                |||||||||  |||||| ||| ||||
                                TCGAAATT   TCAGTT ATA GACG
                                    TAC     C   A
GAM1726  MME      3'  AGTTTTCAGTTTATCCTG    28595    C   AA    AAA
                                AG TTT  AGTT   TATCCTG
                                || |||  ||||   |||||||
                                TC AAA  TCAA   ATAGGAC
                                  _  AG   ___
GAM1726  AIPL1    3'  AGCTCTAAGTGTCCT       40816        A  TAAATA
                                AGCTTTAA GT     TCCT
                                |||||||| ||     ||||
                                TCGAGATT CA     AGGA
                                    _ C_____
GAM1726  DLD      3'  AGCTGTGAGAATATCCTG    6465       TTAA  TTA
                                AGCT   AG   AATATCCTG
                                ||||   ||   |||||||||
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                                TCGA   TC   TTATAGGAC
                                  CAC_ ___
GAM1726 DNMT3B   3' AGCTTTGCAGTTTTCCCTG   27868      AA   AAATA
                                AGCTTT  AGTT    TCCTG
                                ||||||  ||||    |||||
                                TCGAAA  TCAA    GGGAC
                                   CG   AA___
GAM1726 GALNT3   3' AGCTTTAAATGAGTCAAGTATT 21014       ___    A  C
           CTGC                   AGCTTTAA  AGTTAA TAT CTGC
                                ||||||||  |||||| ||| ||||
                                TCGAAATT  TCAGTT ATA GACG
                                    TAC    C  A
GAM1726 MME     3' AGTTTTCAGTTTATCCTG   28595   C  AA   AAA
                                AG TTT  AGTT   TATCCTG
                                || |||  ||||   |||||||
                                TC AAA  TCAA   ATAGGAC
                                 _  AG   ___
GAM1727 ARHGAP6  3' GTTGAATGCCAAGTTCC    30226     C  T
                                GTTGG AT TCAAGTTCC
                                ||||| || |||||||||
                                CAACT TA GGTTCAAGG
                                   _ C
GAM1727 CREM    3' TCTTTCAAGGTTTCAAGTTCC  12438    A  TT  CA
                                TCT TCG  GG  TTTCAAGTTCC
                                ||| |||  ||  ||||||||||
                                AGA AGT  CC  AAAGTTCAAGG
                                  A  T_ __
GAM1727 CYBB    3' TCTATCTTGGCATTGTGTGGTT 44101      G      TCAA_
           C                    TCTATC TTGGCATT    GTTC
                                ||||||| ||||||||    ||||
                                AGATAG AACCGTAA    CAAG
                                   _      CACAC
GAM1727 EXTL2   3' CTAAAGAGGCATTTCAGGTT  11018    TCGTT      A
                                CTA    GGCATTTCA GTT
                                |||    ||||||||| |||
                                GAT    CCGTAAAGT CAA
                                  TTCT_       C
GAM1727 MYCL1   3' TATTATTGGCATTTTAAAGT  23890    CG      C_
                                TAT  TTGGCATTT  AAGT
                                |||  |||||||||  ||||
                                ATA  AACCGTAAA  TTCA
                                  AT       AT
GAM1727 SOCS5   3' TCTTGGAGTTTCAAGTT    30424   G   CA
                                TC TTGG  TTTCAAGTT
                                || ||||  |||||||||
                                AG AACC  AAAGTTCAA
                                 _   TC
GAM1727 SPOCK   3' TATCATTGTTTTTCGAGTT   41742       GCA   A
                                TATCGTTG   TTTC AGTT
                                ||||||||   |||| ||||
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                                ATAGTAAC   AAAG TCAA
                                     AA_    C
GAM1727  GRP58    3'  TTCCATAAACAGTGCAGCTAA  23680          A   TAT
                                TTCCATAAATA TGC   TTGA
                                |||||||||| |||   ||||
                                AAGGTATTTGT ACG   GATT
                                      C   TC_
GAM1728  SS18     3'  TTGAGACCAAAACAATCAA    24844      AT       _
                                TTGA  CCAAAACA TCAG
                                ||||  |||||||| ||||
                                AACT  GGTTTTGT AGTT
                                  CT       T
GAM1728  TLX1     5'  TTGACTCTGGGACATCAATCA  24352      A  CAAA
                                TTGA TC    ACATCAGTTA
                                |||| ||    ||||||||||
                                AACT AG    TGTAGTTAGT
                                  G  ACCC
GAM1728  FUT8     3'  TACTAAAGAATTTGTTCAT    20998     C         _
                                TAC AAAGGATTTGT CAT
                                ||| |||||||||| |||
                                ATG TTTCTTAAACA GTA
                                  A          A
GAM1728  GABRP    3'  ACCGAGGGATTTGTTTAGATTG 30552     AAA       CA  AG
                                ACC   GGATTTGT  TA  TTG
                                |||   ||||||||  ||  |||
                                TGG   CCTAAACA  AT  AAC
                                  CTC       A_  CT
GAM1728  IDH3A    3'  CCAAAGGAGGCCATGAGTTG   24372         TTT    A
                                CCAAAGGA   GTCAT AGTTG
                                ||||||||   ||||| |||||
                                GGTTTCCT   CGGTA TCAAC
                                     C__     C
GAM1728  WBSCR1   3'  TACTGAAGGATTTTTCAT    35272     CA       G
                                TAC  AAGGATTT TCAT
                                |||  |||||||| ||||
                                ATG  TTCCTAAA AGTA
                                  AC       A
GAM1729  ADCY7    3'  AACTTTACGGGGTTCATGGGGA 9977          A  AAC_   T
                                AACTTTATG GG    TGG GA
                                ||||||||| ||    ||| ||
                                TTGAAATGC CC    ACC CT
                                      C  AAGT   C
GAM1729  ASPH     5'  TCCGCGGGGGCTGGTGAG    37140    TA  A  AA
                                TT  TG GG  CTGGTGAG
                                ||  || ||  ||||||||
                                AG  GC CC  GACCACTC
                                 GC  _  CC
GAM1729  ATRN     3'  CTTTATGAGAGGTGAG      40272          AACT
                                CTTTATGAGG    GGTGAG
                                ||||||||||    ||||||
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                                GAAATACTCT   CCACTC
                                      ____
GAM1729 BLAME    3' ACTTTATGAATAGTGGTG   33483        GAAC
                                ACTTTATGAG   TGGTG
                                ||||||||||   |||||
                                TGAAATACTT   ACCAC
                                     ATC_
GAM1729 CLCN1    3' CTTTATGAGGAGGTCGTGGGAG 6352          AC___  T
                                CTTTATGAGGA    TGG GAG
                                ||||||||||     ||| |||
                                GAAATACTCCT    ACC CTC
                                      CCAGC  _
GAM1729 DTR      3' AACTTATGAGGGGAAGTG    12608      T    AACT
                                AACTT ATGAGG   GGTG
                                ||||| ||||||   ||||
                                TTGAA TACTCC   TCAC
                                   _    CCT_
GAM1729 EZH2     3' ACTTTGCAGCTGGTGAGAA   20876      ATGA  AA
                                ACTTT   GG  CTGGTGAGAA
                                |||||   ||  ||||||||||
                                TGAAA   TC  GACCACTCTT
                                   CG__  __
GAM1729 HLA-A    3' TTTAAGAGGGAAGTAAGAA   44861     T   AACT
                                TTTA GAGG   GGTGAGAA
                                |||| ||||   ||||||||
                                AAAT CTCC   TCATTCTT
                                  T   CT__
GAM1729 HLALS    3' ACTCTATGGGGGACAGAGGA  11356       A  A  T  T
                                ACTTTATG GG AC GG GA
                                |||||||| || || || ||
                                TGAGATAC CC TG CT CT
                                     C  C  T  C
GAM1729 KCNJ10   3' AACTTCATGGTGGTGGTGGGA 13865        A_  AAC    A
                                AACTTTATG  GG   TGGTG GA
                                |||||||||  ||   ||||| ||
                                TTGAAGTAC  CC   ACCAC CT
                                     CA  ___    C
GAM1729 LPXN     3' TTTATAAGGAATCTGAAGAG  22069          _   T
                                TTTATGAGGAA CTGG GAG
                                |||||||||| |||| |||
                                AAATATTCCTT GACT CTC
                                      A   T
GAM1729 LRP4     3' CTCTACGCTGGTGAG      42061       AGGAA
                                CTTTATG    CTGGTGAG
                                |||||||    ||||||||
                                GAGATGC    GACCACTC
                                     _____
GAM1729 NDUFA2   3' CTTTATGAGGAATAGGAGAA  14738          C   T
                                CTTTATGAGGAA TGG GAGAA
                                |||||||||||| ||| |||||
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                                GAAATACTCCTT ATC CTCTT
                                             _  _
GAM1729 NR1I2    5' CTTTATGGCAGGTGAG     35101       GA  AACT
                                CTTTAT  GG   GGTGAG
                                ||||||  ||   ||||||
                                GAAATA  CC   CCACTC
                                   __ GT__
GAM1729 UVRAG    3' TTTATAAACCATGGTGAG    17909       GAAC
                                TTTATGAG   TGGTGAG
                                ||||||||   |||||||
                                AAATATTT   ACCACTC
                                     GGT_
GAM1729 ZNF146   3' TTTATGAGGAAACTTTTAA   28361         _ GG
                                TTTATGAGGAA CT  TGA
                                |||||||||| ||  |||
                                AAATACTCCTT GA  ATT
                                       T  AA
GAM1730 INMT     3' CATACTTAACCTTATAGA    27674        TATA
                                TATACTTAAC   CTTATAGA
                                |||||||||    ||||||||
                                GTATGAATTG   GAATATCT
                                             ____
GAM1730 PRKCN    3' TACTGAACAGTCATTATAGACT 25161     T   TATAC
                                TACT AAC    TTATAGACT
                                |||| |||    |||||||||
                                ATGA TTG    AATATCTGA
                                  C  TCAGT
GAM1731 CD74     3' CCTTGCTGCATTGTTATCTGCT 20337       AATAGGC    A
                                TCTTGCTG     TATCT CT
                                ||||||||     ||||| ||
                                GGAACGAC     ATAGA GA
                                     GTAACA_    C
GAM1731 LEF1     3' CTGCTGAACGCATCT      32207        AG  T
                                TTGCTGAAT  GC ATCT
                                |||||||||  || ||||
                                GACGACTTG  CG TAGA
                                             __ _
GAM1731 MUCDHL   3' TCTTGCTGAGGGGCATCGGCT  36321        ATA  T  TA
                                TCTTGCTGA  GGC ATC  CT
                                |||||||||  ||| |||  ||
                                AGAACGACT  CCG TAG  GA
                                     CC_  _  CC
GAM1731 RAD17    5' TCTCGCTGGAAATCTGCT    39414       __  AG
                                TCTTGCTG  AAT  GCT
                                ||||||||  |||  |||
                                AGAGCGAC  TTA  CGA
                                     CT   GA
GAM1731 TPM4     3' TCCTGCTGAGTGGGTCATTACT 17649       ATA  C   C
                                TCTTGCTGA  GG TAT TACT
                                |||||||||  || ||| ||||
```

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                                AGGACGACT   CC GTA ATGA
                                     CAC  A   _
GAM1731  VIM      3'  TCTTGCTGGTAATATATTGCT  45228        __    G___
                                TCTTGCTG  AATA    GCT
                                ||||||||  ||||    |||
                                AGAACGAC  TTAT    CGA
                                     CA    ATAA
GAM1731  ART3     5'  CAAGTCTTCAGGATGGGAT   10137        CAC   T
                                TAAGTCT   TGG GATGGGAT
                                |||||||   ||| ||||||||
                                GTTCAGA   GTC CTACCCTA
                                    A__   _
GAM1731  ATP8A2   3'  GTCTAACACTGATGGGATAC   45264      C  T G
                                GTCT AC G TGATGGGATAC
                                |||| || | ||||||||||
                                CAGA TG T ACTACCCTATG
                                  T  _ G
GAM1731  GEM      5'  GTCCGCGCTGGGATA       23547      CACTG   A
                                GTCT    GTG TGGGATA
                                ||||    ||| |||||||
                                CAGG    CGC ACCCTAT
                                  _____   G
GAM1731  SWAP70   3'  TAAGTCTCGTTGGTCTAATAC  43425         AC    GATGG
                                TAAGTCTC  TGGT    GATAC
                                ||||||||  ||||    |||||
                                ATTCAGAG  ACCA    TTATG
                                     CA    GA___
GAM1732  GNG5     3'  TATTATGGCACATGTGTTACA  23610          _    A
                                TATTATGGCA ATGT TTACA
                                |||||||||| |||| |||||
                                ATAATACCGT TACA AATGT
                                      G   C
GAM1732  SLC22A3  3'  TTATACAGTATTACAACA    35055       G  AT
                                TTATG CA  GTATTACAACA
                                ||||| ||  ||||||||||
                                AATAT GT  CATAATGTTGT
                                  _  __
GAM1732  ADRA1A   3'  CAGTAACAGTAACATGT     37805        GT    T
                                CAGTAA  TGGT AACATGT
                                ||||||  |||| |||||||
                                GTCATT  GTCA TTGTACA
                                  __    _
GAM1732  BDKRB2   3'  TATACAGCAAGTGCTCAATATG 8407            T G    C
            T                    TATACAGTAAGT G TTAA ATGT
                                ||||||||||| | |||| ||||
                                ATATGTCGTTCA C AGTT TACA
                                      _ G    A
GAM1732  MSR1     3'  GTAGGTGTTAACATGT      14661      A  TG
                                GTA GT  GTTAACATGT
                                ||| ||  ||||||||||
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                                CAT CA  CAATTGTACA
                                  C  __
GAM1732  NAGA     3'  TATACAGCAAGTAAAGACATGT 7042            TGGTTA
                                TATACAGTAAGT     ACATGT
                                ||||||||||||     ||||||
                                ATATGTCGTTCA     TGTACA
                                       TTTC__
GAM1732  TTN      3'  TATACAGTATGTACAT      39422          A  TGGTTA
                                TATACAGTA GT     ACAT
                                ||||||||| ||     ||||
                                ATATGTCAT CA     TGTA
                                     A  _______
GAM1733  DMD      5'  TGCCGTGAATAGTGAGGT    19696      AT   TAT
                                TGCT  GTG   ATAGTGAGGT
                                ||||  |||   ||||||||||
                                ACGG  CAC   TATCACTCCA
                                  __   T__
GAM1733  EHD3     3'  TGCATATGTGTGTGTGCAT   31117     _     ATATA   AG
                                TGC TATGTGT    GTG  GTAT
                                ||| |||||||    |||  ||||
                                ACG ATACACA    CAC  CGTA
                                  T      ______   A_
GAM1733  IL20RA   3'  TGCTATGTGCATATGGGAAGT  30882            AGT
                                TGCTATGTGTATAT   GAGGT
                                ||||||||||||||   |||||
                                ACGATACACGTATA   CTTCA
                                       CC_
GAM1733  KAL1     3'  TGTCTGTGTGTATATACATGTA 6877     _  A        GTGAG
              T                  TG CT TGTGTATATA     GTAT
                                || || ||||||||||     ||||
                                AC GA ACACATATAT     CATA
                                 A  C         GTA__
GAM1733  KCNJ3    3'  TGTATGTGTATGTATGTG    13853    C        A  _
                                TG TATGTGTAT TA GTG
                                || |||||||| || |||
                                AC ATACACATA AT CAC
                                 _        C  A
GAM1733  KLRF1    5'  TGTGTATACAGGTA       32414          AGTG
                                TGTGTATAT    AGGTA
                                |||||||||    |||||
                                ACACATATG    TCCAT
                                      ____
GAM1733  PCP4     3'  TGCTATGCGTGTGTGG      26232          ATATA   A
                                TGCTATGTGT    GTG GG
                                ||||||||||    ||| ||
                                ACGATACGCA    CAC CC
                                      ______  A
GAM1733  PPAT     3'  TGTATGTGTACATGTA      15487    C         A
                                TG TATGTGTATAT GTG
                                || ||||||||||| |||
```

```
                                AC ATACACATGTA CAT
                                 _       _
GAM1733  TAT      3'  TGTGTAAAGTGAGGTA      7403        TAT
                                TGTGTA   AGTGAGGTA
                                ||||||   |||||||||
                                ACACAT   TCACTCCAT
                                   T__
GAM1733  VIPR1    3'  TGTATGTGTAGCAGGGTGAGGT 21518    C       _  TA
              AT                  TG TATGTGTA TA  GTGAGGTAT
                                || ||||||||  ||  |||||||||
                                AC ATACACAT GT  CACTCCATA
                                 _      C  CC
GAM1733  IL1RN    3'  TATTGTAAAACAGAGC      8215            ACC
                                TATTGTAAAACA   AGC
                                ||||||||||||   |||
                                ATAACATTTTGT   TCG
                                       C__
GAM1733  KCNAB1   3'  TATATTATAAAATCCCAG    41405           CAA
                                TATATTGTAAAA   CCAG
                                ||||||||||||   ||||
                                ATATAATATTTT   GGTC
                                       AG_
GAM1734  COL6A2   3'  CGGCCTAGAGCTCCTCCTCGGG 38439       CA___       AA
              C                   CGGTC    CTCCTCCTC  GC
                                |||||    |||||||||  ||
                                GCCGG    GAGGAGGAG  CG
                                   ATCTC        CC
GAM1734  EPAC     5'  CCCACCTTCATGTTTCTTTTCA 25916       GG  CACTC_  CC
              AGC                   TCCAC  TC     CT  TCAAGC
                                |||||  ||     ||  ||||||
                                GGGTG  AG     GA  AGTTCG
                                   GA  TACAAA  AA
GAM1734  KCNJ5    3'  GGTTCCTCCCCACAGC      9438      CCAC        _
                                GGT    TCCTCCTCA AGC
                                |||    ||||||||| |||
                                CCA    AGGAGGGGT TCG
                                  _____        G
GAM1734  KCNK7    3'  TCCTGGCTGCTTCCTCCTCA   37860     AC   CCAC
                                TCC  GGT    TCCTCCTCA
                                |||  |||    |||||||||
                                AGG  CCG    AGGAGGAGT
                                  A_   ACGA
GAM1734  NFATC3   5'  GCTGCAGCTCCTCCTCAGGC   21252    C_  _        A
                                GT  CA CTCCTCCTCA GC
                                ||  || ||||||||||  ||
                                CG  GT GAGGAGGAGT CG
                                 AC  C         C
GAM1734  RANBP3   5'  GGGGCTCTTTCTCCTCAAG    28763    TCCA  ___
                                GG    CTC   CTCCTCAAG
                                ||    |||   |||||||||
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                                CC   GAG  GAGGAGTTC
                                 CC__  AAA
GAM1734  RBM6    5'  TCCACGGCCCGCTCCTCC   25105         A
                                TCCACGGTCC CTCCTCC
                                |||||||||| |||||||
                                AGGTGCCGGG GAGGAGG
                                      C
GAM1734  TACC1   5'  TCCTGTGGCCTCCTCAG    26603    AC_  TCCACT      A
                                TCC  GG    CCTCCTCA G
                                |||  ||    |||||||| |
                                AGG  CC    GGAGGAGT C
                                  ACA _______      C
GAM1735  ADCY6   5'  TTAGCCTGGGCCAGGCG    34182       GAA    CA
                                TTAGTCT  GGGTCA  GCG
                                |||||||  ||||||  |||
                                AATCGGA  CCCGGT  CGC
                                   ___     C_
GAM1735  DIO3    3'  TCAGTCTGAAATGGTGGC    10694          _  CACA
                                TTAGTCTGAAG GGT   GC
                                |||||||||| |||   ||
                                AGTCAGACTTT CCA   CG
                                      A  C___
GAM1736  ECM2    3'  TCTGTGTGTTAGTGAATCAG  10812       _ GCCTTA
                                TCTGTG GT    TGAATCAG
                                |||||| ||    ||||||||
                                AGACAC CA    ACTTAGTC
                                   A  ATC___
GAM1736  IAPP    3'  TCTGTGGTCTTTTAATTGAAGA 7666        GC  A  ATC_
            C                    TCTGTGGT  CTT TGA   AGAC
                                |||||||  ||| |||   ||||
                                AGACACCA  GAA ATT   TCTG
                                    __  A  AACT
GAM1736  IL17    3'  TGTGGTGCCTTGATCAGAC   13535         TA  A
                                TGTGGTGCCT  TGA TCAGAC
                                ||||||||||  ||| ||||||
                                ACACCACGGA  ACT AGTCTG
                                    __  _
GAM1736  MBP     3'  TCTGTGCTGCCCCACGTTGGAC 44895       G       AATCA
                                TCTGTG TGCCTTATG    GAC
                                |||||| |||||||||    |||
                                AGACAC ACGGGGTGC    CTG
                                   G       AAC__
GAM1736  SELP    3'  TGGTCTTCTTGTGAGTCAGA  16553     GC_  A  A
                                TGGT  CTT TGA TCAGA
                                ||||  ||| ||| |||||
                                ACCA  GAA ACT AGTCT
                                  GAA  C  C
GAM1736  AOC3    3'  TTCAGTGTCCCCTGTG      19024     T  CTA
                                TTCA GTG  CCTCTGTG
                                |||| |||  ||||||||
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```
                                AAGT CAC   GGGGACAC
                                  _  A__
GAM1736 ARNT2    3' CTCTGTGTCTCTGTG      31356     A   CTAC
                                TTC TGTG   CTCTGTG
                                ||| ||||   |||||||
                                GAG ACAC   GAGACAC
                                  _   A___
GAM1736 ATP11A   3' TCCATGTGCATCTGTG     44184        TACC
                                TTCATGTGC   TCTGTG
                                |||||||||   ||||||
                                AGGTACACG   AGACAC
                                     T___
GAM1736 CASP4    5' TGTGATTTCTGCCTCTGTG   37821     ____ A
                                TGTG   CT CCTCTGTG
                                ||||   || ||||||||
                                ACAC   GA GGAGACAC
                                  TAAA  C
GAM1736 DLEC1    3' TTCATGCGCCATGT       28841         CCTC
                                TTCATGTGCTA   TGT
                                ||||||||||   |||
                                AAGTACGCGGT   ACA
                                      ____
GAM1736 F7       3' TCCATGTGTATATCTGTG    6560        C  CC
                                TTCATGTG TA  TCTGTG
                                |||||||| ||  ||||||
                                AGGTACAC AT  AGACAC
                                     _ AT
GAM1736 FKBP10   3' CTCGCAGTGGGCCTCTGTG   34958    AT_  CTA
                                TTC   GTG   CCTCTGTG
                                |||   |||   ||||||||
                                GAG   CAC   GGAGACAC
                                  CGT   CC_
GAM1736 FKBP1B   3' TTCATGTCTGAGCACCTTGTG 38335       ____ T   C
                                TTCATGT   GC ACCT TGTG
                                |||||||   || |||| ||||
                                AAGTACA   CG TGGA ACAC
                                    GACT  _   _
GAM1736 FOXO1A   3' CTCATGTGAATTCTGTG     12885        CTACC
                                TTCATGTG    TCTGTG
                                ||||||||    ||||||
                                GAGTACAC    AGACAC
                                     TTA__
GAM1736 GDF5     3' TTCCTGACCCCTCTGTG     8149     A  T   A
                                TTC TG GCT CCTCTGTG
                                ||| || ||| ||||||||
                                AAG AC TGG GGAGACAC
                                  G  _   _
GAM1736 HHLA1    5' TTCATGTGCGTCCGTG      25055        TACC
                                TTCATGTGC   TCTGTG
                                |||||||||   ||||||
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                                AAGTACACG   AGGCAC
                                     C___
GAM1736 HRH1    3' TCCATGTGCTATACATATTGTG 9256          CCTC___
                                TTCATGTGCTA     TGTG
                                ||||||||||      ||||
                                AGGTACACGAT     ACAC
                                      ATGTATA
GAM1736 HSD17B3 3' TTCTATGCCTCTGTG      6810     A    TAC
                                TTC TGTGC  CTCTGTG
                                ||| |||||  |||||||
                                AAG ATACG  GAGACAC
                                  _   ___
GAM1736 IARS    3' TTCATGTGTGTGTCTATG    30202       CTACC
                                TTCATGTG    TCTGTG
                                ||||||||    ||||||
                                AAGTACAC    AGATAC
                                     ACAC_
GAM1736 IKBKB   3' TTCTGTCCCTCCTCTGTG    41814    A  G  A
                                TTC TGT CT CCTCTGTG
                                ||| ||| || ||||||||
                                AAG ACA GG GGAGACAC
                                  _  G  A
GAM1736 KCNK10  5' TTCTGTCTCCCTCTGTG     39685    A  G  A
                                TTC TGT CT CCTCTGTG
                                ||| ||| || ||||||||
                                AAG ACA GA GGAGACAC
                                  _  _ G
GAM1736 LIF     3' CTCAAGTACCTCTGTG      14143     T  GCT
                                TTCA GT   ACCTCTGTG
                                ||||  ||  |||||||||
                                GAGT CA   TGGAGACAC
                                  T  ___
GAM1736 LIG4    5' CTCCGTTACCTCTGTG      14164    A  GC
                                TTC TGT  TACCTCTGTG
                                ||| |||  ||||||||||
                                GAG GCA  ATGGAGACAC
                                  _  __
GAM1736 PX19    3' TCACCGCACCTCTGTG      29875     G  T
                                TCAT TGC ACCTCTGTG
                                |||| ||| |||||||||
                                AGTG GCG TGGAGACAC
                                  _  _
GAM1736 SCML1   3' CTCATCCTACCTCTGTG     27560      GTG
                                TTCAT   CTACCTCTGTG
                                |||||   ||||||||||
                                GAGTA   GATGGAGACAC
                                   G__
GAM1736 SULT1C1 3' TTCTGACATCTCCTCTGTG   9844     A  TG__  A
                                TTC TG    CT CCTCTGTG
                                ||| ||    || ||||||||
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                                AAG AC    GA GGAGACAC
                                  _ TGTA  _
GAM1736 TBL1X    5' TTCATGTATGGACCTGTG    24900        CTACC
                                TTCATGTG    TCTGTG
                                ||||||||    ||||||
                                AAGTACAT    GGACAC
                                    ACCT_
GAM1736 TRIM     3' TTCTGTGTCCTCTGTG     32305     A    CTA
                                TTC TGTG   CCTCTGTG
                                ||| ||||   ||||||||
                                AAG ACAC   GGAGACAC
                                  _   A__
GAM1736 TRPM7    3' CTCATACCTCTGTG       41618     TGTGC
                                TTCA    TACCTCTGTG
                                ||||    ||||||||||
                                GAGT    ATGGAGACAC

                                 _____
GAM1736 VSX1     3' TTCATGTGTCTGTA       31098        CTACC
                                TTCATGTG    TCTGTG
                                ||||||||    ||||||
                                AAGTACAC    AGACAT

                                 _____
GAM1736 ZNF236   3' TTCATGTGCAGCTTCATG    28872        TAC  CT
                                TTCATGTGC   CT  GTG
                                |||||||||   ||  |||
                                AAGTACACG   GA  TAC
                                    TC_  AG
GAM1737 ABCD2    3' AAAGTGCATGATTAGGGCAAGT 23145         TATCAATTTT
            C                    AAAGTGCATG        AGTC
                                ||||||||||        ||||
                                TTTCACGTAC        TCAG
                                    TAATCCCGT_
GAM1737 CD8A     3' AAGTGCATGTTTGGGACAGCAG 12086         ATCA_  TT
            T                    AAGTGCATGT    AT  TAGT
                                ||||||||||    ||  ||||
                                TTCACGTACA    TG  GTCA
                                    AACCC  TC
GAM1737 CDK2AP1  3' AAAGATGCAAACAGTTTTAGTC 21592      _   TGTAT  A
                                AAAG TGCA    CA TTTTAGTC
                                |||| ||||    ||  ||||||||
                                TTTC ACGT    GT AAAATCAG
                                  T   TT___  C
GAM1737 DGUOK    3' AGTGCAGGCCCAATTTTGGTC  38959       T  A       A
                                AGTGCA GT TCAATTTT GTC
                                |||||| ||  |||||||| |||
                                TCACGT CG GGTTAAAA CAG
                                   C  _       C
GAM1737 RPIP8    3' AAAGTGCATGCGTTGAAGT   27448          ATCAATTTT
                                AAAGTGCATGT       AGT
                                ||||||||||        |||
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                                TTTCACGTACG        TCA
                                      CAACT_____
GAM1738  CACNA1D   5'  TGAGCGACTACTGTGTGCA   8767      ACC_   G
                                TGA    TTGC TGTGTGCA
                                |||    |||| ||||||||
                                ACT    GATG ACACACGT
                                  CGCT    _
GAM1738  CD34      3'  CCTCTGAGGTGTGTGC      12114        ACCTTGC
                                TCTCTGA      GTGTGTGC
                                |||||||      ||||||||
                                GGAGACT      CACACACG
                                    C_______
GAM1738  CYLN2     3'  CCTCTGTGTGTGTGTG      18048        AACCT  C
                                TCTCTG     TG GTGTGTG
                                ||||||     || |||||||
                                GGAGAC     AC CACACAC
                                   ______  A
GAM1738  LDHB      5'  TCTTTGTGCTTTGCATGTG   14122     C  AACC
                                TCT TG    TTGCGTGTG
                                ||| ||    |||||||||
                                AGA AC    AACGTACAC
                                  A  ACGA
GAM1738  MLLT2     3'  TGAGGCTTCCAATGTGCAA   25513     AC   G  T
                                TGA  CTT CG GTGTGCAA
                                |||  ||| || ||||||||
                                ACT  GAA GT TACACGTT
                                  CC   G  _
GAM1738  RAB36     3'  TCCTGTCCGTGTGTGTGCA   22247    T   AA  TT C
                                TC CTG  CC  G GTGTGTGCA
                                || |||  ||  | |||||||||
                                AG GAC  GG  C CACACACGT
                                 _   A_  __ A
GAM1738  RAG2      5'  TCTCTGAATCTTTGCCGC    44368         C  _  G
                                TCTCTGAA CTT GC TGT
                                |||||||| ||| || |||
                                AGAGACTT GAA CG GCG
                                     A   A  _
GAM1738  SLC6A3    3'  CCTCTGAACAGACTGTGTGTGC 9808          CTT  _
              AA                  TCTCTGAAC   GC GTGTGTGCAA
                                |||||||||   || ||||||||||
                                GGAGACTTG   TG CACACACGTT
                                    TC_  A
GAM1738  ADORA1    3'  CAACACTGAGTCCTTAC     8588          A  GG
                                TAACACTGAG CT  TAC
                                |||||||||| ||  |||
                                GTTGTGACTC GG  ATG
                                     A  A_
GAM1738  AP2B1     3'  TAACACTGCTAAACAGGCTGGT 10491         _______  A
              A                  TAACACTG     AG CTGGTA
                                ||||||||     || ||||||
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                                ATTGTGAC     TC GACCAT
                                     GATTTG  C
GAM1738 ATP6V1A1 3' CAACACTGGAAAAATAC     11778        A  CT
                                TAACACTG GA  GGTAC
                                |||||||| ||  |||||
                                GTTGTGAC CT  TTATG
                                     _  TT
GAM1738 ATP8A2   3' TAACACTGATGGGATAC     45265        GACT
                                TAACACTGA    GGTAC
                                |||||||||    |||||
                                ATTGTGACT    CTATG
                                     ACC_
GAM1738 DAPK1    3' AACACTGAGAGGAGGTAC    22353         CT_
                                AACACTGAGA   GGTAC
                                ||||||||||   |||||
                                TTGTGACTCT   CCATG
                                      CCT
GAM1738 FKBP1A   3' TAACACTGAAAGGATAC     38282         CT
                                TAACACTGAGA  GGTAC
                                ||||||||||| |||||
                                ATTGTGACTTT  CTATG
                                      C_
GAM1738 GAN      3' CAACAGCTGACTGGTAC     35139      _  GA
                                TAACA CT  GACTGGTAC
                                ||||| ||  |||||||||
                                GTTGT GA  CTGACCATG
                                   C  __
GAM1738 HLCS     5' CAACAACCCACTGGTAC     7637       _  GAG
                                TAACA CT   ACTGGTAC
                                ||||| ||   ||||||||
                                GTTGT GG   TGACCATG
                                   T  G__
GAM1738 ITGA11   3' CAACACTACCTGGACTGGT   29194        A___
                                TAACACTG   GACTGGT
                                ||||||||   |||||||
                                GTTGTGAT   CTGACCA
                                     GGAC
GAM1738 MNT      3' ACACTGAAGGCCACTGGT    33699        _____
                                ACACTGAG   ACTGGT
                                ||||||||   ||||||
                                TGTGACTT   TGACCA
                                     CCGG
GAM1738 SIP      3' CAAAACTAACTGGTAC      30842     C   GA
                                TAA ACT  GACTGGTAC
                                ||| |||  |||||||||
                                GTT TGA  TTGACCATG
                                  T  __
GAM1738 SLC25A17 3' CAACACTGAGACATAC      26824          TG
                                TAACACTGAGAC  GTAC
                                ||||||||||||  ||||
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                                GTTGTGACTCTG  TATG
                                      __
GAM1738  SUDD     3'  TAACACTGAAGCAGTGGGTA   19262         _ ACT__
                                TAACACTGA G     GGTA
                                |||||||||  |     ||||
                                ATTGTGACT C     CCAT
                                     T GTCAC
GAM1738  T        3'  TAACCTGAGACTGCCAC     17248      A       G
                                TAAC CTGAGACTG TAC
                                |||| ||||||||| |||
                                ATTG GACTCTGAC GTG
                                  _       G
GAM1738  TEM6     3'  TAACACTGGAGGAATAC     35558        A  CT
                                TAACACTG GA  GGTAC
                                ||||||||  ||  |||||
                                ATTGTGAC CT  TTATG
                                     _  CC
GAM1738  TFAP2C   3'  TAACACTGAAAAAAAAGGTA   17406          CT___
                                TAACACTGAGA     GGTA
                                ||||||||||     ||||
                                ATTGTGACTTT     CCAT
                                       TTTTT
GAM1739  PAH      3'  TATACAGATTTGCTTTTC     7096            A   A
                                TATACAGATTTG TTT TC
                                ||||||||||| ||| ||
                                ATATGTCTAAAC GAA AG
                                     _   A
GAM1739  RNTRE    3'  ACAGATGCCTATATCTATTA   31243       TTGATT
                                ACAGAT     TATCTATTA
                                ||||||     |||||||||
                                TGTCTA     ATAGATAAT
                                   CGGAT_
GAM1739  CALB2    3'  CCTTCCATGTGTGTGATCCACT 11935           ATAAG
                                CTTTCCATGTGT     CTATT
                                ||||||||||     |||||
                                GGAAGGTACACA     GGTGA
                                       CACTA
GAM1739  CD33     3'  TTTCCATGTGTACCTTTATTTA 43945           AAGC
                                TTTCCATGTGTAT    TATTTA
                                ||||||||||||    ||||||
                                AAAGGTACACATG    ATAAAT
                                       GAA_
GAM1739  DNTT     3'  CTTCCCATGTTTCCAAAGTTAT 43817          GTAT_  C
              TTA                 CTTTCCATGT     AAG TATTTA
                                ||||||||||     ||| ||||||
                                GAAGGGTACA     TTC ATAAAT
                                      AAGGT   A
GAM1739  LECT2    5'  TTCCATGGATAGCTATTT     14130        TG ATA
                                TTCCATG  T   AGCTATTT
                                |||||||  |  ||||||||
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                                AAGGTAC  A   TCGATAAA
                                    CT ___
GAM1739  MDM1     3'  TTTCAAGTGTCAAACTATTTA  33521     CAT   A
                                TTTC   GTGT TAAGCTATTTA
                                ||||   |||| ||||||||||
                                AAAG   CACA GTTTGATAAAT
                                  TT_   _
GAM1739  MTMR2    3'  CTTCTCACTATAAGCTATTTA  32066    TC   GTG
                                CTT  CAT   TATAAGCTATTTA
                                |||  |||   ||||||||||||
                                GAA  GTG   ATATTCGATAAAT
                                  GA   ___
GAM1739  ZNF268   3'  CTTTCCATGCGTGCCAC     41762          ATAA
                                CTTTCCATGTGT    GCTAT
                                ||||||||||||    |||||
                                GAAAGGTACGCA    CGGTG
                                                _____
GAM1740  DYT1     3'  TCTATGTAATAATGATGAGAAC 6478           AAC  TT
                                TCTATGTAATAAT   GA  AC
                                ||||||||||||   ||  ||
                                AGATACATTATTA   CT  TG
                                        CTA  CT
GAM1740  XK       3'  TCTATGCACATATGTGATTACA 34371        ATAATAAC
              T                  TCTATGTA       GATTACAT
                                 ||||||||       ||||||||
                                 AGATACGT       CTAATGTA
                                     GTATACA_
GAM1740  STK18    3'  GTCAACAAAAAAGTTATTTATT 30684     T
                                GTTA ATAAAAAAGTTATTTATT
                                |||| ||||||||||||||||||
                                CAGT TGTTTTTTCAATAAATAA
                                  _
GAM1741  FGF2     3'  TCTAGGTAAGCTTCACTGGGT  12844          AGA   CA
                                TCTAGGTAAGTTT   GCT  GGT
                                ||||||||||||   |||  |||
                                AGATCCATTCGAA   TGA  CCA
                                        G__   C_
GAM1741  FLT1     3'  GGTTACTTAGAGCTCAGGT   12913     AAG
                                GGT   TTTAGAGCTCAGGT
                                |||   ||||||||||||||
                                CCA   GAATCTCGAGTCCA
                                  AT_
GAM1741  HMGA2    3'  AGGTAAGTGGTATTCAGGT   18503        TTAGAGC
                                AGGTAAGT      TCAGGT
                                ||||||||      ||||||
                                TCCATTCA      AGTCCA
                                    CCATA__
GAM1741  BLAME    3'  TCTTTTAGAGCCTAGGACTC  33497    CC        CCTA
                                TC  TTAGAGCCTA   GACTC
                                ||  ||||||||||   |||||
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                                AG  AATCTCGGAT   CTGAG
                                 AA        C___
GAM1741  EGFL5    5'  CTCCCTTAGAAGCTTATCCT   44522         _ C _
                                CTCCCTTAGA GC TA CCT
                                |||||||||| || || |||
                                GAGGGAATCT CG AT GGA
                                      T  A  A
GAM1741  KCNA3    3'  CTCCTTAGAGTCTCAGACT   13795     C     C  ACC
                                CTCC TTAGAG CT   TAGACT
                                |||| |||||| ||   ||||||
                                GAGG AATCTC GA   GTCTGA
                                  _     A ___
GAM1741  LAMC2    3'  CTGCCTTAGAGCAGC      33113    C       CTACCT  A
                                CT CCTTAGAGC     AG C
                                || |||||||||     || |
                                GA GGAATCTCG     TC G
                                 C        _______ C
GAM1741  PPP2R5B  5'  CTCGAAAACCTAGACT     26446    TA   CCT
                                CT  GAG   ACCTAGACT
                                ||  |||   |||||||||
                                GA  TTT   TGGATCTGA
                                 GC  ___
GAM1741  TGFB1    3'  CTCCCTTAACCTCTCT     8539        GA    AC
                                CTCCCTTA  GCCT  CT
                                ||||||||  ||||  ||
                                GAGGGAAT  TGGA  GA
                                     __   GA
GAM1741  TPK1     3'  TCCCCTAGAGAGGTTTAGATTC 35356         CCTACC   C
                                TCCCTTAGAG     TAGA TC
                                ||||||||||     |||| ||
                                AGGGGATCTC     ATCT AG
                                      TCCAA_   A
GAM1741  XRCC2    3'  TCCCCTAGAGTTTAAAACT   24095         CCTACCT
                                TCCCTTAGAG      AGACT
                                ||||||||||      |||||
                                AGGGGATCTC      TTTGA
                                      AAAT___
GAM1742  ADAM10   5'  CTGCCGCCGCCCATGG      9970         TCCC
                                CTGCCGCC   GCCTGTGG
                                ||||||||   ||||||||
                                GACGGCGG   CGGGTACC
                                     _____
GAM1742  ADAM10   5'  CCGCCGCCTCCTCACGGGT   9968          _  CT T
                                CTGCCGCCTCC CGC  G GGT
                                |||||||||| |||  | |||
                                GGCGGCGGAGG GTG  C CCA
                                      A  __ _
GAM1742  APLP2    3'  GCCGCCTCCTTGGTGTGGT   44921         CGCC
                                GCCGCCTCC   TGTGGT
                                |||||||||   ||||||
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                                CGGCGGAGG   ACACCA
                                     AACC
GAM1742 ARAF1    5' CTGTCGCCCCCTGCAGCCT   41909    C     C___
                                CTG CGCCTCC   GCCT
                                ||| |||||||   ||||
                                GAC GCGGGGG   CGGA
                                  A      ACGT
GAM1742 ATF4     5' CTGCCGCCGCCATCTTGGT   11723       TCCC  TG__
                                CTGCCGCC   GCC   TGGT
                                ||||||||   |||   ||||
                                GACGGCGG   CGG   ACCA
                                     ____  TAGA
GAM1742 ATP2B2   5' CTGCCGCTGCCGCTGG     11759       CTC   CTG
                                CTGCCGC   CCGC   TGG
                                |||||||   ||||   |||
                                GACGGCG   GGCG   ACC
                                   AC_   ___
GAM1742 BAX      5' CCGCCGCCTCTCGCCGGGT   39871        C   T T
                                CTGCCGCCTC CGCC G GGT
                                |||||||||| |||| | |||
                                GGCGGCGGAG GCGG C CCA
                                     A   _ _
GAM1742 BTAF1    5' CTGCCGCCTACCCGAGCT    43665        _   C_
                                CTGCCGCCT CCCG  CT
                                |||||||| ||||  ||
                                GACGGCGGA GGGC  GA
                                     T   TC
GAM1742 CAPS     3' CTGCCCCTCCCCGCTCTGTGGT 19760      G    _ _
                                CTGCC CCTCCC GC CTGTGGT
                                ||||| |||||| || |||||||
                                GACGG GGAGGG CG GACACCA
                                   _    G  A
GAM1742 CDKN2C   5' TGCCACCTCTCGCGG       38569        C  CTGT
                                TGCCGCCTC CGC   GG
                                |||||||| |||   ||
                                ACGGTGGAG GCG   CC
                                     A  _____
GAM1742 CELSR3   5' CTGCCGCCTCCCGCCGC     10837           T
                                CTGCCGCCTCCCGCC GT
                                |||||||||||||| ||
                                GACGGCGGAGGGCGG CG
                                                _
GAM1742 CLCN7    3' CTGCCGCCTGCCCGCCCAGC   10516        _     _
                                CTGCCGCCT CCCGCCT GT
                                |||||||| ||||||| ||
                                GACGGCGGA GGGCGGG CG
                                     C      T
GAM1742 EGLN2    3' CCGCTGCCTCCCACGG      38819     C       CTGT
                                CTGC GCCTCCCGC   GG
                                |||| |||||||||   ||
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                                GGCG CGGAGGGTG   CC
                                  A      ____
GAM1742  EIF2AK3  5'  CTGCCTCTCCCGCCGC     22107      GC      T
                                CTGCC  CTCCCGCC GT
                                |||||  |||||||| ||
                                GACGG  GAGGGCGG CG
                                  A_      _
GAM1742  FKBP2    5'  CTGCCGCCTCTGCGCAGGCGCG 38391         C_  CT  _
            T                    CTGCCGCCTC  CGC  GTG GT
                                |||||||||  |||  ||| ||
                                GACGGCGGAG  GCG  CGC CA
                                      AC   TC   G
GAM1742  FOXO1A   3'  CTGCCCCAAATACCTGTGGT  12886      G  TCCC
                                CTGCC CC    GCCTGTGGT
                                ||||| ||    |||||||||
                                GACGG GG    TGGACACCA
                                  _ TTTA
GAM1742  FSTL3    3'  TGTCCTCTCCCCATAGCTGGT  25223    _ GC    GCCT _
                                TG CC  CTCCC    G TGGT
                                || ||  |||||    | ||||
                                AC GG  GAGGG    C ACCA
                                 A  A_    GTAT G
GAM1742  FUS1     5'  CCGCCGCCTTCCGCAGGC    28584         C    CTGT
                                CTGCCGCCT CCGC    GGT
                                ||||||||| ||||    |||
                                GGCGGCGGA GGCG    CCG
                                      A    T___
GAM1742  FUT5     3'  CTGTGCCTCCCAGCGG      13022     CC      CCT
                                CTG  GCCTCCCG   GTGG
                                |||  ||||||||   ||||
                                GAC  CGGAGGGT   CGCC
                                  A_      ___
GAM1742  GRB14    5'  CCGCCGCCTCCTCAGG      21029          _  CCTGT
                                CTGCCGCCTCC CG     GG
                                |||||||||| ||     ||
                                GGCGGCGGAGG GT     CC
                                      A _____
GAM1742  GRM1     5'  GCCGCCTCTCCCGGAGTGGT  9136        __    CCT
                                GCCGCC  TCCCG   GTGGT
                                ||||||  |||||   |||||
                                CGGCGG  AGGGC   CACCA
                                   AG    CT_
GAM1742  GSPT1    5'  CTGCCGGCTCCGTGG       13308       C   CGCCT
                                CTGCCG CTCC     GTGG
                                |||||| ||||     ||||
                                GACGGC GAGG     CACC
                                   C    _____
GAM1742  HOXD1    5'  CTGCCGCCGTCTGCGCCGC   35986         _ C_   T
                                CTGCCGCC TC  CGCC GT
                                |||||||| ||  |||| ||
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                                GACGGCGG AG  GCGG CG
                                    C  AC   _
GAM1742  HSF2BP   5'  CTGCCGCCTCCGCTCCGT    28145          C  _
                                CTGCCGCCTCC GC CTGT
                                |||||||||| || ||||
                                GACGGCGGAGG CG GGCA
                                      _  A
GAM1742  IL16     5'  CTGCTGTGTCTTCCTGTGGT   21098     CGCC  CCG
                                CTGC   TC   CCTGTGGT
                                ||||   ||   ||||||||
                                GACG   AG   GGACACCA
                                  ACAC  AA_
GAM1742  IRS1     5'  CTGCCGCCGCCCGCGGGCGCGT 24418        T    CT   _
                                CTGCCGCC CCCGC  GTG GT
                                |||||||| |||||  ||| ||
                                GACGGCGG GGGCG  CGC CA
                                    C    CC   G
GAM1742  LIF      3'  CTGCTGTCTCACCCTGTGGT   14146     CGC   CCG
                                CTGC   CTC   CCTGTGGT
                                ||||   |||   ||||||||
                                GACG   GAG   GGACACCA
                                  ACA   TG_
GAM1742  LOH11CR2A 5'  CTGCCGCCTTCGACCCAGGT   31188         CC  _   T
                                CTGCCGCCT  CG CCTG GGT
                                |||||||||  || |||| |||
                                GACGGCGGA  GC GGGT CCA
                                     A_  T   _
GAM1742  MAN2A1   5'  CTGCCGCCCTCCCCGGGGT   14332        TC  G  T T
                                CTGCCGCC  CC CC G GGT
                                ||||||||  || || | |||
                                GACGGCGG  GG GG C CCA
                                    GA  _  _ C
GAM1742  MAP3K1   5'  CTGCCCGCCTCCCGCAGCAGT  42704       _       CT TG
                                CTGCC GCCTCCCGC  G  GT
                                ||||| |||||||||  |  ||
                                GACGG CGGAGGGCG  C  CA
                                  G        T_ GT
GAM1742  MDS1     5'  CTGCAGCCTCTGGTGTGTGGT  22562     C    CCGCC
                                CTGC GCCTC    TGTGGT
                                |||| |||||    ||||||
                                GACG CGGAG    ACACCA
                                  T    ACCAC
GAM1742  MN1      5'  CTGCCGCTTCTGTTACCACAGG 14578        C _________  CCTG
            CG                    CTGCCGC TC       CCG    TG
                                |||||||  ||       |||    ||
                                GACGGCG AG       GGT    GC
                                   A  ACAAIIIT   GTCC
GAM1742  MTL5     5'  CTGTCGCCCCCCGCGAGC    22269     C        CT
                                CTG CGCCTCCCGC  GT
                                ||| ||||||||||  ||
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                                GAC GCGGGGGGCG  CG
                                  A         CT
GAM1742  NAGLU    5'  CTGCCGCCTCCGGCCACGT   7051          C  _
                                CTGCCGCCTCC GCC TGT
                                |||||||||| ||| |||
                                GACGGCGGAGG CGG GCA
                                      C   T
GAM1742  NUP98    5'  CTGCTGCCACCCGCCGC    32231     C  T    T
                                CTGC GCC CCCGCC GT
                                |||| ||| |||||| ||
                                GACG CGG GGGCGG CG
                                  A  T    _
GAM1742  PITPN    5'  CGTCGCCTCTCGCGCCGC    26335    C    C  _
                                TG CGCCTC CGC CTGT
                                || |||||| ||| ||||
                                GC GCGGAG GCG GGCG
                                 A     A  C
GAM1742  PTPRJ    5'  CTGCCGTCTCCTTCGCCT    15954      C   __
                                CTGCCG CTCC  CGCCT
                                |||||| ||||  |||||
                                GACGGC GAGG  GCGGA
                                   A   AA
GAM1742  RAB4A    5'  GCCGCCTCTCGCCGGGT    21348       C   T T
                                GCCGCCTC CGCC G GGT
                                |||||||| |||| | |||
                                CGGCGGAG GCGG C CCA
                                     A   _ _
GAM1742  RAB6A    5'  CCGCCGCCTCCCGGCAG    16102          CCT TG
                                CTGCCGCCTCCCG  G  G
                                ||||||||||||  |  |
                                GGCGGCGGAGGGC  C  C
                                       ___ GT
GAM1742  RAD23A   3'  CTGTCGCCTCCCAGTCCT   22793    C       __
                                CTG CGCCTCCCG  CCT
                                ||| |||||||||  |||
                                GAC GCGGAGGGT  GGA
                                  A        CA
GAM1742  RAD51L3  3'  GCATCCTCTTTCGCCTGTGGT  39469   CG   C__
                                GC  CCTC   CGCCTGTGGT
                                ||  ||||   ||||||||||
                                CG  GGAG   GCGGACACCA
                                 TA   AAA
GAM1742  RANBP3   3'  CCGCCTCCTCCCCGGT     28755       CG  G
                                CCGCCTCC  CCT TGGT
                                ||||||||  ||| ||||
                                GGCGGAGG  GGG GCCA
                                     A_  _
GAM1742  RNPEPL1  3'  GCCGCCTCTCCCAGCATGGT  32882       _ __ CT
                                GCCGCCTC CC  GC  GTGGT
                                |||||||| ||  ||  |||||
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                                CGGCGGAG GG  CG  TACCA
                                    A  GT  __
GAM1742  SKIV2L   5'  TGCCGCCCCCTCGGG      27972         _  CCTGT
                                TGCCGCCTCC CG    GG
                                |||||||||| ||    ||
                                ACGGCGGGGG GC    CC
                                    A  _____
GAM1742  SLC10A2  3'  CTGCCACCTCCCTGACCATGGT 7815          GC_
                                CTGCCGCCTCCC  CTGTGGT
                                ||||||||||||  |||||||
                                GACGGTGGAGGG  GGTACCA
                                     ACT
GAM1742  SLC18A3  5'  CTGTTGCCGCCCGCCCGC    16831    CC   T
                                CTG  GCC CCCGCCTGT
                                |||  ||| |||||||||
                                GAC  CGG GGGCGGGCG
                                  AA   C
GAM1742  SLC21A9  3'  CTGCTGCCTCCCGAGCAGT   28564    C      CCT TG
                                CTGC GCCTCCCG   G  GT
                                |||| ||||||||   |  ||
                                GACG CGGAGGGC   C  CA
                                  A       T__ GT
GAM1742  SLC7A6   3'  TGCCGCCTCTTTTACCACAGGC 19600        _________  CCTG
            G                    TGCCGCCTC       CCG    TG
                                |||||||||       |||    ||
                                ACGGCGGAG       GGT    GC
                                     AAAAIIIT   GTCC
GAM1742  SMURF1   3'  CCGCCTCCCGCGGGT      45189         CT T
                                CCGCCTCCCGC  G GGT
                                ||||||||||  | |||
                                GGCGGAGGGCG  C CCA
                                     __ _
GAM1742  STAR     5'  CTGCTGCCTCTTCTACCACAGG 7387      C   _________  CCTG
            CG                    CTGC GCCTC       CCG    TG
                                |||| |||||       |||    ||
                                GACG CGGAG       GGT    GC
                                  A    AAGAIIIT   GTCC
GAM1742  STARD5   3'  CTGCCGCCTCTGGTACCACAGG 36125         _________  CCTG
            CG                    CTGCCGCCTC       CCG    TG
                                |||||||||       |||    ||
                                GACGGCGGAG       GGT    GC
                                     ACCAIIIT   GTCC
GAM1742  STXBP1   5'  CCGCCGCCTCCTCAGG      17202         _  CCTGT
                                CTGCCGCCTCC CG    GG
                                |||||||||| ||    ||
                                GGCGGCGGAGG GT    CC
                                     A  _____
GAM1742  TFG      5'  CCGCCGCCTCTCCGCAGGT   25869         _   CTGT
                                CTGCCGCCTC CCGC    GGT
                                |||||||||| ||||    |||
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                                GGCGGCGGAG GGCG    CCA
                                      A    T___
GAM1742  VARS2    3'  TGCTGCCATCCCCATGGT    26664     C   TC  G  T
                                TGC GCC  CC CC GTGGT
                                ||| |||  || || |||||
                                ACG CGG  GG GG TACCA
                                  A   TA  _  _
GAM1742  WASF3    3'  CCGCCGCCTCCTGTG       27381           CGCC
                                CTGCCGCCTCC    TGTG
                                ||||||||||    ||||
                                GGCGGCGGAGG    ACAC
                                          ____
GAM1742  ZNF264   5'  CCGCCGCCTCCTCGG       18269           CGCCTG
                                CTGCCGCCTCC     TGG
                                ||||||||||      |||
                                GGCGGCGGAGG     GCC
                                      A_____
GAM1742  AGRN     3'  TGAGGCTGCCATCCACGCCG   44259       C
                                TGAGGC GCCATCCACGCCG
                                |||||| ||||||||||||
                                ACTCCG CGGTAGGTGCGGC
                                   A
GAM1742  HDLBP    5'  TGAGGCCGCCTCTGTCAGCC   42745          A  ___  C
                                TGAGGCCGCC TC   CA GCC
                                |||||||||| ||   || |||
                                ACTCCGGCGG AG   GT CGG
                                      _  ACA  _
GAM1742  NR2E3    3'  TGAGGTCACTGCCGGT      32287       C   CATCCAC
                                TGAGG CGC      GCCGGT
                                ||||| |||      ||||||
                                ACTCC GTG      CGGCCA
                                   A   A_______
GAM1742  SNAI1    5'  TGGGGTCGCCGATTCGCGCAG  25609    A  C    ATCCA  _
                                TG GG CGCC     CGC CGG
                                || || ||||     ||| |||
                                AC CC GCGG     GCG GTC
                                 C  A    CTAA_   C
GAM1743  ABCD2    5'  TCTGCAGCGTTTCTCTTC     23153     A    A_
                                TCT CAGC  TTTTCTTT
                                ||| ||||  ||||||||
                                AGA GTCG  AAGAGAAG
                                  C    CA
GAM1743  CHC1L    3'  TCTCAGCTAGTGCTTTATAGTT 10421     A    ATTTT
              A                  TCT CAGC     CTTTATAGTTA
                                ||| ||||     ||||||||||
                                AGA GTCG     GAAATATCAAT
                                  _    ATCAC
GAM1743  PAFAH1B1 3'  TACAGTCATTTTCTTACATA   7719        _        _
                                TACAG CATTTTCTT TATA
                                ||||| ||||||||| ||||
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                                ATGTC GTAAAAGAA GTAT
                                  A       T
GAM1743  SERPINH2  3'  CTGCAGCACCTAGTTTTATAGT 10296    A      TC_
             T                   CT CAGCATTT   TTTATAGTT
                                 || ||||||||  |||||||||
                                 GA GTCGTGGA   AAATATCAA
                                  C       TCA
GAM1744  SHOX      5'  TGGCGTCCGTACACCTTGGTGC 7810        T__   GTCCA
                                 TGGCGTCC   CGCC    GC
                                 ||||||||  ||||    ||
                                 ACCGCAGG   GTGG    CG
                                      CAT    AACCA
GAM1744  BACE      3'  CAGATGGATTCTTCCTCATTTC 29043       CGAGAG    CC
                                 CGGATGGA     CCTCA  TC
                                 ||||||||     |||||  ||
                                 GTCTACCT     GGAGT  AG
                                      AAGAA_    AA
GAM1744  DUSP1     3'  GGATGTGAAGAGCCTCACCTCC 20657      GAC
                                 GGATG   GAGAGCCTCACCTCC
                                 |||||  ||||||||||||||||
                                 CCTAC   TTCTCGGAGTGGAGG
                                   AC_
GAM1744  EGR3      3'  CGGATGGAAGACCACCTC    40543       CG   GCC
                                 CGGATGGA  AGA   TCACCTC
                                 ||||||||  |||   |||||||
                                 GCCTACCT  TCT   GGTGGAG
                                      __   ___
GAM1744  GNAS      5'  CGGAGGTCCCAGCCTCACCTCC 38657     T  ACGAG
                                 CGGA GG    AGCCTCACCTCC
                                 |||| ||    ||||||||||||
                                 GCCT CC    TCGGAGTGGAGG
                                   _ AGGG_
GAM1744  GUCY1A2   3'  GAATGGACACATCTTATTTCC  9219        AGAGC  CACC
                                 GGATGGACG    CT    TCC
                                 |||||||||    ||    |||
                                 CTTACCTGT    GA    AGG
                                      GTA__  ATAA
GAM1744  GYS1      3'  CGGATGGAGGGATCCTC     44784       CGA  G
                                 CGGATGGA   GA CCTC
                                 ||||||||   || ||||
                                 GCCTACCT   CT GGAG
                                      CC_  A
GAM1744  IER3      3'  TGGAGGATGCAGTCACCTC   19355     C  GA  C_
                                 TGGA GA  GC  TCACCTC
                                 |||| ||  ||  |||||||
                                 ACCT CT  CG  AGTGGAG
                                   C  A_  TC
GAM1744  LIMK1     3'  GGGTGGGTGGGTCCCACCTCC  32537    A   ACGAGAG  T
                                 GG TGG      CC CACCTCC
                                 || |||      || |||||||
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                                CC ACC      GG GTGGAGG
                                 C  CACCCA_ _
GAM1744 LTF      3' GGATGGGCAATCCCCACCT   14260       A  GAG
                                GGATGG CGA  CCTCACCT
                                ||||||| |||  ||||||||
                                CCTACC GTT  GGGGTGGA
                                   C  A__
GAM1744 PACE4    3' GGATGGATGGGAGTGCCTGCCC 15053       C__  A   CA
             TC                   GGATGGA  GAG GCCT  CCTC
                                ||||||||  ||| ||||  ||||
                                CCTACCT  CTC CGGA  GGAG
                                    ACC  A   CG
GAM1744 SERPINA5 5' CGGGGGACCCACTCACCTC   8414     AT   GAGA  C
                                CGG  GGAC   GC TCACCTC
                                |||  ||||   || |||||||
                                GCC  CCTG   TG AGTGGAG
                                 C_   GG__ _
GAM1745 DNAJB9   3' CATATGGAGTATAATGTGGAAA 29559     _   T____       III
             T                   CAT TGGA    ATGTGGAAA  T
                                ||| ||||    |||||||||  |
                                GTA ACCT    TACACCTTT  A
                                 T   CATAT       III
GAM1745 EGLN1    5' TCGAACACTATGTGGAAA    35180      ___
                                TTGGAT  ATGTGGAAA
                                ||||||  |||||||||
                                AGCTTG  TACACCTTT
                                   TGA
GAM1745 HNF4G    3' CATTGGTTGCATGTGAAA    19973      A__
                                CATTGG  TATGTGGAA
                                ||||||  |||||||||
                                GTAACC  GTACACTTT
                                   AAC
GAM1745 VIM      3' TTGGATACTTGCTGGAAA    45229       G___
                                TTGGATAT   TGGAAA
                                ||||||||   ||||||
                                AACCTATG   ACCTTT
                                    AACG
GAM1746 BAALC    3' GGGAGGGCCAGATCATGTGC  36042      TG       C
                                GGGAGG  CAGATCATG GC
                                ||||||  ||||||||| ||
                                CCCTCC  GTCTAGTAC CG
                                   CG       A
GAM1746 P53AIP1  3' CAGGGAGGTGTAGGCG     35230         C  ATCAT
                                CAGGGAGGTG AG    GCG
                                |||||||||| ||    |||
                                GTCCCTCCAC TC    CGC
                                    A _____
GAM1746 STMN2    5' AGGGATGTGCAGACGC     45406      G       CAT
                                AGGGA GTGCAGAT  GC
                                ||||| ||||||||  ||
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                                TCCCT CACGTCTG   CG
                                  A      ___
GAM1746  PKD2     3'  GCACTGCATGCTCT       41071          CACCG  C
                                GCACTGCAT    GC TCT
                                |||||||||    || |||
                                CGTGACGTA    CG AGA
                                     _____  _
GAM1746  POU3F1   3'  CGCACTGCGTTACCTGTC    40371         ATCACCG    C
                                CGCACTGC     GCCT TC
                                ||||||||     |||| ||
                                GCGTGACG     TGGA AG
                                     CAA____    C
GAM1746  TIMP3    3'  CTGCATCATCTCCGACTCTCT  7451          ___    _
                                CTGCATCA   CCGGC CTCT
                                ||||||||   ||||| ||||
                                GACGTAGT   GGCTG GAGA
                                     AGA    A
GAM1747  CEACAM1  3'  TTTCTTATTTTCTATTTGGAGC 11838         G   TCAGAT
              C                  TTTCTTATT TCT     GAGCC
                                |||||||||| |||     |||||
                                AAAGAATAA AGA     CTCGG
                                     A   TAAAC_
GAM1747  PTGER2   3'  TTGTAACATTTCAGATGAG   9639      C____
                                TTGT    TTCAGATGAG
                                ||||    ||||||||||
                                AACA    AAGTCTACTC
                                  TTGTA
GAM1747  STAU     3'  TTTCTGTTGTCTTCCCTG    32701      TA      AGA
                                TTTCT  TTGTCTTC   TG
                                |||||  ||||||||   ||
                                AAAGA  AACAGAAG   AC
                                  C_       GG_
GAM1748  AHR      3'  TGAAGAAAGTAGGTAAGCAGTG 11551   A        A____
                                A AAGAAAGTAG     CAGTG
                                | ||||||||||     |||||
                                A TTCTTTCATC     GTCAC
                                 C         CATTC
GAM1748  CASP8    3'  TAAGAGAAAGGAGACAGTG   37879     A     T
                                TAA AGAAAG AGACAGTG
                                ||| |||||| ||||||||
                                ATT TCTTTC TCTGTCAC
                                  C     C
GAM1748  EMP1     3'  TAAAGAAAAGTAGGCAAGAT   10898      AG      A   T
                                TAAA  AAAGTAG CAG GAT
                                ||||  ||||||| ||| |||
                                ATTT  TTTCATC GTT CTA
                                  CT      C   _
GAM1748  NLGN2    5'  GAACCAAAGATGGTGATACG   44753     AGT_   CA
                                GAA    AGA  GTGATACG
                                |||    |||  ||||||||
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                                CTT   TCT  CACTATGC
                                  GGTT   AC
GAM1748 PTPRG    3'  TAAAAAAAAGTAGCATGTA   15941          A  _
                                TAAAAGAAAGTAG CA GTG
                                |||||||||||| || |||
                                ATTTTTTTTCATC GT CAT
                                        _  A
GAM1748 SET      3'  CAAGAGAAAGTAGACAGATACA 16559     A         GT
                                TAA AGAAAGTAGACA  GATACG
                                ||| ||||||||||||  ||||||
                                GTT TCTTTCATCTGT  CTATGT
                                  C         __
GAM1749 AKAP13   3'  TCAACCCTTGCATGCACTA   28485        AG   AACA
                                TCAACCCT  GCA   CACTA
                                ||||||||  |||   |||||
                                AGTTGGGA  CGT   GTGAT
                                     A_   AC__
GAM1749 BACE     3'  TAAAACTAGGACTGGTGAG   39968        AA   AA
                                TAAGACTA  ACTG  GAG
                                ||||||||  ||||  |||
                                ATTTTGAT  TGAC  CTC
                                     CC    CA
GAM1749 LPL      3'  TAAGCCTAAAACTGAAGAG   6941       A
                                TAAG CTAAAACTGAAGAG
                                |||| ||||||||||||||
                                ATTC GATTTTGACTTCTC
                                  G
GAM1749 SLC25A12 3'  TAAGACTAAAGCTTGAAACAGC 18979          A  GAA    C
                                TAAGACTAAA CT   GAGAT GC
                                |||||||||| ||   ||||| ||
                                ATTCTGATTT GA   CTTTG CG
                                      C  A__    T
GAM1749 SMARCD2  3'  TAAAACTAAAGCTGGAGAG   16921          A   A
                                TAAGACTAAA CTG AGAG
                                |||||||||| ||| ||||
                                ATTTTGATTT GAC TCTC
                                      C   C
GAM1749 SSR2     3'  AAGGGCTAAGAGAGAAGAGATT 17120     A_   AACT      C
             GC                   AAG  CTAA    GAAGAGAT GC
                                |||  ||||   |||||||| ||
                                TTC  GATT    CTTCTCTA CG
                                  CC    CTCT       A
GAM1750 CACNB1   3'  CAGCGCCCCCTGGAGGACAT   8776          CAAAA
                                CAGCGCCTCC    GACAT
                                ||||||||||    |||||
                                GTCGCGGGGG    CTGTA
                                      ACCTC
GAM1750 DAZ      3'  GCCTCTTCTGGACATATTT    19852       CCAAAA
                                GCCTC     GACATATTT
                                |||||     |||||||||
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                                CGGAG     CTGTATAAA
                                   AAGAC_
GAM1750  HMGB3    3'  CAGCCTCTCCCAAAAGGCAT   23778      GC        A
                                CAGC  CTCCCAAAAG CAT
                                |||||  |||||||||| |||
                                GTCG  GAGGGTTTTC GTA
                                   GA         C
GAM1750  SYN3     3'  CAGCGGTTCCTAAACATATTT  18561       CC   CAAA
                                CAGCG  TCC    AGACATATTT
                                |||||  |||    ||||||||||
                                GTCGC  AGG    TTTGTATAAA
                                   CA   A___
GAM1751  PTGER2   3'  CAGCTTAAATGTTTGTAT    9637        T     _
                                TAGCTT GATGTT GTAT
                                ||||||| ||||||| ||||
                                GTCGAA TTACAA CATA
                                    T     A
GAM1751  ABCA1    3'  GCTGTTGATTCTTTGCCTCT   24271     _       C  A  G
                                GCT TTGATTCTT TG TC TCT
                                ||| ||||||||| || || |||
                                CGA AACTAAGAA AC GG AGA
                                  C       _ _ _
GAM1751  CRACC    3'  CAGTGAATTCTTCTGATTGT   34518     CTTT         C
                                CAG    GATTCTTCTGAT GT
                                |||    |||||||||||| ||
                                GTC    TTAAGAAGACTA CA
                                  AC__          A
GAM1751  DGKB     3'  AGCTTTGATTGTGTTGTC    45210         CTTC  ATC
                                AGCTTTGATT    TG   GTC
                                ||||||||||    ||   |||
                                TCGAAACTAA    AC   CAG
                                      C___  AA_
GAM1751  FBXL2    3'  GCTTTGATTTGATTGT      29121         CTTC    C
                                GCTTTGATT    TGAT GT
                                |||||||||    |||| ||
                                CGAAACTAA    ACTA CA
                                     ____    A
GAM1751  GGPS1    3'  GCTTTTGATTCTTTCAAC    22110       _      CT
                                GCTTT GATTCTT  GAT
                                ||||| |||||||  |||
                                CGAAA CTAAGAA  TTG
                                   A      AG
GAM1751  MAP7     3'  CAGCTTTGGTTCTTCAGA    19571         A     T
                                CAGCTTTG TTCTTC GA
                                |||||||| |||||| ||
                                GTCGAAAC AAGAAG CT
                                     C     T
GAM1751  RGS1     3'  TGACTTTGATTCTTACAGTCT  16310   A         CTG  C
                                C GCTTTGATTCTT   AT GTCT
                                | ||||||||||||   || ||||
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                                A TGAAACTAAGAA   TG CAGA
                                 C          ___  T
GAM1751  SLC5A1   3'  GCTTCTGATTCTTAGTC     7362      _       CTGATC
                                GCT TTGATTCTT     GTC
                                ||| |||||||||     |||
                                CGA GACTAAGAA     CAG
                                  A       T_____
GAM1752  ADAM11   3'  TCTCAGCTGCCTGGT      34661     G    ATTGTC
                                TCT CAGC     TGCCTGGT
                                ||| ||||     ||||||||
                                AGA GTCG     ACGGACCA
                                 _   _______
GAM1752  DBY      3'  CCTGTAGTGAGGCCTGGTC   21657     C  CAT  TCT
                                TCTG AG   TG   GCCTGGTC
                                |||| ||   ||   ||||||||
                                GGAC TC   AC   CGGACCAG
                                  A  ___  TC_
GAM1752  GRB10    5'  TCTGTAGCACTGTCTGCTG   23670     C         C
                                TCTG AGCATTGTCTGC TG
                                |||| |||||||||||| ||
                                AGAC TCGTGACAGACG AC
                                  A         _
GAM1752  TLX1     3'  CTGTGACCCTCTGTCTGGT   24335     CAGC   G    C
                                CTG    ATT TCTG CTGGT
                                |||    ||| |||| |||||
                                GAC    TGG AGAC GACCA
                                  AC__   G    A
GAM1752  ABCC8    5'  CCGCTGGCTCCGCGCGC     7398      A    G
                                TCG CTGGT CTGCGCGC
                                ||| ||||| ||||||||
                                GGC GACCG GGCGCGCG
                                  _     A
GAM1752  BCL11A   3'  TCGACTGGGCGGCACGCG    39721         T  T
                                TCGACTGG GC GCGCGCG
                                |||||||| || |||||||
                                AGCTGACC CG CGTGCGC
                                     _ C
GAM1752  CALM3    5'  TCACTGCCCGCAGCGCGCGC   23246    G    G_   T
                                TC ACTG  TGC GCGCGCGC
                                || ||||  ||| ||||||||
                                AG TGAC  GCG CGCGCGCG
                                 _    GG   T
GAM1752  CDH8     3'  GACTGGTGCTAAACTTGC     12196          C  GC
                                GACTGGTGCTG GC  GC
                                |||||||||| ||  ||
                                CTGACCACGAT TG  CG
                                       T  AA
GAM1752  DHCR7    5'  CTGGCCTGCTTGCGCGCGC    10686       __   _
                                CTGGT  GCT GCGCGCGC
                                |||||  ||| ||||||||
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                                GACCG  CGA CGCGCGCG
                                   GA   A
GAM1752  EDNRA    5'  GACTGTACGCGCGCGC      41994       G   T
                                GACTG TGC GCGCGCGC
                                ||||| ||| ||||||||
                                CTGAC ATG CGCGCGCG
                                  _  _
GAM1752  FACL3    3'  TCAACTGGTGCTACACATGC   20883              C
                                TCGACTGGTGCTGCGCG GC
                                |||||||||||||||| ||
                                AGTTGACCACGATGTGT CG
                                          A
GAM1752  FBXL7    5'  TCGGCTGCCCCTGCGCGC    29412     A   GTG
                                TCG CTG   CTGCGCGC
                                ||| |||   ||||||||
                                AGC GAC   GACGCGCG
                                  C   GGG
GAM1752  GAD2     5'  CGGCTTGGCCCTGCGCGCGC  9054     A  _   G
                                CG CT GGT CTGCGCGCGC
                                || || ||| ||||||||||
                                GC GA CCG GACGCGCGCG
                                 C  A   G
GAM1752  GATM     5'  CCGGCTGGTCCACGCGC     11227     A     G TG
                                TCG CTGGT C  CGCGC
                                ||| ||||| |  |||||
                                GGC GACCA G  GCGCG
                                  C    _ GT
GAM1752  MAPT     5'  GACTGCGAGGGCGCGCGC    32579       G  CT_
                                GACTG TG   GCGCGCGC
                                ||||| ||   ||||||||
                                CTGAC GC   CGCGCGCG
                                   _  TCC
GAM1752  MIPEP    5'  TCGCTGGGAGCGCGCGC     45230     A    TGCT
                                TCG CTGG    GCGCGCGC
                                ||| ||||    ||||||||
                                AGC GACC    CGCGCGCG
                                  _    CT__
GAM1752  MYEOV    3'  TCGGCTGGAGCTGAACTTGC  39880     A    T    C  GC
                                TCG CTGG GCTG GC  GC
                                ||| |||| |||| ||  ||
                                AGC GACC CGAC TG  CG
                                  C    T    T  AA
GAM1752  PCOLCE2  5'  TCGGCTGCCCGCGCGC      30044     A   GTG
                                TCG CTG   CTGCGCGC
                                ||| |||   ||||||||
                                AGC GAC   GGCGCGCG
                                  C   G__
GAM1752  PDGFB    5'  CGGCTGCTCCGCGCGCGC    15175    A   GTG
                                CG CTG   CTGCGCGCGC
                                || |||   ||||||||||
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                                GC GAC   GGCGCGCGCG
                                 C   GA_
GAM1752 PTGFRN   5' TCGGCGGGGGCCGCGCGC    42600     ACT  T
                                TCG   GG GCTGCGCGC
                                |||   || |||||||||
                                AGC   CC CGGCGCGCG
                                  CGC  C
GAM1752 PTP4A2   3' GATGGACACTGCGCGTGC    38631    C  _       C
                                GA TGG TGCTGCGCG GC
                                || ||| ||||||||| ||
                                CT ACC GTGACGCGC CG
                                 _  T       A
GAM1752 SKP2     5' CCATCCCCACTGCGCGCGC   37208     A  GGT
                                TCG CT   GCTGCGCGCGC
                                ||| ||   ||||||||||
                                GGT GG   TGACGCGCGCG
                                  A  GG_
GAM1752 SORBS1   5' CGGGCGGGCTGCGCGCG     26969    AC   T
                                CG  TGG GCTGCGCGCG
                                ||  ||| ||||||||||
                                GC  GCC CGACGCGCGC
                                 CC  _
GAM1752 ZNF278   5' TCGCTGGACTGCGCGC      36808     A    T
                                TCG CTGG GCTGCGCGC
                                ||| |||| |||||||||
                                AGC GACC TGACGCGCG
                                 _   _
GAM1753 AGR2     5' GAGTCGGCGGCTAGGA      26922        AA   TT
                                GAGTCGGC  GCT  GGA
                                ||||||||  |||  |||
                                CTCAGCCG  CGA  CCT
                                    C_   T_
GAM1753 RPP20    3' ATGCAGAGTCCTTTG       25184          GGCAAG
                                ATGCAGAGTC     CTTTG
                                ||||||||||     |||||
                                TACGTCTCAG     GAAAC
                                       _______
GAM1753 SLC6A6   3' GCAGAGTAGATAGCTTTGGA  16791        C  CA
                                GCAGAGT GG  AGCTTTGGA
                                ||||||| ||  |||||||||
                                CGTCTCA TC  TCGAAACCT
                                    _  TA
GAM1753 WNT8B    3' TGGAAAGTGGCAAGCTTTGGA 40590    C    C
                                TG AGAGT GGCAAGCTTTGGA
                                || ||||| ||||||||||||
                                AC TTTCA CCGTTCGAAACCT
                                 C    _
GAM1753 XPNPEP2  5' GCAGAGGAGCTTTGG       18153       TCGGCA
                                GCAGAG     AGCTTTGG
                                ||||||     ||||||||
```

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                                CGTCTC     TCGAAACC
                                   C_____
GAM1754  BARHL1   3'  GGGAGAAAGGGGTTGCCTAG  33469    AG    AA  _
                                GG  GAAAG  GTT CCTGG
                                ||  |||||  ||| |||||
                                CC  CTTTC  CAA GGATC
                                 CT    CC   C
GAM1754  CENPB    3'  GGAGGAAAGAGGATTCTGA   43016         A_   C
                                GGAGGAAAGA  GTTC TGG
                                ||||||||||  |||| |||
                                CCTCCTTTCT  TAAG ACT
                                      CC   _
GAM1754  EN2      3'  GGAGGAGGGAGTTAGGTGCA  10959       AA  A   CCT  _
                                GGAGGA  GA GTT   GGT CA
                                ||||||  || |||   ||| ||
                                CCTCCT  CT CAA   CCA GT
                                   CC  _   T__   C
GAM1754  ETS2     3'  GGAGGCAGCCTGGTCA      23471       AA  AAGTT
                                GGAGG  AG    CCTGGTCA
                                |||||  ||    ||||||||
                                CCTCC  TC    GGACCAGT
                                  G_  _____
GAM1754  FUT3     3'  GGAGGGGAGAGGCTCCTGG   6641        AA   A
                                GGAGG  AGA GTTCCTGG
                                |||||  ||| ||||||||
                                CCTCC  TCT CGAGGACC
                                  CC   C
GAM1754  GFRA2    3'  GGAGGAGACAGGTTCAGCGACA 11267       AAGAA   C_  T
            AG                    GGAGGA    GTTC  TGG CAAG
                                ||||||    ||||  ||| ||||
                                CCTCCT    CAAG  GCT GTTC
                                   CTGTC   TC  _
GAM1754  HEBP1    3'  GAAGGAAAGTTGGTA       31991         AAGTTCC   C
                                GGAGGAAAG      TGGT A
                                |||||||||      |||| |
                                CTTCCTTTC      ACCA T
                                     A_______   A
GAM1754  HEPH     5'  GGAGGGGAGTTCCCATCCA   39859      AAA  A     GT
                                GGAGG   GA GTTCCTG  CA
                                |||||   || |||||||  ||
                                CCTCC   CT CAAGGGT  GT
                                  C__  _      AG
GAM1754  IGFBP4   3'  AGAGGAAGGACGATGGTCAAG  11392       A  AGTTCC
                                GGAGGAA GA     TGGTCAAG
                                |||||||  ||     ||||||||
                                TCTCCTT CT     ACCAGTTC
                                   C  GCT___
GAM1754  IL24     3'  GGAGGGAGGTCCTGGTC     27788       AAA  A  T
                                GGAGG   GA GT CCTGGTC
                                |||||   || ||  |||||||
```

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                                CCTCC   CT CA GGACCAG
                                  ___  C  _
GAM1754  IL6R     3'  GGAGGAGAGAGCTTCTTCCCCC 8178        A   A _______  TG
              AG                    GGAGGA AGA GT     TCC  G
                                |||||| ||| ||      |||  |
                                CCTCCT TCT CG     GGG  C
                                   C   _  AAGAAG   GT
GAM1754  LZTS1    3'  GGAGGAAAAAGAGGTTGG    34271          A TTCC
                                GGAGGAAAGA G    TGG
                                |||||||||| |    |||
                                CCTCCTTTTT C    ACC
                                      _ TCCA
GAM1754  MAML1    3'  GGAGGAAGGGATTCCTGG    31289        A AA
                                GGAGGAA G  GTTCCTGG
                                ||||||| |  ||||||||
                                CCTCCTT C  TAAGGACC
                                    _ CC
GAM1754  MGAT1    3'  GGAGAAGGGGTCTGGTCAAG   14436       AAGAA  TC
                                GGAGGA    GT  CTGGTCAAG
                                ||||||    ||  |||||||||
                                CCTCTT    CA  GACCAGTTC
                                   CCC__  __
GAM1754  MYH11    3'  GGGGAAAGAATTCTCAA     35627    A      G   CTGG
                                GG GGAAAGAA TTC    TCAA
                                || |||||||| |||    ||||
                                CC CCTTTCTT AAG    AGTT
                                 _      _  _____
GAM1754  OGDH     3'  GGAGAAAGAAAGAGTGGT    45014       AG   TTCC
                                GGAGGAA  AAG    TGGT
                                |||||||  |||    ||||
                                CCTCTTT  TTC    ACCA
                                    CT   TC__
GAM1754  OPCML    3'  AGAGGAAAGGGAAGGGTCAAG  14946         __   TTCCT
                                GGAGGAAA  GAAG    GGTCAAG
                                ||||||||  ||||    |||||||
                                TCTCCTTT  CTTC    CCAGTTC
                                    CC   ______
GAM1754  PFKFB2   3'  GGGGAAGAAAGCAGTCAA    26308    A   AG   TCCT
                                GG GGAA  AAGT    GGTCAA
                                || ||||  ||||    ||||||
                                CC CCTT  TTCG    TCAGTT
                                 _    CT   _____
GAM1754  PFN1     3'  GGAGGAAAGGGGTGCAA     22717         AAGTTCCT  _
                                GGAGGAAAG       GGT CAA
                                |||||||||       ||| |||
                                CCTCCTTTC       CCA GTT
                                    C________   C
GAM1754  PPARBP   5'  GGAGGAAACAAGTTGGC     21931         G   TCC
                                GGAGGAAA AAGT   TGGT
                                |||||||| ||||   ||||
```

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                                CCTCCTTT TTCA   ACCG
                                    G   ___
GAM1754  SFRS2IP   5'  GGAGAGAGAAAATGGTCAA   21792      AA    TTCC
                                GGAGG  AGAAG    TGGTCAA
                                |||||  |||||    |||||||
                                CCTCT  TCTTT    ACCAGTT
                                   C_    T___
GAM1754  SLC18A1   3'  GGAGGAAAGAAGATTCCCAG   16821          _   TG
                                GGAGGAAAGAAG TTCC  G
                                |||||||||||| ||||  |
                                CCTCCTTTCTTC AAGG  C
                                       T   GT
GAM1754  SVIL      3'  GGTGGAAAGAAGTTTCCAAACA 34730    A         C TG T
                                GG GGAAAGAAGTT C  G CA
                                || |||||||||| |  | ||
                                CC CCTTTCTTCAA G  T GT
                                 A          A GT T
GAM1754  TCFL1     3'  GCAGGAAAGAAGTTTCTGA   25631   G         C
                                G AGGAAAGAAGTT CTGG
                                | ||||||||||| ||||
                                C TCCTTTCTTCAA GACT
                                 G          A
GAM1754  WNT3A     3'  GAAGGGGCCTTGCCCTGGTCA  37543      AAAGAA  T
                                GGAGG     GT CCTGGTCA
                                |||||     || ||||||||
                                CTTCC     CG GGACCAGT
                                   CCGGAA  _
GAM1755  PACE4     3'  TCATTGATTTCTCTTTCA    39689    C    C
                                TCA TGATT CTTTTTCG
                                ||| ||||| ||||||||
                                AGT ACTAA GAGAAAGT
                                  A    A
GAM1755  RAB30     3'  CTGATTCCTTTTCTTCTCCG   30933          CGATG
                                CTGATTCCTTTTT    CCG
                                ||||||||||||    |||
                                GACTAAGGAAAAG    GGC
                                       AAGA_
GAM1755  ZNF38     3'  CTGATTCCTCGTGC       45361        TTTT   A
                                CTGATTCC   TCG TGC
                                ||||||||   ||| |||
                                GACTAAGG   AGC ACG
                                     _____  _
GAM1755  DUSP4     3'  GCTTTTATTATGTATTC     38420      GGACTC
                                GCTTT     TATGTATTC
                                |||||     |||||||||
                                CGAAA     ATACATAAG
                                   ATA___
GAM1755  NEBL      3'  TAGCTTTGGCCTTTGGACT   26909        A T  A  T
                                TAGCTTTGG C CT TG ATT
                                ||||||||| | || || |||
```

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                                ATCGAAACC G GA AC TGA
                                    _ _  A  C
GAM1755  PRKAR2A  3'  ACTTTGGACTTTGTATCA    20005         CTA    T
                                GCTTTGGACT   TGTAT CA
                                ||||||||||   ||||| ||
                                TGAAACCTGA   ACATA GT
                                     A__    _
GAM1755  SNAI2    3'  GCCTTTGGACTTTATTTGTCA  16882    _      C   GTAT
                                GC TTTGGACT TAT    TCA
                                || ||||||||| |||    |||
                                CG AAACCTGA ATA    AGT
                                 G       A  AAC_
GAM1755  ZNF14    3'  TGAACTCTTTTGTGTATTCAG  34295        A___
                                TGGACTCT    TGTATTCAG
                                ||||||||    |||||||||
                                ACTTGAGA    ACATAAGTC
                                     AAAC
GAM1756  ACK1     5'  CGGGGCCGCTCCCAGGACC    25112     CAAGA      C  CA
                                CGG    CCGCTCCC GG  ACC
                                |||    |||||||| ||  |||
                                GCC    GGCGAGGG CC  TGG
                                  CC___       T  __
GAM1756  ADAMTS8  5'  CGGCGGGAGCGCTCCCCCGGCG 28161      AA  C      _  AA
            GCC                   CGGC  GA CGCTCCCC GGC  CC
                                ||||  || |||||||| |||  ||
                                GCCG  CT GCGAGGGG CCG  GG
                                  CC  C       G   CC
GAM1756  AP2B1    3'  GGGACCGCTCCCCACAA     10488    CAA         G
                                GG   GACCGCTCCCCG CAA
                                ||   ||||||||||||| |||
                                CC   CTGGCGAGGGGT GTT
                                      ___          _
GAM1756  ARHI     5'  CGGAGAGACTGCCGCGGCAACC 21700     CA    C   CCC
                                CGG  AGAC GCT   CGGCAACC
                                |||  |||| |||   ||||||||
                                GCC  TCTG CGG   GCCGTTGG
                                  TC    A   C__
GAM1756  ETV5     5'  CGGTGAACCGCTCCGCGCACC  20850     CAA       C  G  A
                                CGG   GACCGCTCC CG CA CC
                                |||   ||||||||| || || ||
                                GCC   TTGGCGAGG GC GT GG
                                  AC_       C  _ _
GAM1756  GAS11    5'  AGCCACGCCGTTTCCCGGCAAC 11210     AAGA   CTC
            C                    GGC   CCG   CCCGGCAACC
                                |||   |||   ||||||||||
                                TCG   GGC   GGGCCGTTGG
                                  GTGC   AAA
GAM1756  GCH1     3'  GGCAGTACGATCGGCAAC    6703       A AC  CTCCC
                                GGCA G  CG    CGGCAAC
                                |||| |  ||    |||||||
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                                CCGT C  GC    GCCGTTG
                                  _ AT  TA___
GAM1756  MAN2A1   5'  GGCGAGACTCGCCGGCAAC   14334    A   _  TCCC
                                GGC AGAC CGC   CGGCAAC
                                ||| |||| |||   |||||||
                                CCG TCTG GCG   GCCGTTG
                                  C   A  ____
GAM1756  MAP3K9   5'  GGCGAGCTGCTTTCACAGCAAC 41357    A  ACC   CCC_
            C                    GGC AG   GCT   CGGCAACC
                                ||| ||   |||   ||||||||
                                CCG TC   CGA   GTCGTTGG
                                  C  GA_   AAGT
GAM1756  MCM2     3'  GGCAAGATGTTCAGCAAC    42746       CCGCTCCC
                                GGCAAGA       CGGCAAC
                                |||||||       |||||||
                                CCGTTCT       GTCGTTG
                                    ACAA____
GAM1756  PDE1B    3'  AGCTCCCCGCTCCCTGGCAGCC 9561     AAGA      C   A
                                GGC   CCGCTCCC GGCA CC
                                |||   |||||||| |||| ||
                                TCG   GGCGAGGG CCGT GG
                                  AGG_      A   C
GAM1756  PDLIM1   5'  GCAGGGCACCCCCGGCA     34191    A AC   T
                                GCA G  CGC CCCCGGCA
                                ||| |  ||| ||||||||
                                CGT C  GTG GGGGCCGT
                                  _ CC   _
GAM1756  RANBP3   5'  GCAGCATCCCCGGCAGCC    28758    AGACC  _      A
                                GCA    GC TCCCCGGCA CC
                                |||    || |||||||||| ||
                                CGT    CG AGGGGCCGT GG
                                  _____  T       C
GAM1756  S100A10  5'  CGGCAGGGCGCTCCCCCAGC   40391     A AC      _
                                CGGCA G  CGCTCCCC GGC
                                ||||| |  |||||||| |||
                                GCCGT C  GCGAGGGG TCG
                                  _ CC       G
GAM1757  CHRNA3   3'  TGGTGTACTAAGACAGTTATAT 8841     CA      TGT
            T                    TGG  TATTAAG   AGTTATATT
                                |||  |||||||   |||||||||
                                ACC  ATGATTC   TCAATATAA
                                  AC      TG_
GAM1757  ESRRBL1  3'  TGGCATATTTGTCATTGTATT  32844       AAG   A   A
                                TGGCATATT   TGT GTT TATT
                                |||||||||   ||| ||| ||||
                                ACCGTATAA   ACA TAA ATAA
                                     ___   G   C
GAM1757  SLT      3'  TAGCATATTAAGCTCATTGTAT 37178          GTA   A
            T                    TGGCATATTAAGT   GTT TATT
                                ||||||||||||   ||| ||||
```

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                                ATCGTATAATTCG   TAA ATAA
                                      AG_   C
GAM1758  ABCB9    3'  GGAGAGGCCTAGTCTCTGGACA 33355     AA_   CTAC
              T                  GGA   GCTT   CTCTGGACAT
                                 |||   ||||   ||||||||||
                                 CCT   CGGA   GAGACCTGTA
                                   CTC   TCA_
GAM1758  EDNRA    3'  TGGAAAGCATTTCTTCTTGG   42003        __   ACC   _
                                 TGGAAAGC  TTCT   TCT GG
                                 ||||||||  ||||   ||| ||
                                 ACCTTTCG  AAGA   AGA CC
                                      TA   ___   A
GAM1758  GAS11    3'  GGAAAGCTTCTACCCACA    11215            CTGG
                                 GGAAAGCTTCTACCT   ACA
                                 ||||||||||||||    |||
                                 CCTTTCGAAGATGGG   TGT
                                                 _____
GAM1758  LIF      3'  TGGAAACTTCTGCCAGA     14156       G    A  TCT
                                 TGGAAA CTTCT CC   GGA
                                 ||||||  ||||| ||   |||
                                 ACCTTT GAAGA GG   TCT
                                    _    C  ___
GAM1758  TBX3     3'  TGGAAGTTGCTCTGGACA    32441      AGCTTCTAC
                                 TGGAA       CTCTGGACA
                                 |||||       |||||||||
                                 ACCTT       GAGACCTGT
                                   CAAC_____
GAM1758  TCF12    3'  GGAAAGCTTCTGGC        17342        TCTACC    A
                                 GGAAAGCT     TCTGG C
                                 ||||||||     ||||| |
                                 CCTTTCGA     AGACC G
                                      _______    C
GAM1758  BLAME    3'  AATCCAGTTACACCTGGGTGAG 33482         C    GAGA
                                 AATCCAGT ATACT    GTGAG
                                 ||||||||  |||||   |||||
                                 TTAGGTCA TGTGG    CACTC
                                      A    ACC_
GAM1758  DXF68S1E 3'  CAGTGTGGACCATGAGAGTG   41035     CAT_   __
                                 CAGT    ACT  GAGAGTG
                                 ||||    |||  |||||||
                                 GTCA    TGG  CTCTCAC
                                   CACC   TA
GAM1758  EPHB1    3'  CAACTGCAGCCCACTGAGAGTG 20773     C_    A
                                 CAAT  CAGTC TACTGAGAGTG
                                 ||||  ||||| ||||||||||
                                 GTTG  GTCGG GTGACTCTCAC
                                   AC    _
GAM1758  JRK      3'  CAGCCTGGTCAACAGAGTGAG  44496    AT CA    T  TG
                                 CA  C  GTCA AC  AGAGTGAG
                                 ||  |  |||| ||  ||||||||
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                                GT  G  CAGT TG  TCTCACTC
                                 CG AC   _ __
GAM1758 KIF3B    5'  TGATCCAGTCAAATCTTGAG  22044   A       TA_ _
                                C ATCCAGTCA  CT GAG
                                | |||||||||  || |||
                                A TAGGTCAGT  GA CTC
                                 C       TTA  A
GAM1758 KMO      3'  CAGCCTGGTCAACAGAGTGAG  18954    AT CA   T  TG
                                CA  C  GTCA AC  AGAGTGAG
                                ||  |  |||| ||  ||||||||
                                GT  G  CAGT TG  TCTCACTC
                                 CG AC   _ __
GAM1758 MYCL2    3'  TGAGTCACAGCATTGAGAGTG  23912   C      C___
                                C AGTCATA   TGAGAGTG
                                | |||||||   ||||||||
                                A TCAGTGT   ACTCTCAC
                                 C      CGTA
GAM1758 SLC6A6   3'  CCCAGGCTGAGAGTG      16783      TCATA
                                TCCAG    CTGAGAGTG
                                |||||    |||||||||
                                GGGTC    GACTCTCAC
                                   C____
GAM1759 AIM1     3'  TGTTAAGCAGTTTGTTTGCATT 45086        TGAGA  GC
                T                TGTTAAGC    TG  TGCATTT
                                |||||||    ||  |||||||
                                ACAATTCG    AC  ACGTAAA
                                     TCAA_  AA
GAM1759 ALB      3'  TGGTAGGCTGAGATGCT     7882     T  A       G
                                TG TA GCTGAGATG CT
                                || || ||||||||| ||
                                AC AT CGACTCTAC GA
                                 C  C       _
GAM1759 KLK13    3'  TGTTAGCTGAGATTGAGCATTT 31814      A       GGCT
                                TGTTA GCTGAGAT    GCATTT
                                ||||| ||||||||    ||||||
                                ACAAT CGACTCTA    CGTAAA
                                   _       ACT_
GAM1759 CALM1    3'  TGTGTAGCTTGATCTTTA    27864      CAGCT       A
                                TGTG    TAGCTTGA TTTTA
                                ||||    |||||||| |||||
                                ACAC    ATCGAACT GAAAT
                                  _____       A
GAM1759 EVI2A    5'  TGTGCAGCTAGTTTTCCACTTT 30550         T  C  GA_
                                TGTGCAGCT AG TT   ATTTT
                                ||||||||| || ||   |||||
                                ACACGTCGA TC AA   TGAAA
                                     _ A  AGG
GAM1760 TEX14    3'  TCTAGGCACAACCAAAAATTT  36329      A    TC
                                TTTA GTACA  ACCAAAAATTT
                                |||| |||||  ||||||||||
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                                AGAT CGTGT  TGGTTTTTAAA
                                  C    __
GAM1760  UBE2B    3'  TTTAAGTTACACCAAGATTTC  17800        ACAT     AA
                                TTTAAGT    CACCAA  ATTTC
                                |||||||    ||||||  |||||
                                AAATTCA    GTGGTT  TAAAG
                                    AT__     C_
GAM1761  CALU     3'  CTCCTGAACATTTCTTAT    10256      C   GGGT
                                TTCC GAG    CATTTCTTAT
                                |||| |||    ||||||||||
                                GAGG CTT    GTAAAGAATA
                                  A  _____
GAM1761  PRPF18   3'  TTCCCTAAGTTTCTTAT     18952       G   GGTCA
                                TTCCC AGG     TTTCTTAT
                                ||||| |||     ||||||||
                                AAGGG TTC     AAAGAATA
                                  A  ______
GAM1761  WHSC1    3'  TTCTCAGGAGCACTTTCTTATC 39398     C G     CA
             A                   TTC C AGGGGT  TTTCTTATCA
                                ||| | ||||||  ||||||||||
                                AAG G TCCTCG  AAAGAATAGT
                                  A _     TG
GAM1761  AANAT    5'  GGGGCCTGTCCGCAGGC     9900       A       G  CT
                                GGGG CCTGTCCG AG  GC
                                |||| |||||||| ||  ||
                                CCCC GGACAGGC TC  CG
                                  _       G  __
GAM1761  ARHGAP6  5'  GGGCGCCTGAGCTGCG      30224     ACC  T  G
                                GGG   TG CC GAGCTGCG
                                |||   || || ||||||||
                                CCC   GC GG CTCGACGC
                                  ____  _  A
GAM1761  BAI2     5'  GGGGACCTGGCCGGGCGC     11797         T    A  T
                                GGGGACCTG CCGG GC GC
                                ||||||||| |||| || ||
                                CCCCTGGAC GGCC CG CG
                                     C    _ _
GAM1761  CD63     5'  GGGGCTCTCTAGCTGCG      12134      AC  G  CGG
                                GGGG  CT TC   AGCTGCG
                                ||||  || ||   |||||||
                                CCCC  GA AG   TCGACGC
                                  __  G  A__
GAM1761  DPEP1    5'  GGGGACCTGTGTGCACTGC    20636          CCGGA
                                GGGGACCTGT    GCTGC
                                ||||||||||    |||||
                                CCCCTGGACA    TGACG
                                      CACG_
GAM1761  DTNA     3'  GGGGGTCTGTCAGGAGCTGC   37373      AC     C
                                GGGG  CTGTC GGAGCTGC
                                ||||  ||||| ||||||||
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                                CCCC  GACAG CCTCGACG
                                  CA    T
GAM1761  FGF4    5'  GGGGCAGAGCTGCG       12853      ACCTGTC
                                GGGG      CGGAGCTGCG
                                ||||      ||||||||||
                                CCCC      GTCTCGACGC
                                 ________
GAM1761  FOXD1   5'  GGCTGCCGGAGCTGCGC     20930    AC   T
                                GG  CTG CCGGAGCTGCGC
                                ||  ||| ||||||||||||
                                CC  GAC GGCCTCGACGCG
                                 __  _
GAM1761  FZD6    5'  GAGACGGCTCCGGGGTTGCG  18627      CTG    AGC
                                GGGAC   TCCGG   TGCG
                                |||||   |||||   ||||
                                CTCTG   AGGCC   ACGC
                                   CCG    CCA
GAM1761  HAGH    5'  GGCGGCCCGAGAGCTGCGC   23714    _ A    TCC
                                GG GG CCTG   GGAGCTGCGC
                                || || ||||   ||||||||||
                                CC CC GGGC   TCTCGACGCG
                                 G  _   ___
GAM1761  HLCS    3'  GGGGACCCCCAGAGCTGCGC  7644         GT
                                GGGGACCT  CCGGAGCTGCGC
                                ||||||||  ||||||||||||
                                CCCCTGGG  GGTCTCGACGCG
                                   __
GAM1761  ITGA4   5'  GGGAACCTCGGCTGCG     9425         GTC  GA
                                GGGGACCT   CG  GCTGCG
                                ||||||||   ||  ||||||
                                CCCTTGGA   GC  CGACGC
                                   ___  __
GAM1761  MAF     5'  GGGCGTCTGTCCGGGCGGCGC 23836     AC_      A  T
                                GGG   CTGTCCGG GC GCGC
                                |||   |||||||| || ||||
                                CCC   GACAGGCC CG CGCG
                                  GCA       _  C
GAM1761  MGAT4B  5'  GGAGACCTGTGCTGCG     38269         CCGGA
                                GGGGACCTGT    GCTGCG
                                ||||||||||    ||||||
                                CCTCTGGACA    CGACGC
                                   ______
GAM1761  NPC2    5'  GGCGACCTGTCCTCGTGC    26963    G       GGAGC
                                GG GACCTGTCC    TGC
                                || |||||||||    |||
                                CC CTGGACAGG    ACG
                                 G       AGC__
GAM1761  NRXN1   5'  GGGGCTTGTCCGGAAAGGC   22052     ACC       CT
                                GGGG   TGTCCGGAG  GC
                                ||||   |||||||||  ||
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                                CCCC  ACAGGCCTT  CG
                                  GA_       TC
GAM1761  RANBP3   3'  AGGGACCTCGACAGAGCTGTGC 28750        GTC      C
                                GGGGACCT  CGGAGCTG GC
                                ||||||||  |||||||| ||
                                TCCCTGGA  GTCTCGAC CG
                                    GCT       A
GAM1761  RFX2     3'  GGGGCCCTGGTGGCTGCGC   8457      A   TCCGGA
                                GGGG CCTG     GCTGCGC
                                |||| ||||     |||||||
                                CCCC GGAC     CGACGCG
                                  G   CAC___
GAM1761  SERPINE1 3'  GGAGACCTTAAGGGAGTTGTGC 8290        GTCC   C  C
                                GGGGACCT   GGAG TG GC
                                ||||||||   |||| || ||
                                CCTCTGGA   CCTC AC CG
                                    ATTC   A  A
GAM1761  TAPBP    3'  GGAGATCCCTGAGCTGCGC   17306     CCTG  G_
                                GGGGA   TCC  GAGCTGCGC
                                |||||   |||  |||||||||
                                CCTCT   AGG  CTCGACGCG
                                  _____  GA
GAM1761  TARBP2   3'  GGGTACCAGAGCTGCG     39535     GACCTGT
                                GGG     CCGGAGCTGCG
                                |||     ||||||||||
                                CCC     GGTCTCGACGC
                                 AT_____
GAM1761  TNNT1    5'  GGGAACCTAGGCTGCG     17619       GTCC  A
                                GGGGACCT   GG GCTGCG
                                ||||||||   || ||||||
                                CCCTTGGA   TC CGACGC
                                   _____  _
GAM1761  VHL      5'  GGGGCGGAGCTGCG       8114      ACCTGTC
                                GGGG     CGGAGCTGCG
                                ||||     ||||||||||
                                CCCC     GCCTCGACGC
                                  ________
GAM1761  WNT7A    3'  AGGGACCTGGGCTG       21523       GTCC  A
                                GGGGACCT   GG GCTG
                                ||||||||   || ||||
                                TCCCTGGA   CC CGAC
                                   _____  _
GAM1762  SORCS1   3'  TCTTTTGATTTTCCAACACT  38102         A   T
                                TCTTTTGATTT TCCG ACACT
                                |||||||||||| |||| |||||
                                AGAAAACTAAA AGGT TGTGA
                                   _   _
GAM1762  RORB     3'  TTTGAACAATCAACAGGAAAAG 27927       _  TTGGTC
            TA                   TTTGAACA TC     GAAAAGTA
                                |||||||| ||     ||||||||
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                                AAACTTGT AG     CTTTTCAT
                                     T  TTGTC_
GAM1763  KAL1     3'  AATATCTATTATCAGGT     6865        CAAA
                                AATATC    GTTATCAGGT
                                ||||||    ||||||||||
                                TTATAG    TAATAGTCCA
                                   A___
GAM1763  MEL      3'  TCTGAATATACAACGTGTGGGT 23873         C   A  TATCA
                                TCTGAATAT CAA GT    GGT
                                ||||||||| ||| ||    |||
                                AGACTTATA GTT CA    CCA
                                     T   G  CAC__
GAM1763  MLC1     5'  TCTGAATAGTCTGGGTTCAGG  40155        _  CAAA  TA
                                TCTGAATA TC    GT  TCAGG
                                |||||||| ||    ||  |||||
                                AGACTTAT AG    CA  AGTCC
                                     C  ACC_  __
GAM1763  DBT      3'  AAATGATCATTATGAAACCTTC 12550         C  C_
              AT                  AAATGATCA TA  AAACTTTCAT
                                |||||||||  ||  ||||||||||
                                TTTACTAGT AT  TTTGGAAGTA
                                     A  AC
GAM1763  NIPSNAP1 3'  TAAAAGATCACTATCTTTCAT  18873      T       CAAA
                                TAAA GATCACTA    CTTTCAT
                                ||||  ||||||||    |||||||
                                ATTT CTAGTGAT    GAAAGTA
                                   T       A___
GAM1764  MTNR1A   3'  AGATGGGATTTCATCATGTTG  25546    TC       T  _
                                AG  GGGATTTT TCG GTTG
                                ||  |||||||| ||| ||||
                                TC  CCCTAAAG AGT CAAC
                                 TA       T   A
GAM1764  NR1I2    5'  GCTGGGATTTCCTAGGGGTTG  35106    C        C__
                                GT GGGATTTTTT   GGTTG
                                || ||||||||||   |||||
                                CG CCCTAAAGGA   CCAAC
                                 A         TCC
GAM1764  RNF12    5'  GTCAGGATCCGACTCGGTTG   32038          T_
                                GTCGGGATTT  TTCGGTTG
                                ||||||||||  ||||||||
                                CAGTCCTAGG  GAGCCAAC
                                     CT
GAM1764  CAPON    3'  TGTAGCAACATTCAATGT    41937    _  T_
                                TG AGT  CGTTCAATGT
                                || |||  ||||||||||
                                AC TCG  GTAAGTTACA
                                 A  TT
GAM1764  CLN5     3'  TCACTGCCATTCAATGT     27087       AGT
                                TTACTG   TCGTTCAATGT
                                ||||||   ||||||||||
```

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                                AGTGAC  GGTAAGTTACA
                                   ___
GAM1764  DISC1    3'  TTACTGAGTACTGCACTGT   33059       TC_  TCAA
                                TTACTGAGT  GT   TGT
                                |||||||||  ||   |||
                                AATGACTCA  CG   ACA
                                     TGA  TG__
GAM1764  DISC1    3'  TTACTGAGTACTACACTGT   33058       TCGTT  A
                                TTACTGAGT   CA TGT
                                |||||||||   || |||
                                AATGACTCA   GT ACA
                                     TGAT_  G
GAM1764  HUS1     3'  TACTGAATCAGCTTTGATGT  45003       C  CA_
                                TACTGAGTT GTT  ATGT
                                ||||||||| |||  ||||
                                ATGACTTAG CGA  TACA
                                     T  AAC
GAM1764  ICOS     3'  TACTGAGTATGTACTAATGT  29000       TC  TC_
                                TACTGAGT  GT  AATGT
                                ||||||||  ||  |||||
                                ATGACTCA  CA  TTACA
                                     TA  TGA
GAM1764  LRP8     3'  TTACTGAATTCAACCCAAGTGT 37800         _ TT  _
                                TTACTGAGTTC G  CAA TGT
                                |||||||||||  |  ||| |||
                                AATGACTTAAG T  GTT ACA
                                      T GG  C
GAM1764  TCL1B    3'  TCACTGAGGCTCCGGTGT    22256       TTC   AA_
                                TTACTGAG  GTTC  TGT
                                ||||||||  ||||  |||
                                AGTGACTC  CGAG  ACA
                                     ___   GCC
GAM1764  VNN1     3'  TCACTGAGTTGTGTAATGT   21687        C  TC
                                TTACTGAGTT GT  AATGT
                                |||||||||| ||  |||||
                                AGTGACTCAA CA  TTACA
                                      _  CA
GAM1765  EGLN3    3'  CATAACAAAGGAAAATATTTC 35205      TATTA
                                CATAAT    GAAAATATTTC
                                ||||||    ||||||||||
                                GTATTG    CTTTTATAAAG
                                   TTTC_
GAM1765  PRKG2    3'  TCATAAAGGAGAGAAAATATTT 26522      TTATT
           C                     TCATAA    AGAAAATATTTC
                                 ||||||    ||||||||||
                                 AGTATT    TCTTTTATAAAG
                                    TCCTC
GAM1765  SART2    3'  TTCATAATAGAAAATATTT   30040       TTAT
                                TTCATAA   TAGAAAATATTT
                                |||||||   ||||||||||
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                              AAGTATT   ATCTTTTATAAA
                                   ____
GAM1766 BAALC    3' CAAAACATCCTTTTTCTGT   36035       AAC_
                              TAAAACAT   TTTCTGT
                              ||||||||   |||||||
                              GTTTTGTA   AAAGACA
                                   GGAA
GAM1766 COL17A1  3' TCTAAAACATTGCAACTACTG 39083        ___   TT
                              TCTAAAACAT  AACT  CTG
                              ||||||||||  ||||  |||
                              AGATTTTGTA  TTGA  GAC
                                    ACG   T_
GAM1766 CRY1     3' TAAAACATATACTGTCTGT   19835       _  T
                              TAAAACATA ACT TCTGT
                              ||||||||| ||| |||||
                              ATTTTGTAT TGA AGACA
                                    A  C
GAM1766 GRB10    3' CAAAACTCTTTCTGTA     23647      ATAA
                              TAAAAC   CTTTCTGTA
                              ||||||   |||||||||
                              GTTTTG   GAAAGACAT
                                 A___
GAM1766 HNRPA1   3' TCTAAAACATGTCTTCT    36292        AAC
                              TCTAAAACAT  TTTCT
                              ||||||||||  |||||
                              AGATTTTGTA  GAAGA
                                    CA_
GAM1766 ICOS     3' TAAGACATAGCTCTCTAT    28999    A   A
                              TAA ACATA CTTTCTGT
                              ||| ||||| ||||||||
                              ATT TGTAT GAGAGATA
                                C   C
GAM1766 LIF      3' TCTAAGGCAGGAACATCTGTAC 14152     AA  T_  TT
           CA                   TCTAA  CA  AAC  TCTGTACCA
                              |||||  ||  |||  |||||||||
                              AGATT  GT  TTG  AGACATGGT
                                 CC  CC  T_
GAM1766 LPL      3' TCTAAAACATCATTCATAC   6943         AACT  T
                              TCTAAAACAT   TTC GTAC
                              ||||||||||   ||| ||||
                              AGATTTTGTA   AAG TATG
                                    GT__  _
GAM1766 PPEF2    3' TAAAAATAACTTTGCTTTACCA 26403     C      _ G
                              TAAAA ATAACTTT CT TACCA
                              ||||| |||||||| || |||||
                              ATTTT TATTGAAA GA ATGGT
                                 _      C A
GAM1766 SPF30    3' TCCAAAACATGGTACCACTGC  25240        A__  TT
                              TCTAAAACAT  ACT  CTGT
                              ||||||||||  |||  ||||
```

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                                AGGTTTTGTA  TGG  GACG
                                     CCA  T_
GAM1766  TRIM14   3'  TTTGCAAGGTTCTGTCTGCCTG 37713          _____
             GT                   TTTGCAAGGTTCT    CCTGGT
                                  ||||||||||||    ||||||
                                  AAACGTTCCAAGA    GGACCA
                                       CAGAC
GAM1766  ZNF137   5'  TGTAAGGTTCTCTCCAGTA   18338   C       _ TG
                                  TG AAGGTTCTC C  GTA
                                  || |||||||| |  |||
                                  AC TTCCAAGAG G  CAT
                                   A        A GT
GAM1767  MS4A1    3'  TAAACTATCTTTTCCTTCTTT  6601            ATTAT
                                  TAAATTATCTTTT    TTCTTT
                                  ||||||||||||    ||||||
                                  ATTTGATAGAAAA    AAGAAA
                                       GG___
GAM1768  WHN      3'  TAATTTGTGTGTGTGCACGAGG 18754          T    TTT_
             GCT                    TAATTTGTGTGT TGCGC   GCT
                                  |||||||||||| |||||   |||
                                  ATTAAACACACA ACGTG   CGA
                                       C    CTCC
GAM1768  EML1     3'  GTGCACTGTGTCATATATTG  40724      ATCGC_
                                  GTGTA     CATATATTG
                                  |||||     |||||||||
                                  CACGT     GTATATAAC
                                     GACACA
GAM1769  BAT1     5'  CAAGAGCGCAGGCGCAAGGGAC 21586     CA        ___
             CG                     CAAG  CGCAGGTGCAA   ACCG
                                  ||||  ||||||||||   ||||
                                  GTTC  GCGTCCGCGTT   TGGC
                                    TC         CCC
GAM1769  CEP2     5'  GCGCGCAGACGGCAGACCG   28439    A    GT _  A
                                  GC CGCAG  G CA ACCG
                                  || |||||  | || ||||
                                  CG GCGTC  C GT TGGC
                                   C    TG C  C
GAM1769  CTH      5'  TAAAGCACGCAGGTAGAGCCGA 12513   C          CAAA
                                  A AAGCACGCAGGTG   CCGA
                                  | ||||||||||||   ||||
                                  A TTCGTGCGTCCAT   GGCT
                                   T          CTC_
GAM1769  DOM3Z    5'  CAGGCACGCCAGAGGCCGA   24296    A     A  TGCAAA
                                  CA GCACGC GG     CCGA
                                  || |||||| ||     ||||
                                  GT CGTGCG TC     GGCT
                                   C     G  TCC___
GAM1769  LASS1    3'  CACGCAGCAGGGCAGGTCG   34592    A  C    T   AAC
                                  CA GCA GCAGG GCA   CG
                                  || ||| ||||| |||   ||
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                                GT CGT CGTCC CGT   GC
                                 G  _    _  CCA
GAM1769 BAT1    5' CAAGAGCGCAGGCGCAAGGGAC 38745     CA        ___
            CG                   CAAG  CGCAGGTGCAA   ACCG
                                ||||  ||||||||||  ||||
                                GTTC  GCGTCCGCGTT   TGGC
                                  TC         CCC
GAM1769 CEP2    5' GCGCGCAGACGGCAGACCG   28439    A    GT _ A
                                GC CGCAG  G CA ACCG
                                || |||||  | || ||||
                                CG GCGTC  C GT TGGC
                                 C    TG C  C
GAM1769 CTH     5' TAAAGCACGCAGGTAGAGCCGA 12513   C          CAAA
                                A AAGCACGCAGGTG   CCGA
                                | ||||||||||||   ||||
                                A TTCGTGCGTCCAT   GGCT
                                 T          CTC_
GAM1769 DOM3Z   5' CAGGCACGCCAGAGGCCGA   37105    A     A  TGCAAA
                                CA GCACGC GG     CCGA
                                || ||||||  ||     ||||
                                GT CGTGCG TC     GGCT
                                 C     G  TCC___
GAM1769 LASS1   3' CACGCAGCAGGGCAGGTCG   34592    A  C    T   AAC
                                CA GCA GCAGG GCA   CG
                                || ||| ||||| |||   ||
                                GT CGT CGTCC CGT   GC
                                 G  _    _  CCA
GAM1770 CASP10  3' AACAAATTTACTGTACATG   37379        G
                                AACAAATT TATTGTACATG
                                |||||||| ||||||||||
                                TTGTTTAA ATGACATGTAC
                                         _
GAM1770 KLRD1   3' TTAAAACACATTGTTTCACATA 28811        A    AT__
            CATG                  TTAAAACA ATTGT    TGTACATG
                                |||||||| |||||   ||||||||
                                AATTTTGT TAACA    GTATGTAC
                                     G    AAGT
GAM1770 SLC35A1 3' CTAGGACAAAATACTGTACATG 26948     AA    TT
                                TTA  ACAAA  GTATTGTACATG
                                |||  |||||  ||||||||||||
                                GAT  TGTTT  TATGACATGTAC
                                  CC    __
GAM1770 CASP10  3' AACAAATTTACTGTACATG   37379        G
                                AACAAATT TATTGTACATG
                                |||||||| ||||||||||
                                TTGTTTAA ATGACATGTAC
                                         _
GAM1770 KLRD1   3' TTAAAACACATTGTTTCACATA 13966        A    AT__
            CATG                  TTAAAACA ATTGT    TGTACATG
                                |||||||| |||||   ||||||||
```

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                                AATTTTGT TAACA   GTATGTAC
                                    G    AAGT
GAM1770  SLC35A1   3'  CTAGGACAAAATACTGTACATG 26948    AA    TT
                                TTA  ACAAA  GTATTGTACATG
                                |||  |||||  ||||||||||||
                                GAT  TGTTT  TATGACATGTAC
                                  CC    __
GAM1771  MTR       3'  GATGAGTGTATATTTTGCA   7016     C  C   AC
                                GAT GA GTG  TATTTTGCA
                                ||| || |||  |||||||||
                                CTA CT CAC  ATAAAACGT
                                  _ _  AT
GAM1771  Nrap      3'  CAAGATTGGGTGACTACC    40188      CGAC
                                CAAGAT   GTGACTATT
                                ||||||   |||||||||
                                GTTCTA   CACTGATGG
                                   ACC_
GAM1771  ONECUT1   5'  CAACATCGATGTGGCCAGGCA 41625    G    C   A   TTTT
                                CAA ATCGA GTG CTA   GCA
                                ||| ||||| ||| |||   |||
                                GTT TAGCT CAC GGT   CGT
                                  G    A  C   C___
GAM1771  PHKG2     5'  AGGGTCGACGCGAGCTGC    7129     A_      CTATT
                                AG  TCGACGTGA    TTGC
                                ||  |||||||||    ||||
                                TC  AGCTGCGCT    GACG
                                 CC       C____
GAM1771  PIGR      3'  CAGGATCGACATGATTCTG   43699    A       CTA
                                CA GATCGACGTGA   TTTTG
                                || ||||||||||   |||||
                                GT CTAGCTGTACT   AAGAC
                                 C        ___
GAM1771  RRM1      3'  CAAGATGACTTATTTTGC    9755     C    _
                                CGA GTGACT ATTTTGC
                                ||| |||||| |||||||
                                GTT TACTGA TAAAACG
                                  C     A
GAM1771  SPTBN4    3'  GGAGATCGACGTTTTG     36088   A       GACTAT
                                C AGATCGACGT     TTTG
                                | ||||||||||     ||||
                                C TCTAGCTGCA     AAAC
                                 C        _______
GAM1771  HDAC4     3'  GCGTGCATGTGCGTCTC     25772       _   TCACGC
                                GCGTGC TGTG     CGTCTC
                                |||||| ||||     ||||||
                                CGCACG ACAC     GCAGAG
                                   T   _______
GAM1771  HOXD3     3'  AGTGTGTTGTGCCACGCCACC  27894    C   C        GT
                                AG GTG TGTGTCACGCC  C
                                || ||| ||||||||||  |
```

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                                TC CAC ACACGGTGCGG  G
                                 A  A         TG
GAM1771  LIPE     3'  GCGTGCAGGTCCAGCCGTCTCG 23812       TGT   AC
                                GCGTGC   GTC  GCCGTCTCG
                                ||||||   |||  |||||||||
                                CGCACG   CAG  CGGCAGAGC
                                   TC_   GT
GAM1771  RPA3     5'  GCTGTTCACTGCTGTCTC    16380      G   _  C
                                GCTGT TCAC GC GTCTC
                                ||||| |||| || |||||
                                CGACA AGTG CG CAGAG
                                   _   A  A
GAM1772  BCAS1    5'  TGGGAGTATCTTCAGT      18925          G   A
                                TGGGAGTATCT TCA GT
                                |||||||||||| ||| ||
                                ACCCTCATAGA AGT CA

                                      _  _
GAM1772  IRTA1    3'  TGGGATATCTGTCACCTTAAAT 36359       G       AGT___
             ATTC                   TGGGA TATCTGTCA     ATATTC
                                ||||| |||||||||     ||||||
                                ACCCT ATAGACAGT     TATAAG
                                   _       GGAATT
GAM1772  WW45     3'  TGGGAGTAGTTTGTAT     34825        TCT  CAA
                                TGGGAGTA   GT   GTAT
                                ||||||||   ||   ||||
                                ACCCTCAT   CA   CATA
                                     ___  AA_
GAM1772  CYP1B1   3'  CAACTATGCACTGTAGCTAT   6445      CAG  ___
                                CGAC   GC   GTAGCTAT
                                ||||   ||   ||||||||
                                GTTG   CG   CATCGATA
                                  ATA  TGA
GAM1772  F5       5'  TAACCACACTCCGGGCTGT    6555         A_  A  _
                                TAACCACG  CC GGC GT
                                ||||||||  || ||| ||
                                ATTGGTGT  GG CCG CA
                                     GA  C   A
GAM1772  UBE2I    5'  CAACCACGGTTTCAAGGCTGT  17811         ACC___   _
                                TAACCACG     AGGC GT
                                ||||||||     |||| ||
                                GTTGGTGC     TCCG CA
                                     CAAAGT    A
GAM1772  ZNF268   5'  ACCACGACGGGCGATGAACGCT 41757         CA   TA____
             ATC                   ACCACGAC  GGCG     GCTATC
                                ||||||||  ||||     ||||||
                                TGGTGCTG  CCGC     CGATAG
                                     C_    TACTTG
GAM1773  TRRAP    3'  TTTAAATTAGGAAGGTA     18595          AC
                                TTTAAATTAG  AAGGTG
                                ||||||||||  ||||||
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```
                                AAATTTAATC  TTCCAT
                                      C_
GAM1774  AMFR     3'  GACCGCTGTGTAGGAAAA    39935          AGTTA
                                GACCGTTGTGTGG    GAAAA
                                ||||||||||||    |||||
                                CTGGCGACACATC    CTTTT
                                      _____
GAM1774  RPL22    5'  GCGGCAGCGGAGTTAGAAA   9737     T _
                                GT GT GTGGAGTTAGAAA
                                || || ||||||||||||
                                CG CG CGCCTCAATCTTT
                                 C  T
GAM1774  SLC25A17 5'  CGCAGCCAGTGGAGTTAGGAAA 26825     T __        A
            G                    CGT GT  GTGGAGTTAG AAAG
                                ||| ||  |||||||||| ||||
                                GCG CG  CACCTCAATC TTTC
                                  T  GT        C
GAM1774  ST7      3'  GACTGTGCAAGAGTTGGGAGA  30267     CGT    _   ___
                                GAC   TGTGTG GAGTT   AGA
                                |||   |||||| |||||   |||
                                CTG   ACACGT CTCAA   TCT
                                  ___     T    CCC
GAM1774  ABCC1    5'  GGGGCCGCAACGCCGCC     33407     T  CTA
                                GGG CC   CAGCGCCGCC
                                ||| ||   ||||||||||
                                CCC GG   GTTGCGGCGG
                                  C  C__
GAM1774  ACCN2    3'  TGAGGTCCCTTGCCCCG     33455   A      ACA  G
                                C GGGTCCCT   GC CCG
                                | ||||||||   || |||
                                A TCCAGGGA   CG GGC
                                 C       A__  G
GAM1774  ACP5     3'  CAGGGTCCCGGCAGGCC     11513         TA   C
                                CAGGGTCCC  CAG GCC
                                |||||||||  ||| |||
                                GTCCCAGGG  GTC CGG
                                      CC   _
GAM1774  ADARB1   3'  CAGGGCCCTCGCCCGC      31871      T   ACA  G
                                CAGGG CCCT   GC CCGC
                                ||||| ||||   || ||||
                                GTCCC GGGA   CG GGCG
                                   _   G__  _
GAM1774  AKAP1    5'  GGAGTCCGCGCGCCGCC     40226    _   CTACA
                                GG GTCC    GCGCCGCC
                                || ||||    ||||||||
                                CC CAGG    CGCGGCGG
                                 T   CG___
GAM1774  AKT2     5'  CAGCGGCAACGGCGCCGCC   11564     _  CCCT  A
                                CAG GGT    AC GCGCCGCC
                                ||| |||    || ||||||||
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                                GTC CCG    TG CGCGGCGG
                                  G   T___  C
GAM1774  ANK1     3'  CAGGGCCCCTCTCCGC      33852          ACAGCG
                                CAGGGTCCCT     CCGC
                                ||||||||||     ||||
                                GTCCCGGGGA     GGCG
                                     GA____
GAM1774  ARAF1    5'  CAGAGTCCGCCTCCGTCGCC   41908         _  ACAG_
                                CAGGGTCC CT    CGCC
                                |||||||| ||    ||||
                                GTCTCAGG GG    GCGG
                                    C  AGGCA
GAM1774  ASC      5'  CAGGATCCCCGGCCGC      29938          ACAGC
                                CAGGGTCCCT    GCCGC
                                ||||||||||    |||||
                                GTCCTAGGGG    CGGCG
                                     C____
GAM1774  ATP5G3   5'  GGGTCCCTACTGGGCGCCGC   11773          A__
                                GGGTCCCTAC   GCGCCGC
                                ||||||||||   |||||||
                                CCCAGGGATG   CGCGGCG
                                     ACC
GAM1774  BCAS1    5'  GGGTCTCCAGTGCGTGCTGCC  18924       _  TACA  __  C
                                GGGTC CC    GC  GC GCC
                                ||||| ||    ||  || |||
                                CCCAG GG    CG  CG CGG
                                   A  TCA_  CA  A
GAM1774  BLMH     5'  CAGGGTCCTTGGGCGAGCGCC  7550         CTAC___
                                CAGGGTCC      AGCGCC
                                ||||||||      ||||||
                                GTCCCAGG      TCGCGG
                                     AACCCGC
GAM1774  BSN      3'  GGGTCCCTCGGGCACAGCC    18409         ACA    C
                                GGGTCCCT   GCGC GCC
                                ||||||||   |||| |||
                                CCCAGGGA   CGTG CGG
                                     GCC    T
GAM1774  C21orf5  3'  GGGATTACAGGCGCCGCC     23063     TCCC     _
                                GGG    TACAG CGCCGCC
                                |||    ||||| |||||||
                                CCC    ATGTC GCGGCGG
                                  TA__     C
GAM1774  CABC1    5'  CAGGGCCCTGGCCGC       33678       T    ACAGC
                                CAGGG CCCT     GCCGC
                                ||||| ||||     |||||
                                GTCCC GGGA     CGGCG
                                   _    C____
GAM1774  CAPN2    5'  CAGGGCCCGGCGCGCTGC     11964         CTACA    C
                                CAGGGTCC     GCGC GC
                                ||||||||     |||| ||
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                                GTCCCGGG    CGCG CG
                                    CCG__   A
GAM1774 CARKL    3' GGATCCCTACAGGGATGCC   29998          C___
                                GGGTCCCTACAG   GCC
                                ||||||||||||  |||
                                CCTAGGGATGTC   CGG
                                     CCTA
GAM1774 CFTR     5' GGGTCCCTGCTAGGGCCG    7955        AC_ C
                                GGGTCCCT  AG GCCG
                                ||||||||  || ||||
                                CCCAGGGA  TC CGGC
                                    CGA  C
GAM1774 CGTHBA   3' GGGTCCTGCACAGTGGGCC   28964      C_   C__
                                GGGTCC  TACAG  GCC
                                ||||||  |||||  |||
                                CCCAGG  GTGTC  CGG
                                   AC    ACC
GAM1774 CNTN2    3' CAGGGTCCTTGCTGCTGC    22909       CTACA _ C
                                CAGGGTCC    GC GC GC
                                ||||||||    || || ||
                                GTCCCAGG    CG CG CG
                                    AA___  A  A
GAM1774 DAG1     3' CAGGGCCCTGCCCTACCCTGCC 20517      ____    AGC
                                CAGGGT   CCCTAC  GCC
                                ||||||   ||||||  |||
                                GTCCCG   GGGATG  CGG
                                   GGAC    GGA
GAM1774 DBN1     5' GGGTCCCTCAGACCTGCC    38941       A  C  _
                                GGGTCCCT CAG GCC GCC
                                |||||||| ||| ||| |||
                                CCCAGGGA GTC TGG CGG
                                    _  _  A
GAM1774 DDT      5' CAGGGTCCCTGGCACC      10669        ACA
                                CAGGGTCCCT  GCGCC
                                ||||||||||  |||||
                                GTCCCAGGGA  CGTGG
                                     C__
GAM1774 DDX1     5' AGGGCTTCTGGACGCCGCC   22370     CC  ACA
                                AGGGT  CT  GCGCCGCC
                                |||||  ||  ||||||||
                                TCCCG  GA  TGCGGCGG
                                  AA  CC_
GAM1774 DTNBP1   5' GGGTCCCACGCCGC       37013       TACA
                                GGGTCCC   GCGCCGC
                                |||||||   |||||||
                                CCCAGGG   TGCGGCG
                                    ____
GAM1774 DVL3     5' GGGTCCCAGCGCCGCC      20686       TAC
                                GGGTCCC  AGCGCCGCC
                                |||||||  |||||||||
```

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                              CCCAGGG  TCGCGGCGG
                                   ___
GAM1774 EHD1    5' CAGTGGCGGCTAGCGCCGCC  43034    _  CC  AC
                              CAG GGT  CT  AGCGCCGCC
                              ||| |||  ||  |||||||||
                              GTC CCG  GA  TCGCGGCGG
                                A  CC  __
GAM1774 ENG     3' CAGGGTCCTGCCAGGGCC    6492       CTA  C
                              CAGGGTCC  CAG GCC
                              ||||||||  ||| |||
                              GTCCCAGG  GTC CGG
                                   ACG  C
GAM1774 EP300   5' GGGCCGAGCAGCGCCGCC    10991     CCTA
                              GGGTC   CAGCGCCGCC
                              |||||   ||||||||||
                              CCCGG   GTCGCGGCGG
                                 CTC_
GAM1774 FHIT    5' GGGGCCGGAGCGCCGCC    12876    T  CTAC
                              GGG CC   AGCGCCGCC
                              ||| ||   |||||||||
                              CCC GG   TCGCGGCGG
                                C  CC__
GAM1774 FKBP1B  5' GGGTCCCTGCTGCTGCC    38333       ACA  _  C
                              GGGTCCCT  GC GC GCC
                              ||||||||  || || |||
                              CCCAGGGA  CG CG CGG
                                   ___  A  A
GAM1774 FOXF1   3' CAGGGTCCCTGTGACCCGCC  11116       ACA  G
                              CAGGGTCCCT  GC CCGCC
                              ||||||||||  || |||||
                              GTCCCAGGGA  TG GGCGG
                                   CAC  _
GAM1774 GALE    3' CAGGGCCCTGAGTTCCTGCC  41799     T  AC  CG  _
                              CAGGG CCCT  AG  CC GCC
                              ||||| ||||  ||  || |||
                              GTCCC GGGA  TC  GG CGG
                                 _  C_  AA  A
GAM1774 GCGR    5' CAGGGCCCGCGCGGCGCTGC  6692       CTACA  C
                              CAGGGTCC   GCGC GC
                              ||||||||   |||| ||
                              GTCCCGGG   CGCG CG
                                   CGCGC  A
GAM1774 GFRA2   3' CAGAGTCCCTTCCGC      11264       ACAGCG
                              CAGGGTCCCT   CCGC
                              ||||||||||   ||||
                              GTCTCAGGGA   GGCG
                                   A_____
GAM1774 GNAZ    3' CAGGGTCCCAGCAGGGCC    13179       TA  C
                              CAGGGTCCC  CAG GCC
                              |||||||||  ||| |||
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                                GTCCCAGGG  GTC CGG
                                     TC   C
GAM1774  GRF2     3'  CAGGGCCCCTGCAGGACAGGCC 23673          _____   C
                                CAGGGTCCCT    ACAG GCC
                                ||||||||||    |||| |||
                                GTCCCGGGGA    TGTC CGG
                                     CGTCC   _
GAM1774  HPN      5'  AGGGTCCCTGGAAAGCGGGC   13456         AC__   CC
                                AGGGTCCCT   AGCG  GC
                                |||||||||   ||||  ||
                                TCCCAGGGA   TCGC  CG
                                     CCTT   C_
GAM1774  HPS4     5'  AGGTCACGCGCCGC       35214       CCT  A
                                GGGTC   AC GCGCCGC
                                |||||   || |||||||
                                TCCAG   TG CGCGGCG

                                  ___  _
GAM1774  HSD17B1  5'  GGGTCCCTGGCCCGC      7661         ACA  G
                                GGGTCCCT   GC CCGC
                                ||||||||   || ||||
                                CCCAGGGA   CG GGCG
                                     C__  _
GAM1774  HTR4     5'  CAGGGTCCCGCTGCC       9300         TACA  _
                                CAGGGTCCC    GC GCC
                                |||||||||    || |||
                                GTCCCAGGG    CG CGG
                                      _____  A
GAM1774  HYAL2    3'  CAGGGTCCTACATGCC      37633        C    GC
                                CAGGGTCC TACA  GCC
                                |||||||| ||||  |||
                                GTCCCAGG ATGT  CGG
                                     _    A_
GAM1774  IGFBP4   3'  CAGGGCTCTCAGCTGCC     11395        CC  A   _
                                CAGGGT  CT CAGC GCC
                                ||||||  || |||| |||
                                GTCCCG  GA GTCG CGG
                                    A_  _    A
GAM1774  IL6R     3'  CAGGGTCCAGGCTGC       8169         CTAC  C  C
                                CAGGGTCC    AG GC GC
                                ||||||||    || || ||
                                GTCCCAGG    TC CG CG
                                      _____  _  A
GAM1774  ILF1     3'  CAGGGCCCTGCACC        21104       T    ACA
                                CAGGG CCCT   GCGCC
                                ||||| ||||   |||||
                                GTCCC GGGA   CGTGG
                                     _    ____
GAM1774  IRS1     5'  GGGTCCCTGCGGTGCC      24426         ACA   CC
                                GGGTCCCT   GCG  GCC
                                ||||||||   |||  |||
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                                CCCAGGGA  CGC  CGG
                                   ___  CA
GAM1774  JUNB    5'  AGGGTCCCTGCGGGGCCGC   13754        ACAGC
                                AGGGTCCCT    GCCGC
                                |||||||||    |||||
                                TCCCAGGGA    CGGCG
                                     CGCCC
GAM1774  KCNN2   5'  GGGTCCGGAAGGCGCCGCC   34670      CTACA
                                GGGTCC    GCGCCGCC
                                ||||||    ||||||||
                                CCCAGG    CGCGGCGG
                                   CCTTC
GAM1774  KCNQ2   3'  CAGGGCCCTGCCCAGC     41506      T   ACA  G  _
                                CAGGG CCCT   GC CC GC
                                ||||| ||||   || || ||
                                GTCCC GGGA   CG GG CG
                                  _   ___  _  T
GAM1774  KIFC3   5'  CAGGATCCAGGCGTCGCC   24453       CTACA  C
                                CAGGGTCC    GCG CGCC
                                ||||||||    ||| ||||
                                GTCCTAGG    CGC GCGG
                                     TC___  A
GAM1774  KRT16   3'  CAGGGTCCTGACCCAGGCC   45448       CTA__  C
                                CAGGGTCC    CAG GCC
                                ||||||||    ||| |||
                                GTCCCAGG    GTC CGG
                                     ACTGG  _
GAM1774  LARGE   5'  CAGGGTCCCGGCAGGCGCTGCC 21858        TA  _  C
                                CAGGGTCCC  CAG CGC GCC
                                |||||||||  ||| ||| |||
                                GTCCCAGGG  GTC GCG CGG
                                     CC   C   A
GAM1774  LZTR1   5'  CAGGGCGGGAGGCGCCGCC   27633      CCCTACA
                                CAGGGT      GCGCCGCC
                                ||||||      ||||||||
                                GTCCCG      CGCGGCGG
                                   CCCTC__
GAM1774  MAP4    3'  CAGGGCCCTAAGCTGCC     36269      T    C  _
                                CAGGG CCCTA AGC GCC
                                ||||| ||||| ||| |||
                                GTCCC GGGAT TCG CGG
                                  _    _  A
GAM1774  MAPK1   5'  CAGGGACTGCGCCGC       15648      TCCCT  A
                                CAGGG    AC GCGCCGC
                                |||||    || |||||||
                                GTCCC    TG CGCGGCG
                                  _____  A
GAM1774  MECP2   3'  CAGGGCCCCTGCCTGC      22578        ACAGC  _
                                CAGGGTCCCT    GCC GC
                                ||||||||||    ||| ||
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                                GTCCCGGGGA    CGG CG
                                      _____   A
GAM1774  MLC1    3'  CAGGGTCTGCAGGCCGCC   40149       CCTA  C
                                CAGGGTC   CAG GCCGCC
                                |||||||   ||| ||||||
                                GTCCCAG   GTC CGGCGG
                                   AC__   _
GAM1774  MMP25   5'  CAGGGTCGCGCCGC       35377       CCTACA
                                CAGGGTC    GCGCCGC
                                |||||||    |||||||
                                GTCCCAG    CGCGGCG
                                      ______
GAM1774  MOG     3'  AGGTCCCTAGTAGGCTGCC   14608        C_  C  C
                                GGGTCCCTA  AG GC GCC
                                |||||||||  || || |||
                                TCCAGGGAT  TC CG CGG
                                     CA  _  A
GAM1774  MYO1B   3'  AGGTCCCTGCCACCACGCC   29225        A_  G  C
                                GGGTCCCT  CA CGC GCC
                                ||||||||  || ||| |||
                                TCCAGGGA  GT GTG CGG
                                     CG  G  _
GAM1774  OSCAR   3'  CAGGGTCCCAGCTTCTCCGCC  39075        TACAGCG
                                CAGGGTCCC     CCGCC
                                |||||||||     |||||
                                GTCCCAGGG     GGCGG
                                      TCGAAGA
GAM1774  P2RX3   3'  CAGGGTCCTCTGTGGGGAGGCC 14993        _  AC____  C
                                CAGGGTCC CT    AG GCC
                                |||||||| ||    || |||
                                GTCCCAGG GA    TC CGG
                                     A  CACCCC  _
GAM1774  PKIA    5'  AGGTCCCGCGCACGCCGCC   27735       TACA
                                GGGTCCC   GCGCCGCC
                                |||||||   ||||||||
                                TCCAGGG   TGCGGCGG
                                     CGCG
GAM1774  PKIG    3'  CAGGGTCCCTGCCCGGGCCGC  28191         ACAGC_
                                CAGGGTCCCT    GCCGC
                                ||||||||||    |||||
                                GTCCCAGGGA    CGGCG
                                      CGGGCC
GAM1774  PLA2G2D 3'  CAGGGTCCCCAGTGCC     29631        TA  C
                                CAGGGTCCC  CAG GCC
                                |||||||||  ||| |||
                                GTCCCAGGG  GTC CGG
                                     __  A
GAM1774  PRKAR2B 5'  AGGGCCCCGCGGCTGCC    15617        TACA  _ C
                                AGGGTCCC   GCG C GCC
                                ||||||||   ||| | |||
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                                TCCCGGGG   CGC G CGG
                                    ____   C A
GAM1774  PROK1    3'  GGGCTCCCTACACCTGCC    37100    _      GC_
                                GGG TCCCTACA   GCC
                                ||| ||||||||   |||
                                CCC AGGGATGT   CGG
                                  G       GGA
GAM1774  PRX      3'  CAGGGCCCTCCACCCGC     34107      T   ACA  G
                                CAGGG CCCT   GC CCGC
                                ||||| ||||   || ||||
                                GTCCC GGGA   TG GGCG
                                   _   GG_ _
GAM1774  PTEN     5'  GGGTCCCTGGATGTGCCGCC   7219         ACAGC_
                                GGGTCCCT     GCCGCC
                                ||||||||     ||||||
                                CCCAGGGA     CGGCGG
                                     CCTACA
GAM1774  PTGER1   5'  GGGTCCCCATCACCGGCCGC   9636          _  G  _
                                GGGTCCCTA CA CG CCGC
                                ||||||||| || || ||||
                                CCCAGGGGT GT GC GGCG
                                     A  G  C
GAM1774  PTK7     3'  CAGGGATCTTGCCCATCATGC  15857       _ ___   _ _
                                CAGGG TC   CCTA CA GC
                                ||||| ||   |||| || ||
                                GTCCC AG   GGGT GT CG
                                   T  AAC    A  A
GAM1774  PTPN7    5'  CAGGGTCCTCTCCTAACTGC   38723        _  AC_  _
                                CAGGGTCC CT   AGC GC
                                |||||||| ||   ||| ||
                                GTCCCAGG GA   TTG CG
                                     A  GGA   A
GAM1774  PUNC     3'  GGGTCCCTGTCAAGGCTGCC   44882         A_   C  C
                                GGGTCCCT  CAG GC GCC
                                ||||||||  ||| || |||
                                CCCAGGGA  GTT CG CGG
                                     CA   C  A
GAM1774  RAP1B    5'  GGGTCCCTGCAGCCAGCGTCGC 31822         A_____    C
              C                  GGGTCCCT    CAGCG CGCC
                                 ||||||||    ||||| ||||
                                 CCCAGGGA    GTCGC GCGG
                                     CGTCG    A
GAM1774  RBM8A    3'  CAGAGTCCCTGCAAAATGGCC  23010          A   C___
                                CAGGGTCCCT CAG    GCC
                                |||||||||| |||    |||
                                GTCTCAGGGA GTT    CGG
                                     C   TTAC
GAM1774  RGS3     3'  CAGGGCCCCTGACCTGCC     39121          _  AGC
                                CAGGGTCCCT AC   GCC
                                |||||||||| ||   |||
```

```
                              GTCCCGGGGA TG   CGG
                                   C  GA_
GAM1774  SCN4A    3'  AGGTCCCTGACTCCCGC     7317         ACA  G_
                              GGGTCCCT   GC  CCGC
                              ||||||||   ||  ||||
                              TCCAGGGA   TG  GGCG
                                   C__  AG
GAM1774  SCNN1B   3'  CAGGGTCCCTACACC       7334           AGC
                              CAGGGTCCCTAC   GCC
                              ||||||||||||   |||
                              GTCCCAGGGATG   TGG
                                    ____
GAM1774  SH3BP2   3'  CAGGGCCCCTGTGACTGCC   16625          ACA  _
                              CAGGGTCCCT   GC GCC
                              ||||||||||   || |||
                              GTCCCGGGGA   TG CGG
                                   CAC  A
GAM1774  SH3GL1   3'  CAGGGCCCTGCAGGAGACC   16666      T   A   C__
                              CAGGG CCCT CAG   GCC
                              ||||| |||| |||   |||
                              GTCCC GGGA GTC   TGG
                                 _   C   CTC
GAM1774  SLC12A4  3'  CAGGGTCCCACAAGACC     22889        T   C
                              CAGGGTCCC ACAG GCC
                              ||||||||| |||| |||
                              GTCCCAGGG TGTT TGG
                                   _   C
GAM1774  SLC19A1  5'  CAGGGCCCTGCAAACC      16845      T   A   C
                              CAGGG CCCT CAG GCC
                              ||||| |||| ||| |||
                              GTCCC GGGA GTT TGG
                                 _   C   _
GAM1774  SLC4A1   5'  GGGTCCCTGCTCACGAGCC   7357         ACA_  CC
                              GGGTCCCT   GCG  GCC
                              ||||||||   |||  |||
                              CCCAGGGA   TGC  CGG
                                   CGAG  T_
GAM1774  SNL      5'  GGGTCCCTGCGGCGGCGCC   16946        ACA  C
                              GGGTCCCT   GCG CGCC
                              ||||||||   ||| ||||
                              CCCAGGGA   CGC GCGG
                                   CGC  C
GAM1774  SOLH     5'  GGGCCCCTCTCGCCGCC     24832        ACAG
                              GGGTCCCT   CGCCGCC
                              ||||||||   |||||||
                              CCCGGGGA   GCGGCGG
                                   GA__
GAM1774  SOX4     3'  GGGTCCAAAACGCCGCC     16990       CTAC
                              GGGTCC   AGCGCCGCC
                              ||||||   |||||||||
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                                CCCAGG   TTGCGGCGG
                                   TT__
GAM1774  SPAG4    5'  GGGCCTCCTTCAGCCGC     17059      _  A  GC
                                GGGTC CCT CA  GCCGC
                                ||||| ||| ||  |||||
                                CCCGG GGA GT  CGGCG
                                   A  A  __
GAM1774  STAT6    3'  CAGGGTCCCTTGAGCTGC    17150        AC  _
                                CAGGGTCCCT  AGC GC
                                ||||||||||  ||| ||
                                GTCCCAGGGA  TCG CG
                                      AC  A
GAM1774  STK11    5'  CAGGGTCCTGGAGTCCCGCCGC 7830        CTACAG__
              C                  CAGGGTCC      CGCCGCC
                                ||||||||      |||||||
                                GTCCCAGG      GCGGCGG
                                   ACCTCAGG
GAM1774  TBL3     5'  AGGGTCCCGGCAGCCACCGCC  26984       TA   _
                                AGGGTCCC  CAGC GCCGCC
                                ||||||||  |||| ||||||
                                TCCCAGGG  GTCG TGGCGG
                                   CC   G
GAM1774  TFDP1    5'  GGGTCCCTGCCCTGGGCC    28286       ACA  G  ___
                                GGGTCCCT   GC CC   GCC
                                ||||||||   || ||   |||
                                CCCAGGGA   CG GG   CGG
                                   ___  _  ACC
GAM1774  TGFB1    5'  GGGTCCCCAAGTCCTGCC    8550        C  CG  _
                                GGGTCCCTA AG  CC GCC
                                |||||||||  ||  || |||
                                CCCAGGGGT TC  GG CGG
                                   _  A_  A
GAM1774  TMPRSS2  3'  CAAGGTCCCTGGGAATGCTGC  24928         ACAGC_  C
                                CAGGGTCCCT     GC GC
                                ||||||||||     || ||
                                GTTCCAGGGA     CG CG
                                      CCCTTA  A
GAM1774  TNFAIP1  3'  CAGGGCCTCTACAGCACC    34475       C
                                CAGGGTC CTACAGCGCC
                                |||||||  ||||||||||
                                GTCCCGG GATGTCGTGG
                                   A
GAM1774  TOP3B    5'  AGGGTCCCGCAGCCCGCC    19460       TA   G
                                AGGGTCCC  CAGC CCGCC
                                ||||||||  |||| |||||
                                TCCCAGGG  GTCG GGCGG
                                   C_   _
GAM1774  TPTE     5'  GGGTCCCTAGAGCCGCC     30023       AC  C
                                GGGTCCCT  AG GCCGCC
                                ||||||||  || ||||||
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```
                                CCCAGGGA  TC CGGCGG
                                   __  T
GAM1774  WHSC1    3'  CAGGGTCCTTCACAGAGC    39400        C_    C
                                CAGGGTCC  TACAG GC
                                ||||||||  ||||| ||
                                GTCCCAGG  GTGTC CG
                                   AA    T
GAM1774  WHSC1    5'  CAGGGTCCTTCACAGAGC    39356        C_    C
                                CAGGGTCC  TACAG GC
                                ||||||||  ||||| ||
                                GTCCCAGG  GTGTC CG
                                   AA    T
GAM1774  WHSC1L1  5'  GGGTCGCCGCGCCGCC     32820      _  TACA
                                GGGTC CC   GCGCCGCC
                                ||||| ||   ||||||||
                                CCCAG GG   CGCGGCGG
                                  C  ____
GAM1774  XRCC3    3'  CAGGGTCCTGCAGGTGGCC   24101        CTA   C__
                                CAGGGTCC   CAG   GCC
                                ||||||||   |||   |||
                                GTCCCAGG   GTC   CGG
                                   AC_   CAC
GAM1774  YWHAH    5'  CAGGCTGCAGGCAGCGCCGCC  18192      GTCCCTA
                                CAGG      CAGCGCCGCC
                                ||||      ||||||||||
                                GTCC      GTCGCGGCGG
                                  GACGTCC
GAM1774  ZNF2     5'  CAGGATCCAAAATGGCAGCGC  34377        CTA____
                                CAGGGTCC      CAGCGC
                                ||||||||      ||||||
                                GTCCTAGG      GTCGCG
                                   TTTTACC
GAM1774  ZNF2     5'  CAGGGTCCTGGCGACTGCGC   34378        CT___  A
                                CAGGGTCC    AC GCGC
                                ||||||||    || ||||
                                GTCCCAGG    TG CGCG
                                   ACCGC  A
GAM1775  FACL4    3'  TACAACTTTAGTTGAT      35685       G    ACAAA
                                TACAA CTTT    AGTTGAT
                                ||||| ||||    |||||||
                                ATGTT GAAA    TCAACTA
                                  _   _____
GAM1775  HS2ST1   3'  TACAGCTTTACAAATAACCCAT 29336      A        _ GT G
            GG                    TACA GCTTTACAAA A  T ATGG
                                ||||| ||||||||||  |  | ||||
                                ATGT CGAAATGTTT T  G TACC
                                  _        A TG G
GAM1775  LTB4R    5'  TACAAGCTTTGGCAGGAACTGG 8887          ACAAA  TTGA
                                TACAAGCTTT    AG    TGG
                                ||||||||||    ||   |||
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                                ATGTTCGAAA    TC   ACC
                                     CCG__  CTTG
GAM1775  PPP5C    3'  TACAAACTTTACAAAGTAAAAG 26493            A  T  T
             G                   TACAAGCTTTACAAA GT GA GG
                                 ||||||||||||||| || || ||
                                 ATGTTTGAAATGTTT CA TT CC
                                        _  T  T
GAM1776  NBEA     3'  AATCATTTGATAGCCATCATTT 45429       CCAAC   G
             T                   GATCAT    AGC TATCATTTT
                                 ||||||    ||| |||||||||
                                 TTAGTA    TCG GTAGTAAAA
                                    AACTA   _
GAM1776  RFXAP    3'  ATCCAGATTACTTATCATTTT  8050       ACA_  G
                                 ATCCA    GC TATCATTTT
                                 |||||    || |||||||||
                                 TAGGT    TG ATAGTAAAA
                                    CTAA  A
GAM1777  GNAI1    3'  TTATGTTATTTCCAAAGCCATC 13169      A    A      T
                                 TTAT TTATT TCCAAAG CTATC
                                 |||| ||||| ||||||| |||||
                                 AATA AATAA AGGTTTC GGTAG
                                   C    _      _
GAM1778  FGF23    3'  GTTACATTTTTATAAATATCTA 33957    GT__
                                 GT    TTTTTATAAATATCTA
                                 ||    ||||||||||||||||
                                 CA    AAAAATATTTATAGAT
                                  ATGT
GAM1778  GASC1    3'  ATATATTTTATAAATATCTA   42029      T
                                 GTGT TTTTATAAATATCTA
                                 |||| ||||||||||||||
                                 TATA AAAATATTTATAGAT
                                   T
GAM1778  MYBL1    3'  GTGTACGTATAAATATCT    41979      TTTT
                                 GTGT    TATAAATATCT
                                 ||||    ||||||||||
                                 CACA    ATATTTATAGA
                                   TGC_
GAM1779  CARPX    3'  TGATGGAGGTTGTAAGAGT    33579        TC_   AA
                                 TGATGGAG   GTAA  AGT
                                 ||||||||   ||||  |||
                                 ACTACCTC   CATT  TCA
                                      CAA    C_
GAM1779  DAAM2    3'  TGATGGAGTTTTAGAAAAATTT 45182         CG  _
             T                   TGATGGAGT  TA AAAAGTTTT
                                 |||||||||  || |||||||||
                                 ACTACCTCA  AT TTTTTAAAA
                                       AA  C
GAM1779  TBXA2R   5'  ATGGACCTAAGAAGTTTTAT   9846       G  G   A
                                 ATGGA TC TAA AAGTTTTAT
                                 ||||| || ||| |||||||||
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                                TACCT GG ATT TTCAAAATA
                                  _ _  C
GAM1779  DMP1     3'  CGTAAAGAGGAATTTCTTTCTC 20601       A  TTTT  C
                                CGTAAA AG    AT TCTTTCTC
                                |||||| ||    || ||||||||
                                GCATTT TC    TA AGAAAGAG
                                   C  CT__  A
GAM1779  EDNRA    3'  AAAAATTCGATCTTTTTCTC  41990        T    C
                                AAAAGTTT ATCT TTTCTC
                                |||||||| |||| ||||||
                                TTTTTAAG TAGA AAAGAG
                                     C    A
GAM1779  EPM2A    3'  TAAAAAAACACTTCTCTTTCT  24973        TTTTA
                                TAAAAAG    TCTCTTTCT
                                |||||||    |||||||||
                                ATTTTTT    AGAGAAAGA
                                     TGTGA
GAM1780  RLN2     3'  TCTAAGAATTGATGGGACCTAA 39592          TACA__
                                TCTAAGAATT     ATCTAA
                                ||||||||||     ||||||
                                AGATTCTTAA     TGGATT
                                      CTACCC
GAM1781  COL6A2   3'  GGGCGTCGTCCGAGTGAGC   38446      A         C
                                GGGC TTGTCCGAGTGA GC
                                |||| |||||||||||| ||
                                CCCG AGCAGGCTCACT CG
                                  C          _
GAM1781  PLXNB3   5'  GGGCATTGTCCTGGTGGGC   23948          GA   AC
                                GGGCATTGTCC  GTG  GC
                                ||||||||||  |||  ||
                                CCCGTAACAGG  CAC  CG
                                      AC   C_
GAM1781  RAD1     5'  GGGCATCGTCCACTGCGCATTC 15995           AG  A
                                GGGCATTGTCCG  TG CGCATTC
                                ||||||||||||  || |||||||
                                CCCGTAGCAGGT  AC GCGTAAG
                                      G_  _
GAM1781  SLC16A2  3'  GGGCATTGTTGCTCCAGTA   27152        ____   G
                                GGGCATTG    TCC AGTG
                                ||||||||    ||| ||||
                                CCCGTAAC    AGG TCAT
                                     AACG   _
GAM1782  MLLT2    3'  TACAAAATCATTGTGTTGA   25504       T      CTA
                                TACAAA TCATTGT   TGA
                                |||||| |||||||   |||
                                ATGTTT AGTAACA   ACT
                                   T      CA_
GAM1782  RAB1A    3'  CAAATTCATTGCTGTGA     43183          T  A
                                CAAATTCATTG CT TGA
                                |||||||||| || |||
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                                GTTTAAGTAAC GA ACT
                                      _  C
GAM1783  FANCC    3'  CACGAAGCATGTTATATG    43267        TTATT
                                CACGGAGT    TTATATG
                                ||||||||    |||||||
                                GTGCTTCG    AATATAC
                                     TAC__
GAM1783  FANCC    3'  CACGAAGCATGTTATATG    43267        TTATT
                                CACGGAGT    TTATATG
                                ||||||||    |||||||
                                GTGCTTCG    AATATAC
                                     TAC__
GAM1784  ARHGAP6  3'  AAATATATATTATATATGG   30205         C    C
                                AAATATATA TATAT TGG
                                ||||||||| ||||| |||
                                TTTATATAT ATATA ACC
                                      A    T
GAM1784  CNGA3    3'  TAAAATATATACATTTTGAGGA 10537           TATATCT
                                TAAAATATATAC      GGA
                                ||||||||||||      |||
                                ATTTTATATATG      CCT
                                      TAAAACT
GAM1784  CREBL2   3'  AAAATATACTTTATTTGGAA   10572    T     A   C
                                AA ATATACT TAT TGGAA
                                || ||||||| ||| |||||
                                TT TATATGA ATA ACCTT
                                 T     A   A
GAM1784  CYP51    3'  TAAAATTACTATCTGGAA    8959       ATA    TA
                                TAAAAT   TACTA  TCTGGAA
                                ||||||   |||||  |||||||
                                ATTTTA   ATGAT  AGACCTT
                                   ____    __
GAM1784  IQGAP2   3'  TAAAATATATACTTTTATACAG 27373           A_   CT
            AAA                   TAAAATATATACT  TAT  GGAAA
                                ||||||||||||||  |||  |||||
                                ATTTTATATATGA  ATA  TCTTT
                                      AA   TG
GAM1784  ITGA2    3'  TAAAATATACACAAGTGGAA   13603          TATATC
                                TAAAATATATAC     TGGAA
                                ||||||||||||     |||||
                                ATTTTATATGTG     ACCTT
                                      TTC____
GAM1784  NAP1L3   3'  TAAAATATAGACTACCAAGAAA 21212         T    ATCT
                                TAAAATATA ACTAT    GGAAA
                                ||||||||| |||||    |||||
                                ATTTTATAT TGATG    TCTTT
                                     C    GT__
GAM1784  RAB38    3'  AATATATTGAAATCTGGAAA   41261        ACTAT
                                AATATAT    ATCTGGAAA
                                |||||||    |||||||||
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                                TTATATA    TAGACCTTT
                                   ACTT_
GAM1784  RUNX1    3'  CAAGATACATAAATATCTGG   12008     A      CT
                                TAA ATATATA  ATATCTGG
                                ||| |||||||  ||||||||
                                GTT TATGTAT  TATAGACC
                                  C      T_
GAM1784  SACM1L   3'  TACTATAACTACCTGGAA    30427      ____
                                TACTA   TATCTGGAA
                                |||||   |||||||||
                                ATGAT   ATGGACCTT
                                   ATTG
GAM1784  ZFHX1B   3'  TAAAATATATCTATATATTGAA 31340          A     CTG
                                TAAAATATAT CTATAT   GAA
                                |||||||||| ||||||   |||
                                ATTTTATATA GATATA   CTT
                                      _     TAA
GAM1785  ARF3     3'  GGGCCCTGACCTTAGCAGGTTA 11676           GAGT
                                GGGCTCTGACCT    GCAGGTTA
                                ||||||||||||   ||||||||
                                CCCGGGACTGGA    CGTCCAAT
                                      AT__
GAM1785  NPY2R    5'  GAGCTCTGGCTCAGGT      9495         ACCTGA  G
                                GGGCTCTG     GT CAGGT
                                ||||||||     || |||||
                                CTCGAGAC     CG GTCCA
                                     _______ A
GAM1785  NPY2R    3'  GAGCTCTGGCTCAGGT      9495         ACCTGA  G
                                GGGCTCTG     GT CAGGT
                                ||||||||     || |||||
                                CTCGAGAC     CG GTCCA
                                     _______ A
GAM1785  UBE2L6   3'  GGGCTCTGGCCTCAGTCCA   20124        A  G  G
                                GGGCTCTG CCT AGT CA
                                |||||||| ||| ||| ||
                                CCCGAGAC GGA TCA GT
                                     C  G  G
GAM1786  CDK2     3'  GAGGTGGACGTCAGAG      12203    AA       CTT
                                GA  TGGACGTCA   GAG
                                ||  |||||||||   |||
                                CT  ACCTGCAGT   CTC
                                 CC       ___
GAM1786  DSCR3    3'  GACAGGAGGATCACTTGA    25826    AAT   C_
                                GA   GGA  GTCACTTGA
                                ||   |||  |||||||||
                                CT   CCT  TAGTGAACT
                                 GT_   CC
GAM1786  FGF13    3'  AGAAATCTACACTTGAG     37981       GGACGT
                                AGAAAT     CACTTGAG
                                ||||||     ||||||||
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                                TCTTTA     GTGAACTC
                                   GAT___
GAM1786 G1P3     3' GACAGGAGGATCACTTGA    35639    AAT  C_
                                GA  GGA  GTCACTTGA
                                ||  |||  |||||||||
                                CT  CCT  TAGTGAACT
                                 GT_  CC
GAM1786 IFNAR2   3' GAGGAGGGCAGATCACTTGAG 9317     AAT_ AC_
                                GA   GG   GTCACTTGAG
                                ||   ||   ||||||||||
                                CT   CC   TAGTGAACTC
                                 CCTC  GTC
GAM1786 NR3C2    3' AAGAAATGGACGCTAACGAG  9466           CACT
                                AAGAAATGGACGT   TGAG
                                ||||||||||||   ||||
                                TTCTTTACCTGCG   GCTC
                                       ATT_
GAM1786 NR4A2    3' TACAGAAATGGGGGGCAGCTTG 26166     A      AC_  CA
             AG                   TACA GAAATGG   GT  CTTGAG
                                ||||  |||||||   ||  ||||||
                                ATGT CTTTACC   CG  GAACTC
                                  _     CCC  TC
GAM1786 CDK2     3' GAGGTGGACGTCAGAG     12203    AA       CTT
                                GA  TGGACGTCA   GAG
                                ||  |||||||||   |||
                                CT  ACCTGCAGT   CTC
                                 CC       ___
GAM1786 DSCR3    3' GACAGGAGGATCACTTGA    25826    AAT  C_
                                GA   GGA  GTCACTTGA
                                ||   |||  |||||||||
                                CT   CCT  TAGTGAACT
                                 GT_  CC
GAM1786 FGF13    3' AGAAATCTACACTTGAG     37981       GGACGT
                                AGAAAT     CACTTGAG
                                ||||||     ||||||||
                                TCTTTA     GTGAACTC
                                   GAT___
GAM1786 G1P3     3' GACAGGAGGATCACTTGA    35639    AAT  C_
                                GA   GGA  GTCACTTGA
                                ||   |||  |||||||||
                                CT   CCT  TAGTGAACT
                                 GT_  CC
GAM1786 IFNAR2   3' GAGGAGGGCAGATCACTTGAG 9317     AAT_ AC_
                                GA   GG   GTCACTTGAG
                                ||   ||   ||||||||||
                                CT   CC   TAGTGAACTC
                                 CCTC  GTC
GAM1786 NR3C2    3' AAGAAATGGACGCTAACGAG  9466           CACT
                                AAGAAATGGACGT   TGAG
                                ||||||||||||   ||||
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                                TTCTTTACCTGCG   GCTC
                                      ATT_
GAM1786 NR4A2   3' TACAGAAATGGGGGGCAGCTTG 26166     A     AC_ CA
          AG                   TACA GAAATGG  GT  CTTGAG
                               |||| |||||||  ||  ||||||
                               ATGT CTTTACC  CG  GAACTC
                                 _     CCC  TC
GAM1787 ABR     5' GGGCGGGCGGGAGCCGGGGGAG 35015    A   C   CT_
                               GG GCGG CGG  CCGGGGGAG
                               || |||| |||  |||||||||
                               CC CGCC GCC  GGCCCCCTC
                                _   C   CTC
GAM1787 AP2A1   5' GGGGAGGGCTGGCTGGCGGG  39107      C   C   CC _
                               GGGGAG GGC GGCT  GG GGG
                               |||||| ||| ||||  || |||
                               CCCCTC CCG CCGA  CC CCC
                                  _  A   __ G
GAM1787 ATP8A2  3' GGGGTGCGGCGCGGGGGA   45261     A    CGGCTC
                               GGGG GCGGC     CGGGGGA
                               |||| |||||     |||||||
                               CCCC CGCCG     GCCCCCT
                                 A    C_____
GAM1787 BTAF1   5' GGGGAGCGGCCGGTGCGG   43669          CTC
                               GGGGAGCGGCCGG  CGG
                               ||||||||||||  |||
                               CCCCTCGCCGGCC  GCC
                                     AC_
GAM1787 CDK2AP1 5' GGGGCGGCCGGGGCCGGGAG  21601    A      CT
                               GGG GCGGCCGG  CCGGGGG
                               ||| ||||||||  |||||||
                               CCC CGCCGGCC  GGCCCTC
                                 _      CC
GAM1787 CKB     5' GGCGGGCGGCCGGGCGGGGG  12256   _ A      CTC
                               GG GG GCGGCCGG  CGGGGG
                               || || ||||||||  ||||||
                               CC CC CGCCGGCC  GCCCCC
                                G _      C__
GAM1787 DDEF2   5' GGGGAGCGCCGGGCGCGGGAG  19322       G   CTC  G
                               GGGGAGCG CCGG  CG GGGAG
                               ||||||| ||||  || |||||
                               CCCCTCGC GGCC  GC CCCTC
                                    _   C__  G
GAM1787 DLX4    5' GGGAAAGGGGTTCCGGGGG   12577     C  CC  C
                               GGGAG GG  GG TCCGGGGG
                               ||||| ||  || ||||||||
                               CCCTT CC  CC AGGCCCCC
                                  T  __  A
GAM1787 F2RL3   3' GGGGAGGGGCGTGGCTGGGGGA 19525      C  C_   CC
          G                    GGGGAG GGC  GGCT  GGGGGAG
                               |||||| |||  ||||  |||||||
```

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                                CCCCTC CCG  CCGA  CCCCCTC
                                   C   CA   __
GAM1787  FZD4     5'  GGGCAGCGGCCGGCTCTCCAG  29160     G        __
                                GGG AGCGGCCGGC  TCCGG
                                ||| ||||||||||  |||||
                                CCC TCGCCGGCCG  AGGTC
                                  G         AG
GAM1787  GALGT    5'  GGGGGCGGTTGGCGGGG     11189     A    CC   TCC
                                GGGG GCGG  GGC   GGGG
                                |||| ||||  |||   ||||
                                CCCC CGCC  CCG   CCCC
                                  _    AA   ___
GAM1787  GFAP     3'  GGGGAGCAGCTGGGGTGGTGGG 13124          C  CTCCG_
              GAG                   GGGGAGCGGC GG     GGGGAG
                                |||||||||| ||      ||||||
                                CCCCTCGTCG CC     CCCCTC
                                     A  CCACCA
GAM1787  GLTSCR1  3'  GGGGAGAGGTTCGGGGGA    31839       C  CCGGCTC
                                GGGGAG GG      CGGGGGA
                                |||||| ||      |||||||
                                CCCCTC CC      GCCCCCT
                                   T  AA_____
GAM1787  GRB14    5'  GAGGAGCGGCCGGTGGGTGGGG 21034           CTCCG
                                GGGGAGCGGCCGG    GGGG
                                ||||||||||||    ||||
                                CTCCTCGCCGGCC    CCCC
                                       ACCCA
GAM1787  KCNMB4   5'  GGGGAGTGGGCGGCGAGGGGG  30949       C  C    TCC
                                GGGGAG GG CGGC   GGGGG
                                |||||| || ||||   |||||
                                CCCCTC CC GCCG   CCCCC
                                   A  C    CT_
GAM1787  MADH7    3'  GGGGAGAGGCTGAGGGGA    25371       C   C GCTCC
                                GGGGAG GGC G    GGGGGA
                                |||||| ||| |    ||||||
                                CCCCTC CCG C    TCCCCT
                                   T   A _____
GAM1787  MBD3     3'  GGGGGGCCGGCTGGCAGTGGAG 19422      AGC      C_   G
                                GGGG   GGCCGGCT  CGG GGAG
                                ||||   ||||||||  ||| ||||
                                CCCC   CCGGCCGA  GTC CCTC
                                  ___       CC   A
GAM1787  NR1D1    3'  GGGGAGGGTTGTGGGGGA    34704       CGGCC  CTCC
                                GGGGAG    GG    GGGGGA
                                ||||||    ||    ||||||
                                CCCCTC    CC    CCCCCT
                                   _____  AACA
GAM1787  NRXN1    5'  GGGGAGCGGGCGGCGCGGAG   22051         C    TC
                                GGGGAGCGG CGGC  CGGGG
                                |||||||| ||||  |||||
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                                CCCCTCGCC GCCG  GCCTC
                                     C   C_
GAM1787  NRXN2    5'  GGGGAGCGCCCGGGGG      31488        GCCGGC
                                GGGGAGCG     TCCGGGGG
                                ||||||||     ||||||||
                                CCCCTCGC     GGGCCCCC
                                     _______
GAM1787  OTOF     3'  GGGGAGCGGCTGGCGGGAG    22063          C   TCC
                                GGGGAGCGGC GGC   GGGGG
                                |||||||||| |||   |||||
                                CCCCTCGCCG CCG   CCCTC
                                     A  ___
GAM1787  OTP      3'  AGGGGCGGCCGGGAGACGGGGG 36989      A       CTC_
                                GGGG GCGGCCGG    CGGGGG
                                |||| ||||||||    ||||||
                                TCCC CGCCGGCC    GCCCCC
                                  _       CTCT
GAM1787  p100     5'  GGAGCGGCTGGCCGGACTGGAG 41112        C   TC   __
                                GGAGCGGC GGC  CGGG  GGAG
                                |||||||| |||  ||||  ||||
                                CCTCGCCG CCG  GCCT  CCTC
                                     A  __   GA
GAM1787  PCBP1    5'  GCGGGCGGCGTTCGGGGGAG   26219     C    TC_
                                GCGG CGGC   CGGGGGAG
                                |||| ||||   ||||||||
                                CGCC GCCG   GCCCCCTC
                                  C   CAA
GAM1787  PGF      5'  GGGGAGCGGCCCGGCGGGG    15254          _  TCC
                                GGGGAGCGGCC GGC   GGGG
                                |||||||||| |||   ||||
                                CCCCTCGCCGG CCG   CCCC
                                     G  ___
GAM1787  PGM1     5'  AGGGGCGGCCGGCTGAG      15257      A        CC
                                GGGG GCGGCCGGCT  GGG
                                |||| ||||||||||  |||
                                TCCC CGCCGGCCGA  CTC
                                  _       __
GAM1787  RAX      5'  GGGGAGCGCCGGGAGGCGGGAG 30246        G   CTC_
                                GGGGAGCG CCGG    CGGGGG
                                |||||||| ||||    ||||||
                                CCCCTCGC GGCC    GCCCTC
                                     _   CTCC
GAM1787  SCRT1    3'  GGGGAGGGGCCGGCTCCCTGG  36371       C        GG
                                GGGGAG GGCCGGCTCC  GG
                                |||||| ||||||||||  ||
                                CCCCTC CCGGCCGAGG  CC
                                   C         GA
GAM1787  SHOX     3'  GGGAGGCTCCGGGGGG       27824      GCGGCC
                                GGGA     GGCTCCGGGGG
                                ||||     ||||||||||
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                                CCCT     CCGAGGCCCCC
                                  _______
GAM1787 SLC6A8   5' GGGGGGCGGCCGGGCCGGGGG 24782      A      CT
                                GGGG GCGGCCGG  CCGGGGG
                                |||| ||||||||  |||||||
                                CCCC CGCCGGCC  GGCCCCC
                                  C       C_
GAM1787 SLIT3    5' GGGGAGCGGGCGGCGGAG    16873         C    TCC
                                GGGGAGCGG CGGC   GGGG
                                ||||||||| ||||   ||||
                                CCCCTCGCC GCCG   CCTC
                                     C   ___
GAM1787 TAZ      5' GGGGAGCGGTCGCCGGGG    31771         C  GCT
                                GGGGAGCGG CG   CCGGGG
                                ||||||||| ||   ||||||
                                CCCCTCGCC GC   GGCCCC
                                     A  ___
GAM1787 THRA     5' GGGGGCGGGCGGTGGGAG    17523      A   C   CTCC
                                GGGG GCGG CGG    GGGGG
                                |||| |||| |||    |||||
                                CCCC CGCC GCC    CCCTC
                                  _   C  A___
GAM1787 TMEPAI   5' GGGGGCGGCCGGGGGGG     33616      A       CTCC
                                GGGG GCGGCCGG    GGGGG
                                |||| ||||||||    |||||
                                CCCC CGCCGGCC    CCCCC
                                  _      _____
GAM1788 ATP6V1E1 3' CTCAAGAGTGGGGACTGCAGGG 11785      TCTCG     CA
                                CTCG    GGGGAC  CAGGG
                                ||||    ||||||  |||||
                                GAGT    CCCCTG  GTCCC
                                  TCTCA     AC
GAM1788 CA3      5' TCTCTCTCAAAACTGCAGGG   23216      G     GG   CA
                                TCTC TCTCGG  GAC  CAGGG
                                |||| ||||||  |||  |||||
                                AGAG AGAGTT  TTG  GTCCC
                                  _     ___  AC
GAM1788 CANX     5' CCTCCCGGGGACCGCGG     44663    G       G   ACA
                                C TCTCGGGG ACC   GG
                                | ||||||| |||   ||
                                G AGGGCCCC TGG   CC
                                 G       _  CG_
GAM1788 FUT7     3' GTCTCGGGGACCACAGG     20995          G
                                GTCTCGGGG ACCACAGG
                                ||||||||| ||||||||
                                CAGAGCCCC TGGTGTCC
                                          _
GAM1788 JUP      3' GCCAGGGCCACAGGG       13774     TCG    A
                                GTC   GGGG CCACAGGG
                                |||   |||| ||||||||
```

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                                CGG   TCCC GGTGTCCC
                                  ___   _
GAM1788 MTNR1A   5' TCGCGTCCCGGCCGCAGG    25550    T      GGGA  A
                                TC CGTCTCGG    CC CAGG
                                || ||||||||    || ||||
                                AG GCAGGGCC    GG GTCC
                                 C       ____  C
GAM1788 NONO     3' CTCCGTCTCGGGGGCGGG    44356    T        ACCACA
                                CTC CGTCTCGGGGGG     GG
                                ||| ||||||||||      ||
                                GAG GCAGAGCCCCC     CC
                                  _        GC____
GAM1788 RENT1    3' TCTCGCCTCCTGGCCACAGGG  16260         GGG  A
                                TCTCGTCTC   GG CCACAGGG
                                |||||||||   || ||||||||
                                AGAGCGGAG   CC GGTGTCCC
                                     GA_ _
GAM1788 SLC19A1  3' CCCTCGAGGCAGGGGTCGTGGG 16846       TCT     ACCACA
             G                   CTCTCG   CGGGGG     GGG
                                ||||||   ||||||     |||
                                GGGAGC   GTCCCC     CCC
                                   TCC     AGCAC_
GAM1788 TNFRSF5  3' CTCCTGTCTCAAACTGCAGGG  10355    TC     GGG   CA
                                CTC  GTCTCG   GAC  CAGGG
                                |||  ||||||   |||  |||||
                                GAG  CAGAGT   TTG  GTCCC
                                  GA     ___   AC
GAM1788 VANGL2   3' GTCTAAGACCACAGGG     43462      CGG
                                GTCT   GGGACCACAGGG
                                ||||   ||||||||||||
                                CAGA   TTCTGGTGTCCC
                                  ___
GAM1788 ATP6V1E1 3' CTCAAGAGTGGGGACTGCAGGG 11785      TCTCG     CA
                                CTCG    GGGGAC  CAGGG
                                ||||    ||||||  |||||
                                GAGT    CCCCTG  GTCCC
                                  TCTCA     AC
GAM1788 CA3      5' TCTCTCTCAAAACTGCAGGG   23216     G     GG   CA
                                TCTC TCTCGG  GAC  CAGGG
                                |||| ||||||  |||  |||||
                                AGAG AGAGTT  TTG  GTCCC
                                  _     __   AC
GAM1788 CANX     5' CCTCCCGGGGACCGCGG     44663   G      G   ACA
                                C TCTCGGGG ACC   GG
                                | ||||||| |||   ||
                                G AGGGCCCC TGG   CC
                                 G       _  CG_
GAM1788 FUT7     3' GTCTCGGGGACCACAGG     20995         G
                                GTCTCGGGG ACCACAGG
                                ||||||||| ||||||||
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                                CAGAGCCCC TGGTGTCC
                                          _
GAM1788 JUP      3' GCCAGGGCCACAGGG      13774     TCG    A
                                GTC   GGGG CCACAGGG
                                |||   |||| ||||||||
                                CGG   TCCC GGTGTCCC
                                 ___   _
GAM1788 MTNR1A   5' TCGCGTCCCGGCCGCAGG    25550    T      GGGA  A
                                TC CGTCTCGG    CC CAGG
                                || ||||||||    || ||||
                                AG GCAGGGCC    GG GTCC
                                 C       ____ C
GAM1788 NONO     3' CTCCGTCTCGGGGGCGGG    44356    T        ACCACA
                                CTC CGTCTCGGGGGG     GG
                                ||| ||||||||||     ||
                                GAG GCAGAGCCCCC     CC
                                 _        GC____
GAM1788 RENT1    3' TCTCGCCTCCTGGCCACAGGG  16260        GGG  A
                                TCTCGTCTC   GG CCACAGGG
                                |||||||||   || ||||||||
                                AGAGCGGAG   CC GGTGTCCC
                                     GA_ _
GAM1788 SLC19A1  3' CCCTCGAGGCAGGGGTCGTGGG 16846       TCT     ACCACA
           G                     CTCTCG   CGGGGG     GGG
                                ||||||   ||||||     |||
                                GGGAGC   GTCCCC     CCC
                                   TCC     AGCAC_
GAM1788 TNFRSF5  3' CTCCTGTCTCAAACTGCAGGG  10355    TC     GGG   CA
                                CTC  GTCTCG   GAC  CAGGG
                                |||  ||||||   |||  |||||
                                GAG  CAGAGT   TTG  GTCCC
                                 GA     ___   AC
GAM1788 VANGL2   3' GTCTAAGACCACAGGG     43462     CGG
                                GTCT   GGGACCACAGGG
                                ||||   ||||||||||||
                                CAGA   TTCTGGTGTCCC
                                       ___
GAM1789 HCFC1    3' TGCAGCAGTTGGCAGTGCGGCC 43399         AA  TC  C
           T                     TGTAGCAGTT  CG  GC GGCCT
                                ||||||||||  ||  || |||||
                                ACGTCGTCAA  GT  CG CCGGA
                                     CC  CA  _
GAM1789 HCFC1    3' TGCAGCAGTTGGCAGTGCGGCC 43399         AA  TC  C
           T                     TGTAGCAGTT  CG  GC GGCCT
                                ||||||||||  ||  || |||||
                                ACGTCGTCAA  GT  CG CCGGA
                                     CC  CA  _
GAM1790 IL2RA    3' TCTTTATACTACATATAGGGTG 7673       _   CA   CAA
           GA                    TCTTT TAC  ACA   AGGGTGGA
                                ||||| |||  |||   ||||||||
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                                AGAAA ATG  TGT   TCCCACCT
                                  T   A_   ATA
GAM1790  INPP5D   3'  TCTTCTACCAGCACGATGG   44425         A   AAAG
                                TCTTTTACCA CAC    GGTGG
                                |||||||||| |||    |||||
                                AGAAGATGGT GTG    CTACC
                                     C   ____
GAM1790  PLXNA1   3'  TCTCTTGCTGAGGGCAAGGGTG 43630       ACCAACACA
              GA                  TCTTTT        AAGGGTGGA
                                |||||||        |||||||||
                                AGAGAA        TTCCCACCT
                                   CGACTCCCG
GAM1790  PRG4     3'  TCTTTTACAGGTGTGA      25151         CAACACAA  _
                                TCTTTTAC       AGG GTGG
                                ||||||||       ||| ||||
                                AGAAAATG       TCC CACT
                                   _________   A
GAM1790  PRKCN    3'  TCTTTTACAAACACGACTTAAA 25170         C     AAAGGGT
              GA                  TCTTTTAC AACAC      GGA
                                |||||||| |||||       |||
                                AGAAAATG TTGTG      TCT
                                    T    CTGAATT
GAM1790  SUV39H1  3'  TCTTTCACTAGTACAAAG    17227         CAAC
                                TCTTTTAC   ACAAAG
                                ||||||||   ||||||
                                AGAAAGTG   TGTTTC
                                     ATCA
GAM1790  IL2RA    3'  TCTTTATACTACATATAGGGTG 7673       _  CA   CAA
              GA                  TCTTT TAC  ACA   AGGGTGGA
                                ||||| |||  |||   ||||||||
                                AGAAA ATG  TGT   TCCCACCT
                                  T   A_   ATA
GAM1790  INPP5D   3'  TCTTCTACCAGCACGATGG   44425         A   AAAG
                                TCTTTTACCA CAC    GGTGG
                                |||||||||| |||    |||||
                                AGAAGATGGT GTG    CTACC
                                     C   ____
GAM1790  PLXNA1   3'  TCTCTTGCTGAGGGCAAGGGTG 43630       ACCAACACA
              GA                  TCTTTT        AAGGGTGGA
                                |||||||        |||||||||
                                AGAGAA        TTCCCACCT
                                   CGACTCCCG
GAM1790  PRG4     3'  TCTTTTACAGGTGTGA      25151         CAACACAA  _
                                TCTTTTAC       AGG GTGG
                                ||||||||       ||| ||||
                                AGAAAATG       TCC CACT
                                   _________   A
GAM1790  PRKCN    3'  TCTTTTACAAACACGACTTAAA 25170         C     AAAGGGT
              GA                  TCTTTTAC AACAC      GGA
                                |||||||| |||||       |||
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                                AGAAAATG TTGTG      TCT
                                    T    CTGAATT
GAM1790  SUV39H1   3'  TCTTTCACTAGTACAAAG    17227        CAAC
                                TCTTTTAC   ACAAAG
                                ||||||||   ||||||
                                AGAAAGTG   TGTTTC
                                    ATCA
GAM1791  COL4A3    3'  GTGTTATCATCAAGGTAT    36383     CGAT
                                GTGT   TCATCAAGGTAT
                                ||||   ||||||||||||
                                CACA   AGTAGTTCCATA
                                  AT__
GAM1791  GTF2I     5'  GCGTGTCGGTCGCGCTCCTGT  37440        A  CA__  AAG
                                GCGTGTCG TT   TC  GT
                                |||||||| ||   ||  ||
                                CGCACAGC AG   AG  CA
                                    C  CGCG  GA_
GAM1791  COL4A3    3'  GTGTTATCATCAAGGTAT    36383     CGAT
                                GTGT   TCATCAAGGTAT
                                ||||   ||||||||||||
                                CACA   AGTAGTTCCATA
                                  AT__
GAM1791  GTF2I     5'  GCGTGTCGGTCGCGCTCCTGT  37440        A  CA__  AAG
                                GCGTGTCG TT   TC  GT
                                |||||||| ||   ||  ||
                                CGCACAGC AG   AG  CA
                                    C  CGCG  GA_
GAM1792  NRXN2     3'  AGTCAGCCCCGGGACTGAC   31470        G  AAC   AATA
                                AGTCAGCC CG   GGA   AC
                                |||||||| ||   |||   ||
                                TCAGTCGG GC   CCT   TG
                                    G  ___   GAC_
GAM1792  PCTP      3'  AGTCAGCTCTGAACGAAA    34532        CGC
                                AGTCAGC   GAACGGAA
                                |||||||   ||||||||
                                TCAGTCG   CTTGCTTT
                                    AGA
GAM1792  PSCD4     3'  AGTCAGCCTGGGCTCCGCAAAT 30121         ___  GAA  G
            AACG                AGTCAGCC   GC   CG AAATAACG
                                ||||||||   ||   || ||||||||
                                TCAGTCGG   CG   GC TTTATTGC
                                    ACC  AG_  G
GAM1792  NRXN2     3'  AGTCAGCCCCGGGACTGAC   31470        G  AAC   AATA
                                AGTCAGCC CG   GGA   AC
                                |||||||| ||   |||   ||
                                TCAGTCGG GC   CCT   TG
                                    G  ___   GAC_
GAM1792  PCTP      3'  AGTCAGCTCTGAACGAAA    34532        CGC
                                AGTCAGC   GAACGGAA
                                |||||||   ||||||||
```

```
                                TCAGTCG  CTTGCTTT
                                   AGA
GAM1792 PSCD4    3' AGTCAGCCTGGGCTCCGCAAAT 30121       ___ GAA G
           AACG                 AGTCAGCC  GC  CG AAATAACG
                                ||||||||  ||  || ||||||||
                                TCAGTCGG  CG  GC TTTATTGC
                                   ACC AG_ G
GAM1793 B4GALT1  3' TTAAAAGGCACATTCATGC   11294          GGAGAC
                                TTAGAAGGCACG    GC
                                ||||||||||||    ||
                                AATTTTCCGTGT    CG
                                      AAGTA_
GAM1793 GDF2     5' TTAGCGGGCACGGGGAGGAGC 32132     AA      _ AC
                                TTAG GGCACGGG AG GC
                                ||||  |||||||| ||  ||
                                AATC CCGTGCCC TC CG
                                  GC      C CT
GAM1793 MAP4     5' AGGAGGTAGGAGACGTCG    36268    A  CAC      C
                                AG AGG  GGGAGACG CG
                                || |||  |||||||| ||
                                TC TCC  TCCTCTGC GC
                                 C  A__      A
GAM1793 PPP2R5E  5' AGGGGCGGGAGACGGGCGAG  26466    CA       C_
                                AGG CGGGAGACG CGAG
                                |||  |||||||||  ||||
                                TCC GCCCTCTGC GCTC
                                  CC       CC
GAM1793 WHSC1L1  3' TTAGAAGGCACATTGCTGA   35720          GGAGAC C
                                TTAGAAGGCACG    GC GA
                                ||||||||||||    || ||
                                AATCTTCCGTGT    CG CT
                                      AA____ A
GAM1793 BCRP2    3' ATCAACTGCAAGTCTGAGGG  41648        TAAA   TTA
                                ATCAACTGC   CTGA  GGG
                                |||||||||   ||||  |||
                                TAGTTGACG   GACT  CCC
                                     TTCA   ___
GAM1793 MGAT1    3' ATAAACTGCTAGGCTGCAAGG 14424    C      AA  ATT
                                AT AACTGCTA CTG  AGG
                                || ||||||||  |||  |||
                                TA TTGACGAT GAC  TCC
                                 T      CC  GT_
GAM1793 RECQL5   3' TCAGCTGCTTAACTAGG     20171    A    AAAC
                                TCA CTGCT   TGATTAGG
                                ||| |||||   ||||||||
                                AGT GACGA   ATTGATCC
                                  C   _____
GAM1793 STIM1    3' CAACTGCTAGGGGAAGTTGGG 41122        AACT TTA_
                                CAACTGCTA   GA   GGG
                                |||||||||   ||   |||
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                                GTTGACGAT   CT   CCC
                                     CCC_  TCAA
GAM1793  ZNF137   3'  CATCAACTCTAAATGAATGGG  18335       G    C   TTA
                                CATCAACT CTAAA TGA  GGG
                                |||||||| ||||| |||  |||
                                GTAGTTGA GATTT ACT  CCC
                                     _    _  TA_
GAM1794  ACLY     3'  CAAAGTCACAAATATTG    42152       TTT
                                TAAGGTT  ACAAATATTG
                                |||||||  ||||||||||
                                GTTTCAG  TGTTTATAAC
                                     ___
GAM1794  CUBN     3'  GGCCTACAAATATTGA     9890     TT
                                GGT  TTACAAATATTGA
                                |||  ||||||||||||
                                CCG  GATGTTTATAACT
                                     __
GAM1794  NUFIP1   3'  CATAGAATATTTACAAATATTG 29593     AG  T
           AC                     CATA  GT TTTACAAATATTGAC
                                |||||  || ||||||||||||||
                                GTAT  TA AAATGTTTATAACTG
                                  CT  T
GAM1794  SGCG     3'  AGGTTTTTATTGCTTATTGAC  6924        CAAA_
                                AGGTTTTTA    TATTGAC
                                |||||||||    |||||||
                                TCCAAAAAT    ATAACTG
                                     AACGA
GAM1794  SIRT5    3'  GGTTTTTACCCCTTGAC     29265       AAATA
                                GGTTTTTAC    TTGAC
                                |||||||||    |||||
                                CCAAAAATG    AACTG
                                     GGG__
GAM1794  TMOD3    3'  GACTTTTATAAATATTGA    30965   GT    C
                                G  TTTTA AAATATTGA
                                |  ||||| |||||||||
                                C  AAAAT TTTATAACT
                                 TG    A
GAM1795  CENTD2   3'  GTTGGGCCAAGAGGTCT     31602       AACA   TA
                                GTTGGGCCA    AGA  TCT
                                |||||||||    |||  |||
                                CAACCCGGT    TCT  AGA
                                     _____  CC
GAM1795  KCNH3    3'  GTTGGGCCGAACAGCAGAT   42088       A   __
                                GTTGGGCC AACA  AGAT
                                |||||||| ||||  ||||
                                CAACCCGG TTGT  TCTA
                                     C    CG
GAM1795  ORC5L    3'  GCTGGGCCAGCACCTG      14980        AACAA A
                                GTTGGGCCA    G TATCTG
                                |||||||||    | ||||||
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                                CGACCCGGT    C GTGGAC
                                      _____ _
GAM1795 PRV1    3' GTTGGGCCACACAGCCCTG   43877       A  AGATA
                                GTTGGGCCA ACA    TCTG
                                ||||||||| |||    ||||
                                CAACCCGGT TGT    GGAC
                                    G  CG___
GAM1795 ADRBK1  3' TATGGCCCAACCTGCAG    11539         CTCA
                                TATGGCCCAACC   GCAG
                                ||||||||||||   ||||
                                ATACCGGGTTGG   CGTC
                                     A___
GAM1795 BHLHB3  3' ATGGCCCAGCTCCGTGTTTC  36258       ACC  AGCA
                                ATGGCCCA  CTC   GTTTC
                                ||||||||  |||   |||||
                                TACCGGGT  GAG   CAAAG
                                    C__  GCA_
GAM1795 CDKN2B  3' TATGGCATAAGTAAGCAGTTT 38551      CCAACCCTC
                                TATGGC       AGCAGTTT
                                ||||||       ||||||||
                                ATACCG       TCGTCAAA
                                   TATTCAT__
GAM1795 DFFB    3' TGGCCTAGAAAACAGCAGTTTC 44604     CAACCCT
                                TGGCC     CAGCAGTTTC
                                |||||     ||||||||||
                                ACCGG     GTCGTCAAAG
                                  ATCTTTT
GAM1795 DIA1    5' TATGGCCCAACTGTCAGC    28793        CC
                                TATGGCCCAAC  TCAGC
                                ||||||||||  |||||
                                ATACCGGGTTG  AGTCG
                                      AC
GAM1795 MSL3L1  3' CATGGCACCTGTTTTAGCAGTT 38581      _ AACCCTC
            T                    TATGGC CC      AGCAGTTT
                                ||||||  ||      ||||||||
                                GTACCG GG      TCGTCAAA
                                   T  ACAAAA_
GAM1795 PAFAH1B1 3' TGGCTTACCCTTAAACAATTC  7726     CCA    C_
                                TGGC   ACCCT  AGCAGTTT
                                ||||   |||||  ||||||||
                                ACCG   TGGGA  TTGTTAAG
                                  AA_    AT
GAM1795 RYR3    3' TAGCACAGATTTTCAGCAGTTT 9775      C  ACCC_
                                TGGC CA    TCAGCAGTTT
                                |||| ||    ||||||||||
                                ATCG GT    AGTCGTCAAA
                                  T  CTAAA
GAM1795 SORD    3' GGTCCACAAGTAGCAGTTTC  16967    C   ACCCTC
                                GG CCA     AGCAGTTTC
                                || |||     |||||||||
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                                CC GGT     TCGTCAAAG
                                 A  GTTCA_
GAM1796 ALS2     3' TTAGTCCTGCTCGAAAACAC  34097        A  AAC
                                TTAGTCCTG CTC  AATAC
                                ||||||||| |||  |||||
                                AATCAGGAC GAG  TTGTG
                                      _  CTT
GAM1796 FBXL3A   3' ATCCTTCTATAATACCA    29124      GA  CAAC
                                GTCCT  CT   AATACCA
                                |||||  ||   |||||||
                                TAGGA  GA   TTATGGT
                                   A_  TA__
GAM1796 PHKB     3' TTAGCATGACAATACC      7125       CC   TCAAC
                                TTAGT  TGAC    AATACC
                                |||||  ||||    ||||||
                                AATCG  ACTG    TTATGG
                                   T_   _____
GAM1796 COLQ     3' AAGACAGGATGCAGTGGTCC  38689         CT   A
                                AAGACAGGAT  CAGT GTCC
                                ||||||||||  |||| ||||
                                TTCTGTCCTA  GTCA CAGG
                                      C_   C
GAM1796 HS2ST1   3' AAGACAGGGTCAAATTTTAGT  29318        A  TCAG__
                                AAGACAGG TC     TAGT
                                |||||||| ||     ||||
                                TTCTGTCC AG     ATCA
                                     C  TTTAAA
GAM1796 KIF5C    3' TTAAAGTACAGGGAGCAATAGT 21171       _    ATCT
              C                  TTAAAG ACAGG   CAGTAGTC
                                ||||||| |||||   ||||||||
                                AATTTC TGTCC   GTTATCAG
                                   A    CTC_
GAM1796 PIGA     3' ACAGGGATTTCAGTAGTC    33828      _  C
                                ACAGG AT TCAGTAGTC
                                ||||| || |||||||||
                                TGTCC TA AGTCATCAG
                                   C  A
GAM1796 RAP1B    3' TTAAAGACAAGATCACCGTC  31824           TCAGTA
                                TTAAAGACAGGATC     GTC
                                ||||||||||||||     |||
                                AATTTCTGTTCTAG     CAG
                                      TGG___
GAM1796 TPD52L2  3' CTAAAGACAGGGTTT      17634          ATCTCA  AG
                                TTAAAGACAGG     GT  T
                                ||||||||||     ||  |
                                GATTTCTGTCC     CA  A
                                      _______  AA
GAM1796 UBE2B    3' TTAAAGACAGGGTATTGCTC  17799          AT____
                                TTAAAGACAGG     CTC
                                ||||||||||     |||
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                                AATTTCTGTCC     GAG
                                      CATAAC
GAM1797 RGL     3' ACAAATGATTCAGATAAT    31537
                                ATAAATGATTCAGATAAT
                                ||||||||||||||||||
                                TGTTTACTAAGTCTATTA

GAM1797 SYBL1    3' ATAAATGAATCAGGTAGCATGA 24845        T    ATA__
                                ATAAATGA TCAG    ATGA
                                |||||||| ||||    ||||
                                TATTTACT AGTC    TACT
                                     T   CATCG
GAM1798 MYO10    3' TGTGTACACCATTACACA    29578    C   G     TT
                                TG GTA CACCATT  CATA
                                || ||| |||||||  ||||
                                AC CAT GTGGTAA  GTGT
                                 A  _     T_
GAM1798 NAP1L3   3' TGTGTAGCACCAAACTAACAT  21214    C       TTTTCA
                                TG GTAGCACCA     TAACAT
                                || |||||||||     ||||||
                                AC CATCGTGGT     ATTGTA
                                 A       TTG___
GAM1798 SOX11    3' GTAGTCATTCATAACA      17032      _ CCATT
                                GTAG CA    TTCATAACA
                                |||| ||    |||||||||
                                CATC GT    AAGTATTGT
                                  A _____
GAM1798 BLTR2    5' ATGGTGCTAGGTTCCAGG    33361        AGCA   CATCC
                                ATGGTGCTA   CCA    GG
                                |||||||||   |||    ||
                                TACCACGAT   GGT    CC
                                     CCAA  _____
GAM1798 CBFA2T2  3' TGGTGCTGAGCAGCCATCAGG  22981       A   CCA   C
                                TGGTGCT AGCA   CATC GG
                                ||||||| ||||   |||| ||
                                ACCACGA TCGT   GTAG CC
                                    C   CG_   T
GAM1798 CDH4     3' CGGTGCTGGGCAGCGGCCGG   12175       AA   CCACAT
                                TGGTGCT  GCA     CCGG
                                |||||||  |||     ||||
                                GCCACGA  CGT     GGCC
                                    CC   CGCC__
GAM1798 CLTCL1   3' GCTCAAGCACCATGTCTGG   41883     _      CA  C
                                GCT AAGCACCA  TC GG
                                ||| ||||||||  || ||
                                CGA TTCGTGGT  AG CC
                                  G       AC  A
GAM1798 RXRB     3' GTGAGAAGCACCACGTCTGG   35045     CT       A  C
                                GTG  AAGCACCAC TC GG
                                |||  ||||||||| || ||
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                                CAC  TTCGTGGTG AG CC
                                  TC        C  A
GAM1799  HD       3'  CAAGATGTCAGCTGGA      13342           ATACTCC
                                CAAGATGTTAGC      GGA
                                ||||||||||||      |||
                                GTTCTACAGTCG      CCT
                                      A_______
GAM1799  NYX      3'  TGAATGTTAGCATATGAAAGA  35448    A         CTCC
                                A GATGTTAGCATA    GGA
                                | ||||||||||||    |||
                                A TTACAATCGTAT    TCT
                                 C           ACTT
GAM1799  SYBL1    3'  TGAGATGTTAGCAATACT    24848    A         _
                                C AGATGTTAGCA TACT
                                | |||||||||| ||||
                                A TCTACAATCGT ATGA
                                 C          T
GAM1799  TEK      3'  AGATGTTAGCATCCTGGA    7849           TAC   _
                                AGATGTTAGCA   TCC GGA
                                ||||||||||   ||| |||
                                TCTACAATCGT   AGG CCT
                                      ___   A
GAM1799  TEM8     3'  TGAATGTTAGACACTGGGA   32859    A       C     CC
                                A GATGTTAG ATACT  GGA
                                | ||||||| |||||  |||
                                A TTACAATC TGTGA  CCT
                                 C        _     C_
GAM1799  DIAPH2   3'  AAACCACAGAGCATA       28662         TCAA T
                                AAACCACA    G GCATA
                                ||||||||    | |||||
                                TTTGGTGT    C CGTAT
                                     _____ T
GAM1799  MPP3     3'  GAACAAATCAAACAAAGCAT   12567        C  CAT    T
                                GAACAAA CA   CAAG GCAT
                                ||||||| ||   |||| ||||
                                CTTGTTT GT   GTTT CGTA
                                    A  TT_    _
GAM1799  ZNF274   3'  GAACAAACAATATCAAGTGAAT 32248         CAC       C
                                GAACAAAC   ATCAAGTG AT
                                ||||||||   |||||||| ||
                                CTTGTTTG   TAGTTCAC TA
                                     TTA       T
GAM1800  ADCY2    3'  CCTAGGCTGTGAGGACTAATTC 42141        G   C _ CC    CC
              T                  CCTAGG CTG G G  CTAA  CT
                                 |||||| ||| | |  ||||  ||
                                 GGATCC GAC C C  GATT  GA
                                    _  A T CT    AA
GAM1800  AGXT     5'  CCTGGGGCTGCACTGGCC     6190      A      ___
                                CCT GGGCTGC   GGCC
                                ||| |||||||   ||||
```

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                                GGA CCCGACG   CCGG
                                  C      TGA
GAM1800 CELSR1   3' CTAGGCTGTGGCAGGCCTA   30652      G   C  ___
                                CTAGG CTG GGC   CCTA
                                ||||| ||| |||   ||||
                                GATCC GAC CCG   GGAT
                                  _   A   TCC
GAM1800 CYP1A1   3' CCTAAGGACCTCCTAACCCTA  7974        _  GCGGC
                                CCTAGGG CT    CCTAACCCTA
                                ||||||| ||    ||||||||||
                                GGATTCC GG    GGATTGGGAT
                                    T  A____
GAM1800 EIF4EBP2 3' CTAAGGGCTGCTTAGCTCTA   19892     _     __  C
                                CTA GGGCTGC  GGC CTA
                                ||| |||||||  ||| |||
                                GAT CCCGACG  TCG GAT
                                  T      AA   A
GAM1800 GCKR     3' CCTGGGCTGCGGATGCCCT    11240     A      ___
                                CCT GGGCTGCG   GCCCT
                                ||| ||||||||   |||||
                                GGA CCCGACGC   CGGGA
                                  _       CTA
GAM1800 GNPAT    5' CCTAGGGCGGCGGCACCCT    30622        T    CCTA
                                CCTAGGGC GCGGC    ACCCT
                                |||||||| |||||    |||||
                                GGATCCCG CGCCG    TGGGA
                                    C    _____
GAM1800 IMPDH1   3' CCCGGGAGCAGTCCTGACTCT  9405     A   CT   C   A  C
                                CCT GGG  GCGG CCT AC CT
                                ||| |||  |||| ||| || ||
                                GGG CCC  CGTC GGA TG GA
                                  _  T_   A   C  A
GAM1800 MIC2     3' CCTCAGGCAGCTGTTCTAACCC 14502     A   T  GGCC
              T                  CCT GGGC GC    CTAACCCT
                                 ||| |||| ||    ||||||||
                                 GGA TCCG CG    GATTGGGA
                                   G    T  ACAA
GAM1800 SERPINH2 3' CCAGGGGCTGCAGCACCTA   10293    TA       _
                                CC  GGGCTGCGGC CCTA
                                ||  |||||||||| ||||
                                GG  CCCGACGTCG GGAT
                                 TC         T
GAM1800 STIM1    5' CCGGGGCTGCGGCGGCCT    41124    TA       __
                                C  GGGCTGCGGC  CCT
                                |  ||||||||||  |||
                                G  CCCGACGCCG  GGA
                                 GC         CC
GAM1800 TMPRSS2  3' CCAGGGCTGCTAAGGCTCTA  24931          ___  C
                                CTAGGGCTGC   GGC CTA
                                ||||||||||   ||| |||
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                                GGTCCCGACG   CCG GAT
                                     ATT   A
GAM1800  VIPR1    3'  CTAGGGCTGCGTTCTCTA    21507         GCC_
                                CTAGGGCTGCG    CTA
                                ||||||||||    |||
                                GATCCCGACGC    GAT
                                     AAGA
GAM1801  CTSZ     3'  CCTTTTCTTAAACTGCG     41613        GC    C
                                CTTTTTCT  GAGC GCG
                                ||||||||  |||| |||
                                GGAAAAGA  TTTG CGC
                                    A_    A
GAM1801  ESPN     3'  CACTTTTTCTGGGCAACCG   36442          CG_
                                CACTTTTTCTG   AGCCG
                                ||||||||||   |||||
                                GTGAAAAAGAC   TTGGC
                                     CCG
GAM1801  FLRT2    3'  CACTTTTCAAAAGCTGCG    29839        CTGC    C
                                CACTTTTT    GAGC GCG
                                ||||||||    |||| |||
                                GTGAAAAG    TTCG CGC
                                    TT__    A
GAM1801  GRLF1    3'  ACTTTTTCTAGCCGGCG     44219        GCG    _
                                ACTTTTTCT   AGCCG CG
                                |||||||||   ||||| ||
                                TGAAAAAGA   TCGGC GC
                                     ___     C
GAM1801  HS3ST3A1 5'  ACCCCACCTGTGAGCCGCG   25799     TT    C
                                ACTT  TCTG GAGCCGCG
                                ||||  |||| ||||||||
                                TGGG  GGAC CTCGGCGC
                                  GT    A
GAM1801  IRF2     3'  ACTTTTTCCTTTGTACCGCG  13584         GCGA_
                                ACTTTTTCT    GCCGCG
                                |||||||||    ||||||
                                TGAAAAAGG    TGGCGC
                                     AAACA
GAM1801  KCND3    5'  CTTTTTCTTGCAGTGCG     22533         _  G  CC
                                CTTTTTCT GC AG  GCG
                                |||||||| || ||  |||
                                GAAAAAGA CG TC  CGC
                                    A  _  A_
GAM1801  KCNJ6    5'  CTTTTCCTGGCTGCG       13856         CGA  C
                                CTTTTTCTG   GC GCG
                                |||||||||   || |||
                                GAAAAGGAC   CG CGC
                                     ___  A
GAM1801  RENBP    5'  CACTTGTTCCTGCCGCG     16242       T    GCGA
                                CACTT TTCT    GCCGCG
                                |||||  ||||    ||||||
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```
                                GTGAA AAGG   CGGCGC
                                  C   A___
GAM1801 RPS6KA5  5' CTTTTTTTCCGATCCCGCG   21914      CTG  G_
                                CTTTTT  CGA  CCGCG
                                ||||||  |||  |||||
                                GAAAAA  GCT  GGCGC
                                   AAG  AG
GAM1801 TGFB3    3' CACTTTCTTTACCACCG     17458       C  GA
                                CACTTTTT TGC  GCCG
                                |||||||| |||  ||||
                                GTGAAAGA ATG  TGGC
                                    A  G_
GAM1802 GAS41    3' AATAGTACAAATTCCTATTGCT 27199          TTTA   C__
                                AATGGTACAAAT   TCCT  GCT
                                ||||||||||||   ||||  |||
                                TTATCATGTTTA   AGGA  CGA
                                      _____   TAA
GAM1802 NLGN2    5' GGTACAGGCAGTCCTCGCT   44760      AATTTTA
                                GGTACA     TCCTCGCT
                                ||||||     ||||||||
                                CCATGT     AGGAGCGA
                                   CCGTC__
GAM1802 TERF1    3' AATAGTACAAATTTTGTCCC  32738           A
                                AATGGTACAAATTTT TCCT
                                |||||||||||||| ||||
                                TTATCATGTTTAAAA AGGG
                                       C
GAM1803 BTK      5' TTAATGCAGGTAGCTTCC    6296       T  A_
                                TTAAT CA  TAGCTTCC
                                ||||| ||  ||||||||
                                AATTA GT  ATCGAAGG
                                  C  CC
GAM1803 ERBB4    3' TTAGTTAATTTGCTGGTTGCTT 23459        CAATA___
             CC                   TTAGTTAATT      GCTTCC
                                ||||||||||      ||||||
                                AATCAATTAA      CGAAGG
                                     ACGACCAA
GAM1803 F8       3' TAGTTAATTCAGGAGGCT    6568          ATA_
                                TAGTTAATTCA   GCT
                                ||||||||||   |||
                                ATCAATTAAGT   CGA
                                      CCTC
GAM1803 HD       3' GTTATAATTCAGTAGCTTCC  13357     __   A
                                GTTA  ATTCA TAGCTTCC
                                ||||  ||||| ||||||||
                                CAAT  TAAGT ATCGAAGG
                                  AT    C
GAM1803 MYBL1    3' TAGTTAATTTTACTGCTTC   41983        CA  A
                                TAGTTAATT  AT GCTTC
                                |||||||||  || |||||
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                                ATCAATTAA  TG CGAAG
                                     AA  A
GAM1803  NEBL     3'  TCAGTTTACATAGCTTC     26911       AATTCA
                                TTAGTT     ATAGCTTC
                                ||||||     ||||||||
                                AGTCAA     TATCGAAG
                                   ATG___
GAM1803  NRIP1    3'  GCTAGTTCAGTAGTTTCC    40966      A   A   C
                                GTTA TTCA TAG TTCC
                                |||| |||| ||| ||||
                                CGAT AAGT ATC AAGG
                                  C   C   A
GAM1803  PKNOX1   3'  GTCAATTCAGAACATTCC    21309         AT  _
                                GTTAATTCA  AGC TTCC
                                |||||||||  ||| ||||
                                CAGTTAAGT  TTG AAGG
                                     C_  T
GAM1803  TTC3     5'  TTAGTTGCCATAGCTTC     17722       AATTCA
                                TTAGTT     ATAGCTTC
                                ||||||     ||||||||
                                AATCAA     TATCGAAG
                                   CGG___
GAM1804  ADAM19   3'  GGGGACCTTTCCAGTT      37773        CC  CGC   AAC
                                GGGGATCT  CC   GGT   T
                                ||||||||  ||   |||   |
                                CCCCTGGA  GG   TCA   A
                                     AA  ___   ___
GAM1804  TBL1X    3'  GGGGACCTCCCTCACTGG    24893          C   _
                                GGGGATCTCCC CGC GG
                                |||||||||||| ||| ||
                                CCCCTGGAGGG GTG CC
                                      A   A
GAM1805  AXIN1    3'  CCCCTGACTTGGGTACGTGC   41372        GAC__    A
                                TCCCTGAC     TACG GC
                                ||||||||     |||| ||
                                GGGGACTG     ATGC CG
                                     AACCC    A
GAM1805  SLC4A2   5'  CCCGACGACTGCCCCGTGC    16772          A___  A
                                CCTGACGACT    CG GC
                                ||||||||||    || ||
                                GGGCTGCTGA    GC CG
                                      CGGG  A
GAM1805  ZNF135   3'  CCTATGTCCCAGCACATG     18331      ACGA  ACG
                                CCTG    CT   AGCACATG
                                ||||    ||   ||||||||
                                GGAT    GG   TCGTGTAC
                                  ACAG  ___
GAM1805  BACE     3'  TTTGGTGACCTTGGGTGA     39975          CCGAC
                                TTTGGTGACC     GTGA
                                ||||||||||     ||||
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                                AAACCACTGG    CACT
                                     AACC_
GAM1805 MMP16   3' ATTTGGTGTTTTCGAATGCAAT 35436       ACCC  C_ TG  C
            TGT                   ATTTGGTG   CGA  G  AT GT
                                  ||||||||   |||  |  || ||
                                  TAAACCAC   GCT  C  TA CA
                                      AAAA   TA GT  A
GAM1806 ACP5    3' CACCCCGGAACTCAG      11512      TAC  A
                                  TACCC   CG GAACTCAG
                                  |||||   || ||||||||
                                  GTGGG   GC CTTGAGTC
                                    ____ _
GAM1806 EFEMP1  3' TACCCTACAGAAACCAG    33125       CG   CT
                                  TACCCTAC  AGAA  CAG
                                  ||||||||  ||||  |||
                                  ATGGGATG  TCTT  GTC
                                      __   TG
GAM1806 EIF4G2  5' ACCTTCACCGAGAACTCAG  10872    C_
                                  ACC  TACCGAGAACTCAG
                                  |||  ||||||||||||||
                                  TGG  GTGGCTCTTGAGTC
                                    AA
GAM1806 FBXW1B  3' TACTCTACCAAATATCAG   37992    C      AAC
                                  TAC CTACCGAG   TCAG
                                  ||| ||||||||   ||||
                                  ATG GATGGTTT   AGTC
                                    A       AT_
GAM1806 GSTM3   3' TACCCAAGAGAAACTCAG   42764     TACC    _
                                  TACCC    GAGAA CTCAG
                                  |||||    ||||| |||||
                                  ATGGG    CTCTT GAGTC
                                     TT__     T
GAM1806 LSS     3' CCTCTCCCAAGAACTCAG    14247    _  A
                                  CC CT CCGAGAACTCAG
                                  || || ||||||||||||
                                  GG GA GGTTCTTGAGTC
                                   A  G
GAM1806 MAP1A   3' ACCCTGCTAGAACTCAG    14337     ACCG
                                  ACCCT    AGAACTCAG
                                  |||||    |||||||||
                                  TGGGA    TCTTGAGTC
                                     CGA_
GAM1806 PCTP    3' TACCCTACCAAAATTCAG    34535          AC
                                  TACCCTACCGAGA  TCAG
                                  ||||||||||||  ||||
                                  ATGGGATGGTTTT  AGTC
                                         A_
GAM1806 PRCC    3' CACCCCAGAACTCA       25574       ACCG
                                  TACCCT    AGAACTCA
                                  ||||||    ||||||||
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                                GTGGGG   TCTTGAGT
                                    ____
GAM1806  SOX13    3'  CACCCACAGGAACTCAG     25010      T  CGA
                                TACCC AC   GAACTCAG
                                ||||| ||   ||||||||
                                GTGGG TG   CTTGAGTC
                                  _  TC_
GAM1806  ZNF134   3'  ACCCCCAATGAACTCAG     18321      TA   _
                                ACCC  CCGA GAACTCAG
                                ||||  |||| ||||||||
                                TGGG  GGTT CTTGAGTC
                                  __   A
GAM1806  ZNF26    5'  TACCCCACTGATATCAG     43804        C  GAAC
                                TACCCTAC GA    TCAG
                                |||||||| ||    ||||
                                ATGGGGTG CT    AGTC
                                     A  AT__
GAM1806  CAV1     5'  CGCTGGAGGGGGGCGGTGGCTG 11989     C     A_  TCCAC   C
             G                   CGT GGAGGG  GC     GGC GG
                                ||| ||||||  ||     ||| ||
                                GCG CCTCCC  CG     CCG CC
                                  A     CC  CCA__   A
GAM1806  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 31949      GA        A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_        C
GAM1806  FLOT2    3'  GCTGGAGGGAGGGCC       20983    C       CTCCAC
                                GT GGAGGGAG     GGCC
                                || ||||||||     ||||
                                CG CCTCCCTC     CCGG
                                 A      _______
GAM1806  MAPRE3   3'  GCTGGAGGGAGTGGCG      29533    C       CTCCAC   C
                                GT GGAGGGAG     GGC G
                                || ||||||||     ||| |
                                CG CCTCCCTC     CCG C
                                 A       A_____   A
GAM1806  MYO3A    3'  CGTCGGGGGAGGTTTCCCGA   41114       A    C__   A
                                CGTCGG GGGAG   TCC CGG
                                |||||| |||||   ||| |||
                                GCAGCC CCCTC   AGG GCT
                                   _    CAA  _
GAM1806  PPP4C    3'  GTTGGAGGGGGCAGGGGCCGG  15537    C     A  TCCAC
                                GT GGAGGG GC     GGCCGG
                                || |||||| ||     ||||||
                                CA CCTCCC CG     CCGGCC
                                 A     C  TCC__
GAM1806  SLC23A1  5'  CGTTGGGGAGAGCAGCG     44054     C  A     TCCAC   C
                                CGT GG GGGAGC     GGC G
                                ||| || ||||||     ||| |
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                                GCA CC CTCTCG    TCG C
                                  A  C     _____  A
GAM1806  SOX12    3'  ATCGGAGGGGGCTGGCTGCTGG 28029        A   CCACG  C
                                GTCGGAGGG GCT    GC GG
                                ||||||||| |||    || ||
                                TAGCCTCCC CGA    CG CC
                                     C   CCGA_  A
GAM1807  BSN      3'  CATTGCATAGAACGTTAG    18396        AACT
                                CATTGCATA   CGTTAG
                                |||||||||   ||||||
                                GTAACGTAT   GCAATC
                                     CTT_
GAM1807  BTEB1    3'  TTGCTTGCATAAAGACA     10225     A      CT
                                TTGC TTGCATAAA  CG
                                |||| |||||||||  ||
                                AACG AACGTATTT  GT
                                  _       CT
GAM1807  TXNRD2   3'  TTGCATTGCAGAAATGCCAG   26979        T   CTC
                                TTGCATTGCA AAA   GTTAG
                                |||||||||| |||   |||||
                                AACGTAACGT TTT   CGGTC
                                     C   A__
GAM1807  LUM      3'  ATTTAATCCAAGCTTTGAGGA  14268         TAAA
                                GTTTAATCCAA   TTGAGGA
                                ||||||||||   |||||||
                                TAAATTAGGTT   AACTCCT
                                     CGA_
GAM1807  PKHD1    3'  TAGCTTAACTATGGGTTGAGGA 39805        CCAATAAA
                                TAGTTTAAT      TTGAGGA
                                |||||||||      |||||||
                                ATCGAATTG      AACTCCT
                                     ATACCC__
GAM1807  PSG2     3'  ATTTAGTCCAATAACATTGA   36311      A     _
                                GTTTA TCCAATAA ATTGA
                                ||||| |||||||| |||||
                                TAAAT AGGTTATT TAACT
                                  C       G
GAM1807  PSG3     3'  ATTTAGTCCAATAAAATTGGG  34254      A      _  A
                                GTTTA TCCAATAAA TTG GG
                                ||||| ||||||||| ||| ||
                                TAAAT AGGTTATTT AAC CC
                                  C       T  _
GAM1807  PSG5     3'  ATTTAGTCCAATAACATGGA   15801      A      ATTGA
                                GTTTA TCCAATAA    GGA
                                ||||| ||||||||    |||
                                TAAAT AGGTTATT    CCT
                                  C       GTA__
GAM1807  PSG9     3'  ATTTAGTCCAATAACATTGA   15811      A      _
                                GTTTA TCCAATAA ATTGA
                                ||||| |||||||| |||||
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                                TAAAT AGGTTATT TAACT
                                  C       G
GAM1808 CDH13    3' TTAGTTTCCACCCACCTTGC  10374      C  G     GTCC
                                TTAGT TCC ACCCGCC   GC
                                ||||| ||| |||||||   ||
                                AATCA AGG TGGGTGG   CG
                                  A  _     AA__
GAM1808 EYA1     3' TTAGTCTCCGATTCATGAACC 7995          CC  CCGT
                                TTAGTCTCCGA  CG   CC
                                ||||||||||  ||   ||
                                AATCAGAGGCT  GT   GG
                                      AA  ACTT
GAM1808 ACTB     3' TGGGGGACAAAAAGGGGGAAGG 9929     AAGTCTG      A_
             G                   TGG      AAAAAGGG  AAGGG
                                |||      ||||||||  |||||
                                ACC      TTTTTCCC  TTCCC
                                  CCCTG__       CC
GAM1808 ADAM17   3' TGGAGTCTGGGGCGCAGGAAAG 34833     A    AAAAA_
             GG                   TGGA GTCTG     GGGAAAGGG
                                |||| |||||     |||||||||
                                ACCT CAGAC     TCCTTTCCC
                                  _    CCCGCG
GAM1808 ADCY6    3' GGAGGTTGCAGGGAAAGG    34173     A  C  AAAA
                                GGA GT TG    AGGGAAAGG
                                ||| || ||    |||||||||
                                CCT CA AC    TCCCTTTCC
                                  C  _  G___
GAM1808 APLP1    3' TGGAATTTTGGAATTGGAAAGG 23164      GTCT_   AAAG
             G                   TGGAA    GAA    GGAAAGGG
                                |||||    |||    ||||||||
                                ACCTT    CTT    CCTTTCCC
                                   AAAAC   AA__
GAM1808 ARF4L    3' TGGGAGGAAAGGGAGGGGG   43077     A  TCTGAA      AA
                                TGG AG     AAAGGGA  GGG
                                ||| ||     |||||||  |||
                                ACC TC     TTTCCCT  CCC
                                  C  C_____      CC
GAM1808 ARNT     3' GGAACAGCCAGAAGGGAAAGGG 11696     __    T  AAA
                                GGA  AGTC GA   AGGGAAAGGG
                                |||  |||| ||   ||||||||||
                                CCT  TCGG CT   TCCCTTTCCC
                                  TG   T  ___
GAM1808 CACNG3   5' GGAAGGGTTAAGGAAAGGGGAA 27239      TC_   A_     A
             GGG                   GGAAG   TGA  AAAGGG AAGGG
                                |||||   |||  |||||| |||||
                                CCTTC   ATT  TTTCCC TTCCC
                                   CCA   CC     C
GAM1808 CD2AP    3' GAAGTTTGAAAAGCTTTGGG  29071      C     A____
                                GAAGT TGAAAA     GGG
                                ||||| ||||||     |||
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                                CTTCA ACTTTT    CCC
                                   A     CGAAA
GAM1808 CDX2    5' GGGGGCACGAAGGGAAAGGG  10409    AA  C   AAA
                                GG  GT TGA   AGGGAAAGGG
                                ||  || |||   ||||||||||
                                CC  CG GCT   TCCCTTTCCC
                                 CC  T  ___
GAM1808 CEACAM1  3' AGGTTGGGAAAAGGGGAAGGG  11829    TC  A_     A
                                AG  TG  AAAAGGG AAGGG
                                ||  ||  ||||||| |||||
                                TC  AC  TTTTCCC TTCCC
                                 CA  CC      C
GAM1808 CNTN2    5' TGGAGGCTGAGAAAGGACCTGG 22916     A T    A     AAA
             G                    TGGA G CTGA AAAGGG   GGG
                                |||| | |||| ||||||   |||
                                ACCT C GACT TTTCCT   CCC
                                  C _    C     GGA
GAM1808 COX10    3' TGGCAGCGGAGGGAAAGG    10556     A   CTGAAAA
                                TGG AGT      AGGGAAAGG
                                ||| |||      |||||||||
                                ACC TCG      TCCCTTTCC
                                  G   CC_____
GAM1808 CTNS     3' GGAAAGAGAGGGAAGGGG    22348      TCT  AAA     A
                                GGAAG   GA   AGGGAA GGG
                                |||||   ||   |||||| |||
                                CCTTT   CT   TCCCTT CCC
                                   ___  C__     C
GAM1808 DYRK1B   3' TAGAAAAAAAGGGGGAGAGGG  21780       TCT    AA    A
                                TGGAAG   GAAA  GGGA AGGG
                                ||||||   ||||  |||| ||||
                                ATCTTT   TTTT  CCCT TCCC
                                   ___    CC    C
GAM1808 EIF4G2   5' GGAAGGGAGGGGAAAGGG    10877      TCT  AAAA
                                GGAAG   GA    GGGAAAGGG
                                |||||   ||    |||||||||
                                CCTTC   CT    CCCTTTCCC
                                   C__  C___
GAM1808 EIF4G2   5' GGAAAACAAAAAAAAGGGGGAG 10876      TCT_       AA
             GG                   GGAAG    GAAAAAGGG  AGGG
                                |||||    |||||||||  ||||
                                CCTTT    TTTTTTCCC  TCCC
                                   TGTT        CC
GAM1808 ESRRG    3' GGAAAGGAAAGGGGGAAGGG   42446      TCT    AA    A
                                GGAAG   GAAA  GGGAA GGG
                                |||||   ||||  ||||| |||
                                CCTTT   CTTT  CCCTT CCC
                                   C__    CC    _
GAM1808 HCFC1    3' GGAAAGAAGAGGGGGAGGG   43397      TCT   AA    AA
                                GGAAG   GAA  AGGG  AGGG
                                |||||   |||  ||||  ||||
```

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                                CCTTT  CTT  TCCC  TCCC
                                  ___  C_   CC
GAM1808 HDAC5    3' GGACGAAAGAAGGGGAAAGGG 40172    AGTCT  AAA
                                GGA    GAA  GGGAAAGGG
                                |||    |||  |||||||||
                                CCT    CTT  CCCTTTCCC
                                 GCTTT  C__
GAM1808 HMGA2    3' GAAAAGAGAGAGGGAGAGGG  18513     TCT  AAA    A
                                GAAG  GA  AGGGA AGGG
                                ||||  ||  ||||| ||||
                                CTTT  CT  TCCCT TCCC
                                  TCT  C__    C
GAM1808 IL1F5    3' TGGCAGGATTAAAGGGAAGGGG 29361    A  TCTGAA      A
                                TGG AG     AAAGGGAA GGG
                                ||| ||     |||||||| |||
                                ACC TC     TTTCCCTT CCC
                                 G  CTAA__      C
GAM1808 JAG1     5' GCATGGAAAAAGGGGGGAGGG  6857     CT_      AA_
                                GT  GAAAAAGGG  AGGG
                                ||  |||||||||  ||||
                                CG  CTTTTTCCC  TCCC
                                 TAC       CCC
GAM1808 JUP      3' GGGGGTCTGAAACAGGAAGGGG 13779    AA      AA    A
                                GG  GTCTGAAA  GGGAA GGG
                                ||  ||||||||  ||||| |||
                                CC  CAGACTTT  TCCTT CCC
                                 CC       G_    C
GAM1808 KIAA0442 5' GGAGAAAGAAAAGGGGGAAGGG 31790    A TCT    A  A
                                GGA G   GAAAA GGG AAGGG
                                ||| |   ||||| ||| |||||
                                CCT C   CTTTT CCC TTCCC
                                 _ TTT    C  C
GAM1808 LPIN2    3' GAACTGCAAAGAGGGAAAGGG  31208    GT  _  A
                                GAA  CTG AAA AGGGAAAGGG
                                |||  ||| ||| ||||||||||
                                CTT  GAC TTT TCCCTTTCCC
                                  __  G  C
GAM1808 MEF2D    3' GGAAACCTGGGGAGGGGGAGGG 25420     GT  AAAA   AA
                                GGAA  CTG   AGGG  AGGG
                                ||||  |||   ||||  ||||
                                CCTT  GAC   TCCC  TCCC
                                  TG  CCC_   CC
GAM1808 MS4A4A   3' AGAAGGAAAAAGGGAGGGGG  35850      TCT       AA
                                GGAAG  GAAAAAGGGA  GGG
                                |||||  ||||||||||  |||
                                TCTTC  CTTTTTCCCT  CCC
                                  ___        CC
GAM1808 NAV2     3' GGAAGTCTGTGGGAAAGG    41146        AAAAA
                                GGAAGTCTG    GGGAAAGG
                                |||||||||    ||||||||
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                                CCTTCAGAC    CCCTTTCC
                                     A____
GAM1808 NF1     5' GGGAGGGGGAGAGGGAAAGGG 7059    A TCT AAA
                                GG AG  GA  AGGGAAAGGG
                                || ||  ||  ||||||||||
                                CC TC  CT  TCCCTTTCCC
                                 C CCC C__
GAM1808 PAEP    3' TGGAGGTGTGGAAGGGTGG  15071    A C AAA   AAA
                                TGGA GT TG  AAGGG  GG
                                |||| || ||  |||||  ||
                                ACCT CA AC  TTCCC  CC
                                  C C C__   A__
GAM1808 PLCB2   3' TGGAAGCCTGGGGCAGGAGGG 21323        AAAAA  AA__
                                TGGAAGTCTG   GGG   AGGG
                                ||||||||||   |||   ||||
                                ACCTTCGGAC   CCC   TCCC
                                     ______ GTCC
GAM1808 POU3F4  3' GGAAGGGAAGGGAAG      7172      TCT AAA    A
                                GGAAG  GA  AGGGAA G
                                |||||  ||  |||||| |
                                CCTTC  CT  TCCCTT C
                                   C__ ___    C
GAM1808 POU3F4  3' GGAAAGAAAAAGGGGAAAGGG 7171      TCT      _
                                GGAAG  GAAAAAGGG AAAGGG
                                |||||  ||||||||| ||||||
                                CCTTT  CTTTTTCCC TTTCCC
                                     ___       C
GAM1808 RAI14   3' TGGAATCTGAAGGGATGACAGG 31808     G   AAA   A___
            G                    TGGAA TCTGA  AGGGA   AGGG
                                |||||  |||||  |||||   ||||
                                ACCTT AGACT  TCCCT   TCCC
                                  _   ___    ACTG
GAM1808 RBM10   5' TGGAGGCAGATCGGGGGGAGGG 24985    A CT AAAA  AA
                                TGGA GT  GA   GGG  AGGG
                                |||| ||  ||   |||  ||||
                                ACCT CG  CT   CCC  TCCC
                                  C T_  AGC_  CC
GAM1808 RING1   5' TGGGTTAGAGGGAAAGG    16338    AA CT AAAA
                                TGG  GT  GA   GGGAAAGG
                                |||  ||  ||   ||||||||
                                ACC  CA  CT   CCCTTTCC
                                  __ AT  _____
GAM1808 SLC2A3  3' TGTAAGCACCAAGAAGGGAAAG 27984   G   _ TG AA
            GG                    TG AAGT C  A  AAGGGAAAGGG
                                || |||| |  |  ||||||||||
                                AC TTCG G  T  TTCCCTTTCCC
                                 A   T GT C_
GAM1808 SLC9A5  3' TGGCAGCAAAGGGAAGGG   21393    A  CTGAA     A
                                TGG AGT    AAAGGGAA GG
                                ||| |||    |||||||| ||
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                                ACC TCG    TTTCCCTT CC
                                  G _____      C
GAM1808 SMARCD1  3' TGGGGCTCTGAAAGGGAAAGG 40090    AAG    AA
                                TGG  TCTGAA AGGGAAAGG
                                |||  |||||| |||||||||
                                ACC  AGACTT TCCCTTTCC
                                  CCG    __
GAM1808 SUPT6H   3' TGGCAGCAGCAGGGGGGAAAGG 41288    A  CTGAAAAA
           G                     TGG AGT      GGGAAAGGG
                                ||| |||      |||||||||
                                ACC TCG      CCCTTTCCC
                                  G  TCGTCCC_
GAM1808 TP53     3' GGAGAAGGAGGGGAAGG    8097     AGTCT  AA   A
                                GGA    GAA  AGGG AAGG
                                |||    |||  |||| ||||
                                CCT    CTT  TCCC TTCC
                                 _____  CC   C
GAM1808 ZFP36L1  3' GAGGTGCTGGGGGAAAGG    22285    A _  AAAAA
                                GA GT CTG    GGGAAAGG
                                || || |||    ||||||||
                                CT CA GAC    CCCTTTCC
                                 C  C  C____
GAM1809 JAK2     3' TATATAATAATGATATA     22478         C
                                TATATAATAA TGATATA
                                |||||||||| |||||||
                                ATATATTATT ACTATAT
                                          _
GAM1809 LRP2     3' TATACAATATATTTATAGTATT 21186         ACTGA
           A                     TATATAATA    TATAGTATTA
                                |||||||||    ||||||||||
                                ATATGTTAT    ATATCATAAT
                                      ATAA_
GAM1809 PRKCN    3' TATATAGTAACTGGATGCTAGC 25163       A    _ A_
                                TATATA TAACTG AT  TAGT
                                |||||| |||||| ||  ||||
                                ATATAT ATTGAC TA  ATCG
                                   C     C  CG
GAM1810 SHOX     3' GTTCATGCTTGTAATTCTAACA 27827     A  A_
                                GTT ATG  TGTAATTCTAACA
                                ||| |||  ||||||||||||||
                                CAA TAC  ACATTAAGATTGT
                                  G  GA
GAM1811 MOX2     3' ATTTATCTAGCTATAAAAATAA 42513        AA    TGT
           G                     ATTTATCTA  TATGA   ATAAG
                                |||||||||  |||||   |||||
                                TAAATAGAT  ATATT   TATTC
                                      CG    TT_
GAM1812 IL9      3' AAATTGTAGCAACTTAAAGAGA 8234       C   ATAA
                                AAGT GTAG    TTAAAGAGA
                                |||| ||||    |||||||||
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                                TTTA CATC    AATTTCTCT
                                  A    GTTG
GAM1812  PCDH11X   5'  CCAAGATAGTTAAAGAGA    37299     T    A
                                TCG AGATA TTAAAGAGA
                                ||| ||||| |||||||||
                                GGT TCTAT AATTTCTCT
                                  _    C
GAM1812  PCDH11Y   5'  CCAAGATAGTTAAAGAGA    37338     T    A
                                TCG AGATA TTAAAGAGA
                                ||| ||||| |||||||||
                                GGT TCTAT AATTTCTCT
                                  _    C
GAM1812  TNFAIP2   3'  TAAAGTTGCAGATGGAACTAA  26641       C    __
                                TAAAGT GTAGAT  AATTAA
                                |||||| ||||||  ||||||
                                ATTTCA CGTCTA  TTGATT
                                    A     CC
GAM1813  DSG1      3'  TTGTGGACTTGACTATGTAG   12606       GA   A
                                TTGTGGAT  TGA CTATGTAG
                                ||||||||  ||| ||||||||
                                AACACCTG  ACT GATACATC
                                     A_  _
GAM1814  XT3       3'  TGAGCAAAGGAATCTGTATCA  33669          ACCA  AC
                                TGAGCGAAGGAG   CT  ATCA
                                ||||||||||||   ||  ||||
                                ACTCGTTTCCTT   GA  TAGT
                                      A___  CA
GAM1814  C7        3'  GACTCTATAGGATGAA      8229      G  CA   ATTGA
                                GACT TA  AGGA    TGAA
                                |||| ||  ||||    ||||
                                CTGA AT  TCCT    ACTT
                                  G  A_   _____
GAM1814  KIF2      3'  TGTACAATCACTGATGAGGT   21136       GGA      A
                                TGTACAA   ATTGATGA GT
                                |||||||   |||||||| ||
                                ACATGTT   TGACTACT CA
                                    AG_       C
GAM1814  SSRP1     5'  CTGCACAAGGGAAACCAAGT   17121         AATT   G
                                CTGTACAAGG    GAT AAGT
                                ||||||||||    ||| ||||
                                GACGTGTTCC    TTG TTCA
                                      CT__   G
GAM1815  DLEU2     3'  TTTAAACATTTACTTTGCCAA  25694          AC    G
                                TTTAAACATTTA  TTGC GG
                                ||||||||||||  |||| ||
                                AAATTTGTAAAT  AACG TT
                                      GA   G
GAM1815  IL18R1    3'  TTTAAGACATTTAACTTG    19301      _
                                TTTAA ACATTTAACTTG
                                ||||| ||||||||||||
```

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                                AAATT TGTAAATTGAAC
                                   C
GAM1815 LZTFL1   3'  TTTAAACATTTATTTAATATAG 33774          ACTTGCG_
             GTT                  TTTAAACATTTA      GGGTT
                                  ||||||||||||      |||||
                                  AAATTTGTAAAT      TCCAA
                                        AAATTATA
GAM1816 ARHGAP6  3'  TCCCACTCCCATGGGGTCT   30227      CG   TTCT  A
                                  TCCCAC  CCT    GG TCT
                                  ||||||  |||    || |||
                                  AGGGTG  GGG    CC AGA
                                     A_   TAC_  C
GAM1816 ATF5     3'  TCCCACTGGCCTGCTCATCT   28940      C_   _   TGG
                                  TCCCAC  GCCT TTC   ATCT
                                  ||||||  |||| |||   ||||
                                  AGGGTG  CGGA GAG   TAGA
                                     AC    C   ___
GAM1816 BCL2L2   3'  TCCCACCACCACCAGAT     19749         TTT TG
                                  TCCCACCGCC   C  GAT
                                  ||||||||||   |  |||
                                  AGGGTGGTGG   G  CTA
                                        T__ GT
GAM1816 CDH16    3'  TCCTGTCCCCTGCTGGATCT   19789     CA_  G   TT
                                  TCC   CC CCT  CTGGATCT
                                  |||   || |||  ||||||||
                                  AGG   GG GGA  GACCTAGA
                                    ACA  _   C_
GAM1816 CRY2     3'  TCCCACTCTCAGAT       43586       CGCC    T
                                  TCCCAC    TTTC GGAT
                                  ||||||    |||| ||||
                                  AGGGTG    AGAG TCTA
                                     ____    _
GAM1816 CSNK1D   5'  TCCCGGCCGCTTCCTGGGTCT  12468      A_   C      A
                                  TCCC  CCGC TTTCTGG TCT
                                  ||||  |||| ||||||| |||
                                  AGGG  GGCG AAGGACC AGA
                                    CC    _      C
GAM1816 CSNK2A2  3'  CCCGTCGCTTTCCAGTCT    12483     AC   C    TG A
                                  CCC  CGC TTTC  G TCT
                                  |||  ||| ||||  | |||
                                  GGG  GCG AAAG  C AGA
                                    CA   _    GT _
GAM1816 DAAM2    3'  TCCCACTGCCCTAAAC      45179       C   TTT
                                  TCCCAC GCC   CTGGAT
                                  ||||||  |||   ||||||
                                  AGGGTG CGG   GATTTG
                                     A   ___
GAM1816 DAZ      5'  CCCACCACTTCTGGGTCT    19848         CT     A
                                  CCCACCGC  TTCTGG TCT
                                  ||||||||  |||||| |||
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                                GGGTGGTG  AAGACC AGA
                                   __     C
GAM1816  DDAH2    5'  TCCAACCGCTCGGAT      30356     C    CTT  T
                                TCC ACCGC   TC GGAT
                                ||| |||||   || ||||
                                AGG TGGCG   AG CCTA
                                  T   ___ _
GAM1816  DDAH2    5'  TCCTGTCGCGCTGTGATCT   30358     CAC   CTTT  _
                                TCC   CGC   CTG GATCT
                                |||   |||   ||| |||||
                                AGG   GCG   GAC CTAGA
                                  ACA   C___   A
GAM1816  DDOST    3'  TCCCACCCCTTGGCTC      23348       G   TTC   A
                                TCCCACC CCT   TGG TC
                                ||||||| |||   ||| ||
                                AGGGTGG GGA   ACC AG
                                   _  ___  G
GAM1816  EGFL5    3'  TCTCACCACCTTTAATCC    44538    C        CTG
                                TC CACCGCCTTT   GATCT
                                || ||||||||||   |||||
                                AG GTGGTGGAAA   TTAGG
                                 A        ___
GAM1816  EIF2C1   3'  TCCTTGCTTCCTCTGGAT    29184     CACC  C_
                                TCC    GC  TTTCTGGAT
                                |||    ||  |||||||||
                                AGG    CG  GGAGACCTA
                                  AA__  AA
GAM1816  EPB49    3'  TCCCACCCCTGCATC       12735       GCCTT    G
                                TCCCACC     TCTG ATC
                                |||||||     |||| |||
                                AGGGTGG     GGAC TAG
                                   _____    G
GAM1816  EPHB2    3'  TCCCGCCCCCTCCCAGGATCT  32679      A  G   TT T
                                TCCC CC CCT  C GGATCT
                                |||| || |||  | ||||||
                                AGGG GG GGA  G CCTAGA
                                  C  G   GG T
GAM1816  FOXI1    3'  TCTCACTGATCCCTGGATCT   29154    C   CGCC TT
                                TC CAC    T  CTGGATCT
                                || |||    |  ||||||||
                                AG GTG    A  GACCTAGA
                                 A   ACT_ GG
GAM1816  G6PT1    5'  TCTCACAGTTCCCAGATCT    11169    C   CGCC    TG
                                TC CAC    TTTC  GATCT
                                || |||    ||||  |||||
                                AG GTG    AAGG  CTAGA
                                 A   TC__    GT
GAM1816  GGT1     5'  TCCCTCTGCCTCTAGCTGG    23573     ACC     __
                                TCCC   GCCTTT  CTGG
                                ||||   ||||||  ||||
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                                AGGG  CGGAGA  GACC
                                  AGA     TC
GAM1816 GRAF    3' TCCCACCCTCCAACCTTGG  31454       G_  TT  _
                                TCCCACC  CC  TCT GG
                                |||||||  ||  ||| ||
                                AGGGTGG  GG  GGA CC
                                    GA  TT   A
GAM1816 GRM3    5' TCTCATTTCCAAACTGGATCT  9153    C  CCG  TTT
                                TC CA   CC   CTGGATCT
                                || ||   ||   ||||||||
                                AG GT   GG   GACCTAGA
                                 A  AAA  TTT
GAM1816 HIPK2   3' TCCCACCCTCTTTAATCC    35550       GC    CTG
                                TCCCACC  CTTT   GATCT
                                |||||||  ||||   |||||
                                AGGGTGG  GAAA   TTAGG
                                    GA   ___
GAM1816 ID1     3' TCCCACCCCCTAAAGTCT    43117       G   TTCT  A
                                TCCCACC CCT    GG TCT
                                ||||||| |||    || |||
                                AGGGTGG GGA    TC AGA
                                    G   TT__  _
GAM1816 JUN     5' TCTCCGCCGCCTTCTGGTCT   13749    _ A      T    A
                                TC CC CCGCCTT CTGG TCT
                                || || ||||||| |||| |||
                                AG GG GGCGGAA GACC AGA
                                 A  C      _   _
GAM1816 KCNA7   3' TCTCCCCACTCTGGAT      36662    _ A    CTT
                                TC CC CCGC   TCTGGAT
                                || || ||||   |||||||
                                AG GG GGTG   AGACCTA
                                 A  _   ___
GAM1816 KCNJ6   5' TCCCGGCGTCCGCGGGTCT    13862     ACC  C  TC   A
                                TCCC   GC TT  TGG TCT
                                ||||   || ||  ||| |||
                                AGGG   CG AG  GCC AGA
                                  C__  C  GC   C
GAM1816 LILRB5  3' TCCTGTGCCTTCTGGAGTCT   27755     CACC    T    _
                                TCC    GCCTT CTGGA TCT
                                |||    ||||| ||||| |||
                                AGG    CGGAA GACCT AGA
                                  ACA_     _     C
GAM1816 LZTS1   3' TCCCCTCGGGGGTCCTGGGTCT 34274      AC  CCT_     A
                                TCCC  CG    TTCTGG TCT
                                ||||  ||    |||||| |||
                                AGGG  GC    AGGACC AGA
                                  GA  CCCC     C
GAM1816 MAG     5' TCCCCTGCCTTCCAGGGTCT   38749      ACC      T  A
                                TCCC   GCCTTTC GG TCT
                                ||||   ||||||| || |||
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                                AGGG  CGGAAGG CC AGA
                                  GA_     T  C
GAM1816 NUP62    5' TCCAACTGCCTTTCCCGCCCT 29604    C  C      GGA
                                TCC AC GCCTTTCT  TCT
                                ||| || ||||||||  |||
                                AGG TG CGGAAAGG  GGA
                                  T  A      GCG
GAM1816 OTX1     5' CACCATCTACCTGGATCT    30983     C  T
                                CACCG CT TCTGGATCT
                                ||||| || |||||||||
                                GTGGT GA GGACCTAGA
                                   A  T
GAM1816 PIK3R3   5' TCCCACCGCCTCCAAATCT   41449        TT  TG
                                TCCCACCGCC  TC  GATCT
                                ||||||||||  ||  |||||
                                AGGGTGGCGG  AG  TTAGA
                                      __  GT
GAM1816 PIN1     3' TCCCACCACACTGCCCTGGGTC 26321        _ _    A
             T                   TCCCACCGC CT TTCTGG TCT
                                 ||||||||| || |||||| |||
                                 AGGGTGGTG GA GGGACC AGA
                                       T  C     C
GAM1816 PIN1L    3' TCCCACCACATTGCCCTGGGTC 26325        CT__    A
             T                   TCCCACCGC   TTCTGG TCT
                                 |||||||||   |||||| |||
                                 AGGGTGGTG   GGGACC AGA
                                       TAAC     C
GAM1816 POU2AF1  3' TCCCACCCCTTACTACTCT   26377       G   T  GA
                                TCCCACC CCTT CTG  TCT
                                ||||||| |||| |||  |||
                                AGGGTGG GGAA GAT  AGA
                                    _   T  G_
GAM1816 PPP4C    5' TCCGCACCGCACAGGGGTCT  15538    _    CTTTCT  A
                                TCC CACCGC     GG TCT
                                ||| ||||||     || |||
                                AGG GTGGCG     CC AGA
                                  C     TGTC__  C
GAM1816 RAD23B   3' CACTAAGTTTCTGGATCT    16134    CGCC
                                CAC    TTTCTGGATCT
                                |||    ||||||||||
                                GTG    AAAGACCTAGA
                                  ATTC
GAM1816 S100B    5' TCTCACCCCTTCCTGGTCT   26574    C   G      A
                                TC CACC CCTTTCTGG TCT
                                || |||| ||||||||| |||
                                AG GTGG GGAAGGACC AGA
                                 A   _       _
GAM1816 SERPINA5 3' CCAGCCTCTCTGGATCT    8412     CC
                                CCA  GCCTTTCTGGATCT
                                |||  ||||||||||||||
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                                GGT  CGGAGAGACCTAGA
                                  __
GAM1816  SLC19A1   5'  TCCCTCTGGATGCATTCTGGAT 16850     ACC____  CT
                                TCCC      GC  TTCTGGAT
                                ||||      ||  ||||||||
                                AGGG      CG  AAGACCTA
                                  AGACCTA  T_
GAM1816  SLC4A8    3'  TCCCAGCTCACTCATTTCTGGG 22145      C__  C__      A
           TCT                    TCCCA   CGC   TTTCTGG TCT
                                |||||   |||   ||||||| |||
                                AGGGT   GTG   AAAGACC AGA
                                  CGA   AGT     C
GAM1816  SPR      3'  TCCCACCCCTTAAGTTCT    17095       G   TCT  A
                                TCCCACC CCTT   GG TCT
                                ||||||| ||||   || |||
                                AGGGTGG GGAA   TC AGA
                                   _   T__  A
GAM1816  SYNGR1   3'  TCTCACCCTCTCTCATCT    21771    C   GC     GG
                                TC CACC  CTTTCT  ATCT
                                || ||||  ||||||  ||||
                                AG GTGG  GAGAGA  TAGA
                                 A   __     G_
GAM1816  TNS      3'  TCCCACTCCTGCTGGGGTCT   35479      CG   TT   A_
                                TCCCAC  CCT  CTGG  TCT
                                ||||||  |||  ||||  |||
                                AGGGTG  GGA  GACC  AGA
                                   A_   C_   CC
GAM1816  TPI1     3'  CCTGCCTTCTGAGGGGATCT   7475     _     CT___
                                CC GCCTTT    GGATCT
                                || ||||||    ||||||
                                GG CGGAAG    CCTAGA
                                 A     ACTCC
GAM1816  WNT11    3'  TCCCATGCCTGGCATC      21541      CC    TTCT  _
                                TCCCA  GCCT    GG ATC
                                |||||  ||||    || |||
                                AGGGT  CGGA    CC TAG
                                  A_   _____  G
GAM1817  EXTL2    3'  TCTCACAGCTTTGCAATTTT   11021       A   ACT
                                TCTCACA CTTT   GTTTT
                                ||||||| ||||   |||||
                                AGAGTGT GAAA   TAAAA
                                   C    CGT
GAM1817  FZD3     5'  TCTCACAAAAGGCGTTTGTTTT 32632        CTTTAC__
           TG                    TCTCACAA       TGTTTTTG
                                ||||||||       ||||||||
                                AGAGTGTT       ACAAAAAC
                                    TTCCGCAA
GAM1817  HIS1     3'  AATCTCATAATTTCTGTTTTTA 26988        C  C   A
                                AATCTCA AA TTT CTGTTTTTG
                                ||||||| || ||| |||||||||
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                                TTAGAGT TT AAA GACAAAAAT
                                    A  _  _
GAM1817  HTR4     3'  ATCTCACAGCTTGTTT      9299          A  TTAC
                                ATCTCACA CT    TGTTT
                                |||||||| ||    |||||
                                TAGAGTGT GA    ACAAA
                                    C  ____
GAM1817  ITGA1    3'  TCACAACTGTCTTT       41854       ACTTT
                                TCACA    ACTGTTTTT
                                |||||    |||||||||
                                AGTGT    TGACAGAAA
                                  _____
GAM1817  RET      3'  CCACAATTTTGCTGTTTTTG   33929       C   A
                                TCACAA TTT CTGTTTTTG
                                |||||| ||| |||||||||
                                GGTGTT AAA GACAAAAAC
                                    A   C
GAM1817  SCN3A    3'  AATTGCACAACTTTGCCACTTT 27948     CT        A TG
                                AAT  CACAACTTT C  TTTT
                                |||  |||||||||  |  ||||
                                TTA  GTGTTGAAA G  GAAA
                                  AC        C GT
GAM1818  DDX6     3'  GGTAGATTAATCTTTGCCC   20554    C      GTAGA
                                GG AGATTAA    TTGCCC
                                || |||||||    ||||||
                                CC TCTAATT    AACGGG
                                 A      AGA__
GAM1818  GNAO1    3'  CGGCAGATGGGCCCTGCCC   44939        TAA  AGAT
                                CGGCAGAT   GT   TGCCC
                                ||||||||   ||   |||||
                                GCCGTCTA   CG   ACGGG
                                    CC_  GG__
GAM1818  LPIN1    3'  GGCAGATCTGTTTGCC      42640        AA  AGA
                                GGCAGATT  GT   TTGCC
                                ||||||||  ||   |||||
                                CCGTCTAG  CA   AACGG
                                    A_  ___
GAM1818  OAT      3'  AACGGCAGGTTCATAAAC    7084         ATTAA
                                AACGGCAG    GTAGAT
                                ||||||||    ||||||
                                TTGCCGTC    TATTTG
                                    CAAG_
GAM1818  RNPEPL1  5'  ACGGCAGAGTAGGTGC     32874        TTAA   AT
                                ACGGCAGA   GTAG  TGC
                                ||||||||   ||||  |||
                                TGCCGTCT   CATC  ACG
                                    _____   C_
GAM1818  RP2      3'  GGCAGATTCAGTGCC      27934        A   AGATT
                                GGCAGATT AGT    GCC
                                |||||||| |||    |||
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                                CCGTCTAA TCA    CGG
                                    G  _____
GAM1818 SARDH    3' GGTGGATTAGAGACTGCC    28251    CA    A T
                                GG  GATTA G AGATTGCC
                                ||  |||||  | ||||||||
                                CC  CTAAT C TCTGACGG
                                 AC    _ _
GAM1818 TNFRSF4  3' CGGCAGCTCGAGATTGCCC   17763       ATTAAGT
                                CGGCAG      AGATTGCCC
                                ||||||      |||||||||
                                GCCGTC      TCTAACGGG
                                   GAGC___
GAM1819 APPL     3' TAACTGTAAAATCTCTGTTCT  29012   T   A       CA
                                A ATTG TAAAATCTC  TTCT
                                | |||| |||||||||  ||||
                                A TGAC ATTTTAGAG  AAGA
                                 T   _       AC
GAM1819 NCOA3    3' GAATATTGCATTTATCCATTCT 27215        ATAAAATC
                                GAATATTG       TCCATTCT
                                ||||||||       ||||||||
                                CTTATAAC       AGGTAAGA
                                     GTAAAT__
GAM1819 RAB6A    3' AATATTGAGTTTTATTTCCATT 16095        TAAA_  C
             CT                   AATATTGA    AT TCCATTCT
                                ||||||||    || ||||||||
                                TTATAACT    TA AGGTAAGA
                                     CAAAA  A
GAM1820 CHEK1    3' TCAGGAACTACTATTT      10462       CAGAT
                                TTAGGA    ACTACTATTT
                                ||||||    ||||||||||
                                AGTCCT    TGATGATAAA
                                    _____
GAM1820 D12S2489E 3' TAGGATGGATATTACTATTC  28885      CA   C
                                TAGGA  GATA TACTATTT
                                |||||  |||| ||||||||
                                ATCCT  CTAT ATGATAAG
                                   AC   A
GAM1820 SCN1A    3' TTAGTGCAGGTACTACCA    44822     GA   A
                                TTAG  CAG TACTACTA
                                ||||  ||| ||||||||
                                AATC  GTC ATGATGGT
                                  AC   C
GAM1820 WASF3    3' TTAGAATACCACTATTT     27394     GACA
                                TTAG    GATACTACTATTT
                                ||||    ||||||||||||
                                AATC    TTATGGTGATAAA
                                    ____
GAM1820 NPTX1    3' CAAGTGTCAACACAGTGAGGA  14831          TGTAATA
                                TAAGTGTCGAT      AGGA
                                ||||||||||       ||||
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                                GTTCACAGTTG      TCCT
                                      TGTCAC_
GAM1821  BACH1    3'  TCCAAGTTAAAATGATTTGTGT 10151       G     CGT
                                TCCAAG TAAAAT   GTTTGTGT
                                |||||| ||||||   ||||||||
                                AGGTTC ATTTTA   TAAACACA
                                   A     C__
GAM1821  BMP6     3'  TCCAAGGCAGAATGTGT     11869         A   C
                                TCCAAGGTA AAT GTGT
                                ||||||||| ||| ||||
                                AGGTTCCGT TTA CACA
                                      C   _
GAM1821  FZD8     3'  TCCCAGGTGAAATCTGTGT    36613     A    A    _
                                TCC AGGT AAATC GTGT
                                ||| |||| ||||| ||||
                                AGG TCCA TTTAG CACA
                                  G    C     A
GAM1821  LANCL1   3'  CCAAACTCTAATTGTGTTTGTG 25851       GTAA   C
              T                  CCAAG    AAT GTGTTTGTGT
                                 |||||    ||| ||||||||||
                                 GGTTT    TTA CACAAACACA
                                    GAGA   A
GAM1821  MSR1     3'  TCCAAGGTAAGGTTTTGCCT   14662          AATCG
                                TCCAAGGTAA    TGTTT
                                ||||||||||    |||||
                                AGGTTCCATT    ACGGA
                                      CCAAA
GAM1821  NFYA     3'  CAAGGTAAGTGCTTTGTGT    34697         AATC     _
                                CAAGGTAA    GTGTTT GTGT
                                ||||||||    |||||| ||||
                                GTTCCATT    CACGAA CACA
                                     _____      A
GAM1821  RARA     3'  TCCAGTGTGTGTGTGTTTGTGT 9715       AG  AAAATC
                                TCCA  GT     GTGTTTGTGT
                                ||||  ||     ||||||||||
                                AGGT  CA     CACAAACACA
                                  CA  CACA__
GAM1821  SEPX1    3'  TCCAAGGTGGAATGGCCAACGT 32270         AA   C  GTT
              GT                  TCCAAGGT  AAT GT   TGTGT
                                  ||||||||  ||| ||   |||||
                                  AGGTTCCA  TTA CG   GCACA
                                      CC   C  GTT
GAM1821  XT3      3'  TCCCAGGTGAGTGTTTGTG   33668     A   AAAATC
                                TCC AGGT     GTGTTTGTG
                                ||| ||||     |||||||||
                                AGG TCCA     CACAAACAC
                                  G    CT____
GAM1822  SNTB1    3'  TATATCAGATGACAATAT    34283       TAA
                                TATGTT   AGATGACAATAT
                                ||||||   ||||||||||||
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                                ATATAG  TCTACTGTTATA
                                   ___
GAM1822 BTC     3' AAATGGTAGCTTTAT      45537       TGTTG
                                GAATGGT    GGCTTTAT
                                |||||||    ||||||||
                                TTTACCA    TCGAAATA
                                   _____
GAM1822 GAB2    3' CAGAATGGTTGTGCTTT    38675          TGG
                                TAGAATGGTTGT  GCTTT
                                ||||||||||||  |||||
                                GTCTTACCAACA  CGAAA
                                    ___
GAM1822 NRG1    3' TAGAATGATTTTTATTTTATCA 30347        G  GGC
                                TAGAATGGTT TTG  TTTATCA
                                |||||||||| |||  |||||||
                                ATCTTACTAA AAT  AAATAGT
                                      A  A__
GAM1822 ZNF144  3' AGGATGGTGCAGAGCTTTAT  28335   A    T  T
                                AG ATGGT GT GGGCTTTAT
                                || ||||| || |||||||||
                                TC TACCA CG CTCGAAATA
                                 C    _ T
GAM1823 ITGBL1  3' TGATATTCTACCTCCTGTGTGC 21989       _     ATA
          TTG                    TGATATTT ACTTTTT  TGCTTG
                                |||||||| |||||||  ||||||
                                ACTATAAG TGGAGGA  ACGAAC
                                     A      CAC
GAM1823 NRCAM   3' ATATTTACTTTTTAAACT   22688          TAT
                                ATATTTACTTTTTA  GCT
                                ||||||||||||||  |||
                                TATAAATGAAAAAT  TGA
                                       T__
GAM1824 HEM1    5' TGTATCACTTTGATGTGTC  23744        AC  AA
                                TGTATCACTT  GAT  TGTC
                                ||||||||||  |||  ||||
                                ACATAGTGAA  CTA  ACAG
                                      A_  C_
GAM1824 SPARC   3' TAATGTATTCACTTAAATCTAT 17068       _    C  A_
          GT                     TAATGTAT CACTTA GAT  ATGT
                                |||||||| |||||| |||  ||||
                                ATTACATA GTGAAT TTA  TACA
                                     A    _  GA
GAM1825 BCL11A  3' CAGGTTTATTTTATACTCAAC  32846   C        G
                                CA GTTTATTTTATAT TCAAC
                                || ||||||||||||| |||||
                                GT CAAATAAAATATG AGTTG
                                 C          _
GAM1825 GPR85   3' AACACATTTACCTCATGTCAAC 33255          AT
                                AACACGTTTATTTT  ATGTCAAC
                                ||||||||||||||  ||||||||
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                                TTGTGTAAATGGAG  TACAGTTG
                                        __
GAM1825  PRKRA    3'  CATTTTTATTTCATCATCAAC  18972    CG        A
                                CA  TTTATTTTAT TGTCAAC
                                ||  |||||||||| |||||||
                                GT  AAATAAAGTA GTAGTTG
                                 AA        _
GAM1825  SELE     3'  CACATTTATTGTCA       7802          TTTATA
                                CACGTTTAT     TGTCA
                                |||||||||     |||||
                                GTGTAAATA     ACAGT
                                        _______
GAM1826  EBF      5'  TTTAGGCAATTTTGGTTACATT 42370        T    ATAA
                  T                  TTTAGGCA TTTTG    ACATTT
                                |||||||| |||||    ||||||
                                AAATCCGT AAAAC    TGTAAA
                                     T    CAA_
GAM1826  TAF1C    3'  CTTAGGCATGATAAACATT    24990        TTTT
                                TTTAGGCA    TGATAAACATT
                                ||||||||    ||||||||||
                                GAATCCGT    ACTATTTGTAA
                                        _____
GAM1827  CYP4B1   3'  TTGAATAAATGAATGAGC    8937         CAAT
                                TTGAATAAA    TGAGT
                                |||||||||    |||||
                                AACTTATTT    ACTCG
                                     ACTT
GAM1828  FLT1     3'  TCTCCTCAGGACTGCATTT    12914        A_  _
                                TCTCCTCG  ATT CATTT
                                ||||||||  ||| |||||
                                AGAGGAGT  TGA GTAAA
                                     CC   C
GAM1828  SOX12    3'  TCACCTCAAACTTCATTT    28058    T       _
                                TC CCTCGAATT CATTT
                                ||  |||||||| |||||
                                AG GGAGTTTGA GTAAA
                                 T        A
GAM1829  CLECSF12 3'  TGAGTCGAGATTGTGCCACTG  44126        C  CCATC   T
                                TGAGTCGA GA     GCC ACTG
                                |||||||| ||     ||| ||||
                                ACTCAGCT CT     CGG TGAC
                                     _  AACA_  _
GAM1829  FCAR     3'  TGAGTCGAGATCGTGCCACTG  39337        C  CCA   C_
                                TGAGTCGA GA   TCG  CTACTG
                                |||||||| ||   |||  ||||||
                                ACTCAGCT CT   AGC  GGTGAC
                                     _ ____   AC
GAM1829  INMT     3'  TGAGTCGAGATCGCGCCACTG  27683        C  CCA   _
                                TGAGTCGA GA   TCGC CTACTG
                                |||||||| ||   |||| ||||||
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                                ACTCAGCT CT   AGCG GGTGAC
                                   _ ____   C
GAM1829 ABCB4    5' CTCAAATTCTGTTCTTTTAC  7769          AT   CC
                                CTCGAATTC  TTCT  TAC
                                |||||||||  ||||  |||
                                GAGTTTAAG  AAGA  ATG
                                     AC    AA
GAM1829 APPL     3' TCCTTGGTCAACTTCTCCTA  29013     CGAAT  _
                                TCCT    TCA TTTCTCCTA
                                ||||    ||| |||||||||
                                AGGA    AGT GAAGAGGAT
                                  ACC__   T
GAM1829 CALU     3' TCTCCTGAACATTTCT      10264       C   TT
                                TCTCCT GAA  CATTTCT
                                |||||| |||  |||||||
                                AGAGGA CTT  GTAAAGA
                                   _  __
GAM1829 HAP1     3' TCTCCCGGGCTTCTCCT     19506      T  AATTCA
                                TCTCC CG     TTTCTCCT
                                ||||| ||     ||||||||
                                AGAGG GC     GAAGAGGA
                                   _ CC_____
GAM1829 HSD17B1  5' TCTCTCTGACCTTCTCCT    7662      C  GAATTCA
                                TCTC TC      TTTCTCCT
                                |||| ||      ||||||||
                                AGAG AG      GAAGAGGA
                                  _ ACTG___
GAM1829 NR2E1    3' TCTCCTTGAAGTTCCTTCT    17580       C  _  A
                                TCTCCT GAA TTC TTTCT
                                |||||| ||| ||| |||||
                                AGAGGA CTT AAG GAAGA
                                   A  C  _
GAM1829 YWHAZ    3' CCAAGCAATTCATTTTTCCT   18202    TCG_       C
                                CC   AATTCATTT TCCT
                                ||   ||||||||| ||||
                                GG   TTAAGTAAA AGGA
                                 TTCG       A
GAM1830 ABCC5    3' TCTGTGCAGTGGCCAGCCATAG 25026    CA  T      GC_
           GAA                    TC  TGC GTGGCCGGT   AGGAA
                                ||  ||| |||||||||   |||||
                                AG  ACG CACCGGTCG   TCCTT
                                 AC   T       GTA
GAM1830 BECN1    3' CATATTGTTAAGTGCAGGAA   19069     C   GGCC
                                CATG TGT    GGTGCAGGAA
                                |||| |||    ||||||||||
                                GTAT ACA    TCACGTCCTT
                                  A  AT__
GAM1830 DBN1     5' TGCTGTGGCCGGGCCGG     38943          T  A
                                TGCTGTGGCCGG GC GG
                                |||||||||||| || ||
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```
                                ACGACACCGGCC CG CC
                                      _ G
GAM1830 LETM1   3' CCATGCTGCCGAGTGCGGG  29499      GTG  _  A
                                CCATGCT  GCCG GTGC GG
                                |||||||  |||| |||| ||
                                GGTACGA  CGGC CACG CC
                                   ___  T  C
GAM1830 MS4A7   5' TGCTGTGGCTGGGGA     34531        C  TGCA
                                TGCTGTGGC GG   GGA
                                ||||||||| ||   |||
                                ACGACACCG CC   CCT
                                     A ____
GAM1830 MYO6    5' TCCACTGTCACCGGTGCGGGA 22666    AT   G     A
                                TCC  GCTGT GCCGGTGC GGA
                                |||  ||||| |||||||| |||
                                AGG  TGACA TGGCCACG CCT
                                  __   G      C
GAM1830 RAMP3   3' GCTGGGGCTGGTGCAGGA   25201     T  C
                                GCTG GGC GGTGCAGGA
                                |||| ||| |||||||||
                                CGAC CCG CCACGTCCT
                                  C  A
GAM1830 SHANK2  3' TCCCTGAGTTTGCTGGTGCAGG 29469    A  CTGTG  C
                                TCC TG    GC GGTGCAGG
                                ||| ||    || ||||||||
                                AGG AC    CG CCACGTCC
                                  G  TCAAA  A
GAM1830 ST5     3' TCCATGCTCTGGCAGGACAGGA 24048       G   C  T
            A                    TCCATGCT TGGC GG GCAGGAA
                                ||||||||| |||| || |||||||
                                AGGTACGA ACCG CC TGTCCTT
                                     G   T  _
GAM1830 TLL1    3' CTGTTTGATCATGTGCAGGAA  29736     __ GC  _
                                CTGT  G  CG GTGCAGGAA
                                ||||  |  || |||||||||
                                GACA  C  GT CACGTCCTT
                                  AA TA  A
GAM1831 CHC1    3' AGGGGGGAAGTTTTGGT    10423      A  T  CC
                                AGGGGG GAA TTT  GT
                                |||||| ||| |||  ||
                                TCCCCC CTT AAA  CA
                                   _  C  AC
GAM1831 EGR3    3' GGGGAGAAGGTGAGAC     40556       TTTTCC  A
                                GGGGAGAA    GT AGAC
                                ||||||||    || ||||
                                CCCCTCTT    CA TCTG
                                     C_____  C
GAM1831 FOXE1   3' AGGGGGAGAGTTATTGGAC  20937        A  TTCCGTAA
                                AGGGGGAGA TT      GAC
                                ||||||||| ||      |||
```

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                                TCCCCCTCT AA       CTG
                                     C  TAAC_____
GAM1831  MAP3K7   5'  AGGGGAGAATTTTGTGAC    17268           CC  AA
                                GGGGGAGAATTTT  GT  GAC
                                ||||||||||||  ||  |||
                                TCCCCTCTTAAAA  CA  CTG
                                          __  __
GAM1831  PKD2     3'  AGGGGGGGAGTTCTCCATGACT 41068       A  A       AA
                                AGGGGG GA TTTTCCGT  GACT
                                ||||||  || ||||||||  ||||
                                TCCCCC CT AAGAGGTA  CTGA
                                   C  C       __
GAM1832  ARHGEF12 3'  TGTGACGTTAAGAGCAAA    31653        C    T  T
                                TGTGACGT TAAGA GT GA
                                ||||||||  |||||  ||  ||
                                ACACTGCA ATTCT CG TT
                                     _    _  T
GAM1832  EGFR     3'  TGTGGGTCTAAGAGCTAA    23403      AC       T
                                TGTG  GTCTAAGA GTTGA
                                ||||  ||||||||  |||||
                                ACAC  CAGATTCT CGATT
                                  C_       _
GAM1832  HDAC4    3'  TGTGACGTGTGAGAACACTTTG 25791         CTA   TG___
                                TGTGACGT   AGA    TTG
                                ||||||||   |||    |||
                                ACACTGCA   TCT    AAC
                                     CAC   TGTGA
GAM1832  IL8RA    3'  TGTGACGTTCAACGGGAAT   8445         CTAA    TT
                                TGTGACGT   GATG  GAAT
                                ||||||||   ||||  ||||
                                ACACTGCA   TTGC  CTTA
                                     AG__   C_
GAM1832  MCSP     3'  TGTGCTGTCTAAATGTCA    36211      AC    A
                                TGTG  GTCTA GATGTTG
                                ||||  |||||  |||||||
                                ACAC  CAGAT TTACAGT
                                  GA    _
GAM1832  TNFAIP2  3'  TGTGACGTCTAACGCTG     26645          AG
                                TGTGACGTCTA  ATGTTG
                                ||||||||||  ||||||
                                ACACTGCAGAT  TGCGAC
                                          __
GAM1833  CKAP1    5'  TGTAGCGCGGCGGAGCAAGCGC 43887     C       AC  C
            GG                    TGT GCGCGGCG  GC GGCGCGG
                                ||| ||||||||  || |||||||
                                ACA CGCGCCGC  CG TCGCGCC
                                  T       CT  T
GAM1833  FOXD1    5'  TGTGGCGCGGCGGCGGCG    20935     C       AC  C
                                TGT GCGCGGCG  GC GGCG
                                ||| ||||||||  || ||||
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                                ACA CGCGCCGC  CG CCGC
                                  C       __ _
GAM1833  PROS1    5'  TGCTGCGCGGCGGCGCCAG   44614     C       A
                                TGT GCGCGGCG CGCCGG
                                ||| |||||||| ||||||
                                ACG CGCGCCGC GCGGTC
                                  A       C
GAM1834  AIM1     5'  CGGACTGCGGGCGGGCGTCTC  45081     _ G T
                                CGG C G CGGGCGGGCGTCTC
                                ||| | | ||||||||||||||
                                GCC G C GCCCGCCCGCAGAG
                                  T A _
GAM1834  BCL11A   5'  CGGCGGCGGCGGGCGGAC    39708         T
                                CGGCGGCGG CGGGCGGGC
                                ||||||||| |||||||||
                                GCCGCCGCC GCCCGCCTG

                                   _
GAM1834  C1orf6   5'  CGGCGGGCGGTCGGGCGGGC  33526       _
                                CGGCGG CGGTCGGGCGGGC
                                |||||| ||||||||||||
                                GCCGCC GCCAGCCCGCCCG
                                   C
GAM1834  EXTL3    3'  GGCGGCGGCCGGGTCCGG    11036           __
                                GGCGGCGGTCGGG  CGG
                                |||||||||||||  |||
                                CCGCCGCCGGCCC  GCC
                                      AG
GAM1834  FANCE    5'  CGGCGGTGGCGGGCCAGCTC  34897       C  T    G   G
                                CGGCGG GG CGGGC GGC TC
                                |||||| || ||||| ||| ||
                                GCCGCC CC GCCCG TCG AG
                                   A _    G  _
GAM1834  FGD1     5'  CGGCGGCGGCGGGCGGG     20901         T
                                CGGCGGCGG CGGGCGGG
                                ||||||||| ||||||||
                                GCCGCCGCC GCCCGCCC

                                   _
GAM1834  FMR2     5'  CGGCGGCGGGCGGGCGCCT   12961       T
                                CGGCGG CGGGCGGGCGTCT
                                |||||| ||||||||||||
                                GCCGCC GCCCGCCCGCGGA

                                   _
GAM1834  FMR2     5'  CGGCGGCGGCGGGCGGGC    12960         T
                                CGGCGGCGG CGGGCGGGC
                                ||||||||| |||||||||
                                GCCGCCGCC GCCCGCCCG

                                   _
GAM1834  HMGA2    5'  CGGCGGCGGTGGGTGGG     18509         C  C
                                CGGCGGCGGT GGG GGG
                                |||||||||| ||| |||
```

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                                GCCGCCGCCA CCC CCC
                                      _  A
GAM1834  MUC4     3'  CGGTGGCGTTGAACGTCT    32904     C   GTCGGGC
                                CGG GGCG      GGGCGTCT
                                ||| ||||      ||||||||
                                GCC CCGC      CTTGCAGA
                                  A   AA_____
GAM1834  NSEP1    5'  CGGCGGCGGTGGGGCTGCTC   43996         C   GG  G
                                CGGCGGCGGT GGGC  GC TC
                                |||||||||| ||||  || ||
                                GCCGCCGCCA CCCG  CG AG
                                      C   A_ _
GAM1834  PTP4A2   5'  CGGCGGCGGCGGCGGCGCGTCT 38626          CG    _
            C                    CGGCGGCGGT  GGCGG GCGTCTC
                                |||||||||  ||||| |||||||
                                GCCGCCGCCG  CCGCC CGCAGAG
                                      __    G
GAM1834  SLC6A8   5'  CGGCGGCGGCTCGGGCGCGCCT 24760         _     G  G
            C                    CGGCGGCGG TCGGGCG GC TC
                                |||||||| ||||||| || ||
                                GCCGCCGCC AGCCCGC CG AG
                                     G     G  G
GAM1834  SLC9A3   3'  CGGCGGCGGTGGGCGGAC    20049         C
                                CGGCGGCGGT GGGCGGGC
                                |||||||||| ||||||||
                                GCCGCCGCCA CCCGCCTG
                                      _
GAM1835  GA       3'  TGGTGGTTATGGATTACATGTG 29972    A   AAC  TG
                                TG TGGT   TG  TTACATGTG
                                || ||||   ||  |||||||||
                                AC ACCA   AC  AATGTACAC
                                 C   AT_  CT
GAM1835  LRRC2    3'  ATGGTAGCCACATGT      35995       ACTGT
                                ATGGTA    GTTACATGT
                                ||||||    |||||||||
                                TACCAT    CGGTGTACA
                                     _____
GAM1835  MUC3B    5'  TGATGGCAGTTGTGGATGTGC  45347        AC    TTAC
                                TGATGGTA  TGTG   ATGTGC
                                ||||||||  ||||   ||||||
                                ACTACCGT  ACAC   TACACG
                                     CA   C___
GAM1835  PTPRA    5'  TGGTAACTGTGTCATGT     38919          TA
                                TGGTAACTGTGT  CATGT
                                ||||||||||||  |||||
                                ACCATTGACACA  GTACA
                                      __
GAM1835  GA       3'  TGGTGGTTATGGATTACATGTG 29972    A   AAC  TG
                                TG TGGT   TG  TTACATGTG
                                || ||||   ||  |||||||||
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                                AC ACCA   AC  AATGTACAC
                                 C    AT_  CT
GAM1835 LRRC2    3'  ATGGTAGCCACATGT      35995       ACTGT
                                ATGGTA    GTTACATGT
                                ||||||    |||||||||
                                TACCAT    CGGTGTACA
                                  _____
GAM1835 MUC3B    5'  TGATGGCAGTTGTGGATGTGC 45347        AC    TTAC
                                TGATGGTA  TGTG   ATGTGC
                                ||||||||  ||||   ||||||
                                ACTACCGT  ACAC   TACACG
                                     CA   C___
GAM1835 PTPRA    5'  TGGTAACTGTGTCATGT     38919          TA
                                TGGTAACTGTGT  CATGT
                                ||||||||||||  |||||
                                ACCATTGACACA  GTACA
                                      __
GAM1836 ADRA2A   3'  CTGGAGGGAGAGAGGGAAC   8634     TG     A
                                CTG  GGGAGA AGGGAAC
                                |||  |||||| |||||||
                                GAC  CCCTCT TCCCTTG
                                  CT     C
GAM1836 AP2A1    3'  TGGATGGGGAGGGGG       30540      CTG      AAA
                                TGGA   TGGGGAG   GGG
                                ||||   |||||||   |||
                                ACCT   ACCCCTC   CCC
                                  ___      C__
GAM1836 AQP6     3'  TGGGCTGTGGGGTGGGA     38259     A       AGAAA
                                TGG CTGTGGGG    GGGA
                                ||| ||||||||    ||||
                                ACC GACACCCC    CCCT
                                  C       A____
GAM1836 ARIH1    5'  GGAGGAGGGAGGGAGGGA    25092     CTGT     AA
                                GGA    GGGGAG  AGGGA
                                |||    ||||||  |||||
                                CCT    TCCCTC  TCCCT
                                  CC__     CC
GAM1836 ATP1A2   3'  TGGGCATGAAAAGAAAGGGAA 8715      ACT   GG
                                TGG   GTG  GAGAAAGGGAA
                                |||   |||  ||||||||||
                                ACC   TAC  TTCTTTCCCTT
                                  CG_   TT
GAM1836 BCL11A   3'  GGCGATGGGGAAGGGGA     39714    ACT      AAA
                                GG   GTGGGGAG   GGGA
                                ||   ||||||||   ||||
                                CC   TACCCCTT   CCCT
                                 GC_       C__
GAM1836 BRCA1    3'  TGGCTGTGGGGGATCTGGG    28655     A       A  AA_
                                TGG CTGTGGGG GA   GGG
                                ||| |||||||| ||   |||
```

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                                ACC GACACCCC CT   CCC
                                  _       _ AGA
GAM1836 BTG2     3' TGGCTGTGGGGAGGAGAAC   27622     A        AAA
                                TGG CTGTGGGGAG   GGGAAC
                                ||| ||||||||||   ||||||
                                ACC GACACCCCTC   CTCTTG
                                  _        ____
GAM1836 CAPN1    3' GAAGTGGGGAGAGGGGA     23252    CT       AA
                                GA  GTGGGGAGA  GGGA
                                ||  |||||||||  ||||
                                CT  CACCCCTCT  CCCT
                                 T_       C_
GAM1836 CARKL    3' TGGACGTGGGGAACACAGGGA  30005      T      AA_
                                TGGAC GTGGGGAG   AGGGA
                                ||||| ||||||||   |||||
                                ACCTG CACCCCTT   TCCCT
                                   _       GTG
GAM1836 CENTD2   5' TGGCTGGGGAGGGGA      31608     A  GT     AAA
                                TGG CT  GGGGAG   GGGA
                                ||| ||  ||||||   ||||
                                ACC GA  CCCCTC   CCCT
                                  _ __     ____
GAM1836 CKTSF1B1 3' TGGATTGTGAGGAGGAGG    30094      C       AA
                                TGGA TGTGGGGAG  AGG
                                |||| |||||||||  |||
                                ACCT ACACTCCTC  TCC
                                   A        C_
GAM1836 CLCN6    3' GGGGCGGGGAGAGGGGA     34719    ACT       AA
                                GG   GTGGGGAGA  GGGA
                                ||   |||||||||  ||||
                                CC   CGCCCCTCT  CCCT
                                 C__        C_
GAM1836 CPNE7    3' GACTGTGGGGACAGGA      30868          GAAA
                                GACTGTGGGGA    GGGA
                                ||||||||||    ||||
                                CTGACACCCCT    TCCT
                                      G____
GAM1836 CRAT     5' TGGCTGTGGGGCGGGGG     19669     A      AGAAA
                                TGG CTGTGGGG    GGG
                                ||| ||||||||    |||
                                ACC GACACCCC    CCC
                                  _       GCC__
GAM1836 CRHR2    3' TGGCTGGGGAGGGGA       12447     A  GT     AAA
                                TGG CT  GGGGAG   GGGA
                                ||| ||  ||||||   ||||
                                ACC GA  CCCCTC   CCCT
                                  _ __     ____
GAM1836 CRTAP    3' TGGGCTGTTGGGAAAAGGA   26844     A   GG  A
                                TGG CTGT  GG GAAAGGGA
                                ||| ||||  || ||||||||
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                                ACC GACA  CC CTTTTCCT
                                  C   A_  _
GAM1836 DPYS    3'  TGGCTGTGAAGGGAA      10739     A     GGAGAA
                                TGG CTGTGG     AGGGAA
                                ||| ||||||     ||||||
                                ACC GACACT     TCCCTT
                                  _     _______
GAM1836 DYSF    3'  TGGGTTGGGGGAGAAGGAAA  18585     AC  T       A
                                TGG  TG GGGGAGAA GGGAA
                                |||  || |||||||| |||||
                                ACC  AC CCCCTCTT CCTTT
                                  CA  _       _
GAM1836 EPHA8   3'  TGGCTATGGGGAGGGGGGGG   33905     A         AAA
                                TGG CTGTGGGGAG   GGG
                                ||| ||||||||||   |||
                                ACC GATACCCCTC   CCC
                                  _         CCC
GAM1836 F9      3'  GGGTAAAAGGGAGAGAGGGA  6576     ACTGT      A
                                GG    GGGGAGA AGGGA
                                ||    ||||||| |||||
                                CC    TCCCTCT TCCCT
                                 CATTT      C
GAM1836 FN1     5'  GGGTGGGGAAGGGA       38337    ACT      GAA   A
                                GG   GTGGGGA   AGGG A
                                ||   |||||||   |||| |
                                CC   CACCCCT   TCCC T
                                  ___      ___    C
GAM1836 GCN5L1  3'  GGGTTTGGGGAGGGAAC    11246    ACTG     GAAA
                                GG   TGGGGA   GGGAAC
                                ||   ||||||   ||||||
                                CC   ACCCCT   CCCTTG
                                 CAA_    ____
GAM1836 GDF2    3'  TGGGGTGTGGGGAGGGAGAG  32131     AC       AA
                                TGG  TGTGGGGAG  AGGG
                                |||  |||||||||  ||||
                                ACC  ACACCCCTC  TCTC
                                  CC       CC
GAM1836 GDI1    3'  GGGTGGGGAAGGGA       41016    ACT      GAA   A
                                GG   GTGGGGA   AGGG A
                                ||   |||||||   |||| |
                                CC   CACCCCT   TCCC T
                                  ___      ___    C
GAM1836 GNB3    3'  GGACTGTGGGGAGGGAA     13222           GAAA
                                GGACTGTGGGGA   GGGAA
                                ||||||||||||   |||||
                                CCTGACACCCCT   CCCTT
                                     ____
GAM1836 GPR4    5'  GGCTGTGGGGCCACAGGGA   40889    A       AGAA
                                GG CTGTGGGG   AGGGA
                                || ||||||||   |||||
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                                CC GACACCCC   TCCCT
                                 _      GGTG
GAM1836 HADHSC   3' TGTACTGTGTGAGGGAA    23720   G    GG  GAAA
                                TG ACTGTG  GA   GGGAA
                                || ||||||  ||   |||||
                                AC TGACAC  CT   CCCTT
                                 A     A_  _____
GAM1836 HD       3' TGGCTACAGGAGAGGGA    13366    A   TG  G   AA
                                TGG CTG  GG AGA  GGGA
                                ||| |||  || |||  ||||
                                ACC GAT  CC TCT  CCCT
                                  _  GT  _  __
GAM1836 HDAC7A   5' GGACAGAGAGAGGGA     32472    TGT     AA
                                GGAC   GGGGAGA  GGGA
                                ||||   |||||||  ||||
                                CCTG   TCTCTCT  CCCT
                                  ____     __
GAM1836 HERC2    3' GGACACCTGGGAGAGGGGA  21693    TGTG    AA
                                GGAC   GGGAGA  GGGA
                                ||||   ||||||  ||||
                                CCTG   CCCTCT  CCCT
                                  TGGA    C_
GAM1836 HS3ST3A1 5' GGGCGGGAAGGGGAA     25808    ACT     AAA
                                GG   GTGGGGAG   GGGAA
                                ||   ||||||||   |||||
                                CC   CGCCCTTC   CCCTT
                                 ____     ____
GAM1836 IFITM2   3' CGGCTGTGGGGACAGGG    26970    A       GAA
                                TGG CTGTGGGGA   AGGG
                                ||| |||||||||   ||||
                                GCC GACACCCCT   TCCC
                                  _       G__
GAM1836 IL1F5    3' GGATTAAAGGGAAGGG     29354    C  T    GAA
                                GGA TG GGGGA   AGGG
                                ||| || |||||   ||||
                                CCT AT TCCCT   TCCC
                                  A  T    ___
GAM1836 ITGA6    5' GGACGCACGGGGAGGGGA    6831     _ GT    AAA
                                GGAC T  GGGGAG   GGGA
                                |||| |  ||||||   ||||
                                CCTG G  CCCCTC   CCCT
                                  C TG     ___
GAM1836 LDOC1    3' GGGCTGCGGGGAGGGGG    29492    A       AAA
                                GG CTGTGGGGAG   GGG
                                || ||||||||||   |||
                                CC GACGCCCCTC   CCC
                                 C        C__
GAM1836 LGALS3BP 3' GGCTGTGGGGGGATCCCAGAG 42935    A      A  A___
                                GG CTGTGGGG GA    AGGG
                                || |||||||| ||    ||||
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                                CC GACACCCC CT    TCTC
                                 _      C  AGGG
GAM1836 LOH11CR2A 3'  TGAACTCCCTCAAGAAAGGGAA 31193       GTGGG
                                TGGACT    GAGAAAGGGAA
                                ||||||    ||||||||||
                                ACTTGA    TTCTTTCCCTT
                                   GGGAG
GAM1836 LRP1     5'  GGAGGCGGGGAGGGGGG     14214     CT      AAA
                                GGA  GTGGGGAG   GGG
                                |||  ||||||||   |||
                                CCT  CGCCCCTC   CCC
                                  C_       CC_
GAM1836 MADH7    3'  GGCTGGCAGGAAGGGAA     25370    A   TG    GAA
                                GG CTG  GGGA   AGGGAA
                                || |||  ||||   ||||||
                                CC GAC  TCCT   TCCCTT
                                 _   CG    ___
GAM1836 MAN1A1   3'  GGACTGTGGGGGATGGGGA   45097          A  AA
                                GGACTGTGGGG GA  GGGA
                                ||||||||||| ||  ||||
                                CCTGACACCCC CT  CCCT
                                       _ AC
GAM1836 MAP3K14  5'  TGGGTTGGGGGAGAAAGG    19548     AC  T
                                TGG  TG GGGGAGAAAGG
                                |||  || ||||||||||
                                ACC  AC CCCCTCTTTCC
                                  CA  _
GAM1836 MAP3K9   3'  TGGCTGAGGAGAGGGA      41361     A   TG     AA
                                TGG CTG  GGGAGA  GGGA
                                ||| |||  ||||||  ||||
                                ACC GAC  TCCTCT  CCCT
                                  _  __     __
GAM1836 MECP2    3'  GGAAGGGGAAGGGGA       22597     CTGT    A   A
                                GGA    GGGG GAA GGGA
                                |||    |||| ||| ||||
                                CCT    TCCC CTT CCCT
                                  _____   _  C
GAM1836 MUC1     5'  TGGGTGGGGAGGGGG       43772     ACT       AAA
                                TGG   GTGGGGAG   GGG
                                |||   ||||||||   |||
                                ACC   CACCCCTC   CCC
                                  ___       C__
GAM1836 MYOG     3'  TGGATGAGGAAGGGGA      40425     CTG      AAA
                                TGGA   TGGGGAG   GGGA
                                ||||   |||||||   ||||
                                ACCT   ACTCCTT   CCCT
                                  ___       C__
GAM1836 NDRG3    3'  TGGGCTATACAAAAAAGGGG  36749     A    G     A
                                TGG CTGTG GGAGAA GGG
                                ||| ||||| |||||| |||
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                                ACC GATAT TTTTTT CCC
                                  C    G     C
GAM1836 NFIA    5' GGGGTGTGGGGGAGGGGG   43220   AC     A  AA
                                GG  TGTGGGG GA  GGG
                                ||  ||||||| ||  |||
                                CC  ACACCCC CT  CCC
                                 CC      _ CC
GAM1836 NGB     3' GAATGAGGGAAAGGGAA    34584   CT     A
                                GA  GTGGGG GAAAGGGAA
                                ||  |||||| |||||||||
                                CT  TACTCC CTTTCCCTT
                                  __    _
GAM1836 NOS1    5' TGGGTGTGGGGAGGGAGAC  8382     AC       AAA  GA
                                TGG  TGTGGGGAG   GG  AC
                                |||  |||||||||   ||  ||
                                ACC  ACACCCCTC   CC  TG
                                  C_        ___  TC
GAM1836 PBX2    3' GGGTTGTGGGAAGAAGGGGGA 15107   AC        A_
                                GG  TGTGGGGAGAA  GGGA
                                ||  ||||||||||  ||||
                                CC  ACACCCTTCTT  CCCT
                                 CA         CC
GAM1836 PCK1    3' TGGATGGGAAAGGGAA     40946     CTG     GAA
                                TGGA   TGGGGA   AGGGAA
                                ||||   ||||||   ||||||
                                ACCT   ACCCTT   TCCCTT
                                  ___    ___
GAM1836 PPFIA3  3' TGGGCAGGAAAAAGGGGA   41427     ACT TG      A
                                TGG   G  GGGAGAA GGGA
                                |||   |  ||||||| ||||
                                ACC   C  CCTTTTT CCCT
                                  ___ GT     C
GAM1836 PRKY    3' TGGGCATGGAGAGGGA     15713     ACT     GAAA
                                TGG   GTGGGGA   GGGA
                                |||   |||||||   ||||
                                ACC   TACCTCT   CCCT
                                  CG_     _____
GAM1836 PVR     5' TGGGGTGGGAAGGGGAA    27114     ACT      AAA
                                TGG   GTGGGGAG   GGGAA
                                |||   ||||||||   |||||
                                ACC   CACCCTTC   CCCTT
                                  C__       ___
GAM1836 RAB3A   3' GGAAGAGGGGAAAGGGA     16070     CTGT    A
                                GGA    GGGG GAAAGGGA
                                |||    |||| ||||||||
                                CCT    TCCC CTTTCCCT
                                  TC__   _
GAM1836 RTN2    3' CGGGCCGAGGAGGGGG     24724     A  GT     AAA
                                TGG CT  GGGGAG   GGG
                                ||| ||  ||||||   |||
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                                GCC GG  CTCCTC   CCC
                                  C __     C__
GAM1836 RUNX3    3' GGTCCGCGGGGGGGAGAGGG  20323    A      A_ A
                                GG CTGTGGGG  GA AGGG
                                || ||||||||  || ||||
                                CC GGCGCCCC  CT TCCC
                                 A       CC  C
GAM1836 SLC39A4  5' TGGCCTGTGGGGAGGGTCAGGG 39297     A        AA__
                                TGG CTGTGGGGAG    AGGG
                                ||| ||||||||||    ||||
                                ACC GACACCCCTC    TCCC
                                  G         CCAG
GAM1836 SLC7A5   3' TGGGTTGCGGGGAACCGGA   18558     AC       AAA
                                TGG  TGTGGGGAG   GGG
                                |||  |||||||||   |||
                                ACC  ACGCCCCTT   CCT
                                  CA        GG_
GAM1836 SORCS2   3' TGGAGTGGGGAGGGGG      34067     CT      AAA
                                TGGA  GTGGGGAG   GGG
                                ||||  ||||||||   |||
                                ACCT  CACCCCTC   CCC
                                   __       C__
GAM1836 SSRP1    5' GGGGCGCGGGGAGGGGGA    17128    AC       AAA
                                GG  TGTGGGGAG   GGGA
                                ||  |||||||||   ||||
                                CC  GCGCCCCTC   CCCT
                                 CC        C__
GAM1836 SYNGR1   3' TGGGTGTGGAGAGAGGGGA   21773     AC        AA
                                TGG  TGTGGGGAGA  GGGA
                                |||  ||||||||||  ||||
                                ACC  ACACCTCTCT  CCCT
                                  C_        C_
GAM1836 TAGLN2   3' TGGCTATGGGGAAGGGAA    18687     A       GAA
                                TGG CTGTGGGGA   AGGGAA
                                ||| |||||||||   ||||||
                                ACC GATACCCCT   TCCCTT
                                   _       ____
GAM1836 TRPV1    5' TGGACGTGGGGAACACAGGGA  38803      T       AA_
                                TGGAC GTGGGGAG   AGGGA
                                ||||| ||||||||   |||||
                                ACCTG CACCCCTT   TCCCT
                                   _       GTG
GAM1836 TULP1    3' TGGGGCGCGGGGAGGAGGG    17732     AC       AA
                                TGG  TGTGGGGAG  AGGG
                                |||  |||||||||  ||||
                                ACC  GCGCCCCTC  TCCC
                                  CC        C_
GAM1836 XYLB     3' TGGACTGCAAGAAGAGAGAGGG 23029        TG     A__
             AA                   TGGACTG  GGGAGA   AGGGAA
                                |||||||  ||||||   ||||||
```

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                                ACCTGAC  TCTTCT   TCCCTT
                                   GT     CTC
GAM1837  INMT     3'  CCTATTCCTTGACCAAAGCAC  27675    G    CC_  A
                                CC ATTCC   GC CGGAGCAC
                                || |||||   || ||||||||
                                GG TAAGG   TG GTTTCGTG
                                 A    AAC  _
GAM1837  SRGAP2   3'  GATTTCCCACAAAGCAC     43983     C     CG
                                GATT CCCGCA  GAGCAC
                                |||| ||||||  ||||||
                                CTAA GGGTGT  TTCGTG
                                  A     __
GAM1837  INMT     3'  CCTATTCCTTGACCAAAGCAC  27675    G    CC_  A
                                CC ATTCC   GC CGGAGCAC
                                || |||||   || ||||||||
                                GG TAAGG   TG GTTTCGTG
                                 A    AAC  _
GAM1837  SRGAP2   3'  GATTTCCCACAAAGCAC     43983     C     CG
                                GATT CCCGCA  GAGCAC
                                |||| ||||||  ||||||
                                CTAA GGGTGT  TTCGTG
                                  A     __
GAM1838  RUNX1    3'  GCTATTAGCTGTTTACAAAAGT 12024    ATGA   A_
            G                    GC    AGC  TTTACAAAAGTG
                                ||   |||  ||||||||||||
                                CG   TCG  AAATGTTTTCAC
                                 ATAA   AC
GAM1838  RUNX1    3'  GCTATTAGCTGTTTACAAAAGT 12024    ATGA   A_
            G                    GC    AGC  TTTACAAAAGTG
                                ||   |||  ||||||||||||
                                CG   TCG  AAATGTTTTCAC
                                 ATAA   AC
GAM1839  NT5M     5'  CGCCGTGCTGCCGGAT      33649        C     III
                                TGCCGTGC GCCGGA   T
                                |||||||| ||||||   |
                                GCGGCACG CGGCCT   A
                                    A     III
GAM1840  AICDA    3'  CCCGGCCCTCTCTCTTTCTTTT 34039     T  G  GC   CC
            T                    CCCG CT TC  CTCT  CTTTTT
                                |||| || ||  ||||  ||||||
                                GGGC GG AG  GAGA  GAAAAA
                                  C  G  A_   AA
GAM1840  ANKRA2   5'  TGTCCCTCTCTCCTTTTT    35758     G     _
                                TGTC CCTCTC CCTTTTT
                                |||| |||||| |||||||
                                ACAG GGAGAG GGAAAAA
                                  _     A
GAM1840  CDH2     3'  CCCTTTCTTTCCTTTCCTTTTT 12168    G_  GTCG  C  C
            T                    CCC  TCT   CCT TCC TTTTT
                                ||| |||   ||| ||| |||||
```

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                              GGG  AGA    GGA AGG AAAAA
                                AA   AA__   A   A
GAM1840  CDKN2C    5'  CCGGTTTCTTCTCCCTTTT   10391     TCTG  GCC
                              CCG    TC   TCTCCCTTTT
                              |||    ||   ||||||||||
                              GGC    AG   AGAGGGAAAA
                                CAA_  A__
GAM1840  DEC1      5'  CCCTTCAAGTTTTCCCTTTTT  32645     G  TGTCGCCTC
                              CCC TC        TCCCTTTTT
                              ||| ||        |||||||||
                              GGG AG        AGGGAAAAA
                                A  TTCAAA___
GAM1840  GPR17     3'  CCCTTTGTCAGTTCTTCCTTTT 23618     GTC    CC   C
              T                  CCC   TGTCG  TCT CCTTTTT
                              |||   |||||  ||| |||||||
                              GGG   ACAGT  AGA GGAAAAA
                                AA_    CA   A
GAM1840  HMGA2     3'  GTTTGCTTACTTCCCTTTTT   18528    C   CGC  C
                              GT TGT   CT TCCCTTTTT
                              || |||   || |||||||||
                              CA ACG   GA AGGGAAAAA
                               A   AAT  _
GAM1840  MAP1A     3'  GTGGCTCAGCTTCTCCCTTTTT 14347     CTG  _  C
                              GT   TC GC TCTCCCTTTTT
                              ||   || || ||||||||||
                              CA   AG CG AGAGGGAAAAA
                               CCG  T  A
GAM1840  PLXNA2    3'  TCTGTTTTTTTCCCTTTTT    36078      CGCCTC
                              TCTGT     TCCCTTTTT
                              |||||     |||||||||
                              AGACA     AGGGAAAAA
                                 AAAAA_
GAM1840  RAB13     3'  CCCTTCCTCTCTCTTCCTTTTT 16112     G   G  GC    C
                              CCC TCT TC  CTCT CCTTTTT
                              ||| ||| ||  |||| |||||||
                              GGG AGG AG  GAGA GGAAAAA
                                A   _  A_    A
GAM1840  RNF3      5'  CCCGTTTTTTGGGCCCCCCTTT 26744       CTGTC__   T T
              TT                  CCCGT      GCC C CCCTTTTT
                              |||||      ||| | ||||||||
                              GGGCA      CGG G GGGAAAAA
                                 AAAAACC   _ _
GAM1840  SOX4      3'  CGTCTGTCCTTTTCGTTTCTTT 16981         GCC_  TCC_
              TT                  CGTCTGTC    TC    CTTTTT
                              ||||||||    ||    ||||||
                              GCAGACAG    AG    GAAAAA
                                   GAAA  CAAA
GAM1840  TAF5      3'  GCTTTTAGTCTCCCTTTTT    40059    T  GTCGCC
                              G CT      TCTCCCTTTTT
                              | ||      ||||||||||
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                                C GA     AGAGGGAAAAA
                                 _ AAATC_
GAM1840  TEX15    3'  GCTTGACCTTCCCTTTTT    36325    TC  TC    C
                                G  TG  GCCT TCCCTTTTT
                                |  ||  |||| |||||||||
                                C  AC  TGGA AGGGAAAAA
                                 GA  __   _
GAM1841  P2RY12   3'  TCAGTTAATATTTTTACT    35569          CC
                                TTAGTTAATA  TTTACT
                                ||||||||||  ||||||
                                AGTCAATTAT  AAATGA
                                      AA
GAM1841  P2RY12   3'  TCAGTTAATATTTTTACT    35569          CC
                                TTAGTTAATA  TTTACT
                                ||||||||||  ||||||
                                AGTCAATTAT  AAATGA
                                      AA
GAM1842  A1BG     3'  TCATCAACTATTGGTTGATA   39094       T     AAC
                                TCATCA CTATT   TGATA
                                |||||| |||||   |||||
                                AGTAGT GATAA   ACTAT
                                    T    CCA
GAM1842  BDKRB2   3'  AACCTCATCCATTTATTA    8392          _  C
                                AACCTCATC AT TATTA
                                ||||||||| || |||||
                                TTGGAGTAG TA ATAAT
                                      G  A
GAM1842  DCTN1    5'  CTCTCATCTACCTTTCTG    35700     A       AA_
                                CTC TCATCTATT   CTG
                                ||| |||||||||   |||
                                GAG AGTAGATGG   GAC
                                  _       AAA
GAM1842  DTNA     3'  TCATCATCTGTCTGACA     37375         ATTAA
                                TCATCATCT    CTGATA
                                |||||||||    ||||||
                                AGTAGTAGA    GACTGT
                                      CA___
GAM1842  DYRK1A   5'  CTCAGTGTTGTCAACTGATA   38991     TCATCTA
                                CTCA      TTAACTGATA
                                ||||      ||||||||||
                                GAGT      AGTTGACTAT
                                  CACAAC_
GAM1842  HIVEP2   3'  AACCTCACATATATATTGAT   27548       T   C   TAAC
                                AACCTCA CAT TAT    TGAT
                                ||||||| ||| |||    ||||
                                TTGGAGT GTA ATA    ACTA
                                    _  T   TA__
GAM1842  JAK3     3'  AACCTCATCTCTATTAAAAATA 6862          A       CT
                                AACCTCATC TCTATTAA  GATA
                                ||||||||| ||||||||  ||||
```

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                                TTGGAGTAG AGATAATT  TTAT
                                      _      T_
GAM1842 LMO6    3'  CCTCATCATCTACTCTG    26042          AA
                                CCTCATCATCTATT  CTG
                                |||||||||||||  |||
                                GGAGTAGTAGATGA  GAC
                                      __
GAM1842 SLC6A4  3'  AACCTAATCCTAACTGAT   9818      C  ATCTA
                                AACCT ATC    TTAACTGAT
                                ||||| |||    |||||||||
                                TTGGA TAG    GATTGACTA
                                   T  _____
GAM1842 SRD5A2  5'  AACCTCATCATTAATTCTCT  40455        CT  AA
                                AACCTCATCAT  ATT  CT
                                ||||||||||  |||  ||
                                TTGGAGTAGTA  TAA  GA
                                      AT   GA
GAM1842 VLGR1   3'  CATCCTATTAACTGAT     37010     AT
                                CATC  CTATTAACTGAT
                                ||||  ||||||||||||
                                GTAG  GATAATTGACTA
                                   __
GAM1843 ELAC2   3'  CAGCTGAAATACTATTTTCGT  32852     AAT
                                CAGTT   AATACTATTTTCGT
                                |||||   ||||||||||||||
                                GTCGA   TTATGATAAAAGCA
                                   CT_
GAM1844 ME1     3'  AGTGTCCTGTATAAAAATGATG 14404       __   TC    C
            A                    AGTGTCCT  ATGA  AATGA GA
                                ||||||||  ||||  ||||| ||
                                TCACAGGA  TATT  TTACT CT
                                     CA   T_    A
GAM1844 NCOA6   3'  ATGTTCTATGACAATGA    30433     C    T
                                GTGT CTATGA CAATGA
                                |||| |||||| ||||||
                                TACA GATACT GTTACT
                                   A    _
GAM1845 ADH5    5'  AGGGGGGCGGGGCGTGGG    8577         A  A_
                                AGGGGGGCG GGC  GGG
                                |||||||||  |||  |||
                                TCCCCCCGC CCG  CCC
                                     C   CA
GAM1845 ALPL    3'  AGGGGAGCGAGGTGGGC     7883          CA
                                AGGGGGGCGAGG  GGGC
                                ||||||||||||  ||||
                                TCCCCTCGCTCC  CCCG
                                      A_
GAM1845 APOC3   3'  AGGGGGGCCAGGCATGAGGTGG 6214        G   _  CAGC
            G                    AGGGGGGC AGGCA GGG   GGG
                                ||||||||  ||||| |||   |||
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                                TCCCCCCG TCCGT CTC    CCC
                                    G    A   CA__
GAM1845 AR      5'  GGGGGGCGGGTGGGGAGAAGG  6243         A  CA   C  C
                                GGGGGGCG GG  GGG AG GGG
                                |||||||| ||  ||| || |||
                                CCCCCCGC CC  CCC TC TCC
                                    _  AC   _  T
GAM1845 ATBF1   5'  AGGGGGGCGGGCGGGGCGGG  27844         A   A   CA
                                AGGGGGGCG GGC GGG  GCGGG
                                ||||||||| ||| |||  |||||
                                TCCCCCCGC CCG CCC  CGCCC
                                    _  _  __
GAM1845 ATBF1   5'  GGGGCGGGCGGGGCGG      27853       A   A   CA
                                GGGGCG GGC GGG  GCGG
                                |||||| ||| |||  ||||
                                CCCCGC CCG CCC  CGCC
                                    _  _  __
GAM1845 BACE    5'  GAGGGGCGGGCATGGCGG    39961         A   GGGCA
                                GGGGGGCG GGCA    GCGG
                                |||||||| ||||    ||||
                                CTCCCCGC CCGT    CGCC
                                    _   AC___
GAM1845 CACNA1S  5'  AGGGGGCGGGGCAGGAGTGGG  6301         A    GC  C
                                GGGGGGCG GGCAGG  AG GGG
                                |||||||| ||||||  || |||
                                TCCCCCGC CCGTCC  TC CCC
                                    C     __ A
GAM1845 CACNA2D2 5'  GGGGGGCGCGGGCGGCGG    25721        GAG  A   A
                                GGGGGGC   GC GGGC GCGG
                                |||||||   || |||| ||||
                                CCCCCCG   CG CCCG CGCC
                                    ___  _   C
GAM1845 CARKL    5'  AGGGGGGCGGGGCAGGGGCGGG 29986         A     CA
                                AGGGGGGCG GGCAGGG  GCGGG
                                ||||||||| |||||||  |||||
                                TCCCCCCGC CCGTCCC  CGCCC
                                    C     __
GAM1845 CCND2    5'  AGGGAGGCGAGGATTGGGTGGT 12042          CA_  CAGC
          GGG                   AGGGGGGCGAGG  GGG   GGG
                                ||||||||||||  |||   |||
                                TCCCTCCGCTCC  CCC   CCC
                                      TAA  ACCA
GAM1845 COL4A2   3'  AGGGACAACGTGGGGCAGTGGG 12312        GGCA    C
                                GGGGGCGA   GGGCAG GGG
                                ||||||||   |||||| |||
                                TCCCTGTT   CCCGTC CCC
                                    GCAC    A
GAM1845 COPEB    5'  AGGGCGGCGAGGCGCGCGG   44428     G      AGG  A
                                AGGG GGCGAGGC  GC GCGG
                                |||| ||||||||  || ||||
```

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                                TCCC CCGCTCCG   CG CGCC
                                  G       ___  _
GAM1845  CSPG3    3'  GGTGGGGTGGGGCAGGAGTGGG 20490    _   CGA     GC  C
                                GG GGGG   GGCAGG  AG GGG
                                || ||||   ||||||  || |||
                                CC CCCC   CCGTCC  TC CCC
                                 A   ACC     __ A
GAM1845  DLX2     3'  AGGTGGGTGGCGGCAGCGG   20585     G   CGA   AG
                                AGG GGG   GGC  GGCAGCGG
                                ||| |||   |||  ||||||||
                                TCC CCC   CCG  CCGTCGCC
                                  A   A__   __
GAM1845  DUOX2    3'  AGGGGTCAGGGCAGG       30443       CGAGG       C
                                GGGGG    CAGGGCAG G
                                |||||    |||||||| |
                                TCCCC    GTCCCGTC C
                                   A____       A
GAM1845  DYRK1B   5'  AGGGGAGCGAGGCCTGGAGCGG 21776            AG  C
              G                  AGGGGGGCGAGGC  GG AGCGGG
                                 ||||||||||||  || ||||||
                                 TCCCCTCGCTCCG  CC TCGCCC
                                        GA  _
GAM1845  ENIGMA   3'  AGGTGGGTGGGGCAGGGCCCAG 41633     _  GCGA       AG
              G                  AGG GGG   GGCAGGGC  CGGG
                                 ||| |||   ||||||||  ||||
                                 TCC CCC   CCGTCCCG  GTCC
                                  A  ACC_      G_
GAM1845  FBXL11   3'  AGGCGGGGCGGGGTGGGG    29425     _     A  CA
                                AGG GGGGCG GG  GGG
                                ||| |||||| ||  |||
                                TCC CCCCGC CC  CCC
                                  G     C  AC
GAM1845  FOXD2    5'  GGTGGGGCGAGGCGACAGGGGC 20972    _        ___    CA
              GGG                  GG GGGGCGAGGC   AGGG  GCGGG
                                   || ||||||||||   ||||  |||||
                                   CC CCCCGCTCCG   TCCC  CGCCC
                                    A         CTG   __
GAM1845  FSTL1    5'  GGGGGCGCGGGGCAGGACGG   28220       _  A     GCA
                                GGGGG GCG GGCAGG   GCGG
                                ||||| ||| ||||||   ||||
                                CCCCC CGC CCGTCC   TGCC
                                   G   C     ___
GAM1845  FXYD1    3'  AGGGGCGGCGGAGGGGGCGGTG 22759      _   _  CA   AGC
              GG                   AGGGG GGCG AGG  GGGC   GGG
                                   ||||| |||| |||  ||||   |||
                                   TCCCC CCGC TCC  CCCG   CCC
                                     G   C   __    CCA
GAM1845  GFAP     3'  AGGGGAGCAGCTGGGGTGGTGG 13119         GA   A   CAGC_
              G                    AGGGGGGC  GGC GGG     GGG
                                   ||||||||  ||| |||     |||
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                                TCCCCTCG  TCG CCC    CCC
                                    __   A   CACCA
GAM1845  GNA15    5'  GGAGGGCGGGGCGGTGGCGGG  40903        A   A  GCA
                                GGGGGGCG GGC GG   GCGGG
                                |||||||| ||| ||   |||||
                                CCTCCCGC CCG CC   CGCCC
                                    C   _  AC_
GAM1845  GRAF     3'  AGGGGGCTGGCCAGTGGTGGG  31435        GA  _  _  CAGC
                                GGGGGGC  GGC AG GG    GGG
                                |||||||  ||| || ||    |||
                                TCCCCCG  CCG TC CC    CCC
                                   A_   G  A  A___
GAM1845  GSTM3    5'  AAGGGGGCGGGGCCCACGCGCG 42760         A   AGG_  A
              GG                   AGGGGGGCG GGC    GC GCGGG
                                |||||||||  |||    || |||||
                                TTCCCCCGC CCG    CG CGCCC
                                    C   GGTG  _
GAM1845  HS2ST1   5'  GGGGGGCGGGGAGCG       29334         AGGCA   C
                                GGGGGGCG    GGG AGCG
                                ||||||||    ||| ||||
                                CCCCCCGC    CCC TCGC
                                    ______  _
GAM1845  IGF2     3'  GGGGAGGCGGGGCACG      8313      C     A     G
                                GGG GAGGC GGGCA CG
                                ||| ||||| ||||| ||
                                CCC CTCCG CCCGT GC
                                  _     C    _
GAM1845  IGF2     5'  AGGGGGGCAGAGATAGTGG   8308          _   GC  _
                                AGGGGGGC GAG  AG GG
                                |||||||| |||  || ||
                                TCCCCCCG CTC  TC CC
                                    T   TA  A
GAM1845  IMPDH1   5'  GAGGGGCGGGGCGCCGGGGCGG 9408         A   A__   CA
              G                   GGGGGGCG GGC   GGG  GCGGG
                                |||||||| |||   |||  |||||
                                CTCCCCGC CCG   CCC  CGCCC
                                    C   CGG   __
GAM1845  KCNC3    3'  GGGGCGGTGAGGCGGAGG    22514      _ C    A   CAGC
                                GGGG GG GAGGC GGG    GG
                                |||| || ||||| |||    ||
                                CCCC CC CTCCG CCT    CC
                                  G  A    _  _____
GAM1845  KCNC3    5'  AGGAGGGGCGGGGCGGGGC   22491     _     A   A
                                AGG GGGGCG GGC GGGC
                                ||| |||||| ||| ||||
                                TCC CCCCGC CCG CCCG
                                  T     C   C
GAM1845  KCNC3    5'  GGGGGGCGGGGCGGGAGGGGCG 22518         A   A   CA__
              GG                   GGGGGGCG GGC GGG    GCGGG
                                |||||||| ||| |||    |||||
```

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                                CCCCCCGC CCG CCC   CGCCC
                                    C  _  TCCC
GAM1845 KCNJ10   5' GGGCCGCGGGGCAGCGG    13872     GAG A
                                GGGC  GC GGGCAGCGG
                                ||||  || |||||||||
                                CCCG  CG CCCGTCGCC
                                  G__ C
GAM1845 LHX4     3' AGGGGGGCAGGTAGGGTGG   37849       G  C   CAGC
                                AGGGGGGC AGG AGGG   GG
                                |||||||| ||| ||||   ||
                                TCCCCCCG TCC TCCC   CC
                                    _  A   A___
GAM1845 LIMK1    5' GGGGGGCGGGGCCCGGCGGG  32536       A  AG  AGC
                                GGGGGGCG GGC  GGC  GGG
                                |||||||| |||  |||  |||
                                CCCCCCGC CCG  CCG  CCC
                                    C  GG  ___
GAM1845 LMO2     5' AGGGAGGCGGGGTGCCGGGCGG 24535        A  CA__   A
            CGGG                  AGGGGGGCG GG   GGGC GCGGG
                                |||||||||  ||   |||| |||||
                                TCCCTCCGC CC   CCCG CGCCC
                                     C  ACGG   C
GAM1845 LSP1     3' GGGGGGCGGCAAGCAGCGGG  14241       GA    G
                                GGGGGGC  GGCAGG CAGCGGG
                                |||||||  |||||| |||||||
                                CCCCCCG  CCGTTC GTCGCCC
                                   __    _
GAM1845 MGMT     5' AGGGGCGGCGGGGGGGGCGGG  14485     _   A  CA  CA
                                AGGGG GGCG GG  GGG  GCGGG
                                ||||| |||| ||  |||  |||||
                                TCCCC CCGC CC  CCC  CGCCC
                                   G   _ __  C_
GAM1845 MOCS2    3' GGGGCGGTGAGGTGGGGTTGGT 21206     _ C   CA  CAGC_
            GGG                   GGGG GG GAGG  GGG    GGG
                                |||| || ||||  |||    |||
                                CCCC CC CTCC  CCC    CCC
                                  G A   AC  AACCA
GAM1845 NEK4     5' AGCGGCGGGTAGGGCAGCGGG  17189   G   A  C
                                GG GGCG GG AGGGCAGCGGG
                                || |||| || ||||||||||
                                TC CCGC CC TCCCGTCGCCC
                                 G   _ A
GAM1845 NR2C2    5' GGGCTCGCGGGGGCAGCGGG   17674     GAG A
                                GGGC  GC GGGCAGCGGG
                                ||||  || ||||||||||
                                CCCG  CG CCCGTCGCCC
                                  AG_ C
GAM1845 NUP153   3' GGGTGGGTGAGGCAGGGTGGG  23058    _  C       CAGC
                                GGG GGG GAGGCAGGG   GGG
                                ||| ||| |||||||||   |||
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                                CCC CCC CTCCGTCCC   CCC
                                  A  A       A___
GAM1845 OTP     3' AGGGAGGCCAGGGTGGCGG   36988       GAGG    CA
                                AGGGGGGC   CAGGG  GCGG
                                ||||||||   |||||  ||||
                                TCCCTCCG   GTCCC  CGCC
                                     _____    AC
GAM1845 P23     3' AGGGGGACGGGCGAACTGGTGG 27336        A  A   AGC_
             G                   AGGGGGGCG GGC GGGC   GGG
                                ||||||||| ||| ||||   |||
                                TCCCCCTGC CCG CTTG   CCC
                                     _  _   ACCA
GAM1845 PAX2    3' AGGCGGGGCTGGGGGCGGTGGG 19617    _    GA  CA   AGC
                                AGG GGGGC  GG  GGGC   GGG
                                ||| |||||  ||  ||||   |||
                                TCC CCCCG  CC  CCCG   CCC
                                  G    A_ __   CCA
GAM1845 PIGR    3' GGAGGGTGAGGCAGGAGAATGG 43707       C       C  C
                                GGGGGG GAGGCAGGG AG GG
                                |||||| ||||||||| || ||
                                CCTCCC CTCCGTCCT TT CC
                                   A       C  A
GAM1845 POU3F1  3' GGGGGGGCAGGGGCG      40376      CGA      CA
                                GGGGG  GGCAGGG  GCG
                                |||||  |||||||  |||
                                CCCCC  CCGTCCC  CGC
                                     ___     __
GAM1845 PPP2R2B  5' AGGGGGGCAGGGGAGCCAGTGG 21327        G   CA  G   C
             G                   AGGGGGGC AGG  GG CAG GGG
                                |||||||| |||  || ||| |||
                                TCCCCCCG TCC  TC GTC CCC
                                     _  CC  G   A
GAM1845 PPP2R5E  5' GGGGGCGGGCGGCGG      26473       GAGGCA   A
                                GGGGGC     GGGC GCGG
                                ||||||     |||| ||||
                                CCCCCG     CCCG CGCC
                                   _______   C
GAM1845 PROC    3' GGGGGGCGGGGGGG       7192         A  CA   CAGC
                                GGGGGGCG GG  GGG   G
                                |||||||| ||  |||   |
                                CCCCCCGC CC  CCC   C
                                     _ __  _____
GAM1845 RAB3B   5' AGGGGGCCGGGGCGGGGCGCTG 16079       G  A   A   A__
             CGGG                  AGGGGG CG GGC GGGC   GCGGG
                                ||||||| || ||| ||||  |||||
                                TCCCCC GC CCG CCCG   CGCCC
                                   G  C   C   CGA
GAM1845 RCN1    3' GGGGGGGCAGGTCTGCGG    16205      CGA     GCA
                                GGGGG  GGCAGG   GCGG
                                |||||  ||||||   ||||
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                                CCCCC  CCGTCC  CGCC
                                  ___     AGA
GAM1845 RDS     3' AGGAGGGCATATCCTAGGGCAG 7241         AGGC__
            CGGG                  AGGGGGGCG     AGGGCAGCGGG
                                |||||||||     ||||||||||
                                TCCTCCCGT     TCCCGTCGCCC
                                   ATAGGA
GAM1845 RXRA    3' AGGGGTGGAGGGCGGCGG    16413      CGA C    A
                                GGGGG  GG AGGGC GCGG
                                |||||  || ||||| ||||
                                TCCCC  CC TCCCG CGCC
                                  A__ _    C
GAM1845 SCN1B   5' AGCGGGGCGAGAGGCGGCGGG 9777     G      GCA   A
                                AG GGGGCGAG  GGGC GCGGG
                                || ||||||||  |||| |||||
                                TC CCCCGCTC  TCCG CGCCC
                                 G       ___   C
GAM1845 SF1     5' GGGGGCGGGCCGGGGGCGGCGG 21569       A  A__   A
            G                    GGGGGCG GGC   GGGC GCGGG
                                ||||||| |||   |||| |||||
                                CCCCCGC CCG   CCCG CGCCC
                                   _  GCC   C
GAM1845 SH3GL1  3' GAGGGGCGGGGCGGGGACACGG 16669       A  A  CA
            G                    GGGGGGCG GGC GGG  GCGGG
                                |||||||| ||| |||  |||||
                                CTCCCCGC CCG CCC  TGCCC
                                     C  C  TG
GAM1845 SLC6A8  5' GGGGGACGGGGCGGCGG    24781       AGGCA   A
                                GGGGGGCG    GGGC GCGG
                                ||||||||    |||| ||||
                                CCCCCTGC    CCCG CGCC
                                   _____   C
GAM1845 SLC7A4  3' GGAGGGCGGGGCAAGTGTGGG 42187       A     GCAGC
                                GGGGGGCG GGCAGG    GGG
                                |||||||| ||||||    |||
                                CCTCCCGC CCGTTC    CCC
                                     C     ACA__
GAM1845 SNCB    3' GGGGGGCGGGGCAGGGACAGGG 16931       A     _  C
                                GGGGGGCG GGCAGGG CAG GG
                                |||||||| ||||||| ||| ||
                                CCCCCCGC CCGTCCC GTC CC
                                     C      T  _
GAM1845 SOLH    3' AGGGGGGCGGGGGGGCCCATGGG 24823       A  CA   AGC_
                                AGGGGGGCG GG  GGGC   GGG
                                ||||||||| ||  ||||   |||
                                TCCCCCCGC CC  CCCG   CCC
                                   _ __   GGTA
GAM1845 SOX12   3' GAGGGGCGGGGCGGGGCAG   28039       A  A
                                GGGGGGCG GGC GGGCAG
                                |||||||| ||| ||||||
```

```
                                CTCCCCGC CCG CCCGTC
                                     C   C
GAM1845  SOX18    5'  GGAGGGCGGATGGCGGTGGG   32943        A  CAG   AGC
                                GGGGGGCG GG   GGC   GGG
                                |||||||| ||   |||   |||
                                CCTCCCGC CT   CCG   CCC
                                     _  A__   CCA
GAM1845  SP4      5'  GGGGGCGAGGCGGGAG      17049          A   C
                                GGGGGCGAGGC GGG AG
                                |||||||||| ||| ||
                                CCCCCGCTCCG CCC TC
                                       _  _
GAM1845  SPAG11   5'  AGGGTGGGTGGGCAGGCAGCGG 38479      _   CGA     G
              G                  AGGG GGG   GGCAGG CAGCGGG
                                |||| |||   |||||| |||||||
                                TCCC CCC   CCGTCC GTCGCCC
                                  A   AC_     _
GAM1845  TCF20    3'  GGCGGGGCGGGGCAGGGCAGGG 42536    _     A        C
                                GG GGGGCG GGCAGGGCAG GG
                                || |||||| |||||||||| ||
                                CC CCCCGC CCGTCCCGTC CC
                                 G     C        _
GAM1845  TFAP2A   3'  GAGGGGCGGGGCGGGAG     17396         A   A   C
                                GGGGGGCG GGC GGG AG
                                |||||||| ||| ||| ||
                                CTCCCCGC CCG CCC TC
                                     C   _   _
GAM1845  TGFB1    3'  GGCGGGGCGGGGTGGGGCCGG  8544     _     A  CA    AG
                                GG GGGGCG GG  GGGC  CGG
                                || |||||| ||  ||||  |||
                                CC CCCCGC CC  CCCG  GCC
                                 G     C  AC   __
GAM1845  TGFB1    3'  GGGGGCGGGGCGGGGTGGG   8549         A   A   CAGC
                                GGGGGCG GGC GGG    GGG
                                ||||||| ||| |||    |||
                                CCCCCGC CCG CCC    CCC
                                     C   C   A___
GAM1845  THRA     5'  AGGGGGGCGGGCGGTG      17516         A   A  GCAGC
                                AGGGGGGCG GGC GG     G
                                ||||||||| ||| ||     |
                                TCCCCCCGC CCG CC     C
                                       _   _  A____
GAM1845  TK2      3'  GGAAGAGGCAGGGCGGTGGG   21446     C         AGC
                                GGG GAGGCAGGGC   GGG
                                ||| ||||||||||   |||
                                CCT CTCCGTCCCG   CCC
                                  T         CCA
GAM1845  TMEFF2   5'  GGGGGCCGGGCAGCGG      32106       GAGGCA
                                GGGGGC     GGGCAGCGG
                                ||||||     |||||||||
```

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                                CCCCCG    CCCGTCGCC
                                   G_____
GAM1845 TTYH1   5' GGGGGAGGGGGCAGCG     34032     C   CA
                                GGGG GAGG  GGGCAGCG
                                |||| ||||  ||||||||
                                CCCC CTCC  CCCGTCGC
                                  _   __
GAM1845 WNT6    5' AGGGGGCGAGGCTGCG     27177          AGGGCA
                                GGGGGGCGAGGC    GCG
                                ||||||||||||    |||
                                TCCCCCCGCTCCG    CGC
                                      A_____
GAM1845 YY1     5' AGGGGGCGGGCGGCG      18165       GAGGCA   A
                                GGGGGGC    GGGC GCG
                                |||||||    |||| |||
                                TCCCCCG    CCCG CGC
                                   _______   C
GAM1845 ZFP36L1  3' GGGGGGGGGTGGGGGGGCGG   22288      CGA  CA   CA
                                GGGGGG   GG  GGG  GCGG
                                ||||||   ||  |||  ||||
                                CCCCCC   CC  CCC  CGCC
                                   ___  AC   CC
GAM1845 ZNF219   5' GGGGGGCGGCGCGGCGG    32334       GA   AGG  A
                                GGGGGGC  GGC   GC GCGG
                                |||||||  |||   || ||||
                                CCCCCCG  CCG   CG CGCC
                                   __  ___  C
GAM1846 BUB3    3' CAGTCACAAAATGATATTAG  21802      AGTC
                                CAGTCA   AATGATATTAG
                                ||||||   ||||||||||
                                GTCAGT   TTACTATAATC
                                   GTT_
GAM1846 CALCB   3' TACCAGATAAGTCAATGA    44713      TC
                                TACCAG  AAGTCAATGA
                                ||||||  ||||||||||
                                ATGGTC  TTCAGTTACT
                                   TA
GAM1846 MME     3' AGCTAGTGAATGATATTA    28592    CA  C
                                AGT  AGT AATGATATTA
                                |||  ||| ||||||||||
                                TCG  TCA TTACTATAAT
                                  A_   C
GAM1846 SHOC2   5' GTCAATCAATGATTCATTAG  28893      G      __
                                GTCAA TCAATGAT  ATTAG
                                ||||| ||||||||  |||||
                                CAGTT AGTTACTA  TAATC
                                   _       AG
GAM1847 CLASP1  3' TACTGTTCCTATGCACTATGG 42245          ATAT   A
                                TACTGTTCCTA   CAT TATGG
                                ||||||||||    ||| |||||
```

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                                ATGACAAGGAT   GTG ATACC
                                      AC__  _
GAM1847 SEC22L1  3' TACTATTCCCTAATATATATGG 22201        AA  TC
                                TACTGTTCCT  TA  ATATATGG
                                ||||||||||  ||  ||||||||
                                ATGATAAGGG  AT  TATATACC
                                      __  TA
GAM1848 ABCD1    3' GGCGGCTGGCAGTGTAGGC   6198         G  CGGC
                                GGCGGCTGGC AG   GGC
                                |||||||||| ||   |||
                                CCGCCGACCG TC   CCG
                                      _ ACAT
GAM1848 ADCY8    5' GGTGGAGGAGCGGTGGTGG   10015   C  CT  C    C  C
                                GG GG  GG GAGCGG GG GG
                                || ||  || |||||| || ||
                                CC CC  TC CTCGCC CC CC
                                 A __ _    A  A
GAM1848 ADRBK2   5' GGCGGCGGCGGCGGCGG    23131    T   A
                                GGC GGCG GCGGCGGCGG
                                ||| |||| ||||||||||
                                CCG CCGC CGCCGCCGCC
                                  _   _
GAM1848 ANKH     5' GGCGCGGCGGCGGCGG     38321    TG  A
                                GGC  GCG GCGGCGGCGG
                                |||  ||| ||||||||||
                                CCG  CGC CGCCGCCGCC
                                  __  _
GAM1848 AXIN1    5' GGCGGCTGCGGCTCGGCGGCC  41384       G  A  GG
                                GGCGGCTG CG GC  CGGCGGCC
                                |||||||| || ||  ||||||||
                                CCGCCGAC GC CG  GCCGCCGG
                                    _ _  A_
GAM1848 BACH2    5' GGTGGCGAGGGCGGCGGC    34796    C     C
                                GG TGGCGAG GGCGGCGGC
                                || ||||||| |||||||||
                                CC ACCGCTC CCGCCGCCG
                                  _     _
GAM1848 BAI2     5' GGCGCTGGCGGGGGCGGC    11795     G    AGC  C
                                GGCG CTGGCG   GG GGCGGC
                                |||| ||||||   || ||||||
                                CCGC GACCGC   CC CCGCCG
                                  _    ____ _
GAM1848 BAZ1B    5' GGCGGCTGCTGGGGCCGGC   37091       G GAGC  C  _
                                GGCGGCTG C    GG GGC GGC
                                |||||||| |    || ||| |||
                                CCGCCGAC G    CC CCG CCG
                                    _ A___  _   G
GAM1848 BAZ1B    5' GGCGGCGGCGGTGGGACTGGCG 37090       T   AGC_  _
             GC                   GGCGGC GGCG    GGC GGCGGC
                                |||||| ||||    ||| ||||||
```

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                                CCGCCG CCGC   CTG CCGCCG
                                   _   CACC  A
GAM1848 BCL11A   5' GGCGGCGGCGGGCGGACGACGG 39716      T   A   _
            C                    GGCGGC GGCG GCGG CGGCGGC
                                 ||||||| |||| |||| |||||||
                                 CCGCCG CCGC CGCC GCTGCCG
                                   _   C   T
GAM1848 C1orf6   5' GGCGGTGGGCCGGCGGGCGG  33532     CT  GAG    _
                                 GGCGG  GGC  CGGCGG CGG
                                 |||||  |||  |||||| |||
                                 CCGCC  CCG  GCCGCC GCC
                                   AC  ___    C
GAM1848 CACNA1A  5' AGCCCATCGGGCGGCGGCGGC 35724     GG_ A
                                 GGCT  CG GCGGCGGCGGC
                                 ||||  || ||||||||||
                                 TCGG  GC CGCCGCCGCCG
                                   GTA  C
GAM1848 CACNA1A  5' GGGGCTGGGAGCGCGGCGGC  35741   C    C   G
                                 GG GGCTGG GAGCG CGGCGGC
                                 || ||||||| ||||| |||||||
                                 CC CCGACC CTCGC GCCGCCG
                                  _    _   _
GAM1848 CDK5R2   3' GGCGGTAACAGCGGCGGTGGC 19474     C   G     C
                                 GGCGG TGGC AGCGGCGG GGC
                                 ||||| |||| |||||||| |||
                                 CCGCC ATTG TCGCCGCC CCG
                                   _   _      A
GAM1848 CHGA     5' GGCGGCTGGACTGGCGGC    10468       CGAGCG _
                                 GGCGGCTGG     GC GGCGGC
                                 |||||||||     || ||||||
                                 CCGCCGACC     TG CCGCCG
                                     _______ A
GAM1848 CKB      5' GGCGGCGGCGGGCGGGCGGCC 12254      T   A   CG
                                 GGCGGC GGCG GCGG  GCGGCC
                                 |||||| |||| ||||  ||||||
                                 CCGCCG CCGC CGCC  CGCCGG
                                   _   C   __
GAM1848 CNGB1    3' GGCGTGCTGGCGGGACGG    10533     _     AGC
                                 GGCG GCTGGCG   GGCGG
                                 |||| |||||||   |||||
                                 CCGC CGACCGC   CTGCC
                                   A     C__
GAM1848 CRKL     5' GGCGGTAGGGGCGGCGGC    23308      CT  CGAGC
                                 GGCGG  GG    GGCGGCGGC
                                 |||||  ||    |||||||||
                                 CCGCC  CC    CCGCCGCCG
                                   AT  _____
GAM1848 CSDA     5' GCGGCTGGTGGTCGCGGCGGCC 18897       CGAG  G
                                 GCGGCTGG    CG CGGCGGCC
                                 ||||||||    || ||||||||
```

```
                                CGCCGACC   GC GCCGCCGG
                                    ACCA  _
GAM1848 CSDA    5' GCGGCGCAGGCGGCGGCGGCC 18896      TG  A
                                GCGGC  GCG GCGGCGGCGGCC
                                |||||  ||| ||||||||||||
                                CGCCG  CGT CGCCGCCGCCGG
                                   __  C
GAM1848 CSNK1G2  3' GGCGGCTGGCGGGGCGGGGCC 10616          AGC   C
                                GGCGGCTGGCG  GGCGG GGCC
                                ||||||||||  ||||| ||||
                                CCGCCGACCGC  CCGCC CCGG
                                      C__   _
GAM1848 CSNK2A1  5' AGCGGCAGCGGCGGCGGC   12475      TGGCG
                                GGCGGC   AGCGGCGGCGGC
                                ||||||   ||||||||||||
                                TCGCCG   TCGCCGCCGCCG

                                 _____
GAM1848 CTBP2   5' GGCGGTGGCGGTGGCGGCGGC 35601     C   AGC
                                GGCGG TGGCG  GGCGGCGGC
                                ||||| |||||  |||||||||
                                CCGCC ACCGC  CCGCCGCCG
                                   _   CA_
GAM1848 CTBP2   5' GGTGGCGGCGGCTGTGCGGCC 35602   C   A   G__
                                GG TGGCG GCGGC  GCGGCC
                                || ||||| |||||  ||||||
                                CC ACCGC CGCCG  CGCCGG
                                 _   _   ACA
GAM1848 CUL3    5' GGCGGCGGCGGCGGCGGCGGC 18740      T   A
                                GGCGGC GGCG GCGGCGGCGGC
                                |||||| |||| ||||||||||
                                CCGCCG CCGC CGCCGCCGCCG

                                  _  _
GAM1848 CYBB    3' GGCAGCTGGCTGCTGGTGGC  44095       GA _ C
                                GGCGGCTGGC  GC GG GGC
                                ||||||||||  || || |||
                                CCGTCGACCG  CG CC CCG
                                     A_ A  A
GAM1848 CYBB    3' GGTGGCTGGCAGCTGGTGGC  44096   C     G  _ C
                                GG GGCTGGC AGC GG GGC
                                || ||||||| ||| || |||
                                CC CCGACCG TCG CC CCG
                                 A      _  A  A
GAM1848 DYRK2   5' GGCGGCGGGAGCGGCGGC   27040      T  C
                                GGCGGC GG GAGCGGCGGC
                                |||||| || ||||||||||
                                CCGCCG CC CTCGCCGCCG

                                  _ _
GAM1848 EGR1    5' GGCGGCGGATGGCGGCGGCGGC 12662      T  CGA
                                GGCGGC GG  GCGGCGGCGGC
                                |||||| ||  ||||||||||
```

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                                CCGCCG CC   CGCCGCCGCCG
                                   _ TAC
GAM1848  ENO2     5'  GGCGGCGGCGGCTGCGGC    12713       T   A  G
                                GGCGGC GGCG GC GCGGC
                                |||||| |||| || |||||
                                CCGCCG CCGC CG CGCCG
                                   _   _ A
GAM1848  ENO2     5'  GGCAGTGGCGGCGGCGGC    12712       C    A
                                GGCGG TGGCG GCGGCGGC
                                ||||| ||||| ||||||||
                                CCGTC ACCGC CGCCGCCG
                                   _    _
GAM1848  EP300    5'  GGCGGCGGGCGCAGGCGGC    10990       T   AGC
                                GGCGGC GGCG   GGCGGC
                                |||||| ||||   ||||||
                                CCGCCG CCGC   CCGCCG
                                   C   GT_
GAM1848  ETF1     5'  GGCGGCTCGCGGCGGCGGCGGC 21832        G   A
                                GGCGGCT GCG GCGGCGGCGGC
                                ||||||| ||| ||||||||||
                                CCGCCGA CGC CGCCGCCGCCG
                                   G  _
GAM1848  FASN     3'  GGCGGCGGGTGGGTGGGACATG 19940       T  CGAGC  C   _
            CC                    GGCGGC GG     GG GGCG GCC
                                ||||||  ||     ||  |||| |||
                                CCGCCG CC     CC CTGT CGG
                                   C  ACCCA  _    A
GAM1848  FGD1     5'  GGCGGCGGCGGGCGGGAAGGAG 20908       T   A   C_  C
            CC                    GGCGGC GGCG GCGG  GG GGCC
                                |||||| |||| ||||  ||  ||||
                                CCGCCG CCGC CGCC  TC TCGG
                                   _   C   CT  C
GAM1848  FHL1     5'  GGCGGTGGCGGCGGCGGC    11096       C    A
                                GGCGG TGGCG GCGGCGGC
                                ||||| ||||| ||||||||
                                CCGCC ACCGC CGCCGCCG
                                   _    _
GAM1848  FHL2     5'  GGCGGCTGGTGGCTGCGGC    11113         CGAGC  G
                                GGCGGCTGG     GGC GCGGC
                                |||||||||     ||| |||||
                                CCGCCGACC     CCG CGCCG
                                   A____   A
GAM1848  FMR2     5'  GGCGGCGGCGGCAGCGGC    12974       T   A
                                GGCGGC GGCG GCGGCGGC
                                |||||| |||| ||||||||
                                CCGCCG CCGC CGTCGCCG
                                   _   _
GAM1848  FMR2     5'  GGCGGCGGCGGGCGGGCGC   12975       T   A   CG  G
                                GGCGGC GGCG GCGG  GCG C
                                |||||| |||| ||||  ||| |
```

```
                                CCGCCG CCGC CGCC  CGC G
                                   _   C   __  _
GAM1848  FOXE1    5'  GGCGGGCAGCGGCGGTGGCC  20945    T  G      C
                                GGC GGC AGCGGCGG GGCC
                                ||| ||| |||||||| ||||
                                CCG CCG TCGCCGCC CCGG
                                  C  _       A
GAM1848  FTH1     5'  GGCGGCGGCGGCGGCGGTGGC  42789      T   A     C
                                GGCGGC GGCG GCGGCGG GGC
                                |||||| |||| ||||||| |||
                                CCGCCG CCGC CGCCGCC CCG
                                   _   _      A
GAM1848  GNA11    5'  GGCGGCTCGCCAGGCGGCGGCC 44049       G  G GC
                                GGCGGCT GC A  GGCGGCGGCC
                                ||||||| || |  ||||||||||
                                CCGCCGA CG T  CCGCCGCCGG
                                    G  G __
GAM1848  GNAS     5'  GGCGGCGGCGGGGCGCGGC   38662      T   AGC   G
                                GGCGGC GGCG   GGCG CGGC
                                |||||| ||||   |||| ||||
                                CCGCCG CCGC   CCGC GCCG
                                   _   C__   _
GAM1848  GPC1     5'  GCGGTCCAGAGGCGGCGGCGGC 13248     _ TG CGA
              C                  GCGG C  G   GCGGCGGCGGCC
                                 |||| |  |   ||||||||||||
                                 CGCC G  C   CGCCGCCGCCGG
                                   A GT TC_
GAM1848  GTF2IRD1 5'  GGGGCTGGCGCTCGGCGGC   32264    C      AG
                                GG GGCTGGCG  CGGCGGC
                                || ||||||||  |||||||
                                CC CCGACCGC  GCCGCCG
                                 _      GA
GAM1848  HAGH     5'  AGCGGCGGCGGCGGCGGC    23708    T   A
                                GGC GGCG GCGGCGGCGGC
                                ||| |||| ||||||||||
                                TCG CCGC CGCCGCCGCCG
                                  _   _
GAM1848  HDAC4    5'  GACGGTGCTCCGCGGCGGCGGC 25766      CTG  GA_
              C                  GGCGG   GC   GCGGCGGCGGCC
                                 |||||   ||   ||||||||||||
                                 CTGCC   CG   CGCCGCCGCCGG
                                   A__  AGG
GAM1848  HDAC4    5'  ACCGCGGCGGGCGGCGGCGGCC 25740    G  T   A
                                GC GC GGCG GCGGCGGCGGCC
                                || || |||| ||||||||||||
                                TG CG CCGC CGCCGCCGCCGG
                                 G  _   C
GAM1848  HMGA2    5'  GGCGGCGGTGGGTGGGTGC   18525      T  CGAGC  C  CG
                                GGCGGC GG    GG GG  GC
                                |||||| ||    || ||  ||
```

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                                CCGCCG CC    CC CC  CG
                                   _ AC___  A  CA
GAM1848  HPCAL1   5'  GGCGGCTGGCGGCGGCGAC   39548          A
                                GGCGGCTGGCG GCGGCGGC
                                |||||||||| ||||||||
                                CCGCCGACCGC CGCCGCTG
                                          _
GAM1848  IGFBP1   5'  GGTGGCGGCGGGCGGTGGCC  8245    C  T   AGC    C
                                GG GGC GGCG  GGCGG GGCC
                                || ||| ||||  ||||| ||||
                                CC CCG CCGC  CCGCC CCGG
                                 A  _   ___    A
GAM1848  INHBB    5'  GGCGGTTCGGCCGGCGGC    13561      C_   GAG
                                GGCGG  TGGC  CGGCGGC
                                |||||  ||||  |||||||
                                CCGCC  GCCG  GCCGCCG
                                   AA   ___
GAM1848  ITGB1    5'  GGCGCGGCGGGTGGCGGCGGC  38050     G T   AGC
                                GGCG C GGCG  GGCGGCGGC
                                |||| | ||||  |||||||||
                                CCGC G CCGC  CCGCCGCCG
                                  _ _   CCA
GAM1848  KCNS2    5'  GGCGAGCATCGCGGCGGTGGCC 42835    T   A_     C
                                GGC GGCG  GCGGCGG GGCC
                                ||| ||||  ||||||| ||||
                                CCG TCGT  CGCCGCC CCGG
                                  C   AG      A
GAM1848  KPNA3    5'  GCGGCTCCGGCGGCGGC     13983      GGCGAG
                                GCGGCT     CGGCGGCGGC
                                ||||||     ||||||||||
                                CGCCGA     GCCGCCGCCG
                                   G_____
GAM1848  LAMC1    5'  GGCGCGGGCGGTGGCGGCGGC  14088     G T   AGC
                                GGCG C GGCG  GGCGGCGGC
                                |||| | ||||  |||||||||
                                CCGC G CCGC  CCGCCGCCG
                                  _ C   CA_
GAM1848  LTBP2    5'  GGCGGCTGGAGAGTGGTGC   7695         C  C  CG
                                GGCGGCTGG GAG GG  GC
                                ||||||||| ||| ||  ||
                                CCGCCGACC CTC CC  CG
                                     T  A  A_
GAM1848  LTBR     5'  GGCAGCGGTGGCGGCGGC    14257      T  CGAGC
                                GGCGGC GG    GGCGGCGGC
                                |||||| ||    |||||||||
                                CCGTCG CC    CCGCCGCCG
                                   _ A_____
GAM1848  MADH6    3'  GGTGGCGGTGGCCGCGGC    24603    C    AGC   G
                                GG TGGCG   GGC GCGGC
                                || |||||   ||| |||||
```

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                                CC ACCGC   CCG CGCCG
                                 _    CA_  G
GAM1848  MADH6    3'  GGCCGGCAGGTGGCGGTGGCC  24602        AGC    C
                                GGCTGGCG   GGCGG GGCC
                                ||||||||   ||||| ||||
                                CCGGCCGT   CCGCC CCGG
                                     CCA    A
GAM1848  MADH7    5'  GGCAGGAGCGGCGGCGGC    25368      CTGGC
                                GGCGG    GAGCGGCGGCGGC
                                |||||    ||||||||||||||
                                CCGTC    CTCGCCGCCGCCG

                                  ______
GAM1848  MAF      5'  GCGGTGGCGGCGGTGGTGGC  23833     C    A   C  C
                                GCGG TGGCG GCGG GG GGC
                                |||| ||||| |||| || |||
                                CGCC ACCGC CGCC CC CCG
                                  _    _   A  A
GAM1848  MAZ      5'  GGGGCTACGACGGCGGTGGCC  43854    C    G  G    C
                                GG GGCTG CGA CGGCGG GGCC
                                || ||||| ||| |||||| ||||
                                CC CCGAT GCT GCCGCC CCGG
                                 _    _  _     A
GAM1848  MECP2    5'  GCGGCGGCGGCGGCGGCGGCC  22592      T   A
                                GCGGC GGCG GCGGCGGCGGCC
                                ||||| |||| ||||||||||||
                                CGCCG CCGC CGCCGCCGCCGG

                                  _   _
GAM1848  MEN1     5'  GGCGGCGGGCGGTGGGCGGCGG 39191       T   AGC
            CC                    GGCGGC GGCG   GGCGGCGGCC
                                ||||||| ||||   ||||||||||
                                CCGCCG CCGC   CCGCCGCCGG
                                   C   CAC
GAM1848  MEN1     5'  GGCGGCGGGCGGTGGGCGGCGG 39190       T   AGC
            C                     GGCGGC GGCG   GGCGGCGGC
                                ||||||| ||||   |||||||||
                                CCGCCG CCGC   CCGCCGCCG
                                   C   CAC
GAM1848  MEN1     5'  GGCGGCGGGCGGTGGGCGGCGG 39251       T   A___
            CGGC                   GGCGGC GGCG    GCGGCGGCGGC
                                ||||||| ||||    ||||||||||
                                CCGCCG CCGC    CGCCGCCGCCG
                                   C   CACC
GAM1848  MGAT3    5'  GGCGGCAGCAGCGGCGGCGGCG 14463       T__   A
            GC                    GGCGGC   GGCG GCGGCGGCGGC
                                |||||||   |||| ||||||||||
                                CCGCCG   TCGC CGCCGCCGCCG
                                   TCG   _
GAM1848  MGAT3    5'  GGCGGCGGCGGCTCCGCGGCC  14464       T   A  GG  G
                                GGCGGC GGCG GC  CG CGGCC
                                |||||| |||| ||  || |||||
```

```
                                CCGCCG CCGC CG  GC GCCGG
                                   _   _  AG  _
GAM1848 MIC1    5' GGCGGCTGCGGCTGCGGC    30030       GGCGA    G
                                GGCGGCT    GCGGC GCGGC
                                |||||||    ||||| |||||
                                CCGCCGA    CGCCG CGCCG
                                   ______    A
GAM1848 MSF     5' GGCTGGTGGGCAGCGG     44737       CGAGC
                                GGCTGG    GGCGGCGG
                                ||||||    ||||||||
                                CCGACC    CCGTCGCC
                                   AC___
GAM1848 MYC     5' GGCCGGGGCCCGGCGGTGGCGG 14711       _____ A   C
             CC                   GGCTGG   CG GCGG GGCGGCC
                                ||||||   || |||| |||||||
                                CCGGCC   GC CGCC CCGCCGG
                                   CCGG  _   A
GAM1848 NFATC2  5' GGGGCTGGCGGAGGCGGC    29590    C      AGC
                                GG GGCTGGCG   GGCGGC
                                || ||||||||   ||||||
                                CC CCGACCGC   CCGCCG
                                  _       CT_
GAM1848 NFE2L2  5' GGCGGCGGCGGCGGCGGTGGC  26087      T   A     C
                                GGCGGC GGCG GCGGCGG GGC
                                |||||| |||| ||||||| |||
                                CCGCCG CCGC CGCCGCC CCG
                                   _   _      A
GAM1848 NFIA    5' GGCGGCTGCGGCGCCGCGCGGC 43217       G  A   G  _
             C                    GGCGGCTG CG GCG CG GCGGCC
                                |||||||| || ||| || ||||||
                                CCGCCGAC GC CGC GC CGCCGG
                                   _ _  G  G
GAM1848 NPEPPS  5' GGCGGCGGCGAGAGGAGCGGC  26718       T     C  C
                                GGCGGC GGCGAG GG GGCGGC
                                |||||| |||||| || ||||||
                                CCGCCG CCGCTC CC TCGCCG
                                   _     T  _
GAM1848 NR2F2   5' GGCGGCGGCGGGGCGGCGGCGG 34237       T   A_
             C                    GGCGGC GGCG  GCGGCGGCGGC
                                |||||| ||||  ||||||||||
                                CCGCCG CCGC  CGCCGCCGCCG
                                   _   CC
GAM1848 ODC1    5' GGCGGCGGGCGGCGGCGGCGGC 14922       T   A
                                GGCGGC GGCG GCGGCGGCGGC
                                |||||| |||| ||||||||||
                                CCGCCG CCGC CGCCGCCGCCG
                                   C   _
GAM1848 OFD1    5' GGCGGCTGGAGGGCGGGGACC  18813        CG  C    C
                                GGCGGCTGG  AG GGCGG GGCC
                                |||||||||  || ||||| ||||
```

```
                                CCGCCGACC  TC CCGCC CTGG
                                    __ _    C
GAM1848  OTOF     3'  AGCGGCTGGCGGGAGCTGGCGG 22054          AGC  _
              CC                  GGCGGCTGGCG   GGC GGCGGCC
                                  ||||||||||   ||| |||||||
                                  TCGCCGACCGC   TCG CCGCCGG
                                       CC_   A
GAM1848  P3       5'  GCGCGGCGGCGGCGGCGGC   33382     G T   A
                                  GCG C GGCG GCGGCGGCGGC
                                  ||| | |||| ||||||||||
                                  CGC G CCGC CGCCGCCGCCG
                                   _ _   _
GAM1848  PAX2     3'  GGTGGCTGGCGGGCTTCGGGGC 19639    C       A  GG   C
                                  GG GGCTGGCG GC  CGG GGC
                                  || |||||||| ||  ||| |||
                                  CC CCGACCGC CG  GCC CCG
                                   A       C  AA  _
GAM1848  PCTK1    5'  GGCGGCGGCGGCGGCGGTGGC  37477       T   A      C
                                  GGCGGC GGCG GCGGCGG GGC
                                  |||||| |||| ||||||| |||
                                  CCGCCG CCGC CGCCGCC CCG
                                     _   _      A
GAM1848  PCTK1    5'  GGCGCCTGGGGCGGCGGC    26238      G    CGAGC
                                  GGCG CTGG     GGCGGCGGC
                                  |||| ||||     |||||||||
                                  CCGC GACC     CCGCCGCCG
                                    G   ______
GAM1848  PCTK1    5'  GGCGGCTCGCGGCACAGAGCGG 37478        G   A_   C
                                  GGCGGCT GCG  GCGG GGCGG
                                  ||||||| |||  |||| |||||
                                  CCGCCGA CGC  TGTC TCGCC
                                      G  CG   _
GAM1848  PK428    5'  GGCGGCGGCGCGGGCGGC    18809       T   AGC
                                  GGCGGC GGCG   GGCGGC
                                  |||||| ||||   ||||||
                                  CCGCCG CCGC   CCGCCG
                                     _   GC_
GAM1848  PODXL    5'  AGCGGCGGCGGCGGCGGC    23955       T   A
                                  GGCGGC GGCG GCGGCGGC
                                  |||||| |||| ||||||||
                                  TCGCCG CCGC CGCCGCCG
                                     _   _
GAM1848  PPP6C    5'  GCGGCAACAGCGGCGGCGGCGG 15543      T__   A
              C                    GCGGC   GGCG GCGGCGGCGGC
                                   |||||   |||| ||||||||||
                                   CGCCG   TCGC CGCCGCCGCCG
                                     TTG   _
GAM1848  PRKAR1A  5'  GGCGGCGGCGGGCGCGAGGC   15610       T   A  G   C
                                  GGCGGC GGCG GCG CGG GGC
                                  |||||| |||| ||| ||| |||
```

```
                                CCGCCG CCGC CGC GCT CCG
                                   _   C  _  _
GAM1848  PRX     3'  GGGGGGAGGAGCGGCGGCGGCC 34132    C  CT  C
                                GG GG  GG GAGCGGCGGCGGCC
                                || ||  || ||||||||||||||
                                CC CC  TC CTCGCCGCCGCCGG
                                 _  CC  _
GAM1848  PTGIS    5'  GGGGCTGGCGGGGCTGGCGGCC 9675     C       AGC  _
                                GG GGCTGGCG   GGC GGCGGCC
                                || ||||||||   ||| |||||||
                                CC CCGACCGC   CCG CCGCCGG
                                 _      C__   A
GAM1848  PTPRA    5'  GCGGCGGCGGCGGCGGC     38913    T   A
                                GC GGCG GCGGCGGCGGC
                                || |||| ||||||||||
                                CG CCGC CGCCGCCGCCG

                                 _   _
GAM1848  PTPRJ    5'  GGCAGCGGCGGCGGCGGC     15959    T   A
                                GGC GGCG GCGGCGGCGGC
                                ||| |||| ||||||||||
                                CCG TCGC CGCCGCCGCCG

                                  _   _
GAM1848  PTPRJ    5'  GGCGGCGGCGGCCGCGGC     15960    T   A   G
                                GGC GGCG GCGGC GCGGC
                                ||| |||| ||||| |||||
                                CCG CCGC CGCCG CGCCG
                                  _   _    G
GAM1848  RAC3     5'  GGCGGCGGCGGGCGCGGC     22790      T   AGC   G
                                GGCGGC GGCG   GGCG CGGC
                                |||||| ||||   |||| ||||
                                CCGCCG CCGC   CCGC GCCG

                                   _   ____   _
GAM1848  RCN2     5'  GGAGGCTGGCGGGGGCCCGGGC 16214    C       AGC  ___
            GGC                    GG GGCTGGCG   GGC   GGCGGC
                                || ||||||||   |||   ||||||
                                CC CCGACCGC   CCG   CCGCCG
                                 T       CC_   GGC
GAM1848  REV3L    5'  GGCAGCAGCAGCGGCGGCGGC  16265       T   G
                                GGCGGC GGC AGCGGCGGCGGC
                                |||||| ||| ||||||||||||
                                CCGTCG TCG TCGCCGCCGCCG

                                   _   _
GAM1848  RFC1     5'  GCTGGCTGGCGGGTGGGC     16273       GAGC    C__
                                GCTGGC    GGCGG   GGC
                                ||||||    |||||   |||
                                CGACCG    CCGCC   CCG
                                   A___     CAC
GAM1848  RFX2     5'  GGCGGCGGCGGTGGCGGCGGCG 8455        T    A__
            GCC                    GGCGGC GGCG   GCGGCGGCGGCC
                                |||||| ||||   ||||||||||||
```

```
                                CCGCCG CCGC   CGCCGCCGCCGG
                                   _   CAC
GAM1848  RHEB2    5'  GGCGGCGGCGGGCGCGGC    24718       T   A   G
                                GGCGGC GGCG GCG CGGC
                                |||||| |||| ||| ||||
                                CCGCCG CCGC CGC GCCG
                                   _   C   _
GAM1848  RNTRE    5'  GCGGCGCGGCGGCGGCGGCGGC 31255       _    A
                                GCGGC TGGCG GCGGCGGCGGC
                                ||||| ||||| ||||||||||
                                CGCCG GCCGC CGCCGCCGCCG
                                  C    _
GAM1848  ROR1     5'  CGGCGGCGGCGGTGGCGGC   22697     T   A   C
                                CGGC GGCG GCGG GGCGGC
                                |||| |||| |||| ||||||
                                GCCG CCGC CGCC CCGCCG
                                  _   _   A
GAM1848  ROR1     5'  GGCGGCGGCGGCGGCGGC    22701       T   A
                                GGCGGC GGCG GCGGCGGC
                                |||||| |||| ||||||||
                                CCGCCG CCGC CGCCGCCG
                                   _   _
GAM1848  RPS28    5'  GGCGGCGCGGCGGCGG      9753        TGGCGA
                                GGCGGC     GCGGCGGCGG
                                ||||||     ||||||||||
                                CCGCCG     CGCCGCCGCC
                                   _______
GAM1848  RXRA     5'  GGCGGCGGGCGCGGCGGC    16432       T  GAGCG
                                GGCGGC GGC    GCGGCGGC
                                |||||| |||    ||||||||
                                CCGCCG CCG    CGCCGCCG
                                   C  _____
GAM1848  SCN1B    5'  GGCGGCGGGACCTGGCGGCGG  9780        T  C  GC_
                                GGCGGC GG GA   GGCGGCGG
                                |||||| || ||   ||||||||
                                CCGCCG CC CT   CCGCCGCC
                                   _ _ GGA
GAM1848  SEPN1    5'  GGCGGCGGCTGCCGGCGGC   42430       T  GA  GG
                                GGCGGC GGC  GC  CGGCGGC
                                |||||| |||  ||  |||||||
                                CCGCCG CCG  CG  GCCGCCG
                                   _   A_ __
GAM1848  SEPX1    3'  GGCGGCTGGCAGGGGCGGC   32268         AGC  C
                                GGCGGCTGGCG   GG GGCGGC
                                ||||||||||   || ||||||
                                CCGCCGACCGT   CC CCGCCG
                                      ___  _
GAM1848  SLC25A1  5'  GCGGTGGCGGCGGCGGC    25603     C    A
                                GCGG TGGCG GCGGCGGC
                                |||| ||||| ||||||||
```

```
                                CGCC ACCGC CGCCGCCG
                                  _    _
GAM1848 SLC6A8   5' GGCGGCGGCGGCGGCGGCGGC 24776      T   A
                                GGCGGC GGCG GCGGCGGCGGC
                                |||||| |||| ||||||||||
                                CCGCCG CCGC CGCCGCCGCCG
                                  _   _
GAM1848 SLC6A8   5' GGCGGCGGCGGCTGCGGCGGC 24777      T   A  G
                                GGCGGC GGCG GC GCGGCGGC
                                |||||| |||| || ||||||||
                                CCGCCG CCGC CG CGCCGCCG
                                   _   _ A
GAM1848 SLC6A8   5' GCGGCTCGGGCGGCGGCGGC  24772      GG  A
                                GCGGCT  CG GCGGCGGCGGC
                                ||||||  || ||||||||||
                                CGCCGA  GC CGCCGCCGCCG
                                   __  C
GAM1848 SLC6A8   5' GGCGGTGGCGGCGGCGGCGGC 24778     C    A
                                GGCGG TGGCG GCGGCGGCGGC
                                ||||| ||||| ||||||||||
                                CCGCC ACCGC CGCCGCCGCCG
                                  _    _
GAM1848 SOX18    5' GGCGGTGGGGACGGCGGTGG  32944     C  C  G    C
                                GGCGG TGG GA CGGCGG GG
                                ||||| ||| || |||||| ||
                                CCGCC ACC CT GCCGCC CC
                                   _  C  _    A
GAM1848 STIM1    5' GGCGGCTGGCGGTGCCCAGG  41131         AGCG  GGC
                                GGCGGCTGGCG   GC   GG
                                ||||||||||   ||  ||
                                CCGCCGACCGC   CG   CC
                                      CA__  GGT
GAM1848 SYN2     5' GGCGGCTGAGGCGGCGGC   39462        CGAGC
                                GGCGGCTGG    GGCGGCGGC
                                |||||||||    |||||||||
                                CCGCCGACT    CCGCCGCCG
                                             _____
GAM1848 TGFB1    5' GGCGGGGGCGGCGGCGGC   8545      CT   A
                                GGCGG  GGCG GCGGCGGC
                                |||||  |||| ||||||||
                                CCGCC  CCGC CGCCGCCG
                                   C_   _
GAM1848 TNFSF6   5' GGCAGCTGGTGAGTCAGGC   8474         C  _  GCGGC
                                GGCGGCTGG GAG CG    GGC
                                ||||||||| ||| ||    |||
                                CCGTCGACC CTC GT    CCG
                                     A  A _____
GAM1848 TRAP100  5' GGTGGCAGCGGTGGCGGC   31349   C   G   C
                                GG TGGC AGCGG GGCGGC
                                || |||| ||||| ||||||
```

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                                CC ACCG TCGCC CCGCCG
                                 _  _    A
GAM1848 UBE3A   5' GGCGGATGGCGGGCGCCCGCG 39281     C    A  GCG
                                GGCGG TGGCG GCG  GCG
                                ||||| ||||| |||  |||
                                CCGCC ACCGC CGC  CGC
                                   T    C  GGG
GAM1848 UGCG    5' GGCGGCTGCGGGTGCTGCGG  17875       G  AGCG  G
                                GGCGGCTG CG   GC GCGG
                                |||||||| ||   || ||||
                                CCGCCGAC GC   CG CGCC
                                     _ CCA_ A
GAM1848 USF2    3' GGCCGGCGTGGGCGGCGGCGGC 17899       A__
                                GGCTGGCG  GCGGCGGCGGC
                                ||||||||  ||||||||||
                                CCGGCCGC  CGCCGCCGCCG
                                     ACC
GAM1848 USP7    5' GGCGGCGGCGGCGGGGCGGCC  18455      T   A   C
                                GGCGGC GGCG GCGG GGCGGCC
                                |||||| |||| |||| |||||||
                                CCGCCG CCGC CGCC CCGCCGG
                                   _  _  _
GAM1848 WEE1    5' GGCGTCTCTGCGCGGCGGCGGC 18099     G  G_  GA
            C                    GGCG CT  GC  GCGGCGGCGGCC
                                |||| ||  ||  ||||||||||||
                                CCGC GA  CG  CGCCGCCGCCGG
                                  A  GA  __
GAM1848 XK      5' GACGGACGCAGTGGCGGCGGC  34360      CTG  _  C
                                GGCGG  GCG AG GGCGGCGGC
                                |||||  ||| || |||||||||
                                CTGCC  TGC TC CCGCCGCCG
                                   ____  G  A
GAM1848 YWHAG   5' GGCGGCTGCGCGGAGGAGGCGG 29797       _  AGC  C
            C                    GGCGGCTG GCG  GG GGCGGC
                                |||||||| |||  || ||||||
                                CCGCCGAC CGC  CC CCGCCG
                                     G  CT_  T
GAM1848 ZFP103  5' GCCGGCTGGCGGGCGGCGC   24959   G      AGC     G
                                G CGGCTGGCG  GGCGGCG C
                                | |||||||||  ||||||| |
                                C GCCGACCGC  CCGCCGC G
                                 G       ___     _
GAM1848 ZNF219  5' GGCGGCGGCGGGCGGCGGGCC  32333      T   A     CG
                                GGCGGC GGCG GCGGCGG  GCC
                                |||||| |||| |||||||  |||
                                CCGCCG CCGC CGCCGCC  CGG
                                   _   C      __
GAM1848 ZNF278  5' GGCGGTGGCGGCGGCGGCGGC  36802     C    A
                                GGCGG TGGCG GCGGCGGCGGC
                                ||||| ||||| ||||||||||
```

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                                CCGCC ACCGC CGCCGCCGCCG
                                  _    _
GAM1849 ADCY6    3' TGATGCATGAAGATGCCC    31614     GCCT
                                TGA   CATGAAGATGCCC
                                |||   ||||||||||||
                                ACT   GTACTTCTACGGG
                                  AC__
GAM1849 ADORA2A  3' CTGGGCCTCATGCTGC      8601      A      AAGA
                                CTG GCCTCATG   TGC
                                ||| ||||||||   |||
                                GAC CGGAGTAC   ACG
                                  C       G___
GAM1849 AK1      3' CCTCAGCCTCATGAGTAGC    7873      G        AGAT
                                CCT AGCCTCATGA   GC
                                ||| ||||||||||   ||
                                GGA TCGGAGTACT   CG
                                  G        CAT_
GAM1849 CRHR1    5' GCCTGGTGAGGAGATGCC     20443     CA   __
                                GCCT  TGA  AGATGCC
                                ||||  |||  |||||||
                                CGGA  ACT  TCTACGG
                                  CC   CC
GAM1849 FMNL     3' CCTTGAGCCTCAGCC       25295     _      TGAAGAT
                                CCT GAGCCTCA      GCC
                                ||| ||||||||      |||
                                GGA CTCGGAGT      CGG
                                  A       ________
GAM1849 GORASP1  3' CTGGGCCTCATGAAATG     36705     A       A
                                CTG GCCTCATGA GATG
                                ||| ||||||||| ||||
                                GAC CGGAGTACT TTAC
                                  C       _
GAM1849 HFE      5' CCTAGGCTCAGGAGATGCCC   40003     A  C   T  A
                                CCTG GC TCA GA GATGCCC
                                |||| || ||| || |||||||
                                GGAT CG AGT CT CTACGGG
                                  C  _   C  _
GAM1849 PDE4D    3' GCTGTTCGTGAAGATGTCC    43894    C__  A      _
                                GC   TC TGAAGATG CC
                                ||   || ||||||||| ||
                                CG   AG ACTTCTAC GG
                                 ACA  C       A
GAM1849 RABIF    3' CTGAGTTTTGAAAATGC      16125      CCTCA
                                CTGAG     TGAAGATGC
                                |||||     |||||||||
                                GACTC     ACTTTTACG
                                   AAA__
GAM1849 STXBP1   3' CTGACTGAAGATGC         17206      G CTCA
                                CTGA C    TGAAGATGC
                                |||| |    |||||||||
```

```
                                GACT G    ACTTCTACG
                                  _ ____
GAM1850  FOXE1    3'  CCTCTGTGGCCTGCTCG     20941      CAG       T
                                CCTC   GGCCTGCT CG
                                ||||   |||||||| ||
                                GGAG   CCGGACGA GC
                                  ACA       _
GAM1850  LARS2    3'  CCTCTGGGGCGTGCTGCATC   31678      CA   ___    T
                                CCTC  GGGC   CTGC TC
                                ||||  ||||   |||| ||
                                GGAG  CCCG   GACG AG
                                  AC    CAC    T
GAM1850  MUC12    3'  CTTCAGGGCCTGACTTCG     45330    C        _
                                CT CAGGGCCTG CTTCG
                                || |||||||| |||||
                                GA GTCCCGGAC GAAGC
                                 A        T
GAM1850  PKLR     3'  CTTAGGGCCTGCTGAGCAGAT  7147     CC         TCGAC
                                CT  AGGGCCTGCT    GAT
                                ||  ||||||||||    |||
                                GA  TCCCGGACGA    CTA
                                 A_        CTCGT
GAM1850  SPTBN2   3'  CCCCCAGGGCCTGCTTCA    28067
                                CCTCCAGGGCCTGCTTCG
                                ||||||||||||||||||
                                GGGGGTCCCGGACGAAGT

GAM1850  ABCB9    3'  CAGGGACCAGGGGCAAGA    33352         T  AAA
                                CAGGGACC GG   CGAGG
                                |||||||| ||   |||||
                                GTCCCTGG CC   GTTCT
                                     T  CC_
GAM1850  AGRP     5'  ACAGGGACCTAGGAG       28730           AAAC
                                ACAGGGACCTGG    GAG
                                ||||||||||||    |||
                                TGTCCCTGGATC    CTC
                                              _____
GAM1850  ALX4     3'  GGGCCTGGAAAACATGGG     34952     A       _  A
                                GGG CCTGGAAA CG GGG
                                ||| ||||||| || |||
                                CCC GGACCTTT GT CCC
                                  _       T  A
GAM1850  BGN      3'  CAGGGACCCGAGGTGGGGG    11813          AAACGA
                                CAGGGACCTGG     GGG
                                ||||||||||||     |||
                                GTCCCTGGGCT     CCC
                                       CCACC_
GAM1850  CACNG7   3'  GAGCAGGTGGAGAACGAGGGA  36687    A    GACC    _
                                GA CAGG    TGGA AACGAGGGA
                                || ||||    |||| |||||||||
```

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                                CT GTCC   ACCT TTGCTCCCT
                                 C  ____   C
GAM1850  CAPZB   3'  GGGAGGGAAGGGACGAGGGA  22318    CCT  ___
                                GGGA  GGAA  ACGAGGGA
                                ||||  ||||  ||||||||
                                CCCT  CCTT  TGCTCCCT
                                  C__   CCC
GAM1850  CLASP1  3'  GAACAGGGGCCCTGCAGGG  42239      A_  GAAA G
                                GAACAGGG  CCTG   C AGGG
                                ||||||||  ||||   | ||||
                                CTTGTCCC  GGAC   G TCCC
                                    CG   ____ _
GAM1850  CUL5    3'  AGGGACCTGGATAAAGGG   18492       AAC
                                AGGGACCTGGA  GAGGG
                                ||||||||||  |||||
                                TCCCTGGACCT  TTCCC
                                      AT_
GAM1850  DDX26   5'  GGGACCTGGGAGCTGG    29096       AAAC  __
                                GGGACCTGG   GAG  GG
                                |||||||||   |||  ||
                                CCCTGGACC   CTC  CC
                                    ____  GA
GAM1850  DNMT3L  5'  GGGCCATGGAACGAGGGA   30065    A _   A
                                GGG CC TGGAA CGAGGGA
                                ||| || ||||| |||||||
                                CCC GG ACCTT GCTCCCT
                                  _ T   _
GAM1850  EPHA1   5'  GGGACCTGGGACCTGGGA   23435      AA  GA
                                GGGACCTGG  AC  GGGA
                                |||||||||  ||  ||||
                                CCCTGGACC  TG  CCCT
                                    C_  GA
GAM1850  ERBB3   3'  GGGACCTGGGAGAGAGAGGGA 12757      AAAC__
                                GGGACCTGG    GAGGGA
                                |||||||||    ||||||
                                CCCTGGACC    CTCCCT
                                    CTCTCT
GAM1850  FLOT1   5'  CAGGGACCTGGGAGCCGGG   25133       AAACGA
                                CAGGGACCTGG    GGG
                                ||||||||||    |||
                                GTCCCTGGACC    CCC
                                    CTCGG_
GAM1850  GRIK3   3'  GAACAGGGGCTGCCAGGG   9097      AC  GAAA G
                                GAACAGGG  CTG   C AGGG
                                ||||||||  |||   | ||||
                                CTTGTCCC  GAC   G TCCC
                                    C_  G___ _
GAM1850  HOXC13  3'  ACAGGGACTTTGTTGAGGGA  40662      C_  GAAAC
                                ACAGGGAC  TG   GAGGGA
                                ||||||||  ||   ||||||
```

```
                                TGTCCCTG AC    CTCCCT
                                    AA AA___
GAM1850 ICA1    3' GAACGGTGGCCTGGAAAC   22466     AG_ A
                                GAAC  GG CCTGGAAAC
                                ||||  || |||||||||
                                CTTG  CC GGACCTTTG
                                  CCA _
GAM1850 KCNE3   5' AACAGGGATTGAGGTGGGGGA 24189       CCT_ AAACGA
                                AACAGGGA   GG    GGGA
                                ||||||||   ||    ||||
                                TTGTCCCT   CC    CCCT
                                    AACT ACC___
GAM1850 KCNJ10  3' GAACAGAGGCTATGAGGG   13869       AC  GAAAC
                                GAACAGGG CTG   GAGGG
                                |||||||| |||   |||||
                                CTTGTCTC GAT   CTCCC
                                    C_  A____
GAM1850 KIF5C   5' GGGCCGGGAACGACGAGGG  21157    A T  __
                                GGG CC GGAA ACGAGGG
                                ||| || ||||  |||||||
                                CCC GG CCTT TGCTCCC
                                  _ C   GC
GAM1850 MNT     3' GGGACCCGGGATGGG      33719       AAAC _
                                GGGACCTGG   GA GGG
                                |||||||||   || |||
                                CCCTGGGCC   CT CCC
                                    ____ A
GAM1850 RFX2    3' CAGGGACCTGGGGACCCAGA  8449         AA GA
                                CAGGGACCTGG AC GGG
                                |||||||||||  ||  |||
                                GTCCCTGGACC TG TCT
                                     CC GG
GAM1850 RNH     5' CAGGAACCTGGAGAGGA    40602         AAC
                                CAGGGACCTGGA  GAGGG
                                ||||||||||||  |||||
                                GTCCTTGGACCT  CTCCT
                                    ___
GAM1850 RNMT    3' ACAGGGGCTTGGGGCCGGGGG 19146      ACC  AAA A
                                ACAGGG  TGG  CG GGG
                                ||||||  |||  || |||
                                TGTCCC  ACC  GC CCC
                                   CGA  CCG  C
GAM1850 RNPEP   3' GAACAGGAATTTGGGAACA  42158       CC  A
                                GAACAGGGA TGG AACG
                                |||||||||  ||| ||||
                                CTTGTCCTT ACC TTGT
                                     AA  C
GAM1850 SOLH    3' ACAGGGACCCGGGCTCTGGGGG 24820         AAACGA_
            A                    ACAGGGACCTGG     GGGA
                                ||||||||||||     ||||
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                                TGTCCCTGGGCC      CCCT
                                      CGAGACC
GAM1850  SOX10    3'  CAGGGGCTGGGCGGGG     27997      AC    AAA  A
                                CAGGG  CTGG   CG GGG
                                |||||  ||||   || |||
                                GTCCC  GACC   GC CCC
                                   C_    C__  _
GAM1850  SPN      3'  GGGTGGAAACATGGGA      17087     ACC       A
                                GGG   TGGAAACG GGGA
                                |||   |||||||| ||||
                                CCC   ACCTTTGT CCCT
                                  ___       A
GAM1850  SSX4     3'  GAACAGGAAACAGAGTGAGGG  45415         CCT   AAC
                                GAACAGGGA   GGA   GAGGG
                                |||||||||   |||   |||||
                                CTTGTCCTT   TCT   CTCCC
                                      TG_   CA_
GAM1850  SUV39H2  5'  GAACAGGGAAGGCGAGGG    36013         CCT  AAA
                                GAACAGGGA   GG   CGAGGG
                                |||||||||   ||   ||||||
                                CTTGTCCCT   CC   GCTCCC
                                      T__  ___
GAM1850  SYK      3'  GAAAGGGATTTGGAAACA    17236     C    CC
                                GAA AGGGA  TGGAAACG
                                ||| |||||  ||||||||
                                CTT TCCCT  ACCTTTGT
                                  _     AA
GAM1850  TERF1    3'  GAACAGGATTTGGGGGTGGGGA 32741         ACC   AAACGA
                                GAACAGGG   TGG     GGGA
                                ||||||||   |||     ||||
                                CTTGTCCT   ACC     CCCT
                                     AA_   CCCAC_
GAM1850  TIMP3    3'  CAGGTCTGGAACGAGGG     7444       GAC     A
                                CAGG   CTGGAA CGAGGG
                                ||||   |||||| ||||||
                                GTCC   GACCTT GCTCCC
                                  A__     _
GAM1850  TNFRSF10B 3'  GACAAGGGACCTGGGACCGGA  19286    AC        AA  GA
                                GA  AGGGACCTGG  AC  GGG
                                ||  ||||||||||  ||  |||
                                CT  TCCCTGGACC  TG  CCT
                                 GT        C_  G_
GAM1850  WFS1     3'  GAACAGGGTGCTTGAAGGTGGG 25640         AC  G   ACGA_
            GGA                   GAACAGGG  CT GAA    GGGA
                                ||||||||  || |||    ||||
                                CTTGTCCC  GA CTT    CCCT
                                     AC  A   CCACC
GAM1851  HOXC5    3'  TATTTGATATGACAAAATAT   33248     C     C
                                TAT TGATAT ACAAAATAT
                                ||| |||||| |||||||||
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                                ATA ACTATA TGTTTTATA
                                  A     C
GAM1851  CBLB     3'  CACAAAACCTTAATGTAT    20332        ATCAA
                                CACAAAAT    TAATGTAT
                                ||||||||    ||||||||
                                GTGTTTTG    ATTACATA
                                    GA___
GAM1851  MADH5    3'  CATCACAAAATACAAATGTAT  25355           CAAT
                                TATCACAAAATAT    AATGTAT
                                ||||||||||||    |||||||
                                GTAGTGTTTTATG    TTACATA
                                       T___
GAM1851  MAGEC1   3'  ACAAAATATCAAACTGT     24164          TAA
                                ACAAAATATCAA   TGT
                                ||||||||||||  |||
                                TGTTTTATAGTT   ACA
                                       TG_
GAM1851  RRM2B    3'  ACAGAATACCAAATAATAATGT 42708     A     ____
                AT                ACA AATATCA    ATAATGTAT
                                ||| |||||||    |||||||||
                                TGT TTATGGT    TATTACATA
                                  C      TTAT
GAM1852  BIN3     3'  GGTTCAGGGCCTCTCCCAG    33084       ACTC
                                GGTTTG    GCCTCTCCCAG
                                ||||||    ||||||||||
                                CCAAGT    CGGAGAGGGTC
                                   CC__
GAM1852  PKIB     5'  GGTTTTCTGCTTCTCCCAG    37165      GA  C  C
                                GGTTT  CT GC TCTCCCAG
                                |||||  || || ||||||||
                                CCAAA  GA CG AGAGGGTC
                                   A_  _  A
GAM1852  SLC6A6   3'  GAGGGCTTGGCAGGAGTCTCCC 16789    A     ACTCGCC
                AG                GA GGTTTG      TCTCCCAG
                                || ||||||      ||||||||
                                CT CCGAAC      AGAGGGTC
                                 C     CGTCCTC
GAM1852  SPS2     3'  AGGCTTGCTCTGCCTCTCCCAG 29301        A  _
                                AGGTTTG CTC GCCTCTCCCAG
                                ||||||| ||| ||||||||||
                                TCCGAAC GAG CGGAGAGGGTC
                                   _  A
GAM1853  ABCD1    3'  ACAGGGCCCAGTCACTGTG   6192     ACC   TT
                                ACA   CCCA  TCACTGTG
                                |||   ||||  ||||||||
                                TGT   GGGT  AGTGACAC
                                  CCC   C_
GAM1853  DISC1    3'  CACAGCCTCACTGTG      33026      A  CCCATT
                                CACA CC     TCACTGTG
                                ||||  ||     ||||||||
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                                GTGT GG     AGTGACAC
                                  C _______
GAM1853  FPGS     3'  ACCTGGTCCAGTGTCACTGTGA 22422     C___   TT_
                A                  ACC   CCA   TCACTGTGAA
                                   |||   |||   ||||||||||
                                   TGG   GGT   AGTGACACTT
                                     ACCA   CAC
GAM1853  GNA11    3'  ACATCCCCTGATAACTGTGAA  44024     A   CATTTC
                                   ACA CCCC     ACTGTGAA
                                   ||| ||||     ||||||||
                                   TGT GGGG     TGACACTT
                                     A   ACTAT_
GAM1853  H3F3B    3'  ACAAGACTCCCCACCACTTGTG 23702     CA _     TT   _
                AA                 ACA  AC CCCCAT  CACT GTGAA
                                   |||  || ||||||  |||| |||||
                                   TGT  TG GGGGTG  GTGA CACTT
                                     TC  A     __    A
GAM1853  MSL3L1   3'  CACGAATATTTCACTGTGAA   38580     AACCCCC
                                   CAC      ATTTCACTGTGAA
                                   |||      ||||||||||||
                                   GTG      TAAAGTGACACTT
                                     CTTA___
GAM1853  PML      3'  ACACAGACTTCACCAGTGTGAA 37721       ACCCCC       ___
                                   ACACA     ATTTCACT   GTGAA
                                   |||||     ||||||||   |||||
                                   TGTGT     TGAAGTGG   CACTT
                                      C_____       TCA
GAM1853  PTEN     3'  ACACAACCTTTTTTCAACTGGA 7195         CCCA    _  T
                                   ACACAACC    TTTCA CTG GA
                                   ||||||||    ||||| ||| ||
                                   TGTGTTGG    AAAGT GAC CT
                                        AAA_    T  _
GAM1853  RBM3     5'  CAACCCCCATTGTG        43252          TTCAC
                                   CAACCCCCAT     TGTG
                                   ||||||||||     ||||
                                   GTTGGGGGTA     ACAC
                                                 _____
GAM1853  SCN4A    3'  CAATTCCCATTTCCCATG     7318      CC       A
                                   CAA  CCCATTTC CTGTG
                                   |||  |||||||| |||||
                                   GTT  GGGTAAAG GGTAC
                                     AA       _
GAM1853  SLC9A6   3'  ACACAACATCACTGTG      26826        CCCCATT
                                   ACACAAC      TCACTGTG
                                   |||||||      ||||||||
                                   TGTGTTG      AGTGACAC
                                      T_______
GAM1854  CLTC     3'  TATGCATAATGGGGAAACCTGC 22154      _   GC  A    A
                                   TATG ATAA  GG GGAAA CCTGC
                                   |||| ||||  || ||||| |||||
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                                ATAC TATT  CC CCTTT GGACG
                                  G   A_ _   _
GAM1854  EMX2    3'  TGATAAACGGAATACCTGC   44699          GAAA
                                TGATAAGCGGAG   ACCTGC
                                ||||||||||||  ||||||
                                ACTATTTGCCTT   TGGACG
                                       A___
GAM1854  GYG2    3'  TGATGGGAGGAAATTTGC    19392     AAGC      ACC
                                TGAT   GGAGGAAA  TGC
                                ||||   ||||||||  |||
                                ACTA   CCTCCTTT  ACG
                                  C___      AA_
GAM1854  PXR1    3'  CATGATGAGCAGAGAGATCTG  7232       A     _  AAAC
                                TATGAT AGCGGAG GA   CTG
                                |||||| ||||||| ||   |||
                                GTACTA TCGTCTC CT   GAC
                                   C      T  A___
GAM1854  HNF3A   3'  GGGTTGGGGTCCTTGTAACT   40729    CG   A      C
                                GGG  GGG TCCTTGTG GCT
                                |||  ||| ||||||||  |||
                                CCC  CCC AGGAACAT TGA
                                 AA   C      _
GAM1854  MCOLN1  3'  GGGCGGGGGTCTCTGCAGT   33919        A  CT G   CT
                                GGGCGGGG TC  T TGCG  GT
                                |||||||| ||  | ||||  ||
                                CCCGCCCC AG  A ACGT  CA
                                     C  __ G   __
GAM1855  PHTF1   3'  GTTGCCAAAAAGACTATGT   27355     AGA         C
                                GTTG   TTAAAAAGACTA GT
                                ||||   ||||||||||||  ||
                                CAAC   GGTTTTTCTGAT CA
                                  ___          A
GAM1856  CYLN2   3'  TGGCAGGGCGAGGGGTTG    18069      ___    AT
                                TGGCA   TGAGG  GGTTG
                                |||||   |||||  |||||
                                ACCGT   GCTCC  CCAAC
                                   CCC    __
GAM1856  G6PC    3'  TGTTATGAGCAGGATGGTTG   6663     GC   ___
                                TG  ATGA   GGATGGTTG
                                ||  ||||   |||||||||
                                AC  TACT   CCTACCAAC
                                 AA    CGT
GAM1856  SLC22A3 3'  TGTCATGAGAATCAGGTTG   35054    G       __
                                TG CATGAGGAT  GGTTG
                                || |||||||||  |||||
                                AC GTACTCTTA  CCAAC
                                 A        GT
GAM1856  SMP1    3'  TGGCATTACAAAAGGTTG    30720       GA_   T
                                TGGCAT   GGA GGTTG
                                ||||||   ||| |||||
```

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                                ACCGTA   TTT CCAAC
                                   ATG   T
GAM1856 UBE4A    3'  TGGCTGTGGACAAGGTTG    21980      A  A   __
                                TGGC TG GGAT  GGTTG
                                |||| || ||||  |||||
                                ACCG AC CCTG  CCAAC
                                  _ A    TT
GAM1856 XT3      3'  TGGAAGATGAGATGGTTG    33670     C__    G
                                TGG   ATGAG ATGGTTG
                                |||   ||||| |||||||
                                ACC   TACTC TACCAAC
                                  TTC    _
GAM1856 CRADD    3'  CTGTTTTCTCCTTCCATCTG   19177      CCCGGCGTG  _
                                CTGT        CCT CCATCTG
                                ||||        ||| |||||||
                                GACA        GGA GGTAGAC
                                  AAAGA____   A
GAM1856 SLC22A1LS 5'  CTGTTCCTCCTGCCCTCCATCT 28254      C  GGCG   _
              G                  CTGT CC    TGCC TCCATCTG
                                |||| ||    |||| ||||||||
                                GACA GG    ACGG AGGTAGAC
                                  A  AGG_    G
GAM1856 TEM5     3'  TGTCCCGGTGTGCCACCTCTG  37248         C    T  A
                                TGTCCCGG GTGCC CC TCTG
                                |||||||| ||||| || ||||
                                ACAGGGCC CACGG GG AGAC
                                     A    T  _
GAM1857 GAB2     3'  TCCAGAGTTCTGGGGACCCA   38683     C      A
                                TCC GAGTTCT GGGACCTA
                                ||| ||||||| ||||||||
                                AGG CTCAAGA CCCTGGGT
                                  T      C
GAM1857 LRRC2    3'  TCCTGGGCTCAAACAACCTGCT 35999     CGA    T  G    A
              TG                   TCC   GTTC AG GACCT CTTG
                                |||   |||| || ||||| ||||
                                AGG   CGAG TT TTGGA GAAC
                                  ACC    T  G    C
GAM1857 DMRT2    3'  CATAAGTCTCCGCTGGAATGGG 27259         _  AGTTCTC
                                CATAAGTC CCG       GGG
                                |||||||| |||       |||
                                GTATTCAG GGC       CCC
                                     A   GACCTTA
GAM1857 RHBDL    3'  CAAGTCCTGGGAGTGGGGG    19552        C__   TCTC
                                TAAGTCC   GAGT    GGG
                                |||||||   ||||    |||
                                GTTCAGG   CTCA    CCC
                                     ACC    CC__
GAM1858 ADD2     3'  GGCCATCAGACATTGTCCTC   32730        _   CCGC
                                GGCCGTC GACA    CCTC
                                ||||||| ||||    ||||
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                                CCGGTAG CTGT   GGAG
                                    T   AACA
GAM1858  ALEX3   5'  AGGCCGGCCCGCCCTC     32482      TCGACA
                                AGGCCG     CCGCCCTC
                                ||||||     ||||||||
                                TCCGGC     GGCGGGAG
                                   CG____
GAM1858  ALK     5'  GAGGCCGTTTACACTGCTCTC  43836       CG   C  C
                                GAGGCCGT  ACAC GC CTC
                                ||||||||  |||| || |||
                                CTCCGGCA  TGTG CG GAG
                                     AA   A  A
GAM1858  CASP6   5'  GGCCCGGCCCCGCCCTC    37421     GT  ACA
                                GGCC  CG   CCGCCCTC
                                ||||  ||   ||||||||
                                CCGG  GC   GGCGGGAG
                                  __  CGG
GAM1858  CCND1   3'  GGGGCCGGCTCCGCCCTC    38215   A    TCGACA
                                G GGCCG     CCGCCCTC
                                | |||||     ||||||||
                                C CCGGC     GGCGGGAG
                                 C    CGA___
GAM1858  CCND2   3'  GAGACCGCCCTGCCT       12047       CGACA _  C
                                GAGGCCGT    CC GCC T
                                ||||||||    || ||| |
                                CTCTGGCG    GG CGG A
                                     _____  A   A
GAM1858  CSHL1   3'  GAAGCCACAGCTGCCCTC    35455       T  ACACC
                                GAGGCCG CG    GCCCTC
                                |||||||  ||    ||||||
                                CTTCGGT GT    CGGGAG
                                   _  CGA__
GAM1858  CST3    3'  AAGGCCGCCTGCTGCCTTC   6434        GACACC   C
                                GAGGCCGTC     GCC TC
                                |||||||||     ||| ||
                                TTCCGGCGG     CGG AG
                                     ACGA__   A
GAM1858  CTSD    5'  GAGGCCGTGCGCTTCCTC    12527       _  ACACCGC
                                GAGGCCGT CG      CCTC
                                ||||||||  ||     ||||
                                CTCCGGCA GC      GGAG
                                     C  GAA____
GAM1858  DDX5    3'  AAGGCCATGCATTGCCTTC   20533       CGA  CC   C
                                GAGGCCGT   CA  GCC TC
                                ||||||||   ||  ||| ||
                                TTCCGGTA   GT  CGG AG
                                     C__   AA   A
GAM1858  EFEMP2  3'  GGCCTGGAGTCCGCCCTC    32621     GTC  CA
                                GGCC   GA  CCGCCCTC
                                ||||   ||  ||||||||
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                                CCGG  CT  GGCGGGAG
                                  AC_  CA
GAM1858  FKBP2    5'  AGGCCGGGCCACGCCGCCCTC  38389      __  G  A
                                AGGCC  GTC AC CCGCCCTC
                                |||||  ||| || ||||||||
                                TCCGG  CGG TG GGCGGGAG
                                   CC  _  C
GAM1858  G6PD     5'  GGCCTCGGCCACCACCCC    7607      G  A_
                                GGCC TCG  CACCGCCCT
                                ||||  |||  |||||||||
                                CCGG AGC  GTGGTGGGG
                                  _  CG
GAM1858  GADD45G  3'  GAGGCCGCGCCTCCT      27461       T  ACA  GC
                                GAGGCCG CG  CC  CCT
                                |||||||  ||  ||  |||
                                CTCCGGC GC  GG  GGA
                                   _  ___  A_
GAM1858  GH1      3'  GAAGCCACAGCTGCCCTC    8011        T  ACACC
                                GAGGCCG CG    GCCCTC
                                |||||||  ||    ||||||
                                CTTCGGT GT    CGGGAG
                                   _  CGA__
GAM1858  GH2      3'  GAAGCCACAGCTGCCCTC    35435       T  ACACC
                                GAGGCCG CG    GCCCTC
                                |||||||  ||    ||||||
                                CTTCGGT GT    CGGGAG
                                   _  CGA__
GAM1858  GNAS     3'  GGGTCCTCTTCGCCGCCCTC  38664   A  _  G  GACA
                                G GG CC TC    CCGCCCTC
                                |  ||  ||  ||    ||||||||
                                C CC GG AG    GGCGGGAG
                                 _  A  _  AAGC
GAM1858  HCFC1    5'  GAGGCCGCCATCTTAACTGCCC 43392          AC___  C
            TC                    GAGGCCGTCG    AC GCCCTC
                                |||||||||||    || ||||||
                                CTCCGGCGGT    TG CGGGAG
                                      AGAAT  A
GAM1858  HOXB3    5'  AAGGCCATTGCCGTTCTC    13437        CGACA  CC
                                GAGGCCGT    CCG  CTC
                                ||||||||    |||  |||
                                TTCCGGTA    GGC  GAG
                                   AC___  AA
GAM1858  HRMT1L1  5'  AGCCTGAGCCACCGCCCTC   42178     GTCGA
                                GGCC    CACCGCCCTC
                                ||||    ||||||||||
                                TCGG    GTGGCGGGAG
                                  ACTCG
GAM1858  HSPA6    3'  GAGGATGAACCGCCCT     44065     CC  C  C
                                GAGG  GT GA ACCGCCCT
                                ||||  ||  || ||||||||
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                                CTCC  TA CT TGGCGGGA
                                  __  _  _
GAM1858  IHPK1    3'  GAACCCAGGCGCCGCCCTC   45487    G   T_  ACA
                                GAG CCG  CG   CCGCCCTC
                                ||| |||  ||   ||||||||
                                CTT GGT  GC   GGCGGGAG
                                  G   CC  ___
GAM1858  IL17R    5'  GAGGCTTTCTTTTCCGCCCTC  30741      CG  GACA
                                GAGGC  TC    CCGCCCTC
                                |||||  ||   ||||||||
                                CTCCG  AG   GGCGGGAG
                                   AA  AAAA
GAM1858  KCNS2    5'  GGCCGCCGAGCGTCTC      42834        CAC  CC
                                GGCCGTCGA   CG  CTC
                                |||||||||   ||  |||
                                CCGGCGGCT   GC  GAG
                                     C__  A_
GAM1858  MID2     5'  AGGCCGCCGCCCGCCTTC    29220        ACA    C
                                AGGCCGTCG   CCGCC TC
                                |||||||||   ||||| ||
                                TCCGGCGGC   GGCGG AG
                                     G__     A
GAM1858  MOG      3'  GAGACCATCCTGTGTTGCTCTC 14612        GACACC_  C
                                GAGGCCGTC      GC CTC
                                |||||||||      || |||
                                CTCTGGTAG      CG GAG
                                     GACACAA  A
GAM1858  MTCP1    5'  GGCCGGCCACCGCCCTC     30583      TCGA
                                GGCCG    CACCGCCCTC
                                |||||    ||||||||||
                                CCGGC    GTGGCGGGAG
                                   CG__
GAM1858  MTMR1    5'  GGGCCCCCGCCGCCCTC     43157   A   G   ACA
                                G GGCC TCG   CCGCCCTC
                                | |||| |||   ||||||||
                                C CCGG GGC   GGCGGGAG
                                 _   G   ___
GAM1858  MUS81    5'  GAGAGCCTGCGGCCGCCCTC   36063    _  GT  ACA
                                GAG GCC  CG   CCGCCCTC
                                ||| |||  ||   ||||||||
                                CTC CGG  GC   GGCGGGAG
                                  T   AC  C__
GAM1858  NUP62    5'  GAGGCCGCCGCCGCCTCTC   29601        ACA    _
                                GAGGCCGTCG   CCGCC CTC
                                ||||||||||   ||||| |||
                                CTCCGGCGGC   GGCGG GAG
                                     ___     A
GAM1858  NXT1     5'  GAGCGCCCCGGCGCCGCCCTC  29909    _   G   ACA
                                GAG GCC TCG   CCGCCCTC
                                ||| ||| |||   ||||||||
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                                CTC CGG GGC   GGCGGGAG
                                  G  _  CGC
GAM1858  PPARBP   5'  GAGGCCGCCGCCATC      21930       TCGACA    C
                                GAGGCCG     CCGCC TC
                                |||||||     ||||| ||
                                CTCCGGC     GGCGG AG
                                   _______    T
GAM1858  PPP4C    5'  GGCCGCCGCCCCCT       15535       ACA  G
                                GGCCGTCG   CC CCCT
                                ||||||||   || ||||
                                CCGGCGGC   GG GGGA
                                   ___  _
GAM1858  PSME3    5'  GACCCGACCGCCCT       25124     GT   CA
                                GGCC  CGA  CCGCCCT
                                ||||  |||  |||||||
                                CTGG  GCT  GGCGGGA
                                  __   __
GAM1858  PTPRE    5'  GCCTGCCCGCCGCCCTC     27105     _  GACA
                                GCC GTC    CCGCCCTC
                                ||| |||    ||||||||
                                CGG CGG    GGCGGGAG
                                  A  GC__
GAM1858  RPA3     5'  GGTTGTGATACCCGCCCCC    16382    CC  CG_  A
                                GG  GT   AC CCGCCCTC
                                ||  ||   || ||||||||
                                CC  CA   TG GGCGGGGG
                                 AA  CTA  _
GAM1858  SDC1     3'  AGGCCCCTGCCGCCCTC     16497      G  GACA
                                AGGCC TC    CCGCCCTC
                                |||||  ||    ||||||||
                                TCCGG GG    GGCGGGAG
                                   _  AC__
GAM1858  SMURF1   5'  GACGCCCGCCGCCCT      45195    G   GT  ACA
                                GA GCC  CG   CCGCCCT
                                || |||  ||   |||||||
                                CT CGG  GC   GGCGGGA
                                 G   __  ____
GAM1858  SNX6     5'  GGGCCGTCGTCCAGGCCTTC  34565   A      A_  CC   C
                                G GGCCGTCG  CA  GCC TC
                                | ||||||||  ||  ||| ||
                                C CCGGCAGC  GT  CGG AG
                                _       AG  C_   A
GAM1858  TDG      5'  GAGGCCGCTGATGCGGCGGCTC 17356        C  CACC  C_
                                GAGGCCGT GA    GC  CTC
                                |||||||| ||    ||  |||
                                CTCCGGCG CT    CG  GAG
                                     A  ACGC  CC
GAM1858  TFG      5'  GAGGCCGCGGCCGCCGCC    25872        T  ACA    _
                                GAGGCCG CG   CCGCC CT
                                ||||||| ||   ||||| ||
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                                CTCCGGC GC   GGCGG GG
                                   _ C__     C
GAM1858 TNFRSF8  3' GAGGCCGTGGTGCCTCTC    10320        CGACACC  _
                                GAGGCCGT      GCC CTC
                                ||||||||      ||| |||
                                CTCCGGCA      CGG GAG
                                    CCA_____  A
GAM1858 TOP3A    3' AAGGCCAACACTGTCCTC    21461       GTC    CGC
                                GAGGCC   GACAC   CCTC
                                ||||||   |||||   ||||
                                TTCCGG   TTGTG   GGAG
                                   ___     ACA
GAM1858 WNT3A    3' GAGGCGCTCCGCCCT       37544       C  CGACA
                                GAGGC GT    CCGCCCT
                                ||||| ||    |||||||
                                CTCCG CG    GGCGGGA
                                  _ A_____
GAM1858 BCAT1    3' TGTCTGAGAGTTGACCTTCC   42386      C _ CC    _
                                TGTC GA AG  GACCT CC
                                |||| || ||  ||||| ||
                                ACAG CT TC  CTGGA GG
                                  A  C  AA    A
GAM1859 CABC1    3' CCAGCAGCAGCGAGCCTGTG   33679       CTTCTA     C
                                CCGGT     CGAGCC GTG
                                |||||     |||||| |||
                                GGTCG     GCTCGG CAC
                                   TCGTC_     A
GAM1859 CLCN7    3' CCCTGGTGCTACGAGTCCGTG  10512     C   CTT      C
                                CCC GGT   CTACGAG CCGTG
                                |||  |||   ||||||| |||||
                                GGG CCA   GATGCTC GGCAC
                                  A   C__      A
GAM1859 EDAR     3' CCTTCTGTCTTCTACTGGAG   35304    CCCG       __
                                CC    GTCTTCTAC  GAG
                                ||    |||||||||  |||
                                GG    CAGAAGATG  CTC
                                 AAGA        AC
GAM1859 HR       5' CCTGGTCCTCTCCAT       32915    C       ACGAGC
                                CC GGTCTTCT      CCGT
                                || ||||||||      ||||
                                GG CCAGGAGA      GGTA
                                 A       _______
GAM1859 LATS2    3' CCCTCGGCTTCCCTATTGGCCT 31020     _   T    ACGA__   C
            GTG                    CCC CGG CTTCT     GCC GTG
                                ||| ||| |||||     ||| |||
                                GGG GCC GAAGG     CGG CAC
                                  A   _     GATAAC   A
GAM1859 RALB     5' GGTCTTCTGAGGCTGTG     16147        AC   CCC
                                GGTCTTCT  GAG   GTG
                                ||||||||  |||   |||
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                                CCAGAAGA CTC  CAC
                                   __  CGA
GAM1859 SLC1A4   3' CCCCTGGTCTACCGACTCTGTG 16744     C    TCTA  GCCC
                                CCCC GGTCT   CGA   GTG
                                |||| |||||   |||   |||
                                GGGG CCAGA   GCT   CAC
                                  A    TG__  GAGA
GAM1859 TNFRSF6B 5' CCCGGTCTTCTCGGACCGTG  32349         A  AG  C
                                CCCGGTCTTCT CG  CC GTG
                                |||||||||| ||  || |||
                                GGGCCAGAAGA GC  GG CAC
                                      _ CT  _
GAM1859 BRF1     5' CACCGGGACCACGGCGGGGACG 11328          A  TCTC_
           CG                    TACCGGGACCACG GT    CGCG
                                ||||||||||||| ||    ||||
                                GTGGCCCTGGTGC CG    GCGC
                                      _ CCCCT
GAM1859 SGT      3' GGGACCACGGCGCCG      16620         A  TCT
                                GGGACCACG GT  CCG
                                ||||||||| ||  |||
                                CCCTGGTGC CG  GGC
                                   _ C__
GAM1859 TRPS1    5' CAGGACCTCAGTCTCCGCG   30458       A G  T
                                CGGGACC C AGT CTCCGCG
                                ||||||| | ||| |||||||
                                GTCCTGG G TCA GAGGCGC
                                   A _  _
GAM1860 IRS2     5' TCGGGGTCCGCGCCGCCGCCGG 40716     AC_    T  GA_
           G                     TCGG  CCGCGC CG  CCGGG
                                ||||  |||||| ||  |||||
                                AGCC  GGCGCG GC  GGCCC
                                  CCA    _ GGC
GAM1860 MUS81    5' CCGGCCCAGGCGGACCGGG   36061     A   C  TC
                                TCGG CCCG GC  GGACCGGG
                                |||| |||| ||  ||||||||
                                GGCC GGGT CG  CCTGGCCC
                                  _   C  __
GAM1860 TBX1     3' TCGGGGCTGTGCAGGACCGGG  25627     ACCCGC  TC
                                TCGG    GC  GGACCGGG
                                ||||    ||  ||||||||
                                AGCC    CG  CCTGGCCC
                                  CCGACA  T_
GAM1860 BRAF     5' GGCCCGAGCGGCCGCTGTCG   20263      __      CGC
                                GGTCC  GCGGCCGC   CG
                                |||||  ||||||||   ||
                                CCGGG  CGCCGGCG   GC
                                   CT      ACA
GAM1860 EN2      5' ACGCTCCGGCCGCCGC      10928     G  GC
                                GCG TCC  GGCCGCCGC
                                ||| |||  |||||||||
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                                TGC AGG  CCGGCGGCG
                                  G  __
GAM1860  FLT1    5'  AGCCGCCGCCGCTGCCG     12904    T   G    C
                                GG CCGC GCCGC GCCG
                                || |||| ||||| ||||
                                TC GGCG CGGCG CGGC
                                  _   G    A
GAM1860  JUND    5'  GAGTGGCCGCGGCCTCCCG   23802    C  T      G_
                                GAG GG CCGCGGCC  CCG
                                ||| || ||||||||  |||
                                CTC CC GGCGCCGG  GGC
                                  A  _       AG
GAM1860  MIF     5'  GCGCCGCGGCCGCCGCTGAG  14511    GT          C
                                GCG  CCGCGGCCGCCGC GAG
                                |||  |||||||||||| |||
                                CGC  GGCGCCGGCGGCG CTC
                                  __           A
GAM1860  MSF     3'  GAGCAGTCTGCGGATGGCTGAG 44728         C    CCGCC  C
                                GAGCGGTC GCGG    GC GAG
                                |||||||| ||||    || |||
                                CTCGTCAG CGCC    CG CTC
                                     A   TAC__  A
GAM1860  NFRKB   5'  GCGGTCGCGGCCGTGAC    26096       C      CC
                                GCGGTC GCGGCCG  GC
                                |||||| |||||||  ||
                                CGCCAG CGCCGGC  TG
                                   _      AC
GAM1860  NPY2R   5'  GGGCGGTTGGCGCTGCCG    9500    A    CCGC   C  C
                                G GCGGT   GGC GC GCCG
                                | |||||   ||| || ||||
                                C CGCCA   CCG CG CGGC
                                 C    A___   _ A
GAM1860  RNF12   5'  GGTTCGGCCGCCGCCGCCGAG  32036    _ C  G
                                GGT C GC GCCGCCGCCGAG
                                ||| | || ||||||||||||
                                CCA G CG CGGCGGCGGCTC
                                  A C  G
GAM1860  SART1   5'  CGAGCCCGGCTGCCGCCGA   23110    GT  G   C
                                CG  CC CGGC GCCGCCGA
                                ||  || |||| ||||||||
                                GC  GG GCCG CGGCGGCT
                                 TC  _   A
GAM1860  SOD3    3'  GGTCCCTGGCCGCCGCCG    16957      GC
                                GGTCC  GGCCGCCGCCG
                                |||||  ||||||||||
                                CCAGG  CCGGCGGCGGC
                                   GA
GAM1861  PIK3R3  3'  CTGTATCTGTATTTCCA     41442         GCGG
                                CTGTATCTG   TTCCG
                                |||||||||   |||||
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                                GACATAGAC    AAGGT
                                     ATA_
GAM1862  DDX15    3'  AGAAGCATTTTCAACCATTT   10677        CGGG
                                AGAGGCAT    GGCCATTT
                                ||||||||    ||||||||
                                TCTTCGTA    TTGGTAAA
                                     AAAG
GAM1862  PPP3CA   3'  TCAAAGGCATTAAGCATTT    9617          CG  GGC
                                TCAGAGGCAT  GG   CATTT
                                ||||||||||  ||   |||||
                                AGTTTCCGTA  TC   GTAAA
                                     AT  ___
GAM1862  RANBP3   5'  TCTTCAGAGGCATTGCTGGACT 28769     _       CGG_   _
           CATTT                    TCT CAGAGGCAT    GGGC CATTT
                                ||| |||||||||    |||| |||||
                                AGA GTCTCCGTA    CCTG GTAAA
                                  A        ACGA    A
GAM1862  SUV39H2  3'  TCAGAGGCATCGGTAATACATT 36018           GGGC_
           T                     TCAGAGGCATCGG    CATTT
                                ||||||||||||     |||||
                                AGTCTCCGTAGCC    GTAAA
                                      ATTAT
GAM1862  WASF1    3'  GAGGAAAAGGGTCATTT     19446      CATC    C
                                GAGG    GGGGG CATTT
                                ||||    ||||| |||||
                                CTCC    TTCCC GTAAA
                                  TT__     A
GAM1863  CCND2    5'  ATTGGGTGGTGGGCGA      12046       C  CGAG    C
                                ATTGGG GG    GGGC GA
                                ||||||  ||   ||||  ||
                                TAACCC CC    CCCG CT
                                   A  A___    _
GAM1863  ENG      3'  CTGGGCGAGCGCGGGGGGCCG  6496         _   A__
                                TTGGGCG GCG   GGGGCCG
                                |||||||  |||   |||||||
                                GACCCGC CGC   CCCCGGC
                                     T   GCC
GAM1863  RAB26    5'  TTGGGCGGCGCGTCGGGGC    30752          A___
                                TTGGGCGGCG    GGGGC
                                ||||||||||    |||||
                                AACCCGCCGC    CCCCG
                                      GCAG
GAM1863  SHMT2    3'  TTGAGCAAGTTGGGGCCGAA   24013        CGA
                                TTGGGCGG   GGGGCCGAA
                                ||||||||   |||||||||
                                AACTCGTT   CCCCGGCTT
                                     CAA
GAM1864  APG5L    3'  CTTTAAACTTCAAAAGACTG   22131        C   TGT
                                CTTTAAAC TTA   AGACTG
                                ||||||||  |||   ||||||
```

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                              GAAATTTG AGT   TCTGAC
                                  A  TT_
GAM1864  GALR1    3'  CTTTAAAATGTAGACT     11201       CCTT
                              CTTTAAA   ATGTAGACT
                              |||||||   |||||||||
                              GAAATTT   TACATCTGA
                                  ____
GAM1864  MTMR6    3'  TACCTTTAAATCATATA     45278         CC
                              TACCTTTAAA  TTATGTA
                              ||||||||||  |||||||
                              ATGGAAATTT  AGTATAT
                                  __
GAM1864  TRPM7    3'  TACCTTTAAAATTTCTCAGCTG 41620         CC  ATG   A
                              TACCTTTAAA  TT   TAG CTG
                              ||||||||||  ||   ||| |||
                              ATGGAAATTT  AA   GTC GAC
                                   TA  GA_  _
GAM1864  USH2A    3'  CCTTTAAATTTTGTGACCG    28304        CC  A   A
                              CCTTTAAA  TT TGT GACTG
                              ||||||||  || ||| |||||
                              GGAAATTT  AA ACA CTGGC
                                  __  A  _
GAM1864  ZNF36    3'  CCTTTGGAACTGTAGACT    45291      A_  CTTA
                              CCTTT  AAC   TGTAGACT
                              |||||  |||   ||||||||
                              GGAAA  TTG   ACATCTGA
                                 CC  ____
GAM1864  ABCB1    3'  TTGCTACTTCTATAATCTTTT  9575     TC   TT   T
                              TTG  ACT  TCT TAATCTTTT
                              |||  |||  ||| |||||||||
                              AAC  TGA  AGA ATTAGAAAA
                                GA  __  T
GAM1864  FCMD     3'  CTTGTCACATTTTTTCTTT   27518        ___
                              CTTGTCAC   TTTTCTTT
                              ||||||||   ||||||||
                              GAACAGTG   AAAAGAAA
                                  TAA
GAM1864  PCDH11X  3'  TTGTCACTATTGGTTCTTT   37322        T____
                              TTGTCACT    TTCTTT
                              ||||||||    ||||||
                              AACAGTGA    AAGAAA
                                  TAACC
GAM1864  PCDH11Y  3'  TTGTCACTATTGGTTCTTT   37367        T____
                              TTGTCACT    TTCTTT
                              ||||||||    ||||||
                              AACAGTGA    AAGAAA
                                  TAACC
GAM1864  SULT1C1  3'  CTTTTCACTTTTCTTTTCTTTT 9839      G         AA
                              CTT TCACTTTTCTTT  TCTTTT
                              ||| ||||||||||||  ||||||
```

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                                GAA AGTGAAAAGAAA  AGAAAA
                                  A         __
GAM1864  VAX2     3'  CTTGTCATTGTTTTCCTT    29779        C__
                                CTTGTCA   TTTTCTTT
                                |||||||   ||||||||
                                GAACAGT   AAAAGGAA
                                    AAC
GAM1865  CREBL2   3'  TCAGAGCCTGTCAGGAAATTCA 10586        ATG   TA
              T                  TCAGAGC   GTC  GAAATTCAT
                                |||||||   |||  |||||||||
                                AGTCTCG   CAG  CTTTAAGTA
                                    GA_   TC
GAM1865  GABRE    3'  GCATGTCCAAATTCAT      35083       G    GA
                                GCATG TCTA  AATTCAT
                                ||||| ||||  |||||||
                                CGTAC AGGT  TTAAGTA

                                  _   __
GAM1865  RAB11A   3'  AGGCATTTTAGAAATTCAT   21677     A    GGTC
                                AG GCAT    TAGAAATTCAT
                                || ||||    ||||||||||
                                TC CGTA    ATCTTTAAGTA
                                 _    AA__
GAM1865  RAB11A   3'  AGGACATGGAAAAATTCAT   21676     AG    TCT
                                AG  CATGG   AGAAATTCAT
                                ||  |||||   ||||||||||
                                TC  GTACC   TTTTTAAGTA
                                 CT    ___
GAM1866  COL5A1   5'  CCGTTCTTCTTTGTGGCGGCGG 6414          ___   A
                                CCGTTCTT   TGT GCGGCGG
                                ||||||||   ||| |||||||
                                GGCAAGAA   ACA CGCCGCC
                                    GAA   C
GAM1866  PRKAR2A  5'  TCGCGCCGCTCTTTGGCCGG   20008             TAG
                                TCGCGCCGTTCTTTG   CGG
                                ||||||||||||||   |||
                                AGCGCGGCGAGAAAC   GCC
                                         CG_
GAM1867  AICDA    3'  CATCCTACCTAAAAGTCATAGA 34037      AAGAAG       C
                                CATC      AAAAGTCA AGA
                                ||||      |||||||| |||
                                GTAG      TTTTCAGT TCT
                                  GATGGA       A
GAM1867  BCAT1    3'  ACATCAGGAAGAAAACAG     42373        A      AGTC
                                ACATCA GAAGAAA    ACAG
                                ||||||| |||||||    ||||
                                TGTAGT CTTCTTT    TGTC
                                  C      _____
GAM1867  CLTB     3'  TACATCAGGAGGGACAGTCACA 28228         A  AGAAA
                                TACATCA GA     AGTCACA
                                ||||||| ||     |||||||
```

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                                ATGTAGT CT    TCAGTGT
                                    C  CCCTG
GAM1867  DNM1    3'  TACAACAGATTAAGTCACAGA  20604     TCA   AGAA
                                TACA   AGA   AAGTCACAGA
                                ||||   |||   ||||||||||
                                ATGT   TCT   TTCAGTGTCT
                                  TG_   AA__
GAM1867  GRM1    3'  TACATCAAGGTGAAGAGT    9140         AA   A
                                TACATCAAG  GAA AGT
                                |||||||||  ||| |||
                                ATGTAGTTC  CTT TCA
                                     CA   C
GAM1867  KRT2A   5'  TCCAGGGAGGAAAGTCACAG   7687     A  A_  A
                                TC AG  AG AAAGTCACAG
                                || ||  || ||||||||||
                                AG TC  TC TTTCAGTGTC
                                 G  CC  C
GAM1867  MAN1A1  3'  CATAAGGAGGCTGTCACAGA   45093     C   A  AAAA
                                CAT AAG AG    GTCACAGA
                                ||| ||| ||    ||||||||
                                GTA TTC TC    CAGTGTCT
                                  _   C  CGA_
GAM1867  PCP4    3'  ACATCAAGGAAAATAGTTGCAG 26230        A    A   CA
                                ACATCAAG AGAA AGT  CAG
                                |||||||| |||| |||  |||
                                TGTAGTTC TTTT TCA  GTC
                                     C    A   AC
GAM1867  PEX1    3'  AAGAAGAAATTCATAGA     7870         AG   C
                                AAGAAGAAA  TCA AGA
                                |||||||||  ||| |||
                                TTCTTCTTT  AGT TCT
                                     A_   A
GAM1867  PXN     3'  AAAGAGGGGGAGTCACAGA   16023      AA___
                                GAAGA    AGTCACAGA
                                |||||    |||||||||
                                TTTCT    TCAGTGTCT
                                   CCCCC
GAM1867  SLC21A9 3'  TCACAAAGGTCACAG      28570     A   AAAA
                                TCA GAAG    GTCACAG
                                ||| ||||    |||||||
                                AGT TTTC    CAGTGTC
                                  G   ____
GAM1867  STX1A   3'  TCAAGAAGGCAACACGGA    21414        AAA  T   A
                                TCAAGAAG   AG CAC GA
                                ||||||||   || ||| ||
                                AGTTCTTC   TT GTG CT
                                     CG_  _   C
GAM1867  TLX1    5'  TCAAGAAGTAAAATCCTACAG  24346        A     __
                                TCAAGAAG AAAGTC  ACAG
                                |||||||| ||||||  ||||
```

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                                AGTTCTTC TTTTAG  TGTC
                                    A     GA
GAM1868  ANGPT1   5'  AAAACTTGAGATATTTATTGCA 40235        C   _   CC
                                AAAACTTG AGAT TTTA  GCA
                                |||||||| |||| ||||  |||
                                TTTTGAAC TCTA AAAT  CGT
                                    _   T   AA
GAM1868  ATP11B   3'  TGAAAGCTTGCAGACTGC    44310      A       TTACC
                                TGAAA CTTGCAGATT    GC
                                ||||| ||||||||||    ||
                                ACTTT GAACGTCTGA    CG
                                  C       _____
GAM1868  MDS1     3'  ACTTGCAGGTACGGCA     22558        ATTT  C
                                ACTTGCAG   TAC GCA
                                ||||||||   ||| |||
                                TGAACGTC   ATG CGT
                                    C___  C
GAM1868  NEBL     3'  AACGACAGATTTTATTGCA   26894     TT       CC
                                AAC  GCAGATTTTA  GCA
                                |||  ||||||||||  |||
                                TTG  TGTCTAAAAT  CGT
                                  C_        AA
GAM1868  PYCS     3'  TGAAACTTGCATCTCCTGCTGC 16040      A     GA   ACC
           A                     TGAAA CTTGCA  TTTT   GCA
                                |||||  ||||||  ||||  |||
                                ACTTT GAACGT  AGGA   CGT
                                  _     AG   CGA
GAM1868  ZNF142   3'  TGAGAACTTGCAGGTTAAAAAC 22928     A       A  TTAC_
           GCA                    TGA AACTTGCAG TT    CGCA
                                ||| |||||||| ||    ||||
                                ACT TTGAACGTC AA    GCGT
                                  C       C  TTTTT
GAM1869  FRAT2    3'  TATCCCAGGTCCTTGGGCT   28975        A  AGAATATA
                                TATCTCAG TC       GGCT
                                |||||||| ||       ||||
                                ATAGGGTC AG       CCGA
                                    C  GAAC____
GAM1869  KCNA3    3'  TATGTCAGATCAGGACAT    13797     C       A
                                TAT TCAGATCAG ATAT
                                ||| |||||||| ||||
                                ATA AGTCTAGTC TGTA
                                  C       C
GAM1869  MIPOL1   3'  TATCTCAGCTTGGAATGTGG   44199       ATCA   ATA
                                TATCTCAG   GAAT   GG
                                ||||||||   ||||  ||
                                ATAGAGTC   CTTA   CC
                                    GAAC   CA_
GAM1869  USH2A    3'  TATCTCAGTTAGAATAT     28305        ATC
                                TATCTCAG   AGAATAT
                                ||||||||   |||||||
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                                ATAGAGTC  TCTTATA
                                    AA_
GAM1870 EBI2    3' AAGGGAAGTCCTGCAAAGTTT 22393      C  _
                                AAGGGG AGTC TGCAAAGTTT
                                |||||| |||| ||||||||||
                                TTCCCT TCAG ACGTTTCAAA
                                   _  G
GAM1870 POLR2H  3' GGAGGGGCAGTCTGAAAAAGT 26354  A       C_
                                A AGGGGCAGTCTG AAAGT
                                | ||||||||||| |||||
                                C TCCCCGTCAGAC TTTCA
                                 C         TT
GAM1870 RARRES3 3' AAGGGGCAGATGGCTGTTTAT 42841       TCT AAA
                                AAGGGGCAG  GC  GTTTAT
                                |||||||||  ||  ||||||
                                TTCCCCGTC  CG  CAAATA
                                     TAC A__
GAM1870 RNH     5' GGGGTGGTCTGTGAGCCT   40610    CA   CAA
                                GGGG GTCTG  AGTTT
                                |||| |||||  |||||
                                CCCC CAGAC  TCGGA
                                  AC   AC_
GAM1870 RPS5    3' AAAGGGCAGACAGGTTTA   9745       TCT  AA
                                AAGGGGCAG  GCA GTTTA
                                |||||||||  |||  |||||
                                TTTCCCGTC  TGT CAAAT
                                    ___  C_
GAM1870 SHMT1   3' GGGGCAGTGTGTACAAGCT  20023      C CA_
                                GGGGCAGT TG  AAGTT
                                |||||||| ||  |||||
                                CCCCGTCA AC  TTCGA
                                    C ATG
GAM1871 COL4A4  3' TGAGTGCAAGAAGCTGTG   6409       ____
                                TGAGTGCGA   TTGTG
                                |||||||||   |||||
                                ACTCACGTT   GACAC
                                     CTTC
GAM1871 DGCR2   3' AGTGCAACCGTTGTGACA   23084      ___
                                AGTGCGAT  TGTGACA
                                ||||||||  |||||||
                                TCACGTTG  ACACTGT
                                    GCA
GAM1871 JUN     3' TGAATACATTTATTGTGACA 13750      ___
                                TGAGTGCG  ATTGTGACA
                                ||||||||  |||||||||
                                ACTTATGT  TAACACTGT
                                    AAA
GAM1871 LOXL3   3' TGAGTGCGGTTGCTGACA   37202      A  _
                                TGAGTGCG TTG TGACA
                                |||||||| ||| |||||
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```
                                ACTCACGC AAC ACTGT
                                    C   G
GAM1872  ADH5    3'  ATGTAGTTCACTATACTAGAAA 8578     A   CCTTTG
              T                  ATG AGT     ATACTAGAAAT
                                 ||| |||     ||||||||||
                                 TAC TCA     TATGATCTTTA
                                   A   AGTGA_
GAM1872  TPST2   3'  ATGAAGTCATTTGCGGAGA   18757       C    ATACT
                                 ATGAAGTC TTTG     AGA
                                 |||||||| ||||     |||
                                 TACTTCAG AAAC     TCT
                                     T    GCC__
GAM1872  WIG1    3'  TGAAATCCACAACTGGAAAT   45388       TTTGAT   A
                                 TGAAGTCC     ACT GAAAT
                                 ||||||||     ||| |||||
                                 ACTTTAGG     TGA CTTTA
                                     TGT___   C
GAM1872  IMPA1   3'  TTGAAACTAAAGAGAAAT    24393          AG
                                 TTGAAACTGAAGA  AGT
                                 ||||||||||||  |||
                                 AACTTTGATTTCT  TTA
                                       CT
GAM1872  VHL     3'  TTGAAACTAAGGAAGGAACCAG 8123          A   _ GT  C
              TC                   TTGAAACTGA GAAG A  CG GTC
                                 |||||||||| |||| |  || |||
                                 AACTTTGATT CTTC T  GT CAG
                                     C    C TG  _
GAM1873  EXT2    3'  TGATGTAAATAACTAAAA    7592    A   GG
                                 C GTG  AATAACTAAAA
                                 | |||  ||||||||||
                                 A TAC  TTATTGATTTT
                                  C   AT
GAM1873  PAFAH1B1 3'  TACAGTGGGAAGATAAAAAG   7721          TAACT
                                 TACAGTGGGAA     AAAAG
                                 ||||||||||     |||||
                                 ATGTCACCCTT     TTTTC
                                       CTAT_
GAM1873  PSAP    3'  TATTACAGTGGGAATTAC    42971           A
                                 TATTACAGTGGGAAT AC
                                 |||||||||||||| ||
                                 ATAATGTCACCCTTA TG
                                       A
GAM1873  CCRL1   3'  TGTTATTCACTTATGCCTGTTA 32433       TC  GGATCA
                                 TGTTATT  CT     CCTGTTA
                                 |||||||  ||     |||||||
                                 ACAATAA  GA     GGACAAT
                                    GT  ATAC__
GAM1873  DAB1    3'  TGCTATTTCTTAGGTCTGTT   34351       C   ATCAC
                                 TGTTATTTC TGG    CTGTT
                                 |||||||| |||    |||||
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                                ACGATAAAG ATC    GACAA
                                    A  CA___
GAM1873 LAPTM5   3' TGTTATTTCCTGGAGCTAATTG 27610          TCACC_
            TT                   TGTTATTTCCTGGA    TGTT
                                 ||||||||||||||    ||||
                                 ACAATAAAGGACCT    ACAA
                                       CGATTA
GAM1873 PKIG     3' TTATTTCCTGGGTCCTA    28196        ATCA
                                 TTATTTCCTGG   CCTG
                                 ||||||||||    ||||
                                 AATAAAGGACC   GGAT
                                     CA__
GAM1874 A1BG     3' AGGAACTAGATATTACTA   39086        _
                                 AGGAACTA ATATTACTA
                                 |||||||| |||||||||
                                 TCCTTGAT TATAATGAT
                                     C
GAM1874 AGR2     3' TAGAGGAATTCCATATATTA  26924        __  _
                                 TAGAGGAA  CTA ATATTA
                                 ||||||||  ||| ||||||
                                 ATCTCCTT  GGT TATAAT
                                     AA  A
GAM1874 MDM1     3' AGGACAGTATAATATTACTA  33513     AC___
                                 AGGA    TAATATTACTA
                                 ||||    ||||||||||
                                 TCCT    ATTATAATGAT
                                   GTCAT
GAM1874 SERPINB13 3' ATAGAGGAGGATTACT     29619       ACTAAT
                                 ATAGAGGA    ATTACT
                                 ||||||||    ||||||
                                 TATCTCCT    TAATGA
                                     CC____
GAM1875 ABCC5    3' TTCACATTTTCAGATTTT    25029       GC  C
                                 TTCACATT  CAG TTTT
                                 ||||||||  ||| ||||
                                 AAGTGTAA  GTC AAAA
                                     AA  T
GAM1875 CASP2    3' TTCACTTGTCAGGCTCTT    37404      A  C  _
                                 TTCAC TTG CAG CTTTT
                                 ||||| ||| ||| |||||
                                 AAGTG AAC GTC GAGAA
                                   _  A  C
GAM1875 MYO5A    3' CATATTGCCAGTTTATTTC   40753    C      CT   C
                                 CA ATTGCCAG  TTTA TTC
                                 || ||||||||  |||| |||
                                 GT TAACGGTC  AAAT AAG
                                  A       __   A
GAM1875 PCSK1    3' TTACCAACCATACTTCA     7758         TT
                                 TTGCCAGCT  TACTTCA
                                 |||||||||  |||||||
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```
                                AATGGTTGG  ATGAAGT
                                     T_
GAM1875  QDPR     3'  CTCGCATTGTCTTACTTC    7237      A    CCAGC
                                TTC CATTG    TTTTACTTC
                                ||| |||||    |||||||||
                                GAG GTAAC    AGAATGAAG
                                  C    _____
GAM1875  RNF18    3'  TTCCATTGATTTTTACTTC   33778     A    CCAGC
                                TTC CATTG    TTTTACTTC
                                ||| |||||    |||||||||
                                AAG GTAAC    AAAATGAAG
                                  _    TA___
GAM1875  SHOC2    3'  TTCACTTTGCCAGTTTTTTTTT 28899      A     C   AC_
              TCA                  TTCAC TTGCCAG TTTT   TTCA
                                ||||| ||||||| ||||   ||||
                                AAGTG AACGGTC AAAA   AAGT
                                   A      A    AAA
GAM1875  TMOD     3'  TTCATGCTGCCAGCATTTT   17605     CA      _
                                TTCA  TTGCCAGC TTTT
                                ||||  |||||||| ||||
                                AAGT  GACGGTCG AAAA
                                  AC       T
GAM1875  TPST1    3'  TTCACATTGAAAGCTTTTA   18763        CC
                                TTCACATTG  AGCTTTTA
                                |||||||||  ||||||||
                                AAGTGTAAC  TCGAAAAT
                                     TT
GAM1875  VIL2     3'  TTGCAAAGCTTTTATTTCA   18002     C_      C
                                TTGC  AGCTTTTA TTCA
                                ||||  |||||||| ||||
                                AACG  TCGAAAAT AAGT
                                  TT       A
GAM1875  SNX6     3'  TACTTGGTTTAGTCTACAAG  34566         T   A
                                TATTTGGTTT GTC TACAAG
                                |||||||||| ||| ||||||
                                ATGAACCAAA CAG ATGTTC
                                     T   _
GAM1876  ARHGEF12 3'  AAACTTGTTAAGTTGCAGT   31629           _
                                AAACTTGTTAAGT GCGGT
                                |||||||||||| |||||
                                TTTGAACAATTCA CGTCA
                                       A
GAM1876  LNPEP    3'  CAAAATGAGGTGCGGTTGTG  24557     CT  TTAA
                                CAAA  TG   GTGCGGTTGTG
                                ||||  ||   ||||||||||
                                GTTT  AC   CACGCCAACAC
                                  T_  TC__
GAM1876  MDM1     3'  TCAAACTTTTTAAAAATTGTG 33519        G    TGC
                                TCAAACTT TTAAG   GGTTGTG
                                |||||||| |||||   |||||||
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                                AGTTTGAA AATTT   TTAACAC
                                    A    ___
GAM1876  TEGT     3'  TCAAACTGTGCACTGGTTGTG  42099       T  TAA TG _
                                TCAAACT GT   G  C GGTTGTG
                                ||||||| ||   |  | |||||||
                                AGTTTGA CA   C  G CCAACAC
                                    _ ___ GT A
GAM1876  BMP1     3'  TCGTACCAGCACAGGCGGCTGC 25994        AA    A___
              G                  TCGTACCA  CACA    GCTGCG
                                ||||||||  ||||   ||||||
                                AGCATGGT  GTGT    CGACGC
                                    C_    CCGC
GAM1876  XRCC5    3'  GCTCAACACAAGTTGTGA    34491    ACCA       C  C
                                GT    AACACAAG TG GA
                                ||    |||||||| || ||
                                CG    TTGTGTTC AC CT
                                 AG__       A  A
GAM1876  ZNF219   3'  AATCGTACCAAAAATAGCG   32313           CAC  GCT
                                AATCGTACCAAA   AA   GCG
                                ||||||||||||   ||   |||
                                TTAGCATGGTTT   TT   CGC
                                       ___ AT_
GAM1877  ACVR1B   3'  TGCCATTAGGAGGTAAAT    33765         A  TC
                                TGCCATTAG AG  AAAT
                                ||||||||| ||  ||||
                                ACGGTAATC TC  TTTA
                                     C  CA
GAM1877  RB1CC1   3'  CATTAACTTGTCAAATTCAG   31308       AA_
                                CATTAG   GTCAAATTCAG
                                ||||||   ||||||||||||
                                GTAATT   CAGTTTAAGTC
                                   GAA
GAM1877  SPG4     3'  TGCCATGTATAAAAATTCAG   31403       TAGAAGTC
                                TGCCAT       AAATTCAG
                                ||||||       ||||||||
                                ACGGTA       TTTAAGTC
                                   CATATT__
GAM1877  LDHB     5'  TGAGTAGTTACTCTGTGGACAT 14124       AGCT    AA
              G                  TGAGTG    TTCT  TGGACATG
                                ||||||    ||||  ||||||||
                                ACTCAT    GAGA  ACCTGTAC
                                   CAAT    C_
GAM1877  PLCB4    3'  TGAGTGAGTCTTTTGATG    9586         _   CTA
                                TGAGTGAG CTTT   ATG
                                |||||||| ||||   |||
                                ACTCACTC GAAA   TAC
                                     A   AC_
GAM1877  PSMD7    3'  TGGGTCAGCTTTCTAATAAGCA 15840    A  G         GA
              TG                   TG GT AGCTTTCTAATG  CATG
                                || || ||||||||||||  ||||
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                                AC CA TCGAAAGATTAT  GTAC
                                 C  G          TC
GAM1877 RGS1     3'  TGAGGGGCTTTCTAATA     16311      TGA
                                TGAG   GCTTTCTAATG
                                ||||   ||||||||||
                                ACTC   CGAAAGATTAT
                                  CC_
GAM1877 ZNF268   3'  TGAATGAGTTTTCTGGTG    41764        C     AA
                                TGAGTGAG TTTCT  TG
                                |||||||| |||||  ||
                                ACTTACTC AAAGA  AC
                                     A     CC
GAM1878 ATP6V1G2 3'  TTACAATGGGAAAGTAA     39631           TA
                                TTACAGTGGGAA  AGTAA
                                ||||||||||||  |||||
                                AATGTTACCCTT  TCATT
                                              __
GAM1878 BSN      3'  TTACAGCATGGGGGTGGGTAA  18425        __   AATAA
                                TTACAGT  GGG    GTAA
                                |||||||  |||    ||||
                                AATGTCG  CCC    CATT
                                    TA   CCACC
GAM1878 CALM1    3'  GCAAGAGGTAAGTAAAAG    27859   TG   A_
                                G  GGA  TAAGTAAAAG
                                |  |||  ||||||||||
                                C  TCT  ATTCATTTTC
                                 GT   CC
GAM1878 CPA3     3'  CTACTGAAAGTAAGTAAAAG   12416     AG  GG A
                                TTAC  TG  A TAAGTAAAAG
                                ||||  ||  | ||||||||||
                                GATG  AC  T ATTCATTTTC
                                  __  TT C
GAM1878 PAFAH1B1 3'  TACAGTGGGAAGATAAAAA   7720           TAA
                                TACAGTGGGAA   GTAAAAG
                                ||||||||||   |||||||
                                ATGTCACCCTT   TATTTTT
                                      C__
GAM1878 CHD3     5'  ACCCTTTGTTTCCCGATC    10456     C  A      G
                                ACCC TT TTTCCTG ATC
                                |||| || ||||||| |||
                                TGGG AA AAAGGGC TAG
                                  A  C      _
GAM1878 CPT2     5'  AACCTCTATTTCCTCACC    6429      CC       TGGA
                                AACC  TTATTTCC   TCACC
                                ||||  ||||||||   |||||
                                TTGG  GATAAAGG   AGTGG
                                  A_      _____
GAM1878 DMD      3'  AACCCCTTGTTTTAAATC    19671        A   CC
                                AACCCCTT TTT  TGGATC
                                |||||||| |||  ||||||
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                                TTGGGGAA AAA  ATTTAG
                                    C  __
GAM1878  ESR1    3'  CCCTTATTTGTTCAGCCC    6528        TCC  GA  _
                                CCCTTATT  TG  TCA CCT
                                ||||||||  ||  ||| |||
                                GGGAATAA  AC  AGT GGG
                                    ____ A_  C
GAM1878  EVI2B   3'  CTTATTCCTCTCCACCC    27092       T  GGA
                                CTTATT CCT  TCACCT
                                |||||| |||  ||||||
                                GAATAA GGA  GGTGGG
                                   _  GA_
GAM1878  FGF7    3'  CCCCTTATTCTTAACTGCATC  12857         C___  G
                                CCCCTTATTT   CTG ATC
                                ||||||||||   ||| |||
                                GGGGAATAAG   GAC TAG
                                     AATT  G
GAM1878  LCP1    5'  AACCCCTTCTTTCTGATC    14101        A   CTG
                                AACCCCTT TTTC  GATC
                                |||||||| ||||  ||||
                                TTGGGGAA AAAG  CTAG
                                    G   A__
GAM1878  MYOD1   3'  CCTTTATTTTGATCACCT    42130    C    CCTG
                                CC TTATTT   GATCACCT
                                || ||||||   ||||||||
                                GG AATAAA   CTAGTGGA
                                 A     A___
GAM1878  NPHP1   3'  CTTTCTCAAATGGATCAC    41680    A   C__
                                CTT TTTC  TGGATCAC
                                ||| ||||  ||||||||
                                GAA AGAG  ACCTAGTG
                                  _   TTT
GAM1878  SFRS7   3'  CCTCTTATGCTGATCACCT   40467    C   TTC  G
                                CC CTTAT  CTG ATCACCT
                                || |||||  ||| |||||||
                                GG GAATA  GAC TAGTGGA
                                 A   C__  _
GAM1878  XPNPEP2 3'  CCCTGTGTTTCCTGGGGCCT  18152    TA_     ATCA
                                CCCT  TTTCCTGG   CCT
                                ||||  ||||||||   |||
                                GGGA  AAAGGACC   GGA
                                  CAC      CC__
GAM1879  FCAR    3'  AGTGAGCTTTTCTCTCTTGTG  39333        _____  CA
                                AGTGAGCTT    TC  GTG
                                |||||||||    ||  |||
                                TCACTCGAA    AG  CAC
                                     AAGAG  AA
GAM1879  PLCB4   3'  TGAGTGAGTCTTTTGATG    9586         _   CCA
                                TGAGTGAG CTTT  GTG
                                |||||||| ||||  |||
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                                ACTCACTC GAAA   TAC
                                    A   AC_
GAM1879  TRPS1    3'  TGAGGAGCTTTCCCTTCAT   30470     T       AGTGGA
                                TGAG GAGCTTTCC     CAT
                                |||| |||||||||     |||
                                ACTC CTCGAAAGG     GTA
                                  _       GAA___
GAM1879  ZNF239   3'  TGAGTGATTTTTCAGTG    24979       GC   C
                                TGAGTGA  TTTC AGTG
                                |||||||  |||| ||||
                                ACTCACT  AAAG TCAC
                                    AA   _
GAM1879  ZNF268   3'  TGAATGAGTTTTCTGGTG    41764        C   CA
                                TGAGTGAG TTTC  GTG
                                |||||||| ||||  |||
                                ACTTACTC AAAG  CAC
                                    A   AC
GAM1879  GRB10    3'  TCAGAGTCAAGCTTTT     23668     G    AATTC
                                TCAG AGTCA    AGCTTTT
                                |||| |||||    |||||||
                                AGTC TCAGT    TCGAAAA
                                  _    _____
GAM1879  MIR16    3'  AAGAGTCAGGTTCTCACT    32494       AA  A_
                                AGGAGTCA  TTC  GCT
                                ||||||||  |||  |||
                                TTCTCAGT  AAG  TGA
                                    CC   AG
GAM1879  PCNA     3'  AGAGTCAAGACCCTTTTG    15117       AT  AG
                                GGAGTCAA  TC  CTTTTG
                                ||||||||  ||  ||||||
                                TCTCAGTT  GG  GAAAAC
                                    CT  __
GAM1880  CASP3    5'  AGCCACAGGTATGAGCTGCGA  37414      TAT   ACACA
                                AGTCG   CAG    AGCTGCGA
                                |||||   |||    ||||||||
                                TCGGT   GTC    TCGACGCT
                                  ___   CATAC
GAM1880  XRCC5    3'  GCTCAACACAAGTTGTGA    34491    A   A     C  C
                                GT TCAG CACAAG TG GA
                                || |||| |||||| || ||
                                CG AGTT GTGTTC AC CT
                                  _   _     A  A
GAM1881  ING1     3'  TACTGAATTGTTATATGG    24399          TGT
                                TACTGAATTGTT   TGG
                                ||||||||||||   |||
                                ATGACTTAACAA   ACC
                                      TAT
GAM1881  TMEPAI   3'  CATGTTGGGTTGTTTATTGG  33593     AC  AA
                                CAT  TG  TTGTTTGTTGG
                                |||  ||  ||||||||||
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                                GTA  AC  AACAAATAACC
                                  CA  CC
GAM1882 ACP5     3'  CATCAGCTGTGTTTCCCC    11514    _  G_  AAC
                                CA CGG  GTG   TTCCCC
                                || |||  |||   ||||||
                                GT GTC  CAC   AAGGGG
                                 A   GA   A__
GAM1882 ADRA1B   5'  TCCCCCGTGGTCTTCTTCC    8621     A  A  G   GAA
                                TCC CC CG GGT   CTTCC
                                ||| || || |||   |||||
                                AGG GG GC CCA   GAAGG
                                  _ _  A   GAA
GAM1882 ATP8B2   3'  TCCCTGCCAAGACTTCCCC    42216    ACCA   GTGA
                                TCC   CGGG   ACTTCCCC
                                |||   ||||   ||||||||
                                AGG   GTTC   TGAAGGGG
                                  GACG   _____
GAM1882 CELL     3'  TCCACCACAGTCTTCTTC     12229         GGTGAA
                                TCCACCACGG     CTTC
                                ||||||||||     ||||
                                AGGTGGTGTC     GAAG
                                      AGAA__
GAM1882 COPA     3'  TCCATCACAGAGTTTTCC     20411      C       GAAC
                                TCCA CACGGGGT    TTCC
                                |||| ||||||||    ||||
                                AGGT GTGTCTCA    AAGG
                                  A       A___
GAM1882 CTBP2    3'  TCTACCACAGGCAAACAGTTTT 35604    C      G TG  _____  C
            CTCC                  TC ACCACGG G  AAC    TTC CC
                                || ||||||| |  |||    ||| ||
                                AG TGGTGTC C  TTG    AAG GG
                                 A      _ GT   TCAA   A
GAM1882 CTBP2    3'  TCTACCACAGGCAAACAGTTTT 35605    C      G TG  _______
            TTCC                  TC ACCACGG G  AAC     TTCC
                                || ||||||| |  |||     ||||
                                AG TGGTGTC C  TTG     AAGG
                                 A      _ GT   TCAAAA
GAM1882 DYRK1A   3'  TCCTGTCATGGGGGACTCTTC  39000     AC_  C    T  A_
                                TCC   CA GGGG GA  CTTC
                                |||   || |||| ||  ||||
                                AGG   GT CCCC CT  GAAG
                                  ACA  A    _  GA
GAM1882 EN2      5'  ACCGTGGGGCGAAATCCC    10927     AC       CT
                                ACC  GGGGTGAA  TCCC
                                |||  ||||||||  ||||
                                TGG  CCCCGCTT  AGGG
                                  CA       T_
GAM1882 GOLGA4   5'  CCAAGATGTGAACTTCCC    41056     C GG
                                CCA G  GTGAACTTCCC
                                ||| |  ||||||||||
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                                GGT C  CACTTGAAGGG
                                  T TA
GAM1882  GRM1     5'  TCCACCACCGCCTCCTTCCCC  9144          GGG  GAA
                                TCCACCAC  GT  CTTCCCC
                                ||||||||  ||  |||||||
                                AGGTGGTG  CG  GAAGGGG
                                    G__  GAG
GAM1882  ISLR     3'  TCCACCACTGAGGCTTCTCCC  24437         _    GAA
                                TCCACCAC GGGGT  CTTCC
                                |||||||| |||||  |||||
                                AGGTGGTG CTCCG  GAGGG
                                    A    AA_
GAM1882  MOCS2    3'  TCTACCACAGATATCTTTCC  21207    C      GTGAAC
                                TC ACCACGGG     TTCC
                                || ||||||||     ||||
                                AG TGGTGTCT     AAGG
                                 A       ATAGA_
GAM1882  PLAUR    5'  TCCGCCACAAACTTCC      15371     A   GGGGT
                                TCC CCAC    GAACTTCC
                                ||| ||||    ||||||||
                                AGG GGTG    TTTGAAGG
                                  C   _____
GAM1882  PLOD     5'  TCGGCCGCGGGGTGAACCT   7159     CA  A
                                TC  CC CGGGGTGAACTT
                                ||  || ||||||||||||
                                AG  GG GCCCCACTTGGA
                                 CC  C
GAM1882  TADA2L   5'  TCCTTACGGGGTGGGACCGGCC 39428    ACC      A_  TC
                                TCC   ACGGGGTG  ACT  CC
                                |||   ||||||||  |||  ||
                                AGG   TGCCCCAC  TGG  GG
                                  AA_      CC   CC
GAM1882  TCIRG1   5'  CCCGTCACGGGGTGCTCC    25838     AC       AAC
                                TCC  CACGGGGTG   TTCC
                                |||  |||||||||  ||||
                                GGG  GTGCCCCAC   GAGG
                                  CA       ___
GAM1882  CALM1    3'  TATCCTTCACCCATTTTTCTGC 27862           CCGCTAC
                                TATCCTTCACCCG      CTGC
                                ||||||||||||       ||||
                                ATAGGAAGTGGGT      GACG
                                       AAAAA__
GAM1882  FN14     5'  TCCTGCGCCCGCCGCTGTCTGC 32492      TCA       AC
                                TCCT   CCCGCCGCT  CTGC
                                ||||   |||||||||  ||||
                                AGGA   GGGCGGCGA  GACG
                                  CGC        CA
GAM1882  LRP4     3'  TATCCTTCATCCCTGTCGC   42066         _  GCC____
                                TATCCTTCA CCC      GC
                                |||||||| |||      ||
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                                ATAGGAAGT GGG      CG
                                     A   ACAGIII
GAM1882  NOS2A    3'  CATCTTTCACCCACTTGC    8417      C       C_
                                TATC TTCACCCGC  GC
                                |||| |||||||||  ||
                                GTAG AAGTGGGTG  CG
                                  A        AA
GAM1882  SLC7A6   3'  TCCTTCATCCTACCTG      19596       C  GCCGC
                                TCCTTCA CC    TACCTG
                                |||||||  ||    ||||||
                                AGGAAGT GG    ATGGAC
                                   A _____
GAM1882  UPF3B    3'  TATCCTTCACTGTACCTG    38767         CCGCCGC
                                TATCCTTCAC      TACCTG
                                ||||||||||      ||||||
                                ATAGGAAGTG      ATGGAC
                                     AC_____
GAM1883  DMP1     3'  TTACTGGTGTCACTCCACAG  20602      ACC    C
                                TTACT   GTCAC TCCACAG
                                |||||   ||||| |||||||
                                AATGA   CAGTG AGGTGTC
                                   CCA    _
GAM1883  EPHA3    3'  CTACGCCTTCCACAGC      23440      C   ACC
                                CTAC GTC   TCCACAGC
                                |||| |||   ||||||||
                                GATG CGG   AGGTGTCG
                                  _   A__
GAM1883  HKR3     5'  CTCCGTCGCCTCCACAGC    23774    A    A
                                CT CCGTC CCTCCACAGC
                                || ||||| ||||||||||
                                GA GGCAG GGAGGTGTCG
                                 _    C
GAM1883  NDUFV1   5'  TCACGCTGTCACCTTCATAGC  28253      TACC      C  C
                                TTAC    GTCACCT CA AGC
                                ||||    ||||||| || |||
                                AGTG    CAGTGGA GT TCG
                                  CGA_      A  A
GAM1883  WASF3    3'  CATTCCTACCGTCACCTC    27378      A
                                CATT CTACCGTCACCTC
                                |||| ||||||||||||
                                GTAA GATGGCAGTGGAG
                                  G
GAM1883  C18orf2  3'  GCAAATCTGAAGAAGAGA    36407        C  C    AA
                                GCAAGTCT GG AGAA  AGA
                                |||||||| || ||||  |||
                                CGTTTAGA CT TCTT  TCT
                                     _ _    C_
GAM1883  COL1A1   3'  CCCAACGGGCAGAAAGGGA   6369     G   GTCTC       AA
                                CC CAA     GGCAGAAA  GA
                                || |||     ||||||||  ||
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                                GG GTT    CCGTCTTT  CT
                                 _  GC___      CC
GAM1883  GOLGA5   3'  CCCAAGTCTAGAAAAAGA   23048   G     CGGC
                                CC CAAGTCT   AGAAAAAGA
                                || |||||||   |||||||||
                                GG GTTCAGA   TCTTTTTCT
                                 _     ____
GAM1883  HOXD4    3'  CGTGAGGGCGTCAGAAAAAGAC 31173   CA  TCT  G
                                CG  AG   CG CAGAAAAAGAC
                                ||  ||   || ||||||||||
                                GC  TC   GC GTCTTTTTCTG
                                 AC  CC_  A
GAM1883  LUZP1    3'  CACAGGTTTCTCATCAAAAAGA 37956     AG__    GCAG
           C                     CGCA   TCTCG   AAAAAGAC
                                ||||   |||||   ||||||||
                                GTGT   AGAGT   TTTTTCTG
                                  CCAA    AG__
GAM1883  MAP3K14  3'  GCAGGGGCAGAAAAAGA    19540    A TCTC
                                GCA G   GGCAGAAAAAGA
                                ||| |   ||||||||||||
                                CGT C   CCGTCTTTTTCT
                                 _ C___
GAM1883  MKI67    3'  ACAAGTCTGAAGCTGGAGAAAG 14512       C_  A_  A
           A                     GCAAGTCT  GGC  GA AAAGA
                                ||||||||  |||  || |||||
                                TGTTCAGA  TCG  CT TTTCT
                                     CT   AC  C
GAM1883  MTR      3'  GCAATCATCCAAGAAAAAGA   7017     G  _  GGC
                                GCAA TC TC   AGAAAAAGA
                                ||||  ||  ||   |||||||||
                                CGTT AG AG   TCTTTTTCT
                                  _  T  GT_
GAM1883  NCOA6    5'  GCAAATCTTAAAGGAAAAGA   30437       CG C  A
                                GCAAGTCT  G AG AAAAGA
                                ||||||||  | || ||||||
                                CGTTTAGA  T TC TTTTCT
                                     AT _  C
GAM1883  NPAS1    5'  CCGAGTCTCCTGCAGCGGGAG  40870    CA    G_   AAAA
                                CCG  AGTCTC  GCAG   AG
                                |||  ||||||  ||||   ||
                                GGC  TCAGAG  CGTC   TC
                                  __     GA   GCCC
GAM1883  PLIN     3'  CCACAAGTTTGGTTAAAGAGA  15397       CTC  CAG   A
                                CCGCAAGT   GG   AAA AGA
                                ||||||||   ||   ||| |||
                                GGTGTTCA   CC   TTT TCT
                                     AA_  AA_   C
GAM1883  RERE     3'  AGCCCAGCAGGAAGA      29020     T     AAA
                                AGTC CGGCAG   AAGA
                                ||||  ||||||   ||||
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```
                                TCGG GTCGTC   TTCT
                                  _     C__
GAM1883  SNX3     3'  ACAAGCCTGGAGGAAGA     19134        C  C  AAA
                                GCAAGTCT GG AG   AAGA
                                |||||||| || ||   ||||
                                TGTTCGGA CC TC   TTCT
                                    _ _  C__
GAM1883  TAL1     3'  CCCCAGGTCTTAGGAAAGA   17280    G  A    CG CAGAA
                                CC CA GTCT  G     AAAGA
                                || || ||||  |     |||||
                                GG GT CAGA  C     TTTCT
                                 G  C    AT C____
GAM1883  TEM6     3'  CCGCAAGTTAGAGAAGGAG   35553        CTC  C    AA
                                CCGCAAGT   GG AGAA  AG
                                ||||||||   || ||||  ||
                                GGCGTTCA   TC TCTT  TC
                                     A__  _    CC
GAM1883  TNS      3'  ACAGGTGGCCAGAAAAAGA   35461     A  CTC   _
                                GCA GT   GGC AGAAAAAGA
                                ||| ||   ||| |||||||||
                                TGT CA   CCG TCTTTTTCT
                                  C  ___   G
GAM1883  TPD52L2  3'  AGCTCCTGAGAAAAAGAC    17631     CT GGC
                                AGT  C   AGAAAAAGAC
                                |||  |   ||||||||||
                                TCG  G   TCTTTTTCTG
                                  AG AC_
GAM1884  APPBP2   3'  TGCAATAAATCCTAAAGC    26884          ATTC
                                TGCAATAGATC    AGT
                                ||||||||||    |||
                                ACGTTATTTAG    TCG
                                      GATT
GAM1884  GALNT7   5'  TGCAACAGGTCATGTTCAA   38362        A   __
                                TGCAATAG TCAT  TCAG
                                |||||||| ||||  ||||
                                ACGTTGTC AGTA  AGTT
                                     C    CA
GAM1884  LAMC2    3'  TGCAATAGGTGTTCAGT     33123        ATCA
                                TGCAATAG    TTCAGT
                                ||||||||    ||||||
                                ACGTTATC    AAGTCA
                                     CAC_
GAM1884  MAGEB3   3'  TGCAACAGATCACTAAATAA   14326            C
                                TGCAATAGATCATT AGTAA
                                |||||||||||||| |||||
                                ACGTTGTCTAGTGA TTATT
                                         T
GAM1884  MAP3K7   3'  TGCAATGAAACAGTAAAA    17274       A  TCATT
                                TGCAAT GA    CAGTAAAA
                                |||||| ||    ||||||||
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```
                                ACGTTA CT    GTCATTTT
                                   _ TT___
GAM1884 MBNL    3' ACAGTACAATCAGTAAAA   34305     AT  T
                                ATAG  CA TCAGTAAAA
                                ||||  || |||||||||
                                TGTC  GT AGTCATTTT
                                  AT  T
GAM1884 MCCC1   3' GCATACAATCATTTAGTAAAAC 33561    ATA     C
                                GCA   GATCATT AGTAAAAC
                                |||   ||||||| ||||||||
                                CGT   TTAGTAA TCATTTTG
                                  ATG      A
GAM1884 PCDH11X 3' TAGATCATCAGAAAAC     37309       T   T
                                TAGATCAT CAG AAAAC
                                |||||||| ||| |||||
                                ATCTAGTA GTC TTTTG

                                   _  _
GAM1884 PCDH11Y 3' TAGATCATCAGAAAAC     37350       T   T
                                TAGATCAT CAG AAAAC
                                |||||||| ||| |||||
                                ATCTAGTA GTC TTTTG

                                   _  _
GAM1884 PIK3R3  3' GCTTGGTATTATTCAGTAAAAC 41443   AATAG  C
                                GC    AT ATTCAGTAAAAC
                                ||    || ||||||||||||
                                CG    TA TAAGTCATTTTG
                                 AACCA  A
GAM1884 RP2     3' TGCAAAGATCATTTGTAAA   27938     T      CA
                                TGCAA AGATCATT  GTAAA
                                ||||| ||||||||  |||||
                                ACGTT TCTAGTAA  CATTT
                                   _      A_
GAM1885 ADAMTS4 3' GAGGCCGAGGCAGGTCGAT   23006     AA   TA
                                GAGG  CCGG  TGGGTCGAT
                                ||||  ||||  |||||||||
                                CTCC  GGCT  GTCCAGCTA
                                  __   CC
GAM1885 NTRK2   5' TGGGGGTCCGGTATGCACCTCG 26149   A  AA      G __
                                TG GG  CCGGTATG G  TCG
                                || ||  |||||||| |  |||
                                AC CC  GGCCATAC T  AGC
                                 C  CA       G GG
GAM1885 ADAT1   3' CTTTGATTCTCTTGGC     28994    C      C  TGAC
                                CT TGATTCTC TG    GC
                                || |||||||| ||    ||
                                GA ACTAAGAG AC    CG
                                 A       A _____
GAM1885 AOAH    3' CCTTTGGGCCTGTGACG     45019    C  ATTCT
                                CCT TG    CCTGTGACG
                                ||| ||    |||||||||
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                                GGA AC    GGACACTGC
                                  A  CC___
GAM1885  BCL9    3'  CTCTGTTCTCCTATTGCA    20238      A       GAC
                                CTCTG TTCTCCTGT   GCA
                                ||||| |||||||||   |||
                                GAGAC AAGAGGATA   CGT
                                   _       A__
GAM1885  BMP6    3'  TCTAACCCTGTGGCG      11870      TCT     A
                                TCTGAT   CCTGTG CG
                                ||||||   |||||| ||
                                AGATTG   GGACAC GC
                                   ___     C
GAM1885  CAPS    3'  GACCTCTGGTCAGCATGGCG   19761        AT  TCC    A
                                GACCTCTG  TC   TGTG CG
                                ||||||||  ||   |||| ||
                                CTGGAGAC  AG   GTAC GC
                                     C_  TC_    C
GAM1885  GNRH1   5'  CCTCTAATTTTCTAATGA    9076         C  CT
                                CCTCTGATT TC  GTGA
                                ||||||||| ||  ||||
                                GGAGATTAA AG  TACT
                                     A  AT
GAM1885  PIGR    3'  GACCTCTATTCTTCTCCGTA   43704        A__     T
                                GACCTCTG   TTCTCC GTG
                                ||||||||   |||||| |||
                                CTGGAGAT   AAGAGG CAT
                                     AAG     _
GAM1885  SCG3    5'  CTGAAGTTCCTGTGACGC    29886     TTC
                                CTGA   TCCTGTGACGC
                                ||||   ||||||||||
                                GACT   AGGACACTGCG
                                  TCA
GAM1885  TNFAIP2  5'  CCTCTGACTCTGCCTCTGA   26635          _   G
                                CCTCTGATTCT CCT TGA
                                |||||||||| ||| |||
                                GGAGACTGAGA GGA ACT
                                      C   G
GAM1886  ATP2B4   3'  TGACAATGAAAAGTCCCA    43202         CAAA
                                TGACAATGAA    CCTA
                                |||||||||    ||||
                                ACTGTTACTT    GGGT
                                     TTCA
GAM1886  CANX    3'  CATGAAAAAACAAACCTAAGA  44662      CAAT
                                CATGA    GAACAAACCTAAGA
                                |||||    ||||||||||||||
                                GTACT    TTTGTTTGGATTCT
                                  TT__
GAM1886  CIT     3'  ATGAGAATGAACAGGAACAAG  43040      C       AACC
                                ATGA AATGAACA    TAAG
                                |||| ||||||||    ||||
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                                TACT TTACTTGT   GTTC
                                  C      CCTT
GAM1886 CLDN11   3' TGACGAGCAAACCTA      24664     AAT  A
                                TGAC   GA CAAACCTA
                                |||| || ||||||||
                                ACTG   CT GTTTGGAT
                                  ___  C
GAM1886 GNAI3    3' ATAACATAAAACCTAAG     27096       A   CAA
                                ATGACA TGAA   ACCTAAG
                                |||||| ||||  |||||||
                                TATTGT ATTT   TGGATTC
                                  _   ___
GAM1886 IL8RA    3' CATACAGTGAACAAACC     8441       A  A
                                CATG CA TGAACAAACC
                                |||| || ||||||||||
                                GTAT GT ACTTGTTTGG
                                  _ C
GAM1886 JRK      3' TGACTTACGTGCAAACCTAAGA 44503      A_   AA
             C                   TGAC  ATG  CAAACCTAAGAC
                                |||| ||| ||||||||||||
                                ACTG  TGC  GTTTGGATTCTG
                                  AA   AC
GAM1886 MAN1A1   3' ATGATAATAAACATAAAAGAC  45091     C       AACCT
                                ATGA AATGAACA    AAGAC
                                |||| ||||||||    |||||
                                TACT TTATTTGT    TTCTG
                                  A       ATT__
GAM1886 NRCAM    3' GACAATGACAGTAATCTAGGAC 22693        ACAAAC_   A
                                GACAATGA      CTA GAC
                                ||||||||      ||| |||
                                CTGTTACT      GAT CTG
                                    GTCATTA   C
GAM1886 PRKWNK3  3' TGAAAGGTAAACCTAAGAC   41539     C___
                                TGAA    AAACCTAAGAC
                                ||||    ||||||||||
                                ACTT    TTTGGATTCTG
                                  TCCA
GAM1886 PSCDBP   3' TGGGCATAAGCAAACCTAAGA  20182    ACA    A
                                TG   ATGA CAAACCTAAGA
                                ||   |||| ||||||||||
                                AC   TATT GTTTGGATTCT
                                 CCG    C
GAM1886 ROBO1    3' ATGACAATGACTAGACAA    39478         _____
                                ATGACAATGA    ACAA
                                ||||||||||    ||||
                                TACTGTTACT    TGTT
                                      GATC
GAM1887 ACHE     3' AGAGGAGGGGCCCCTGTGGC   8557         C  G __  C
                                AGAGGAGG GG T  TG GGC
                                |||||||| || |  || |||
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                                TCTCCTCC CC G  AC CCG
                                     _ G GG  A
GAM1887 ADAM19   3' TGAGAGGACGCGTTGGG    37780       G  GG   C
                                TGAGAGGA GC  GTTG GG
                                |||||||| ||  |||| ||
                                ACTCTCCT CG  CAA CC
                                     G __   _
GAM1887 ASPH     3' GAGAGGAGGGAAGGTGG    37136       C_   TGC
                                GAGAGGAGG  GGGT  GG
                                |||||||||  ||||  ||
                                CTCTCCTCC  TCCA  CC
                                     CT  ___
GAM1887 BAAT     3' TGAGAGAAGGTCCCGG     11792       AGGC   G
                                TGAGAGG   GGGTT CGG
                                |||||||   ||||| |||
                                ACTCTCT   TCCAG GCC
                                    ____   G
GAM1887 BCL10    5' GAGAGGAGGCGGAGCGG    19406          TT
                                GAGAGGAGGCGGG  GCGG
                                ||||||||||||  ||||
                                CTCTCCTCCGCCT  CGCC
                                      __
GAM1887 BMP1     3' CGGGAGGAGGCAGGGTGGC   25978    A     _   T
                                TG GAGGAGGC GGGT GC
                                || |||||||| |||| ||
                                GC CTCCTCCG CCCA CG
                                 C      T   C
GAM1887 CAPN1    3' TGGTAGGAGGCGAGGC     23258    AG       TT
                                TG  AGGAGGCGGG  GC
                                ||  ||||||||||  ||
                                AC  TCCTCCGCTC  CG
                                 CA       __
GAM1887 CBFA2T3  3' TGAGAGGAGTGGAGGGAGGG  23270       GC__  TTGC
                                TGAGAGGAG   GGG   GG
                                |||||||||   |||   ||
                                ACTCTCCTC   CCC   CC
                                     ACCT  TC__
GAM1887 CD1A     3' TGACGAGGAGGCTCATGGT   43409    _     G___
                                TGA GAGGAGGC   GGT
                                ||| ||||||||   |||
                                ACT CTCCTCCG   CCA
                                  G      AGTA
GAM1887 CDKN1A   3' AGAGGAGGGGGCGG       38501       C  GTT
                                AGAGGAGG GG   GCGG
                                |||||||| ||   ||||
                                TCTCCTCC CC   CGCC
                                     _ ___
GAM1887 CDKN2A   3' AAGCGGGGTGGGTTGTGGC   38464    A  A  C    C
                                GAG GG GG GGGTTG GGC
                                ||| || || |||||| |||
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                                TTC CC CC CCCAAC CCG
                                  G _ A     A
GAM1887 CELSR1   3' TGAGGGGAGGGGGTGG     30655     A    C   TGC
                                TGAG GGAGG GGGT   GG
                                |||| ||||| ||||   ||
                                ACTC CCTCC CCCA   CC
                                  C    _   ____
GAM1887 CLDN14   5' TGAGAGGAGGTGGCTTGGC   40325        CG   GC
                                TGAGAGGAGG  GGTT  GGC
                                ||||||||||  ||||  |||
                                ACTCTCCTCC  CCGA  CCG
                                      A_    A_
GAM1887 CLTB     3' TGAGAGGAGGCGTGAGGGGC  28229          GGTTGC
                                TGAGAGGAGGCG     GGC
                                ||||||||||||     |||
                                ACTCTCCTCCGC     CCG
                                       ACTCC_
GAM1887 COL4A3   3' TGAGTGGAGGCCAGTGG     36386     A     G   TGC
                                TGAG GGAGGC GGT   GG
                                |||| ||||||  |||   ||
                                ACTC CCTCCG TCA   CC
                                  A     G   ____
GAM1887 COL5A3   3' TGAGAGGAGGCTGGAC      31856          G  TT
                                TGAGAGGAGGC GG  GC
                                |||||||||||  ||  ||
                                ACTCTCCTCCG CC  TG
                                       A  __
GAM1887 COL6A2   3' TGGCAGGAGGCGTGGGGGC   38451    AG       _ TT
                                TG  AGGAGGCG GG  GC
                                ||  ||||||||  ||  ||
                                AC  TCCTCCGC CC  CG
                                 CG       A  CC
GAM1887 CTF1     3' CGGGAGGAGGCGGGGC      10626    A         TT
                                TG GAGGAGGCGGG  GC
                                ||  ||||||||||  ||
                                GC CTCCTCCGCCC  CG
                                 C          __
GAM1887 CXCL1    5' TGAGAGGAGCGGAAGAGC    11322         G   TT_
                                TGAGAGGAG CGGG   GC
                                |||||||||  ||||   ||
                                ACTCTCCTC GCCT   CG
                                      _    TCT
GAM1887 CYP8B1   3' TGAGAGGAGGGTTCGG      20511        GGC    G
                                TGAGAGGA   GGGTT CGG
                                ||||||||   |||||  |||
                                ACTCTCCT   CCCAA GCC
                                        ___    _
GAM1887 DTR      5' GAGAGGAGGCGGCGAGGC    12613           GT  C
                                GAGAGGAGGCGG  TG GGC
                                ||||||||||||  ||  |||
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                                CTCTCCTCCGCC  GC CCG
                                      __  T
GAM1887  EPHA8    3'  TGAGAGGAGGGCAGAGGC    33902         _   TTGC
                                TGAGAGGAGG CGGG   GGC
                                |||||||||| ||||   |||
                                ACTCTCCTCC GTCT   CCG
                                     C   ____
GAM1887  EPS15    5'  GAGGAGGCGGAGGGAGCGGC   12743          TT__
                                GAGGAGGCGGG   GCGGC
                                ||||||||||   |||||
                                CTCCTCCGCCT   CGCCG
                                      CCCT
GAM1887  EXO1     5'  TGAGCGGAGCCGATTGCGG   25700     A   G G
                                TGAG GGAG C GGTTGCGG
                                |||| |||| | ||||||||
                                ACTC CCTC G CTAACGCC
                                  G   _ G
GAM1887  F2RL3    3'  TGAGGGGATGAGGTTGCGG   19532     A   GGC
                                TGAG GGA   GGGTTGCGG
                                |||| |||   |||||||||
                                ACTC CCT   TCCAACGCC
                                  C   AC_
GAM1887  FBXL11   3'  GAGGGCAGGCTCTCCTGGC   29429     AG      GC___
                                GAGG  GCGGGTT    GGC
                                ||||  |||||||    |||
                                CTCC  CGTCCGA    CCG
                                  __      GAGGA
GAM1887  FGFR2    3'  TGAGAGGGGTTACA       35670       AGGCG
                                TGAGAGG    GGTTGCG
                                |||||||    |||||||
                                ACTCTCC    CCAATGT
                                     _____
GAM1887  FHIT     3'  GAGAGGCGGGGGGGCGG     12869       A  C   TT
                                GAGAGG GG GGG  GCGG
                                |||||| || |||  ||||
                                CTCTCC CC CCC  CGCC
                                   G  _   C_
GAM1887  FLOT2    3'  GAGGGAGGGCCGGGTGGC    20982     A    __    T
                                GAG GGAGG  CGGGT GC
                                ||| |||||  ||||| ||
                                CTC CCTCC  GCCCA CG
                                  _    CG    C
GAM1887  FOXD2    5'  GAGAGGTGAGATTGCGGC    20963       A GC
                                GAGAGG G  GGGTTGCGGC
                                |||||| |  ||||||||||
                                CTCTCC C  TCTAACGCCG
                                   A __
GAM1887  FZD3     3'  TGAGAGGAAGGTGTTAGGC   32633         CGG   C
                                TGAGAGGAGG   GTTG GGC
                                ||||||||||   |||| |||
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                                ACTCTCCTTC   CAAT CCG
                                     CA_   _
GAM1887  GBF1     3'  TGGAGGAGGTGGCCCAGGGC   20082    A      C  G   C
                                TG GAGGAGG GG TTG GGC
                                || ||||||| || ||| |||
                                AC CTCCTCC CC GGT CCG
                                 _      A  G   C
GAM1887  GFRA2    5'  GAGAGGCGGGCGATGGGC    11265    G      __ C
                                GAG AGGCGGGT  TG GGC
                                ||| ||||||||  || |||
                                CTC TCCGCCCG  AC CCG
                                  _       CT  _
GAM1887  GGA1     3'  TGGAGGAGGCCTAAGCTG    30050    A      __
                                TG GAGGAGGC  GGGTTG
                                || ||||||||  ||||||
                                AC CTCCTCCG  TTCGAC
                                 _       GA
GAM1887  GPC1     3'  TGGGAGGAGGCGGGGAGGAAGG 13264    A         TTGC__
                C                TG GAGGAGGCGGG     GGC
                                || ||||||||||      |||
                                AC CTCCTCCGCCC     CCG
                                 C          CTCCTT
GAM1887  GPC1     3'  TGGGAGCAGGCGGGTCCTGGC  13262    A  G       GC
                                TG GAG AGGCGGGTT  GGC
                                || ||| |||||||||  |||
                                AC CTC TCCGCCCAG  CCG
                                 C  G        GA
GAM1887  GSPT1    5'  TGAGGGAAGGCGGCGGGGC   13313     A      GT  C
                                TGAG GGAGGCGG  TG GGC
                                |||| ||||||||  || |||
                                ACTC CTTCCGCC  GC CCG
                                  C       __ C
GAM1887  HDAC5    5'  GAGGGGGTGGAGCTGCGG    40166     A  C  _
                                GAGG GG GG GTTGCGG
                                |||| || || |||||||
                                CTCC CC CC CGACGCC
                                  C  A  T
GAM1887  IL21R    3'  GAGGGGAGGCGACTTGGC    34755     A      G  _
                                GAG GGAGGCGG TTG C
                                ||| ||||||| ||| |
                                CTC CCTCCGCT AAC G
                                  C       G  C
GAM1887  INSRR    3'  GAGAGGAGGCGGAAGGAGGGC 42844           TTGC_
                                GAGAGGAGGCGGG    GGC
                                ||||||||||||    |||
                                CTCTCCTCCGCCT    CCG
                                        TCCTC
GAM1887  JPH3     5'  GAGAGGAGGACGCGG       34018         CGGGT
                                GAGAGGAGG    TGCGG
                                |||||||||    |||||
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                                CTCTCCTCC    GCGCC
                                     T____
GAM1887  KCNK4    3'  GAGGAGGCGGAGAGGC     37832         TTGC
                                GAGGAGGCGGG   GGC
                                ||||||||||   |||
                                CTCCTCCGCCT   CCG
                                     CT__
GAM1887  KIFC3    3'  TGAGGGGAGACGGGGC     24467     A       TT
                                TGAG GGAGGCGGG  GC
                                |||| |||||||||  ||
                                ACTC CCTCTGCCC  CG
                                  C       __
GAM1887  LBX1     3'  GAGGAGGCGGGAGTGGC     27283         TTGC
                                GAGGAGGCGGG   GGC
                                ||||||||||   |||
                                CTCCTCCGCCC   CCG
                                     TCA_
GAM1887  LFG      3'  GAGAGGAGGTGGAGGAGGG   44134        C   TTGC
                                GAGAGGAGG GGG   GG
                                ||||||||| |||   ||
                                CTCTCCTCC CCT   CC
                                     A   CCTC
GAM1887  LFG      3'  TGAGAGGATGTGGGTCTCGG  44155       GGC   TG
                                TGAGAGGA   GGGT  CGG
                                ||||||||   ||||  |||
                                ACTCTCCT   CCCA  GCC
                                     ACA    GA
GAM1887  LPIN2    3'  TGGGAGAAGGCTCATGTGG   31226    A      GGGT  C
                                TG GAGGAGGC    TG GG
                                || ||||||||    || ||
                                AC CTCTTCCG    AC CC
                                 C       AGT_  A
GAM1887  MAD2L2   3'  GAGAAGTCGAGGTTGCGGC   26804       G  _
                                GAGGAG CG GGTTGCGGC
                                |||||| || |||||||||
                                CTCTTC GC CCAACGCCG
                                    A  T
GAM1887  MAP1B    5'  TGAGAGAGGGCGGGGAGGC   25399       GA     TTGC
                                TGAGAG  GGCGGG   GGC
                                ||||||  ||||||   |||
                                ACTCTC  CCGCCC   CCG
                                    TC     CT__
GAM1887  MAP4     3'  TGAGAGGAGGTGTGGGGC    36275         C__   TT
                                TGAGAGGAGG   GGG  GC
                                ||||||||||   |||  ||
                                ACTCTCCTCC   CCC  CG
                                     ACA   __
GAM1887  MBP      3'  TGGGAGGAAGCCATGCCTGGC  44897    A       GG_   GC
                                TG GAGGAGGC   GTT  GGC
                                || ||||||||   |||  |||
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                                AC CTCCTTCG  CGG  CCG
                                 C       GTA  A_
GAM1887  MSI1     3'  TGCAGGGGAGGGGGCGGC    14651    _ A    C   T
                                TG AG GGAGG GGGT GC
                                || || ||||| |||| ||
                                AC TC CCTCC CCCG CG
                                 G  C    _   C
GAM1887  MSI1     3'  GAGGGAGGCGGCCAGGGGC   14641     A      GTTGC
                                GAG GGAGGCGG    GGC
                                ||| ||||||||    |||
                                CTC CCTCCGCC    CCG
                                  _      GGTCC
GAM1887  MUS81    5'  GAGAGGAGAGCCTGCGGC    36064        GC  G
                                GAGAGGAG  GG TTGCGGC
                                ||||||||  || |||||||
                                CTCTCCTC  TC GACGCCG
                                    __  G
GAM1887  MYF5     5'  TGAGAGGCAGGCGGTGC     24636        _     GT
                                TGAGAGG AGGCGG  TGC
                                ||||||| ||||||  |||
                                ACTCTCC TCCGCC  ACG
                                    G    __
GAM1887  NFIA     5'  GAGGGGGCGGCTGCGGC     43213      A    G
                                GAGG GGCGG TTGCGGC
                                |||| ||||| |||||||
                                CTCC CCGCC GACGCCG
                                  C    _
GAM1887  OAS2     3'  GAGAGGAGGGCTAGTGGC    32551         _ G   T
                                GAGAGGAGG C GGT GC
                                ||||||||| | ||| ||
                                CTCTCCTCC G TCA CG
                                     C A   C
GAM1887  OTP      3'  GAGGGGAGGCGGCGGGC     36993     A      GT  C
                                GAG GGAGGCGG  TG GGC
                                ||| ||||||||  || |||
                                CTC CCTCCGCC  GC CCG
                                  C       __ _
GAM1887  PACSIN1  3'  TGGGAGGGGAGGGGCGGC    45167    A   A  C   TT
                                TG GAGG GG GGG  GCGGC
                                || |||| || |||  |||||
                                AC CTCC CC CCC  CGCCG
                                 C    _ T   __
GAM1887  PHKG2    5'  TGAAGGAGGCGGGGG       7133      G        TTGC
                                TGA AGGAGGCGGG   GG
                                ||| ||||||||||   ||
                                ACT TCCTCCGCCC   CC
                                  _       _____
GAM1887  PPFIA3   5'  CGGGAGGAGGCGGGGG      41419    A         TTGC
                                TG GAGGAGGCGGG   GG
                                || ||||||||||   ||
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                                GC CTCCTCCGCCC   CC
                                 C        ____
GAM1887 PPP3R1   5' GAGAGGGGGCGAAGACGGC   44075      A    TT
                                GAGAGG GGCGGG  GCGGC
                                |||||| ||||||  |||||
                                CTCTCC CCGCTT  TGCCG
                                   C     C_
GAM1887 PPT2     3' TGGAAGGAGACCCCTGTGG   39930    AG     GGG  C
                                TG  AGGAGGC   TTG GG
                                ||  |||||||   ||| ||
                                AC  TCCTCTG   GAC CC
                                 CT      GG_  A
GAM1887 PRV1     3' GAGGGGCAGGAGGCGGC     43875     A    TT
                                GAGG GGCGGG  GCGGC
                                |||| ||||||  |||||
                                CTCC CCGTCC  CGCCG
                                  _     TC
GAM1887 RAD51L3  3' TGGAGGAGGCGGGAAGC     39475    A        TT
                                TG GAGGAGGCGGG  GC
                                || ||||||||||  ||
                                AC CTCCTCCGCCC  CG
                                 _         TT
GAM1887 RFNG     3' GAGGGGCACTGCGGC       44769     A   GG
                                GAGG GGCG  TTGCGGC
                                |||| ||||  |||||||
                                CTCC CCGT  GACGCCG
                                  _   __
GAM1887 RNH      5' GAGAGGAGGCTTGGATGGC   40603          __   T
                                GAGAGGAGGC  GGGT GC
                                ||||||||||  |||| ||
                                CTCTCCTCCG  CCTA CG
                                      AA   C
GAM1887 SH3GL1   3' GAGGCGGGGGTGCATTGGC   16668        T_  ___
                                GAGGCGGG  TGC   GGC
                                ||||||||  |||   |||
                                CTCCGCCC  ACG   CCG
                                     CC   TAA
GAM1887 SIX1     5' AGGGAGGGGGGCGCGG      25595    A    C   T
                                AG GGAGG GGG TGCGG
                                || ||||| ||| |||||
                                TC CCTCC CCC GCGCC
                                 _    _  C
GAM1887 SLC21A9  3' AGAGGAGGTACTGCTGTGGC   28557        CGG_   C
                                AGAGGAGG    GTTG GGC
                                ||||||||    |||| |||
                                TCTCCTCC    CGAC CCG
                                     ATGA    A
GAM1887 SLC22A12 3' TGGGAGGAGGCAGGCTTGTGGC 40338    A          _ C
                                TG GAGGAGGCGGGTT G GGC
                                || ||||||||||||| | |||
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                                AC CTCCTCCGTCCGA C CCG
                                 C          A A
GAM1887 SMG1    5' TGAGAGAGGCGGATGAAGGC  31513      G      TGC
                                TGAGAG AGGCGGGT  GGC
                                |||||| ||||||||  |||
                                ACTCTC TCCGCCTA  CCG
                                   _      CTT
GAM1887 SORCS2  3' TGAGAGGGAGGCCACGG    34066       A GC   TG
                                TGAGAGG G  GGGT  CGG
                                ||||||| |  ||||  |||
                                ACTCTCC C  TCCG  GCC
                                   _ __   GT
GAM1887 SOST    3' GAGGGGGGCCTTGCCGGC   36104     C   __  _
                                GAGG GGGT  TGC GGC
                                |||| ||||  ||| |||
                                CTCC CCCG  ACG CCG
                                  C   GA  G
GAM1887 SOX11   3' GAGGGGAGGCGGGAAGGGC  17020    A       TTGC
                                GAG GGAGGCGGG   GGC
                                ||| |||||||||   |||
                                CTC CCTCCGCCC   CCG
                                 C       TTC_
GAM1887 TFAP4   5' TGGGAGGGGCGGGAGGGAGG  17419   A   A    TTGC_
                                TG GAGG GGCGGG    GG
                                || |||| ||||||    ||
                                AC CTCC CCGCCC    CC
                                 C  _     TCCCT
GAM1887 TK1     3' GAGAGGAGGGAGCATGCGGC  17553       C   _
                                GAGAGGAGG GGGT TGCGGC
                                ||||||||| |||| ||||||
                                CTCTCCTCC CTCG ACGCCG
                                   _  T
GAM1887 TRIM8   3' GAGGGGAGGCGAGGAAGG   36282    A       TTGC
                                GAG GGAGGCGGG   GG
                                ||| |||||||||   ||
                                CTC CCTCCGCTC   CC
                                 C       CTT_
GAM1887 WHSC1L1 5' GAGAGGAGCCTGCGG      35711       G GGG
                                GAGAGGAG C  TTGCGG
                                |||||||| |  ||||||
                                CTCTCCTC G  GACGCC
                                   _ ___
GAM1887 ZNF2    5' GAGAGCGAGCCGTTGTGGC  34380     _  G GG   C
                                GAGAG GAG C  GTTG GGC
                                ||||| ||| |  |||| |||
                                CTCTC CTC G  CAAC CCG
                                  G  G __   A
GAM1888 CARPX   5' TGGCTGCTGCGCTCCG     33580        GTCTC
                                TGGCTGCTGC    GCTCCG
                                ||||||||||    ||||||
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                                ACCGACGACG    CGAGGC
                                      _____
GAM1888 CD53    3' TGGCTGCTGCCGTCAGTGAGT 8155         _  TCGCTCC
                                TGGCTGCTGC GTC      GAGT
                                |||||||||| |||      ||||
                                ACCGACGACG CAG      CTCA
                                      G  TCA____
GAM1888 DNMT3L  5' GGCTGCTGCCACGGCTCCGGGT 30062        GTCTC    A
                                GGCTGCTGC    GCTCCG GT
                                |||||||||    |||||| ||
                                CCGACGACG    CGAGGC CA
                                     GTGC_    C
GAM1888 ZFP36L1  3' GGCTGCTGGTTCCG       22287        C  CTCGC
                                GGCTGCTG GT    TCCG
                                |||||||| ||    ||||
                                CCGACGAC CA    AGGC
                                      _ _____
GAM1889 ACAA1   3' CCTGGGTGACCCAGGCTGC   11492    GC  AA       C
                                CC  GG  GACCCAGGC GC
                                ||  ||  |||||||||| ||
                                GG  CC  CTGGGTCCG CG
                                 A_  CA       A
GAM1889 ANKTM1   5' GCGGAAGCCCTGGAGAACTTC  28805       A   A  CC_  C
                                GCGGAAG CCC GG   GC TC
                                ||||||| ||| ||   || ||
                                CGCCTTC GGG CC   TG AG
                                    _  A  TCT  A
GAM1889 EN2     5' TCCGGCGGGGACGCGGGCCGCC 10963     _  AA   CCA
            TC                   TCCG CGG  GAC   GGCCGCCTC
                                ||||  |||  |||   |||||||||
                                AGGC GCC  CTG   CCGGCGGAG
                                  C   C_   CGC
GAM1889 M11S1   5' TCCGTGGGCGCAGGCCGCTTC  25331     C  AAGACC      C
                                TCCG GG     CAGGCCGC TC
                                |||| ||     |||||||| ||
                                AGGC CC     GTCCGGCG AG
                                  A  CGC___       A
GAM1889 OGG1    5' CGCCCTCCTTGGGCCGCCTC   32561    GGAAGA  CA_
                                CGC     CC   GGCCGCCTC
                                |||     ||   |||||||||
                                GCG     GG   CCGGCGGAG
                                  GGA___  AAC
GAM1890 AMPD3    5' CGCGGGGGCCGGGCGTTCAGAG 7896     AGCA   A  ____  CTC
            GG                   CGC    GCC GGC    AGA   GGG
                                |||    ||| |||    |||   |||
                                GCG    CGG CCG    TCT   CCC
                                  CCCC   C   CAAG  ___
GAM1890 CAPN7    5' GCGGCGGCGAGGACTCGG    30711    A  A  C   CAG
                                GC GC GC AGG   ACTCGG
                                || || || |||   ||||||
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                                CG CG CG TCC   TGAGCC
                                 C  C  C  ___
GAM1890 CDKN2A   3' GCAGCAGCTCCGCCACTCGGG 38473       CAG  AG
                                GCAGCAGC   GC  ACTCGGG
                                ||||||||   ||  |||||||
                                CGTCGTCG   CG  TGAGCCC
                                    AGG  G_
GAM1890 CHRNA5   5' AGCAGCTTCTGGCGGGCTCGGG 40746      CA__   AGA
                                AGCAGC   GGC   CTCGGG
                                ||||||   |||   ||||||
                                TCGTCG   CCG   GAGCCC
                                   AAGA   CCC
GAM1890 COL18A1  3' GCAGCCAGGTCCTGGG     39055        CAGA  C
                                GCAGCCAGG   CT GGG
                                |||||||||   || |||
                                CGTCGGTCC   GA CCC
                                    AG__  _
GAM1890 CSNK2A1  3' GCAGCAGCCGGGATTGAGG   12476        A  CA_  CTC
                                GCAGCAGCC GG   GA   GG
                                ||||||||| ||   ||   ||
                                CGTCGTCGG CC   CT   CC
                                    C  TAA  ___
GAM1890 DDX11    3' GCAGCAGCTGGGAATGG    36175        CA  CA  CTC
                                GCAGCAGC  GG  GA   GG
                                ||||||||  ||  ||   ||
                                CGTCGTCG  CC  CT   CC
                                    A_  __  TA_
GAM1890 FASN     3' GCCGCAGCCAGCAGGCTTGGG  19938    A      G   A  C
                                GC GCAGCCAG CAG CT GGG
                                || |||||||| ||| || |||
                                CG CGTCGGTC GTC GA CCC
                                 G       _  C  A
GAM1890 FOSB     3' CAGGGATGGGCGGACTCGGG   27532    CAGCCA   A
                                CAG     GGC GACTCGGG
                                |||     ||| ||||||||
                                GTC     CCG CTGAGCCC
                                  CCTAC_   C
GAM1890 FOXG1B   5' CGCAGTTGGACGCAGGCTCGGG 23500      CAGCCAG    A
                                CGCAG      GCAG CTCGGG
                                |||||      |||| ||||||
                                GCGTC      CGTC GAGCCC
                                   AACCTG_    C
GAM1890 HCFC1    3' GCAGCAGTTGGCAGTGCGG    43394       CCA    ACT
                                GCAGCAG   GGCAG   CGG
                                |||||||   |||||   |||
                                CGTCGTC   CCGTC   GCC
                                    AA_    AC_
GAM1890 HOXA3    3' CGCAGCAGCTGGGAACCGGG   36193        CA  CA   T
                                CGCAGCAGC  GG  GAC CGGG
                                |||||||||  ||  ||| ||||
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                                GCGTCGTCG  CC  TTG GCCC
                                     AC  __  _
GAM1890  ITCH    5'  GCATGGTACCGGGACTCGGG  36455    GCA_  A  CA
                                GCA   GCC GG  GACTCGGG
                                |||   ||| ||  ||||||||
                                CGT   TGG CC  CTGAGCCC
                                  ACCA  _ __
GAM1890  MAT1A   3'  CAGCAGCCAGGCGTCTGGG   44902         AGA  C
                                CAGCAGCCAGGC  CT GGG
                                ||||||||||||  || |||
                                GTCGTCGGTCCG  GA CCC
                                      CA_  _
GAM1890  ORM1    5'  ACGTGGAGCCAGGCAGTGCTGG 8296     CAGC       A_  C
                                ACG   AGCCAGGCAG  CT GG
                                |||   ||||||||||  || ||
                                TGC   TCGGTCCGTC  GA CC
                                  ACC_        AC  _
GAM1890  PKM2    3'  GCAGCCAGGCTCTGGG     15333         AGA  C
                                GCAGCCAGGC  CT GGG
                                ||||||||||  || |||
                                CGTCGGTCCG  GA CCC
                                     A__  _
GAM1890  PTK2B   3'  GCAGTGGCCAGGCAGCAG   19920     CA       ACT
                                GCAG  GCCAGGCAG  CGG
                                ||||  |||||||||  |||
                                CGTC  CGGTCCGTC  GTC
                                  AC       ___
GAM1890  RARA    3'  ACCCAGTGGTCAGGCAGAGGG 9700    G  CAGC      CTC
                                AC CAG   CAGGCAGA  GGG
                                || |||   ||||||||  |||
                                TG GTC   GTCCGTCT  CCC
                                 G  ACCA      ___
GAM1890  SNCG    3'  GCAGCAGCACAGGTGGACAGG 16933       _   CA  TC
                                GCAGCAGC CAGG  GAC  GG
                                |||||||| ||||  |||  ||
                                CGTCGTCG GTCC  CTG  CC
                                     T   AC  T_
GAM1890  TGFBR3  3'  GCATTTGCATCTTGCTACAG  17491       C  CG  ACT
                                GCATTTGCA CT  GC  CGG
                                ||||||||| ||  ||  |||
                                CGTAAACGT GA  CG  GTC
                                     A  A_  AT_
GAM1891  ABCA3   5'  CTCCGCACAGAGGGCTCCGG  9903       CA  CCGCT
                                CTCCGCAC  AG   CTCCGG
                                ||||||||  ||   ||||||
                                GAGGCGTG  TC   GAGGCC
                                     TC  CC___
GAM1891  CACNG3  5'  CTCCGCGCAAAGTTTCTGG  27234      AC   CCGC  CC
                                CTCCGC  CAAG   TCT  GG
                                ||||||  ||||   |||  ||
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                                GAGGCG  GTTT   AGA  CC
                                   C_   CAA_  __
GAM1891  CHRNA5   5'  CTCCGCGCCACAGCTCCCGCCG 40749      A  _  CG  T
            G                    CTCCGC CCA AGC  CTC CCGG
                                 |||||| ||| |||  ||| ||||
                                 GAGGCG GGT TCG  GGG GGCC
                                    C  G  A_  C
GAM1891  DPYD     5'  TCCGCACCAGCTCTG      41295        AGCC    CC
                                 TCCGCACCA   GCTCT  G
                                 |||||||||   |||||  |
                                 AGGCGTGGT   CGAGA  C
                                      ____   __
GAM1891  DUSP7    5'  CCCCGCACCGGGCTCG     42262        AAGCC   TCC
                                 CTCCGCACC    GCTC   G
                                 |||||||||    ||||   |
                                 GGGGCGTGG    CGAG   C
                                      CC___   ___
GAM1891  EGLN1    5'  CTCCGCACTCGGCGGGGCCGG  35164       CAA  CGCTCT
                                 CTCCGCAC   GC     CCGG
                                 ||||||||   ||     ||||
                                 GAGGCGTG   CG     GGCC
                                      AGC  CCCC__
GAM1891  MAN2A2   5'  CTCCGCGCCGCTCCG      25947       ACCAA    TC
                                 CTCCGC    GCCGC  TCCG
                                 ||||||    |||||  ||||
                                 GAGGCG    CGGCG  AGGC
                                      _____    __
GAM1891  MPHOSPH6 3'  CACCAAGCACCCCTGGG     25126        C    CC
                                 CACCAAGC GCTCT  GG
                                 |||||||| |||||  ||
                                 GTGGTTCG TGGGG  CC
                                      _    AC
GAM1891  NUMA1    5'  CTCTGCCTCGCGATTCTCCGGA 45241     C  ACCAA  CGC
                                 CTC GC    GC   TCTCCGGA
                                 ||| ||    ||   ||||||||
                                 GAG CG    CG   AGAGGCCT
                                   A  GAG__  CTA
GAM1891  PAX7     5'  CTCCACGCCTTCTTTCTCCGGA 30331       ACCAA   GC___
                                 CTCCGC    GCC    TCTCCGGA
                                 ||||||    |||    ||||||||
                                 GAGGTG    CGG    AGAGGCCT
                                      _____  AAGAA
GAM1891  PIK3R3   5'  TCTACACAGTCGCTCTCCGG   41450    CG   CA  C
                                 TC  CAC  AG CGCTCTCCGG
                                 ||  |||  || ||||||||||
                                 AG  GTG  TC GCGAGAGGCC
                                  AT   __  A
GAM1891  PRX      3'  CCGCACCAGGCCAAACCGG   34110        A   CTCT
                                 CCGCACCA GCCG   CCGG
                                 |||||||| ||||   ||||
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                                GGCGTGGT CGGT   GGCC
                                    C   TT__
GAM1891 PSCDBP   3' TCCCACCAAGCTGGGATCTGG 20181    G      CGCTC  C
                                TCC CACCAAGC    TC GG
                                ||| ||||||||    || ||
                                AGG GTGGTTCG    AG CC
                                  _      ACCCT  A
GAM1891 RAB36    3' CTCCGCACCACAGTCACGG   22240        AAGCC  TC  _
                                CTCCGCACC    GC  TC CGG
                                |||||||||    ||  || |||
                                GAGGCGTGG    TG  AG GCC
                                     _____ TC  T
GAM1891 RDS      3' GCACCAAGTGACACTTTGGA  7244         CC  T  CC
                                GCACCAAG  GC CT  GGA
                                ||||||||  || ||  |||
                                CGTGGTTC  TG GA  CCT
                                    AC  T  AA
GAM1891 STK11    3' CTCCGGCCGGGCCGCCAAAGCG 7832       CA  AA     CTC_
             G                   CTCCG  CC  GCCGCT   CGG
                                 |||||  ||  ||||||   |||
                                 GAGGC  GG  CGGCGG   GCC
                                   C_  CC     TTTC
GAM1891 TEAD3    5' CTCCGGCCGGGCCGCTCCGCCG 17373      CA  AA      _
             G                   CTCCG  CC  GCCGCTCT CCGG
                                 |||||  ||  |||||||| ||||
                                 GAGGC  GG  CGGCGAGG GGCC
                                   C_  CC       C
GAM1892 ADAM20   5' AGAGAACAAGGTGTGAGGCACT 19210          CG_  ATA
             G                   AGAGAACAAGG   GA   CACTG
                                 ||||||||||   ||   |||||
                                 TCTCTTGTTCC   CT   GTGAC
                                      ACA  CC_
GAM1892 AIM1     3' AGGAACAAGACAGATATGTTGG 45076    A         ATACAC
                                AG GAACAAGGCGGA     TGG
                                || ||||||||||||     |||
                                TC CTTGTTCTGTCT     ACC
                                 _          ATACA_
GAM1892 BACE2    5' GAGAAGGCGGAGGCCGG     39989     ACA      ATACA
                                GAGA   AGGCGGA    CTGG
                                ||||   |||||||    ||||
                                CTCT   TCCGCCT    GGCC
                                  ___      CC___
GAM1892 IL18     5' GAGGGCAAAATGCACTG     11454     AACAA      A
                                GAG    GGCGGAAT CACTG
                                |||    |||||||| |||||
                                CTC    CCGTTTTA GTGAC
                                  ______       C
GAM1892 LYZ      3' AAAGAACGGAATGTACTG    6951       ACAAG      AC
                                AGAGA    GCGGAAT  ACTG
                                |||||    |||||||  ||||
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                                TTTCT    TGCCTTA  TGAC
                                  _____      CA
GAM1892  MEN1     3'  GACTAAGGCGGAGCCTGG    39180    AC       ATACA
                                GA  AAGGCGGA    CTGG
                                ||  ||||||||    ||||
                                CT  TTCCGCCT    GACC
                                 GA       CG___
GAM1892  PABPN1   3'  AAGGGGAATTTACACTGG    21603     C   __
                                AAGG GGAA  TACACTGG
                                |||| ||||  ||||||||
                                TTCC CCTT  ATGTGACC
                                  _   AA
GAM1892  PCLO     3'  AGAGAACAGGGTGAGCAGA   45302        A____
                                AGAGAACA    GGCGGA
                                ||||||||    ||||||
                                TCTCTTGT    TCGTCT
                                     CCCAC
GAM1892  PLCB4    5'  GAGAACAAGGGGCAAGCGGCAC 9584          C  AATA___
            TGG                   GAGAACAAGG GG      CACTGG
                                ||||||||||  ||      ||||||
                                CTCTTGTTCC CC      GTGACC
                                     _  GTTCGCC
GAM1892  RAP1GDS1 3'  AGAGAATGAAGCGGAAGAAGCC 34507       CA       TACA___
            GCTGG                 AGAGAA  AGGCGGAA      CTGG
                                ||||||  ||||||||      ||||
                                TCTCTT  TTCGCCTT      GACC
                                   AC       CTTCGGC
GAM1892  SLC4A7   3'  AGAGAACAGAGTGGGAATCATT 18819        AG C_    A  C
            GG                    AGAGAACA  G  GGAAT CA TGG
                                ||||||||  |  ||||| || |||
                                TCTCTTGT  C  CCTTA GT ACC
                                     CT AC    _  A
GAM1892  SMARCA1  3'  AGAGTACCATGAATACACTGG  40049     A  AAGGCG
                                AGAG AC     GAATACACTGG
                                |||| ||     ||||||||||
                                TCTC TG     CTTATGTGACC
                                  A  GTA___
GAM1892  SPTBN4   3'  AGAGATCAAGGCAGCATTG    36082      A       AATA  C
                                AGAGA CAAGGCGG    CA TG
                                ||||| ||||||||    || ||
                                TCTCT GTTCCGTC    GT AC
                                  A       _____  A
GAM1892  TGM2     3'  AGAGGAGAAGGCAGTCGCTGG  21437      AAC      AATACA
                                AGAG   AAGGCGG     CTGG
                                ||||   |||||||     ||||
                                TCTC   TTCCGTC     GACC
                                  CTC      AGC___
GAM1892  THRA     5'  AGAGACTGGGGTGGGCACACTG 17515       ACAA  C  AA
            G                     AGAGA    GG GG  TACACTGG
                                |||||    || ||  ||||||||
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                                TCTCT   CC CC  GTGTGACC
                                  GACC  A  C_
GAM1892  TPD52L2  3'  AGAGAAGCAGGTTTTGTACACT 17630      CA   CGGAA
             GG                   AGAGAA  AGG    TACACTGG
                                |||||| |||    ||||||||
                                TCTCTT  TCC    ATGTGACC
                                  CG   AAAAC
GAM1893  ABR     3'  CAGTAGAAGGAACAGTCA    35006       A   ATAC
                                CAGTAGAA GAA    TCA
                                |||||||| |||    |||
                                GTCATCTT CTT    AGT
                                    C   GTC_
GAM1893  ACT     5'  TGAGTAGAATACTCAA     33886   C     AAGAA
                                A AGTAGA    ATACTCAA
                                | ||||||    ||||||||
                                A TCATCT    TATGAGTT
                                C     _____
GAM1893  AF1Q    3'  CACAGTAGGGAGAGAACA    27723       AA  _
                                TACAGTAG  AGA AATA
                                ||||||||  ||| ||||
                                GTGTCATC  TCT TTGT
                                    CC   C
GAM1893  ARCN1   3'  ATAGAAAGAAAAACCTAAAG   11647         T  TC
                                GTAGAAAGAAA AC  AAAG
                                |||||||||| ||  ||||
                                TATCTTTCTTT TG  TTTC
                                      T  GA
GAM1893  BCL9    3'  CAGTTGAAAGAAAATAGTCCAA 20235     A      TAC__
             AG                   CAGT GAAAGAAA    TCAAAG
                                |||| ||||||||    ||||||
                                GTCA CTTTCTTT    GGTTTC
                                  A       TATCA
GAM1893  CALB1   3'  TACATAGAAAGAAAATCCA   22313     G       TAC
                                TACA TAGAAAGAAA   TCA
                                |||| ||||||||||  |||
                                ATGT ATCTTTCTTT   GGT
                                  _        TA_
GAM1893  EIF2S3  3'  CAGCCTGGAGGTACTCAAAG  10863     AGAAA  AA
                                CAGT    GA  TACTCAAAG
                                ||||    ||  |||||||||
                                GTCG    CT  ATGAGTTTC
                                  GAC__  CC
GAM1893  ITPKB   3'  GCAGAGAAACTCAA       13645      AA   AT
                                GTAGA  GAA  ACTCAA
                                |||||  |||  ||||||
                                CGTCT  CTT  TGAGTT
                                   __  __
GAM1893  NARS    3'  AGTAGAAAGAAAAACAGAAAG  21216         T  TC
                                AGTAGAAAGAAA AC  AAAG
                                |||||||||||| ||  ||||
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                                TCATCTTTCTTT TG  TTTC
                                       T  TC
GAM1893  WNT1     3'  TACAGTGGAAGGAAATACT   24086       A   A
                                TACAGT GAA GAAATACT
                                |||||| ||| ||||||||
                                ATGTCA CTT CTTTATGA
                                   C   C
GAM1893  ZNF24    3'  TACAGTGGAAGAAATACC    28089       A   A
                                TACAGT GAA GAAATACT
                                |||||| ||| ||||||||
                                ATGTCA CTT CTTTATGG
                                   C   _
GAM1894  CORO2A   3'  CTCCCAGAGTGCTGGGA     18076         C    A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _    C
GAM1894  EGFL5    5'  TCCCAGAACTGTTGCACGGT   44536           CTAGGAAC
                                TCCCAGAGCTG       CGGT
                                ||||||||||        ||||
                                AGGGTCTTGAC       GCCA
                                      AACGT___
GAM1894  ITCH     3'  CTCCCAGAGTGCTAGGA     36454         C
                                CTCCCAGAG TGCTAGGA
                                ||||||||| ||||||||
                                GAGGGTCTC ACGATCCT
                                      _
GAM1894  KDR      5'  CCCAGAACTCGGGAGCCGGT   13940         GCTA   A
                                CCCAGAGCT    GGA CCGGT
                                |||||||||    ||| |||||
                                GGGTCTTGA    CCT GGCCA
                                     GC__   C
GAM1894  PLAT     3'  CCAAAGCTGCTCACGG      37446           AGGAAC
                                CCAGAGCTGCT      CGG
                                ||||||||||       |||
                                GGTTTCGACGA      GCC
                                      GT_____
GAM1894  TBX6     3'  CTCCCAGAGTGCTGGGA     38855         C    A
                                CTCCCAGAG TGCT GGA
                                ||||||||| |||| |||
                                GAGGGTCTC ACGA CCT
                                      _    C
GAM1894  BDKRB1   5'  TGTAGTTGGGTTTTCTGA    8737       C  T    CAAC
                                TGTAG TG GGTT    CTGA
                                ||||| || ||||    ||||
                                ACATC AC CCAA    GACT
                                   A  _    AA__
GAM1894  CCND1    3'  GTAGCTGTGGGTTGAACCTGGA 38217           _  C      A
              C                  GTAGCTGTGG TT AACCTG AC
                                ||||||||||  || ||||||  ||
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                                CATCGACACC AA TTGGAC TG
                                      C  C     C
GAM1894  CCND3    3'  TGTGGTGTGGTTCCTG      12066     AGC      CAA
                                TGT   TGTGGTT   CCTG
                                |||   |||||||   ||||
                                ACA   ACACCAA   GGAC
                                  CC_      ___
GAM1894  EGFR     3'  TGTGGCTTGGTCCTG       23402     A   G    TCAA
                                TGT GCT TGGT    CCTG
                                ||| ||| ||||    ||||
                                ACA CGA ACCA    GGAC
                                  C  _   ____
GAM1894  FLG      5'  TGTGGCTGTGATGGGACCCTGA 43366     A       TCAA_
                                TGT GCTGTGGT    CCTGA
                                ||| ||||||||    |||||
                                ACA CGACACTA    GGACT
                                  C       CCCTG
GAM1894  FLG      3'  TGTGGCTGTGATGGGACCCTGA 43366     A       TCAA_
                                TGT GCTGTGGT    CCTGA
                                ||| ||||||||    |||||
                                ACA CGACACTA    GGACT
                                  C       CCCTG
GAM1894  GABRE    3'  GTGGCTGTGGTTTTGAAC    35077     A       CAACC
                                GT GCTGTGGTT    TGAAC
                                || |||||||||    |||||
                                CA CGACACCAA    ACTTG
                                 C       A____
GAM1894  LAD1     3'  TGTGCTGTGACCTG        24495     A     GTTCA
                                TGT GCTGTG    ACCTG
                                ||| ||||||    |||||
                                ACA CGACAC    TGGAC
                                 _     ______
GAM1894  NPEPPS   3'  TAGAGATATTCAACCTGAACA  26721     CTGTG
                                TAG    GTTCAACCTGAACA
                                |||    ||||||||||||||
                                ATC    TAAGTTGGACTTGT
                                  TCTA_
GAM1894  PRODH    3'  TGCAGCTGTGGTGATGGCCTG  32280           TCAA_
                                TGTAGCTGTGGT    CCTG
                                ||||||||||||    ||||
                                ACGTCGACACCA    GGAC
                                      CTACC
GAM1894  SCAMP1   3'  TGCAGCTGCGGTCTGGAC     38068           TCAAC   A
                                TGTAGCTGTGGT    CTG AC
                                ||||||||||||    ||| ||
                                ACGTCGACGCCA    GAC TG
                                      ______  C
GAM1894  SRR      3'  TGTGCTGTGGTTTAAACC     34969     A       C_
                                TGT GCTGTGGTT  AACC
                                ||| |||||||||  ||||
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                                ACA CGACACCAA  TTGG
                                  _       AT
GAM1894 WHSC1L1  5' TGCGGCTGGCAGCCCGGCCTG 35717    TA  _ TG   AA
                                TG  GCT G  GTTC  CCTG
                                ||  ||| |  ||||  ||||
                                AC  CGA C  CGGG  GGAC
                                 GC   C GT    CC
GAM1895 ADAMTS3  3' TCTTTGGTGATTTCTTCC    30645     A   A
                                TCT TTG TGATTTCTTTT
                                ||| ||| ||||||||||
                                AGA AAC ACTAAAGAAGG
                                  _  C
GAM1896 B3GALT3  3' TGGAATATGACACTC       37671          TCAA
                                TGGAATATGA    CATTT
                                ||||||||||    |||||
                                ACCTTATACT    GTGAG

                                      ____
GAM1896 CD3E     3' GGCCTCTGTCAACATTTA    8814     AATA  A
                                GG    TG TCAACATTTA
                                ||    || ||||||||||
                                CC    AC AGTTGTAAAT
                                 GGAG  _
GAM1896 CFTR     3' TGTCCCATGTCAACATTTA   7960     GAA    A
                                TG   TATG TCAACATTTA
                                ||   |||| ||||||||||
                                AC   GTAC AGTTGTAAAT
                                 AGG   _
GAM1896 ESR1     3' TGGAACATGGCAGCATTTA   6541          AT  A
                                TGGAATATG  CA CATTTA
                                |||||||||  || ||||||
                                ACCTTGTAC  GT GTAAAT
                                     C_  C
GAM1896 GAN      3' GAAATGAGTCAACATTTA    35144     T   _
                                GAA ATGA TCAACATTTA
                                ||| |||| ||||||||||
                                CTT TACT AGTTGTAAAT
                                  _   C
GAM1896 HNRPH2   3' TGGTATAAGAGCAACATTTA  33333     A   T  T
                                TGG ATA GA CAACATTTA
                                ||| ||| || |||||||||
                                ACC TAT CT GTTGTAAAT
                                  A   T  C
GAM1896 IMPG2    5' GGAAAGACCTAACATTTA    32188      TAT   _
                                GGAA   GATC AACATTTA
                                ||||   |||| ||||||||
                                CCTT   CTGG TTGTAAAT
                                  T__    A
GAM1896 LY94     3' GGAATATACAACCATTTA    22104         ATCAA
                                GGAATATG    CATTTA
                                ||||||||    ||||||
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                                CCTTATAT    GTAAAT
                                    GTTG_
GAM1896 NCALD    3' TGGAATATGTTACCATTT    36774        ATCAA
                                TGGAATATG    CATTT
                                |||||||||    |||||
                                ACCTTATAC    GTAAA
                                    AATG_
GAM1896 OLR1     3' GGAATATTCAACATTTA     14941       GA
                                GGAATAT  TCAACATTTA
                                |||||||  ||||||||||
                                CCTTATA  AGTTGTAAAT
                                  __
GAM1896 TDG      3' GGATATATCAACATTTA     17358     A   A
                                GGA TATG TCAACATTTA
                                ||| |||| ||||||||||
                                CCT ATAT AGTTGTAAAT
                                  _  _
GAM1896 VLGR1    3' TGGAATATGAACATCC      37012        TCA
                                TGGAATATGA   ACATTT
                                ||||||||||   ||||||
                                ACCTTATACT   TGTAGG
                                   ___
GAM1897 CRY2     3' CCTTCCCACTCTCAGATTTGC 43582          ATCATA
                                CCTTTCCACTCT     TTGC
                                ||||||||||||     ||||
                                GGAAGGGTGAGA     AACG
                                    GTCTA_
GAM1897 MGAM     3' CTTCCACTCTCCTCTTGC    43654        ATCATA
                                TTTCCACTCT     TTGC
                                ||||||||||     ||||
                                GAAGGTGAGA     AACG
                                    GGAG__
GAM1897 NBEA     3' TTTCCACCAGAGATATTGC   45434        CTATC
                                TTTCCACT    ATATTGC
                                ||||||||    |||||||
                                AAAGGTGG    TATAACG
                                    TCTC_
GAM1897 SFPQ     3' ACCTTTCCACTTTTCAAAAGC 22856          CTA  TATT
                                ACCTTTCCACT  TCA   GC
                                ||||||||||   |||   ||
                                TGGAAAGGTGA  AGT   CG
                                    AA_  TTT_
GAM1897 OPHN1    3' GTGGTTCTTGACTTTTTTGG  14969     A  G  T
                                GTG TTC TGA CTTTTTTGG
                                ||| ||| ||| |||||||||
                                CAC AAG ACT GAAAAAACC
                                  C  A  _
GAM1898 MORC     3' TACTATGACTAAATAATAAAAT 30875       TGGCT
                TA                TACTATG    ATAATAAAATTA
                                  |||||||    ||||||||||||
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                                ATGATAC    TATTATTTTAAT
                                    TGATT
GAM1898  CASQ2    3'  ATTATACTGCACACTTAACA   10281        A    GTTG
                                ATTATACT CACAC    TAACA
                                |||||||| |||||    |||||
                                TAATATGA GTGTG    ATTGT
                                     C    A___
GAM1898  NAP1L3   3'  TATTATACTACAACAGCC    21213          _ C
                                TATTATACTACA CA GTT
                                |||||||||||| || |||
                                ATAATATGATGT GT CGG
                                       T _
GAM1898  TEX15    3'  TATTAACTATAAATGCTGTAAC 36326      T   CACAC
             A                   TATTA ACTA    GTTGTAACA
                                |||||| ||||    |||||||||
                                ATAAT TGAT    CGACATTGT
                                  _   ATTTA
GAM1899  CCND1    3'  TTAAAAATAAACTGTAT     38229          A
                                TTAAAAATAGA CTGTAT
                                |||||||||| ||||||
                                AATTTTTATTT GACATA
                                          _
GAM1899  P29      3'  TTAAAAAGGGAACTGTACA   31773        TA
                                TTAAAAA  GAACTGTATA
                                |||||||  ||||||||||
                                AATTTTT  CTTGACATGT
                                    CC
GAM1899  CLN2     3'  TTCAAGAGAATATAGCCC    7560       _      A
                                TTTAA AGAATATA CCC
                                ||||| |||||||| |||
                                AAGTT TCTTATAT GGG
                                   C       C
GAM1900  HMOX1    3'  TGGTCATGGCCGTGTCAAC   13413     C   AT   A
                                TGG CATG  CGT TCAAT
                                ||| ||||  ||| |||||
                                ACC GTAC  GCA AGTTG
                                  A   CG   C
GAM1900  IGFBP4   3'  TGGCTGTGACCACAAATGGGGT 11410     CA     TAT   TAA_
                                TGGC  TGATCG   CAA    GGT
                                ||||  ||||||   |||    |||
                                ACCG  ACTGGT   GTT    CCA
                                  AC      ___   TACC
GAM1900  RASSF1   3'  TGGCTTTGATTAGCAAATAAGG 28428     CA   C_   TC
             T                   TGGC  TGAT  GTA  AATAAGGT
                                ||||  ||||  |||  ||||||||
                                ACCG  ACTA  CGT  TTATTCCA
                                  AA   AT   __
GAM1900  AGA      3'  CGTACATGTACATTTATTAA  6184     AAA
                                CG   ATGTACATTTATTAA
                                ||   ||||||||||||||
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                                GC   TACATGTAAATAATT
                                 ATG
GAM1900  TFDP2    5'  CCAACATTCACATTTATT    26618      AAATG
                                CCGA    TACATTTATT
                                ||||    ||||||||||
                                GGTT    GTGTAAATAA
                                  GTAA_
GAM1901  IDH3A    3'  TACATTTGTGTCTTTGTA    24376      C  C
                                TACGT TG GTCTTTGTA
                                ||||| || |||||||||
                                ATGTA AC CAGAAACAT
                                   A  A
GAM1901  INHBB    3'  CGTCTCTGTCTTTGTGCTTT  13555      GC       AA
                                CGTCT  GTCTTTGT  GTTTT
                                |||||  ||||||||  |||||
                                GCAGA  CAGAAACA  CGAAA
                                   GA       __
GAM1902  AXIN1    3'  GTGGACGTGTCGGTGGTGG   41392           CGACA
                                GTGGACGTGTCG    TGG
                                ||||||||||||    |||
                                CACCTGCACAGC    ACC
                                      CACC_
GAM1902  AXIN1    3'  GTGGACGTGGTGGTGGACG   41391         TCGCGACA
                                GTGGACGTG       TGGACG
                                |||||||||       ||||||
                                CACCTGCAC       ACCTGC
                                     CACC_____
GAM1903  CMKLR1   5'  CTGTGACCAACAGAAAGT    19826    A       TAAC
                                CT TGACCAACA    AAGT
                                || |||||||||    ||||
                                GA ACTGGTTGT    TTCA
                                 C       CT__
GAM1903  NT5E     3'  CACTATGCTTAACAAGT     14858        ACCAACA
                                CACTATG      TAACAAGT
                                |||||||      ||||||||
                                GTGATAC      ATTGTTCA
                                    GA_____
GAM1903  NUP62    3'  CACAGGATAGCATAACAAGT  29599     TAT  CCAA
                                CAC   GA   CATAACAAGT
                                |||   ||   ||||||||||
                                GTG   CT   GTATTGTTCA
                                  TC_  ATC_
GAM1903  NXT1     3'  ACTATGACAAACAAGT      29907        CAACAT
                                ACTATGAC     AACAAGT
                                ||||||||     |||||||
                                TGATACTG     TTGTTCA
                                     T_____
GAM1903  PFKFB4   3'  CACTATGGCTAACAAAT     21286        ACCAACA
                                CACTATG      TAACAAGT
                                |||||||      ||||||||
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                                GTGATAC      ATTGTTTA
                                   CG_____
GAM1903  RNMT     3'  ACACTATGTTTTTAAAACAAGT 19144        ACCAACAT
             A                   ACACTATG       AACAAGTA
                                 ||||||||       ||||||||
                                 TGTGATAC       TTGTTCAT
                                    AAAAATT_
GAM1903  SMG1     3'  ACTGTTGCCAAGCAACAAGT   31498     A_ A   CA
                                 ACT  TG CCAA  TAACAAGT
                                 |||  || ||||  ||||||||
                                 TGA  AC GGTT  GTTGTTCA
                                   CA  _   C_
GAM1903  TIRAP    3'  CCATGATATAACAAGT      38091       CCAAC
                                 CTATGA    ATAACAAGT
                                 ||||||    |||||||||
                                 GGTACT    TATTGTTCA
                                    A____
GAM1904  DSC1     3'  TAGCAGATGCTGCTAACA    35933        C
                                 TAGCAGA GCTGCTAACA
                                 ||||||| ||||||||||
                                 ATCGTCT CGACGATTGT
                                    A
GAM1905  CLASP1   5'  TCAATATCACTTCGAGA     42247       C       A
                                 TCAATA CATTTCGA GA
                                 |||||| |||||||| ||
                                 AGTTAT GTGAAGCT CT
                                    A      _
GAM1905  DDX4     3'  AACACCATTTGTAT        35927          CGAAGA
                                 AATACCATTT     GTAT
                                 ||||||||||     ||||
                                 TTGTGGTAAA     CATA
                                        _______
GAM1905  HEPH     3'  TCAATACCTTCCAAGTGT    31344         AT   G   A
                                 TCAATACC  TTC AAG GT
                                 ||||||||  ||| ||| ||
                                 AGTTATGG  AAG TTC CA
                                    __   G   A
GAM1905  ZNF215   3'  AATATCAACTCCAAGAGTAT   29913      C  T   G
                                 AATA CA TTC AAGAGTAT
                                 |||| || ||| ||||||||
                                 TTAT GT GAG TTCTCATA
                                   A  T   G
GAM1905  SYT4     3'  TTGCATATTTAATAATTCAACT 41666         CCAACAA__
             G                   TTGCATGT       CAACTG
                                 ||||||||       ||||||
                                 AACGTATA       GTTGAC
                                    AATTATTAA
GAM1905  UCP3     3'  TTGCATGTCATAGCACCCCTG  17860         CAACA  AA
                                 TTGCATGTC    AC  CTG
                                 |||||||||    ||  |||
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                                AACGTACAG    TG  GAC
                                     TATCG  GG
GAM1906 ADRBK2   3'  AGCTGACCCCAAGCCGAAGGGT 23128    A_      AAGCT  _
             CC                   GGC  ACCCCAAGC    GG CC
                                  |||  |||||||||    || ||
                                  TCG  TGGGGTTCG    CC GG
                                    AC       GCTTC  A
GAM1906 ARHGEF12 3'  AGGTGCGTCATAAAAGCTGGCC 31634    CAACCC  AGC
                                  AGG     CA   AAGCTGGCC
                                  |||     ||   |||||||||
                                  TCC     GT   TTCGACCGG
                                    ACGCA_  ATT
GAM1906 B4GALT2  3'  AGGCAGTGCAGGGGCTGGCCC  36134     ACCCCAA   A__
                                  AGGCA     GCA   GCTGGCCC
                                  |||||     |||   ||||||||
                                  TCCGT     CGT   CGACCGGG
                                     CA_____   CCC
GAM1906 BRF1     3'  GGCTGCCCCAAGCCTG     11338     AA      AAG
                                  GGC  CCCCAAGC   CTG
                                  |||  ||||||||   |||
                                  CCG  GGGGTTCG   GAC
                                    AC       ___
GAM1906 CACNB1   3'  AGGCAACCCCTGGGCACCATCC 8774          AA_  AA   GG
                                  AGGCAACCCC   GC  GCT  CC
                                  ||||||||||   ||  |||  ||
                                  TCCGTTGGGG   CG  TGG  GG
                                       ACC  __   TA
GAM1906 CHD2     3'  AGACAACTTCAAGCAAGCT   10437        CC
                                  AGGCAAC  CAAGCAAGCT
                                  |||||||  ||||||||||
                                  TCTGTTG  GTTCGTTCGA
                                     AA
GAM1906 CREBL2   5'  AGGCGGCCCCAAACGC      10574     AA      AAGCTG
                                  AGGC  CCCCAAGC     GC
                                  ||||  ||||||||     ||
                                  TCCG  GGGGTTTG     CG
                                    CC       _______
GAM1906 DBH      5'  GGCCGGGCAGGCTGGCCC    8971     AACCCCAA   A
                                  GGC       GCA GCTGGCCC
                                  |||       ||| ||||||||
                                  CCG       CGT CGACCGGG
                                    GCC_____   C
GAM1906 DGCR6    3'  AAGCAGACAGCAGCAGGCTGGC 24981      _  CCCA    A
             CC                   AGGCA AC    AGCA GCTGGCCC
                                  |||||  ||    |||| ||||||||
                                  TTCGT  TG    TCGT CGACCGGG
                                     C  TCG_    C
GAM1906 DGKG     5'  GGGGACCGAAGCTGGCC     10656    CA   CCAAGC
                                  GG  ACC     AAGCTGGCC
                                  ||  |||     |||||||||
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                                CC  TGG     TTCGACCGG
                                 CC   C_____
GAM1906  EFNB1    3'  GCACAGCGGGCTGGCCC     20718     A CCCA   AA
                                GCA C    AGC  GCTGGCCC
                                ||| |    |||  ||||||||
                                CGT G    TCG  CGACCGGG
                                 _ ____   CC
GAM1906  EGFL4    3'  GGCTGACCCCAGGCAGGCGCC  41576     A_     A   A  TG
                                GGC  ACCCCA GCA GC  GCC
                                |||  |||||| ||| ||  |||
                                CCG  TGGGGT CGT CG  CGG
                                  AC     C  C  __
GAM1906  EIF4G1   3'  AGGCAGCCCCAAGCCATCCTGC 22406       A       AAG  G
              C                  AGGCA CCCCAAGC   CT GCC
                                |||||| ||||||||   || |||
                                TCCGT GGGGTTCG   GG CGG
                                   C       GTA  A
GAM1906  EN1      5'  GGCGCCTCGGCGCTGGCC    10917     AAC  CAA  AA
                                GGC   CC   GC  GCTGGCC
                                |||   ||   ||  |||||||
                                CCG   GG   CG  CGACCGG
                                  C__  AGC  __
GAM1906  GFRA2    3'  AGCCAGCCTCAGGCACAGCCC  11260    G  A  C  A   AGC
                                AG CA CC CA GCA   TGGCCC
                                || || || || |||   ||||||
                                TC GT GG GT CGT   GTCGGG
                                 G  C  A  C  ___
GAM1906  GGT1     5'  AGGGGCCCCAAGCCTTGCC    23571     CAA       AAGCTG
                                AGG   CCCCAAGC     GCC
                                |||   ||||||||     |||
                                TCC   GGGGTTCG     CGG
                                  CC_       GAA___
GAM1906  GLP1R    3'  GGGAACCCCAAGGGC       13140     C        CAAGCT
                                GG AACCCCAAG     GGC
                                || |||||||||     |||
                                CC TTGGGGTTC     CCG
                                 C        _______
GAM1906  GNA15    5'  GGCAACCCCCAGCCCAGCCGGC 40904          A   A_
              CC                  GGCAACCCC AGC  AGCTGGCCC
                                |||||||||| |||  |||||||||
                                CCGTTGGGG TCG  TCGGCCGGG
                                     G   GG
GAM1906  GNB2     5'  AGGCAGCTCCTGGCCGCTGGCC 23595       ACC  AA  AA
              C                   AGGCA   CC  GC  GCTGGCCC
                                |||||   ||  ||  ||||||||
                                TCCGT   GG  CG  CGACCGGG
                                   CGA  AC  G_
GAM1906  HIP12    3'  AGGGAGCCCCACGCTGGCC   42392     CAA    AGCAA
                                AGG   CCCCA    GCTGGCC
                                |||   |||||    |||||||
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                                TCC  GGGGT   CGACCGG
                                  CTC   G____
GAM1906 HOXA3   3' GGCAGCCCAGCTGGCC     36194     A  CAAGCA
                                GGCA CCC    AGCTGGCC
                                |||| |||    ||||||||
                                CCGT GGG    TCGACCGG
                                  C  _______
GAM1906 HOXD4   5' AGCTGGGACTGGGCAAGCTGGC 31166    AACCCCAA_
             C                   GGC       GCAAGCTGGCC
                                |||       ||||||||||
                                TCG       CGTTCGACCGG
                                  ACCCTGACC
GAM1906 LCP1    3' GGAAGCCACAACAAGCTGG   14107   C  C  CA
                                GG AA CC  AGCAAGCTGG
                                || || ||  ||||||||||
                                CC TT GG  TTGTTCGACC
                                 _  C  TG
GAM1906 LTK     3' AGGCCAGCCCCGAGACAGGCCC 14264     AA_   A  CAA  T
                                AGGC  CCCC AG  GC GGCCC
                                ||||  |||| ||  || |||||
                                TCCG  GGGG TC  TG CCGGG
                                  GTC   C ___  T
GAM1906 LZTS1   3' AGCAGCCCCGCTGGC      34260     A   AAGCAA
                                GGCA CCCC    GCTGGC
                                |||| ||||    ||||||
                                TCGT GGGG    CGACCG
                                  C  _______
GAM1906 NDUFA10 3' GGCTGCCGAGAGCTGGCC   21234    AACC  A  CA
                                GGC   CC AG  AGCTGGCC
                                |||   || ||  ||||||||
                                CCG   GG TC  TCGACCGG
                                  AC__  C  __
GAM1906 OAS2    3' AGCTAACCCCACGGTTGGC   32547    _     AGCAAGC
                                GGC AACCCCA     TGGC
                                ||| |||||||     ||||
                                TCG TTGGGGT     ACCG
                                  A     GCCA___
GAM1906 PCSK5   5' GGCGCCCCCTCTGCTGGCCC  26235    AA   AAGCAA
                                GGC  CCCC    GCTGGCCC
                                |||  ||||    ||||||||
                                CCG  GGGG    CGACCGGG
                                  CG   AGA___
GAM1906 PIK3R3  3' AGCCAGCCCCAAGCTGCT   41433   G  A     AA
                                AG CA CCCCAAGC  GCT
                                || || ||||||||  |||
                                TC GT GGGGTTCG  CGA
                                 G  C      A_
GAM1906 PMP2    3' GGAGCCCCTTCAAGCTGGC   15421   CAA   AAG
                                GG  CCCC  CAAGCTGGC
                                ||  ||||  |||||||||
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                                CC  GGGG  GTTCGACCG
                                 TC_   AA_
GAM1906 POU5F1   5' AGGCGCCCCAAGCCGGGGGCC 15466     AA      AAGCT
                                AGGC CCCCAAGC   GGCC
                                |||| |||||||   ||||
                                TCCG GGGGTTCG   CCGG
                                  C_      GCCC_
GAM1906 PREB     3' AGGCAACCTCAGCTGTGGACCC 30138       CCA  AAGC  _
                                AGGCAACC  AGC   TGG CCC
                                ||||||||  |||   ||| |||
                                TCCGTTGG  TCG   ACC GGG
                                    AG_  AC__  T
GAM1906 PRKCABP  3' AGGCGCCCCAAGCCAGCAGGCC 29667     AA      A  T
                                AGGC CCCCAAGC AGC GGCC
                                |||| |||||||| ||| ||||
                                TCCG GGGGTTCG TCG CCGG
                                  C_      G  T
GAM1906 PRKY     3' AGCTGGTCTCAAACTCCTGGCC 15685    AACCC_   AAG
                                GGC    CAAGC  CTGGCC
                                |||    |||||  ||||||
                                TCG    GTTTG  GACCGG
                                 ACCAGA   AG_
GAM1906 PSEN1    3' AAGCAACCTCAGGTTCAGACTG 28734       C  AG__  AG
           GCC                   AGGCAACC CA   CA  CTGGCC
                                |||||||| ||   ||  ||||||
                                TTCGTTGG GT   GT  GACCGG
                                    A  CCAA  CT
GAM1906 RAD9     3' GGCAACCCTAGCCACACACT  21374       CA  AA___
                                GGCAACCC  AGC   GCT
                                ||||||||  |||   |||
                                CCGTTGGG  TCG   TGA
                                    A_  GTGTG
GAM1906 RCN1     5' GGCTAACCCCAGGCGGCC   16204    _    A  AAGCT
                                GGC AACCCCA GC   GGCC
                                ||| ||||||| ||   ||||
                                CCG TTGGGGT CG   CCGG
                                 A     C _____
GAM1906 RXRA     3' GGAGGCCCCAAGCCCCGCCC  16429   CAA     AAG  G
                                GG  CCCCAAGC  CT GCCC
                                ||  ||||||||  || ||||
                                CC  GGGGTTCG  GG CGGG
                                 TCC      ___  G
GAM1906 SFTPD    5' AGGAGCTCCAAGCAAACT   16600    CAACC
                                AGG   CCAAGCAAGCT
                                |||   ||||||||||
                                TCC   GGTTCGTTTGA
                                 TCGA_
GAM1906 SH3GL1   3' AGGCAGATCCCAGCTGGCC  16664     AC_   AGCAA
                                AGGCA  CCCA   GCTGGCC
                                |||||  ||||   |||||||
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                                TCCGT  GGGT   CGACCGG
                                  CTA  _____
GAM1906 TFEB    5' GGCAGCCCCAAGCCAGGCCC  45136    A      AAGCT
                                GGCA CCCCAAGC   GGCCC
                                |||| ||||||||   |||||
                                CCGT GGGGTTCG   CCGGG
                                  C      GT___
GAM1906 TNFRSF8  3' AGGGGCCCCGGGAGCTGGCC  10309    CAA   AAGCA
                                AGG  CCCC   AGCTGGCC
                                |||  ||||   ||||||||
                                TCC  GGGG   TCGACCGG
                                 CC_  CCC__
GAM1906 UROS    3' AGGCCAGCCCCAGGTCAGGTCC 7505     AA_   AG_ AGCT _
                                AGGC  CCCCA  CA   GG CC
                                ||||  |||||  ||   || ||
                                TCCG  GGGGT  GT   CC GG
                                  GTC   CCA  ____ A
GAM1906 USP6    5' AGGCAACCCAGGCAGAGCT   45023       CAA  _
                                AGGCAACCC  GCA AGCT
                                |||||||||  ||| ||||
                                TCCGTTGGG  CGT TCGA
                                     TC_  C
GAM1906 ZNF134   5' AGCAACCCCGAGCTTCTG    18322       A  AAG
                                GGCAACCCC AGC  CTG
                                ||||||||| |||  |||
                                TCGTTGGGG TCG  GAC
                                     C  AA_
GAM1906 B4GALT6  3' CCACTAAGAGCGCG      40847       CAAGCG
                                CCACTAAGA    GCGCG
                                |||||||||    |||||
                                GGTGATTCT    CGCGC
                                          _______
GAM1906 CCNA1    3' TGTCATAAGACAAGCAG    19387    C  C
                                TG CA TAAGACAAGCGG
                                || || ||||||||||||
                                AC GT ATTCTGTTCGTC
                                 A  _
GAM1906 CD5     3' TGCCACTCGGGGCAGCAGCGC  30547      AAGACA
                                TGCCACT    AGCGGCGC
                                |||||||    ||||||||
                                ACGGTGA    TCGTCGCG
                                    GCCCCG
GAM1906 CHAC    3' TACCACTGAGGCAATGTTGG  37816      A  A  GC_____
                                TGCCACT AG CAA     GG
                                ||||||| || |||     ||
                                ATGGTGA TC GTT     CC
                                    C  C  ACAAIII
GAM1906 DDX10   3' TGCCAGTAAGACAAAGGCA  20576      C       C
                                TGCCA TAAGACAAG GGCG
                                ||||| ||||||||| ||||
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                                ACGGT ATTCTGTTT CCGT
                                  C       _
GAM1906 FOXO1A   5' TGCTCTCCCCAGCGGCGCGCC 12892    CA  AAGACA
                                TGC  CT     AGCGGCGCGCC
                                |||  ||     ||||||||||
                                ACG  GA     TCGCCGCGCGG
                                  A_  GGGG__
GAM1906 KCNA6    5' GCCACTAGGACGGCGC      13813        A   AAGC
                                GCCACTA GAC    GGCGC
                                ||||||| |||    |||||
                                CGGTGAT CTG    CCGCG
                                    C  ____
GAM1906 LHCGR    3' TGCACTGAGACAGGG       6933      C   A     A C
                                TGC ACT AGACA G GG
                                ||| ||| ||||| | ||
                                ACG TGA TCTGT C CC
                                  _  C    _ _
GAM1906 MN1      3' TGCCACTAAGCAGGTAC     14598          A  AGC  CG
                                TGCCACTAAG CA   GG  C
                                |||||||||| ||   ||  |
                                ACGGTGATTC GT   CC  G
                                      _ ___  AT
GAM1906 PDE4B    3' TGCCATCAAGGCAAGTCAAC   15154      C    A   _
                                TGCCA TAAG CAAG CGGC
                                ||||| |||| |||| ||||
                                ACGGT GTTC GTTC GTTG
                                   A    C    A
GAM1906 SOX12    3' CCATTAAGGCAGCGACGCC   28032     C    ACAA     _
                                CCA TAAG    GCGGCG CGCC
                                ||| ||||    |||||| ||||
                                GGT ATTC    CGTCGC GCGG
                                  A   _____      T
GAM1907 CACNB2   5' AGCCATTCTCAACTCGGGAGA 8790           CCAGTA
                                AGCCATTCTTAAT     GAGA
                                ||||||||||||      ||||
                                TCGGTAAGAGTTG     CTCT
                                      AGCC__
GAM1907 ERBB4    3' GCCATTCTTACTTGCTAGGAC  23456         ATCCAG   A
                                GCCATTCTTA     TAG GAC
                                ||||||||||     ||| |||
                                CGGTAAGAAT     ATC CTG
                                     GAACG_  _
GAM1907 HIP1     3' AGCCATTCTAATCTGAGC    23748         T   C_
                                AGCCATTCT AATC  AGT
                                ||||||||| ||||  |||
                                TCGGTAAGA TTAG  TCG
                                     _   AC
GAM1907 MYBL1    3' GCAACCTAATTTAGTAGAGAC 41978    CATT     CC
                                GC   CTTAAT  AGTAGAGAC
                                ||   ||||||  |||||||||
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                                CG   GGATTA  TCATCTCTG
                                 TT__     AA
GAM1907  TCF1    3'  AGCCTTCCCAGTAGAG     8085      A   TTAAT
                                AGCC TTC    CCAGTAGAG
                                |||| |||    |||||||||
                                TCGG AAG    GGTCATCTC
                                  _  _____
GAM1907  TPMT    3'  AGCCATTTTTAGTAAAGA    7492        C  AATCC
                                AGCCATT TT    AGTAGAGA
                                ||||||| ||    ||||||||
                                TCGGTAA AA    TCATTTCT
                                   A _____
GAM1908  ABH     3'  CGTGGGTTCCAAGGCAA     40740      AAC      T
                                CGTG   TCCAAGG CGA
                                ||||   ||||||| |||
                                GCAC   AGGTTCC GTT
                                  CCA      _
GAM1908  CACNB2  5'  CGTGTGGCTTCACCAAGCT   8792      AA_  C  AGG
                                CGTG   CT CA   TCGAGCT
                                ||||   || ||   |||||||
                                GCAC   GA GT   GGTTCGA
                                  ACC  A  ___
GAM1908  CLTCL1  3'  CACCTGAACTCCATCAGCT   41880     G       AGG  G
                                CAC TGAACTCCA   TC AGCT
                                ||| |||||||||   || ||||
                                GTG ACTTGAGGT   AG TCGA
                                 G        ___  _
GAM1908  HOXD4   5'  GTGAACTCGCCTCTGAG     31179       CAAG  ___
                                GTGAACTC    GTC   GAG
                                ||||||||    |||   |||
                                CACTTGAG    CGG   CTC
                                     _____  AGA
GAM1909  ALDH3A2  3'  TTTCTTACTATTTTTGGTATGA 42924        TAAGGA_
           T                     TTTCTTATT      GTATGAT
                                 |||||||||      |||||||
                                 AAAGAATGA      CATACTA
                                      TAAAAAC
GAM1909  COX10   3'  TTTCTTATTTGGGGAGCAT   10557         AA
                                TTTCTTATTT  GGAGTAT
                                ||||||||||  |||||||
                                AAAGAATAAA  CCTCGTA
                                     CC
GAM1909  EEF1B2  3'  TTATTTAAATGCCATGATCC  34432        GAG
                                TTATTTAAG   TATGATCC
                                |||||||||   ||||||||
                                AATAAATTT   GTACTAGG
                                     ACG
GAM1909  ETFA    3'  TTTCTTTTTAAGGCATGATCC  6546       A     AG
                                TTTCTT TTTAAGG  TATGATCC
                                ||||||  |||||||  ||||||||
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                                AAAGAA AAATTCC  GTACTAGG
                                   _     __
GAM1909  ETV3     3'  TTTCTTGGGCAGGAGTATGAT  23480       ATTTA
                                TTTCTT    AGGAGTATGAT
                                ||||||    ||||||||||
                                AAAGAA    TCCTCATACTA
                                   CCCG_
GAM1909  NCSTN    5'  TTATTTAAGGGGATATATATC  43944         A_   _
                                TTATTTAAGG  GTATG ATC
                                ||||||||||  ||||| |||
                                AATAAATTCC  TATAT TAG
                                      CC    A
GAM1909  SEC22L1  3'  TCTTTTGTTTAAGGAGTA    22203     A__
                                TCTT   TTTAAGGAGTA
                                ||||   ||||||||||
                                AGAA   AAATTCCTCAT
                                  AAC
GAM1910  CDH17    3'  TTTGCAGAGTAGGTTGT     19792       GA  A
                                TTTGCGG  TA GGTTGT
                                |||||||  || ||||||
                                AAACGTC  AT CCAACA
                                    TC  _
GAM1910  FOSL1    5'  TCTGCGGGGTACACGGCT    24140        __  A
                                TTTGCGGG  ATA GGTT
                                ||||||||  ||| ||||
                                AGACGCCC  TGT CCGA
                                     CA   G
GAM1910  FPRL1    5'  TTTGCAAATAGGTTGT      11151        ATA
                                TTTGCGGG   AGGTTGT
                                ||||||||   |||||||
                                AAACGTTT   TCCAACA
                                     A__
GAM1910  FZD1     3'  TTTGCAGGAGCTGAGTTGT   18623         TAA_
                                TTTGCGGGA    GGTTGT
                                |||||||||    ||||||
                                AAACGTCCT    TCAACA
                                      CGAC
GAM1910  NFYA     3'  TTTGGTTGAGAAGGTTGT    14769     CGG  T
                                TTTG   GA AAGGTTGT
                                ||||   || ||||||||
                                AAAC   CT TTCCAACA
                                  CAA  C
GAM1910  PCDHA1   3'  TTGGTTAGAGAAGGTTGT    36401     CG_  T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA10  3'  TTGGTTAGAGAAGGTTGT    36568     CG_  T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
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                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA11  3'  TTGGTTAGAGAAGGTTGT    36583    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA12  3'  TTGGTTAGAGAAGGTTGT    33136    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA13  3'  TTGGTTAGAGAAGGTTGT    33137    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA2   3'  TTGGTTAGAGAAGGTTGT    36470    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA3   3'  TTGGTTAGAGAAGGTTGT    33142    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA4   3'  TTGGTTAGAGAAGGTTGT    36492    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA5   3'  TTGGTTAGAGAAGGTTGT    36501    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA6   3'  TTGGTTAGAGAAGGTTGT    33147    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA7   3'  TTGGTTAGAGAAGGTTGT    36523    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910  PCDHA8   3'  TTGGTTAGAGAAGGTTGT    36531    CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
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                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910 PCDHA9   3' TTGGTTAGAGAAGGTTGT    30419     CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910 PCDHAC1  3' TTGGTTAGAGAAGGTTGT    36624     CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910 PCDHAC2  3' TTGGTTAGAGAAGGTTGT    36634     CG_   T
                                TTG   GGA AAGGTTGT
                                |||   ||| ||||||||
                                AAC   TCT TTCCAACA
                                  CAA   C
GAM1910 SLC1A3   3' TTGTGGGATGAAAATTGT    20047     C     _
                                TTG GGGAT AAGGTTGT
                                ||| ||||| ||||||||
                                AAC CCCTA TTTTAACA
                                  A     C
GAM1910 BRIP1    3' ACTTACAACAGAGTTTAAC    36780     GC  G
                                AC  AC AACAGAGTTTAAC
                                ||  || ||||||||||||
                                TG  TG TTGTCTCAAATTG
                                 AA  _
GAM1910 CCND2    3' ACCCGCATGGAGTTTA       12041     A    CGAACA
                                GCC CGCA     GAGTTTA
                                ||| ||||     |||||||
                                TGG GCGT     CTCAAAT
                                  _    AC____
GAM1910 F2RL3    3' GCCCAGGAAGCAGAGTTT     19518     ACG  C   _
                                GCC   CA GAA CAGAGTTT
                                |||   || ||| ||||||||
                                CGG   GT CTT GTCTCAAA
                                  ___  C   C
GAM1910 ICMT     3' GCCACGCACAGGGCAGGC     29653          AA_   A
                                GCCACGCACG   CAG GT
                                ||||||||||   ||| ||
                                CGGTGCGTGT   GTC CG
                                      CCC   _
GAM1910 PTPN2    5' AGCTGGCGCGAGCAGAGC     15908     CAC  A   A
                                AGC   GC CGA CAGAGT
                                |||   || ||| ||||||
                                TCG   CG GCT GTCTCG
                                  AC_  C   C
GAM1910 RP2      3' GCCACGCACAGGGTGAGC     27932          AACA
                                GCCACGCACG    GAGT
                                ||||||||||    ||||
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                                CGGTGCGTGT   CTCG
                                     CCCA
GAM1910 ZFHX1B   3' CACGTGCATGAACAGCTTAAC 31337    __  C    GA
                                CAC  GCA GAACA  GTTTAAC
                                |||  ||| |||||  |||||||
                                GTG  CGT CTTGT  CGAATTG
                                  CA   A    __
GAM1911 DNAI2    3' TAATTTTACAAGAATTAGGA  35747          TTA
                                TAATTTTACAAG   TAGGA
                                ||||||||||||   |||||
                                ATTAAAATGTTC   ATCCT
                                       TTA
GAM1911 KRAS2    3' TGTAACTTTACATTCATCAGG 37888          AG   _
                                TGTAATTTTACA  TTAT AGG
                                ||||||||||||  |||| |||
                                ACATTGAAATGT  AGTA TCC
                                       A_    G
GAM1912 CSPG2    3' TACAGTAGGCTGGTATACATTA 20479        AGA    A  A
              G                  TACAGTA   TGGTG TA ATTAG
                                |||||||   ||||| || |||||
                                ATGTCAT   ACCAT AT TAATC
                                    CCG    _ G
GAM1912 RPA3     5' TAAGTAAGAAGAATGTGGTAAA 16383   C      TG___   A
              TTAG                  A AGTAAGA    GTG TAAATTAG
                                | |||||||    ||| |||||||||
                                A TCATTCT    CAC ATTTAATC
                                 T      TCTTA   C
GAM1912 ZNF141   3' TACAGTAAGATGTGACAA    18347          G
                                TACAGTAAGATG TGATAA
                                |||||||||||| ||||||
                                ATGTCATTCTAC ACTGTT
                                       _
GAM1913 ENTPD1   5' TAATAGGAGAAAAGGCATA   12126          AA
                                TAATAGGAGAAAA  TATA
                                ||||||||||||  ||||
                                ATTATCCTCTTTT  GTAT
                                       CC
GAM1913 SCN3A    3' ATAGGAGTTTATATAATG    27950       AAAAAA
                                ATAGGAG     TATATAATG
                                |||||||     |||||||||
                                TATCCTC     ATATATTAC
                                    AA____
GAM1914 CDKN2B   3' TCCGCTTCTCTGTGTTTCG   38552    A  AG  AC
                                TCC GT  TT  GTGTTTCG
                                ||| ||  ||  ||||||||
                                AGG CG  GA  CACAAAGC
                                  _ AA  GA
GAM1914 GABRR2   3' TCCAGTAGCTGCTGCATT    13044         AC_
                                TCCAGTAGTT   GTGTT
                                |||||||||   |||||
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                                AGGTCATCGA  CGTAA
                                      CGA
GAM1914 GPRC5B   3' TCTGGTATTACGTGTCT    32178   CA  G
                                TC  GTA TTACGTGTTT
                                ||  ||| ||||||||||
                                AG  CAT AATGCACAGA
                                 AC  _
GAM1914 HGF      3' TCCAGTAGTTGTCT       45323        TACG
                                TCCAGTAGT   TGTTT
                                |||||||||   |||||
                                AGGTCATCA   ACAGA
                                           ____
GAM1914 MEIS2    3' CAGTAGTTATAACTCTCG   33538        CGTG
                                CAGTAGTTA   TTTCG
                                |||||||||   |||||
                                GTCATCAAT   AGAGC
                                      ATTG
GAM1914 PTGS1    3' TCCAGTGTTGCCTC       38743       A  TACG
                                TCCAGT GT   TGTTTC
                                |||||| ||   ||||||
                                AGGTCA CA   ACGGAG
                                  _ ____
GAM1914 SLC38A2  3' TCCAGTAGGTGAGCATTT   33277        TTAC
                                TCCAGTAG   GTGTTT
                                ||||||||   ||||||
                                AGGTCATC   CGTAAA
                                     CACT
GAM1914 SPK      5' TCCAGTAGTGTGGGTC     22072        TAC  TT
                                TCCAGTAGT  GTG  TC
                                |||||||||  |||  ||
                                AGGTCATCA  CAC  AG
                                     ___  CC
GAM1915 KIR2DL5  3' TAAGTTTCACTGCTGACT   33923          _
                                TAAGTTTTATTGCT ACT
                                |||||||||||||| |||
                                ATTCAAAGTGACGA TGA
                                         C
GAM1915 ZNF141   3' TATTAAGTATGAACATTGCTA 18348        TT___
                                TATTAAGT    TATTGCTA
                                ||||||||    ||||||||
                                ATAATTCA    GTAACGAT
                                     TACTT
GAM1916 ADCY6    5' GGTAGGCAACAAGGGTA    34175     A   AAATC
                                GGTA GCAG    CAAGGGTA
                                |||| ||||    ||||||||
                                CCAT CGTT    GTTCCCAT
                                  C  _____
GAM1916 BTAF1    5' GGTAAGCAGGGGTCCAAGA  43670        AAA
                                GGTAAGCAG   TCCAAGG
                                |||||||||  |||||||
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                                CCATTCGTC   AGGTTCT
                                     CCC
GAM1916  CX3CR1    3'  TGGAAAGCAGAAGTCTAAGAGG 43300     T       A  C  _
              C                   TGG AAGCAGAA TC AAG GGT
                                  ||| |||||||| || ||| |||
                                  ACC TTCGTCTT AG TTC CCG
                                    T       C  A   T
GAM1916  FMOD      3'  TGGTAAGCAAAGTCTGGC     12933          AATCCAAG
                                  TGGTAAGCAGA       GGT
                                  ||||||||||        |||
                                  ACCATTCGTTT       CCG
                                        CAGA____
GAM1916  NFE2L1    3'  TGGTAGGCAGAGGCCCGAG    17337       A     AA   A
                                  TGGTA GCAGA  TCC AG
                                  ||||| |||||  ||| ||
                                  ACCAT CGTCT  GGG TC
                                     C    CC   C
GAM1916  SCN8A     3'  TGGTAAGCAGACGACGTTTGGT 30535          AATCCAAG
              A                   TGGTAAGCAGA       GGTA
                                  ||||||||||        ||||
                                  ACCATTCGTCT       CCAT
                                        GCTGCAAA
GAM1917  BCAS2     3'  TTGAAAGCTTTAAATAAGGATC 25243         ATT_    A_
              CTT                   TTGAAAGC    GATGA  ATCCTT
                                  ||||||||    |||||  ||||||
                                  AACTTTCG    TTATT  TAGGAA
                                       AAAT     CC
GAM1917  DAPP1     3'  TTGAAAGAAAATCCT       30818        CATTGAT
                                  TTGAAAG      GAAATCCT
                                  |||||||      ||||||||
                                  AACTTTC      TTTTAGGA
                                       ________
GAM1917  OCLN      3'  AAAGCATAAAATCCTT      14899        TGAT
                                  AAAGCAT    GAAATCCTT
                                  |||||||    |||||||||
                                  TTTCGTA    TTTTAGGAA
                                       ____
GAM1917  CHES1     3'  GGTAATTTTGGCTTTTTCG   23285         CTCG  AC_
                                  GGTAATTTT    GG   TTTCG
                                  |||||||||    ||   |||||
                                  CCATTAAAA    CC   AAAGC
                                       ____ GAA
GAM1918  ATP11A    3'  TGTGTGCATGCATG        44193       CTAAA
                                  TGTGT     GCATGCGTG
                                  |||||     |||||||||
                                  ACACA     CGTACGTAC
                                       _____
GAM1918  KIF5A     3'  CTTTGTGTGTGTGCATGCGTG 22547     A     CTAAA
                                  CT TGTGT     GCATGCGTG
                                  || |||||     |||||||||
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                                GA ACACA    CGTACGCAC
                                 A    CACA_
GAM1918 MHC2TA   3' CTGGTGTGTGCACGCGTG   6981    A_   CTAAA
                                CT  TGTGT    GCATGCGTG
                                ||  |||||    |||||||||
                                GA  ACACA    CGTGCGCAC
                                 CC    _____
GAM1918 UC28     3' CTATGTGTCAGGCACTGTG   34687       TAAA   GC
                                CTATGTGTC    GCAT  GTG
                                |||||||||    ||||  |||
                                GATACACAG    CGTG  CAC
                                      TC__    A_
GAM1918 ADRB3    3' AAGAGGATGGTGAAAACCCACT 6173      A   AAGA GG
             T                   AAGA GAT    G  AATCCACTT
                                ||||  |||    |  |||||||||
                                TTCT CTA    C  TTGGGTGAA
                                  C   CCA_ TT
GAM1918 ANKTM1   3' AGAGGATAAAAGATGGTTTACT 28801     A       GAATCC
             T                   AGA GATAAGAGG     ACTT
                                |||  |||||||||      ||||
                                TCT CTATTTTCT     TGAA
                                  C        ACCAAA
GAM1918 ARHGEF12 3' GAGAAGAAAGCTTCCACT    31639    T      AA
                                GA AAGAGGG  TCCACT
                                ||  |||||||  ||||||
                                CT TTCTTTC  AGGTGA
                                 C      GA
GAM1918 BACH2    3' AAGAAGAGGAGAGGTCACT    34767       TA    GAATC
                                AAGAAGA  AGAGG    CACT
                                |||||||  |||||    ||||
                                TTCTTCT  TCTCC    GTGA
                                    CC    A____
GAM1918 CTSZ     3' AAGAAGACTGAGGTCCCA    41608       AA    GAA
                                AAGAAGAT  GAGG   TCCA
                                ||||||||  ||||   ||||
                                TTCTTCTG  CTCC   GGGT
                                     A_   A__
GAM1918 FCMD     3' AAGGAGGAAAGAGGGAAC    27507     A  AT
                                AAG AG  AAGAGGGAAT
                                |||  ||  ||||||||||
                                TTC TC  TTCTCCCTTG
                                  C  CT
GAM1918 FGF7     3' AGAAGAAAGAAAACAGTCCACT 12855       T      AA_
             T                   AGAAGA AAGAGGG   TCCACTT
                                ||||||  |||||||   |||||||
                                TCTTCT TTCTTTT   AGGTGAA
                                   _      GTC
GAM1918 GABRE    3' AAGAAGAGGGAGGTGGCCCA   35072       TAA    GAA
                                AAGAAGA   GAGG   TCCA
                                |||||||   ||||   ||||
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                                TTCTTCT  CTCC  GGGT
                                   CC_   ACC
GAM1918 GUCY1A2  3' AAGAAAACATGGAATC     9212        AGAG
                                AAGAAGATA   GGAATC
                                |||||||||   ||||||
                                TTCTTTTGT   CCTTAG
                                    A___
GAM1918 JAM3     3' AAGAGGAACAGTGGGATCCA  37257     A  TA  A   A
                                AAGA GA  AG GGGA TCCA
                                |||| ||  || |||| ||||
                                TTCT CT  TC CCCT AGGT
                                  C  TG  A   _
GAM1918 LANCL1   3' AAGAAAGTAACCCTAGATCCAC 25845      A  GAG_  A
             TT                  AAGAAG TAA   GGA TCCACTT
                                |||||| |||   ||| |||||||
                                TTCTTT ATT   TCT AGGTGAA
                                   C  GGGA  _
GAM1918 MAP3K7IP2 3' AAGAAGAAAAGAAATCACT   31516       TAA       C
                                AAGAAGA  GAGGGAATC ACT
                                |||||||  ||||||||| |||
                                TTCTTCT  TTTCTTTAG TGA
                                   ___       _
GAM1918 MAP3K7IP2 3' AGAAGATACAGGGCCA     31518       AG   AAT
                                AGAAGATA  AGGG  CCA
                                ||||||||  ||||  |||
                                TCTTCTAT  TCCC  GGT
                                    G_   ___
GAM1918 MARK1    5' AAGAGGAGGGGGAGCCGCT   33007     TA  A   AT  A
                                AAGA  AG GGGA  CC CT
                                ||||  || ||||  || ||
                                TTCT  TC CCCT  GG GA
                                  CC  C   C_  C
GAM1918 MYBL1    3' AAGAAAATATATGAGAATTTAC 41968        AGA    CC
             TT                  AAGAAGATA  GGGAAT  ACTT
                                |||||||||  ||||||  ||||
                                TTCTTTTTAT  CTCTTA  TGAA
                                     ATA    AA
GAM1918 NEBL     3' AAGAAGACATGAAGGATTC   26895        A    A
                                AAGAAGATA GAGGGA TC
                                |||||||||  ||||||  ||
                                TTCTTCTGT CTTCCT AG
                                     A    A
GAM1918 NEUROD2  5' GAGAAGAGGGATCTTCTC    26059    T      A  CA
                                GA AAGAGGGA TC  CTT
                                || ||||||||  ||  |||
                                CT TTCTCCCT AG  GAG
                                 C       _  AA
GAM1918 STE      5' AAAAAGATGAGAACCACT    24049        AAGA    T
                                AAGAAGAT   GGGAA CCACT
                                ||||||||   ||||| |||||
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                                TTTTTCTA   CTCTT GGTGA
                                    ____   _
GAM1918 TMC2    3' GGAAAGAGGGGAGAGAACC   38850   A    TAA
                                A GAAGA   GAGGGAATC
                                | |||||   |||||||||
                                C TTTCT   CTCTCTTGG
                                 C    CCC
GAM1918 TMSB4Y  5' AAGAGAATAGGAAAGCCACTT  20085     A  TAAG     T
                                AAGA GA    AGGGAA CCACTT
                                |||| ||    |||||| ||||||
                                TTCT CT    TCCTTT GGTGAA
                                   _ TA__     C
GAM1918 XYLB    3' AAGAAGAGAGAGGGAAT     23018       TA
                                AAGAAGA  AGAGGGAAT
                                |||||||  |||||||||
                                TTCTTCT  TCTCCCTTA
                                    C_
GAM1919 PPP3R1  3' TGGCACTTTTGTACTCTAT   44086        GTAATAA
                                TGGCATTTT      TGCTCTGT
                                |||||||||      ||||||||
                                ACCGTGAAA      ATGAGATA
                                     AC_____
GAM1919 CLOCK   3' TTAAGTGTGGTATG       22222         ATAA
                                TTAAGTGTG   GTGTG
                                |||||||||   |||||
                                AATTCACAC   CATAC
                                    ____
GAM1919 EHD4    3' TTAAGTATGATAAGTGGGC   40210             T
                                TTAAGTGTGATAAGTG GC
                                |||||||||||||||| ||
                                AATTCATACTATTCAC CG
                                          C
GAM1919 FGF12   3' TTAAGTGTGCTAATCTTTGTGC 34304         ATAAG___
                                TTAAGTGTG       TGTGC
                                |||||||||       |||||
                                AATTCACAC       ACACG
                                     GATTAGAA
GAM1919 IRF2    5' TAAGTGTTGCTAGGGTGTG   13588       GA_  A_
                                TAAGTGT   TA  GTGTG
                                |||||||   ||  |||||
                                ATTCACA   AT  CACAC
                                    ACG  CC
GAM1919 KCNS2   3' CTAAGTGTTCCATGTGC     42824        GATAA
                                TTAAGTGT    GTGTGC
                                ||||||||    ||||||
                                GATTCACA    TACACG
                                     AGG__
GAM1919 MLLT2   3' TCAATTGTAGTAAGTGTGC   25507     G   A
                                TTAA TGTG TAAGTGTGC
                                |||| |||| |||||||||
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                                AGTT ACAT ATTCACACG
                                  A   C
GAM1919 PAX6    5' TCAAGTGTGTTAATGTG    7098        ATA
                                TTAAGTGTG  AGTGTG
                                |||||||||  ||||||
                                AGTTCACAC  TTACAC
                                     AA_
GAM1919 PLAG1   3' CTAAGTGCAATCTGAGTGTGC 15348      TG A__
                                TTAAGTG AT  AGTGTGC
                                |||||||  ||  |||||||
                                GATTCAC TA  TCACACG
                                   GT  GAC
GAM1919 SCN8A   3' CTAAATGTGAGTGTG     30531        TAA
                                TTAAGTGTGA  GTGTG
                                ||||||||||  |||||
                                GATTTACACT  CACAC

                                    ___
GAM1919 SORCS3  3' TCAAAAATAAGTGTGC     31428     TGT
                                TTAAG  GATAAGTGTGC
                                |||||  ||||||||||||
                                AGTTT  TTATTCACACG

                                  ___
GAM1919 WHN     3' TTAAGTGTGGATGAGTGT   18756       _ A
                                TTAAGTGTG AT AGTGT
                                ||||||||| || |||||
                                AATTCACAC TA TCACA
                                     C  C
GAM1920 ADCY2   3' TGTAATAATTCTCTTGCTT  42148     A  CTC
                                TGTGA TAA  TCTCTTGTTT
                                ||||| |||  ||||||||||
                                ACATT ATT  AGAGAACGAA
                                  _  A__
GAM1920 BTAF1   3' TGAGAATAACTTGTTT     43673   T     CTCTCT
                                TG GAATAACT     TGTTT
                                || ||||||||     |||||
                                AC CTTATTGA     ACAAA
                                 T      _______
GAM1920 CEP1    5' TGTGGATAACCTCTGCCTC  28140     A    T   CTT
                                TGTG ATAAC CTCT  GTTTC
                                |||| ||||| ||||  |||||
                                ACAC TATTG GAGA  CGGAG
                                  C   _   ____
GAM1920 COL19A1 3' TGTGGATACAGCCTTGTTTC  12389     A  ACTCTC
                                TGTG ATA     TCTTGTTTC
                                |||| |||     |||||||||
                                ACAC TAT     GGAACAAAG
                                  C  GTC___
GAM1920 DLD     3' TGAATGACTGACTTGTTTCC  6468      A  CTCT
                                TGAAT ACT   CTTGTTTCC
                                ||||| |||   |||||||||
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                              ACTTA TGA    GAACAAAGG
                                 C   CT__
GAM1920 IL1F8    3'  TGAATAATTCTGCTGTTTC   30895        C   CTC
                              TGAATAA TCT   TTGTTTC
                              ||||||| |||   |||||||
                              ACTTATT AGA   GACAAAG
                                  A   C__
GAM1920 NDUFV3   5'  GTGAATGAACACCCTTGTTTC 34342       _   TCT
                              GTGAAT AAC   CTCTTGTTTC
                              |||||| |||   ||||||||||
                              CACTTA TTG   GGGAACAAAG
                                 C   T__
GAM1920 PARK2    3'  TGTGAGAACTCTCTCTC     21279      AT
                              TGTGA  AACTCTCTCTT
                              |||||  ||||||||||
                              ACACT  TTGAGAGAGAG
                                 C_
GAM1920 PCDH9    5'  TGTGAATGGCTGTCTCCT    44413       AA  C
                              TGTGAAT  CT TCTCTT
                              |||||||  || ||||||
                              ACACTTA  GA AGAGGA
                                  CC  C
GAM1920 SPI1     3'  TGAGAATAACTTTACTTGTTT  17084    T      CTCT
                              TG GAATAACT    CTTGTTT
                              || ||||||||    |||||||
                              AC CTTATTGA    GAACAAA
                               T       AAT_
GAM1920 STC1     3'  TGTGAATAACCTCTCCC     17187          T
                              TGTGAATAAC CTCTCTT
                              |||||||||| |||||||
                              ACACTTATTG GAGAGGG
                                      _
GAM1920 TRAM     3'  TGTAAATAGTTTTCTCTCC   30705        AC__
                              TGTGAATA    TCTCTCT
                              ||||||||    |||||||
                              ACATTTAT    AGAGAGG
                                   CAAA
GAM1920 VHL      3'  TGGAATTTCACTCTTGTTTCC  8121     T   AAC  T
                              TG GAAT   TC CTCTTGTTTCC
                              || ||||   || ||||||||||
                              AC CTTA   AG GAGAACAAAGG
                               _    A__  T
GAM1920 DYRK1A   3'  AAATGGTAGGCTCTTCTAAT   38986         _  GATC
                              AAATGGTAG TTC    CTAAT
                              ||||||||| |||    |||||
                              TTTACCATC GAG    GATTA
                                   C   AA__
GAM1920 MRE11A   3'  AAAATGGTAGCTTTATTTTAAT 24627           CG  CC
                              AAAATGGTAGTT  AT  TAAT
                              ||||||||||||  ||  ||||
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                                TTTTACCATCGA  TA  ATTA
                                      AA  AA
GAM1920  SCA7     5'  TCAAAATGAGACACGATCCT   7309         TAGTT
                                TCAAAATGG    CGATCCT
                                |||||||||    |||||||
                                AGTTTTACT    GCTAGGA
                                     CTGT_
GAM1921  CELSR1   3'  TGATTTTAAGACAAGGGGTGC  30656     CAC       C  C
                                TGA   TAAGACAAG GG GC
                                |||   ||||||||| || ||
                                ACT   ATTCTGTTC CC CG
                                  AAA       C  A
GAM1921  ITPKB    3'  TGACACTAAAGGCAAGC     13659         ACAAGC    C
                                TGACACTAAG     GGCG GC
                                ||||||||||     |||| ||
                                ACTGTGATTT     CCGT CG
                                      _______   T
GAM1921  LHCGR    3'  TGCACTGAGACAGGG       6933     A    A    A C
                                TG CACT AGACA G GG
                                || |||| ||||| | ||
                                AC GTGA TCTGT C CC
                                 _   C    _ _
GAM1921  PER2     3'  TGACACTAAGAGGCGC      35621          CAAGC
                                TGACACTAAGA    GGCGC
                                ||||||||||    |||||
                                ACTGTGATTCT    CCGCG
                                      _____
GAM1921  RNGTT    5'  TAACGTCAGGGGCGGCGCGCC  19165     ACTA  ACAA
                                TGAC    AG    GCGGCGCGCC
                                ||||    ||    ||||||||||
                                ATTG    TC    CGCCGCGCGG
                                  CAG_  CC__
GAM1921  WNT3A    3'  TGGCACAGGCGTCGGCGCGCC  37553    A   TAAGACAAG
                                TG CAC        CGGCGCGCC
                                || |||        |||||||||
                                AC GTG        GCCGCGCGG
                                 C   TCCGCA___
GAM1922  ENG      5'  TTGCTGTCCGAAGGATGGGCGG 6512      AA__   TTAAA
                                TTGT    CGG    ATGGGCGG
                                ||||    |||    ||||||||
                                AACG    GCT    TACCCGCC
                                  ACAG   TCC__
GAM1923  ATP1B1   3'  AACACCAGTCTATGGGGTAC   11729         ACAA_  C
                                AACATCAGTC    GG AC
                                ||||||||||    || ||
                                TTGTGGTCAG    CC TG
                                      ATACC  A
GAM1923  ATP2A2   3'  CCCAACATCAGTCATGCAC    11744           CAAG
                                TCCAACATCAGTCA    GCAC
                                ||||||||||||||    ||||
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                                GGGTTGTAGTCAGT   CGTG
                                      A___
GAM1923 CD97    3' TCTGACATCAGTCTTAGC   38524   CA      ACAA
                                TC  ACATCAGTC   GGC
                                ||  |||||||||   |||
                                AG  TGTAGTCAG   TCG
                                 AC       AA__
GAM1923 CEBPA   3' ACATTGCACAAGGCAC     20381     CA T
                                ACAT  G CACAAGGCAC
                                ||||  | ||||||||||
                                TGTA  C GTGTTCCGTG
                                  A_ _
GAM1923 KITLG   3' TCCAACATCAGCTGCAAG   19647          CA
                                TCCAACATCAGT  CAAG
                                ||||||||||||  ||||
                                AGGTTGTAGTCG  GTTC
                                      AC
GAM1923 PCDH9   5' TCCCACATCAGTAGG      44410    A      CACA
                                TCC ACATCAGT   AGG
                                ||| ||||||||   |||
                                AGG TGTAGTCA   TCC
                                  G      _____
GAM1923 PRKY    3' TCCGGCAGCAGTCACAGG   15708    AA  T      A
                                TCC  CA CAGTCACA GG
                                |||  || |||||||| ||
                                AGG  GT GTCAGTGT CC
                                  CC  C       _
GAM1923 ST5     3' TCAGGCTCTGCAAGGCAC   24047     __  A_
                                TCAG  TC  CAAGGCAC
                                ||||  ||  ||||||||
                                AGTC  AG  GTTCCGTG
                                   CG  AC
GAM1924 CARPX   3' TGTGTGTTTGTGAGTATGTGTG 33583    A       AAAT   _
            AG                    TGT TGTTTGTGA   TGTG GAG
                                ||| |||||||||   |||| |||
                                ACA ACAAACACT   ACAC CTC
                                  C       CAT_   A
GAM1924 CNGB3   3' TGTAGGTTCCGGAAATTGTGG  33312     T   G  A
                                TGTA GTTT TG AAATTGTGG
                                |||| |||| || |||||||||
                                ACAT CAAG GC TTTAACACC
                                  C   _  C
GAM1924 IL1RAP  3' TTTGTGTTTGTGGAG      13513       AAAA
                                TTTGTG   TTGTGGAG
                                ||||||   ||||||||
                                AAACAC   AACACCTC
                                   A___
GAM1924 SERPINB4 5' TGTGTGTCTGTGGAATGAAG  42229    A      AAAATT
                                TGT TGTTTGTG    GTGGAG
                                ||| ||||||||    ||||||
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                                ACA ACAGACAC     TACTTC
                                  C       CT____
GAM1924  SLC39A4   3'  TGTAGGTTTGTGAGGTGTGG  32816     T      AAAT
                                TGTA GTTTGTGA   TGTGG
                                |||| ||||||||   |||||
                                ACAT CAAACACT   ACACC
                                  C       CC__
GAM1924  TACC1     3'  TGTATGTGTGTGAGAGTG    26607       T    AAATT
                                TGTATGT TGTGA    GTG
                                ||||||| |||||    |||
                                ACATACA ACACT    CAC
                                    C    CT___
GAM1925  FOXO1A    3'  AAATCTCCCCAATTTTTAA   12878       ATTA
                                AAATCT   CAATTTTTAA
                                ||||||   ||||||||||
                                TTTAGA   GTTAAAAATT
                                   GGG_
GAM1925  HPGD      3'  TAATTTATGGAGATCAGA    9243        TA
                                TAATTTAT  AGATCAGA
                                ||||||||  ||||||||
                                ATTAAATA  TCTAGTCT
                                     CC
GAM1925  SNX9      3'  TTATTAAGGTCAGAAAAAT   32164       A    TG
                                TTATTAAG TCAGA  GAT
                                ||||||| |||||  |||
                                AATAATTC AGTCT  TTA
                                     C    TT
GAM1926  ANGPT1    3'  TATATATTTCCCTTACATATAA 40244          TC
            T                    TATATATTTCTCTT  TATATAAT
                                ||||||||||||||  ||||||||
                                ATATATAAAGGGAA  GTATATTA
                                        T_
GAM1926  DPYSL2    3'  TATAGGGCCTCTTTCTAT    10756     TT_
                                TATA   TCTCTTTCTAT
                                ||||   ||||||||||
                                ATAT   GGAGAAAGATA
                                  CCC
GAM1926  MTAP      3'  TATATATATTTCTTTCTA    14680       TTC
                                TATATAT   TCTTTCTA
                                |||||||   ||||||||
                                ATATATA   AGAAAGAT
                                    TAA
GAM1926  FACL2     3'  TAAGGCAGATTTTTAAAT    34437      TG  A
                                TAAGG  GA TTTTAAAT
                                |||||  || ||||||||
                                ATTCC  CT AAAATTTA
                                   GT  A
GAM1926  TNFRSF6   3'  TAAGGAGAATCTTAAAT     6222       T
                                TAAGG GGAATTTTAAAT
                                ||||| ||||||||||||
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                                ATTCC TCTTAGAATTTA
                                  _
GAM1927 ACK1    5' TCTCCCACTGCCGCTCCCCCAG 25120    TT   A
                                TTT  CGCT CCGCTCCCCCAG
                                |||  |||| ||||||||||||
                                AGA  GTGA GGCGAGGGGGTC
                                  GG   C
GAM1927 FZD1    5' TTTCGGCCCGCTCCCCCGGC  18622     CTA       A
                                TTTCG   CCGCTCCCCC GC
                                |||||   |||||||||| ||
                                AAAGC   GGCGAGGGGG CG
                                   CG_       C
GAM1927 GAMT    3' TTTTTCACTGCCGACTGGCC  39889        A  _  CC
                                TTTTTCGCT CCG CT  CC
                                ||||||||| ||| ||  ||
                                AAAAAGTGA GGC GA  GG
                                      C   T  CC
GAM1927 GYPC    3' TTTCCTTGCTTCCCCAGCC   13327     G  ACC   C
                                TTTC CT   GCT CCCCAGCC
                                |||| ||   ||| ||||||||
                                AAAG GA   CGA GGGGTCGG
                                  _ A__   A
GAM1928 AOX1    3' TGCCTTTCACTATATGGT    10110    G   CGT
                                TG CTT   TTATATGGT
                                || |||   |||||||||
                                AC GAA   GATATACCA
                                 G   AGT
GAM1928 ATP2B2  5' TGGCATCTACATGGT       11766     TTC
                                TGGC   GTTTATATGGT
                                ||||   ||||||||||
                                ACCG   TAGATGTACCA
                                  ___
GAM1928 B3GAT1  3' TGGCCTCACTCCTGTGTGGT  38306         ATA__
                                TGGCTTCGTTT    TGGT
                                ||||||||||    ||||
                                ACCGGAGTGAG    ACCA
                                      GACAC
GAM1928 BCL2    3' TGGCTTCATACCACAGGT    8527          _    T
                                TGGCTTCGT TTATA GGT
                                ||||||||| ||||| |||
                                ACCGAAGTA GGTGT CCA
                                      T    _
GAM1928 CD83    3' TGGCCTCATGCTATGTGGT   20143         _   A
                                TGGCTTCGT TTAT TGGT
                                ||||||||| |||| ||||
                                ACCGGAGTA GATA ACCA
                                      C   C
GAM1928 CLECSF5 3' TGGTCTTCCTTATGGT      29931     _   G TTA
                                TGG CTTC T   TATGGT
                                ||| |||| |   ||||||
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                                ACC GAAG A   ATACCA
                                  A   G ___
GAM1928 GPR4     3'  TGGCTCACATTTGTGGT     40894       _    ATA
                                TGGCTT CGTTT   TGGT
                                |||||| |||||   ||||
                                ACCGAG GTAAA   ACCA
                                   T    C__
GAM1928 MAP3K7IP1 3'  TGGCTTGTCCAAGGT      25935       C    TAT
                                TGGCTT GTTTA   GGT
                                |||||| |||||   |||
                                ACCGAA CAGGT   CCA
                                   _    T__
GAM1928 MEF2B    5'  TGGCATTCATATGGT      25414     TTC
                                TGGC   GTTTATATGGT
                                ||||   ||||||||||
                                ACCG   TAAGTATACCA
                                  ___
GAM1928 OPTN     5'  TGGCTTCGCTCAGGGT     35070          TAT
                                TGGCTTCGTTTA   GGT
                                ||||||||||||   |||
                                ACCGAAGCGAGT   CCA
                                      C__
GAM1928 PDGFRA   3'  TGTTTCATTCATATGGT    26288    GC
                                TG  TTCGTTTATATGGT
                                ||  ||||||||||||||
                                AC  AAGTAAGTATACCA
                                 A_
GAM1928 SCN7A    5'  TGGCATTCACATGGT      16483     TTC
                                TGGC   GTTTATATGGT
                                ||||   ||||||||||
                                ACCG   TAAGTGTACCA
                                  ___
GAM1928 SLC18A3  3'  TGGCTTCGCTGGCCTCGGT   16840         TATA_
                                TGGCTTCGTT    TGGT
                                |||||||||     ||||
                                ACCGAAGCGA    GCCA
                                     CCGGA
GAM1928 TFAP4    3'  TGGCTTCGTTCAAAGGT     17417          TAT
                                TGGCTTCGTTTA   GGT
                                ||||||||||||   |||
                                ACCGAAGCAAGT   CCA
                                      TT_
GAM1929 B4GALT6  3'  AAAACTAAACTTAAAATTTGT  40841           TTACA
                                AAAACTAAACTTG    TTGT
                                ||||||||||||     ||||
                                TTTTGATTTGAAT    AACA
                                      TTTA_
GAM1929 CLCN3    3'  TTAAAACCAAGCTTCATTG   12273         ACTT   A
                                TTAAAACTAA    GTT CATTG
                                |||||||||    ||| |||||
```

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                                AATTTTGGTT   CGA GTAAC
                                     ____  A
GAM1929 JPH3    3' ACTGAACAAGTTACATTGT   34014    A  TT
                                ACT AAC  GTTACATTGT
                                ||| |||  ||||||||||
                                TGA TTG  CAATGTAACA
                                  C  TT
GAM1929 SLC38A2 3' TTAAAACAAACATACATTG   33279      T   TTGT
                                TTAAAAC AAAC   TACATTG
                                ||||||| ||||   |||||||
                                AATTTTG TTTG   ATGTAAC
                                    _  T___
GAM1930 MECP2   3' ACAAATTTCCTTAATAAAT   22565     GG
                                GCGAG  TTCCTTAATAAAT
                                |||||  ||||||||||||
                                TGTTT  AAGGAATTATTTA
                                   A_
GAM1930 LDB3    3' GGGGATGTTGGATG       44110        CTTGG
                                GGGGATGTT    GGATG
                                |||||||||    |||||
                                CCCCTACAA    CCTAC
                                     _____
GAM1930 PCLO    3' GGGGATGTTCTTGCTGTGTGCT 45305          GGGA_
          T                      GGGGATGTTCTTG    TGCTT
                                 ||||||||||||    |||||
                                 CCCCTACAAGAAC    ACGAA
                                       GACAC
GAM1931 ASTN    3' GCTGAAGGTGTGTGTTCAGG  42949   GTACAA  AC
                                GC     TGT  GTGTTCAGG
                                ||     |||  |||||||||
                                CG     ACA  CACAAGTCC
                                 ACTTCC  __
GAM1931 FGFRL1  3' GCGTGTGTATGTTCAGG    34911    ACAA  AC
                                GCGT   TGT  GTGTTCAGG
                                ||||   |||  |||||||||
                                CGCA   ACA  TACAAGTCC
                                  C___  __
GAM1931 CDH12   5' TATTTTGTTTGTTCTTTT    19777       G
                                TATTTTGT TGTTCTTTT
                                |||||||| |||||||||
                                ATAAAACA ACAAGAAAA
                                     A
GAM1931 TSN     3' TATTTTGTGTGTGCTTTC    21499         T
                                TATTTTGTGTGT CTTTT
                                |||||||||||| |||||
                                ATAAAACACACA GAAAG
                                       C
GAM1932 DPEP1   3' CGGGTCTTCCCGGAGCTC    20635    A   ATAA
                                CGG TCTT   TCGGAGCTC
                                ||| ||||   |||||||||
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                                GCC AGAA   GGCCTCGAG
                                  C   G___
GAM1932 EP300   5' CCGAGGTCTCTCGGAGCTC  10975    _ A   ATAA
                                CCG G TCTT   TCGGAGCTC
                                ||| | ||||   |||||||||
                                GGC C AGAG   AGCCTCGAG
                                  T C   ____
GAM1932 SRGAP1  3' CGGATCTTTGGAGGAGTTC  43600       ATAATC   C
                                CGGATCTT     GGAG TC
                                ||||||||     |||| ||
                                GCCTAGAA     CCTC AG
                                     ACCT__   A
GAM1932 TCIRG1  5' ACTGGACAAGGAGTCGGAGCTC 25834   C   CTTATAA
                                AC GGAT      TCGGAGCTC
                                || ||||      |||||||||
                                TG CCTG      AGCCTCGAG
                                 A   TTCCTC_
GAM1933 ADCY2   3' CATCTCAATATTGGCTTCT   42140       C  CA   A
                                TATCTCAA AT  GCT CT
                                |||||||| ||  ||| ||
                                GTAGAGTT TA  CGA GA
                                     A  AC   A
GAM1933 COG3    3' CCTTAACATCAGCGGC     36414    C       TACTA
                                TCT AACATCAGC    GGC
                                ||| |||||||||    |||
                                GGA TTGTAGTCG    CCG
                                  A      _____
GAM1933 DLG5    5' TCAACACCTGCTGCTGCTGGGC 44464       A___   A  A
           A                     TCAACATC   GCT CT GGCA
                                ||||||||   ||| || ||||
                                AGTTGTGG   CGA GA CCGT
                                     ACGA   C  C
GAM1933 FBP1    3' TATCTTAACACCAGTGGC    8005      C      CTACTA
                                TATCT AACATCAG     GGC
                                ||||| ||||||||     |||
                                ATAGA TTGTGGTC     CCG
                                   A      A_____
GAM1933 KLHL1   3' TCAACATCAGTAGG       34083         CTAC
                                TCAACATCAG   TAGG
                                ||||||||||   ||||
                                AGTTGTAGTC   ATCC
                                     ____
GAM1933 NRIP1   3' TATTTCAACATCACCAG    40986    C      AGCT
                                TAT TCAACATC   ACTAG
                                ||| ||||||||   |||||
                                ATA AGTTGTAG   TGGTC
                                  A      ____
GAM1933 PDGFRL  3' CTTGACATCAGCCTCTGGCA  26293   CA       A  A
                                CT  ACATCAGCT CT GGCA
                                ||  |||||||| || ||||
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                                GA  TGTAGTCGG GA CCGT
                                 AC        A  _
GAM1933  SH2D1A    3'  TCCAATATCAGAACACTAGGCA 14291    T   C     C_
                                TC CAA ATCAG  TACTAGGCA
                                || ||| |||||  |||||||||
                                AG GTT TAGTC  GTGATCCGT
                                 _  A    TT
GAM1933  STX7      3'  TATCCTTAGTAATTTTACTAGG 18697      CAACATCAGC
              CA                  TATCT        TACTAGGCA
                                |||||        |||||||||
                                ATAGG        ATGATCCGT
                                   AATCATTAAA
GAM1934  LGALS3BP  3'  GCGATCTGAGCCGCCAGA    42934     CAATGC
                                GCG     GAGCCGCCAGA
                                |||     ||||||||||
                                CGC     CTCGGCGGTCT
                                  TAGA__
GAM1934  PCM1      5'  AGCGCAATGCGAGCTAGA    26223            CGCC
                                AGCGCAATGCGAGC    AGA
                                ||||||||||||||    |||
                                TCGCGTTACGCTCG    TCT
                                        A___
GAM1934  TAF15     5'  GCGCGGCGGCCGGAG       18559      AAT   A    CCA
                                GCGC   GCG GCCG   GAG
                                ||||   ||| ||||   |||
                                CGCG   CGC CGGC   CTC
                                  C__   _   ____
GAM1934  ACCN2     5'  GCCGGAGCCCGCGGCCGCCGC  33447    A_    AGA   _
                                GC  GAGC   GCG CCGCCGC
                                ||  ||||   ||| |||||||
                                CG  CTCG   CGC GGCGGCG
                                 GC    GG_   C
GAM1934  ADAM23    5'  CGCGCATGGTGCCGCCGC    19202     AGA   GAGC
                                CGC   GCA    GCCGCCGC
                                |||   |||    ||||||||
                                GCG   CGT    CGGCGGCG
                                  ____   ACCA
GAM1934  AMPH      5'  CGAAGAGCAGAGCGCGCA    11598    C          CGCC
                                CG AGAGCAGAGCGC    GCA
                                || ||||||||||||    |||
                                GC TCTCGTCTCGCG    CGT
                                 T          _____
GAM1934  BIG1      5'  ACGCAGAGAAGGAGGCTGC    26953         CA_   C  C
                                ACGCAGAG   GAG GC GC
                                ||||||||   ||| || ||
                                TGCGTCTC   CTC CG CG
                                     TTC   _  A
GAM1934  CPNE7     5'  GCGAGTCGCGCCGCCGC     30869     A   CAGA
                                GC GAG    GCGCCGCCGC
                                || |||    ||||||||||
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```
                                CG CTC    CGCGGCGGCG
                                 _   AG__
GAM1934  CTBP1    3'  ACACAGGGCAGAGCGCCCACAG 42747       A        GC
                                ACGCAG GCAGAGCGCC  CGCAG
                                |||||| ||||||||||  |||||
                                TGTGTC CGTCTCGCGG  GTGTC
                                   C         __
GAM1934  CXX1     3'  AGAGCAGAGCAGAATGCAG   19427          CCGCC
                                AGAGCAGAGCG    GCAG
                                ||||||||||    ||||
                                TCTCGTCTCGT    CGTC
                                      CTTA_
GAM1934  DPYSL3   3'  GCAGAGCAGAGAGTGCAG    10770          CGCCGCC
                                GCAGAGCAGAG     GCAG
                                ||||||||||     ||||
                                CGTCTCGTCTC     CGTC
                                      TCA____
GAM1934  EHD1     5'  GCGGCTAGCGCCGCCGC     43035    AGA  AG
                                GC   GC  AGCGCCGCCGC
                                ||   ||  ||||||||||
                                CG   CG  TCGCGGCGGCG
                                 C__  A_
GAM1934  EPO      5'  CGGAGCAGAGCGGGCGC     9031     CA       C_
                                CG  GAGCAGAGCG  CGC
                                ||  ||||||||||  |||
                                GC  CTCGTCTCGC  GCG
                                 __         CC
GAM1934  GRF2     3'  CGCGGGGCAGAGCACCAGCTGC 23675     AGA        _  C
                                CGC   GCAGAGCGCC GC GC
                                |||   |||||||||| || ||
                                GCG   CGTCTCGTGG CG CG
                                  CCC         T  A
GAM1934  GTF2I    5'  CGCGGGCTGCGGCCGCCGC    37435     AGA  AGA  _
                                CGC   GC   GCG CCGCCGC
                                |||   ||   ||| |||||||
                                GCG   CG   CGC GGCGGCG
                                  CC_  A__   C
GAM1934  HCN2     5'  GCGGAGCGGAGCCGCCGCCGC  10169    A   A   _
                                GC GAGC GAGC GCCGCCGC
                                || |||| |||| ||||||||
                                CG CTCG CTCG CGGCGGCG
                                 C    C    G
GAM1934  IGF1     3'  GCAGAGCAAAGGATCCTGC    8340           CG_  _
                                GCAGAGCAGAG   CC GC
                                ||||||||||   || ||
                                CGTCTCGTTTC   GG CG
                                      CTA  A
GAM1934  KIAA0857 5'  ACCAACTCTGAGCGCCGCCGCA 42463    G   AGCA
            G                    AC CAG    GAGCGCCGCCGCAG
                                || |||    ||||||||||||||
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                                TG GTT    CTCGCGGCGGCGTC
                                 _   GAGA
GAM1934  KIFC3    5'  GCAGGATCCAGGCGTCGCCGCA 24460      _ G_   A   C
              G                   GCAG A  CAG GCG CGCCGCAG
                                  |||| |  ||| ||| ||||||||
                                  CGTC T  GTC CGC GCGGCGTC
                                    C AG   _   A
GAM1934  LTB4R    5'  CAGAGCAGAGATGACCTCGCAG 8880          C__   GC
                                  CAGAGCAGAG   GCC  CGCAG
                                  ||||||||||   |||  |||||
                                  GTCTCGTCTC   TGG  GCGTC
                                        TAC   A_
GAM1934  MARK3    5'  CGCAAGACAGGCCGCCGC    14356      AG   AGC
                                  CGCAG  CAG   GCCGCCGC
                                  |||||  |||   ||||||||
                                  GCGTT  GTC   CGGCGGCG
                                     CT   ___
GAM1934  MYO10    5'  CGCGGAAGTCAGCGCCGCCGC  29570     A   CAG
                                  CGC GAG   AGCGCCGCCGC
                                  ||| |||   ||||||||||
                                  GCG CTT   TCGCGGCGGCG
                                    C   CAG
GAM1934  NAP1L3   5'  CGCAGAGCGGAGCTGGAGC   21210        A   GCC_
                                  CGCAGAGC GAGC    GC
                                  |||||||| ||||    ||
                                  GCGTCTCG CTCG    CG
                                       C    ACCT
GAM1934  NDST1    5'  GCAGAGCAGAAGTGCCCCA   11368         _ C   G
                                  GCAGAGCAGA G GCC CCG
                                  |||||||||| | ||| |||
                                  CGTCTCGTCT C CGG GGT
                                        T A   _
GAM1934  PTBP1    5'  ACACAGAGCAGACCCGC     15850          G G
                                  ACGCAGAGCAGA C CCGC
                                  |||||||||||| | ||||
                                  TGTGTCTCGTCT G GGCG
                                              _ _
GAM1934  SDC2     5'  CGGAGCAGAGTACCGC      42564    CA      CG
                                  CG  GAGCAGAG  CCGC
                                  ||  ||||||||  ||||
                                  GC  CTCGTCTC  GGCG
                                    __       AT
GAM1934  SREBF1   5'  CGCAGAGCACAGTCCTGCTGCA 45371         G  CG  _  C
              G                   CGCAGAGCA AG  CC GC GCAG
                                  |||||||||  ||  ||  ||  ||||
                                  GCGTCTCGT TC  GG CG CGTC
                                        G  A_  A  A
GAM1935  CALD1    3'  TGAGTTATCTAAAATGTG    37632    T      __
                                  TG GTTATCT  GATGTG
                                  ||  |||||||  ||||||
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                                AC CAATAGA  TTACAC
                                 T      TT
GAM1935 DISC1    3' TGTGTTACTGAGCA       33057        T   TGT
                                TGTGTTA CTGA   GCG
                                ||||||| ||||   |||
                                ACACAAT GACT   CGT
                                    _   ___
GAM1935 EMP2     3' TGGTTATCTGAATGTGGATT   10901    T       _   C
                                TG GTTATCTGA TGTG GATT
                                || ||||||||| |||| ||||
                                AC CAATAGACT ACAC CTAA
                                 _       T   _
GAM1935 CX3CR1   5' TCAGCCACCCTGTCCT      43298     A      CGC
                                TCA CCACCCTG   CCT
                                ||| ||||||||   |||
                                AGT GGTGGGAC   GGA
                                  C       A__
GAM1935 EGLN2    5' CCAGCCGCCCTGCGCAGTG    38818     A  A      CCT
                                TCA CC CCCTGCGC   AGTG
                                ||| || ||||||||   ||||
                                GGT GG GGGACGCG   TCAC
                                  C  C      ___
GAM1935 NCF4     5' CCAGCCACCCTGCGTCT      30200     A        CC
                                TCA CCACCCTGCG  CT
                                ||| ||||||||||  ||
                                GGT GGTGGGACGC  GA
                                  C         A_
GAM1936 AF1Q     5' ACTGAGTCTGTCAGTT       27722       TCA
                                ATTGG   TCTGTCAGTT
                                |||||   ||||||||||
                                TGACT   AGACAGTCAA
                                   C__
GAM1936 ATP2B1   3' ACTGTTTATCTGTCAGTT     11746      GTC
                                ATTG   ATCTGTCAGTT
                                ||||   ||||||||||
                                TGAC   TAGACAGTCAA
                                   AAA
GAM1936 CEACAM5  3' TCATGAAGCTGTCAGTT      20377      T  TCAT
                                TCAT GG    CTGTCAGTT
                                |||| ||    |||||||||
                                AGTA CT    GACAGTCAA
                                  _  TC__
GAM1936 CHRNA3   3' TCATTGGCATCTAGTGAGTT   8839         T    _  C
                                TCATTGG CATCT GT AGTT
                                ||||||| ||||| || ||||
                                AGTAACC GTAGA CA TCAA
                                    _    T  C
GAM1936 CXCL13   5' TCATTAGCAGAGTCAGTT     26952        T  TCT
                                TCATTGG CA   GTCAGTT
                                ||||||| ||   |||||||
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                                AGTAATC GT   CAGTCAA
                                   _ CT_
GAM1936 DDX10    3' ATTGATCATCTCAATT     20573        TG
                                ATTGGTCATC  TCAGTT
                                ||||||||||  ||||||
                                TAACTAGTAG  AGTTAA
                                   __
GAM1936 DLG2     5' CCGTTCCCTCTGTCAGTT    10697     G  A_
                                TTG TC  TCTGTCAGTT
                                ||| ||  ||||||||||
                                GGC AG  AGACAGTCAA
                                  A  GG
GAM1936 EFG2     5' TCATTGGTAACGCCAA      37033        CATC
                                TCATTGGT   TGTCAG
                                ||||||||   ||||||
                                AGTAACCA   GCGGTT
                                     TT__
GAM1936 FACL3    3' ACTAATCCTGTCAGTT      20879       AT
                                ATTGGTC  CTGTCAGTT
                                |||||||  |||||||||
                                TGATTAG  GACAGTCAA
                                   __
GAM1936 MAML1    3' TCACTGGTGTTACTGTTGGTT 31295       CAT_   CA
                                TCATTGGT   CTGT  GTT
                                ||||||||   ||||  |||
                                AGTGACCA   GACA  CAA
                                     CAAT   AC
GAM1936 NEDD4L   3' TCATTGGTAACAAAACTCAGTT 31621       __ TCTG
                                TCATTGGT  CA   TCAGTT
                                ||||||||  ||   ||||||
                                AGTAACCA  GT   AGTCAA
                                     TT  TTTG
GAM1936 NFIA     3' ATTGATTCCTGTCAGTT     43206      CA
                                ATTGGT  TCTGTCAGTT
                                ||||||  ||||||||||
                                TAACTA  GGACAGTCAA
                                   A_
GAM1936 RAB27A   3' ATTGGTCAATCCAGTT      21358       TCTG
                                ATTGGTCA   TCAGTT
                                ||||||||   ||||||
                                TAACCAGT   GGTCAA
                                     TA__
GAM1936 RCN2     3' CATTGTCCTGTCAGTT      16212      G  AT
                                CATTG TC  CTGTCAGTT
                                |||||  ||  |||||||||
                                GTAAC AG  GACAGTCAA
                                   _  __
GAM1936 SOD3     5' TCATTGTCATTGTCGTT     16959       G   C   A
                                TCATTG TCAT TGTC GTT
                                ||||||  ||||  ||||  |||
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                                AGTAAC AGTA ACAG CAA
                                  _   _   _
GAM1936  SOX12    3'  TCTTTGGTCATTCAGTT     28061    A      CTG
                                TC TTGGTCAT   TCAGTT
                                || ||||||||   ||||||
                                AG AACCAGTA   AGTCAA
                                 A      ____
GAM1936  USP7     3'  TCATTGGCATCCAAGCT     18456       T     TC
                                TCATTGG CATCTG  AGTT
                                ||||||| ||||||  ||||
                                AGTAACC GTAGGT  TCGA
                                  _     ___
GAM1936  WISP1    3'  TCTTGGTCATTTCAGT      38903    A      CTG
                                TC TTGGTCAT   TCAGT
                                || ||||||||   |||||
                                AG AACCAGTA   AGTCA
                                 _       A__
GAM1936  YWHAG    3'  CAAAAGCATCTGTCAGTT    29789    TT  T
                                CA  GG CATCTGTCAGTT
                                ||  || ||||||||||||
                                GT  TC GTAGACAGTCAA
                                 TT  _
GAM1936  B4GALT1  3'  TTTGACCCTGAGTGCCACA   11295          A  ACGA
                                TTTGACCCTGA TG    ATA
                                |||||||||| ||    |||
                                AAACTGGGACT AC    TGT
                                      C  GG__
GAM1936  IL1RN    3'  TTTGATCCTGAATGCAGA    8219       C      AC
                                TTTGA CCTGAATG  GA
                                ||||| ||||||||  ||
                                AAACT GGACTTAC  CT
                                   A       GT
GAM1936  P2RY12   5'  TCTGACCCTGGACATGAGA   35570         A__    C
                                TTTGACCCTG   ATGA GA
                                ||||||||||   |||| ||
                                AGACTGGGAC   TACT CT
                                      CTG   _
GAM1936  TBR1     3'  TTTGTGCCTTGACGAGAATAAA 27318     AC   GA   C
                A                TTTG  CCT  ATGA GAATAAAA
                                ||||  |||  |||| ||||||||
                                AAAC  GGA  TGCT CTTATTTT
                                  AC   AC   _
GAM1937  PDE4B    3'  TCTAATGTGAGAATATTGTTT  15153        A  T   T
                                TCTAATGT GA AAT TTGTTT
                                |||||||| || ||| ||||||
                                AGATTACA CT TTA AACAAA
                                     _ C   T
GAM1937  RAD17    5'  TCTAATGTAGAAGGCCCATTT  39413          TAAT  TG
                                TCTAATGTAGA    TT  TTT
                                ||||||||||    ||  |||
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                                AGATTACATCT   GG  AAA
                                      TCC_  GT
GAM1938  EPHA3    3'  TTAGTGCAGCATTCTATATAG  23444        A    AAGAT
                                TTAGTGTA CATTT    TAG
                                |||||||| |||||    |||
                                AATCACGT GTAAG    ATC
                                    C    ATAT_
GAM1938  INPP4A   3'  ATGTAACAGCTAATTAGA    19708        TTTAA
                                GTGTAACA    GATTAGA
                                ||||||||    |||||||
                                TACATTGT    TTAATCT
                                    CGA__
GAM1938  ADCY9    3'  CATAACACCACGTCCGGGGA  10017        G   TAC   AA
                                TATAACAC ATGT   CCG  GA
                                |||||||| ||||   |||  ||
                                GTATTGTG TGCA   GGC  CT
                                    G   ___   CC
GAM1938  DYRK1A   5'  TATAACACTGTGTGAAGA    38998        GA   TACCC
                                TATAACAC  TGT    GAAGA
                                ||||||||  |||    |||||
                                ATATTGTG  ACA    CTTCT
                                    AC  _____
GAM1938  TEX13A   5'  TAACACGCCCGAAG       36330        ATGTTA
                                TAACACG     CCCGAAG
                                |||||||     |||||||
                                ATTGTGC     GGGCTTC
                                      _______
GAM1939  GNRHR    5'  TTTGCATATACATCATGTCAGT 7621             _   _
           T                     TTTGCATATACAT ATG CGGTT
                                |||||||||||| ||| |||||
                                AAACGTATATGTA TAC GTCAA
                                      G   A
GAM1939  KL       3'  TTTGCATATAGTTTCTGTGTTT 22008          CATATGCG
           TA                     TTTGCATATA       GTTTTA
                                ||||||||||       ||||||
                                AAACGTATAT       CAAAAT
                                     CAAAGACA
GAM1939  SHOC2    3'  TTGTATATACATATATAG    28900     C        CG
                                TTG ATATACATATG  G
                                ||| ||||||||||  |
                                AAC TATATGTATAT  C
                                  A         AT
GAM1939  SRGAP2   3'  TTTGCATAAATGAAAACTGGTT 43994         TACATAT  _
           TTA                    TTTGCATA      GC GGTTTTA
                                ||||||||      || |||||||
                                AAACGTAT      TG CCAAAAT
                                    TTACTTT  A
GAM1939  NET1     3'  GCCATTAAAAAAAG        25229          TGGC
                                GCCGTTAAG   GAAAG
                                |||||||||   |||||
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                                CGGTAATTT   TTTTC
                                     ____
GAM1940 RAB11A   3' TTTGATGCTTACAAAAA    21681       GTATT
                                TTTGATGC    CAAAAA
                                ||||||||    ||||||
                                AAACTACG    GTTTTT
                                    AAT__
GAM1940 SURF4    3' TTTGATGTGTTTCCAAAAATCA 37663       C  A     AA
                                TTTGATG GT TTCAAAA  ATCA
                                ||||||| || |||||||  ||||
                                AAACTAC CA AGGTTTT  TAGT
                                    A  A     __
GAM1941 ABL1     3' GCGAGTGCACCCCACCCCGG   28716    AAA     _ A_
                                GC   TGTATTCC CC  GG
                                ||   |||||||| ||  ||
                                CG   ACGTGGGG GG  CC
                                 CTC       T  GG
GAM1941 AQP8     3' GCAGCGTGTTCCCCAGG     10116     AA   A
                                GCA  TGT TTCCCCAGG
                                |||  ||| |||||||||
                                CGT  GCA AAGGGGTCC
                                  C_   C
GAM1941 BTNL3    3' TGACTAGCAAATGAGGAGCCTG 27465      A      TATTC  CA
           GG                     TGAC AGCAAATG    CC  GG
                                |||| ||||||||    ||  ||
                                ACTG TCGTTTAC    GG  CC
                                  A       TCCTC  AC
GAM1941 CELSR2   3' TGAGGGGCAGGCCCCCCAG   10858    CAA   AAT  AT
                                TGA   GCA   GT  TCCCCAG
                                |||   |||   ||  |||||||
                                ACT   CGT   CG  GGGGGTC
                                  CCC   C__  __
GAM1941 DSCR1    3' TGCTGAGTGAATGCATTCCAGG 20639    ACA  CA       CC
                                TG   AG  AATGTATTCC  AGG
                                ||   ||  ||||||||||  |||
                                AC   TC  TTACGTAAGG  TCC
                                 GAC  AC        __
GAM1941 EMS1     3' TGATGAGAAAATGCACCTCAGG 23429     CA  C      TT  C
                                TGA  AG AAATGTA  CC CAGG
                                |||  || |||||||  || ||||
                                ACT  TC TTTACGT  GG GTCC
                                  AC  T      __  A
GAM1941 JAM3     3' GACAAGCAGGGTTCCTCAGG   37263        AATGTA   C
                                GACAAGCA     TTCC CAGG
                                ||||||||     |||| ||||
                                CTGTTCGT     AAGG GTCC
                                    CCC____    A
GAM1941 NOTCH2   3' TGACAGATGCTTTTTCCCCAGG 35915       A CAA   A__
                                TGACA G   ATGT   TTCCCCAGG
                                ||||| |   ||||   |||||||||
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                                ACTGT C   TACG   AAGGGGTCC
                                  _ ___    AAA
GAM1941  PNOC     3'  TGGCAAGTCAAAACCCCAG   26353    A   _   TGTATT
                                TG CAAG CAAA     CCCCAG
                                || |||| ||||     ||||||
                                AC GTTC GTTT     GGGGTC
                                 C   A   T_____
GAM1941  SORCS1   3'  TGACAAACAAATGTGAAGACAG 38103           ATTCCC
           G                     TGACAAGCAAATGT     CAGG
                                ||||||||||||||     ||||
                                ACTGTTTGTTTACA     GTCC
                                       CTTCT_
GAM1941  WIF1     5'  GCAAATACATTTTCCAGG    41166         CC
                                GCAAATGTATT  CCAGG
                                ||||||||||  |||||
                                CGTTTATGTAA  GGTCC
                                       AA
GAM1941  ATP11B   3'  TGTATTGTGGTAGTTTGC    44311      ACAGGC   C
                                TGTAT     TGGT AGTTTGC
                                |||||     |||| |||||||
                                ACATA     ACCA TCAAACG
                                  AC_____   _
GAM1941  COL19A1  3'  TGTATTTCTGTTAGTTTGCT   12388     ACAGG   GTC
                                TGTAT    CTG   AGTTTGCT
                                |||||    |||   ||||||||
                                ACATA    GAC   TCAAACGA
                                  AA___   AA_
GAM1941  KLRF1    5'  TGTATACAGGTATGTTTTG   32413        CTG  CAG
                                TGTATACAGG   GT   TTTG
                                ||||||||||   ||   ||||
                                ACATATGTCC   CA   AAAC
                                      ATA  ___
GAM1942  ESRRBL1  3'  TAATTTCTTTATTAAACA    32842          T
                                TAATTTCTTTATT GATA
                                |||||||||||| ||||
                                ATTAAAGAAATAA TTGT
                                       T
GAM1942  SLC22A12 3'  TCATTTGTTTCTTTATTCAAT  40335      AA       TG
                                TCATT  TTTCTTTATT  AT
                                |||||  ||||||||||  ||
                                AGTAA  AAAGAAATAA  TA
                                  AC        GT
GAM1943  ELMO2    3'  AAAAGGTGAGTGGCTGTT    35219        ATT  AT
                                AAAAGGTGA   TG  TGTT
                                |||||||||   ||  ||||
                                TTTTCCACT   AC  ACAA
                                     C__  CG
GAM1943  GYPA     3'  TAAAAGGTAAATTTCTGTT   44624           GA
                                TAAAAGGTGAATTT  TTGTT
                                ||||||||||||||  |||||
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                                ATTTTCCATTTAAA  GACAA
                                      __
GAM1943  MBTPS1   5'  AAAAGTGAATTTTTGTT     19130          GA
                                AAAGGTGAATTT  TTGTT
                                ||||||||||||  |||||
                                TTTTCACTTAAA  AACAA
                                      __
GAM1943  SFRS7    3'  TAAAGGGTGAACTTGAGAGCT  40470      A         TT
                                TAAA GGTGAATTTGA  GTT
                                ||||| ||||||||||  |||
                                ATTT CCACTTGAACT  CGA
                                  C          CT
GAM1944  EGFL5    3'  AGCCTTGAACAAGATATTTAGC 44514      C_       C____
                                AGCT  GAACAAGA    GGC
                                ||||  ||||||||    |||
                                TCGG  CTTGTTCT    TCG
                                  AA       ATAAA
GAM1944  HLF      3'  TAAGCTCGAACATGAAGC    13393          A  C
                                TAAGCTCGAACA GA GGC
                                |||||||||||| || |||
                                ATTCGAGCTTGT CT TCG
                                       A  _
GAM1944  HSPA4    3'  TAAGCTCAGTAAGACTAACTGG 44854         AAC    _   AA
           GC                     TAAGCTCG   AAGAC GGCT  GC
                                ||||||||   ||||| ||||  ||
                                ATTCGAGT   TTCTG TTGA  CG
                                     CA_    A    CC
GAM1945  FLRT2    3'  TGATAGGTGCTAGTAGAAAAT  29861        TAACT   A
                                TGGTAGGT    GTA AAAAT
                                ||||||||    ||| |||||
                                ACTATCCA    CAT TTTTA
                                     CGAT_   C
GAM1946  EIF3S10  3'  AAAAAAACTCAGCGATA     43471       T   AC
                                AAAAAG ACT  CAGCGATA
                                ||||||  |||  ||||||||
                                TTTTTT TGA  GTCGCTAT
                                     _  __
GAM1946  LFNG     3'  TAAAAAAATACTGTCACAATA  45218          ACCA
                                TAAAAAAGTACT    GCGATA
                                ||||||||||||    ||||||
                                ATTTTTTTATGA    TGTTAT
                                       CAG_
GAM1946  MAGOH    3'  TAAAAAAATACTGCCCTGATA  14330          A  AGC
                                TAAAAAAGTACT CC   GATA
                                |||||||||||| ||   ||||
                                ATTTTTTTATGA GG   CTAT
                                       C  GA_
GAM1946  PCDHB11  3'  TAAAAAAGTACATGCAA     33182          TACCA
                                TAAAAAAGTAC    GCGA
                                ||||||||||     ||||
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                                ATTTTTTCATG    CGTT
                                       TA___
GAM1946 SOX11    3' TGCTTTATTTTTTCATTTTCA 17042        AC
                                TGCTTTATT  TTCATTTTTA
                                |||||||||  ||||||||||
                                ACGAAATAA  AAGTAAAAGT
                                     AA
GAM1947 BRCA1    3' TATTCACTACTTTTCTGTG   28643     A  ATAAT
                                TAT CA    CTTTTCTGTG
                                ||| ||    ||||||||||
                                ATA GT    GAAAAGACAC
                                  A  GAT__
GAM1947 IMPDH1   3' TAATACACAATGACGCAACTGT 9414          A  CTTTT
             G                   TAATATACAAT AT    CTGTG
                                ||||||||||| ||    |||||
                                ATTATGTGTTA TG    GACAC
                                       C  CGTT_
GAM1948 GLUL     3' TACATTTAAATATAAAAAT    13157
                                TACATTTAAATATAAAAAT
                                ||||||||||||||||||
                                ATGTAAATTTATATTTTTA

GAM1948 ZNF256   3' TGTCCATTTAAACACAAAGAAT 25098     A          _
             TTT                  TGT CATTTAAATATAAA AATTTT
                                ||| ||||||||||||| ||||||
                                ACA GTAAATTTGTGTTT TTAAAA
                                  G           C
GAM1949 GLUL     3' TACATTTAAATATAAAAAT    13157
                                TACATTTAAATATAAAAAT
                                ||||||||||||||||||
                                ATGTAAATTTATATTTTTA

GAM1949 ZNF256   3' TGTCCATTTAAACACAAAGAAT 25098     A          _
             TTT                  TGT CATTTAAATATAAA AATTTT
                                ||| ||||||||||||| ||||||
                                ACA GTAAATTTGTGTTT TTAAAA
                                  G           C
GAM1950 B3GNT3   3' TATTCCACCACCTC       30681       GCAT
                                TATTTT    GCCACCTC
                                ||||||    ||||||||
                                ATAAGG    TGGTGGAG
                                     _____
GAM1950 BMP8     5' CCCTGCCGTGCCACCTCC    11875       A_
                                TTTTGC  TGCCACCTCC
                                ||||||  ||||||||||
                                GGGACG  ACGGTGGAGG
                                   GC
GAM1950 CD3Z     5' TATTCTGCAGCTACCTCCC    8821         T  C
                                TATTTTGCA GC ACCTCCC
                                ||||||||| || |||||||
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                                ATAAGACGT CG TGGAGGG
                                     _ A
GAM1950 CD68     3' ATTTTGCTGCTCTCC      40782       A  CAC
                                ATTTTGC TGC  CTCC
                                ||||||| |||  ||||
                                TAAAACG ACG  GAGG
                                   _  A__
GAM1950 CRY2     3' CATTTTGCCTGCAACCATC   43578       A  C  _
                                TATTTTGC TGC ACC TC
                                |||||||| ||| ||| ||
                                GTAAAACG ACG TGG AG
                                     G  T  T
GAM1950 DNASE1L1 3' TATTTTGCCAAACATACCT   27501       AT_ C_
                                TATTTTGC  GC  ACCT
                                ||||||||  ||  ||||
                                ATAAAACG  TG  TGGA
                                     GTT  TA
GAM1950 DOK1     3' ATCCCTAGTGCCACCTCCC   10722     GCA
                                ATTTT  TGCCACCTCCC
                                |||||  ||||||||||||
                                TAGGG  ACGGTGGAGGG
                                   ATC
GAM1950 EGR1     3' TATTTTGCTCCCAAAGCCTCCC 12667       ATG  ___
                                TATTTTGC  CCA  CCTCCC
                                ||||||||  |||  ||||||
                                ATAAAACG  GGT  GGAGGG
                                     AG_  TTC
GAM1950 ELAC2    3' TATCCTGAGCTGCCTCC    32855      CAT  CA
                                TATTTTG  GC  CCTCC
                                |||||||  ||  |||||
                                ATAGGAC  CG  GGAGG
                                     T__  AC
GAM1950 EPB49    3' TATTTCCACCCCACCTCC   12734      G  G
                                TATTTT CAT CCACCTCC
                                |||||| ||| ||||||||
                                ATAAAG GTG GGTGGAGG
                                   _  G
GAM1950 EPHA1    3' TTCTACCCCCACCTCCC    23437      ATG
                                TTTTGC  CCACCTCCC
                                ||||||  |||||||||
                                AAGATG  GGTGGAGGG
                                   GG_
GAM1950 GNB1     3' TATCTTGCATCCAGCTTCC   13208       G  C  _
                                TATTTTGCAT CCA CT CC
                                |||||||||| ||| || ||
                                ATAGAACGTA GGT GA GG
                                     _  C  A
GAM1950 GNRH1     5' CATTTTGCCTTAACATTTCCC 9075       ATGC_ CC
                                TATTTTGC   CA  TCCC
                                ||||||||   ||  ||||
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                                GTAAAACG    GT  AGGG
                                    GAATT  AA
GAM1950  HLCS     3'  TATTCTGCAGATGCCCTCTC   7646          __    AC
                                TATTTTGCA  TGCC  CTC
                                |||||||||  ||||  |||
                                ATAAGACGT  ACGG  GAG
                                    CT    GA
GAM1950  IL18R1   3'  TATTTTGCATCACGTCC     19296         GC   C
                                TATTTTGCAT  CAC TCC
                                ||||||||||  ||| |||
                                ATAAAACGTA  GTG AGG
                                    __  C
GAM1950  MEIS1    3'  TACTTTGCAGCCTTCC      14417         T   ACC
                                TATTTTGCA GCC   TCC
                                |||||||||| |||   |||
                                ATGAAACGT CGG   AGG
                                    _  A__
GAM1950  MGAM     3'  ATTTTCCACACCTCCC      43651       G  TGC
                                ATTTT CA   CACCTCCC
                                ||||| ||   ||||||||
                                TAAAA GT   GTGGAGGG
                                  G  ___
GAM1950  MLLT2    3'  TATTCTGCCGTTACACCTCC   25505         ATGC_
                                TATTTTGC    CACCTCC
                                ||||||||    |||||||
                                ATAAGACG    GTGGAGG
                                    GCAAT
GAM1950  MRE11A   3'  TATCTTGCATGTTTCTC     24628          CCAC
                                TATTTTGCATG    CTC
                                ||||||||||    |||
                                ATAGAACGTAC    GAG
                                    AAA_
GAM1950  MSN      3'  TTTTGCACTCACTCCC      41254         GC   C
                                TTTTGCAT  CAC TCCC
                                ||||||||  ||| ||||
                                AAAACGTG  GTG AGGG
                                    A_  _
GAM1950  MSX2     3'  CATTTTGCAAATAATTTGTCTC 42292         TGCCAC____
            CC                    TATTTTGCA        CTCCC
                                |||||||||         |||||
                                GTAAAACGT         GAGGG
                                    TTATTAAACA
GAM1950  PCDH11X  3'  TATTCTGCATCCAATTTTCC   37311          G   CC__
                                TATTTTGCAT CCA    TCC
                                |||||||||| |||    |||
                                ATAAGACGTA GGT    AGG
                                    _  TAAA
GAM1950  PCMT1    3'  TACTTTGCATCCTTCC      23942          G  ACC
                                TATTTTGCAT CC   TCC
                                |||||||||| ||   |||
```

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                                ATGAAACGTA GG   AGG
                                      _ A__
GAM1950 RGS16    3' CTTTGCAGAACCTGCCTCCC  16321       T_  A_
                                TTTTGCA  GCC  CCTCCC
                                |||||||  |||  ||||||
                                GAAACGT  TGG  GGAGGG
                                    CT   AC
GAM1950 RNF14    3' TACTTTGCTACCAAGCCTCCC 20185        A    __
                                TATTTTGC TGCCA  CCTCCC
                                |||||||| |||||  ||||||
                                ATGAAACG ATGGT  GGAGGG
                                    _    TC
GAM1950 RUNX1    3' TTTTGCACATTCATTTCCC   12035       GC_ CC
                                TTTTGCAT   CA  TCCC
                                ||||||||   ||  ||||
                                AAAACGTG   GT  AGGG
                                     TAA  AA
GAM1950 SIAH1    3' TATTTTACAATGCTTCCT    16715        _  CA
                                TATTTTGCA TGC  CCT
                                ||||||||| |||  |||
                                ATAAAATGT ACG  GGA
                                     T   AA
GAM1950 SLC5A5   5' TCTGTCCTGCCACCTCCC    7828      CA_
                                TTTG   TGCCACCTCCC
                                ||||   ||||||||||
                                AGAC   ACGGTGGAGGG
                                  AGG
GAM1950 SOX2     3' TTTTGCACCCCTCCC       45477       AT   A
                                TTTTGC  GCC CCTCCC
                                ||||||  ||| ||||||
                                AAAACG  TGG GGAGGG
                                   __   _
GAM1950 STXBP1   3' TATCCTGATTGTCACCTCCC  17208       CA  C
                                TATTTTG  TG CACCTCCC
                                |||||||  || ||||||||
                                ATAGGAC  AC GTGGAGGG
                                    TA  A
GAM1950 TRIM37   3' TAAACTGTGCCACCTTCC    31626    TT   CA      _
                                TA  TTG  TGCCACCT CC
                                ||  |||  |||||||| ||
                                AT  GAC  ACGGTGGA GG
                                 TT  __       A
GAM1950 DES      3' CCTGCAGCAGGGGAGGGGAGGG 43561         AAA   AACTT
           C                     TCTGCAGCA   GAGG    GC
                                |||||||||   ||||    ||
                                GGACGTCGT   CTCC    CG
                                     CCC    CCTCC
GAM1950 JAM3     3' TCTGTGGCAAAGAGGAAC    37267      CA    A
                                TCTG  GCAAA GAGGAAC
                                ||||  ||||| |||||||
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                                AGAC  CGTTT CTCCTTG
                                  AC    _
GAM1950  KCNN3    3'  TCTGCAGCAAGGGCCCTGC   13921        AAAG   AA
                                TCTGCAGCA   AGG  CTTGC
                                |||||||||   |||  |||||
                                AGACGTCGT   TCC  GGACG
                                     ____   CG
GAM1950  KRT6A    3'  TCTGCAGCCAGAGAGGGGC   24477       AAA    AACTT
                                TCTGCAGC   AGAGG    GC
                                ||||||||   |||||    ||
                                AGACGTCG   TCTCC    CG
                                     GTC    C____
GAM1950  LIF      3'  CATCAAAGAGGAATTTG     14140    GCA       C
                                CA   AAAGAGGAA TTG
                                ||   ||||||||| |||
                                GT   TTTCTCCTT AAC
                                 AG_       A
GAM1950  NPAS1    5'  CCTGCAGCGGGAGGGGGC    40871       AAAA    AACTT
                                TCTGCAGC    GAGG    GC
                                ||||||||    ||||    ||
                                GGACGTCG    CTCC    CG
                                     CC__    CC___
GAM1950  PCTK1    5'  TCCGCAGCGGGAGGGGACGCGG 37479        AAA  A   ACTT
              CC                  TCTGCAGC   AG GGA    GCC
                                |||||||   || |||   |||
                                AGGCGTCG   TC CCT    CGG
                                     CCC  C   GCGC
GAM1950  SMARCA3  3'  TCTGCAGCAAATAAGTTTGC  40056         A   GAAC
                                TCTGCAGCAAA GAG    TTGC
                                ||||||||||| |||    ||||
                                AGACGTCGTTT TTC    AACG
                                      A   A___
GAM1950  SOX11    3'  TCTGCAGCAAAAGCTTGC    17040          AGGAA
                                TCTGCAGCAAAAG    CTTGC
                                ||||||||||||    |||||
                                AGACGTCGTTTTC    GAACG
                                      _____
GAM1950  ZNF35    5'  TCTGCAGCAGGAGGCTGGC   18285        AAA    AA  T
                                TCTGCAGCA   GAGG  CT GC
                                |||||||||   ||||  || ||
                                AGACGTCGT   CTCC  GA CG
                                     C__    __  C
GAM1951  CNTNAP2  3'  TTGAAATTTTGGTGAGAGG   30500        C  A
                                TTGAGATT TG TGAGAGG
                                |||||||| || |||||||
                                AACTTTAA AC ACTCTCC
                                     A  C
GAM1951  THY1     3'  AGATTCCAGAGGCTTG      26623        GATG
                                AGATTCT    AGAGGCTTG
                                |||||||    |||||||||
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                                TCTAAGG   TCTCCGAAC
                                   ____
GAM1951 BCAS2   3' GATGATGATGATAATGATAACT 25242          CAACCGC
            GT                   GATGATGATGA     GGCTGT
                                 ||||||||||      ||||||
                                 CTACTACTACT     TTGACA
                                      ATTACTA
GAM1951 DYRK1A  3' TGATGATGCAATGCATTCTGT 39003       A  CC  G_
                                 TGATGATG CAA  GCG  CTGT
                                 |||||||| |||  |||  ||||
                                 ACTACTAC GTT  CGT  GACA
                                      _  A_  AA
GAM1951 EFNB2   3' GATGATGATGGAATTACAGCC 19880       ACAACC
                                 GATGATGATG    GCGGCT
                                 ||||||||||    ||||||
                                 CTACTACTAC    TGTCGG
                                      CTTAA_
GAM1951 MEL     3' GAGGACCATGTGACGGCTGT  23868   T  G  ACAACC
                                 GA GAT ATG    GCGGCTGT
                                 || ||| |||    ||||||||
                                 CT CTG TAC    TGCCGACA
                                  C  G  AC____
GAM1951 PCTP    3' GATGATGAGGAAAAATGTGGTT 34534       T  CAACCGC  C
            GT                   GATGATGA GA     GG TGT
                                 |||||||| ||     || |||
                                 CTACTACT CT     CC ACA
                                      C  TTTTACA  A
GAM1951 PTPRM   3' GATTTGGCAACTGTGGCTGT  15972    GA  A   CGC
                                 GAT  TG CAAC   GGCTGT
                                 |||  || ||||   ||||||
                                 CTA  AC GTTG   CCGACA
                                   A_  C   ACA
GAM1951 TCEA1   3' GATGATGATCACGG        44326        GACAAC
                                 GATGATGAT     CGCGG
                                 |||||||||     |||||
                                 CTACTACTA     GTGCC
                                    _______
GAM1951 TPK1    3' GATGATGATGCAGACT      35354         A  ACCGC
                                 GATGATGATG CA    GGCT
                                 |||||||||| ||    ||||
                                 CTACTACTAC GT    CTGA
                                    _ ______
GAM1952 SCRT1   3' ACCTGAGTCCCTGCGACG    36361     TTA_
                                 ACCT   CCCTGCGACG
                                 ||||   ||||||||||
                                 TGGA   GGGACGCTGC
                                   CTCA
GAM1952 SOX11   3' CCACCTTCGTTGCGGCG     17008        ACCC   A
                                 CCACCTTT   TGCG CG
                                 ||||||||   |||| ||
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                                GGTGGAAG   ACGC GC
                                    CA__   C
GAM1952 JUP     3' AGTCTGAAGCTTTAGTG    13771        CTTTA
                                AGTCTGAAGC    TGGTG
                                ||||||||||    |||||
                                TCAGACTTCG    ATCAC
                                     AA___
GAM1952 PLN     5' AGTCTGAAGTTTTAAGTG    15402        CC   T
                                AGTCTGAAG  TTTA GGTG
                                |||||||||  |||| ||||
                                TCAGACTTC  AAAT TCAC
                                     A_   _
GAM1952 PPP1R7   3' ATCTGAAAATGGTGT      15508        CCTTT
                                GTCTGAAG    ATGGTGT
                                ||||||||    |||||||
                                TAGACTTT    TACCACA
                                     _____
GAM1953 DFFB    3' AGCTGTTCAACAGACATTG   44594        TTTGA    C
                                AGCTGTTCA    AGACA TG
                                |||||||||    ||||| ||
                                TCGACAAGT    TCTGT AC
                                     TG___    A
GAM1953 LGALS3BP 3' GAGCTGTTGGTGTCCAGGGCAC 42931        CATTTGA  A_
           TG                    GAGCTGTT      AG  CACTG
                                |||||||      ||  |||||
                                CTCGACAA      TC  GTGAC
                                    CCACAGG  CC
GAM1953 RBM3    3' GAGCTGATGAAGATGCTG    43256       TTCATT     CA
                                GAGCTG     TGAAGA  CTG
                                ||||||     ||||||  |||
                                CTCGAC     ACTTCT  GAC
                                   T_____     AC
GAM1953 XT3     3' GCTGCAAGGTGGGGACACTGA  33666      TCATT  AA
                                GCTGT    TG  GACACTGA
                                |||||    ||  ||||||||
                                CGACG    AC  CTGTGACT
                                   TTCC_  CC
GAM1953 ABCA4    3' TGTGTTTGTTTTCTGCTGCAGT 42557      G    CCTA
                                TGTGT TGTT    TGTTGCAGT
                                ||||| ||||    |||||||||
                                ACACA ACAA    ACGACGTCA
                                   A    AAG_
GAM1953 ATP11A   3' TGTGTGTGTGCATGTGTGCAGT 44196         TCC    _
                                TGTGTGTGT   TATGT TGCAGT
                                |||||||||   ||||| ||||||
                                ACACACACA   GTACA ACGTCA
                                     C__    C
GAM1953 BCL2    3' TGTGTGTGTCTGTC       8528          CCTA
                                TGTGTGTGTT    TGTT
                                ||||||||||    ||||
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                              ACACACACAG   ACAG
                                    ____
GAM1953 BCRP2   3' ATGTGTGTGTCTTATGGGGC  41649        CC   TT
                              ATGTGTGTGTT  TATG  GC
                              ||||||||||  ||||  ||
                              TACACACACAG  ATAC  CG
                                    A_   CC
GAM1953 CARPX   3' TGTGTGTGTTTGTGA     33582        CCTA   T C
                              TGTGTGTGTT   TGT G A
                              ||||||||||   ||| | |
                              ACACACACAA   ACA C T
                                    ____  _ _
GAM1953 CDH13   3' TGTGTGTGTGCATGTGCGGT  10373       TCC    T  A
                              TGTGTGTGT   TATGT GC GT
                              |||||||||   ||||| || ||
                              ACACACACA   GTACA CG CA
                                    C__    _ C
GAM1953 DMD     3' TGTGTGTGTTTGTT      19700         CCTA
                              TGTGTGTGTT   TGTT
                              ||||||||||   ||||
                              ACACACACAA   ACAA
                                    ____
GAM1953 EHD3    3' TGTGTGTGTGTGTGTGTAGT 31124        TCCTA  _ C
                              TGTGTGTGT    TGT TG AGT
                              |||||||||    ||| || |||
                              ACACACACA    ACA AC TCA
                                    CAC__  C  A
GAM1953 LUM     3' ATGTGTGTGTTCTTGT     14267         CTA
                              ATGTGTGTGTTC  TGT
                              ||||||||||||  |||
                              TACACACACAAG  ACA
                                    A__
GAM1953 MEL     3' GTGGAGCTTTGTGTTGCAGT  23870    TGT  CCTA
                              GTG  GTT   TGTTGCAGT
                              |||  |||   |||||||||
                              CAC  CGA   ACAACGTCA
                                CT_  AAC_
GAM1953 MS4A3   3' ATGTGTGAGTTCCAGCAG   26008      T    TATGTT
                              ATGTGTG GTTCC    GCAG
                              ||||||| |||||    ||||
                              TACACAC CAAGG    CGTC
                                  T    T_____
GAM1953 OLR1    3' TGTGTGTGTCTGTC       14944         CCTA
                              TGTGTGTGTT   TGTT
                              ||||||||||   ||||
                              ACACACACAG   ACAG
                                    ____
GAM1953 PBX2    3' ATGTGTATGTTTCTGTGT   15102         C  A
                              ATGTGTGTGTT CT TGT
                              |||||||||| || |||
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                                TACACATACAA GA ACA
                                      A  C
GAM1953  SNAP25   3'  TGTGTGTGTTGTCTCATCAGT  39264          C_  ATGTTG
                                TGTGTGTGTT  CT     CAGT
                                ||||||||||  ||     ||||
                                ACACACACAA  GA     GTCA
                                      CA  GTA___
GAM1953  TFAP4    5'  TGTGTGTGTGTTTGCAG     17423          TCCTATG
                                TGTGTGTGT      TTGCAG
                                |||||||||      ||||||
                                ACACACACA      AACGTC
                                     CA_____
GAM1954  DSCR1    3'  TGATGTCTTCGTGGGG      20638      CA       TCA
                                TGATG  CTTCGTGG   GG
                                |||||  ||||||||   ||
                                ACTAC  GAAGCACC   CC
                                   A_      ___
GAM1954  EGLN2    5'  TGATGCACGTGGATGGGTGGC  38838        TTC    TCA___
                                TGATGCAC   GTGG     GGC
                                ||||||||   ||||     |||
                                ACTACGTG   CACC     CCG
                                     ___    TACCCA
GAM1955  PPP2CA   3'  CCTTGATTTTTATTTTACCTAC 15515    G       A   AC
              A                  C TTGATTTT TGT  TACCTACA
                                | ||||||||  |||  ||||||||
                                G AACTAAAA ATA  ATGGATGT
                                 G       _  AA
GAM1955  USP6     3'  CATTGGTAATTACTACCTA    45025      ATTTTATG
                                CGTTG       TACTACCTA
                                |||||       |||||||||
                                GTAAC       ATGATGGAT
                                   CATTA___
GAM1956  ATP2C1   5'  AAACTGCACTCGGGTTGATGGC 30783        ATACCGCC
                                AAGCTGCA       GATGGC
                                ||||||||       ||||||
                                TTTGACGT       CTACCG
                                     GAGCCCAA
GAM1956  BBS4     3'  AGCTGCAATACTCAGCAGGC   37495          _ _  CGAT
                                AGCTGCAATAC C GC    GGC
                                ||||||||||| | ||    |||
                                TCGACGTTATG G CG    CCG
                                      A T  T___
GAM1956  BNC      5'  GCTGCGCAGCACGATGGCC    11853      AATACC  _
                                GCTGC     GC CGATGGCC
                                |||||     || ||||||||
                                CGACG     CG GCTACCGG
                                   CGT___  T
GAM1956  CACNA1G  3'  GCTGCAATGTGCTCGCGG    33131        ACC  _  A
                                GCTGCAAT   GC CG TGG
                                ||||||||   || || |||
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                                CGACGTTA   CG GC GCC
                                    CA_  A  _
GAM1956  CLCN6    3'  AAGCTGCGACTGCGGCAATGGC 34711        A  AC  C
              C                  AAGCTGC AT  CG CGATGGCC
                                 ||||||| ||  || ||||||||
                                 TTCGACG TG  GC GTTACCGG
                                    C  AC  C
GAM1956  EPB49    3'  AAGCTGCAGTGCAGGAAAGC   12719        ATACC  C_  T
                                 AAGCTGCA    GC  GA GGC
                                 ||||||||    ||  || |||
                                 TTCGACGT    CG  CT TCG
                                    CA___  TC  T
GAM1956  LZTFL1   3'  AAGCTGCATTGTGATGGC    33766        ATACCGCC
                                 AAGCTGCA       GATGGC
                                 ||||||||       ||||||
                                 TTCGACGT       CTACCG
                                    AACA____
GAM1956  MMP19    5'  GCTGCAATGATGCGC       35589        ACCGCC   _
                                 GCTGCAAT     GATG GC
                                 ||||||||     |||| ||
                                 CGACGTTA     CTAC CG
                                    _______   G
GAM1956  RGS3     3'  AGCTGCAAGCTCCAATGGCC   39120        TACCG
                                 AGCTGCAA    CCGATGGCC
                                 ||||||||    |||||||||
                                 TCGACGTT    GGTTACCGG
                                    CGA__
GAM1956  RNF26    3'  AAGCTGCAAGCCCCTGGGCC   36750        TA  G  GAT
                                 AAGCTGCAA  CC CC   GGCC
                                 |||||||||  || ||   ||||
                                 TTCGACGTT  GG GG   CCGG
                                    C_  _  AC_
GAM1956  SIP      3'  AAGCTGCAGTACAGTGGC    30841        A   CGCCGA
                                 AAGCTGCA TAC     TGGC
                                 |||||||| |||     ||||
                                 TTCGACGT ATG     ACCG
                                    C   TC____
GAM1956  THBS1    3'  AAGGTGCAATACCAGCATTGG  17508     C        C  A
                                 AAG TGCAATACCG CG TGG
                                 ||| |||||||||| || |||
                                 TTC ACGTTATGGT GT ACC
                                   C         C  A
GAM1956  ALS2     3'  GCAAAACACTGAAATGTTGA   34094      _      CGC
                                 GCAGA CACTGAAA   TGA
                                 ||||| ||||||||   |||
                                 CGTTT GTGACTTT   ACT
                                    T       ACA
GAM1956  MRPS12   5'  TCGCGGACACGCTGA       37892      A    TGAAAC
                                 TCGC GACAC     GCTGA
                                 |||| |||||     |||||
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                                AGCG CTGTG     CGACT
                                  C    _______
GAM1956 SLC1A5   5'  TCTTGGACACTGAGGGCTG   24751    GCA      AAC
                                TC   GACACTGA   GCTG
                                ||   ||||||||   ||||
                                AG   CTGTGACT   CGAC
                                 AAC       CC_
GAM1957 CLASP1   3'  AGCAAAGTCCTGGT       42231      ATTTA
                                AGCAA    AGTCCTGGT
                                ||||||    |||||||||
                                TCGTT    TCAGGACCA
                                   ______
GAM1957 HFE      5'  GCCCAGTAAAACTTCCTGGTG  40006    _ C   TTTAAG
                                GCC AG AAA     TCCTGGTG
                                ||| || |||     ||||||||
                                CGG TC TTT     AGGACCAC
                                  G  A   TGA___
GAM1957 KCNA7    3'  GCTATTTCCTTTGGGTCCTGGT 36659    CAGCAAA   AA
              G                  GC      TTT  GTCCTGGTG
                                ||      |||  |||||||||
                                CG      AAA  CAGGACCAC
                                 ATAAAGG   CC
GAM1957 PCK1     5'  CGCCAGCAAGTTTGTGTTCCCA 40943         A   AAG_   TG
              GTG                  CGCCAGCAA TTT    TCC  GTG
                                |||||||||  |||    |||  |||
                                GCGGTCGTT AAA    AGG  CAC
                                     C   CACA   GT
GAM1957 PCSK1N   3'  GCTGGCGGGGAGCAGTCCTGGT 29976    CA  AAATTTA
              G                  GC  GC      AGTCCTGGTG
                                ||  ||      ||||||||||
                                CG  CG      TCAGGACCAC
                                 AC  CCCCTCG
GAM1957 CD28     3'  AGTGGGTTTAAATTTGTGTT   26015         CTGGCC   C
                                AGTGGGTTTG     TTG GTT
                                ||||||||||     ||| |||
                                TCACCCAAAT     AAC CAA
                                     TTA___   A
GAM1958 TDRD1    5'  TACTTGGCAATACAAACT    36333      A
                                TATTT GCAATACAAATT
                                ||||| ||||||||||||
                                ATGAA CGTTATGTTTGA
                                   C
GAM1959 CLN2     3'  GTAGTAGCAGTGGGGATATAAG 7557      TG   __   A
                                GTA  AGC  TGG GATATAAG
                                |||  |||  ||| ||||||||
                                CAT  TCG  ACC CTATATTC
                                  CA   TC   C
GAM1959 COL4A3   3'  AATTGTATAAGCTACTCATAAG 36375            GAGA
                                AATTGTATGAGCTG    TATAAG
                                ||||||||||||||    ||||||
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                                TTAACATATTCGAT   GTATTC
                                       GA__
GAM1959 IL1RAP   3' TTGTGTTTGTGGAGATATAAG 13512     ATGAGC
                                TTGT     TGGAGATATAAG
                                ||||     ||||||||||||
                                AACA     ACCTCTATATTC
                                  CAAAC_
GAM1959 MSR1     3' ATTGTATGAGTTTTAGAT    14657         CTGG
                                ATTGTATGAG    AGAT
                                ||||||||||    ||||
                                TAACATACTC    TCTA
                                      AAAA
GAM1960 IL22RA2  5' AGGACCAAAGAGGAAACA    38131         A___
                                AGGACCAAA    AAACA
                                |||||||||    |||||
                                TCCTGGTTT    TTTGT
                                     CTCC
GAM1960 AQP6     3' GGTGAGAGGATGGGAGGG    38254     AAA      A
                                GGT   AGGGTGG AGGG
                                |||   ||||||| ||||
                                CCA   TCCTACC TCCC
                                  CTC      C
GAM1960 ATP1A1   5' GGCGGGAGGGTGGGAGGG    8698      AAA      A
                                GGT   AGGGTGG AGGG
                                |||   ||||||| ||||
                                CCG   TCCCACC TCCC
                                  CCC      C
GAM1960 ATP2A3   3' GGCAAGGGTGGGGGGCG     23197     AA      AA
                                GGTA  AGGGTGG  GGGTG
                                ||||  |||||||  |||||
                                CCGT  TCCCACC  CCCGC
                                   __      C_
GAM1960 CACNG6   3' GGTCAAAGGGCTCGGTGGTTG  36700     A      GGAAG
                                GGT AAAGGGT    GGTGGTTG
                                ||| |||||||    ||||||||
                                CCA TTTCCCG    CCACCAAC
                                  G      AG___
GAM1960 CALR     3' GGAGGGGGTGGGGGAGAGTG   41771    TAAAA     A__
                                GG    GGGTGG   AGGGTG
                                ||    ||||||   ||||||
                                CC    CCCACC   TCTCAC
                                 TCC__     CCC
GAM1960 CSF3     3' GGTGAAGAGGTGGAGGGTG    8903      A  AG     A
                                GGT AA  GGTGGA GGGTG
                                ||| ||  |||||| |||||
                                CCA TT  CCACCT CCCAC
                                  C  CT     _
GAM1960 CYP17    3' GGAGAAGGGTGGGGGGTT     6439     TAA       AAG  T
                                GG   AAGGGTGG   GG GGTT
                                ||   ||||||||   || ||||
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                                CC   TTCCCACC   CC CCAA
                                 TC_       ___  _
GAM1960  DYT1     3'  GGTGGAAGTGTGGAAGGACTG  6476      AA   G       _
                                GGT  AAG GTGGAAGGG TG
                                |||  ||| |||||||||  ||
                                CCA  TTC CACCTTCCT AC
                                  CC   A        G
GAM1960  MAL      3'  GGCAGTGGGGGGGGTGGTT    35334     AAAAG    AA
                                GGT    GGTGG  GGGTGGTT
                                |||    |||||  ||||||||
                                CCG    TCACC  CCCACCAA
                                  ______    CC
GAM1960  MSN      3'  GGTGGGGGGTGTGGAAGGG    41246     AAAA  _
                                GGT    GG GTGGAAGGG
                                |||    ||  |||||||||
                                CCA    CC CACCTTCCC
                                  CCC_  A
GAM1960  NONO     3'  GGTGAAAGGGGGAAGAGATTG  44358     A     T      TG
                                GGT AAAGGG GGAAGGG  GTTG
                                ||| |||||| |||||||  ||||
                                CCA TTTCCC CCTTCTC  TAAC
                                  C     _      __
GAM1960  SUOX     3'  GGAAAGGGGTGGAGGTG     7839     T   A      AG
                                GG AAA GGGTGGA  GGTG
                                ||  ||| |||||||  ||||
                                CC TTT CCCACCT  CCAC
                                 _   C       __
GAM1961  COL15A1  3'  AGCAGTCCTGTTTCTGT     12349         TATATC
                                AGCAGTCTT     TTCTGT
                                |||||||||     ||||||
                                TCGTCAGGA     AAGACA
                                     CA_____
GAM1961  DCX      5'  AAGCAGTCTTTGCATTTCAGT  8142           A   C   T
                                AAGCAGTCTTT TAT TTC GT
                                |||||||||||  ||| ||| ||
                                TTCGTCAGAAA GTA AAG CA
                                      C   _   T
GAM1961  FANCC    3'  GCGCTCTCCGCCTCTTCTGTAT 43277    AG     ATA
                                GC  TCTTT   TCTTCTGTAT
                                ||  |||||   ||||||||||
                                CG  AGAGG   AGAAGACATA
                                 CG    CGG
GAM1961  MAPK1    3'  GCAGTCTTTATATAACCCAT   15651           CT
                                GCAGTCTTTATAT  TCTGT
                                ||||||||||||  |||||
                                CGTCAGAAATATA  GGGTA
                                        TT
GAM1961  MELK     3'  AACAGTCTTTATGTAGGCTGTA 31332           ATCTT
              T                  AGCAGTCTTTAT    CTGTAT
                                 ||||||||||||    ||||||
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                                TTGTCAGAAATA    GACATA
                                      CATCC
GAM1962 CAPZB    3' CTCTATGGAAATGTGGAGA   22317    GGAT
                                CTT   TGGAAATGTGGAGA
                                |||   ||||||||||||||
                                GAG   ACCTTTACACCTCT
                                  AT__
GAM1962 CBFA2T1  5' TGCACTTGGAGCAGAAATGTGG 20311    _     TT
             AG                   TG ACTTGGA  GGAAATGTGGAG
                                || |||||||  ||||||||||||
                                AC TGAACCT  TCTTTACACCTC
                                 G      CG
GAM1962 CHRM1    3' TGGGTTGGATTGGGGAG    45426    AC       AAATGT
                                TG  TTGGATTGG     GGAG
                                ||  |||||||||     ||||
                                AC  AACCTAACC     CCTC
                                 CC       _______
GAM1962 CLECSF5  3' TGTCTTGTGAGTGTGGAG    29932    GA  _  AA
                                TG  TTG GA  TGTGGAG
                                ||  ||| ||  |||||||
                                AC  AAC CT  ACACCTC
                                 AG   A  C_
GAM1962 CMRF35   3' GGATTCCAGGAGATGTGGAGA  27435      ___  A
                                GGATT   GGA ATGTGGAGA
                                |||||   ||| |||||||||
                                CCTAA   CCT TACACCTCT
                                   GGT   C
GAM1962 DGKG     3' CCTGTGGGAATGTGGAG     10652      GAT   A
                                CTTG   TGG AATGTGGAG
                                ||||   ||| |||||||||
                                GGAC   ACC TTACACCTC
                                  ___   C
GAM1962 MOCS1    3' TGCTTGGATTGGCTGGTGGGGA 45127    A        AAAT    A
                                TG CTTGGATTGG    GTGG GA
                                || ||||||||||    |||| ||
                                AC GAACCTAACC    CACC CT
                                 _         GAC_    C
GAM1962 PGM1     3' TGACTTGGATGGGTCCGGG    15259          T  AAA  T
                                TGACTTGGAT GG   TG GG
                                |||||||||| ||   || ||
                                ACTGAACCTA CC   GC CC
                                      C  AG_  _
GAM1962 PTPN1    3' TGACTTGGAATGGCGGAG     15907         T   AAATG
                                TGACTTGGA TGG     TGGAG
                                ||||||||| |||     |||||
                                ACTGAACCT ACC     GCCTC
                                      T  ______
GAM1962 TKTL1    3' TGACTTGAACAGTACAGTGTGG 29316          TGGAAA_
             AG                   TGACTTGGAT      TGTGGAG
                                ||||||||||      |||||||
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                                ACTGAACTTG      ACACCTC
                                     TCATGTC
GAM1962 TLR5     5' TGGTTTGGTGACTGTGGAG   44292     A   AAA_
                                TGG TTGG    TGTGGAG
                                ||| ||||    |||||||
                                ACC AACC    ACACCTC
                                  A    ACTG
GAM1962 TNFSF4   3' TGATTTGGATCGGGATTGGA  17758     C       AAATG
                                TGA TTGGATTGG     TGGA
                                ||| |||||||||     ||||
                                ACT AACCTAGCC     ACCT
                                  A       CTA__
GAM1962 ACP2     3' CTCCCTCCCAAGTACAGAC   11507     ACAA
                                TTC    TCCAAGTACAGAC
                                |||    ||||||||||||
                                GAG    GGGTTCATGTCTG
                                  GGA_
GAM1962 CD83     3' TTCACAATGCTATCTCACTACA 20144       _____  _ AG
             GA                   TTCACA    ATC CA  TACAGA
                                ||||||    ||| ||  ||||||
                                AAGTGT    TAG GT  ATGTCT
                                   TACGA   A  G_
GAM1962 CSNK1A1  3' TTCACAATTACAGA       12466        CCAAG
                                TTCACAAT    TACAGA
                                ||||||||    ||||||
                                AAGTGTTA    ATGTCT
                                     _____
GAM1962 EDNRA    5' TCCACAATCGTCAGA      41998        CAA  A
                                TTCACAATC   GT CAGA
                                |||||||||   || ||||
                                AGGTGTTAG   CA GTCT
                                     ___  _
GAM1962 EN2      3' TTCACATGCATACAGAC     10969       ATCCAA
                                TTCACA     GTACAGAC
                                ||||||     ||||||||
                                AAGTGT     TATGTCTG
                                   ACG___
GAM1962 FABP2    3' TTCACAACCAGTTCAA      6589        T   A  A
                                TTCACAA CCA GT CAG
                                ||||||| ||| || |||
                                AAGTGTT GGT CA GTT
                                   _  _  A
GAM1962 FAT      3' TCACAAATATACAGAC      23491       TCCAA
                                TCACAA    GTACAGAC
                                ||||||    ||||||||
                                AGTGTT    TATGTCTG
                                   TA___
GAM1962 GUCY2F   5' TTCACAATCCTGTCAAGGAC  11342         AAG  CA
                                TTCACAATCC   TA  GAC
                                ||||||||||   ||  |||
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                                AAGTGTTAGG  GT  CTG
                                     ACA  TC
GAM1962 HMGCR   3' TCCACAATAACAATGCAGAC  9238       CCA  A
                                TTCACAAT  AGT CAGAC
                                ||||||||  ||| |||||
                                AGGTGTTA  TTA GTCTG
                                    TTG  C
GAM1962 IRS2    3' TCCATGATCAATACAGAC   40714    CA  CA
                                TTCA  ATC  AGTACAGAC
                                ||||  |||  |||||||||
                                AGGT  TAG  TTATGTCTG
                                  AC  __
GAM1962 MMP13   3' TCACAATCTAGTAGAC     14555      CA  AC
                                TCACAATC  AGT  AGAC
                                ||||||||  |||  ||||
                                AGTGTTAG  TCA  TCTG
                                    A_  __
GAM1962 NAPB    3' TTCACAGCAACACAGAC    43182     ATC  G
                                TTCACA  CAA TACAGAC
                                ||||||  ||| |||||||
                                AAGTGT  GTT GTGTCTG
                                   C__  _
GAM1962 NT5E    3' TTCACAATACACACACAGA   14866       C  AG
                                TTCACAAT CA  TACAGA
                                |||||||| ||  ||||||
                                AAGTGTTA GT  GTGTCT
                                    T  GT
GAM1962 NUP62   3' CTCACAATCTAACAGCGAGAC 29600       CA__  AC
                                TTCACAATC   AGT  AGAC
                                |||||||||   |||  ||||
                                GAGTGTTAG   TCG  TCTG
                                     ATTG  C_
GAM1962 POV1    3' TTCACACATACACAGAC    18845     ATC  AG
                                TTCACA  CA  TACAGAC
                                ||||||  ||  |||||||
                                AAGTGT  GT  GTGTCTG
                                   ___  AT
GAM1962 PTPRO   3' CTCACAACCCATGCAGA    36224        AGTA
                                TTCACAATCCA   CAGA
                                ||||||||||   ||||
                                GAGTGTTGGGT   GTCT
                                     AC__
GAM1962 SNTB2   3' CCAAAATCCAAGTATAGA   39292    C       C
                                TCA AATCCAAGTA AGA
                                ||| |||||||||| |||
                                GGT TTAGGTTCAT TCT
                                  T       A
GAM1962 UTX     5' TTCACAACTCCAACGCCGAC  41604       _   GTACA
                                TTCACAA TCCAA   GAC
                                ||||||| |||||    |||
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                                AAGTGTT AGGTT    CTG
                                   G    GCGG_
GAM1962  WHSC1    3'  TTCACAACTTGAATACGAC   39397       CCA    A
                                TTCACAAT   AGTAC GAC
                                ||||||||   ||||| |||
                                AAGTGTTG   TTATG CTG
                                    AAC    _
GAM1962  ZFP93    3'  TTCACAATCATCAGCATGGAC  20149       CA_   CA
                                TTCACAATC   AGTA  GAC
                                |||||||||   ||||  |||
                                AAGTGTTAG   TCGT  CTG
                                     TAG    AC
GAM1963  CD5L     3'  TTCAAATGTTCCTTTC      25320         AA
                                TTCAAATGTT  TCTTTC
                                ||||||||||  ||||||
                                AAGTTTACAA  GGAAAG
                                            __
GAM1963  FHL1     3'  TTCAAATGTTAATTTTC     11102          C
                                TTCAAATGTTAAT TTTC
                                |||||||||||| ||||
                                AAGTTTACAATTA AAAG
                                            _
GAM1963  JJAZ1    3'  CTCAAATGCGTTCTTTC     31689        TAA
                                TTCAAATGT   TCTTTC
                                |||||||||   ||||||
                                GAGTTTACG   AGAAAG
                                     CA_
GAM1963  OPHN1    3'  TTCAAATGTTTGCCTTTC    14977         AA
                                TTCAAATGTT  TCTTTC
                                ||||||||||  ||||||
                                AAGTTTACAA  GGAAAG
                                      AC
GAM1963  PCSK2    3'  TTCAAACGTGCCCCTTTC    15139        TAA
                                TTCAAATGT   TCTTTC
                                |||||||||   ||||||
                                AAGTTTGCA   GGAAAG
                                     CGG
GAM1963  SNAI2    3'  TTCAAAGCTAATCTTTC     16889       T
                                TTCAAA GTTAATCTTTC
                                ||||||  ||||||||||
                                AAGTTT CGATTAGAAAG
                                           _
GAM1963  BCL11A   3'  CATACAAATAATTTGCACTATA 39706     T       CC_
                                CAT ACAAATAAT   TACTATA
                                |||  |||||||||   |||||||
                                GTA TGTTTATTA   GTGATAT
                                  _       AAC
GAM1963  C5       3'  TTACAAATAAGACCAGCTAT   11916         TC  _
                                TTACAAATAA  CTA CTAT
                                ||||||||||  |||  ||||
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                                AATGTTTATT  GGT GATA
                                     CT   C
GAM1963 JRKL     3'  AACATTACAAAACCTGTACTAT 19088          TAAT  __
             A                    AACATTACAAA   CCT  ACTATA
                                  ||||||||||    |||  ||||||
                                  TTGTAATGTTT   GGA  TGATAT
                                       T___   CA
GAM1963 SHANK2   3'  ATCACAAATAATTCACT    29449          CC
                                  ATTACAAATAAT  TACT
                                  ||||||||||||  ||||
                                  TAGTGTTTATTA  GTGA
                                       A_
GAM1963 TAX1BP1  3'  AACATTGAAATAATCCT    25695       AC
                                  AACATT  AAATAATCCT
                                  ||||||  ||||||||||
                                  TTGTAA  TTTATTAGGA
                                     C_
GAM1963 WHSC1    3'  AACATCACAAACATTTACT   39346           ATCC
                                  AACATTACAAATA   TACT
                                  ||||||||||||    ||||
                                  TTGTAGTGTTTGT   ATGA
                                       AA__
GAM1964 EBAG9    5'  AAAAATCGGCCTGGAGA     20114         GA  A
                                  AAAAATCGGC  TG AGA
                                  ||||||||||  || |||
                                  TTTTTAGCCG  AC TCT
                                       G_  C
GAM1964 FBXL3A   3'  TAAAAAAAATTCGGAGAT    29129         A   C
                                  TAAGAAAAA TCGG GAT
                                  |||||||||  |||| |||
                                  ATTTTTTTT AGCC CTA
                                       A   T
GAM1964 PTGFRN   3'  AGAAAAAAAATTAGATGAAG  42583        TCGGC
                                  AGAAAAAA    GATGAAG
                                  ||||||||    |||||||
                                  TCTTTTTT    CTACTTC
                                       TTAAT
GAM1964 AXIN2    3'  TCTCTTAGTTTATGGATTTC  21641         A   TT
                                  TCTCTTAG TTAT  GTTTT
                                  ||||||| ||||  |||||
                                  AGAGAATC AATA  TAAAG
                                       A   CC
GAM1964 KLK4     3'  TCTCTTAGACTTTATTTC    41756         TA
                                  TCTCTTAGAT  TTTGTTTT
                                  ||||||||||  ||||||||
                                  AGAGAATCTG  AAATAAAG
                                              __
GAM1964 NXF5     5'  TCTCTCAGACCTAGTGTTTTCC 37621          ATT
             AG                     TCTCTTAGATT   TGTTTTCCAG
                                  ||||||||||   ||||||||||
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                                AGAGAGTCTGG   ACAAAAGGTC
                                      ATC
GAM1964  RPH3AL   3'  TCTCTTCAGGGAAGGGTTTTCC 28105       AGATTATTT
             AG                   TCTCTT       GTTTTCCAG
                                  ||||||       |||||||||
                                  AGAGAA       CAAAAGGTC
                                     GTCCCTTCC
GAM1964  TMEPAI   3'  TCTCTTAGCTTGTGCATTC   33624        ATTATT   T
                                  TCTCTTAG     TGT TTC
                                  ||||||||     ||| |||
                                  AGAGAATC     ACG AAG
                                       GAAC__   T
GAM1964  TRPS1    3'  TCTTATGGATTATTTCCCCAG  30468      __      TGT TT
                                  TCTTA  GATTATT   T  CCAG
                                  |||||  |||||||  |  ||||
                                  AGAAT  CTAATAA   A  GGTC
                                     AC      ___ GG
GAM1965  ADAM11   3'  TCCACATAGCTCAGGTCAGAGC 34660        A  CC___    A
             CGTC                    TCCACGTA GC     TCAGA CCGTC
                                  ||||||||  ||     |||||  |||||
                                  AGGTGTAT CG     AGTCT GGCAG
                                       _  AGTCC     C
GAM1966  APBB1    5'  GACGGAGGTGGCTCAGGC    10115     AT      GGT
                                  GAC  AGGTGGCT   GGT
                                  |||  ||||||||   |||
                                  CTG  TCCACCGA   CCG
                                    CC       GT_
GAM1966  IRTA2    3'  CAACAGCAGCTGGTGGTGCT   36337      TAG TG
                                  CGACA   G  GCTGGTGGTGCT
                                  |||||   |  ||||||||||||
                                  GTTGT   C  CGACCACCACGA
                                     ___ GT
GAM1966  MFGE8    3'  GACTGTGTGGTGGTGCT     25461     ATAG   GC
                                  GAC    GTG  TGGTGGTGCT
                                  |||    |||  ||||||||||
                                  CTG    CAC  ACCACCACGA
                                    A___   __
GAM1966  PLA2G10  5'  CAGAGGTGGGACGGTGCT    18671    T     CT GT
                                  CA AGGTGG  G  GGTGCT
                                  || ||||||  |  ||||||
                                  GT TCCACC  C  CCACGA
                                   C      __ TG
GAM1966  PNUTL1   3'  GACCTGGGAGGGGGTGGTGCT  15429     ATA  T  CT
                                  GAC   GG GG  GGTGGTGCT
                                  |||   || ||  |||||||||
                                  CTG   CC CC  CCACCACGA
                                    GAC  T  C_
GAM1966  SOX10    3'  CATAGGTGGCATGGGC      27999          TG    T
                                  CATAGGTGGC  GTGG GC
                                  ||||||||||  |||| ||
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                                GTATCCACCG  TACC CG
                                  __   _
GAM1967  DCK     3'  AAAGAAACTTATATTAATATGA 8976      TTTAG   C
             AG                   AGAG    TATA TAATATGAAG
                                  ||||    |||| ||||||||||
                                  TTTC    ATAT ATTATACTTC
                                    TTTGA   A
GAM1967  OTX1    3'  AGAGTTTAGTAGGGGCTGAAG  30979          TACTAATA
                                  AGAGTTTAGTA      TGAAG
                                  ||||||||||       |||||
                                  TCTCAAATCAT      ACTTC
                                       CCCCG___
GAM1967  SART1   3'  GAGCTTTATTTAATATGAAG  23111       A  ATAC
                                  GAGTTT GT   TAATATGAAG
                                  |||||| ||   ||||||||||
                                  CTCGAA TA   ATTATACTTC
                                     A  A___
GAM1968  ATP5J   5'  GGGCCTTTTCCCCCACAAG   11771      ACCC      C
                                  GGGC   TCCCCCAC GAG
                                  ||||   |||||||| |||
                                  CCCG   AGGGGGTG TTC
                                    GAAA      _
GAM1968  GRN     3'  AGGGCACCCTCCGAG       13289           CCCACC
                                  AGGGCACCCTCC     GAG
                                  ||||||||||||     |||
                                  TCCCGTGGGAGG     CTC
                                       _______
GAM1968  MATK    3'  GGGCCAAGGGCCCCACCGGGTG 40314      ACCCTC      A
                                  GGGC     CCCCACCG GTG
                                  ||||     |||||||| |||
                                  CCCG     GGGGTGGC CAC
                                    GTTCCC       C
GAM1968  STAU    3'  AGGGACCGCCAGGTCACCGAGT 32690     C  _  CCCC
             G                     AGGG ACC CT   CACCGAGTG
                                  |||| ||| ||   |||||||||
                                  TCCC TGG GG   GTGGCTCAC
                                    _  C  TCCA
GAM1968  UBE2I   5'  CAGGATGTCCTTCCCCAC    17815      CAC   C
                                  CAGGG   CCT CCCCAC
                                  |||||   ||| ||||||
                                  GTCCT   GGA GGGGTG
                                     ACA   A
GAM1968  XPNPEP1  3'  GGGCATCTTCCTTTCACCAAGT 33782      CCC   CC_
             G                     GGGCA   TCC   CACCGAGTG
                                  |||||   |||   |||||||||
                                  CCCGT   AGG   GTGGTTCAC
                                     AGA   AAA
GAM1968  ZNF215  3'  CAGGGCACACTTCCTCAC    29916        C  C  C
                                  CAGGGCAC CT CC CAC
                                  |||||||| || || |||
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                                GTCCCGTG GA GG GTG
                                     T  A  A
GAM1969  AHSG     3'  TCAGGCACTTTCATTAACA   11559      T  C  AA
                                TCAG GC AC  TTTCATTAACA
                                |||| || ||  ||||||||||
                                AGTC CG TG  AAAGTAATTGT
                                  _  _  __
GAM1969  CX3CR1   3'  GTGCCACAATATGAACA     43296          TTCATT
                                GTGCCACAAT     AACA
                                ||||||||||     ||||
                                CACGGTGTTA     TTGT
                                     TAC___
GAM1969  GSTM3    3'  TCAGTACCACAGTTTTACT   42765           A   C
                                TCAGTGCCACA TTT ATT
                                |||||||||||| ||| |||
                                AGTCATGGTGT AAA TGA
                                     C   A
GAM1969  RTN3     3'  GTACACACAGTTTCATTA    43961      _   A
                                GTGC CACA TTTCATTA
                                |||| |||| ||||||||
                                CATG GTGT AAAGTAAT
                                  T   C
GAM1969  TUFT1    3'  AGTGTCACTCTGACATTAACAA 33508      C   AATTT
                                AGTG CAC    CATTAACAA
                                |||| |||    |||||||||
                                TCAC GTG    GTAATTGTT
                                  A  AGACT
GAM1970  GAS11    3'  TCTTGCTCATGGGATAAATTGT 11221        TTAGTTAGTC
           G                     TCTTGCTC        ATTGTG
                                ||||||||        ||||||
                                AGAACGAG        TAACAC
                                    TACCCTATT_
GAM1970  TMEFF1   3'  TTGCTGTGGTCATTGT      18976      CTTA  TA
                                TTGCT   GT  GTCATTGT
                                |||||   ||  ||||||||
                                AACGA   CA  CAGTAACA
                                  _____  C_
GAM1970  CYP1A1   3'  TAGAATAGAAGGATTGTT    7976          A_
                                TAGAGTAGAA  ATTGTT
                                ||||||||||  ||||||
                                ATCTTATCTT  TAACAA
                                     CC
GAM1970  EIF1A    3'  AAGTAGAAAAACTAATGTT   44804          _  T
                                GAGTAGAAAA TTG TGTT
                                |||||||||| ||| ||||
                                TTCATCTTTT GAT ACAA
                                     T  T
GAM1970  GRIA2    3'  GAGTAGAAAAAGATGTT     9083          TTGT
                                GAGTAGAAAA   TGTT
                                ||||||||||   ||||
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                                CTCATCTTTT   ACAA
                                     TCT_
GAM1970 INPP5B   3' AGAGTAGAAATGACCTGTT   45469        ATTG
                                AGAGTAGAAA   TTGTT
                                ||||||||||   |||||
                                TCTCATCTTT   GACAA
                                     ACTG
GAM1970 MPHOSPH1 3' CAGAGTAGAAGAATGGTT   32114         _  T
                                TAGAGTAGAA AAT GTT
                                |||||||||| ||| |||
                                GTCTCATCTT TTA CAA
                                     C  C
GAM1970 NID      3' GAGGGAAAAGTTGTTGTT   14796    TA   A
                                GAG  GAAA TTGTTGTT
                                |||  |||| ||||||||
                                CTC  TTTT AACAACAA
                                  CC   C
GAM1970 NXF5     5' TAGAGTATACTTTTGTTGTT  37623      GAAAA
                                TAGAGTA    TTGTTGTT
                                |||||||    ||||||||
                                ATCTCAT    AACAACAA
                                    ATGAA
GAM1970 PCSK2    3' TAGAGTAAAAAAGATTGTT   15130         TT
                                TAGAGTAGAAAA  GTTGTT
                                ||||||||||||  ||||||
                                ATCTCATTTTTT  TAACAA
                                     C_
GAM1970 PLAG1    3' GAGTAGGACTGTTGTT     15352      AAA
                                GAGTAG   ATTGTTGTT
                                ||||||   |||||||||
                                CTCATC   TGACAACAA
                                   C__
GAM1970 SMARCA3  3' AGAGTAGACTGTGTTGTT   40053       AAAT
                                AGAGTAGA   TGTTGTT
                                ||||||||   |||||||
                                TCTCATCT   ACAACAA
                                     GAC_
GAM1970 TRPM6    3' TAGAATAGGATAAAGTTGTT  32794       AAAATT
                                TAGAGTAG     GTTGTT
                                ||||||||     ||||||
                                ATCTTATC     CAACAA
                                     CTATTT
GAM1971 LIMK1    3' TCCTGGATGGGGGTGGGT    32540    C  T  ATTTTT
                                TCC GG TG     GGGTGGGT
                                ||| || ||     ||||||||
                                AGG CC AC     CCCACCCA
                                  A  T  C_____
GAM1971 OXTR     3' AGTTGATTTTTGCACATAGTG  9520          G TG_
                                GGTTGATTTTTG G   GGTG
                                ||||||||||| |   ||||
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                                TCAACTAAAAAC T   TCAC
                                      G GTA
GAM1971  WT1     5'  TCCCGGCTCTGGGTGGGT    35972       TGATT
                                TCCCGGT    TTTGGGTGGGT
                                |||||||    ||||||||||
                                AGGGCCG    AGACCCACCCA
                                     _____
GAM1971  APM1    3'  AGCCTTTAATTGACTTTGG   22009        CTAC   AAA
                                AGCCTTTAA   ATT   TTGG
                                |||||||||   |||   ||||
                                TCGGAAATT   TGA   AACC
                                     AAC_  ___
GAM1971  PTP4A2  5'  AGCCTTTACTACATTTAG    38619        A      AAAT
                                AGCCTTTA CTACATT    TGG
                                |||||||| |||||||    |||
                                TCGGAAAT GATGTAA    ATC
                                     _     ____
GAM1972  CUL3    3'  TGAGAATTTTAATTTTCCCACA 18749     A       A    T
                TT                  TGA AATTTTAAT TTTCT CATT
                                ||| ||||||||| ||||| ||||
                                ACT TTAAAATTA AAGGG GTAA
                                  C       A    T
GAM1972  IL1RAP  3'  TGAAAACTTTCATATTTTTCAT 13507         A     C
                T                   TGAAAATTTT ATATTT TTCATT
                                |||||||||| |||||| ||||||
                                ACTTTTGAAA TATAAA AAGTAA
                                     G    _
GAM1972  ATRX    3'  AGTAAAACTAATATGGAAGATT 39602      T      A
                                AGTGA ACTAATAT GAAGATT
                                ||||| |||||||| |||||||
                                TCATT TGATTATA CTTCTAA
                                   T      C
GAM1973  ALS2    3'  ATAACACAAAGTCCTTTCCA   34091        TCT    C_
                                ATAACACAA   GGTCT  TCCA
                                |||||||||   |||||  ||||
                                TATTGTGTT   TCAGG  AGGT
                                     ___    AA
GAM1973  CD28    3'  TACATACACTTGGTCTCT    26024     _   AATC
                                TATA ACAC    TGGTCTCT
                                |||| ||||    ||||||||
                                ATGT TGTG    ACCAGAGA
                                  A   A___
GAM1973  CYBB    3'  ATAACACAGGGCAGATCTCTC  44092       ATCT_
                                ATAACACA    GGTCTCTC
                                ||||||||    ||||||||
                                TATTGTGT    CTAGAGAG
                                     CCCGT
GAM1973  EBF     3'  TAGCAGAATCCAACCTCTTCA  42369    A  C    GG    C
                                TA CA AATCT  TCTCT CA
                                || || |||||  ||||| ||
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                                AT GT TTAGG  GGAGA GT
                                 C  C     TT     A
GAM1973  ESR1     3'  TATAACCAATGACCTCTC    6537        A   TC  GT
                                TATAAC CAA  TG  CTCTC
                                |||||| |||  ||  |||||
                                ATATTG GTT  AC  GAGAG
                                   _   __  TG
GAM1973  F12      3'  ACACAATCTTGCCTTCCA    7996          G    C
                                ACACAATCT GTCT TCCA
                                ||||||||| |||| ||||
                                TGTGTTAGA CGGA AGGT
                                      A    _
GAM1973  FMR2     3'  TATAACACTGTCTCATCT    12981         AA   G
                                TATAACAC  TCT GTCT
                                ||||||||  ||| ||||
                                ATATTGTG  AGA TAGA
                                     AC   G
GAM1973  GPC4     3'  ATAACACAAACAACCTCT    11083         TC GG
                                ATAACACAA  T  TCTCT
                                |||||||||  |  |||||
                                TATTGTGTT  G  GGAGA
                                      T_ TT
GAM1973  GRIA2    3'  CATAACACGTCCATTTTCTCCA 9081          AA    GTC
                                TATAACAC  TCTG   TCTCCA
                                ||||||||  ||||   ||||||
                                GTATTGTG  AGGT   AGAGGT
                                     C_    AAA
GAM1973  JDP1     3'  TATAATACAATCTACTCT    34761       C       G
                                TATAA ACAATCTG TCT
                                ||||| |||||||| |||
                                ATATT TGTTAGAT AGA
                                   A       G
GAM1973  LEPR     3'  TATAACACAAATCTGAAGGTTT 14134           _  ____  C   C
              CTTCA                  TATAACACAA TCT   GGT TCT CA
                                |||||||||| |||   ||| ||| ||
                                ATATTGTGTT AGA   CCA AGA GT
                                      T   CTT   A   A
GAM1973  NPY2R    3'  AACACAATCTCTCTCTCTCTCC 9486           GG___
              A                   AACACAATCT     TCTCTCCA
                                ||||||||||     ||||||||
                                TTGTGTTAGA     AGAGAGGT
                                     GAGAG
GAM1973  PCDH11X  3'  TAAACACAATCTAAGTCT    37305    T        _
                                A AACACAATCTG GTCT
                                | ||||||||||| ||||
                                A TTGTGTTAGAT CAGA
                                 T         T
GAM1973  PCDH11Y  3'  TAAACACAATCTAAGTCT    37345    T        _
                                A AACACAATCTG GTCT
                                | ||||||||||| ||||
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```
                                A TTGTGTTAGAT CAGA
                                 T         T
GAM1973 RAD54B   3' TAACACAATCTGAACTTTC   39583          GT  C
                                TAACACAATCTG  CT TC
                                ||||||||||||  || ||
                                ATTGTGTTAGAC  GA AG
                                       TT  A
GAM1973 RNF26    3' CACAGTCTGCCCTCTCCA    36752     A    G
                                CACA TCTG TCTCTCCA
                                |||| |||| ||||||||
                                GTGT AGAC GGAGAGGT
                                  C    G
GAM1973 SMARCA3  3' TATAACACAACATTGTCTCC  40054          CTG
                                TATAACACAAT   GTCTCT
                                ||||||||||   ||||||
                                ATATTGTGTTG   CAGAGG
                                       TAA
GAM1973 SORBS1   3' TAAACACAACACTTCTCT    31712    T      CTGG
                                A AACACAAT    TCTCT
                                | ||||||||    |||||
                                A TTGTGTTG    AGAGA
                                 T       TGA_
GAM1973 PCDHB9   3' GCTGGGTGCGGTGGCTCATG  33322        AATC_
                                GCTGGGTG    GCTCATG
                                ||||||||    |||||||
                                CGACCCAC    CGAGTAC
                                     GCCAC
GAM1974 OGT      5' TTGCGCTACTGCAGGGTCACAG 18793         CGATTCT
                                TTGCGCTAC      TCACAG
                                |||||||||      ||||||
                                AACGCGATG      AGTGTC
                                      ACGTCCC
GAM1975 ARHGEF12 3' TCTCTGACCACACCACCT    31652    C   G   C
                                TC CTGA CCAC ATCACCT
                                || |||| |||| |||||||
                                AG GACT GGTG TGGTGGA
                                 A   _   _
GAM1975 BAZ2A    5' TCCCTGAGCCTCAAG       30315         ACCA   CCT
                                TCCCTGAGCC    TCA   AG
                                ||||||||||    |||   ||
                                AGGGACTCGG    AGT   TC
                                      _____   ___
GAM1975 DDEF2    3' CTGAGCCATCATCCCAGA    19318        C    A  T
                                CTGAGCCA CATC CC AGA
                                |||||||| |||| || |||
                                GACTCGGT GTAG GG TCT
                                     A    _  _
GAM1975 EDG8     3' TCCCTGACCACCATCAC     44208        G
                                TCCCTGA CCACCATCAC
                                ||||||| ||||||||||
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                                AGGGACT GGTGGTAGTG
                                      _
GAM1975 IL2RB    3' TCCCTGAGCTGCAGAGGAGAC 9394         CAC  TCACCT
                                TCCCTGAGC   CA     AGAC
                                |||||||||   ||     ||||
                                AGGGACTCG   GT     TCTG
                                     AC_  CTCC__
GAM1975 LPIN2    3' TCCCTGAGCCGTCACCC     31220          ACCA
                                TCCCTGAGCC    TCACCT
                                ||||||||||    ||||||
                                AGGGACTCGG    AGTGGG
                                      C___
GAM1975 ORC2L    3' TCCCTGAGCACACTGTTCA   26195         _  CA_
                                TCCCTGAGC CAC   TCA
                                ||||||||| |||   |||
                                AGGGACTCG GTG   AGT
                                      T   ACA
GAM1975 PPARA    5' CCCTGAGCTTCAGCCT      22767        CACCA  _
                                CCCTGAGC    TCA CCT
                                ||||||||    ||| |||
                                GGGACTCG    AGT GGA
                                     A____   C
GAM1975 PSMB8    3' TCCCTGAGTCGGCCAAGA    45548        CCACCA  A_  T
                                TCCCTGAG     TC  CC AGA
                                ||||||||     ||  || |||
                                AGGGACTC     AG  GG TCT
                                     _______  CC  T
GAM1975 ZFHX1B   3' TCTCTGAACCACACAGTTTTTA 31343    C       _  TCACC
             G                   TC CTGAGCCAC CA     TAG
                                 || |||||||| ||     |||
                                 AG GACTTGGTG GT     ATC
                                  A        T  CAAAA
GAM1976 LTBP2    3' TGTTTATGTAATAGA       7697          AAT
                                TGTTTATGTA   ATAGA
                                ||||||||||   |||||
                                ACAAATACAT   TATCT
                                      ___
GAM1976 RFXAP    3' AATGTTTATGTTCTACAG    8049          AAA
                                AATGTTTATGT   TATAG
                                ||||||||||   |||||
                                TTACAAATACA   ATGTC
                                      AG_
GAM1977 HAS3     3' TGTGCACTTTTAAAAGCAG   39779      A  __
                                TGTG ACT  TAAAAGCAG
                                |||| |||  |||||||||
                                ACAC TGA  ATTTTCGTC
                                  G   AA
GAM1977 SOX15    3' TATGTTGTGCGGCTCTCCCTGG 28021         AA___  AAAA
             C                   TATGTTGTG    CTT   GC
                                 |||||||||    |||   ||
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                                ATACAACAC    GAG   CG
                                     GCCGA  GGAC
GAM1978 KCND2    3' GATGATTGATCCTGTGATAT  29365         AACAAC
                                GATGATTGAT     GATAT
                                ||||||||||     |||||
                                CTACTAACTA     CTATA
                                     GGACA_
GAM1978 MADH4    3' TATGATCATTGATGGCAA    23819       G     AA
                                TATGAT ATTGAT  CAA
                                |||||| ||||||  |||
                                ATACTA TAACTA  GTT
                                   G     CC
GAM1979 CDC7L1   3' ATTATTTTAAATTCCCAACT  18601       A_
                                ATTATT  AAATTTCCAACT
                                ||||||  ||||||||||||
                                TAATAA  TTTAAGGGTTGA
                                   AA
GAM1979 SLC4A7   3' TATCATTATTAAAGTTTC    18825           A
                                TATCATTATTAAA TTTC
                                |||||||||||| ||||
                                ATAGTAATAATTT AAAG
                                       C
GAM1980 ARSD     3' TGTAGAGATGGGGGGGGGGGC 28930      ____
                                TGTGG   GGGGGGGGGGGC
                                |||||   ||||||||||||
                                ACATC   CCCCCCCCCCCG
                                   TCTA
GAM1980 BCL7A    3' TGTGGTGGGGGGGAGGGC    34225      _
                                TGTGG GGGGGGGGGGGC
                                ||||| ||||||||||||
                                ACACC CCCCCCCTCCCG
                                   A
GAM1980 CAPZA1   5' TCCAACCCCGGGGGGGGGGGC 43720     TATGTGG
                                TCC      GGGGGGGGGGGC
                                |||      ||||||||||||
                                AGG      CCCCCCCCCCCG
                                  TTGGGG_
GAM1980 CD68     3' TCCTGCTGGGGGGGGGGGGGGG 40784     A_ T
             C                   TCCT  TG GGGGGGGGGGGGC
                                ||||  || ||||||||||||||
                                AGGA  AC CCCCCCCCCCCCCG
                                  CG  C
GAM1980 GRIN2D   5' CTGTTGGGGGGATGGCGGGGGG 9129     ATG     _____
             GC                  CT  TGGGGGG    GGGGGGGC
                                ||  |||||||    ||||||||
                                GA  ACCCCCC    CCCCCCCG
                                 CA_      TACCG
GAM1980 HDAC7A   3' TCCTATGTGGGGTGGGAA    32474          G
                                TCCTATGTGGGG GGGGG
                                |||||||||||| |||||
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                                AGGATACACCCC CCCTT
                                      A
GAM1980 KCNJ3    5' TCCTGGGTGGGGGGGG      13852     ATGT  GG    G
                                TCCT   GGG  GGGGGG G
                                ||||   |||  |||||| |
                                AGGA   CCC  CCCCCC C
                                  ____  A_    G
GAM1980 NME4     3' TCCTGCGTGGGGGATGGGG   22684     A     GG
                                TCCT TGTGGGGG  GGGG
                                |||| ||||||||  ||||
                                AGGA GCACCCCC  CCCC
                                  C       TA
GAM1980 OAS2     3' TCCTGGGTGGGGGGGATAAAGGC 32554     AT       GG
                                TCCT  GTGGGGGGG  GGGGC
                                ||||  |||||||||  |||||
                                AGGA  CACCCCCCT  TTCCG
                                  CC        AT
GAM1980 PDE4B    3' TCCTGTGGGGGGCAGGG     15152     AT      G
                                TCCT  GTGGGGGG GGGG
                                ||||  |||||||| ||||
                                AGGA  CACCCCCC TCCC
                                  __       G
GAM1980 POLA     3' TATGTGGGGGGGACATAGGC  32618          GG_
                                TATGTGGGGGGGG  GGGC
                                ||||||||||||  ||||
                                ATACACCCCCCCT  TCCG
                                      GTA
GAM1980 PTPRCAP  3' CCTGTGGTTGGGGGGGGC   24692    AT   GGG
                                CCT  GTGG  GGGGGGGGC
                                |||  ||||  |||||||||
                                GGA  CACC  CCCCCCCCG
                                  __   AA_
GAM1980 RAI14    3' CTGTGCGGGGGCAGAAGGGGC 31802    A     _
                                CT TGTGGGGG GGGGGGGGC
                                || |||||||| |||||||||
                                GA ACGCCCCC TCTTCCCCG
                                 C       G
GAM1980 TCOF1    3' TCCTGTGTTGGGGGAGTGGGG 7410      A  G     _
                                TCCT TGT GGGGGGG GGGG
                                |||| ||| ||||||| ||||
                                AGGA ACA CCCCCTC CCCC
                                  C  A      A
GAM1980 TEC      3' TCCTATGTGAGGTGGGGG    17389          G
                                TCCTATGTGGGG GGGGG
                                |||||||||||| |||||
                                AGGATACACTCC CCCCC
                                      A
GAM1980 TRH      3' CCTGTGGTGGGGGGGG      28289     AT   G
                                CCT  GTGG GGGGGGGG
                                |||  |||| ||||||||
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                                GGA  CACC CCCCCCCC
                                  __   A
GAM1981  GLI2    5'  CGGTGCCTTGAACGTTTTA   36117        __    CG
                                CGGTGCCT  GACGT  TA
                                ||||||||  |||||  ||
                                GCCACGGA  TTGCA  AT
                                    AC    AA
GAM1981  MTMR8   3'  GGTGATCCTTTGTATTTTAA  31752     __  GACGTC
                                GGTG  CCT    GTATTTTAA
                                ||||  |||    |||||||||
                                CCAC  GGA    CATAAAATT
                                  TA  AA____
GAM1981  TXK     3'  GGAGCTTGATGTCACATTT   17767    T  C   C
                                GG GC TGA GTCGTATTT
                                || || ||| |||||||||
                                CC CG ACT CAGTGTAAA
                                 T  A   A
GAM1982  ANKH    3'  GTCCAGGGGAGGAGGACAC   38324      A___
                                GTCCG   AGGAGGACAC
                                |||||   ||||||||||
                                CAGGT   TCCTCCTGTG
                                   CCCC
GAM1982  BACE    3'  AGCTCTTGTGGTGGAGGACA  39947    A  C  CCGAA
                                AGC CT GT    GGAGGACA
                                ||| || ||    ||||||||
                                TCG GA CA    CCTCCTGT
                                  A  A  CCA__
GAM1982  BFSP2   3'  AAGCATTTATTTGAAGGAGGAC 18699      CTCGTCC
                                AAGCA      GAAGGAGGAC
                                |||||      ||||||||||
                                TTCGT      CTTCCTCCTG
                                   AAATAAA
GAM1982  HS3ST3B1 5' GCGCTCGGGGCCAGGAGGAC  25795    A   TCCGA
                                GC CTCG    AGGAGGAC
                                || ||||    ||||||||
                                CG GAGC    TCCTCCTG
                                 C   CCCGG
GAM1982  IRS1    5'  GCAGCTGAAGGAGGAC     24424     CTC  CC
                                GCA   GT  GAAGGAGGAC
                                |||   ||  ||||||||||
                                CGT   CG  CTTCCTCCTG
                                  ___  A_
GAM1982  NDRG1   3'  GCACCCGTTTGAACCAGGA   40578       CC   GG
                                GCACTCGT  GAA  AGGA
                                ||||||||  |||  ||||
                                CGTGGGCA  CTT  TCCT
                                    AA   GG
GAM1982  PFKP    3'  GCACTCGCCGATTAGG      15241       T   AGG
                                GCACTCG CCGA   AGG
                                ||||||| ||||   |||
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                                CGTGAGC GGCT   TCC
                                   _   AA_
GAM1982 CRSP8    3' CTTCTTTGCCTTCAGTCCGC  44338      C   G
                                CTTCTT GCCT CAGTCCGC
                                |||||| |||| ||||||||
                                GAAGAA CGGA GTCAGGCG
                                   A   A
GAM1982 EIF2B1   3' CTTTTCGCCTGCATCTCG    40644    C       G _
                                CTT TTCGCCTGCA TC CG
                                ||| |||||||||| || ||
                                GAA AAGCGGACGT AG GC
                                  _       _ A
GAM1982 EPB41    5' TACTTCTTTGCCTTCTTCCTCG 20768       C   GCAG  GC
                                TACTTCTT GCCT   TCC  CG
                                |||||||| ||||   |||  ||
                                ATGAAGAA CGGA   AGG  GC
                                    A   AGA_  A_
GAM1982 FCN2     3' TACTTCTCCGCCTCGTC     31895          GCA
                                TACTTCTTCGCCT   GTC
                                ||||||||||||   |||
                                ATGAAGAGGCGGA   CAG
                                       G__
GAM1982 MTR      3' CTTCTTCGTCTTCATCCTTCG  7014        C  GCA   GC
                                CTTCTTCG CT   GTCC  CG
                                |||||||| ||   ||||  ||
                                GAAGAAGC GA   TAGG  GC
                                    A  AG_   AA
GAM1982 RRM2B    5' CTTTCTCGCCTGTCCA     42719    CT    GCA
                                CTT  TCGCCT   GTCCG
                                |||  ||||||   |||||
                                GAA  AGCGGA   CAGGT
                                  AG     ___
GAM1983 EDG8     3' TCTTTTCCGACTGCACCT    44210     CC    G
                                TCTTT  CTGAC GCATCT
                                |||||  ||||| ||||||
                                AGAAA  GGCTG CGTGGA
                                   A_    A
GAM1983 HIP1     3' TCTTCCCTGATGGGAGCA    23760     T    C___
                                TCTT CCCTGA   GGCA
                                |||| ||||||   ||||
                                AGAA GGGACT   TCGT
                                  _     ACCC
GAM1983 RPS6KA5  5' TCTTTCCCGCTCTGC      21916       TGACG  A  AA
                                TCTTTCCC    GC TCT  C
                                ||||||||    || |||  |
                                AGAAAGGG    CG AGA  G
                                    _____ _  CC
GAM1983 ADRA2A   3' AGGCACAGGAAAAAAAT     8624       CGTA
                                AGGCAC   AGGGAAAAAAT
                                ||||||   ||||||||||
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                                TCCGTG   TCCTTTTTTTA
                                   ____
GAM1983 CSRP1    3' TCAGGGCAAAGGGAAA     19844      _ CCGT
                                TCAGG CA   AAGGGAAA
                                ||||| ||   ||||||||
                                AGTCC GT   TTCCCTTT
                                   C ____
GAM1983 DNMT3B   3' GGGTTTGTGGGGGAAAAAAT  27879    CACC  AA
                                GG   GT  GGGAAAAAAT
                                ||   ||  ||||||||||
                                CC   CA  CCCTTTTTTA
                                 CAAA  CC
GAM1983 SUPT5H   3' CCAGGGAGGGAAAAA      17216      CACCGTA      A
                                TCAGG      AGGGAAAA A
                                |||||      |||||||| |
                                GGTCC      TCCCTTTT T
                                   C_______       C
GAM1984 ADRA2B   3' TCGGGGTAGGAATTCACACAC  8652      AACA_  GCA
                                TTGG    GAA   TTACACAC
                                ||||    |||   ||||||||
                                AGCC    CTT   AGTGTGTG
                                  CCATC   A__
GAM1984 CCND1    3' TTGGAATAGAGCAGTAATCACA 38230       C   A   T  CA
                                TTGGAA AGA GCA TA  CACA
                                |||||| ||| ||| ||  ||||
                                AACCTT TCT CGT AT  GTGT
                                   A   _   C  TA
GAM1984 EMS1     3' TTGGGGAAGAACACACAC    23430     AACA   CAT
                                TTGG   GAAG   TACACAC
                                ||||   ||||   |||||||
                                AACC   CTTC   GTGTGTG
                                  C___    TT_
GAM1984 MME      3' TTAGAAATTAAGCATTATGTAC 28615       CAG      C__
            AC                    TTGGAA   AAGCATTA   ACAC
                                ||||||   ||||||||   ||||
                                AATCTT   TTCGTAAT   TGTG
                                   TAA       ACA
GAM1984 MYLK     3' TTGGAATGTTACACACA     38169       CAGAAGCA
                                TTGGAA       TTACACACA
                                ||||||       |||||||||
                                AACCTT       AATGTGTGT
                                   AC_______
GAM1984 PDYN     3' TGGAGTAGAAGCATGATAC    35924      AC      __
                                TGGA  AGAAGCAT  TAC
                                ||||  ||||||||  |||
                                ACCT  TCTTCGTA  ATG
                                  CA       CT
GAM1984 SH3BP4   3' TTGGGTACAGAAAACACACAC  30964      A_      CATT
                                TTGG  ACAGAAG   ACACACAC
                                ||||  |||||||   ||||||||
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                                AACC  TGTCTTT    TGTGTGTG
                                  CA      ____
GAM1984  SLBP     3'  GAACAGAAAATCTGTACACA  27195         CAT__
                                GAACAGAAG     TACACA
                                |||||||||     ||||||
                                CTTGTCTTT     ATGTGT
                                     TAGAC
GAM1984  TCP1     3'  TTGTGACCCTGTTACACACAC  36246     GA  AGAAGCA
                                TTG  AC      TTACACACAC
                                |||  ||      ||||||||||
                                AAC  TG      AATGTGTGTG
                                  AC  GGAC___
GAM1984  CDC2L1   5'  TCCTCTTGTTCCTTCCTTCGTT 37913    G   CTA    GCA
                                TC CTC   TTCC   CCTTCGTT
                                || |||   ||||   ||||||||
                                AG GAG   AAGG   GGAAGCAA
                                 _   AAC    AA_
GAM1984  CDC2L2   5'  TCCTCTTGTTCCTTCCTTCGTT 37943    G   CTA    GCA
                                TC CTC   TTCC   CCTTCGTT
                                || |||   ||||   ||||||||
                                AG GAG   AAGG   GGAAGCAA
                                 _   AAC    AA_
GAM1984  SHMT2    3'  TCCCATTCTACCTTGTT     24010         CGC     C
                                TCCTATTC   ACCTT GTT
                                ||||||||   ||||| |||
                                AGGGTAAG   TGGAA CAA
                                     A__     _
GAM1985  ATF5     3'  TAGCGTAGTGTCCCAAGGTCAC 28939      ACGCG__  A GAG
                                TAGC      CC C   GAGGTCAC
                                ||||      || |   ||||||||
                                ATCG      GG G   TTCCAGTG
                                  CATCACA  _ ___
GAM1985  FOXE1    5'  GCACGCGCTGGAGGC       20943         CACGA
                                GCACGCGC     GGAGGT
                                ||||||||     ||||||
                                CGTGCGCG     CCTCCG
                                     A____
GAM1985  GNAZ     3'  TAGCACGCGTTGGGGC       13183         CCACGA  A
                                TAGCACGCG     GG GGT
                                |||||||||     || |||
                                ATCGTGCGC     CC CCG
                                     AA____  _
GAM1985  HAP1     3'  GCATGCGCCATAAAGGTCA    19500     C     CGA
                                GCA GCGCCA   GGAGGTCA
                                ||| ||||||   ||||||||
                                CGT CGCGGT   TTTCCAGT
                                  A     A__
GAM1986  ADA      5'  GCCAGCGGTGGCCGCGGCCG   41547      C   CGCAA
                                GCCG GCG    CCGCGGCCG
                                |||| |||    |||||||||
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                                CGGT CGC    GGCGCCGGC
                                  _  CACC_
GAM1986 ADAM12   5' GCGTCGCGCGCGCCG    18474    C      AACCGCG
                                GCG CGCGCGCGC     GCCG
                                ||| |||||||||     ||||
                                CGC GCGCGCGCG     CGGC
                                  A      ________
GAM1986 BRF1    5' CGCCGCGCGCGCCCGGGCCG  11330          AA  C
                                CGCCGCGCGCGC  CCG GGCCG
                                ||||||||||||  ||| |||||
                                GCGGCGCGCGCG  GGC CCGGC
                                      __  _
GAM1986 BTEB1   5' GCCTCGCGGTCCCGTGGCCG  10216    G   CGCAA  C
                                GCC CGCG    CCG GGCCG
                                ||| ||||    ||| |||||
                                CGG GCGC    GGC CCGGC
                                  A   CAG__  A
GAM1986 CCND1   3' GCGCCGCGGTGCAACCA    38209       CGC
                                GCGCCGCG  GCAACCG
                                ||||||||  |||||||
                                CGCGGCGC  CGTTGGT
                                    CA_
GAM1986 CCND3   5' GCCCGCGCGCGCGCGC     12060    G       AACC  G
                                GC CCGCGCGCGC   GCG C
                                || ||||||||||   ||| |
                                CG GGCGCGCGCG   CGC G
                                _       _____  _
GAM1986 CDK2AP1  5' GCCCGCGCGCGTCCGGGCGGC 21598    G       CAA __
                                GC CCGCGCGCG   CC  GCGGC
                                || |||||||||   ||  |||||
                                CG GGCGCGCGC   GG  CGCCG
                                  _       A__  CC
GAM1986 CLCN4   5' GCCGCATCGCGCCCGCGGCCG 12286      _    AA
                                GCCGCG CGCGC  CCGCGGCCG
                                ||||||| |||||  |||||||||
                                CGGCGT GCGCG  GGCGCCGGC
                                   A    __
GAM1986 CYLN2   5' GCCTGCGCGCCCCGCGGCC   18053    GC    AA
                                GCC  GCGCGC  CCGCGGCC
                                |||  ||||||  ||||||||
                                CGG  CGCGCG  GGCGCCGG
                                  A_     G_
GAM1986 DAG1    5' GCGCCGCGCCGCAGCC     20522        GCGCAAC
                                GCGCCGCGC      CGCGGCC
                                |||||||||      |||||||
                                CGCGGCGCG      GCGTCGG
                                       ________
GAM1986 DSCAM   5' GCGCCGCGCCCCACGCTGCGGC 10805         ___   AACC
            CG                    GCGCCGCGC   GCGC   GCGGCCG
                                ||||||||||  ||||   |||||||
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                                CGCGGCGCG  TGCG   CGCCGGC
                                     GGG   A___
GAM1986  FBXL5   5'  CGCCTCAGCAGCCGCGGCCG  37947     G  CGC   A
                                CGCC CG   GCA CCGCGGCCG
                                |||| ||   ||| |||||||||
                                GCGG GT   CGT GGCGCCGGC
                                  A ___   C
GAM1986  FGFR1   5'  CGGCGCGCTCGCGGC      31935    C     AAC
                                CG GCGCGC   CGCGGC
                                || ||||||   ||||||
                                GC CGCGCG   GCGCCG
                                 _     A__
GAM1986  FOP     5'  GCTCCGCGCGCGGGCTACGCGG 28188    G       CAAC_
            CCG                    GC CCGCGCGCG    CGCGGCCG
                                || |||||||||    ||||||||
                                CG GGCGCGCGC    GCGCCGGC
                                 A       CCGAT
GAM1986  G1P3    5'  GCGCCGCGCGCGGGCTCC    35640          CAACC  GG
                                GCGCCGCGCGCG    GC  CC
                                ||||||||||||    ||  ||
                                CGCGGCGCGCGC    CG  GG
                                       C____  A_
GAM1986  GAD2    5'  GCCCTGCGCGCGCGTGCGTGCC 9055    G _      AACC  _
            G                   GC CC GCGCGCGC   GCG GCCG
                                || || ||||||||   ||| ||||
                                CG GG CGCGCGCG   CGC CGGC
                                 _ A      CA__  A
GAM1986  GRIN2A  5'  GCGCTGCGCGCACGAGCA   9111      C      AACC
                                GCGC GCGCGCGC   GCG
                                |||| ||||||||   |||
                                CGCG CGCGCGTG   CGT
                                  A      CT__
GAM1986  GTF2I   5'  GCCGCGCGCGGGCTGCGGCCG  37438        CAACC
                                GCCGCGCGCG    GCGGCCG
                                ||||||||||    |||||||
                                CGGCGCGCGC    CGCCGGC
                                      CCGA_
GAM1986  HBQ1    5'  GCGCCGCGCCGCAGCTTCG   23730        G   ACCG
                                GCGCCGCGC CGCA   CG
                                |||||||| ||||   ||
                                CGCGGCGCG GCGT   GC
                                      _   CGAA
GAM1986  HRB     5'  GCCGCCCTGGCCGCGGCCG   21087      GCGCGCAA
                                GCCGC      CCGCGGCCG
                                |||||      |||||||||
                                CGGCG      GGCGCCGGC
                                   GGACC___
GAM1986  HTR2C   5'  GCGCTGCGCGCCGCAACCTCG  9287      C    _    G
                                GCGC GCGCGC GCAACC CG
                                |||| |||||| |||||| ||
```

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                                CGCG CGCGCG CGTTGG GC
                                  A     G     A
GAM1986  HTR2C    5'  GCGCTGCGCTGCGCGC      9288       C   _   AACCGCG
                                GCGC GCGC GCGC      GC
                                |||| |||| ||||      ||
                                CGCG CGCG CGCG      CG
                                  A   A   ________
GAM1986  INPP4A   5'  GCGACGCGCGCGCCTGGC     19709     C       AACCGC
                                GCG CGCGCGCGC     GGC
                                ||| |||||||||     |||
                                CGC GCGCGCGCG     CCG
                                  T       GA____
GAM1986  JAG1     5'  GCGCCGCGCGCCGCGG      6858           GCAAC
                                GCGCCGCGCGC    CGCGG
                                ||||||||||    |||||
                                CGCGGCGCGCG    GCGCC

                                      ______
GAM1986  JAG2     5'  GCGCCGCGGCGCGCGGGCC   13725        C   AAC  C
                                GCGCCGCG GCGC   CG GGCC
                                |||||||| ||||   || ||||
                                CGCGGCGC CGCG   GC CCGG
                                     _   C__  _
GAM1986  JUND     5'  GCGCCCGCCCCGGCCGCGGCCG 23804      G   G_  CAA
                                GCGCC CGC  CG   CCGCGGCCG
                                ||||| |||  ||   |||||||||
                                CGCGG GCG  GC   GGCGCCGGC
                                   _   GG  C__
GAM1986  LY6E     5'  GCGCGCTCTGGACCGCGGC   14279       GCA__
                                GCGCGC    ACCGCGGC
                                ||||||    ||||||||
                                CGCGCG    TGGCGCCG
                                   AGACC
GAM1986  NFRKB    5'  GCCCGCGGGGCGGTCGCGGCCG 26095    G    C_   CAAC
                                GC CCGCG  GCG    CGCGGCCG
                                || |||||  |||    ||||||||
                                CG GGCGC  CGC    GCGCCGGC
                                 _    CC   CA__
GAM1986  NPY2R    5'  GCGCCGCGCGGGCGGGCAGCCG 9497           C  AACC
                                GCGCCGCGCG GC    GCGGCCG
                                |||||||||| ||    |||||||
                                CGCGGCGCGC CG    CGTCGGC
                                      C  CC__
GAM1986  PDGFB    5'  GCTCCGCGCGCGCGGCGTGCC  15181    G        AACC  _
                                GC CCGCGCGCGC    GCG GCC
                                || ||||||||||    ||| |||
                                CG GGCGCGCGCG    CGC CGG
                                 A        C___   A
GAM1986  PFKFB3   5'  GCGCCGGCGCGCGGC       44436       C     AACCGC
                                GCGCCG GCGCGC     GGC
                                ||||||| ||||||     |||
```

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                                CGCGGC CGCGCG     CCG
                                  _    ______
GAM1986 PK428    5' GCGCCGCGCGGGCAGAGAGCC 18807         C   ACCGC
                                GCGCCGCGCG GCA    GGCC
                                |||||||||| |||    ||||
                                CGCGGCGCGC CGT    TCGG
                                     C  CTC__
GAM1986 POU4F1   5' GCGCCGCGCGCCGGCC     26389          GCAACCG
                                GCGCCGCGCGC     CGGCC
                                ||||||||||      |||||
                                CGCGGCGCGCG     GCCGG
                                                _______
GAM1986 PPP1R7   3' GCGTCGCGCGCGCCAGC     15511     C       AACCG
                                GCG CGCGCGCGC    CGGC
                                ||| |||||||||    ||||
                                CGC GCGCGCGCG    GTCG
                                  A       _____
GAM1986 PRKCI    5' GCGCTTGCCGGAGAACCGCGGC 15633     C_  G  CGC
             CG                   GCGC  GC CG   AACCGCGGCCG
                                ||||  || ||   ||||||||||
                                CGCG  CG GC   TTGGCGCCGGC
                                  AA  _  CTC
GAM1986 PTGER3   5' CCGCTGCTGGGACCGCGGCCG 9644      GC  GCA_
                                CCGC  GC   ACCGCGGCCG
                                ||||  ||   ||||||||||
                                GGCG  CG   TGGCGCCGGC
                                  A_  ACCC
GAM1986 PTPN18   5' GCCCCGCGCGCGCGGCGA    30768    G       AACC
                                GC CCGCGCGCGC   GCGG
                                || ||||||||||   ||||
                                CG GGCGCGCGCG   CGCT
                                 G       C___
GAM1986 RAD23A   5' GCGCCGCGCGCCGACCACTTCC 22796          GCA    GG
             G                   GCGCCGCGCGC   ACCGC  CCG
                                ||||||||||   |||||  |||
                                CGCGGCGCGCG   TGGTG  GGC
                                     GC_    AA
GAM1986 RAD23A   5' GCGCCGCGCCGCGCGC     22795        G   AACC   G
                                GCGCCGCGC CGC   GCG C
                                |||||||| |||   ||| |
                                CGCGGCGCG GCG   CGC G
                                  _  _____  _
GAM1986 RPS6KA2  5' GCCGCGCCGGCCACCGCGGCCG 34464       GC  A
                                GCCGCGC  GC ACCGCGGCCG
                                |||||||  || ||||||||||
                                CGGCGCG  CG TGGCGCCGGC
                                    GC  G
GAM1986 SFRP1    5' GCGTTGCCCGGCTCCGCGGCCG 16575     CC  G  C  AA
                                GCG  GC CG GC  CCGCGGCCG
                                |||  || || ||  |||||||||
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                                CGC  CG GC CG  GGCGCCGGC
                                  AA  G  _  A_
GAM1986  SLC30A4   5'  GCGCTGCTCCACCCGCGGCCG  30017      C  GCG   AA
                                GCGC GC   CGC  CCGCGGCCG
                                |||| ||   |||  |||||||||
                                CGCG CG   GTG  GGCGCCGGC
                                  A  AG_   __
GAM1986  SMS       5'  GCGCGGCGTGTCAGGCTGCGGC 21396      C  ___  C  AACC
                CG                GCGC GCG   CG GC    GCGGCCG
                                |||| |||   || ||    |||||||
                                CGCG CGC   GT CG    CGCCGGC
                                  C   ACA  C  A___
GAM1986  TBL1X     5'  GCGCCGCGCGCCCGGCCGCGCT 24884          GCAA    G_
                CCG                 GCGCCGCGCGC    CCGCG  CCG
                                ||||||||||    |||||  |||
                                CGCGGCGCGCG    GGCGC  GGC
                                      GGCC     GA
GAM1986  ZIC1      5'  GCGCCGCGCGGCGCTGGCC    18236          C  AACC  _
                                GCGCCGCGCG GC    GC GGCC
                                |||||||||| ||    || ||||
                                CGCGGCGCGC CG    CG CCGG
                                      _  _____  A
GAM1986  ZNF134    5'  GCGCCGGGCCCATCACCGCGGC 18328       C  G  CA
                CG                  GCGCCG GC CG  ACCGCGGCCG
                                |||||| || ||  ||||||||||
                                CGCGGC CG GT  TGGCGCCGGC
                                   C  G  AG
GAM1986  ZNF278    5'  GCGCCGGCGCGCAGCCA     36796       C      A
                                GCGCCG GCGCGCA CCG
                                |||||| ||||||| |||
                                CGCGGC CGCGCGT GGT
                                   _      C
GAM1986  ZYX       5'  GCGCCGCGTCTCGGGTGGCCG  18436        CG_  CAACCGC
                                GCGCCGCG   CG      GGCCG
                                ||||||||   ||      |||||
                                CGCGGCGC   GC      CCGGC
                                     AGA  CCA_____
GAM1987  SCA2      3'  AATTATGGAATAGCCCCCAA   16475           A_
                                AATTATGGAATA  CCTTAA
                                ||||||||||||  ||||||
                                TTAATACCTTAT  GGGGTT
                                      CG
GAM1988  HCS       3'  TTTTAATTATCTTTAGTCT    33240            __
                                TTTTGATTATCTTT  TCT
                                ||||||||||||||  |||
                                AAAATTAATAGAAA  AGA
                                      TC
GAM1988  TSN       3'  TTTTAATTATCTATTTTTATAC 21502           _  C
                                TTTTGATTATCT TTT TATAC
                                |||||||||||| ||| |||||
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                                AAAATTAATAGA AAA ATATG
                                      T   A
GAM1989  KCNK2    3'  AATTTCTTGTCATTTACAAAAA 30564       GTAA    C
                                AATTTC   GTCGT TACAAAAA
                                ||||||   ||||| ||||||||
                                TTAAAG   CAGTA ATGTTTTT
                                   AA__    A
GAM1989  SRGAP2   3'  AATTTCGCAGGTTGGTCCA   43973        A  C_
                                AATTTCGTA GT  GTCTA
                                ||||||||| ||  |||||
                                TTAAAGCGT CA  CAGGT
                                     C  AC
GAM1990  ACTB     5'  CGGCGGATCGGCAAAGGCGAGG 9924      A_   CCT  C__    A
            C                    CGGC  GTC   GC   GGCGA GC
                                ||||  |||   ||   ||||| ||
                                GCCG  TAG   CG   CCGCT CG
                                  CC   C__  TTT    C
GAM1990  AQP6     5'  GGCAGCCCTTGTCCCCAGC   11642        C ___
                                GGCAGTCC TG   CCGGC
                                |||||||| ||   |||||
                                CCGTCGGG AC   GGTCG
                                    A  AGG
GAM1990  BGN      3'  CGGCAGCCCTGGCAGAGC    11815       T   GCC   A
                                CGGCAG CCCT   GGCG AGC
                                |||||| ||||   |||| |||
                                GCCGTC GGGA   CCGT TCG
                                  _   ____   C
GAM1990  ENG      5'  ACGGCGTCCCTGCTCCAGC   6489       A      __
                                ACGGC GTCCCTGC  CGGC
                                ||||| ||||||||  ||||
                                TGCCG CAGGGACG  GTCG
                                  _      AG
GAM1990  FOXE3    5'  CGGCAGCCCCTGCCCGCGCGGC 29143            G   AA
                                CGGCAGTCCCTGCC GCG  GC
                                |||||||||||||| |||  ||
                                GCCGTCGGGGACGG CGC  CG
                                       G   GC
GAM1990  FXR2     5'  ACGGCGGCCCTGCCACAGC   22156      A T      G GA
                                ACGGC G CCCTGCCG C  AGC
                                ||||| | |||||||| |  |||
                                TGCCG C GGGACGGT G  TCG
                                  C _      _ __
GAM1990  GEMIN5   5'  ACGGAGGTCCGCGCGGCGAAGC 44841     CA   CT  _
            C                    ACGG  GTCC  GC CGGCGAAGCC
                                ||||  ||||  || ||||||||||
                                TGCC  CAGG  CG GCCGCTTCGG
                                  TC    __  C
GAM1990  GNB1     5'  GCAGGTGCGCGCCGGCGAGGC  13205     TCCC_       A
                                GCAG    TGCCGGCGA GC
                                ||||    ||||||||| ||
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                                CGTC    GCGGCCGCT CG
                                  CACGC       C
GAM1990  GPX3    3'  GGCATCCCTGCCCAGGGGC   13279     G      ____
                                GGCA TCCCTGCC   GGC
                                |||| ||||||||   |||
                                CCGT AGGGACGG   CCG
                                  _      GTCC
GAM1990  HRMT1L1  3'  ACGGCAGCTCCTGCCGAGC   42177       TC     GCGA
                                ACGGCAG  CCTGCCG   AGC
                                |||||||  |||||||   |||
                                TGCCGTC  GGACGGC   TCG
                                   GA     ____
GAM1990  IL1RN   3'  GGCAGTCCCTGCAGTCGGCTTG 8213          C_______  GAA
                                GGCAGTCCCTGC     GGC  G
                                ||||||||||||     |||  |
                                CCGTCAGGGACG     CCG  C
                                       TCAGIII  AAG
GAM1990  KCNK5   3'  GGCGGCCTCTGCAAACGGC   19039    A  C   ___
                                GGC GTC CTGC   CGGC
                                ||| ||| ||||  ||||
                                CCG CGG GACG   GCCG
                                  C  A   TTT
GAM1990  MBD3    3'  ACGTGGTCCCCACCTGGAGC   19414    GCA   TG  _  CGA
                                ACG   GTCCC  CC GG   AGC
                                |||   |||||  || ||   |||
                                TGC   CAGGG  GG CC   TCG
                                  AC_    GT  A  ___
GAM1990  MEN1    5'  CGGCGGCCCCTGCCCCGCAGAG 39175     A       G_  A
            CC                    CGGC GTCCCTGCC  GCG AGCC
                                |||| |||||||||  ||| ||||
                                GCCG CGGGGACGG  CGT TCGG
                                  C       GG   C
GAM1990  MPP5    3'  GGCAGTTTTTGCCAGATCAAG  35398      CCC    CG_
                                GGCAGT   TGCCGG   AAG
                                ||||||   ||||||   |||
                                CCGTCA   ACGGTC   TTC
                                   AAA     TAG
GAM1990  PAWR    5'  ACAGCAGCCGGCGGG      15095      GTCCCT     AA
                                ACGGCA     GCCGGCG  G
                                ||||||     |||||||  |
                                TGTCGT     CGGCCGC  C
                                  _______     CC
GAM1990  PTGS2   3'  AGCAGTCCTGAGCTGAG    9684        C  CC   GA
                                GGCAGTCC TG  GGC  AG
                                |||||||| ||  |||  ||
                                TCGTCAGG AC  TCG  TC
                                    _ __   AC
GAM1990  RALBP1  3'  GCAGTTCCCACCGGAGC    27700      C  TG   CGA
                                GCAGT CC  CCGG   AGC
                                ||||| ||  ||||   |||
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                                CGTCA GG  GGCC   TCG
                                  A  GT   ___
GAM1990  SOX18    5'  CGGTGGTCCCTGCAGCG     32941     CA       C
                                CGG  GTCCCTGC GGCG
                                |||  |||||||| ||||
                                GCC  CAGGGACG TCGC
                                  AC       _
GAM1990  SUFU     3'  GGCATCCCTGCTGGTGC     32094     G      C  CGAA
                                GGCA TCCCTGC GG    GC
                                |||| ||||||| ||    ||
                                CCGT AGGGACG CC    CG
                                  _      A  A___
GAM1990  TFDP1    5'  CGGGGTCCCTGCCCTGGGC    28276     CA       ___
                                CGG  GTCCCTGCC   GGC
                                |||  |||||||||   |||
                                GCC  CAGGGACGG   CCG
                                  C_        GAC
GAM1990  TIMP3    5'  GCGCGCCGCCGGCGGGGC    7458     A  C  T      AA
                                GC GT CC GCCGGCG  GC
                                || || || |||||||  ||
                                CG CG GG CGGCCGC  CG
                                 _ C  _      CC
GAM1990  TMEPAI   3'  ACGGCAGACCCCTGAAACGAAG 33587        _     CC
                  C                ACGGCAG TCCCTG  GGCGAAGC
                                   ||||||| ||||||  ||||||||
                                   TGCCGTC GGGGAC  TTGCTTCG
                                       T     T_
GAM1991  CST4     3'  ACTACAGTGGGTGGGAGTGGGT 12497          A   TACACA_
                  GG                 ATTACAGTG GGT      GGTGG
                                   |||||||||| |||      |||||
                                   TGATGTCAC CCA      CCACC
                                        _  CCCTCAC
GAM1991  HCS      3'  CAGTGAGATTGCACCACTG    33224          A   AGG
                                   CAGTGAGGTT CAC   TG
                                   |||||||||| |||   ||
                                   GTCACTCTAA GTG   AC
                                         C   GTG
GAM1991  TEM8     3'  TTACAATGAGGTTACCCATGG  38195             ACAG
                                   TTACAGTGAGGTTAC    GTGG
                                   ||||||||||||||    ||||
                                   AATGTTACTCCAATG    TACC
                                            GG__
GAM1992  LETM1    3'  AAAGATGAGTGTGACACA    29494         CGCGA   CGT
                                   GAAGATGAG    GAC   ACA
                                   |||||||||    |||   |||
                                   TTTCTACTC    CTG   TGT
                                        ACA__   ____
GAM1993  APPBP2   3'  ACTGCAGTTTTCTGTCTGCA  26870         C_  GTG
                                   ACTGCAGT  TC   CTGCA
                                   ||||||||  ||   |||||
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                                TGACGTCA AG  GACGT
                                    AA ACA
GAM1993 RAB7    5' CTGTGTCCCATATCTGCAT  21576    CA     _
                                CTG GTCTCGTG CTGCAT
                                ||| |||||||| ||||||
                                GAC CAGGGTAT GACGTA
                                  A_      A
GAM1993 TNXB    5' CTGTGGCCTCGTGACTCCTGC 37155    CA     ____
                                CTG GTCTCGTG  CTGC
                                ||| |||||||  ||||
                                GAC CGGAGCAC  GACG
                                  AC      TGAG
GAM1994 ARPC2   3' CTCGTTTCTGCAGATTATT  25063     G   A
                                CTTGTT TTGTA GATTATT
                                |||||| ||||| |||||||
                                GAGCAA GACGT CTAATAA
                                   A   _
GAM1994 CCR2    3' TTGTTGTTATATACAGATT  8506        ___
                                TTGTTGTTGTA  AGATT
                                ||||||||||  |||||
                                AACAACAATAT  TCTAA
                                      ATG
GAM1994 PTPRG   3' TTGCTGTTGTATAAGATT   15945       __
                                TTGTTGTTGTA AGATT
                                |||||||||| |||||
                                AACGACAACAT TCTAA
                                      AT
GAM1994 RPS17   3' TTGCTGTTGTCCCAGATT   9748        A__
                                TTGTTGTTGT  AGATT
                                |||||||||  |||||
                                AACGACAACA  TCTAA
                                     GGG
GAM1994 TRIM9   5' CTTGTTGTTGTTGGGGACT  31566        AA__
                                CTTGTTGTTGT  GATT
                                ||||||||||  ||||
                                GAACAACAACA  CTGA
                                      ACCC
GAM1994 XRCC2   3' CTCGTTGTTGTTTCGATT   24092        AA_
                                CTTGTTGTTGT  GATT
                                ||||||||||  ||||
                                GAGCAACAACA  CTAA
                                      AAG
GAM1995 TLR4    3' TTGATGAGGTAAGAGTTGAAAT 39725      ___ CC  A
          GACTT                 TTGATGAG  AG  TT AAATGACTT
                                |||||||  ||  || |||||||||
                                AACTACTC  TC  AA TTTACTGAA
                                    CAT  TC  C
GAM1996 C18orf2 3' AAAATTCTAGAGGAGAAAAAG 36405      A   A
                                AAAATTT AGAG AGAAAAAG
                                ||||||| |||| ||||||||
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                                TTTTAAG TCTC TCTTTTTC
                                    A   C
GAM1996  CNGB3    3'  TAGAAAGATTTAAAAAGAAAAA 33310       _     GA
              G                  TAGAAA ATTTAA  GAAGAAAAAG
                                 |||||| ||||||  ||||||||||
                                 ATCTTT TAAATT  TTTCTTTTTC
                                    C     __
GAM1996  CSN1     3'  GAAAATTTAGCTTAAGAAAAAG 12460          A AG_
                                 GAAAATTTA G   AAGAAAAAG
                                 ||||||||| |   |||||||||
                                 CTTTTAAAT C   TTCTTTTTC
                                       _ GAA
GAM1996  F9       3'  TAGAAGATTCAAGATAGAA    6578        A       GA
                                 TAGAA ATTTAAGA  AGAA
                                 ||||| ||||||||  ||||
                                 ATCTT TAAGTTCT  TCTT
                                    C       A_
GAM1996  HPSE     3'  AAAATTTAAGAGTATTGAAA   27412           AA__
                                 AAAATTTAAGAG    GAAA
                                 ||||||||||||    ||||
                                 TTTTAAATTCTC    CTTT
                                       ATAA
GAM1996  ITGAM    3'  GAAAACTCGCGGGGGAGAAGAA 43513         AA____
                                 GAAAATTT      GAGAAGAA
                                 ||||||||      ||||||||
                                 CTTTTGAG      CTCTTCTT
                                     CGCCCC
GAM1996  KCNMB1   3'  TAGAGAATTCAAACAAAGAA   19981      A       A
                                 TAGA AATTTAAG GAAGAA
                                 |||| |||||||| ||||||
                                 ATCT TTAAGTTT TTTCTT
                                   C       G
GAM1996  KRTHB6   3'  CAGAAGGTAGGAGGAAGAAAAA 14030       AATTTA  A
              G                  TAGAA      AG GAAGAAAAAG
                                 |||||      || ||||||||||
                                 GTCTT      TC CTTCTTTTTC
                                    CCATCC  _
GAM1996  MAX      3'  AAAAATTTAAAAAAAAAA     40362
                                 GAAAATTTAAGAGAAGAA
                                 ||||||||||||||||||
                                 TTTTTAAATTTTTTTTTT


GAM1996  NTRK2    3'  AGAAAATTTAAAAAAAGAAAAA 26141
              G                   AGAAAATTTAAGAGAAGAAAAAG
                                  |||||||||||||||||||||||
                                  TCTTTTAAATTTTTTTCTTTTTC


GAM1996  PBX2     3'  AGAAAGACAGAGGAGAAAAAG  15101       ATTTA    A
                                 AGAAA     AGAG AGAAAAAG
                                 |||||     |||| ||||||||
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                                TCTTT    TCTC TCTTTTTC
                                   CTG__   C
GAM1996  PMX1     5'  CAGAAGAAGAGAGAAGAA    35503      AATTTA
                                TAGAA     AGAGAAGAA
                                |||||     |||||||||
                                GTCTT     TCTCTTCTT
                                   CTTC__
GAM1996  POLA     3'  TAGAAAACTTTATTCTTAAGAA 32617          AA_____
                GAA                TAGAAAATTT      GAGAAGAA
                                |||||||||||      ||||||||
                                ATCTTTTGAA      TTCTTCTT
                                      ATAAGAA
GAM1996  SCD      3'  AGAAAACGTTCAGGGAAGAGAA 22817        TTA_  A    A
                AG                   AGAAAAT   AG GAAGA AAAG
                                |||||||   || ||||| ||||
                                TCTTTTG   TC CTTCT TTTC
                                    CAAG  C    C
GAM1996  SIX2     3'  CAGAAAAAAGAAAAGAGAAG   32601       TTT__
                                TAGAAAA    AAGAGAAG
                                |||||||    ||||||||
                                GTCTTTT    TTCTCTTC
                                    TTCTT
GAM1996  SIX3     5'  AGAAAATTCAGGGAGAGGAA   24014         A_   A
                                AGAAAATTTA  GAGA GAA
                                ||||||||||  |||| |||
                                TCTTTTAAGT  CTCT CTT
                                      CC   C
GAM1996  TBR1     3'  AGAAAATTAAAAGAGAGA    27310        T_    A
                                AGAAAATT  AAGAGA GA
                                ||||||||  |||||| ||
                                TCTTTTAA  TTCTCT CT
                                    TT    _
GAM1996  TRIM37   3'  GAAAATAAAGAAGAAAA     31624       TTA
                                GAAAAT   AGAGAAGAAAA
                                ||||||   ||||||||||||
                                CTTTTA   TTTCTTCTTTT
                                   ___
GAM1996  WIF1     3'  TAGAAAACTTAAAAGGAAGA   41169            _
                                TAGAAAATTTAAGAG AAGA
                                |||||||||||||| ||||
                                ATCTTTTGAATTTTC TTCT
                                      C
GAM1996  ZFHX1B   5'  CAGAAATGGTGAGAAGAAAAAG 31338       ATTTAA
                                TAGAAA     GAGAAGAAAAAG
                                ||||||     ||||||||||||
                                GTCTTT     CTCTTCTTTTTC
                                   ACCA__
GAM1997  ADH7     5'  CAAACATAGACTTTTTCT    8585          C  GC
                                TAAACATAGAC TT  CT
                                ||||||||||| ||  ||
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                                GTTTGTATCTG AA  GA
                                      A  AA
GAM1998 ITGA1    3'  TTTTGGATAATGCATGAC    41864         AT    G
                                TTTTGGATA  GTGCA GAC
                                |||||||||  ||||| |||
                                AAAACCTAT  TACGT CTG
                                     __    A
GAM1998 NPTX1    3'  TGCGTGTGCGTGTGCAGG    14843      TT  GATAA
                                TGCGT  TG    TGTGCAGG
                                |||||  ||    ||||||||
                                ACGCA  AC    ACACGTCC
                                   C_  GC___
GAM1998 PLAB     5'  TGCTTTTGGATGAGGTTGGGG  42319     G       AAT  GCA
                                TGC TTTTGGAT   GT   GG
                                ||| ||||||||   ||   ||
                                ACG AAAACCTA   CA   CC
                                  _       CTC  ACC
GAM1998 SRGAP1   5'  TGTGTTTTGGAAAATGAGA   43612    C       T    TGCA
                                TG GTTTTGGA AATG    GGA
                                || |||||||| ||||    |||
                                AC CAAAACCT TTAC    TCT
                                 A       T    _____
GAM1999 M6PR     3'  TAACTCTGACTTACAAC     14307      G   A
                                TAAC TCT ACTTACAAC
                                |||| ||| |||||||||
                                ATTG AGA TGAATGTTG
                                   _  C
GAM1999 XK       3'  GCCTAGAAGAACACAACATGGT 34363       ACT___      C
                                GTCTA     TACAACA GGT
                                |||||     ||||||| |||
                                CGGAT     GTGTTGT CCA
                                   CTTCTT      A
GAM2000 ATP10C   3'  TCAGGTATTAATCA       35983         TAACG
                                TCAGGTATT    AATCA
                                |||||||||    |||||
                                AGTCCATAA    TTAGT
                                     ______
GAM2000 CBFB     3'  CAGGTATTATAATCAT      35631         TAACG
                                CAGGTATT    AATCAT
                                ||||||||    ||||||
                                GTCCATAA    TTAGTA
                                     TA___
GAM2000 COG8     3'  TTCAGGTATTTGGGGACTACAT 37040          AAC  AT_
                                TTCAGGTATTT   GA   CAT
                                ||||||||||   ||   |||
                                AAGTCCATAAA   CT   GTA
                                      CCC  GAT
GAM2000 DUSP5    3'  TTCAAGTATGACTAAGAATCAT 20664         __    C
                                TTCAGGTAT  TTAA GAATCAT
                                |||||||||  |||| |||||||
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                                AAGTTCATA  GATT CTTAGTA
                                     CT   _
GAM2000  SECTM1   3'  TTCAGATATTCGAGTCAT    16546         TAA   A
                                TTCAGGTATT   CGA TCAT
                                ||||||||||   ||| ||||
                                AAGTCTATAA   GCT AGTA
                                     ____  C
GAM2000  SGK      3'  AGGCATCTGAATACGAGTCAT  24740        A___   A
                                AGGTATTT    ACGA TCAT
                                ||||||||    |||| ||||
                                TCCGTAGA    TGCT AGTA
                                     CTTA   C
GAM2000  SMARCC1  3'  TTCAGGTATTTTGTAGAAT   16908          AAC_
                                TTCAGGTATTT    GAAT
                                ||||||||||    ||||
                                AAGTCCATAAA    CTTA
                                       ACAT
GAM2000  DPYSL3   3'  TAGTTATTTTAATAACCA    10777       C
                                TAGTTA TTTAATAACCG
                                |||||| ||||||||||
                                ATCAAT AAATTATTGGT
                                   A
GAM2000  LANCL1   3'  TTAGTTACTACCATGTTGTTAG 25860         TTAATAACC
                                TTAGTTACT       GTTAG
                                |||||||||       |||||
                                AATCAATGA       CAATC
                                     TGGTACAA_
GAM2000  PTGS2    3'  TTAGTTACTTCTAATGCATCA  9697          AATAAC
                                TTAGTTACTTT     CGTTA
                                ||||||||||     |||||
                                AATCAATGAAG     GTAGT
                                       ATTAC_
GAM2001  PTPN1    3'  TAGTGCACTATGGATGCCTTTG 15905         CAAACAG  GA_
              G                  TAGTGTACTA     GC   TGG
                                ||||||||||     ||   |||
                                ATCACGTGAT     CG   ACC
                                     ACCTA__  GAA
GAM2002  CYP1B1   3'  GTCAGTTGTAATGGGAGTTCTG 6452         __   TA  CC
                                GTCAGTTG  GTG  AG  CTG
                                ||||||||  |||  ||  |||
                                CAGTCAAC  TAC  TC  GAC
                                     AT   CC  AA
GAM2002  EZH1     3'  TCTTTCAGTTTGAGCCCTG    12788     G     GGTGTA
                                TCT TCAGTT     AGCCCTG
                                ||| ||||||     |||||||
                                AGA AGTCAA     TCGGGAC
                                  A     AC____
GAM2002  F9       3'  AGTTAGTGAGAGGCCCTG     6572          TAA_
                                AGTTGGTG    GCCCTG
                                ||||||||    ||||||
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                                TCAATCAC   CGGGAC
                                    TCTC
GAM2002  METTL1   3'  TGTCAGCTGGCCCT       23877        GTGTAA
                                TGTCAGTTG    GCCCT
                                |||||||||    |||||
                                ACAGTCGAC    CGGGA
                                             _____
GAM2003  BDKRB2   3'  GGGAGCCATAAAATCCT     8404      AA  TCGAAA
                                GGGA  CC     AAAATCCT
                                ||||  ||     ||||||||
                                CCCT  GG     TTTTAGGA
                                  C_  TA____
GAM2003  CHRNA4   3'  GGAAACCCTCAGGGTCCT    8853       _    AAAAAAA
                                GGAAA CCTCG      TCCT
                                |||||  |||||     ||||
                                CCTTT GGAGT      AGGA
                                   G    CCC____
GAM2003  HRMT1L2  3'  GGGAGCCCCGAAACCGCCTA  11361     AA      AAAAT
                                GGGA  CCTCGAAA    CCTA
                                ||||  ||||||||    ||||
                                CCCT  GGGGCTTT    GGAT
                                  C_      GGC__
GAM2003  LIMD1    3'  GGGCAAAAAAAAAAATCCT   30632     AAACCTC
                                GGG      GAAAAAAATCCT
                                |||      ||||||||||||
                                CCC      TTTTTTTTAGGA
                                  GTTT___
GAM2003  WHSC1    3'  AGGAAACCACGGAGTCCT    39351        T  AAAAAAA
                                GGGAAACC CG      TCCT
                                ||||||||  ||     ||||
                                TCCTTTGG GC      AGGA
                                    T  CTC_____
GAM2004  ALDH2    3'  TTTTTCTTGGTTTTGTTGCTGA 40690           CGG  G
           T                     TTTTTCTTGGTTTT   GT TGAT
                                 ||||||||||||||   || ||||
                                 AAAAAGAACCAAAA   CG ACTA
                                        CAA  _
GAM2004  GOLGA4   3'  TTTTTCTTGGTCTTTTGGC   41065           CG
                                TTTTTCTTGGTTTT  GGT
                                ||||||||||||||  |||
                                AAAAAGAACCAGAA  CCG
                                        AA
GAM2005  BDKRB2   3'  AGTTATTGGTTGAGCTGGA   8395     C      C   GACC
                                GG TATTGGTT GGGC    GGA
                                || ||||||||  ||||    |||
                                TC ATAACCAA CTCG    CCT
                                 A       _    A___
GAM2005  DNM2     3'  GGCTGTGTGGTTAATATGGCCG 22386      AT_    CG___   GAC
           G                     GGCT   TGGTT    GGC   CGG
                                 ||||   |||||    |||   |||
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                                CCGA  ACCAA   CCG  GCC
                                  CAC   TTATA  ___
GAM2005 FZD10   3' GACTATTGGTGAAGGCCGGA  28454       TC   GAC
                                GGCTATTGGT  GGGC  CGGA
                                ||||||||||  ||||  ||||
                                CTGATAACCA  TCCG  GCCT
                                     CT   ___
GAM2005 NEK6    5' GCTGGCCCGCGGGCGGCTGGA  30825    ATT  __    ACC
                                GCT  GGTT  CGGGCG  GGA
                                |||  ||||  ||||||  |||
                                CGA  CCGG  GCCCGC  CCT
                                  ___  GC    CGA
GAM2005 PCDHGA1  3' AGTTATTGGTTTATGGCTGGAA 33150   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA10 3' AGTTATTGGTTTATGGCTGGAA 36870   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA11 3' AGTTATTGGTTTATGGCTGGAA 36879   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA12 3' AGTTATTGGTTTATGGCTGGAA 36888   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA2  3' AGTTATTGGTTTATGGCTGGAA 33155   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA3  3' AGTTATTGGTTTATGGCTGGAA 33159   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA4  3' AGTTATTGGTTTATGGCTGGAA 33166   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA5  3' AGTTATTGGTTTATGGCTGGAA 36828   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
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                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA6 3' AGTTATTGGTTTATGGCTGGAA 36836   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA7 3' AGTTATTGGTTTATGGCTGGAA 36844   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA8 3' AGTTATTGGTTTATGGCTGGAA 36853   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGA9 3' AGTTATTGGTTTATGGCTGGAA 36862   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGB1 3' AGTTATTGGTTTATGGCTGGAA 36897   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGB2 3' AGTTATTGGTTTATGGCTGGAA 36906   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGB3 3' AGTTATTGGTTTATGGCTGGAA 36915   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGB4 3' AGTTATTGGTTTATGGCTGGAA 36924   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGB5 3' AGTTATTGGTTTATGGCTGGAA 36933   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
                                TC ATAACCAA  CCG   CCTT
                                 A      ATA  A___
GAM2005 PCDHGB6 3' AGTTATTGGTTTATGGCTGGAA 33176   C     CG_  GACC
                                GG TATTGGTT  GGC   GGAA
                                || ||||||||  |||   ||||
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                                TC ATAACCAA   CCG    CCTT
                                 A       ATA   A___
GAM2005  PCDHGB7   3'  AGTTATTGGTTTATGGCTGGAA 36947    C      CG_   GACC
                                GG TATTGGTT   GGC    GGAA
                                || ||||||||   |||    ||||
                                TC ATAACCAA   CCG    CCTT
                                 A       ATA   A___
GAM2005  PCDHGC3   3'  AGTTATTGGTTTATGGCTGGAA 37048    C      CG_   GACC
                                GG TATTGGTT   GGC    GGAA
                                || ||||||||   |||    ||||
                                TC ATAACCAA   CCG    CCTT
                                 A       ATA   A___
GAM2005  PCDHGC4   3'  AGTTATTGGTTTATGGCTGGAA 33179    C      CG_   GACC
                                GG TATTGGTT   GGC    GGAA
                                || ||||||||   |||    ||||
                                TC ATAACCAA   CCG    CCTT
                                 A       ATA   A___
GAM2005  PCDHGC5   3'  AGTTATTGGTTTATGGCTGGAA 37077    C      CG_   GACC
                                GG TATTGGTT   GGC    GGAA
                                || ||||||||   |||    ||||
                                TC ATAACCAA   CCG    CCTT
                                 A       ATA   A___
GAM2006  POR       5'  TGGAGCTGGTGTCCAC      45301    A   CGA
                                TG AGT   GGTGTCCAC
                                || |||   |||||||||
                                AC TCG   CCACAGGTG
                                 C   A__
GAM2006  SMAC      5'  TTGAAGCCGGGAGGCACA    39901        A  TGTC
                                TTGAAGTCG GG    CACA
                                ||||||||| ||    ||||
                                AACTTCGGC CC    GTGT
                                      _  TCC_
GAM2006  ATP8B2    3'  TGTGCCATTGCACTCTTGCC   42223      ACCTAA
                                TGTGT     CGCTCTTGCC
                                |||||     ||||||||||
                                ACACG     GTGAGAACGG
                                   GTAAC_
GAM2006  GABRG3    3'  TGTGTACCAAATGCTCTT    37714        T  C
                                TGTGTACC AA GCTCTT
                                |||||||| || ||||||
                                ACACATGG TT CGAGAA
                                     T  A
GAM2006  SNTB1     3'  TGCGTACCTGGTGAACAAGTTG 34284         ____    CTC
              CC                  TGTGTACCT   AACG   TTGCC
                                |||||||||   ||||  |||||
                                ACGCATGGA   TTGT   AACGG
                                     CCAC   TC_
GAM2006  THBD      3'  TGTGTACCTAGCCTT       7436          AC  T
                                TGTGTACCTA  GC CTT
                                ||||||||||  || |||
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                                ACACATGGAT  CG GAA
                                          __  _
GAM2006  ZNF134   5'  GTGTACCCTGGTGTTCATCCAG 18329        AACGCTC  GC
                                GTGTACCT      TT  CCAG
                                ||||||||      ||  ||||
                                CACATGGG      AG  GGTC
                                     ACCACA_  TA
GAM2007  ACCN2    3'  GGAGGAGAGAGGGGCAGC    33451          ATA
                                GGAGGAGAGAGG   CGGC
                                ||||||||||||   ||||
                                CCTCCTCTCTCC   GTCG
                                       CC_
GAM2007  ADAR     3'  TGAAGAGGAGAGGGGCTGC   31911      G      A  ATACG
                                TGAAG AGGAGAG GG     GC
                                ||||| ||||||| ||     ||
                                ACTTC TCCTCTC CC     CG
                                   _      C  GA___
GAM2007  ADCY8    5'  AGGAGGAGGAGGGGGTCACGG  9995        A   A___
                                AGGAGGAG GAGG    TACGG
                                |||||||| ||||    |||||
                                TCCTCCTC CTCC    GTGCC
                                     _   CCCA
GAM2007  ADCY8    5'  GGAGGAGAAGGGAGGC      10008         A  TAC
                                GGAGGAGAG GGA   GGC
                                ||||||||| |||   |||
                                CCTCCTCTT CCT   CCG
                                      C  ___
GAM2007  BAT3     3'  TGAAGGAAGAGGGGGGAAACG  38788         AGA  T
                                TGAAGGAGGAG   GGA ACG
                                ||||||||||   ||| |||
                                ACTTCCTTCTC   CCT TGC
                                       CCC   T
GAM2007  C1orf6   5'  AGGAGGAGGAGGGGCGGGC   33524        A   ATAC
                                AGGAGGAG GAGG    GGC
                                |||||||| ||||    |||
                                TCCTCCTC CTCC    CCG
                                     _   CCGC
GAM2007  CDC25B   5'  GAGGGAGGAGAGGGATGCG   34848    A       A   A
                                GA GGAGGAGAG GGAT CG
                                || |||||||| |||| ||
                                CT CCTCCTCTC CCTA GC
                                 C       _   C
GAM2007  CDX1     3'  GGAGGAGGAGGTGGGGC     12217       A   ATAC
                                GGAGGAG GAGG    GGC
                                |||||||| ||||    |||
                                CCTCCTC CTCC    CCG
                                     _   ACC_
GAM2007  EN2      3'  GAAGGAGGAGGGAGTTAGG   10950         A  GA  C
                                GAAGGAGGAG GAG  TA GG
                                |||||||||| |||  || ||
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                                CTTCCTCCTC CTC  AT CC
                                      C   A_ _
GAM2007 HLF      3'  TGAAGGAGGGAGGGGAT     13397         A   A
                                TGAAGGAGG GAG GGAT
                                ||||||||| ||| ||||
                                ACTTCCTCC CTC CCTA
                                     _  C
GAM2007 HMGA1    3'  TGAAGGAGCAGAGAGGGC    44164         G      ATACG
                                TGAAGGAG AGAGAGG    GC
                                |||||||| |||||||    ||
                                ACTTCCTC TCTCTCC    CG
                                     G      _____
GAM2007 LASS1    3'  AGGAGGAGGAGGAGGTGG    34590         A    TAC
                                AGGAGGAG GAGGA   GG
                                |||||||| |||||   ||
                                TCCTCCTC CTCCT   CC
                                     _    CCA
GAM2007 MUC3B    3'  TGAGGAGAGGAGGGAGGAT   45345     A_      A
                                TGA  GGAGGAG GAGGAT
                                |||  ||||||| ||||||
                                ACT  TCTCCTC CTCCTA
                                  CC      C
GAM2007 NEDD4    5'  TGGAGGAGGAGGAGGAGAAGCG 43104    A       A     TAC
                                TG AGGAGGAG GAGGA   GGCG
                                || |||||||| |||||   ||||
                                AC TCCTCCTC CTCCT   TCGC
                                 C       _    CT_
GAM2007 NPEPPS   5'  AGGAGGAGGGGAGGAGGC    26716         A_    TAC
                                AGGAGGAG  GAGGA   GGC
                                ||||||||  |||||   |||
                                TCCTCCTC  CTCCT   CCG
                                     CC    ___
GAM2007 NPR1     3'  GGAGGGGAGGGGATCAG     44584       A   A   A
                                GGAGG GAG GGAT CGG
                                ||||| ||| |||| |||
                                CCTCC CTC CCTA GTC
                                   C   C   _
GAM2007 PAFAH1B1 5'  GAAGGAGGGGGGGAGGATGGCG  7707          AGA     AC
                                GAAGGAGG   GAGGAT  GGCG
                                ||||||||   ||||||  ||||
                                CTTCCTCC   CTCCTA  CCGC
                                     CCC     __
GAM2007 PCTK1    5'  TGAGGAGGAGGAGGCGGC    37481     A      A   ATA
                                TGA GGAGGAG GAGG   CGGC
                                ||| ||||||| ||||   ||||
                                ACT CCTCCTC CTCC   GCCG
                                  _     _   ____
GAM2007 PCTK1    5'  AGGAGGAGGAGGCGGCGGC   37462         A   ATA
                                AGGAGGAG GAGG   CGGC
                                |||||||| ||||   ||||
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                                TCCTCCTC CTCC   GCCG
                                     _   GCC
GAM2007  PIM1     3'  TGAAGGAGGGGGTGAGGGA   44973        A___   A
                                TGAAGGAGG   GAG GGA
                                |||||||||   ||| |||
                                ACTTCCTCC   CTC CCT
                                     CCCA  _
GAM2007  POLR2A   5'  GGAGGAGGGGAAGGTGGC    9600        A_   ATAC
                                GGAGGAG  GAGG   GGC
                                |||||||  ||||   |||
                                CCTCCTC  CTTC   CCG
                                    CC   CA__
GAM2007  POU2F2   3'  TGGAGGAGGAGGAGGAT     15465    A      A
                                TG AGGAGGAG GAGGAT
                                || |||||||| ||||||
                                AC TCCTCCTC CTCCTA
                                 C      _
GAM2007  PPP3R1   5'  AGGAGGGGGAGAGGGGGC    44072      A_     ATAC
                                AGGAGG  GAGAGG   GGC
                                ||||||  ||||||   |||
                                TCCTCC  CTCTCC   CCG
                                   CC     C___
GAM2007  PTPRF    3'  GGAGGAGAGGGGAGC       15929        A   TACG
                                GGAGGAGAG GGA   GC
                                ||||||||| |||   ||
                                CCTCCTCTC CCT   CG
                                     C  _____
GAM2007  SEZ6L    5'  TGGAGGAGGAGAGGAGAT    34427    A       AG
                                TG AGGAGGAGAG  GAT
                                || ||||||||||  |||
                                AC TCCTCCTCTC  CTA
                                 C         CT
GAM2007  SF1      5'  GAGGGAGGAGAGAGGGCAC   21563    A         A
                                GA GGAGGAGAGAGG TAC
                                || ||||||||||| |||
                                CT CCTCCTCTCTCC GTG
                                 C          C
GAM2007  SLC18A3  3'  TGGAGGAGGAGTGGGGAT    16838    A      AGA
                                TG AGGAGGAG   GGAT
                                || ||||||||   ||||
                                AC TCCTCCTC   CCTA
                                 C       ACC
GAM2007  SMG1     5'  AGGAGGAGGAGGCGGCGGC   31500        A   ATA
                                AGGAGGAG GAGG   CGGC
                                ||||||||| ||||   ||||
                                TCCTCCTC CTCC   GCCG
                                     _   GCC
GAM2007  SMG1     5'  AGGAGGAGGAGGAGGCGGC   31499        A    TA
                                AGGAGGAG GAGGA  CGGC
                                ||||||||| |||||  ||||
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                                TCCTCCTC CTCCT  GCCG
                                    _    CC
GAM2007  SPTBN4   3'  GGAGGAGAGAGGAAAACAG   36089          T_
                                GGAGGAGAGAGGA  ACGG
                                |||||||||||||  ||||
                                CCTCCTCTCTCCT  TGTC
                                      TT
GAM2007  SYN3     3'  GAGGCAGGAGGGGGACGA    18563     _ A   AT_
                                GAGG AG GAGG   ACGG
                                |||| || ||||   ||||
                                CTCC TC CTCC   TGCT
                                  G _   CCC
GAM2007  TCIRG1   5'  TGAAGGAGGAGGCGGGGC    25843         AGA  ATAC
                                TGAAGGAGGAG   GG   GGC
                                ||||||||||   ||   |||
                                ACTTCCTCCTC   CC   CCG
                                      CG_  ____
GAM2007  XYLB     3'  TGAAGGAGGGGGAGAGGA    23028        A_
                                TGAAGGAGG  GAGAGGA
                                |||||||||  |||||||
                                ACTTCCTCC  CTCTCCT
                                     CC
GAM2007  MYH1     3'  TGCATTTCTTTGGTCACCTTT  25562         C  GG  G
                                TGCATTTCTT GG  AC TTT
                                |||||||||| ||  || |||
                                ACGTAAAGAA CC  TG AAA
                                      A  AG  G
GAM2007  MYH4     3'  TCGTGCATTTCTTTGGTCACAT 32754    T       C  GG
              TT                  TC TGCATTTCTT GG  ACGTTT
                                || ||||||||||  ||  ||||||
                                AG ACGTAAAGAA CC  TGTAAA
                                 C        A  AG
GAM2008  FBLN1    3'  TGATACATGTTGGCCTTATG   27050      _  GAT
                                TGATA ATG   TTGGCCTTATG
                                |||||  |||   ||||||||||
                                ACTAT TAC   AACCGGAATAC
                                   G  ___
GAM2008  COX11    3'  CAAAGTAATTATTCAGAACTCT 20417        CA_   CCC
                                CAAAGTAAT   TCGG   ACTCT
                                |||||||||   ||||   |||||
                                GTTTCATTA   AGTC   TGAGA
                                      ATA    T__
GAM2008  HNRPH2   3'  AAAATAATCTCAACTTCCACT  33329        A    __
                                AAAGTAATC TCGGC  CCACT
                                ||||||||| |||||  |||||
                                TTTTATTAG AGTTG  GGTGA
                                      _    AA
GAM2008  TOP2A    3'  AAATAATCACATAACTACTCT  9881          C_   CC
                                AAGTAATCAT  GGC  ACTCT
                                ||||||||||  |||  |||||
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                                TTTATTAGTG  TTG  TGAGA
                                     TA   A_
GAM2009  C7      3'  GTATCCACAGAATAGGGAAA   8230       ATTGT
                                GTATT    AATAGGGAAA
                                |||||    ||||||||||
                                CATAG    TTATCCCTTT
                                   GTGTC
GAM2009  FLRT2    3'  GCATTATTTCTCACAGGG    29849        GTA_
                                GTATTATT    ATAGGG
                                ||||||||    ||||||
                                CGTAATAA    TGTCCC
                                     AGAG
GAM2009  ITGA11   3'  TCGTACTATGCACAGGG     29205         T   A
                                TCGTATTAT GTA TAGGG
                                ||||||||| ||| |||||
                                AGCATGATA CGT GTCCC
                                          _   _
GAM2010  SHOX     3'  AGATGGATCTTCTCGGAGGT   27814      A  CCGCGA
                                AGAT GA     CTCGGAGGT
                                |||| ||     |||||||||
                                TCTA CT     GAGCCTCCA
                                  C  AGAA__
GAM2011  AP3S1    3'  AGAAGTCCAGTTACCTTGGA   10504         AGC  GTCG
                                AGAAGTCCA   GC    TGGA
                                |||||||||   ||    ||||
                                TCTTCAGGT   TG    ACCT
                                     CAA  GA__
GAM2011  F2RL3    3'  TCAGACACCAGTGCGTCGTGG  19531       AGT   A C
                                TCAGA   CCA G GCGTCGTGG
                                |||||   ||| | |||||||||
                                AGTCT   GGT C CGCAGCACC
                                   GT_   _ A
GAM2011  PPP2R2B  3'  TCAGAAGTTCAAGTCAACTATG 21336         C    _  C TC
            GA                    TCAGAAGT CAAG CG G  GTGGA
                                |||||||| |||| || |  |||||
                                AGTCTTCA GTTC GT T  TACCT
                                     A    A  _ GA
GAM2011  SLC9A1   5'  CAGGGGTCCAGGCGCGCCG   43231     AA    A
                                CAG  GTCCA GCGCGTCG
                                |||  ||||| ||||||||
                                GTC  CAGGT CGCGCGGC
                                  CC    C
GAM2011  SNX15    3'  TCAGAAGTGTGAGTCCTGG   43937        CCAAGCGC   G
                                TCAGAAGT       GTC TGG
                                ||||||||       ||| |||
                                AGTCTTCA       CAG ACC
                                     CACT_____   G
GAM2011  UBE2V1   3'  CCAGAAGTTCAACTACGTGGA 35344         CCA   GCGT
                                TCAGAAGT   AGC    CGTGGA
                                ||||||||   |||    ||||||
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                                GGTCTTCA  TTG   GCACCT
                                    AG_  AT__
GAM2012 AP2S1   3' GTGAAGTCTCCTCCC     34645         ATAGAGTG
                                GTGAAGTCTCC      CCT
                                ||||||||||      |||
                                CACTTCAGAGG      GGG
                                     A_______
GAM2012 GAGED2  5' GTGAGGTTCCCTCGTGCCTTA 39416     A  CT  ATAGA
                                GTGA GT  CC    GTGCCTTA
                                |||| ||  ||    ||||||||
                                CACT CA  GG    CACGGAAT
                                  C  AG  AG___
GAM2012 ITGA2   3' GTGAAATCCTGAGAGTG    13602        CCAT
                                GTGAAGTCT   AGAGTG
                                |||||||||   ||||||
                                CACTTTAGG   TCTCAC
                                     AC__
GAM2012 JPH2    3' TGGGGTCTCCATAGAATG   45381    AA
                                TG  GTCTCCATAGAGTG
                                ||  ||||||||||||||
                                AC  CAGAGGTATCTTAC
                                 CC
GAM2013 ACADVL  3' AAGGGGCTTCGGCTTTGGC   6155       AGC  GA
                                AGGGGG   CG  GCTTTGGC
                                ||||||   ||  ||||||||
                                TTCCCC   GC  CGAAACCG
                                   GAA  __
GAM2013 BCL11B  5' GGGGGAGCCGGGGGAGGGGGTC 39752          AGCTTT_  C
           CG                   GGGGGAGCCGG      GG CCG
                                ||||||||||      || |||
                                CCCCCTCGGCC      CC GGC
                                     CCCTCCC  A
GAM2013 CRHR1   3' AGGGGAAGCTGGCCTGGCC   20434        C  AGC
                                AGGGGGAGC GG   TTTGGCC
                                |||||||||  ||   |||||||
                                TCCCCTTCG CC   GGACCGG
                                     A  ___
GAM2013 DRD2    3' GAGGGAGCTAAGGTTTTTGGC  9015        CG   C__
                                GGGGGAGC  GAG   TTTGGC
                                |||||||  |||   ||||||
                                CTCCCTCG  TTC   AAACCG
                                    A_   CAA
GAM2013 GALE    3' AGGGGAGGCCTTGGC      41798       CCGGA
                                GGGGGAG    GCTTTGGC
                                |||||||    ||||||||
                                TCCCCTC    CGGAACCG
                                     _____
GAM2013 MAPK7   3' AGGGGGAGTTGGGGTCTCCCG  40043       CC_  AG  TTGG
                                AGGGGGAG   GG  CT   CCCG
                                |||||||   ||  ||   ||||
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                                TCCCCCTC  CC  GA   GGGC
                                    AAC  CA  ____
GAM2013  MUC3B   3'  AGGGGGAGTCGGGGGCAGAACC 45336       C  A_  TTT
                                AGGGGGAG CGG  GC  GGCC
                                |||||||| |||  ||  ||||
                                TCCCCCTC GCC  CG  TTGG
                                    A  CC  TC_
GAM2013  NR2C2   5'  GGCGGGAGCCGGGGGCCGCGGG 17672   _      A_  TT_  C
           CTCG                   GG GGGAGCCGG  GCT  GGC CG
                                || |||||||||  |||  ||| ||
                                CC CCCTCGGCC  CGG  CCG GC
                                 G       CC  CGC  A
GAM2013  PDE4A   5'  AGGGGGAGCCGCGGAGGGGCC  26248         __  CTTT
                                AGGGGGAGCC  GGAG   GGCC
                                ||||||||||  ||||   ||||
                                TCCCCCTCGG  CCTC   CCGG
                                     CG   C___
GAM2013  PIK3R2   3'  AGGGGAAGTTGGAGTCTG   22741       CC   C
                                AGGGGGAG  GGAG TTTG
                                ||||||||  |||| ||||
                                TCCCCTTC  CCTC AGAC
                                    AA   _
GAM2013  PKIA    5'  GGGGGAGCGGGGCCGCTCCCG  27744       C  A  TTGG
                                GGGGGAGC GG GCT   CCCG
                                |||||||| || |||   ||||
                                CCCCCTCG CC CGG   GGGC
                                    C  _  CGA_
GAM2013  PLXNB2   3'  GAGGGAGCTGGGGCTGGGGC  29646       C  A  TT
                                GGGGGAGC GG GCT  GGC
                                |||||||| || |||  |||
                                CTCCCTCG CC CGA  CCG
                                    A  C  CC
GAM2013  PRX     3'  AGGCGGAGCCGGGGCTCCG   34102    G      A
                                AGG GGAGCCGG GCTTTG
                                ||| |||||||| ||||||
                                TCC CCTCGGCC CGAGGC
                                  G       C
GAM2013  PTGDS   3'  GGGGAGCCGGGGCAGGGGCTCG 9635         A  TTT  C
                                GGGGAGCCGG GC   GGC CG
                                |||||||||| ||   ||| ||
                                CCCCTCGGCC CG   CCG GC
                                     C  TCC   A
GAM2013  RAPSN   5'  GGTGGGAGCCGGAATGGGGCC  37217   _       CTTT
                                GG GGGAGCCGGAG   GGCC
                                || ||||||||||   ||||
                                CC CCCTCGGCCTT   CCGG
                                 A         ACC_
GAM2013  RENT1   3'  AGGGGAAGCTGGAGGCC    16246        C  GCTTT
                                AGGGGGAGC GGA    GGCC
                                |||||||| |||    ||||
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                                TCCCCTTCG CCT    CCGG
                                    A  _____
GAM2013  RGS19IP1  3'  AGGGGGGCCGGGGACCC    41693      A    AGCTTT
                                AGGGGG GCCGG    GGCCC
                                |||||| |||||     |||||
                                TCCCCC CGGCC    CTGGG
                                   _    C_____
GAM2013  RPH3AL   3'  GGAGGAGCCGGGCAGGG    28102         A  TTT
                                GGGGGAGCCGG GC   GG
                                |||||||||| ||   ||
                                CCTCCTCGGCC CG   CC
                                      _ TC_
GAM2013  RXRA     3'  GGAGGGGCCGGGGCACTCTG   16431      A    A__
                                GGGGG GCCGG   GCTTTG
                                ||||| |||||   ||||||
                                CCTCC CGGCC   TGAGAC
                                   C    CCG
GAM2013  SIX2     5'  GGCGGGGCTGGCCCCCTGGCCC 32610    _  A  C  AG
             G                   GG GGG GC GG  CTTTGGCCCG
                                 || ||| || ||  ||||||||||
                                 CC CCC CG CC  GGGACCGGGC
                                  G   _  A  GG
GAM2013  WISP2    3'  AGGGGAAGTCGGAGAGAAAGCT 19308        C    CTTT   C
             CG                    AGGGGGAG CGGAG    GGC CG
                                 |||||||| |||||    ||| ||
                                 TCCCCTTC GCCTC    TCG GC
                                     A    TCTT   A
GAM2013  WSX1     5'  AGGGGGAGTGGGGAGGCGGCC  22115        CC_   CTT
                                AGGGGGAG   GGAG   TGGCC
                                ||||||||   ||||   |||||
                                TCCCCCTC   CCTC   GCCGG
                                     ACC    C__
GAM2013  ACVR1B   3'  GGCCCAAAGCCTTTTCTTC    33760        T  CCTC
                                GGCCCGAA CC    CTTC
                                |||||||| ||    ||||
                                CCGGGTTT GG    GAAG
                                     C  AAAA
GAM2013  ADD1     3'  GGCTTCCTCCTCCTTC      30510     CCGAA  _
                                GGC    TCC CCTCCTTC
                                |||    ||| ||||||||
                                CCG    AGG GGAGGAAG
                                  A____   A
GAM2013  ALPP     3'  GGCCTGAGCCCCCTCCTTTCC  42870      C  AT       C
                                GGCC GA  CCCCTCCTT CC
                                |||| ||  ||||||||| ||
                                CCGG CT  GGGGAGGAA GG
                                  A  CG       A
GAM2013  APAF1    5'  CCGGCCTGTGGCGCCCTTCCCC 29817       CGAATCCCC
                                CCGGCC       TCCTTCCCC
                                ||||||       |||||||||
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                              GGCCGG       GGGAAGGGG
                                 ACACCGC__
GAM2013 AQP6    3' CCGGCTGGGATTCCTTCTTC  38239      CC_ A  CCTC
                              CCGGC  GA TCC   CTTC
                              |||||  || |||   ||||
                              GGCCG  CT AGG   GAAG
                                 ACC  A  AA__
GAM2013 ARF3    5' CCGGCTCCCTCCTTCC      11672      CCGAATC
                              CCGGC      CCCTCCTTCC
                              |||||      ||||||||||
                              GGCCG      GGGAGGAAGG
                                 A_______
GAM2013 ATP8B2  5' AGCCCGCGCCCTCCTT      42199       AATC
                              GGCCCG   CCCTCCTT
                              ||||||   ||||||||
                              TCGGGC   GGGAGGAA
                                 GC__
GAM2013 CA3     5' CCTGCTTCCTCTCTCCTTCC  23210   G  CCGAA  C__
                              CC GC    TCC   CTCCTTCC
                              || ||    |||   ||||||||
                              GG CG    AGG   GAGGAAGG
                               A  A_____  AGA
GAM2013 CDH6    5' CCAGCCTCATTCCTCCTTCC  22324      CGA  CC
                              CCGGCC   AT  CCTCCTTCC
                              ||||||   ||  |||||||||
                              GGTCGG   TA  GGAGGAAGG
                                 AG_  A_
GAM2013 CDKN2A  5' CCAGCCAGCCCCTCCTC     38467      CGAAT
                              CCGGCC     CCCCTCCTT
                              ||||||     |||||||||
                              GGTCGG     GGGGAGGAG
                                 TC____
GAM2013 CEBPA   3' GGCCTGCTCCCCTCCTTC    20397     CGAA
                              GGCC    TCCCCTCCTTC
                              ||||    ||||||||||
                              CCGG    AGGGGAGGAAG
                                ACG_
GAM2013 CLCA2   3' GGTCCGACTTTACCCTTCCC  27225    C   ATCCCC
                              GG CCGA      TCCTTCCC
                              || ||||      ||||||||
                              CC GGCT      GGGAAGGG
                               A   GAAAT_
GAM2013 CLOCK   3' GCTGGAACTTTCCCTCCTTTCC 22216   CC   C__      C
                              GC  GAAT   CCCTCCTT CC
                              ||  ||||   |||||||| ||
                              CG  CTTG   GGGAGGAA GG
                               AC    AAA       A
GAM2013 CNTNAP2 5' CCCGCTTCCTCTTCTTCCC   30484     AA  C  C
                              CCCG  TCC CT CTTCCC
                              ||||  ||| || ||||||
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                                GGGC  AGG GA GAAGGG
                                  GA   A  A
GAM2013  COX10    5'  CCGCCATCTTCCTTCC      10548     G  CGA   CCC
                                CCG CC   ATC   TCCTTCC
                                ||| ||   |||   |||||||
                                GGC GG   TAG   AGGAAGG
                                  _ ___   A__
GAM2013  CSK      3'  CCGCTCCGTGGCCTCCTTCC  20459     GC   AATCC
                                CCG  CCG    CCTCCTTCC
                                |||  |||    |||||||||
                                GGC  GGC    GGAGGAAGG
                                  GA   ACC__
GAM2013  CTNND2   3'  CCGGCCCGAATGCCTCGTCTC  10634          CC   __
                                CCGGCCCGAAT  CCTC  CTT
                                ||||||||||  ||||  |||
                                GGCCGGGCTTA  GGAG  GAG
                                       C_    CA
GAM2013  DLEC1    3'  CCTGCTGCCTCCTTCTTCCC   28823    G  CCGAAT  _   C
                                CC GC     CC CCT CTTCCC
                                || ||     || ||| ||||||
                                GG CG     GG GGA GAAGGG
                                 A  AC____  A   A
GAM2013  DMXL1    5'  CCCTCCCTCCTTCCC      24290     GAATC
                                CCC    CCCTCCTTCCC
                                |||    ||||||||||
                                GGG    GGGAGGAAGGG
                                  A____
GAM2013  DNAJB9   5'  CCGACCTAGCGCTCCTCCTTCC 29560       CGAATCC
              CC                  CCGGCC      CCTCCTTCCCC
                                |||||      ||||||||||
                                GGCTGG      GGAGGAAGGGG
                                   ATCGCGA
GAM2013  DNASE2   3'  CCGTCCCCCGCCCCCCC     10711     AA     C
                                CCG  TCCCCT CTTCCCC
                                |||  |||||| |||||||
                                GGC  AGGGGG GGGGGGG
                                  __      C
GAM2013  DPYSL3   5'  GGCTCCCTCCCTCCTTC     10774     _  GAATC
                                GGC CC    CCCTCCTTC
                                ||| ||    |||||||||
                                CCG GG    GGGAGGAAG
                                  A  GA___
GAM2013  DRD2     3'  CAGCTTCCCCTCCTTCC     9011      CCGAA
                                CGGC    TCCCCTCCTTCC
                                ||||    ||||||||||||
                                GTCG    AGGGGAGGAAGG
                                  A____
GAM2013  EDARADD  5'  CCGCCTTCCCCTCCCT      38845     G  CGAA
                                CCG CC    TCCCCTCCTT
                                ||| ||    ||||||||||
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                                GGC GG   AGGGGAGGGA
                                  _ A___
GAM2013 EPHB1   3' GGTCCTTTTCCCTCCTCTCCTT 20776   C GAA  ____
            CCCC                  GG CC  TCCC   CTCCTTCCCC
                                || ||  ||||  ||||||||||
                                CC GG  AGGG   GAGGAAGGGG
                                 A AAA   AGGA
GAM2013 EPHB6   5' CCGGCCCGGGTCCGTTCGGCGC 20796       AA  CC  CTTC
            C                  CCGGCCCG TCC TC   CC
                                |||||||| ||| ||   ||
                                GGCCGGGC AGG AG   GG
                                    CC  CA CCGC
GAM2013 F2RL3   3' CCGGCCCGGTCCCTGACCC  19515       AA   CTCCTT
                                CCGGCCCG TCCC    CCC
                                |||||||| ||||    |||
                                GGCCGGGC AGGG    GGG
                                    C_   ACT___
GAM2013 FGF1    3' CAGCCAGTTTCCCTTTCTTTC 37566     CGAA   C_ C
                                CGGCC   TCCC TC TTC
                                |||||   ||||  || |||
                                GTCGG   AGGG AG AAG
                                   TCAA   AA A
GAM2013 FZD1    5' GCCTCCGCCTCCTTCTCC   18614    CGAA  _     _
                                GCC   TCC CCTCCTTC CC
                                |||   ||| |||||||| ||
                                CGG   AGG GGAGGAAG GG
                                  ____  C      A
GAM2013 G6PD    3' GGCGCCCTCCTCCTTCC    7608     CCGAA  _
                                GGC   TCC CCTCCTTCC
                                |||   ||| |||||||||
                                CCG   GGG GGAGGAAGG
                                  C____  A
GAM2013 G6PT1   3' CCAGGCAGGCCCCTCCTT   11160   _  CCGAAT
                                CC GGC    CCCCTCCTT
                                || |||    |||||||||
                                GG CCG    GGGGAGGAA
                                 T  TCC___
GAM2013 GAN     5' CCGGCCCGGCTCTCCGCGCTC 35141       AA  _  ___
                                CCGGCCCG TC CC  CTC
                                |||||||| || ||  |||
                                GGCCGGGC AG GG  GAG
                                    CG  A  CGC
GAM2013 GCN5L1  3' CAGCCTCCCTCCTTCCCC   11244     CGAATC
                                CGGCC    CCCTCCTTCCCC
                                |||||    ||||||||||||
                                GTCGG    GGGAGGAAGGGG
                                  A_____
GAM2013 GDF2    3' CGGCCTGCTCCTTCCC     32124     CGAATCCC
                                CGGCC     CTCCTTCCC
                                |||||     |||||||||
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                                GCCGG       GAGGAAGGG
                                  AC_______
GAM2013  GFRA1    5'  CCCGCCCCCTCCTTCC      23563      AA
                                CCCG  TCCCCTCCTTCC
                                ||||  ||||||||||||
                                GGGC  GGGGGAGGAAGG
                                  __
GAM2013  GNGT2    5'  GCCTGCTTTCTCCTCCTTCCC  36485     CGAA_  C
                                GCC    TC CCTCCTTCCC
                                |||    || ||||||||||
                                CGG    AG GGAGGAAGGG
                                  ACGAA  A
GAM2013  GTF2F1   5'  CCGACCCGGGTTCCTTTCGTCT 13320         AA_   CC  C_
              CC                  CCGGCCCG   TCC  TC  TTCC
                                ||||||||   |||  ||  ||||
                                GGCTGGGC   AGG  AG  GAGG
                                     CCA   AA  CA
GAM2013  HDAC5    3'  CCAGTCCTCTCCTTCCC     24192      CCCGAA   C
                                CCGG     TCC CTCCTTCCC
                                ||||     ||| |||||||||
                                GGTC     AGG GAGGAAGGG
                                  _______  A
GAM2013  HS2ST1   5'  GCCCGCCTCCCTCTCTTCCTTC 29330       AA   _ ___
              C                   GCCCG  TCCC C   TCCTTCC
                                |||||  |||| |   |||||||
                                CGGGC  AGGG G   AGGAAGG
                                   GG    A AGA
GAM2013  HYAL2    3'  CCAGCTGTACCCTCCTTCCCC  37634      CCGAATC
                                CCGGC      CCCTCCTTCCCC
                                |||||      ||||||||||||
                                GGTCG      GGGAGGAAGGGG
                                   ACAT___
GAM2013  ITPR2    5'  GCTCCTCCTCCTCCTCCTTCCC 13678    _  GAA  _
                                GC CC   TCC CCTCCTTCCC
                                || ||   ||| ||||||||||
                                CG GG   AGG GGAGGAAGGG
                                 A  AGG   A
GAM2013  KCNK3    3'  CCTGCCTGTCCCTCCTTC    13901    G   CGAATC
                                CC GCC     CCCTCCTTC
                                || |||     |||||||||
                                GG CGG     GGGAGGAAG
                                 A   ACA___
GAM2013  KCNMB3   5'  GCTCCTCTCACCCTCCTTCTCC 30839    _  GAA  _       _
                                GC CC   TC CCCTCCTTC CC
                                || ||   || |||||||| ||
                                CG GG   AG GGGAGGAAG GG
                                 A  AG_  T       A
GAM2013  KLF4     5'  GGCCGAGATCCTTCTTC     20155      C  _   CCTC
                                GGCC GA ATCC    CTTC
                                ||||  || ||||   ||||
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                                CCGG CT TAGG    GAAG
                                  _ C    AA__
GAM2013  KLK8     5'  CCTGCTCCTCCTCCTTCTCC   40326    GAA  _      _
                                CC   TCC CCTCCTTC CC
                                ||   ||| |||||||| ||
                                GG   AGG GGAGGAAG GG
                                 ACG   A       A
GAM2013  KPNB1    5'  CGGTCCGGCTCCCCTTCCTCTC 13967     C   AA     _   TC
              C                  CGG CCG  TCCCCT CCT  CC
                                ||| |||  |||||| |||  ||
                                GCC GGC  AGGGGA GGA  GG
                                  A   CG     A   GA
GAM2013  LAMB2    5'  CGGCCCGAGCCCTCCTC     14072         ATC
                                CGGCCCGA   CCCTCCTT
                                ||||||||   ||||||||
                                GCCGGGCT   GGGAGGAG
                                     C__
GAM2013  LRP2     5'  CCGGCCTCGCCGTTCCTTCCCC 21185        _ AAT  CC
                                CCGGCC CG   CC  TCCTTCCCC
                                |||||| ||   ||  |||||||||
                                GGCCGG GC   GG  AGGAAGGGG
                                   A  ___  CA
GAM2013  MAML1    3'  CCGGCCTACGGCCTCCTTCCCC 31280       CGAATCC
                                CCGGCC      CCTCCTTCCCC
                                ||||||      ||||||||||
                                GGCCGG      GGAGGAAGGGG
                                   ATGCC__
GAM2013  MARK3    5'  GGCCCCCTCACCTCCTTCTCC  14359      GAA  C      _
                                GGCCC   TC CCTCCTTC CC
                                |||||   || |||||||| ||
                                CCGGG   AG GGAGGAAG GG
                                   GG_  T       A
GAM2013  MGAT1    5'  GGCCCGCCTCCTTTCCC     14438       AATCC     _
                                GGCCCG    CCTCCTT CCC
                                ||||||    ||||||| |||
                                CCGGGC    GGAGGAA GGG
                                   _____       A
GAM2013  MGAT3    5'  CCGGCCCCGATCCCCTCCCCCC 14458       GA
                                CCGGCCC  ATCCCCTCCTTCC
                                |||||||  ||||||||||||
                                GGCCGGG  TAGGGGAGGGGGG
                                    GC
GAM2013  MN1      3'  ACACGCAGTCCCCTCCTTC   14568    C  AA_
                                GC CG   TCCCCTCCTTC
                                || ||   ||||||||||
                                TG GC   AGGGGAGGAAG
                                 T  GTC
GAM2013  MPP6     5'  CCAAATCCCTTTCTTCTCC   32391         CTC   _
                                CCGAATCCC   CTTC CC
                                |||||||||   |||| ||
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                                GGTTTAGGG  GAAG GG
                                     AAA   A
GAM2013  MYC     5'  GCTCCGGATCTCCCTTCCC   14709    _  A  CCC
                                GC CCG ATC  TCCTTCCC
                                || ||| |||  ||||||||
                                CG GGC TAG  GGGAAGGG
                                 A  C  A__
GAM2013  MYO10   3'  GGTTCCTCCCCTCCTT     29575    C_ GAA
                                GG  CC  TCCCCTCCTT
                                ||  ||  ||||||||||
                                CC  GG  AGGGGAGGAA
                                 AA  ___
GAM2013  NAPB    3'  GGCCCTTCCCACTTCCTTTCC 43175      GAA  _ _  C
                                GGCCC  TCCC CT CCTT CC
                                |||||  |||| || |||| ||
                                CCGGG  AGGG GA GGAA GG
                                   A__   T A   A
GAM2013  NDST1   5'  GGTCACGCTCCTTCCTTCC   11371    CC  AA_  CC
                                GG  CG  TCC  TCCTTCC
                                ||  ||  |||  |||||||
                                CC  GT  AGG  AGGAAGG
                                 A_  GCG  A_
GAM2013  NNMT    5'  GCCCTCCTTCTCTTTCC     26120     GAA  C_  C
                                GCCC  TCC  CTC TTCC
                                ||||  |||  ||| ||||
                                CGGG  AGG  GAG AAGG
                                  ___  AA  A
GAM2013  NRXN2   3'  GGCCTGAGCCCCTTCCC     31485     C  ATCCC
                                GGCC GA   CTCCTTCCC
                                |||| ||   |||||||||
                                CCGG CT   GGGGAAGGG
                                  A  C____
GAM2013  OXTR    5'  CGGTTGGAATCCCCTCGCC   9523     CCC       CTT
                                CGG  GAATCCCCTC  CC
                                |||  ||||||||||  ||
                                GCC  CTTAGGGGAG  GG
                                  AAC       C__
GAM2013  PACSIN3  5'  CCGGCCCGAGTCCTCCTC   32141        A  _
                                CCGGCCCGA TCC CCTC
                                ||||||||| ||| ||||
                                GGCCGGGCT AGG GGAG
                                     C  A
GAM2013  PAFAH1B1 5'  CCGAGCGCTCCCCTCCTTCTCC 7703     _  CCGAA        _
                                CCG GC   TCCCCTCCTTC CC
                                ||| ||   |||||||||| ||
                                GGC CG   AGGGGAGGAAG GG
                                  T  CG___        A
GAM2013  PAX9    5'  CCGGCCCCAGTTCCGCACTCC  26203       GAA_  C__
                                CCGGCCC   TCC  CTCC
                                |||||||   |||  ||||
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                                GGCCGGG   AGG  GAGG
                                    GTCA  CGT
GAM2013 PIG3    5' CCGACCCGGGTCCCCGGCGCCC 22191       AA   TCCTT
                                CCGGCCCG TCCCC   CCC
                                |||||||| ||||| |||
                                GGCTGGGC AGGGG   GGG
                                    CC   CCGC_
GAM2013 PIP5K1A 3' CCAGGCCCCCTTCTTCCC   18650   _   GAATCC  C
                                CC GGCCC    CCT CTTCCC
                                || |||||    ||| ||||||
                                GG CCGGG    GGA GAAGGG
                                 T   _______  A
GAM2013 PKM2    3' CCAGTCCAGCATTCCTCCTTC 15331    C  AATCC
                                CCGG CCG    CCTCCTTC
                                |||| |||    ||||||||
                                GGTC GGT    GGAGGAAG
                                  A  CGTAA
GAM2013 POU4F1  3' CGGGTCTCCGCTTTCCTTCCCC 26384    CCCGAA  CC__
                                CGG    TCC   TCCTTCCCC
                                |||    |||   |||||||||
                                GCC    AGG   AGGAAGGGG
                                 CAG___  CGAA
GAM2013 PPP1R11 3' GCTCCCTCCCTCTTCCTTCC  45509   _ GAA   _ _
                                GC CC  TCCC CT CCTTCC
                                || ||  |||| || ||||||
                                CG GG  AGGG GA GGAAGG
                                 A G__   A  A
GAM2013 PPP2R4  5' CGGTGACCTCCTCCTTCC   41328    CCC  AT  _
                                CGG  GA  CC CCTCCTTCC
                                |||  ||  || |||||||||
                                GCC  CT  GG GGAGGAAGG
                                 A__  __ A
GAM2013 PPP5C   3' GCTCCACCTCCTTCC      26491    CCGAA  _
                                GC    TCC CCTCCTTCC
                                ||    ||| |||||||||
                                CG    AGG GGAGGAAGG
                                 _____  T
GAM2013 PSG5    5' GCTGTCCTTCCTCCTTCCCC  15803    CCGAA  __
                                GC    TCC  CCTCCTTCCCC
                                ||    |||  ||||||||||
                                CG    AGG  GGAGGAAGGGG
                                 AC___  AA
GAM2013 PTPRG   5' CGGCCCGAGTCCCCTTGGAATC 15934       A    CCT__
            C                    CGGCCCGA TCCCCT    TCC
                                |||||||| ||||||    |||
                                GCCGGGCT AGGGGA    AGG
                                    C     ACCTT
GAM2013 RAB2L   5' CCGGACCGAGTCCCCTCCCC  21917     C   A
                                CCGG CCGA TCCCCTCCTT
                                |||| |||| ||||||||||
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                                GGCC GGCT AGGGGAGGGG
                                  T   C
GAM2013  RBM6     5'  CGGCCCGCTCCTCCTTCTCC   25103        AATCC      _
                                CGGCCCG    CCTCCTTC CC
                                |||||||    |||||||| ||
                                GCCGGGC    GGAGGAAG GG
                                   GA___       A
GAM2013  RFX5     3'  GGCTTCCCTCTCCTTCC     7796      CCGAA   _
                                GGC    TCCC CTCCTTCC
                                |||    |||| ||||||||
                                CCG    AGGG GAGGAAGG
                                 A____    A
GAM2013  RPS6KA2  5'  CGCTCCCTCCGCCTCCTTCTCC 34459    G_   GAA   _      _
                                CG  CCC   TCC CCTCCTTC CC
                                ||  |||   ||| |||||||| ||
                                GC  GGG   AGG GGAGGAAG GG
                                 GA  ___   C       A
GAM2013  RRM2B    3'  ACCACAGAATCCCCTTTTTCCC 42709     _ _       CC
              C                  GCC C GAATCCCCT  TTCCCC
                                 ||| | |||||||||  ||||||
                                 TGG G CTTAGGGGA  AAGGGG
                                  T T        AA
GAM2013  RTN3     3'  GGCGGAGCCTTTCCTTCCC    43960     CC  AT  CC
                                GGC  GA  CC  TCCTTCCC
                                |||  ||  ||  ||||||||
                                CCG  CT  GG  AGGAAGGG
                                  C_  C_  AA
GAM2013  SDC2     3'  CCTGCCTACCCTCCTTCCC    42563    G   CGAATC
                                CC GCC     CCCTCCTTCCC
                                || |||     ||||||||||
                                GG CGG     GGGAGGAAGGG
                                 A  AT_____
GAM2013  SDC2     5'  CCGGGTCCTCCTCCTTCTCC   42561     AA   _      _
                                CCG  TCC CCTCCTTC CC
                                |||  ||| |||||||| ||
                                GGC  AGG GGAGGAAG GG
                                  CC   A       A
GAM2013  SLC12A7  3'  CGGGTCCGTGTCCTCCTTCCC  27328     C_   AATCC
                                CGG  CCG    CCTCCTTCCC
                                |||  |||    ||||||||||
                                GCC  GGC    GGAGGAAGGG
                                  CA   ACA__
GAM2013  SLC19A2  5'  CCGGCCCGGCCCCTTCCTTCTC 42886         AAT    _    _
              C                   CCGGCCCG   CCCCT CCTTC CC
                                  ||||||||   ||||| ||||| ||
                                  GGCCGGGC   GGGGA GGAAG GG
                                     C__     A    A
GAM2013  SLC21A9  3'  GGCCTGAGTCTCCCTCCCT    28566      C  A  _
                                GGCC GA TC CCCTCCTT
                                |||| || || ||||||||
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                                CCGG CT AG GGGAGGGA
                                  A  C  A
GAM2013  SLC4A1   3'  GACACGCCTTCCTTCCCC    7355     C  AATC  C
                                GGC CG   CC TCCTTCCCC
                                ||| ||   || |||||||||
                                CTG GC   GG AGGAAGGGG
                                  T  ____  A
GAM2013  SLC6A8   3'  CCCGTCTCTCCCTCCTTCCC  24755     AA  _
                                CCCG  TC CCCTCCTTCCC
                                ||||  || ||||||||||||
                                GGGC  AG GGGAGGAAGGG
                                  AG  A
GAM2013  SPAG8    3'  GGCTTGGTCCCCTTCCTCCC  29695     CCGAA     C
                                GGC    TCCCCT CTTCCC
                                |||    |||||| ||||||
                                CCG    AGGGGA GGAGGG
                                  AACC_     A
GAM2013  STC1     5'  CCTGCCCCCCTTTCCTCTTTCC 17174    G   GAA  ___   C
              C                  CC GCCC   TCC   CCTC TTCCC
                                 || ||||   |||   |||| |||||
                                 GG CGGG   GGG   GGAG AAGGG
                                  A   ___   AAA   A
GAM2013  STK10    3'  CAGCCTCCCTCTTTCCC     25615      CGAATC    C
                                CGGCC     CCCTC TTCCC
                                |||||     ||||| |||||
                                GTCGG     GGGAG AAGGG
                                  A_____    A
GAM2013  SYNGR1   3'  CCGGCCCAGTCCCTTCTCC    21755        AA   __
                                CCGGCCCG  TCCC  CTCC
                                ||||||||  ||||  ||||
                                GGCCGGGT  AGGG  GAGG
                                    C_   AA
GAM2013  TARBP2   5'  CCGTCCCGCCTCCTTCC     39529     G   AATCC
                                CCG CCCG    CCTCCTTCC
                                ||| ||||    |||||||||
                                GGC GGGC    GGAGGAAGG
                                  A   _____
GAM2013  TCF15    3'  GGCTCCTGGCCTCCTTCTCC   21423     _  GAATCC      _
                                GGC CC     CCTCCTTC CC
                                ||| ||     |||||||| ||
                                CCG GG     GGAGGAAG GG
                                  A  ACC___      A
GAM2013  TGT      3'  CCAGCCCCTCCCTCCCTTCCTT 36303       GAA__   C
              CC                  CCGGCCC    TCCC TCCTTCC
                                  |||||||    |||| |||||||
                                  GGTCGGG    AGGG AGGAAGG
                                     GAGGG   A
GAM2013  THRA     3'  GGCACTCCTTCTCCTTCCCC  17519     CCGAA  C_
                                GGC    TCC  CTCCTTCCCC
                                |||    |||  ||||||||||
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                                CCG    AGG  GAGGAAGGGG
                                  TG___  AA
GAM2013  TNFRSF13C 3'  GGCTTAATGGTGCCTTCCCC  38119    CCG  CCCCT
                                GGC  AAT   CCTTCCCC
                                |||  |||   ||||||||
                                CCG  TTA   GGAAGGGG
                                  AA_  CCAC_
GAM2013  TNFRSF6B  5'  GACCGCCCCCTCTCCTTCC   32354     CGAA  _
                                GGCC   TCCC CTCCTTCC
                                ||||   |||| ||||||||
                                CTGG   GGGG GAGGAAGG
                                  CG__   A
GAM2013  TRC8    5'  CCGCCCCTGCCCTCCTTCC   28510    G  GAATC
                                CCG CCC    CCCTCCTTCC
                                ||| |||    ||||||||||
                                GGC GGG    GGGAGGAAGG
                                  G  AC___
GAM2013  TRIM9   3'  CCAGCTTTTCTCTCCTCCTTCT 31555      CCGAA  C      _
            CC                    CCGGC    TC CCTCCTTC CC
                                |||||    || |||||||| ||
                                GGTCG    AG GGAGGAAG GG
                                   AAAAG  A       A
GAM2013  WRN     5'  CCGGCCCGGCTCGCCTTTCTC  8136         AA  C  CC
                                CCGGCCCG  TC CCT  TTC
                                ||||||||  || |||  |||
                                GGCCGGGC  AG GGA  GAG
                                     CG  C   AA
GAM2013  WW45    5'  CCGGCGCCGCCGCCTCCTTCCC 34816      _  AAT  _
                                CCGGC CCG   CC CCTCCTTCCC
                                ||||| |||   || ||||||||||
                                GGCCG GGC   GG GGAGGAAGGG
                                   C   ___  C
GAM2013  ZIC1    5'  CCGGCCCGGCTCGCACTTTCTC 18229         AA  CC_  CC
                                CCGGCCCG  TC   CT  TTC
                                ||||||||  ||   ||  |||
                                GGCCGGGC  AG   GA  GAG
                                     CG  CGT  AA
GAM2013  ZIC1    5'  CAGCCGCCCCTCCTTCC     18226      CGAAT
                                CGGCC    CCCCTCCTTCC
                                |||||    ||||||||||
                                GTCGG    GGGGAGGAAGG
                                   C____
GAM2014  BSN     3'  CCAGGGAGACAGAGAT     18397     TGT  AAA
                                CTAG  AGA  CAGAGAT
                                ||||  |||  |||||||
                                GGTC  TCT  GTCTCTA
                                  CC_  ___
GAM2014  HYOU1   3'  TGAATGGGGAAAACAGAG   40642   T   TA
                                C AGTG  GAAAACAGAG
                                | ||||  ||||||||||
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                                A TTAC  CTTTTGTCTC
                                 C    CC
GAM2014  ITGB1    3'  ACTAGTGTGAAACAAGAT    38042        A    A  G
                                ACTAGTGT GAAA CA AGAT
                                |||||||| |||| || ||||
                                TGATCACA CTTT GT TCTA
                                      _    _ _
GAM2014  MAGEA4   3'  TGTAAAAGGAAACAGAGATA   14325        ___
                                TGTAGAA   AACAGAGATA
                                |||||||   ||||||||||
                                ACATTTT   TTGTCTCTAT
                                    CCT
GAM2014  PTTG1IP  3'  ACTAAATCTAGAAACAGAGAT  20278      _ G     A
                                ACTAG T TAGAAA CAGAGAT
                                ||||| | |||||| |||||||
                                TGATT A ATCTTT GTCTCTA
                                   T G     _
GAM2014  RAB27A   3'  GCTGGTAAAGACAGAGAT    21362    __     AA
                                GT  GTAGA  ACAGAGAT
                                ||  |||||  ||||||||
                                CG  CATTT  TGTCTCTA
                                 AC     C_
GAM2014  SALL2    5'  ACTGTGAAGCAGAGAT      41894     A   T  AAAA
                                ACT GTG AG    CAGAGAT
                                ||| ||| ||    |||||||
                                TGA CAC TC    GTCTCTA
                                  _   T  _____
GAM2014  SFRS7    3'  TAACTAATGTAGAAAGCA    40471            A
                                TAACTAGTGTAGAAA CA
                                |||||||||||||| ||
                                ATTGATTACATCTTT GT
                                          C
GAM2014  SGT      3'  AGTGGAGGAGGGCAGAGATA   16607      T  AAAA_
                                AGTG AG     CAGAGATA
                                |||| ||     ||||||||
                                TCAC TC     GTCTCTAT
                                  C  CTCCC
GAM2014  SLC19A2  3'  TAACTATGTAGAAAGAC     42892       G     AAACA
                                TAACTA TGTAGA     GAGAT
                                |||||| ||||||     |||||
                                ATTGAT ACATCT     TTCTG
                                      _     ______
GAM2015  XKRY     5'  TAAGCTGTGGAGTTCAAGTAAA 21705         A  AAGAT
            T                    TAAGTTGTG AG     AGTAAAT
                                |||||||||  ||     |||||||
                                ATTCGACAC TC     TCATTTA
                                      C  AAGT_
GAM2015  APOBEC2  3'  GACTGGAGCCCATGTATG    27705     __       AC
                                GGC  GAGCCCAT  ATG
                                |||  ||||||||  |||
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                                CTG  CTCGGGTA  TAC
                                  AC       CA
GAM2015  EPS15    3'  TTTATAGGTGAAAAACATGA   12751        C   CCCAT
                                TTTATAGG GAG     ACATGA
                                |||||||| |||     ||||||
                                AAATATCC CTT     TGTACT
                                    A   TT___
GAM2015  FGFR2    3'  TTTATAAGCTCATATACATG   35672         GAGCCC
                                TTTATAGGC      ATACATG
                                |||||||||      |||||||
                                AAATATTCG      TATGTAC
                                    AGTA__
GAM2015  HSF2BP   3'  TTTATAGGTGAACCTACA    28150         C     CA
                                TTTATAGG GAGCC  TACA
                                |||||||| |||||  ||||
                                AAATATCC CTTGG  ATGT
                                    A    __
GAM2015  MEN1     3'  TAGGTCACTGCATACATGA    39201      _  AGCC
                                TAGG CG    CATACATGA
                                |||| ||    |||||||||
                                ATCC GT    GTATGTACT
                                  A  GAC_
GAM2016  COL4A4   5'  TAGTACTTAAAAAATATT     6406         C
                                TAGTAC TAAAGGATATT
                                |||||| ||||||||||
                                ATCATG ATTTTTTATAA
                                    A
GAM2016  PCDH15   3'  TATAGCACCTGAGATTTATT   37508          AAA    A
                                TATAGTACCT   GGAT TTATT
                                ||||||||||   |||| |||||
                                ATATCGTGGA   TCTA AATAA
                                    C__    _
GAM2016  ZNF26    3'  AATACTGGGGGATATTATTC   43790       CTAAA
                                AGTAC     GGATATTATTC
                                |||||     ||||||||||
                                TTATG     CCTATAATAAG
                                  ACCC_
GAM2017  BDNF     3'  TATAATCTAATCTATACAACA  40595        A
                                TATAAT TAATCTATATAATA
                                |||||| ||||||||||||||
                                ATATTA ATTAGATATGTTGT
                                    G
GAM2017  IRAK4    3'  TAACATAATCTAATAAT      41460           T
                                TAATATAATCTA ATAAT
                                |||||||||||| |||||
                                ATTGTATTAGAT TATTA
                                                _
GAM2017  MADH6    3'  TATAATATATATTTCCATATAA 24605          A___
                TA                  TATAATATA    TCTATATAATA
                                |||||||||    ||||||||||
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                                ATATTATAT   AGGTATATTAT
                                     ATAA
GAM2017 RGS1    3' TACAAACTATATAATAAT   16309      T
                                TATAA CTATATAATAAT
                                ||||| ||||||||||||
                                ATGTT GATATATTATTA
                                   T
GAM2018 LPHH1   3' TGATTGCTAGTGGTTAAGCATG 29390   A      CAT___  C
           TTTT                  A GTTGCTAGT     GCA GTTTT
                                | |||||||||     ||| |||||
                                A TAACGATCA     CGT CAAAA
                                 C       CCAATT   A
GAM2019 PAG     3' TGGGATCTTTTGTGGGTG    32960         _  TC
                                TGGGATCTTT GTG  TG
                                |||||||||| |||  ||
                                ACCCTAGAAA CAC  AC
                                      A   CC
GAM2019 SYNGR3  3' GGGAGGTGTCTGTCTGAT   20097     TCTTT       A
                                GGGA    GTGTCTGTCT AT
                                ||||    |||||||||| ||
                                CCCT    CACAGACAGA TA
                                  C____        C
GAM2020 APRT    3' CAGCTGGAGATGTTGGGCT   7927     AA  C   CA
                                CAG  GG GGA  TTGGGCT
                                |||  || |||  |||||||
                                GTC  CC TCT  AACCCGA
                                  GA  _  AC
GAM2020 BF      5' GAAGGCAGGAGAGAAGCTG   11810       ACATT
                                GAAGGCGG    GGGCTG
                                ||||||||    ||||||
                                CTTCCGTC    TTCGAC
                                     CTCTC
GAM2020 CAPN9   5' CAGAGGGCCACTGGGCT    27356     A   GGA
                                CAGA GGC   CATTGGGCT
                                |||| |||   |||||||||
                                GTCT CCG   GTGACCCGA
                                  C  ___
GAM2020 CAV1    5' GAGGAGGTTTCCCTGGGCTG   11991    A  C  ACA__
                                GA GG GG    TTGGGCTG
                                || || ||    ||||||||
                                CT CC CC    GACCCGAC
                                 _  T  AAAGG
GAM2020 ENC1    3' ACCAGAAGTGGAGGGCT    18858       GC   CATT
                                ACCAGAAG  GGA   GGGCT
                                ||||||||  |||   |||||
                                TGGTCTTC  CCT   CCCGA
                                     A_  _____
GAM2020 HCS     3' CCTGGAAGGCGGAGGTTG    33229    A_      CA
                                CC  GAAGGCGGA  TTG
                                ||  |||||||||  |||
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                                GG  CTTCCGCCT  AAC
                                 AC        CC
GAM2020  HCS      3'  ACTGGAAGGCGGAGGTTG    33218    CA       CA
                                AC  GAAGGCGGA  TTG
                                ||  |||||||||  |||
                                TG  CTTCCGCCT  AAC
                                 AC        CC
GAM2020  IRAK1    3'  CCAGAGGCCTGGGC       11470      A   GGACA
                                CCAGA GGC    TTGGGC
                                |||||| |||    ||||||
                                GGTCT CCG    GACCCG
                                   _  ______
GAM2020  KIF5C    3'  AGAGCAGGTATATTGGGCTG   21142    _    AC__
                                AG GCGG    ATTGGGCTG
                                || ||||    |||||||||
                                TC CGTC    TAACCCGAC
                                 T    CATA
GAM2020  KMO      3'  AGAGGGTAACTCTGGGCTG    18953     A  CG   A
                                AGA GG  GAC TTGGGCTG
                                ||| ||  ||| ||||||||
                                TCT CC  TTG GACCCGAC
                                  _ CA   A
GAM2020  LAMB3    3'  CACCAGGGGTGGTCCAGGCTG  6905        AA  C  ACA TG
                                CACCAG  GG GG   T  GGCTG
                                ||||||  || ||   |  |||||
                                GTGGTC  CC CC   G  CCGAC
                                   C_  A  A__ GT
GAM2020  MAFF     5'  CAGAAGGTGCCCTCTGGGCTG  29510       CGGACA
                                CAGAAGG     TTGGGCTG
                                |||||||     ||||||||
                                GTCTTCC     GACCCGAC
                                    ACGGGA
GAM2020  PKIG     3'  CCAGAAGATTGGGC       28192        GCGGAC
                                CCAGAAG     ATTGGGC
                                |||||||     |||||||
                                GGTCTTC     TAACCCG
                                   _______
GAM2020  POLL     3'  CACTGGGAGCCGGGCAGACACT 29979     C___  AA_
           G                     CAC    AG   GGCGGACATTG
                                |||    ||   ||||||||||||
                                GTG    TC   CCGTCTGTGAC
                                  ACCC  GGC
GAM2020  PVALB    5'  CACTGAAAGGCTGGGC      15998     CA     GGACAT
                                CAC  GAAGGC     TGGGC
                                |||  ||||||     |||||
                                GTG  TTTCCG     ACCCG
                                  AC     _______
GAM2020  PYGM     5'  CAGGAGGGCGGGCCGGACTG  24695     AA_    ACA
                                CAG   GGCGG   TTGGGCTG
                                |||   |||||   ||||||||
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                                GTC  CCGCC  GGCCTGAC
                                  CTC    C__
GAM2020 RFP     3' CACTGGAGGTGGACATC    27128    CA  A  C
                                CAC  GA GG GGACATT
                                |||  || || |||||||
                                GTG  CT CC CCTGTAG
                                  AC  _  A
GAM2020 SLC1A5  5' CCGGGAGGCGGGGACCCGGGCT 24745   AGA    ACA_
          G                      CC  AGGCGG   TTGGGCTG
                                ||  ||||||  ||||||||
                                GG  TCCGCC   GGCCCGAC
                                 CCC    CCTG
GAM2020 SLC7A5  3' CACCAGGCAGGTGGGGCACCAG 18539     A_  C  A_  TG G
          CTG                     CACCAG  AGG GG  CAT  G CTG
                                ||||||  ||| ||  |||  | |||
                                GTGGTC  TCC CC  GTG  C GAC
                                   CG   A  CC   GT _
GAM2020 SMOH    5' GGGGCCCATGTTGGGCTG   24815    C  A_  __
                                GG GG  CAT  TGGGCTG
                                || ||  |||  |||||||
                                CC CC  GTA  ACCCGAC
                                 _ GG   CA
GAM2020 TGFB1   5' ACCAGAAGGTGGGTGGTCT   8532        C  ACAT   G
                                ACCAGAAGG GG   TGG CT
                                |||||||||  ||   ||| ||
                                TGGTCTTCC CC   ACC GA
                                     A  C___   A
GAM2021 ABCD1   3' TTTACTGGGGGGGACTGGGGG  6210        AAT    C
                                TTTATTGGG   ATTGG GGG
                                |||||||||   ||||| |||
                                AAATGACCC   TGACC CCC
                                     CCC    _
GAM2021 AQP7    3' TTTATTGGGGAATGGATGGGAT 10120       AATAT   CG
                                TTTATTGGG    TGG  GGGAT
                                |||||||||    |||  |||||
                                AAATAACCC    ACC  CCCTA
                                     CTT__   TA
GAM2021 CASP4   5' TTTATTGGGGGATATTTGG   37823        A_    _
                                TTTATTGGG  ATATT GG
                                |||||||||  ||||| ||
                                AAATAACCC  TATAA CC
                                     CC    A
GAM2021 CRP     3' TATTGGGAATGCGGGGA    43445        ATTG
                                TATTGGGAAT   GCGGGGA
                                ||||||||||   |||||||
                                ATAACCCTTA   CGCCCCT
                                             ____
GAM2021 GAGEB1  3' TTTATTGGGAGAATTTTAATGG 19120        AT   GGCG_
                                TTTATTGGGA  ATT    GG
                                ||||||||||  |||    ||
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                                AAATAACCCT TAA   CC
                                     CT  AATTA
GAM2021 GRM1    3' TTTATTGGTGGTAAAAAGGGAT 9148       GAATATTGGC
                                TTTATTGG       GGGGAT
                                ||||||||       ||||||
                                AAATAACC       TCCCTA
                                    ACCATTTT__
GAM2021 IL16    5' TTTATCGGGGATGTTTGGG  21101       AATAT GCG
                                TTTATTGGG   TG  GGG
                                |||||||||   ||  |||
                                AAATAGCCC   AC  CCC
                                     CT___ AAA
GAM2021 LDHA    3' TTTATTGGGGGTTTTAGTTGG 24521       AATA  CG
                                TTTATTGGG   TTGG GG
                                |||||||||   ||||  ||
                                AAATAACCC   AATC CC
                                     CCAA   AA
GAM2021 TULP1   3' TTTATTGGGGATGTGGG    17733       AATAT GC
                                TTTATTGGG   TG  GGG
                                |||||||||   ||  |||
                                AAATAACCC   AC  CCC
                                     CT___ A_
GAM2022 CTSD    3' GCTCAGCCCAGCGGGCGCTG  12529       GT_   A
                                GCTCGGTT  TGGGC CTG
                                ||||||||  ||||| |||
                                CGAGTCGG  GCCCG GAC
                                     GTC   C
GAM2022 ESRRA   3' GCTCGTTGGGAGCTGAT    20832    GGTT    CA
                                GCTC   GTTGGG  CTGAT
                                ||||   ||||||  |||||
                                CGAG   CAACCC  GACTA
                                  ____    TC
GAM2022 KRT6B   3' AGCTCAGTGGAACAGGTATTGA 24478       TGT_  CAC
            T                    AGCTCGGT   TGGG  TGAT
                                ||||||||   ||||  ||||
                                TCGAGTCA   GTCC  ACTA
                                     CCTT   ATA
GAM2022 MECP2   3' AGCTGTAGACGGGGCACTGAT 22572      T____
                                GGTTGT   GGGCACTGAT
                                ||||||   ||||||||||
                                TCGACA   CCCGTGACTA
                                   TCTGC
GAM2022 PPP1R12B 3' GATTACTGGGTGTTGATA   36975       CAC
                                GGTTGTTGGG  TGATA
                                ||||||||||  |||||
                                CTAATGACCC  ACTAT
                                      ACA
GAM2023 ARHGAP6 3' TGTGAGGCACTGCCTTT    30233   C  CTT
                                TG TG  TACTGCCTTT
                                || ||  ||||||||||
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                              AC AC   GTGACGGAAA
                               _ TCC
GAM2023 ATP6V0A4 5' GCTGCTTTACATTCCTTT    39289        TG_
                              GCTGCTTTAC   CCTTT
                              ||||||||||   |||||
                              CGACGAAATG   GGAAA
                                    TAA
GAM2023 C6      5' TGTGCATACTGCCTTT     45405    C   TT
                              TG TGC  TACTGCCTTT
                              || |||  ||||||||||
                              AC ACG  ATGACGGAAA
                               _  T_
GAM2023 CACNA1G  3' TGCTGCTTTTAACTCTCTTT  33133        __  GC
                              TGCTGCTTT  ACT  CTTT
                              |||||||||  |||  ||||
                              ACGACGAAA  TGA  GAAA
                                    AT   GA
GAM2023 CASQ1    3' ATGCTGCCCCAGATGTCTTT  10279         C_ C
                              ATGCTGCTTTA  TG CTTT
                              ||||||||||  ||  ||||
                              TACGACGGGGT  AC GAAA
                                    CT  A
GAM2023 CD59     3' ATACCTGAACTGCCTTT     8305       GCTTT
                              ATGCT    ACTGCCTTT
                              |||||    |||||||||
                              TATGG    TGACGGAAA
                                 ACT__
GAM2023 COL8A1   5' ATGCTGCTCTGCCTT      12334        TTA
                              ATGCTGCT   CTGCCTT
                              ||||||||   |||||||
                              TACGACGA   GACGGAA
                                   ___
GAM2023 FGF1     5' TGCTGCTTGTGGCGCTTT    37574        TACT _
                              TGCTGCTT    GC CTTT
                              ||||||||    ||  ||||
                              ACGACGAA    CG GAAA
                                   CAC_ C
GAM2023 FOXF2    3' TGTGCTTAGCACTGCCTTT   11132    C    __
                              TG TGCTT  TACTGCCTTT
                              || |||||  ||||||||||
                              AC ACGAA  GTGACGGAAA
                               _    TC
GAM2023 GRPR     5' TGCTGCTCTGGCTTT      23684       TTA  C
                              TGCTGCT   CTG CTTT
                              |||||||   |||  ||||
                              ACGACGA   GAC GAAA
                                  ___  C
GAM2023 ITGB4    3' TGCTGCTCCCAGCTCTTT    6848         ACT _
                              TGCTGCTTT   GC CTTT
                              |||||||||   ||  ||||
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                                ACGACGAGG  CG GAAA
                                     GT_  A
GAM2023 LYL1    3' ATGTTGCTTTGCCGACCT   24574    C    A  _
                                ATG TGCTTT CTG CCT
                                ||| |||||| ||| |||
                                TAC ACGAAA GGC GGA
                                  A    C  T
GAM2023 NFATC3  3' ATGCTGCTCCTGTTCTTT   21248       TA  C_
                                ATGCTGCTT  CTG  CTTT
                                |||||||||  |||  ||||
                                TACGACGAG  GAC  GAAA
                                     __  AA
GAM2023 NUMB    3' ATACTGCTTTTCCTTT     19048        ACTG
                                ATGCTGCTTT   CCTTT
                                ||||||||||   |||||
                                TATGACGAAA   GGAAA
                                     A___
GAM2023 PPT1    3' TGCTACTTCCCTCCTTT    41555       TA  G
                                TGCTGCTT  CT CCTTT
                                ||||||||  || |||||
                                ACGATGAA  GA GGAAA
                                     GG  _
GAM2023 PRKACA  3' GCTGCTTTGTCTGGCTTT   15579       A_  C
                                GCTGCTTT  CTG CTTT
                                ||||||||  ||| ||||
                                CGACGAAA  GAC GAAA
                                     CA  C
GAM2023 ROR2    3' TGCCTCCTCGCTGCCTTT   21265    G  TA
                                TGCT CTT  CTGCCTTT
                                ||||  |||  ||||||||
                                ACGG GGA  GACGGAAA
                                  A  GC
GAM2023 SHB     3' TGCCGCCCTTCTGTCTTT   16691       A  C
                                TGCTGCTTT CTG CTTT
                                ||||||||| ||| ||||
                                ACGGCGGGA GAC GAAA
                                     A  A
GAM2023 SLC2A5  5' TGCCGCTCACCTCCTTT    16769       T  G
                                TGCTGCTT ACT CCTTT
                                |||||||| ||| |||||
                                ACGGCGAG TGG GGAAA
                                     _  A
GAM2023 TFCP2   5' ACGCTGCTTTTGCACCTTT  24919        AC
                                ATGCTGCTTT  TGCCTTT
                                ||||||||||  |||||||
                                TGCGACGAAA  GTGGAAA
                                      AC
GAM2023 TOP3B   5' TGCGCTTCCCGCCTTT     19468    T   A
                                TGC GCTTT CTGCCTTT
                                ||| ||||| ||||||||
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                                ACG CGAAG GGCGGAAA
                                  _   _
GAM2024 CEACAM6  3' TGTACATTTGAACACACGGCTG 14734        CCA__   T
                                TGTACATT    ACAC GCTG
                                ||||||||    |||| ||||
                                ACATGTAA    TGTG CGAC
                                     ACTTG   C
GAM2024 CTBP2    3' TGTAGTTTCAACACTGCAAC  35606     CA  C      T
                                TGTA  TTC AACACTGC GC
                                ||||  ||| |||||||| ||
                                ACAT  AAG TTGTGACG TG
                                  CA  _      T
GAM2024 CTGF     3' TATACATTCTGGTGCTG     12507        CAACAC
                                TGTACATTC     TGCTG
                                |||||||||     |||||
                                ATATGTAAG     ACGAC
                                     ACC___
GAM2024 CUL5     3' TGTACATTTACAGTATTTGCTG 18494       CCA  C____
             C                   TGTACATT   ACA    TGCTGC
                                ||||||||   |||    ||||||
                                ACATGTAA   TGT    ACGACG
                                     A__   CATAA
GAM2024 GAS1     3' TGTACATTTCTACAACGTCCAT 13077       CCA  CT  TG
                                TGTACATT   ACA  GC  CCAT
                                ||||||||   |||  ||  ||||
                                ACATGTAA   TGT  TG  GGTA
                                     AGA   __  CA
GAM2024 GPR81    3' TGCACATTCTGTCCCCTGCCAT 37192        CAACA  G
                                TGTACATTC     CT CTGCCAT
                                |||||||||     || |||||||
                                ACGTGTAAG     GG GACGGTA
                                     ACA__  G
GAM2024 MAX      3' TGTACATTTCCATGTGAATAAG 14375       _   ACACTGCT_
             CCAT                    TGTACATT CCA       GCCAT
                                ||||||||| |||       |||||
                                ACATGTAA GGT       CGGTA
                                     A   ACACTTATT
GAM2024 NET1     3' TGTATATCTTTAGCTGCCA   25231     C   CCAACACT
                                TGTA ATT       GCTGCCA
                                ||||| |||      |||||||
                                ACAT TAG       CGACGGT
                                  A   AAAT____
GAM2024 PRKWNK3  3' TGTACATTTTGACATTGCC   41541       CCA  C
                                TGTACATT   ACA TGCT
                                ||||||||   ||| ||||
                                ACATGTAA   TGT ACGG
                                     AAC   A
GAM2024 PTGFRN   3' TGTAGATTCCAGGGCTGCCAT  42604     C     ACACT
                                TGTA ATTCCA    GCTGCCAT
                                |||| ||||||    ||||||||
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                                ACAT TAAGGT    CGACGGTA
                                  C     CC___
GAM2025  PTPRB    3'  TAAATTATACATAGTATCAA   15926          _
                                TAAATTATACA AGTATTAA
                                |||||||||||  ||||||||
                                ATTTAATATGT TCATAGTT
                                      A
GAM2026  ACADSB   3'  TCTGAACTATTATTCAGGATAA 11501    CA      C  CA
                                TC  AACTATTA TC  GGGATAA
                                ||  ||||||||  ||  |||||||
                                AG  TTGATAAT AG  TCCTATT
                                 AC       A  __
GAM2026  AP2B1    3'  TCCAAATGACCAGGGATA    10492       CTATTACT
                                TCCAAA       CCAGGGATA
                                ||||||       |||||||||
                                AGGTTT       GGTCCCTAT
                                   ACT_____
GAM2026  BNC      3'  TCCAAACACAGGGAT       11855        TATTACTC
                                TCCAAAC      CAGGGAT
                                |||||||      |||||||
                                AGGTTTG      GTCCCTA
                                   T________
GAM2026  BYSL     3'  TCAGAACTAAACAGGGATA   19757    CA    TTACTC
                                TC  AACTA    CAGGGATA
                                ||  |||||    ||||||||
                                AG  TTGAT    GTCCCTAT
                                 TC    TT____
GAM2026  CDH19    5'  TCCAACTATTACTCTTCAG   34504      A       __
                                TCCAA CTATTACTC  CAG
                                |||||  |||||||||  |||
                                AGGTT GATAATGAG  GTC
                                   _       AA
GAM2026  CR1      3'  TCCAAACTATTTTCTATCTCC  8202          A_____
                                TCCAAACTATT     CTCC
                                ||||||||||     ||||
                                AGGTTTGATAA     GAGG
                                      AAGATA
GAM2026  DSC3     3'  AAACTATCACTTAAAGTGA   35940          CC  _
                                AAACTATTACT  AGG GA
                                ||||||||||  ||| ||
                                TTTGATAGTGA  TTC CT
                                      AT   A
GAM2026  EFG2     5'  TCCAAACTGTTACTGTCTCGG  37034        A    CCA__
                                TCCAAACT TTACT    GG
                                ||||||||  |||||    ||
                                AGGTTTGA AATGA    CC
                                   C    CAGAG
GAM2026  IL1R1    3'  TCCAGGTGACCTCAGGGATAA  9367       AACTATT  TC
                                TCCA      AC  CAGGGATAA
                                ||||      ||  |||||||||
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                                AGGT      TG  GTCCCTATT
                                  CCAC___  GA
GAM2026  PSCDBP   3'  CTCAATTATTCACAGGGATAA  20180    __    C  _
                                CT  ATTA TC CAGGGATAA
                                ||  |||| || |||||||||
                                GA  TAAT AG GTCCCTATT
                                 GT    A  T
GAM2026  RFP      3'  TCCCAGAATCCTTCCAGGGAT  27133     AAACT   AC
                                TCC    ATT  TCCAGGGAT
                                |||    |||  |||||||||
                                AGG    TAG  AGGTCCCTA
                                  GTCT_  GA
GAM2026  SRR      3'  CCAGTCAGTACTCCAGGGAT   34964     AAC  T
                                CCA   TA TACTCCAGGGAT
                                |||   || ||||||||||||
                                GGT   GT ATGAGGTCCCTA
                                  CA_  C
GAM2026  ZNF207   3'  TCCAAACCTATTAGACTGGAT  18386        _    CTCCAG
                                TCCAAAC TATTA     GGAT
                                ||||||| |||||     ||||
                                AGGTTTG ATAAT     CCTA
                                    G    CTGA__
GAM2027  REGL     3'  CATTAGATGGCCATTAGT    27121       A   AT
                                CATTA ATG  GTTATTAGT
                                ||||| |||  |||||||||
                                GTAAT TAC  CGGTAATCA
                                  C  __
GAM2027  RHO      3'  TTACATTAATTGATGTTATT   8065         A
                                TTACATTAA TGATGTTATT
                                ||||||||| ||||||||||
                                AATGTAATT ACTACAATAA
                                     A
GAM2028  MFI2     3'  TTCCCACATAACAATATTTT   25472        TT_
                                TTCCCAC   ATAATATTTT
                                |||||||   ||||||||||
                                AAGGGTG   TGTTATAAAA
                                    TAT
GAM2028  NEK2     3'  TACTCTTCCTGCATAAATATTT 14748         CACTTAT
           T                    TACTCTTCC      AATATTTT
                                |||||||||      ||||||||
                                ATGAGAAGG      TTATAAAA
                                     ACGTAT_
GAM2028  PLXNA1   3'  TTCCCACTGCCTTCATTTT   43631        TATAA
                                TTCCCACT    TATTTT
                                ||||||||    ||||||
                                AAGGGTGA    GTAAAA
                                    CGGAA
GAM2028  PRKCN    3'  TACTCTTCCTTTTGTAACAT  25160         CAC  A
                                TACTCTTCC   TT TAATAT
                                |||||||||   || ||||||
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                                ATGAGAAGG   AA ATTGTA
                                     AA_  C
GAM2028 RAD51L1  3' ACTCTTTCCCAATATTT     39448       _   CTTATA
                                ACTCTT CCCA     ATATTT
                                |||||| ||||     ||||||
                                TGAGAA GGGT     TATAAA
                                   A   _______
GAM2028 SUSP1    3' TACTCTTTCCTCTTAAATATTT 31795        C  A    T
                                TACTCTT CC CTTA AATATTT
                                ||||||| || |||| |||||||
                                ATGAGAA GG GAAT TTATAAA
                                    A  A   _
GAM2029 FABP5    3' TATTTATTAACCAAAGGGATGA 11067          ATATA__  C
           TCC                    TATTTATTAA      GA GATCC
                                |||||||||||      || |||||
                                ATAAATAATT      CT CTAGG
                                      GGTTTCC  A
GAM2029 ALOX12B  3' TAGGGCACAGAATGGGGAGA   10072     TT       A  A
                                TAG  TATAGAAT GG AGA
                                |||  |||||||| || |||
                                ATC  GTGTCTTA CC TCT
                                  CC       C  C
GAM2029 ALX3     3' TCAGTTTGTGGTAGGAAGA    27066        ATAGAA
                                TTAGTTT     TAGGAAGA
                                |||||||     ||||||||
                                AGTCAAA     ATCCTTCT
                                    CACC__
GAM2029 BACE     3' TAGCCTAATAGGAAGA       39970        TAGA
                                TAGTTTA    ATAGGAAGA
                                |||||||    |||||||||
                                ATCGGAT    TATCCTTCT
                                     ____
GAM2029 DLEC1    3' ATCCACAGAGTAGGAGGA     28815         A    A
                                GTTTATAGA TAGGA GA
                                ||||||||| ||||| ||
                                TAGGTGTCT ATCCT CT
                                     C    C
GAM2029 EHHADH   3' TTAGTTCATAGACATTTGG    12686          ATA__
                                TTAGTTTATAGA    GG
                                ||||||||||||    ||
                                AATCAAGTATCT    CC
                                      GTAAA
GAM2029 GPC5     3' TTAATTTAGAAAGGAAG      20921        TA    T
                                TTAGTT  TAGAA AGGAAG
                                ||||||  ||||| ||||||
                                AATTAA  ATCTT TCCTTC
                                    __    _
GAM2029 GPR23    3' TTAGTTTATAGCATAGGA     41318          A
                                TTAGTTTATAG ATAGGA
                                |||||||||| ||||||
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                                AATCAAATATC TATCCT
                                      G
GAM2029  GRAF    3'  TAGCTAATAGGAAG       31453      TATAG
                                TAGTT    AATAGGAAG
                                |||||    |||||||||
                                ATCGA    TTATCCTTC
                                  _____
GAM2029  PIM1    3'  AGCTTGGAATAGGAAG     44962      ATA
                                AGTTT  GAATAGGAAG
                                |||||  ||||||||||
                                TCGAA  CTTATCCTTC
                                  C__
GAM2029  SRGAP2  3'  CTAGTTAAATAGGAAG     43978      TATA
                                TTAGTT   GAATAGGAAG
                                ||||||   ||||||||||
                                GATCAA   TTTATCCTTC
                                  ____
GAM2029  TLR4    3'  TTAGCTTATAGGCAAGA     17567        AA
                                TTAGTTTATAG  TAGGA
                                ||||||||||  |||||
                                AATCGAATATC  GTTCT
                                      C_
GAM2029  UBL3    3'  TTAGTTTACAGGAAG       28270        AGAAT
                                TTAGTTTAT    AGGAAG
                                |||||||||    ||||||
                                AATCAAATG    TCCTTC
                                  _____
GAM2030  ITGA9   3'  GGTCATGTGACTGGTG      13613          TCC
                                GGTCATGTGACT  GGTG
                                ||||||||||||  ||||
                                CCAGTACACTGA  CCAC
                                    ___
GAM2030  PRKAB1  3'  TCATGTGACTTCTAGACGTG  26505          CGGT
                                TCATGTGACTTC   GACGTG
                                ||||||||||||   ||||||
                                AGTACACTGAAG   CTGCAC
                                      AT__
GAM2031  AGC1    3'  GCTCAGCGTCCTGGGTGCG   29813    GA  A   C
                                GCT  CAG GTCC TGGGTGCG
                                |||  ||| |||| ||||||||
                                CGA  GTC CAGG ACCCACGC
                                  __  G   _
GAM2031  GAS7    3'  GCTGCAAAGGATTCTGGGTGCG 25274     A    TCC_
                                GCTG CAGAG   CTGGGTGCG
                                |||| |||||   |||||||||
                                CGAC GTTTC   GACCCACGC
                                  _   CTAA
GAM2031  MYBL2   3'  AAGCTGACGGAGCTCCCTG   14699       A  _
                                AAGCTGAC GAG TCCCTG
                                |||||||| ||| ||||||
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                                TTCGACTG CTC AGGGAC
                                    C   G
GAM2031  NRGN     3'  AGCTGCATGCTGGGTGC     26124       A  GAGTCC
                                AGCTG CA     CTGGGTGC
                                ||||| ||     ||||||||
                                TCGAC GT     GACCCACG
                                  _  AC____
GAM2031  SERPIND1 3'  AGTGACAGAGTCAGGTG     6771     C        CCT
                                AG TGACAGAGTC   GGGTG
                                || ||||||||||   |||||
                                TC ACTGTCTCAG   TCCAC
                                 _       ___
GAM2031  SGCG     3'  AGCTGCTCCCTGGGTG      6923       ACAGAG
                                AGCTG     TCCCTGGGTG
                                |||||     ||||||||||
                                TCGAC     AGGGACCCAC
                                   G_____
GAM2031  SSPN     5'  GCTGGGTGGGTGGGTGGGTGCG 22937      ACAGA  CCC
                                GCTG    GT   TGGGTGCG
                                ||||    ||   ||||||||
                                CGAC    CA   ACCCACGC
                                  CCACC  CCC
GAM2031  WWOX     3'  GCTGTGCAGGGTCCCAGGTGCG 39116      A_   A    T
                                GCTG  CAG GTCCC GGGTGCG
                                ||||  ||| ||||| |||||||
                                CGAC  GTC CAGGG TCCACGC
                                  AC   C    _
GAM2031  ZNF274   5'  AAGTGGGCAGAGTCCCGGCG   32245     C  A_       TG
                                AAG TG  CAGAGTCCC  GGTG
                                ||| ||  |||||||||  ||||
                                TTC AC  GTCTCAGGG  CCGC
                                  _  CC        __
GAM2031  LANCL1   3'  TAAAGTTAAAAGACTTCCT    25854          CTC   C
                                TAAAGTTAAA   ACT CCT
                                ||||||||||   ||| |||
                                ATTTCAATTT   TGA GGA
                                      TC_   A
GAM2031  MSN      3'  GTCCTGTCTCATTCCCTAGAC  41247     AAA_   C
                                GTT    CTCA TCCCTAGAC
                                |||    |||| |||||||||
                                CAG    GAGT AGGGATCTG
                                  GACA    A
GAM2031  NHLH1    5'  CAAAGTTAGTGACCAGCTTTCT 24649        A__   CA  CC
            AGAC                   TAAAGTTA   ACT  CT  CTAGAC
                                ||||||||   |||  ||  ||||||
                                GTTTCAAT   TGG  GA  GATCTG
                                     CAC   TC  AA
GAM2032  ASH1     3'  ATGGGGTAGGAATAGGGAT    32973      TAACT      A
                                ATGG    GGAATAG GAT
                                ||||    ||||||| |||
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                                TACC    CCTTATC CTA
                                  CCAT_     C
GAM2032 GFI1    3' TAACATGGTGCCTGGTAC   23556        AA   A
                                TAACATGGT  CTGG AT
                                |||||||||  |||| ||
                                ATTGTACCA  GACC TG
                                     CG   A
GAM2032 SHMT2   3' TAACATGGTGGGTTGGAGTTAG 24008        AAC_   A_  A
           GAT                   TAACATGGT   TGGA  TAG GAT
                                |||||||||   ||||  ||| |||
                                ATTGTACCA   ACCT  ATC CTA
                                     CCCA   CA  _
GAM2032 SLC29A1  3' TAACGTGGCAACTGTACAG   22418     A       GA
                                TAAC TGGTAACTG  ATAG
                                |||| |||||||||  ||||
                                ATTG ACCGTTGAC  TGTC
                                  C       A_
GAM2032 SP110   3' CAACATGGTGACTGAGAG    38652        A   GAAT
                                TAACATGGT ACTG   AGAG
                                ||||||||| ||||   ||||
                                GTTGTACCA TGAC   TCTC
                                     C   _____
GAM2032 HS3ST3A1 5' TGCTTAAGAAACCATCGTCTTA 25809    C_   TTCT      C
                                TGT  AAGA   CTATCGTC TA
                                |||  ||||   |||||||| ||
                                ACG  TTCT   GGTAGCAG AT
                                  AA   TT__      A
GAM2032 MAPK4   5' TGTCAAGTTTTCTACCAT    15674       A  C
                                TGTCAAG TT TCTATCGT
                                ||||||| || ||||||||
                                ACAGTTC AA AGATGGTA
                                    _  A
GAM2032 RAB6A   3' TGTTGAGATTTCCATCAT    16110     CA    C
                                TGT  AGATT TCTATCGT
                                |||  ||||| ||||||||
                                ACA  TCTAA AGGTAGTA
                                  AC    _
GAM2032 SMP1    3' AAGATTCTTTCTCATGCT    30715       CTA   C
                                AAGATTCT   TCGT CT
                                ||||||||   |||| ||
                                TTCTAAGA   AGTA GA
                                     AAG   C
GAM2032 ZFP93   3' TGTCAAGATTCTTTGAAGCTCT 20147          CTATC TC
           A                    TGTCAAGATTCT    G  CTA
                                ||||||||||||    |  |||
                                ACAGTTCTAAGA    C  GAT
                                       AACTT GA
GAM2033 BSN     3' TAGAGCCTGAGACTAGGCCTGC 18413          TGTTC_
           T                    TAGAGCCTGGG     CCTGCT
                                ||||||||||      ||||||
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                                ATCTCGGACTC     GGACGA
                                      TGATCC
GAM2033  CNN1     3'  GCTCTGGGGGCTTTGCT     10540    _    T   CCC
                                GC CTGGG GTT   TGCT
                                || ||||| |||   ||||
                                CG GACCC CGA   ACGA
                                 A    C   A__
GAM2033  DIAPH2   3'  TAGAACCTGTTTTCCCTGCTAG 28678          GGTG
                                TAGAGCCTG    TTCCCTGCTAG
                                |||||||||    ||||||||||
                                ATCTTGGAC    AAGGGACGATC
                                      AA__
GAM2033  POLS     3'  TAAAGCTTGTCCTTGCT     28122       C  GGTGT   C
                                TAGAGC TG    TCC TGCT
                                |||||| ||    ||| ||||
                                ATTTCG AC    AGG ACGA
                                   A _____   A
GAM2033  TBXA2R   3'  CAGAGCCTTCCCTG       9847         GGGTGT
                                TAGAGCCT     TCCCTG
                                ||||||||     ||||||
                                GTCTCGGA     AGGGAC
                                      _______
GAM2033  CHST6    3'  TGAGCCCTGGGACTC       34684           GGTT
                                TGAGCCCTGGGA   CTC
                                ||||||||||||   |||
                                ACTCGGGACCCT   GAG
                                      _____
GAM2033  ENG      3'  CTGGGCCCTCTTCTCT      6495     A    GGGAGG
                                TTG GCCCT     TTCTCT
                                ||| |||||     ||||||
                                GAC CGGGA     AAGAGA
                                  C    G_____
GAM2033  EPB41    5'  GATTGGTTTTTGGGAAGCT   20766       AGCCC
                                GATTG    TGGGAGGTT
                                |||||    |||||||||
                                CTAAC    ACCCTTCGA
                                   CAAAA
GAM2033  FUS1     3'  GATTGAGCCTGGGAGTTTCT  28585         C     G
                                GATTGAGCC TGGGAG TTCT
                                ||||||||| |||||| ||||
                                CTAACTCGG ACCCTC AAGA
                                      _     A
GAM2033  FZD10    3'  TGGGCCCTGGGGATGGCTC   28462    A      A__
                                TG GCCCTGGG   GGTTC
                                || ||||||||   |||||
                                AC CGGGACCC   CCGAG
                                 C       CTA
GAM2033  LRP1     5'  GATGGAGCTCTGGGGGCTC   14211     T   C    A
                                GAT GAGC CTGGG GGTTC
                                ||| |||| ||||| |||||
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                                CTA CTCG GACCC CCGAG
                                  C   A    _
GAM2033  LY94     3'  GACTGAGCCTATGTGGTT    22103         C  GGA
                                GATTGAGCC TG   GGTT
                                ||||||||| ||   ||||
                                CTGACTCGG AT   CCAA
                                     _  ACA
GAM2033  PLD2     3'  GATGAGCTCTGGGACTCTC    15379     T   C     GG
                                GAT GAGC CTGGGA  TTCTC
                                ||| |||| ||||||  |||||
                                CTA CTCG GACCCT  GAGAG
                                  _   A    __
GAM2033  TRPS1    3'  AATTGAGTTTTGGGACTC    30455       CCC    GGTT
                                GATTGAG   TGGGA   CTC
                                |||||||   |||||   |||
                                TTAACTC   ACCCT   GAG
                                    AAA   _____
GAM2034  GPR62    3'  GCCCTTAGGGCCCTCTTC    44876     TG   AA
                                GCT  CTTA  GCCCTCTTC
                                |||  ||||  |||||||||
                                CGG  GAAT  CGGGAGAAG
                                  __   CC
GAM2034  HMGA2    3'  TTGCTTACTTCCCT        18535         AAAG
                                TTGCTTGCTT   CCCT
                                ||||||||||   ||||
                                AACGAATGAA   GGGA
                                             _____
GAM2034  NEBL     3'  ACTTGCTTGCTTGGTTTTCTT  26898          AAAGCCC
                                GCTTGCTTGCTT     TCTT
                                ||||||||||||     ||||
                                TGAACGAACGAA     AGAA
                                      CCAAA__
GAM2034  NT5C2    3'  GCTTACAGAGCCCTCT     29231       TTAA
                                GCTTGC   AGCCCTCT
                                ||||||   ||||||||
                                CGAATG   TCGGGAGA
                                   TC__
GAM2034  PPP2R5E  3'  GCTGTTTGCTCAACTCTT   26470     T C      AGCC
                                GCT G TTGCTTAA   CTCTT
                                ||| | ||||||||   |||||
                                CGA C AACGAGTT   GAGAA
                                  _ A      _____
GAM2034  RASGRP1  3'  GCTTGATAAGCCAAAGCC   25079      CTT_  T
                                GCTTG   GCT AAAGCC
                                |||||   ||| ||||||
                                CGAAC   CGG TTTCGG
                                  TATT  _
GAM2034  TRIM9    5'  GCTTTCTTGCTTTCCT     31573      G      AAAGC
                                GCTT CTTGCTT    CCT
                                ||||  |||||||   |||
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                                CGAA GAACGAA    GGA
                                  A     A____
GAM2034 ACVR1    3' CCATTTTAGAGTATAGT    9959         A  AGC
                                CCATTTTAGA GTA  TAGT
                                |||||||||| |||  ||||
                                GGTAAAATCT CAT  ATCA
                                       _  ___
GAM2034 CDH5     3' TGCCATTTTTGGAGGCTGTG  12195       AGA  TAA  A
                                TGCCATTTT  AG  GCT GTG
                                |||||||||  ||  ||| |||
                                ACGGTAAAA  TC  CGA CAC
                                     ACC ___  _
GAM2034 ESR1     3' TGCCATTTTAGAAATGGCT   6540           AA
                                TGCCATTTTAGAAGT  GCT
                                ||||||||||||||  |||
                                ACGGTAAAATCTTTA  CGA
                                        C_
GAM2034 STARD4   3' CCATTTTAGAAGTAAACTAG  40122
                                CCATTTTAGAAGTAAGCTAG
                                ||||||||||||||||||
                                GGTAAAATCTTCATTTGATC

GAM2035 SLC10A2  3' GGGGCCCTTCTGACTTTTGGG 7817    AC      _  _
                                GG  CCTTTCTG CTTT GGG
                                ||  |||||||| |||| |||
                                CC  GGGAAGAC GAAA CCC
                                 CC      T   A
GAM2035 ARHGEF12 3' AAGCAGGAAGATGTCTGACAG 31630       A  CC  AG
                                AAGCAGGAA AT  CT  CAG
                                ||||||||| ||  ||  |||
                                TTCGTCCTT TA  GA  GTC
                                     C  CA  CT
GAM2035 GRM6     3' AAACAGGAAAATCTTTAG    9163          CC
                                AAGCAGGAAAATC  TAG
                                ||||||||||||  |||
                                TTTGTCCTTTTAG  ATC
                                       AA
GAM2035 IRS2     3' AAGCAGGAAGACTTTTGCA   40691       A  CCCTA
                                AAGCAGGAA AT    GCA
                                ||||||||| ||    |||
                                TTCGTCCTT TG    CGT
                                     C  AAAA_
GAM2035 MTL5     5' AGCAAGAAGATTCTGCAAA   22267       A  CC  A
                                AGCAGGAA AT  CT GCAGA
                                |||||||| ||  || |||||
                                TCGTTCTT TA  GA CGTTT
                                     C  A_  _
GAM2035 PMX1     3' AAGCAGCAAGATCCCTAA    35492      G  A
                                AAGCAG AA ATCCCTAG
                                |||||| || ||||||||
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                                TTCGTC TT TAGGGATT
                                   G  C
GAM2035  PPP4R1   3'  AAGCAGGAAAGACACCGAGATT 23073          _ TC  TAGC
                                AAGCAGGAAA A  CC    AGATT
                                |||||||||| |  ||    |||||
                                TTCGTCCTTT T  GG    TCTAA
                                     C GT  C___
GAM2035  PSME1    3'  AAGCAGGAAGGTCTCTGC    26525         AA  C  A
                                AAGCAGGAA  TC CT GC
                                |||||||||  || || ||
                                TTCGTCCTT  AG GA CG
                                     CC  A  _
GAM2035  SSPN     3'  AAGCAGGAAAATGTTTTCCT   22933           C____
                                AAGCAGGAAAAT    CCT
                                ||||||||||||    |||
                                TTCGTCCTTTTA    GGA
                                      CAAAA
GAM2035  STAU     5'  AAGTGGGAAAATCGCTGAC   32687     CA       C  AG
                                AAG  GGAAAATC CT  C
                                |||  |||||||| ||  |
                                TTC  CCTTTTAG GA  G
                                  AC       C  CT
GAM2035  TAF6     5'  AGCAGGAAAACTCTAGC     24858           CC
                                AGCAGGAAAAT  CTAGC
                                ||||||||||  |||||
                                TCGTCCTTTTG  GATCG
                                      A_
GAM2036  EIF1A    3'  GAGACCATTTCCATTATTTATG 44807    AA_       C
                                GA   TATTTCCA TATTTATG
                                ||   |||||||| ||||||||
                                CT   GTAAAGGT ATAAATAC
                                 CTG       A
GAM2036  EPHA3    3'  TATAAATGTTTCCACTAC    23443       ATA
                                TATGAA   TTTCCACTAT
                                ||||||   ||||||||||
                                ATATTT   AAAGGTGATG
                                   AC_
GAM2037  AHSG     3'  TTGGACAAAATGGTGGC     11560          ACGTA
                                TTGGATAGAA    GTGGC
                                ||||||||||    |||||
                                AACCTGTTTT    CACCG
                                      AC___
GAM2037  APPBP2   3'  CTAGCCAGGCGTGGTGGC    26879      A   AAA   A
                                TTGG TAG   CGT GTGGC
                                |||| |||   ||| |||||
                                GATC GTC   GCA CACCG
                                  G   C__   C
GAM2037  CDH1     3'  TTAGTCATGCGTAGTGG     20371      A  GAAA
                                TTGG TA    CGTAGTGG
                                |||| ||    ||||||||
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                                AATC GT    GCATCACC
                                  A  AC__
GAM2037  CHRNA3   3'  TTAGATAGAAGGTGG       8843          ACGTA
                                TTGGATAGAA     GTGG
                                ||||||||||     ||||
                                AATCTATCTT     CACC
                                     C____
GAM2037  CLECSF11 5'  TGGCCAGGTGTAGTGGC     39045     A   AAAC
                                TGG TAG    GTAGTGGC
                                ||| |||    ||||||||
                                ACC GTC    CATCACCG
                                  G   CA__
GAM2037  DTNA     3'  TTGGACAGGTTGTGG       37378         AAAC  A
                                TTGGATAG    GT GTGG
                                ||||||||    || ||||
                                AACCTGTC    CA CACC
                                    ____  A
GAM2037  DYRK1A   5'  TTGGTAGAATTCCAAGTGG   39010      A    ACGT_
                                TTGG TAGAA     AGTGG
                                |||| |||||     |||||
                                AACC ATCTT     TCACC
                                  _     AAGGT
GAM2037  F2R      3'  TGGAGCAAATGTAGTGGC    12800      _   AAC
                                TGGA TAGA   GTAGTGGC
                                |||| ||||   ||||||||
                                ACCT GTTT   CATCACCG
                                  C    A__
GAM2037  GRM6     3'  TTGGATAAAGTGTGG       9179          AAC  A
                                TTGGATAGA   GT GTGG
                                |||||||||   || ||||
                                AACCTATTT   CA CACC
                                    ___  _
GAM2037  HOXC6    3'  TTGGATAGGAACACTGAC    21079         A    TAG
                                TTGGATAG AACG   TGGC
                                |||||||| ||||   ||||
                                AACCTATC TTGT   ACTG
                                     C    G__
GAM2037  IL18R1   3'  TTGGATAAGGTTCCAGAGGC  19300         AAACG   T
                                TTGGATAG     TAG GGC
                                ||||||||     ||| |||
                                AACCTATT     GTC CCG
                                     CCAAG   T
GAM2037  IL2RB    3'  TTGGACAGAGCTTGG       9397          AAC  AG
                                TTGGATAGA   GT  TGG
                                |||||||||   ||  |||
                                AACCTGTCT   CG  ACC
                                    ___  A_
GAM2037  KCNA6    3'  TGGATAGATGGCAGTGG     13823         AAC
                                TGGATAGA   GTAGTGG
                                ||||||||   |||||||
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                                ACCTATCT  CGTCACC
                                   AC_
GAM2037 MATN1   3' TTGGAGAGGCCACAGTGG   14370     T AAA
                                TTGGA AG  CGTAGTGG
                                ||||| ||  ||||||||
                                AACCT TC  GTGTCACC
                                  C CG_
GAM2037 NCOR2   3' TGGATGGAGGCGCAGGC    26742     A AA  GT
                                TGGAT GA CGTA GGC
                                ||||| || |||| |||
                                ACCTA CT GCGT CCG
                                  C CC  __
GAM2037 PCDHB16 3' TTGGATGGGCACATTGGC   34151      AGAA  AG
                                TTGGAT   ACGT TGGC
                                ||||||   |||| ||||
                                AACCTA   TGTA ACCG
                                   CCCG  __
GAM2037 PIGA    3' TTGAATAGAATAATGGC    33835       AAC
                                TTGGATAGA  GTAGTGGC
                                |||||||||  ||||||||
                                AACTTATCT  TATTACCG
                                          ___
GAM2037 PKD2    3' TTGGATAAAAACTTTCAGT  41082        G__
                                TTGGATAGAAAC  TAGT
                                ||||||||||||  ||||
                                AACCTATTTTTG  GTCA
                                      AAA
GAM2037 PTGFRN  5' TTGAACATTTGTAGTGGC   42609      GAAAC
                                TTGGATA   GTAGTGGC
                                |||||||   ||||||||
                                AACTTGT   CATCACCG
                                   AAA__
GAM2037 PTPN13  3' TTGGATAGAGAGCAGGAG   38783       AAC  TG
                                TTGGATAGA  GTAG G
                                |||||||||  |||| |
                                AACCTATCT  CGTC C
                                     CT_  CT
GAM2037 PVR     3' TTAGCCAGACGTGGTGGC   27116    A  AA A
                                TTGG TAGA CGT GTGGC
                                |||| |||| ||| |||||
                                AATC GTCT GCA CACCG
                                  G  __ C
GAM2037 RP2     3' TTAGCCAGGTGTAGTGGC   27939    A AAAC
                                TTGG TAG  GTAGTGGC
                                |||| |||  ||||||||
                                AATC GTC  CATCACCG
                                  G CA__
GAM2037 SIGLEC6 3' TTGGACAGAAGTCCTGTGG  40937       ACGTA
                                TTGGATAGAA   GTGG
                                ||||||||||   ||||
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                                AACCTGTCTT    CACC
                                     CAGGA
GAM2037 SLC19A2  3' TTGAATAGAGGCAGATGC    42896        AAC   TG
                                TTGGATAGA   GTAG  GC
                                |||||||||   ||||  ||
                                AACTTATCT   CGTC  CG
                                     C__    TA
GAM2037 SYNGR3   3' GGATGGGAACAGTGGC      20096     A_  ACG
                                GGAT  GAA   TAGTGGC
                                ||||  |||   |||||||
                                CCTA  CTT   GTCACCG
                                  CC  ___
GAM2038 GAD1     3' TACTTCATATATAAATAAGAT  30293         CTATTT
                                TATTTCATATA     ATAAGAT
                                ||||||||||      |||||||
                                ATGAAGTATAT     TATTCTA
                                      ATT___
GAM2038 OCM      3' TTAGGTAGGGATGGGATGTGG  26191     TA   ACAT   AT
                                TTAG  AGG    TGG  ATGTGG
                                ||||  |||    |||  ||||||
                                AATC  TCC    ACC  TACACC
                                  CA  CT__   C_
GAM2039 SCN1A    5' CTATTTTCCTAAGAGGATT    44814        G  ACT  C
                                CTATTTTC TA   GG GGATT
                                |||||||| ||   || |||||
                                GATAAAAG AT   TC CCTAA
                                     G  ___  T
GAM2040 AKAP2    3' GCCATCCTAACTGCCACT     28495         TA
                                GTCATCCTGG  GCCACT
                                ||||||||||  ||||||
                                CGGTAGGATT  CGGTGA
                                      GA
GAM2040 AKAP2    3' ATCATCCTGAAACACACT     28492         T  _
                                GTCATCCTGG AGC CACT
                                |||||||||| ||| ||||
                                TAGTAGGACT TTG GTGA
                                     _  T
GAM2040 APOL1    3' ATCATCAGGAAGCCGCT      18932       CT  T   A
                                GTCATC  GG AGCC CT
                                ||||||  || |||| ||
                                TAGTAG  CC TCGG GA
                                   T_  T   C
GAM2040 BLAME    3' TCATCCTGAGCTGAGCTGCT   33495         _ __  CA
                                TCATCCTG GT  AGC  CT
                                ||||||||  ||  |||  ||
                                AGTAGGAC CG  TCG  GA
                                     T  AC   AC
GAM2040 CARD4    3' GTCACCCTTCAGCTGCT      25893         GG   CA
                                GTCATCCT  TAGC  CT
                                ||||||||  ||||  ||
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                                CAGTGGGA GTCG GA
                                    A_   AC
GAM2040 CDH5    3' GTCACTCCTGATCTCCACT  12192    _    AG
                                GTCA TCCTGGT CCACT
                                |||| ||||||| |||||
                                CAGT AGGACTA GGTGA
                                  G     GA
GAM2040 EVI2A   3' ATCATCTAACCACT      30549      CTGG
                                GTCATC   TAGCCACT
                                ||||||   ||||||||
                                TAGTAG   ATTGGTGA
                                    ____
GAM2040 GGA1    3' GTCACCCCCCAGTCACT    30049       GG  C
                                GTCATCCT TAG CACT
                                |||||||| ||| ||||
                                CAGTGGGG GTC GTGA
                                    G_  A
GAM2040 HCS     3' GTCAATACAGTAGCCACT   33231     TCC
                                GTCA  TGGTAGCCACT
                                ||||  ||||||||||
                                CAGT  GTCATCGGTGA
                                  TAT
GAM2040 ISLR    3' GCCATACCAGCCACT      24436     _ TGGT
                                GTCAT CC   AGCCACT
                                ||||| ||   |||||||
                                CGGTA GG   TCGGTGA
                                  T ____
GAM2040 LFG     3' GCCATCCTGCCCACCCACT  44138       G_ G
                                GTCATCCTG TA CCACT
                                ||||||||| || |||||
                                CGGTAGGAC GT GGTGA
                                     GG G
GAM2040 MMP25   3' GTCGTCCCTCCAGCCACT   35392    A  GG
                                GTC TCCT TAGCCACT
                                ||| |||| ||||||||
                                CAG AGGG GTCGGTGA
                                  C  AG
GAM2040 PCDH11X 3' ATCACAATAGCCACT      37294     CCT
                                GTCAT  GGTAGCCACT
                                |||||  ||||||||||
                                TAGTG  TTATCGGTGA
                                   ___
GAM2040 PCDH11Y 3' ATCACAATAGCCACT      37328     CCT
                                GTCAT  GGTAGCCACT
                                |||||  ||||||||||
                                TAGTG  TTATCGGTGA
                                   ___
GAM2040 PCDH9   5' GTCCCTGGCAGTTACT     44405    AT     CC
                                GTC CCTGGTAG ACT
                                ||| |||||||| |||
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                                CAG  GGACCGTC  TGA
                                  __       AA
GAM2040  PCDHB14   3'  GTCATTATAGCCACT      33189      CCTG
                                GTCAT    GTAGCCACT
                                |||||    |||||||||
                                CAGTA    TATCGGTGA
                                  A___
GAM2040  RCN1      3'  GTATCCTAGCCACT       16206    C    GGT
                                GT ATCCT   AGCCACT
                                || |||||   |||||||
                                CA TAGGA   TCGGTGA
                                 _    ___
GAM2040  SERPINF2  3'  GTCTCCTGGCAGAACT     9594      A       CC
                                GTC TCCTGGTAG  ACT
                                ||| |||||||||  |||
                                CAG AGGACCGTC  TGA
                                  _       T_
GAM2040  SHANK2    3'  GTCACCCAGCCACT       29465       TGGT
                                GTCATCC    AGCCACT
                                |||||||    |||||||
                                CAGTGGG    TCGGTGA
                                     _____
GAM2040  TIM3      3'  GTAATCCCAGCCACT      37251    C    GGT
                                GT ATCCT   AGCCACT
                                || |||||   |||||||
                                CA TAGGG   TCGGTGA
                                 T    ___
GAM2040  TPST1     5'  CATCCTGGCCTCAGCCGCT   18760         ___   A
                                CATCCTGGT   AGCC CT
                                |||||||||   |||| ||
                                GTAGGACCG   TCGG GA
                                     GAG    C
GAM2040  ZNF2      5'  GTCACCCTGAAGTACT      34383          T  CC
                                GTCATCCTGG AG  ACT
                                |||||||||| ||  |||
                                CAGTGGGACT TC  TGA
                                     _  A_
GAM2041  CNTNAP2   3'  GGGATCTCAAGACTTTT     30488    T    ACT
                                GG ATCT   GGACTTTT
                                || ||||   ||||||||
                                CC TAGA   TCTGAAAA
                                 C    GT_
GAM2041  KCNH1     3'  AGGTATCTGTCTCTGACTTTT  13841        A_  G_
                                AGGTATCT  CT  GACTTTT
                                ||||||||  ||  |||||||
                                TCCATAGA  GA  CTGAAAA
                                     CA  GA
GAM2041  NFKBIA    3'  TGACAGGTAGTAACTTTT    33908         TCTACTG
                                TGACAGGTA      GACTTTT
                                |||||||||      |||||||
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                                ACTGTCCAT      TTGAAAA
                                     CA_____
GAM2041  TOP1     3'  TAACAGGTGCGCTGGGTTTTT  17627        ATCTA    AC
                                TGACAGGT    CTGG  TTTT
                                ||||||||    ||||  ||||
                                ATTGTCCA    GACC  AAAA
                                     CGC__    CA
GAM2041  WISP3    3'  TGACAGGATTGACTAACTTTTC 38978        T  CT    G
                                TGACAGG AT  ACTG ACTTTTC
                                ||||||| ||  |||| |||||||
                                ACTGTCC TA  TGAT TGAAAAG
                                     _ AC   _
GAM2041  AK2      3'  CGCCGCGGGGTGATGAGCAGTG 30189      AGA       CT_ _ C
            TTGC                   CGCC   GGGTGATG   GG GT GC
                                ||||   ||||||||   || || ||
                                GCGG   CCCACTAC   TC CA CG
                                  CGC       TCG  A  A
GAM2041  CIAO1    5'  CGCCGGAGGACCTGGGTCGC   43682     A    TGATG
                                CGCC GAGGG    CTGGGTCGC
                                |||| |||||    |||||||||
                                GCGG CTCCT    GACCCAGCG
                                  C    G____
GAM2041  ETF1     3'  GCTGGAGGGTGAGGCACG    21831    CA      T  _
                                GC  GAGGGTGA GC TG
                                ||  |||||||| || ||
                                CG  CTCCCACT CG GC
                                 AC       C  T
GAM2041  JPH3     5'  CGCCGGCGGCCCTGGGTCG   34016     AGAG   ATG
                                CGCC   GGTG   CTGGGTCG
                                ||||   ||||   ||||||||
                                GCGG   CCGC   GACCCAGC
                                  ____   CGG
GAM2041  SHOX     3'  CGCGAGGGTCTGGCTGGGTCG  27818     CA     GAT
                                CGC  GAGGGT   GCTGGGTCG
                                |||  ||||||   |||||||||
                                GCG  CTCCCA   CGACCCAGC
                                  __     GAC
GAM2041  SOX11    3'  CGCCAGCGGGATGGGTCG    17015       A   TGATGC
                                CGCCAG GGG     TGGGTCG
                                |||||| |||     |||||||
                                GCGGTC CCC     ACCCAGC
                                   G   T_____
GAM2041  ZNF289   3'  GCCAGAGGGTGAGGCCCAC    42255          TGCT  G
                                GCCAGAGGGTGA    GG TCGC
                                ||||||||||||    || ||||
                                CGGTCTCCCACT    CC GGTG
                                       ____  G
GAM2042  BTEB1    3'  TGCATTTATATCCATCTAAGT  10220        A  C    GC
                                TGCATTTA TA CCATC  AGT
                                ||||||||  || |||||  |||
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                                ACGTAAAT AT GGTAG  TCA
                                    _ A    AT
GAM2042  SIM2    3'  TGCATTTAATGCCTATTCAAT  22884         A  CATCG
                                TGCATTTAAT CC    CAGT
                                |||||||||| ||    ||||
                                ACGTAAATTA GG    GTTA
                                     C  ATAA_
GAM2042  WT1     3'  TGCATCTAGTACTTATACAGT  35969        A   CC  C
                                TGCATTTA TAC  AT GCAGT
                                |||||||| |||  || |||||
                                ACGTAGAT ATG  TA TGTCA
                                    C   AA  _
GAM2043  EPHB6   5'  GTGGACCTGACGCTG       20800       AACGAG
                                GTGGAC     CTGACGCTG
                                ||||||     |||||||||
                                CACCTG     GACTGCGAC

                                _______
GAM2043  PCDH9   5'  TGTAGACAAGGCTGGCGCTG  44412         CGA   A
                                TGTGGACAA   GCTG CGCTG
                                |||||||||   |||| |||||
                                ACATCTGTT   CGAC GCGAC
                                     C__   C
GAM2043  SQSTM1  3'  TGTGGACAGTGAGCAGCCAA  19378         AC   TGAC  TG
                                TGTGGACA  GAGC   GC  A
                                ||||||||  ||||   ||  |
                                ACACCTGT  CTCG   CG  T
                                    CA   T___  GT
GAM2043  WHSC1   3'  TGAGGGTAGCGACGCTGA    39388    T  ACAACG   T
                                TG GG     AGC GACGCTGA
                                || ||     ||| ||||||||
                                AC CC     TCG CTGCGACT
                                 T  CA____  _
GAM2043  RARB    3'  TGCATCTTGAGTGTTCAAA   32063     CG   CATCA
                                TGCA  TTGA    TGTTCAAA
                                ||||  ||||    ||||||||
                                ACGT  AACT    ACAAGTTT
                                  AG   C____
GAM2043  XPNPEP2 3'  TGCACTTTGGAAAGTTCAAAG  18156      G   ACATCAT
                                TGCAC TTG      GTTCAAAG
                                ||||| |||      ||||||||
                                ACGTG AAC      CAAGTTTC
                                   A   CTTT___
GAM2044  RAP1A   3'  TAAAGTATAATGGTTCAACT   16151          A   GT
                                TAGAGTATAATG TTTA  T
                                |||||||||||| ||||  |
                                ATTTCATATTAC AAGT  A
                                      C   TG
GAM2044  ZNF9    3'  TTGATTTCTGTGAAAATGCATT 18281       _ A    C
            TC                    TTGATT CT TGAAAA TGTGTTTC
                                |||||| || |||||| ||||||||
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                                AACTAA GA ACTTTT ACGTAAAG
                                   A  C     _
GAM2045  FLT1    3'  CACAGGTGGTTTGCGTAT    12907          AAT  C
                                CACAGGTGGT   CG TAT
                                ||||||||||   || |||
                                GTGTCCACCA   GC ATA
                                     AAC  _
GAM2045  MATK    5'  GCACAGGAGGTAGGGAGCT   40310        T   ATC_
                                GCACAGG GGTA   GCT
                                |||||||  ||||   |||
                                CGTGTCC CCAT   CGA
                                   T   CCCT
GAM2045  SDC4    3'  CCAGCACAGCTGAGGCT    16520         G   TAATC
                                CCAGCACAG TGG    GCT
                                |||||||||  |||    |||
                                GGTCGTGTC ACT    CGA
                                     G   C____
GAM2045  TNXB    5'  CAGACAATGAAGTCGCT    37149     C   G   TAA
                                CAG ACAG TGG   TCGCT
                                |||  ||||  |||   |||||
                                GTC TGTT ACT   AGCGA
                                  _   _  TC_
GAM2045  EIF2C1  3'  GTCTGTCTTGCTGGCC     29181     ATCG   CG
                                GTCT   GTC  GCTGGCC
                                ||||   |||  |||||||
                                CAGA   CAG  CGACCGG
                                  ____   AA
GAM2045  NAPB    3'  TACAGTCTGTCCTTGGCTGGCC 43177    _   ATCG   __
            C                    TAC GTCT   GTCC  GGCTGGCCC
                                |||  ||||   ||||  |||||||||
                                ATG CAGA   CAGG  CCGACCGGG
                                  T   ____   AA
GAM2045  PTPN18  3'  GTCTATCAAGCTGTTGGCTGG  30770       _  CC__
                                GTCTATCG GT   GGCTGG
                                |||||||  ||   ||||||
                                CAGATAGT CG   CCGACC
                                     T  ACAA
GAM2045  SUV39H2  5'  CACGTCGCCATCTGGCTGGCCC 36010      TATCG   C
                                TACGTC    GTC GGCTGGCCC
                                ||||||    ||| |||||||||
                                GTGCAG    TAG CCGACCGGG
                                   CGG__   A
GAM2045  UCP2    5'  GTCTGTCGGCTGGC       17847     ATCG   C
                                GTCT   GTC GGCTGGC
                                ||||   ||| |||||||
                                CAGA   CAG CCGACCG
                                  ____   _
GAM2046  DUSP4   5'  CCTCCGGCGCTCAGCCCTCGT  38415         GAATA
                                CCTCCGGTGT    AGCCCTCGT
                                ||||||||||    |||||||||
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                                GGAGGCCGCG    TCGGGAGCA
                                     AG___
GAM2046 LRP4    3' CCTTTGTGTGAATGAGC    42060    CCG      A
                                CCT  GTGTGAAT AGC
                                |||  |||||||| |||
                                GGA  CACACTTA TCG
                                  AA_      C
GAM2046 APPBP2  3' ATTAAACTAAAATCCC     26875         AC
                                GTTAAACTGAG  GTCCC
                                ||||||||||  |||||
                                TAATTTGATTT  TAGGG
                                      __
GAM2046 LRP1    3' ATTAAAACGTTCACGTCCC   14207      C  AG_
                                GTTAAA TG   ACGTCCC
                                |||||| ||   |||||||
                                TAATTT GC   TGCAGGG
                                    T  AAG
GAM2046 MADH3   3' GTTGGACTGTGACATCCC    25351    AA   A
                                GTT  ACTG GACGTCCC
                                |||  |||| ||||||||
                                CAA  TGAC CTGTAGGG
                                  CC    A
GAM2046 MECP2   3' CGTTGGAGGACGTCCC     22586     AAACT  _
                                CGTT    GAG ACGTCCC
                                ||||    ||| |||||||
                                GCAA    CTC TGCAGGG
                                  C_____  C
GAM2046 RAD18   3' GTGAACTGACATCCC      33556    TA   GA
                                GT  AACT  GACGTCCC
                                ||  ||||  ||||||||
                                CA  TTGA  CTGTAGGG
                                 C_   __
GAM2046 TMPRSS2 3' CCTTAAACTGAGCATCC    24933   G       A
                                C TTAAACTGAG CGTCC
                                | ||||||||| |||||
                                G AATTTGACTC GTAGG
                                 G        _
GAM2047 BTG1    3' TATGGCACTGTCACTTAAAA  11913       ACGC
                                TATGGCA   CGCTTAAAA
                                |||||||   |||||||||
                                ATACCGT   GTGAATTTT
                                    GACA
GAM2047 CHAD    3' GGCATGGGCTTTAAAACCCT  10416     ACGCC   _
                                GGCA    GCTT AAAACCCT
                                ||||    |||| ||||||||
                                CCGT    CGAA TTTTGGGA
                                  ACC__   A
GAM2047 KIT     3' TATGGCAAGACAAAACTC    6898        C  C__
                                TATGGCAA GC   GCTT
                                |||||||| ||   ||||
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                                ATACCGTT TG   TGAG
                                    C  TTT
GAM2047  AGTR1    5'  GACAGCTAGGTGGGCAGTGGTG 28911        TGC    TGACAA
             C                   GACAGCTA   GGGT     TGC
                                 ||||||||   ||||     |||
                                 CTGTCGAT   CCCG     ACG
                                    CCA    TCACC_
GAM2047  NRF1     3'  GACAGTGAAATTGACAATG    41093      CTA  C
                                 GACAG   TG GGGTTGACAATG
                                 ||||||   || ||||||||||||
                                 CTGTC   AC TTTAACTGTTAC
                                   ____ _
GAM2047  RAGE     3'  CAGCTGCGCGGGCCGCGGGTGC 30602      A       ACAA
                                 CAGCT TGCGGGTTG    TGC
                                 ||||| |||||||||    |||
                                 GTCGA GCGCCCGGC    ACG
                                    C        GCCC
GAM2048  ACPT     3'  GTGACATTCCCTCCATCTTTGG 38892           __   A_
             C                   GTGGCATTCCCTCC  CTT  GC
                                 ||||||||||||||  |||  ||
                                 CACTGTAAGGGAGG  GAA  CG
                                        TA   AC
GAM2048  AKAP13   3'  GTGGTGTGCCCTCACCCAGCA  40352      CATT    C
                                 GTGG    CCCTC CTTAGCA
                                 ||||    ||||| |||||||
                                 CACC    GGGAG GGGTCGT
                                   ACAC     T
GAM2048  ANGPT2   5'  GTGTTGTTCCCTCCCTCA    10088     GCA
                                 GTG   TTCCCTCCCTTA
                                 |||   ||||||||||||
                                 CAC   AAGGGAGGGAGT
                                   AAC
GAM2048  BACE     3'  GTGGCATTTTCACTTCATGGTA 39967        CCC  C   AGC___
             GCA                   GTGGCATT   TC CTT     AGCA
                                 ||||||||   || |||     ||||
                                 CACCGTAA   AG GAA     TCGT
                                      A__  T   GTACCA
GAM2048  DMD      3'  GTGGCATTGCTAGCAG      19688        CCCTCCC
                                 GTGGCATT      TTAGCAG
                                 ||||||||      |||||||
                                 CACCGTAA      GATCGTC
                                      C_______
GAM2048  GARP     3'  GTGGCATTTTCACTTTCTCGCA 24315        __  C  CC   A
                                 GTGGCAT  TC CT  CTT GCA
                                 |||||||  || ||  ||| |||
                                 CACCGTA  AG GA  GAG CGT
                                      AA  T  AA  _
GAM2048  HMGN1    3'  GTGGGATTCCCTCCTTCTTA   22450      C       __
                                 GTGG ATTCCCTCC  CTTA
                                 |||| |||||||||  ||||
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                                CACC TAAGGGAGG  GAAT
                                  C       AA
GAM2048  INPP4A   5'  GTGGCATTTCTTCATAGAAGCA 19711        CC  CCCT   C
                                GTGGCATT  CT    TAG AGCA
                                ||||||||  ||    ||| ||||
                                CACCGTAA  GA    ATC TCGT
                                    A_  AGT_   T
GAM2048  INPP5D   3'  GCATTCCCTTCTGCA      44421         CC  TA
                                GCATTCCCT  CT  GCA
                                |||||||||  ||  |||
                                CGTAAGGGA  GA  CGT
                                     A_  __
GAM2048  ITGA1    3'  GTGGCATCTTTCTCTGC     41851        TCC  CC   A
                                GTGGCAT   CT  CTT GC
                                |||||||   ||  ||| ||
                                CACCGTA   GA  GAG CG
                                   ___  AA   A
GAM2048  LASS1    3'  GTGGCATCTTCCTCCCAGGC   34616        C_     TTA
                                GTGGCATT  CCTCCC   GC
                                ||||||||  ||||||   ||
                                CACCGTAG  GGAGGG   CG
                                     AA     TC_
GAM2048  PHKB     3'  GTGGCATTCACCTCCCCAGCA  7123          _      T
                                GTGGCATTC CCTCCCT AGCA
                                ||||||||| ||||||| ||||
                                CACCGTAAG GGAGGGG TCGT
                                     T      _
GAM2048  PRKAR1A  3'  TGGCATTTCTCCCTTTAGCAGC 15615        CC      _
            A                    TGGCATT  CTCCCTT AGCAGCA
                                 |||||||  ||||||| |||||||
                                 ACCGTAA  GAGGGAA TCGTCGT
                                    A_      A
GAM2048  ABL1     3'  AGGGGAAGGGCCCTTCAGGGC  28702        AAA     _
                                AGGGGAA   TCCTTC GGGT
                                |||||||   |||||| ||||
                                TCCCCTT   GGGAAG CCCG
                                    CCC     T
GAM2048  CCND2    3'  AGGGGAAAAACTTCAAG     12043          TC
                                AGGGGAAAAA  CTTCGGG
                                ||||||||||  |||||||
                                TCCCCTTTTT  GAAGTTC
                                           __
GAM2048  CCND2    3'  AGGGGAGGAGTATTCAGCATGA 12045       AAAATCC    _
            C                    AGGGGA      TTCGG GTGAC
                                 ||||||      ||||| |||||
                                 TCCCCT      AAGTC TACTG
                                    CCTCAT_    G
GAM2048  CEP1     5'  AAGGGGAAAGACCTAGGC    28136         AAT   TC
                                AAGGGGAAA   CCT  GGGT
                                |||||||||   |||  ||||
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                                TTCCCCTTT  GGA  TCCG
                                     CT_  __
GAM2048  CREBL2   3'  AGGGGAGAAAGCTCAAATGAC  10575      A  TCC
                                AGGGGA AAA  TTCGGGTGAC
                                |||||| |||  ||||||||||
                                TCCCCT TTT  GAGTTTACTG
                                   C  C__
GAM2048  DLEC1    3'  AGGCGGAGCTCCTTTGGGTG  28844    _  AAAA   C
                                AGG GGA   TCCTT GGGTG
                                ||| |||   ||||| |||||
                                TCC CCT   AGGAA CCCAC
                                  G  CG__   A
GAM2048  FZD1     5'  GGGGAGAACCCGGGTG     18617      AA   TTC
                                GGGGA  AATCC  GGGTG
                                |||||  |||||  |||||
                                CCCCT  TTGGG  CCCAC
                                   C_   ___
GAM2048  GPRK5    3'  AAGGAGAAGGGTCTGGGC   23630       AAA  CTTC
                                AAGGGGAA  TC   GGGT
                                ||||||||  ||   ||||
                                TTCCTCTT  AG   CCCG
                                     CCC  A___
GAM2048  LAPTM5   5'  AAGGGGAAAGAGCCTGGT   27601       AAT  TCG
                                AAGGGGAAA  CCT  GGT
                                |||||||||  |||  |||
                                TTCCCCTTT  GGA  CCA
                                     CTC  ___
GAM2048  MFGE8    3'  AAGGGGAAGTGTCTTGGGGAC  25457      AAATC  C  T
                                AAGGGGAA   CTT GGG GAC
                                ||||||||   ||| ||| |||
                                TTCCCCTT   GAA CCC CTG
                                     CACA_  _  _
GAM2048  MFRP     3'  AAGGGGAAGAGGCCTGGAT   36422       AAAT  TC
                                AAGGGGAA   CCT  GGGT
                                ||||||||   |||  ||||
                                TTCCCCTT   GGA  CCTA
                                     CTCC  __
GAM2048  MKI67    3'  GGGGAGGAATCCAGACAGGTGA 14526     AA   TT_
                                GGGGA  AATCC  CGGGTGA
                                |||||  |||||  |||||||
                                CCCCT  TTAGG  GTCCACT
                                   CC   TCT
GAM2048  NRXN3    5'  AGGTGGAAGAGTTCTTCGGGT  39938    _  AAATC
                                AGG GGAA   CTTCGGGT
                                ||| ||||   ||||||||
                                TCC CCTT   GAAGCCCA
                                  A  CTCAA
GAM2048  PABPC4   5'  AAGGGTAAAAATCCTTTAAGAG 19218     G       C___
            GC                   AAGGG AAAAATCCTT   GGGT
                                |||||  ||||||||||  ||||
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                                TTCCC TTTTTAGGAA   TCCG
                                   A        ATTC
GAM2048 PAG     3' GGGGAAAAAGCCTTAAAGT   32956        T   CG
                                GGGGAAAAA CCTT  GGT
                                ||||||||| ||||  |||
                                CCCCTTTTT GGAA  TCA
                                     C   TT
GAM2048 PCSK1N  3' AGGGGGTAGGGATCCTCGGGT 29975      AAAA__    T
                                AGGGG     ATCCT CGGGT
                                |||||     ||||| |||||
                                TCCCC     TAGGA GCCCA
                                  CATCCC    _
GAM2048 PIGR    3' GGAGGGAAAAATTCTGTTGAC 43706   A       CCT  GGG
                                A GGGGAAAAAT   TC   TGAC
                                | ||||||||||   ||   ||||
                                C TCCCTTTTTA   AG   ACTG
                                 C         ___  ACA
GAM2048 PPP1R8  3' GGGGAAAGAGCCTCCAAACTGA 39731       AAT      _
             C                   GGGGAAA   CCTTCGGG TGAC
                                 |||||||   |||||||| ||||
                                 CCCCTTT   GGAGGTTT ACTG
                                     CTC       G
GAM2048 SGT     3' AAGGGGAAAATCCATCTTGAC  16604         A   T  GGG
                                AAGGGGAAAA TCC TC   TGAC
                                |||||||||| ||| ||   ||||
                                TTCCCCTTTT AGG AG   ACTG
                                      _  T  A__
GAM2048 SOX4    3' AAGGGGGAGACTCCTTCAAGT  16973       AAAAA
                                AAGGGG    TCCTTCGGGT
                                ||||||    ||||||||||
                                TTCCCC    AGGAAGTTCA
                                   CTCTG
GAM2048 SPOCK   3' GGGGAAAAAGTACAGTGTG   41738        TCCTT  _
                                GGGGAAAAA    CGG GTG
                                |||||||||    ||| |||
                                CCCCTTTTT    GTC CAC
                                      CAT__   A
GAM2048 UBE2V1  3' AAGGGGAAGGGCCTGTGGT   35340        AAAT  TCG
                                AAGGGGAA   CCT   GGT
                                ||||||||   |||   |||
                                TTCCCCTT   GGA   CCA
                                     CCC_   CA_
GAM2049 CYP7B1  3' CTGCCACCATCCTGTT     22076      TAGCTA
                                CTGCC     CATCCTGTT
                                |||||     |||||||||
                                GACGG     GTAGGACAA
                                  TG_____
GAM2049 TNXB    5' TGTCCCCGCTCATTTTGTTT  37161    _  A  A  CC
                                TG CCT GCT CAT  TGTTT
                                || ||| ||| |||  |||||
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                                AC GGG CGA GTA  ACAAA
                                 A  G  _  AA
GAM2050 IL22RA2  3' TGTTTTATTAAGTCAGGCT   38136     A        AT
                                TGTT TATTAAGTCA  CT
                                |||| ||||||||||  ||
                                ACAA ATAATTCAGT  GA
                                  A        CC
GAM2050 MAP3K12  3' CATCTTTCTGTTGATTATGTGG 26680      CATTAT        A
             C                   TATCT     TTGATTATGT GC
                                |||||     |||||||||| ||
                                GTAGA     AACTAATACA CG
                                  AAGAC_        C
GAM2051 IL22RA2  3' ACCATAAATGAATTTTGTTTTA 38130        AATGTCG
                                ACCATAAAT      TTGTTTTA
                                |||||||||      ||||||||
                                TGGTATTTA      AACAAAAT
                                     CTTAA__
GAM2051 LYPLA1   3' CCATAAATAATATCTTG     26757           G
                                CCATAAATAATGTC TTG
                                |||||||||||||| |||
                                GGTATTTATTATAG AAC
                                                _
GAM2051 NAPB     3' ACCATAAATAATTATATTTT   43165          GTCGT
                                ACCATAAATAAT    TGTTTT
                                ||||||||||||    ||||||
                                TGGTATTTATTA    ATAAAA
                                      AT___
GAM2051 PMCHL1   3' ATAAATAATAAGTCGTTTTA   36666         TC
                                ATAAATAATG  GTTGTTTTA
                                ||||||||||  |||||||||
                                TATTTATTAT  CAGCAAAAT
                                     T_
GAM2051 SGK      3' CATAAATAATGCCCATTTTA   24741          GTT
                                CATAAATAATGTC   GTTTTA
                                ||||||||||||   ||||||
                                GTATTTATTACGG   TAAAAT
                                       G__
GAM2052 MBNL     3' ACTGCAGTAATAATAAAATA   34307       A   AA
                                ACTGCAG TGA  AATAAAATA
                                ||||||| |||  |||||||||
                                TGACGTC ATT  TTATTTTAT
                                   _  A_
GAM2052 NPTX2    3' AACATGTATGAAAAATAAAATA 45204     TGCAG
                                AAC    ATGAAAAATAAAATA
                                |||    ||||||||||||||
                                TTG    TACTTTTTATTTTAT
                                  TACA_
GAM2052 RNF4     3' ACTGCAGATCAATGATAA    16349         G  AA
                                ACTGCAGAT AA  ATAA
                                ||||||||| ||  ||||
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                                TGACGTCTA TT  TATT
                                     G  AC
GAM2052  RRM2     3'  TACAGTGAGAAATAAAAT    9761       A   A
                                TGCAG TGA AAATAAAAT
                                ||||| ||| |||||||||
                                ATGTC ACT TTTATTTTA
                                   _  C
GAM2052  SCN1A    3'  TGCTGAAAAATAAAATA     44819     AGA
                                TGC   TGAAAAATAAAATA
                                |||   ||||||||||||||
                                ACG   ACTTTTTATTTTAT
                                 ___
GAM2052  SMARCA2  3'  TGCCTGATGAAAAATAAAATA  16895     A_
                                TGC  GATGAAAAATAAAATA
                                |||  ||||||||||||||||
                                ACG  CTACTTTTTATTTTAT
                                  GA
GAM2053  GALGT    5'  CGGGGAGGGCTCTGGCC     11181    A   AA  G
                                CG GGAG  CT CTGGCC
                                || ||||  || ||||||
                                GC CCTC  GA GACCGG
                                 C   CC  _
GAM2053  OTOF     3'  GGGCAGGGTCTGGCCCCTGCTG 22061     AGAACTG      _
                                GG      CTGGCCC TGCTG
                                ||      ||||||| |||||
                                CC      GACCGGG ACGAC
                                 CGTCCCA      G
GAM2053  PGLS     3'  CGGGTAGGGCTGCTGGCCGGAG 28983    A  _  AA       CT__
            GCTG                    CG GG AG  CTGCTGGCC    GCTG
                                || || ||  |||||||||    ||||
                                GC CC TC  GACGACCGG    CGAC
                                 _  A  CC        CCTC
GAM2053  PIK3CD   3'  GAGGAGAACAGTCTTTGCTG   22727         _______
                                GAGGAGAAC      TGCTG
                                |||||||||      |||||
                                CTCCTCTTG      ACGAC
                                     TCAGAA
GAM2053  PIST     5'  CGAAGGGAACTGCTGGGACTG  33791       A         CC
                                CGAGG GAACTGCTGG  CTG
                                ||||| ||||||||||  |||
                                GCTTC CTTGACGACC  GAC
                                   C         CT
GAM2053  PPP1R12B 3'  CGAGGAAAATTTTCTTGCTG   36956         _____  _
                                CGAGGAGAA    CT GCTG
                                |||||||||    || ||||
                                GCTCCTTTT    GA CGAC
                                     AAAA  A
GAM2053  TCF3     3'  CGAGGGGACACCCTGC      43320       A  A TGCTG
                                CGAGG GA C    GCCCTGC
                                ||||| || |    |||||||
```

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                                GCTCC CT G    TGGGACG
                                  C  _ _____
GAM2053  TNFRSF6B  5'  GGGGGGTGGCCATAGCCCTGCT 32361   AGAACT  __
              G                    GG    GCT  GGCCCTGCTG
                                   ||    |||  ||||||||||
                                   CC    CGG  TCGGGACGAC
                                    CCCCAC   TA
GAM2053  VCL      3'  CGGGAGTGGCCCTGC      30407   A   AACTGC
                                   CG GGAG    TGGCCCTGC
                                   || ||||    |||||||||
                                   GC CCTC    ACCGGGACG
                                    _   _______
GAM2053  ZNF147   3'  CAAGGAGAGTTCTGCCTGCTG  22929       ACTG  GC
                                   CGAGGAGA   CTG  CCTGCTG
                                   ||||||||   |||  |||||||
                                   GTTCCTCT   GAC  GGACGAC
                                        CAA_  __
GAM2053  ZNF278   3'  CGAGGAGAGACATGTTCTGCTG 36816       ACT  _  GCC
                                   CGAGGAGA   GC TG   CTGCTG
                                   ||||||||   || ||   ||||||
                                   GCTCCTCT   TG AC   GACGAC
                                        C__   T  AA_
GAM2053  AQP6     5'  CAACAGCCAGCCCCTCTG    38236       AG
                                   CAGCAGC  TAGCCCCTCTG
                                   |||||||  ||||||||||
                                   GTTGTCG  GTCGGGGAGAC
                                             __
GAM2053  ARL2     3'  AGCAGCAGTAGCAGCTCC    11690          CC
                                   AGCAGCAGTAGC  CTCT
                                   ||||||||||||  ||||
                                   TCGTCGTCATCG  GAGG
                                          TC
GAM2053  B4GALT7  3'  GCTGGCTGTTCCCCCTCTGT   28546    A_  A  AG
                                   GC  GC GT  CCCCTCTGT
                                   ||  || ||  |||||||||
                                   CG  CG CA  GGGGAGACA
                                    AC  A  AG
GAM2053  BPGM     5'  CAGCAGCAGCAGCAGCCGCT   11892              C
                                   CAGCAGCAGCAGTAGCC CT
                                   |||||||||||||||| ||
                                   GTCGTCGTCGTCGTCGG GA
                                              C
GAM2053  C18orf1  3'  CAGCAGCAGCAGCAGCAAATGA 41213             CCCT__
              CTGT                    CAGCAGCAGCAGTAGC     CTGT
                                   ||||||||||||||||     ||||
                                   GTCGTCGTCGTCGTCG     GACA
                                              TTTACT
GAM2053  CARPX    5'  GCGGCGGCAGCAGCCACCT   33572    A  A       _
                                   GC GC GCAGTAGCC CCT
                                   || || ||||||||| |||
```

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                                CG CG CGTCGTCGG GGA
                                 C  C        T
GAM2053  CCR9     3'  AGCAGCAGCCAGTGCTTCTGT  36293         _   A  CCC
                                AGCAGCAGC AGT GC   TCTGT
                                ||||||||| ||| ||   |||||
                                TCGTCGTCG TCA CG   AGACA
                                    G   _  A__
GAM2053  CYLN2    3'  GCGTGCACACGTGGTCCCTCTG 18054    A_   G  _  AGC
              T                  GC  GCA CA GT   CCCTCTGT
                                 ||  ||| || ||   ||||||||
                                 CG  CGT GT CA   GGGAGACA
                                  CA   _  G  CCA
GAM2053  CYP17    5'  CAGCAGTGGAGTAGAAGAGCTG 6438        C__     CCCCT
              T                  CAGCAG   AGTAG     CTGT
                                 ||||||   |||||     ||||
                                 GTCGTC   TCATC     GACA
                                    ACC     TTCTC
GAM2053  EGLN1    3'  ACAGCAGTCAAAATCTTCTGT  35158        _   TAGCCCC
                                 GCAGCAG CAG       TCTGT
                                 ||||||| |||       |||||
                                 TGTCGTC GTT       AGACA
                                    A   TTAGA__
GAM2053  FGF1     3'  AGAAGCAATTTGGTCCCTCTGT 9036     C      AGC__
                                 AG AGCAGT     CCCTCTGT
                                 || ||||||     ||||||||
                                 TC TCGTTA     GGGAGACA
                                  T     AACCA
GAM2053  GRM1     3'  CAGCAGCAGCAGCGGTCTCC   9132            CC_
                                 CAGCAGCAGTAGC   CTCT
                                 ||||||||||||   ||||
                                 GTCGTCGTCGTCG   GAGG
                                         CCA
GAM2053  GTF2H1   5'  GCCGCAGCAGTAGCCACCGCCT 23690     A          ____
              CTGT                  GC GCAGCAGTAGCC    CCTCTGT
                                 || ||||||||||||    |||||||
                                 CG CGTCGTCATCGG    GGAGACA
                                  G          TGGC
GAM2053  H4F2     3'  CAGCAGCCAGTGACTTCTG    40436        AG    AG CCC
                                 CAGCAGC  CAGT  C   TCTG
                                 |||||||  ||||  |   ||||
                                 GTCGTCG  GTCA  G   AGAC
                                    __    CT A__
GAM2053  ICA1     3'  CAACAGCAGCAGGTCATCTTTG 22463           TAGCCC  C
              T                  CAGCAGCAGCAG     CT TGT
                                 ||||||||||||     || |||
                                 GTTGTCGTCGTC     GA ACA
                                        CAGTA_  A
GAM2053  IL16     5'  AGCAGCAGTGGCAGCAGC    21093         ___
                                 AGCAGCA   GCAGTAGC
                                 |||||||   ||||||||
```

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                                TCGTCGT  CGTCGTCG
                                    CAC
GAM2053  MADH7    5'  CAGCAGCAGCAGGGGCCC    25363          TA
                                CAGCAGCAGCAG  GCCC
                                ||||||||||||  ||||
                                GTCGTCGTCGTC  CGGG
                                      CC
GAM2053  MYL1     3'  AGAGCAGCAGACACTTTG    38604    C      TA  CC  C
                                AG AGCAGCAG  GC  CT TG
                                || ||||||||  ||  || ||
                                TC TCGTCGTC  TG  GA AC
                                 _       __  T_  A
GAM2053  NRG1     5'  CAGCAGCGGCGGCAGGAGAGGC 30338       A  A   CCCCT_
            TGT                   CAGCAGC GC GTAG     CTGT
                                |||||||  || ||||      ||||
                                GTCGTCG CG CGTC     GACA
                                    C  C    CTCTCC
GAM2053  PSMD7    5'  GCAGCAGTAGCGGTCACCG   15837          CCCT_
                                GCAGCAGTAGC    CTG
                                ||||||||||     |||
                                CGTCGTCATCG    GGC
                                      CCAGT
GAM2053  PTGER4   5'  GCAGCAGCGGTGGCAGCC    9653         A___
                                GCAGCAGC   GTAGCC
                                ||||||||   ||||||
                                CGTCGTCG   CGTCGG
                                    CCAC
GAM2053  RAB11A   5'  AGCAGCAGTGGTATCTGT    21675        CA   GCCCC
                                AGCAGCAG  GTA    TCTGT
                                ||||||||  |||    |||||
                                TCGTCGTC  CAT    AGACA
                                    AC  _____
GAM2053  REPS2    5'  CAGCAGCGGCGGCGGCCC    21806        A  A TA
                                CAGCAGC GC G  GCCC
                                |||||||  || |  ||||
                                GTCGTCG CG C  CGGG
                                    C  C GC
GAM2053  REV3L    5'  CAGCAGCGGCGGCGGCTCCCT  16263        A  A TA  _
                                CAGCAGC GC G  GC CCCT
                                |||||||  || |  ||  ||||
                                GTCGTCG CG C  CG GGGA
                                    C  C GC  A
GAM2053  TCF2     3'  CAGCACAGCAGCCACCTCTGT  27019      G       _
                                CAGCA CAGTAGCC CCTCTGT
                                |||||  ||||||||  |||||||
                                GTCGT GTCGTCGG GGAGACA
                                  _       T
GAM2053  TMPRSS3  5'  CAATGGCAGCAGTGACAGGATC 37059     CA       AG CCC_
            TGT                   CAG  GCAGCAGT  C    TCTGT
                                |||  ||||||||  |    |||||
```

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                                GTT  CGTCGTCA  G    AGACA
                                  AC       CT TCCT
GAM2053  VSNL1    3'  CAGGAGCCAAGGGTCCCTCTGT 18036     C   AGT  C__
                                CAG AGC   AG   CCCTCTGT
                                ||| |||   ||   ||||||||
                                GTC TCG   TC   GGGAGACA
                                  C   GT_  CCA
GAM2053  WFS1     3'  ACAGCAGCCTTCCCTTTG    25636        AGC    C
                                GCAGCAGT   CCCT TG
                                ||||||||   |||| ||
                                TGTCGTCG   GGGA AC
                                     GAA    A
GAM2054  ARF4L    5'  ACCGCAGCCGCCCCGCG     43069           ATGACA
                                GCCGCAGCCGCC     GCG
                                ||||||||||||     |||
                                TGGCGTCGGCGG     CGC
                                      GG_____
GAM2054  ARNT2    3'  CAGCCGCGGCTGCAGGGGAGAG 31354        A  C  CAT_  C
                                CAGCCGC GC GC    GA AG
                                ||||||| || ||    || ||
                                GTCGGCG CG CG    CT TC
                                    C  A  TCCC  C
GAM2054  ATP5A1   5'  CAGCCGCAGCCTCCGGAC    42408           G  AT
                                CAGCCGCAGCC CC  GAC
                                |||||||||||  ||  |||
                                GTCGGCGTCGG GG  CTG
                                      A  C_
GAM2054  CD47     5'  CAGCCGCCGCCGCCGTTACAG  12129        A     ATG
                                CAGCCGC GCCGCC   ACAG
                                ||||||| ||||||   ||||
                                GTCGGCG CGGCGG   TGTC
                                    G     CAA
GAM2054  CUL3     5'  CAGCCGCGGCGGCGGCG     18731        A  C  CATGACA
                                CAGCCGC GC GC      GCG
                                ||||||| || ||      |||
                                GTCGGCG CG CG      CGC
                                    C  C  C_______
GAM2054  CYB561   3'  AGCCACAGCCAGCAGCAGCG   12539           C  TGA
                                AGCCGCAGCCG CA   CAGCG
                                ||||||||||| ||   |||||
                                TCGGTGTCGGT GT   GTCGC
                                      C  C__
GAM2054  EGLN1    5'  CAGCCGCAAGCGGGTAGCG    35161         C  CCATGAC
                                CAGCCGCAG CG      AGCG
                                |||||||| ||      ||||
                                GTCGGCGTT GC      TCGC
                                      C  CCA_____
GAM2054  ELMO3    3'  GCCGCAGCTGTGGCCCATG    36022         C___   _
                                GCCGCAGC    GCC ATG
                                ||||||||    ||| |||
```

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                                CGGCGTCG   CGG TAC
                                    ACAC   G
GAM2054  EYA4    5'  GCCGCAGTCGTCACTCCCCG  19908       C  C   GACAG
                                GCCGCAG CG CAT    CG
                                ||||||| || |||    ||
                                CGGCGTC GC GTG    GC
                                   A  A   AGGG_
GAM2054  FCN2    3'  GCCGCAGCCAGTTGGCCTG  31890        _____  A
                                GCCGCAGCC    GCC TG
                                |||||||||    ||| ||
                                CGGCGTCGG    CGG AC
                                     TCAAC   _
GAM2054  FOXD2   5'  CAGCCGCAGCCAGGGAAGTGGC 20954          CCATGACA
           G                     CAGCCGCAGCCG      GCG
                                ||||||||||||      |||
                                GTCGGCGTCGGT      CGC
                                      CCCTTCAC
GAM2054  FZD1    5'  ACCGCAGCCGCCGCCGCCGCG  18607          A_  ACA
                                GCCGCAGCCGCC  TG   GCG
                                ||||||||||||  ||   |||
                                TGGCGTCGGCGG  GC   CGC
                                      CG  GG_
GAM2054  GCH1    5'  GCCGCAGCCGCTGCCGTTCG  6702          CA  ACAG_
                                GCCGCAGCCGC  TG    CG
                                ||||||||||  ||    ||
                                CGGCGTCGGCG  AC    GC
                                     __  GGCAA
GAM2054  GRHPR   5'  CAGTGCAGCCGCCGACCCG   29191    CC       AT   AG
                                CAG  GCAGCCGCC  GAC  CG
                                |||  |||||||||  |||  ||
                                GTC  CGTCGGCGG  CTG  GC
                                  A_       __   G_
GAM2054  HADHSC  5'  GCAGCGGCGGCGACAGCGA   23717      C  CA
                                GCAGC GC  TGACAGCGA
                                |||||  ||  |||||||||
                                CGTCG CG  GCTGTCGCT
                                   C  CC
GAM2054  ING1L   5'  GCCGCGGCCGCCGCG       11459      A     ATGACA
                                GCCGC GCCGCC     GCG
                                |||||  ||||||     |||
                                CGGCG CGGCGG     CGC
                                   C     _______
GAM2054  KCNA6   5'  GCCGCAGCTGCAGC        13814         CGCCA  A
                                GCCGCAGC    TG CAGC
                                ||||||||    || ||||
                                CGGCGTCG    AC GTCG
                                      ______  _
GAM2054  KCND2   5'  CAGCCGCCGCCGCCGTGGCG  29364        A     A  ACA
                                CAGCCGC GCCGCC TG   GCG
                                |||||||  ||||||  ||   |||
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                                GTCGGCG CGGCGG AC   CGC
                                   G     C ___
GAM2054  LIPE     3'  CAGCAGCAGCAAAAGGCAGCG  23811      C     CGCCATGA
                                CAGC GCAGC       CAGCG
                                |||| |||||       |||||
                                GTCG CGTCG       GTCGC
                                  T    TTTTCC__
GAM2054  LRPAP1   3'  CAGCCCCAGCCACCCTGACGGC 14234      G       A   A
              G                  CAGCC CAGCCGCC TGAC GCG
                                |||||| |||||||| |||| |||
                                GTCGG GTCGGTGG ACTG CGC
                                   G       G   C
GAM2054  NME1     5'  GCTGCAGCCGCCAGCACCCGA  7071     C        TG  AG
                                GC GCAGCCGCCA  AC  CGA
                                || ||||||||||  ||  |||
                                CG CGTCGGCGGT  TG  GCT
                                 A         CG  G_
GAM2054  OTOF     3'  AGCCGCAGCCTGGGGCAGTGA  22053          GCCATGA   C
                                AGCCGCAGCC      CAG GA
                                ||||||||||      ||| ||
                                TCGGCGTCGG      GTC CT
                                      ACCCC__   A
GAM2054  PHEMX    3'  AGCTGCAGCCACAGC      40020     C     GCCATG
                                AGC GCAGCC     ACAGC
                                ||| ||||||     |||||
                                TCG CGTCGG     TGTCG
                                  A     _______
GAM2054  POLR2E   3'  CAGCCACAGCGGCAGTGA    40913          C  CA
                                CAGCCGCAGC GC  TGA
                                |||||||||| ||  |||
                                GTCGGTGTCG CG  ACT
                                      C  TC
GAM2054  POU2F2   3'  CAGCCGCAGCCGCTGCTGA   15459            CA_
                                CAGCCGCAGCCGC   TGA
                                ||||||||||||   |||
                                GTCGGCGTCGGCG   ACT
                                        ACG
GAM2054  POU4F1   5'  CAGCCGCGGCGGTCGCGGCG   26382        A ___   CATGACA
                                CAGCCGC GC   CGC      GCG
                                ||||||| ||   |||      |||
                                GTCGGCG CG   GCG      CGC
                                   C  CCA   C_______
GAM2054  PPP1R2   5'  GCCGCAACTGCTGCCTCG    26419        C  CA  ACAG
                                GCCGCAGC GC  TG    CG
                                |||||||| ||  ||    ||
                                CGGCGTTG CG  AC    GC
                                     A  __  GGA_
GAM2054  PPP3CC   5'  CAGCCGCGGCTGCTCGCG    24674        A  C  CATGACA
                                CAGCCGC GC GC      GCG
                                ||||||| || ||      |||
```

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                                GTCGGCG CG CG      CGC
                                    C  A  AG_____
GAM2054  PTBP1    3'  CAGCCGCGGCCGCCGCG     36715        A     ATGACA
                                CAGCCGC GCCGCC     GCG
                                ||||||| ||||||     |||
                                GTCGGCG CGGCGG     CGC
                                    C     _______
GAM2054  PTEN     5'  AGCTGCAGCCGCCGC       7199      C       ATGACA
                                AGC GCAGCCGCC     GC
                                ||| |||||||||     ||
                                TCG CGTCGGCGG     CG
                                  A       _______
GAM2054  SFRP5    5'  CAGCCGCCGCCGCCGCCGCCGC 16589        A     A_  ACA
              G                   CAGCCGC GCCGCC  TG   GCG
                                ||||||| ||||||  ||   |||
                                GTCGGCG CGGCGG  GC   CGC
                                    G     CG  GG_
GAM2054  SGT      3'  GCCGCAGCTGGCAGG       16613         CGCCA  A   C
                                GCCGCAGC    TG CAG G
                                ||||||||    || ||| |
                                CGGCGTCG    AC GTC C
                                     _____  C   A
GAM2054  SNL      3'  GCCGCAGCCGCTGACCCGA    16941           CA    AG
                                GCCGCAGCCGC  TGAC  CGA
                                ||||||||||  ||||  |||
                                CGGCGTCGGCG  ACTG  GCT
                                     __    G_
GAM2054  SYK      5'  GCCTCAGCCGCCGGGCCCGCG  17238     G       ATGACA
                                GCC CAGCCGCC     GCG
                                ||| ||||||||     |||
                                CGG GTCGGCGG     CGC
                                  A       CCCGGG
GAM2054  USP11    5'  CAGCAGCAGCTGTAGAAGCG   21629      C     CGCCAT  C
                                CAGC GCAGC     GA AGCG
                                |||| |||||     || ||||
                                GTCG CGTCG     CT TCGC
                                  T    ACAT__  _
GAM2054  WEE1     5'  CAGCCGCGGCGTCTCTGCGCGG 18082        A  CGCCA  ACA_
              CG                    CAGCCGC GC    TG    GCG
                                ||||||| ||    ||    |||
                                GTCGGCG CG    AC    CGC
                                    C  CAGAG  GCGC
GAM2054  HMGA2    5'  CGCCGCTACCGCCGC       18507        TGACAGC
                                CGTCGCT      ACCGCCGC
                                |||||||      ||||||||
                                GCGGCGA      TGGCGGCG
                                             _______
GAM2054  KCNA6    5'  TCGCTGCCGCCGCCGCA     13820       TGACA  A_
                                TCGCT    GC  CCGCCGCA
                                |||||    ||  ||||||||
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                                AGCGA    CG  GGCGGCGT
                                  _____  GC
GAM2054  LASS1    3'  GTCCTCATACTGCCGCA     34615     G  TGA  GC  C
                                GTC CT   CA  AC GCCGCA
                                ||| ||   ||  || ||||||
                                CAG GA   GT  TG CGGCGT
                                  _ ___  A_  A
GAM2054  MTA1L1   5'  CGCGCTGTCGCCGCCGCA    21884    T   TGACAGCA
                                CG CGCT       CCGCCGCA
                                || ||||       ||||||||
                                GC GCGA       GGCGGCGT
                                  _   CAGC____
GAM2054  PIK3R2   3'  CGTGGCTCCCGCCGCCGCA   22747     C   GACAGCA
                                CGT GCTT      CCGCCGCA
                                ||| ||||      ||||||||
                                GCA CGAG      GGCGGCGT
                                  C   GGC____
GAM2054  PTEN     5'  CGCCGCTGCCGCCGCCGCA   7208        TGACA  A_
                                CGTCGCT    GC  CCGCCGCA
                                |||||||    ||  ||||||||
                                GCGGCGA    CG  GGCGGCGT
                                   _____  GC
GAM2054  WNT10B   5'  CGCTTCCCCAGCGCCGCCGC   18144      GA_   A
                                CGCTT   CAGC CCGCCGC
                                |||||   |||| |||||||
                                GCGAA   GTCG GGCGGCG
                                   GGG   C
GAM2055  CANX     3'  AGGCATGACATATACT      44660        G    CTAA  T
                                AGGCATG ACATA    TA CT
                                ||||||| |||||    || ||
                                TCCGTAC TGTAT    AT GA
                                   _    ____  _
GAM2055  SLA      3'  GGCATGAACCATTGTGTCTGT  27565         ATACTAATA
                                GGCATGGAC        TCTGT
                                |||||||||        |||||
                                CCGTACTTG        AGACA
                                     GTAACAC__
GAM2055  VHL      3'  AGGGAGACTATACTAATGTTTG 8106      CAT   _      ATC
              T                  AGG   GGAC ATACTAAT   TGT
                                 |||   |||| ||||||||   |||
                                 TCC   TCTG TATGATTA   ACA
                                   C__    A       CAA
GAM2055  BCR      3'  CCAGACCTGGGCAGATCTGCC  34631         A  A  TAT   A
                                CCAGACCT GG GC   TCT CC
                                |||||||| || ||   ||| ||
                                GGTCTGGA CC CG   AGA GG
                                     _ _  TCT   C
GAM2055  CCR2     3'  GATTTAGGAGTTCCCAC     8500     CC     CTA
                                GA  TAGGAG   TTCTAC
                                ||  ||||||   ||||||
```

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                                CT  ATCCTC   AGGGTG
                                 AA     A__
GAM2055  DAZL     3'  ACCAGTTCTAGGAGCAAAC   42773      AC      TATTCT
                                ACCAG  CTAGGAGC     AC
                                |||||  ||||||||     ||
                                TGGTC  GATCCTCG     TG
                                  AA       TT____
GAM2055  GJA1     3'  CAGGCCTAGAAAGCTTACC   6729      A     _  ATTC
                                CAG CCTAGGA GCT    TACC
                                ||| ||||||| |||    ||||
                                GTC GGATCTT CGA    ATGG
                                  C      T  _____
GAM2055  HIVEP3   5'  CAGGGCCCACGCTATTCTA   35989     A_   GGA
                                CAG  CCTA   GCTATTCTA
                                |||  ||||   |||||||||
                                GTC  GGGT   CGATAAGAT
                                  CC    G__
GAM2055  LASS2    3'  AGAATTAGTTGCCATTCTAC   42667     CC   GA
                                AGA  TAG  GCTATTCTAC
                                |||  |||  ||||||||||
                                TCT  ATC  CGGTAAGATG
                                  TA   AA
GAM2055  LUZP1    3'  ACCACGCCTGGCCAGAATTCTA 37955      GA   A  AGCT_
              CC                  ACCA  CCT GG    ATTCTACC
                                ||||  ||| ||    ||||||||
                                TGGT  GGA CC    TAAGATGG
                                  GC  _ GGTCT
GAM2055  MYOC     3'  CCAGAGGAGCTATTCT      7030       CCTA
                                CCAGA    GGAGCTATTCT
                                |||||    ||||||||||
                                GGTCT    CCTCGATAAGA
                                   _____
GAM2055  NXF2     5'  ACCAACCTGGGAGCTACACT   35185      A  A      T
                                ACCAG CCT GGAGCTAT CT
                                ||||| ||| |||||||| ||
                                TGGTT GGA CCTCGATG GA
                                  _  C       T
GAM2055  PCOLN3   3'  ACCACGTCTAGGACCTACC    15742     GAC     G
                                ACCA   CTAGGA CTATT
                                ||||   |||||| |||||
                                TGGT   GATCCT GATGG
                                  GCA     G
GAM2055  RAB7L1   3'  CCAGATTTGGGAACCACT    19431      CCTA
                                CCAGA    GGAGCTATT
                                |||||    |||||||||
                                GGTCT    CCTTGGTGA
                                   AAAC
GAM2055  RARA     3'  CCAGGTCTGGGAAAACTCT   9704      AC  A   CT
                                CCAG  CT GGAG  ATTCT
                                ||||  || ||||  |||||
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                                GGTC  GA CCTT  TGAGA
                                  CA  C    T_
GAM2055  RAX      3'  CCAAGTTTAGGAGCTTCAGCC  30243      ACC       AT  TA
                                CCAG   TAGGAGCT  TC  CC
                                ||||   ||||||||  ||  ||
                                GGTT   ATCCTCGA  AG  GG
                                  CAA       __  TC
GAM2056  CSHL1    3'  TGTGGAGCAGCTCTAAGTTG   35458      AG ATCTAA
                                TGTG  G     CTCTAAGTTG
                                ||||  |     ||||||||||
                                ACAC  C     GAGATTCAAC
                                  CT GTC___
GAM2056  FOXO1A   3'  TGTAAGAATTTTAAGTTG    12894         CTAACTC
                                TGTGAGGAT      TAAGTTG
                                |||||||||      |||||||
                                ACATTCTTA      ATTCAAC
                                     AA_____
GAM2056  ADD2     3'  CTTACTCAGGGGAAGCCTT    32727            TT
                                CTTACTCAGGGGAA  GTTTT
                                ||||||||||||||  |||||
                                GAATGAGTCCCCTT  CGGAA
                                                __
GAM2056  ALDH3A2  3'  TGACTTGCTCAGGGGATCCTCT 42921    A    A        A  G
           T                     A ACTT CTCAGGGGA TT TTTT
                                 | |||| |||||||||  || ||||
                                 A TGAA GAGTCCCCT AG AGAA
                                  C   C         _  G
GAM2056  BACE     3'  AAACTGACTCAGTATTCTTGTT 39945       T     GGGAA
           TT                     AAACT ACTCAG     TTGTTTT
                                  |||||  ||||||     |||||||
                                  TTTGA TGAGTC     AACAAAA
                                    C      ATAAG
GAM2056  DDX6     3'  TTACTTGGGATTGTTTT     20571       CAG    A
                                  TTACT   GGGA TTGTTTT
                                  |||||   ||||  |||||||
                                  AATGA   CCCT  AACAAAA
                                    A__   _
GAM2056  SMARCA3  3'  AAACTTACTTATGAGTGTGTTT 16897         CAG   AAT
           T                      AAACTTACT   GGG   TGTTTT
                                  |||||||||   |||   ||||||
                                  TTTGAATGA   CTC   ACAAAA
                                       ATA   AC_
GAM2056  SNK      3'  CCACAGGGGAATTGTTTT    27359    _
                                  CT CAGGGGAATTGTTTT
                                  || ||||||||||||||
                                  GG GTCCCCTTAACAAAA
                                   T
GAM2056  TKTL1    3'  AAACTTACTATCAGGTGGTTGT 29314         __     _  AA
           TTT                      AAACTTAC  TCAGG GG  TTGTTTT
                                  ||||||||  |||||  ||  |||||||
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                                TTTGAATG  AGTCC CC  AACAAAA
                                    AT    A  __
GAM2056  TMEPAI   3'  AAACTGTGCTCAGGTTTTTGTT 33585      TA_     GGAA
              TT                  AAACT   CTCAGG   TTGTTTT
                                  |||||  ||||||  |||||||
                                  TTTGA  GAGTCC   AACAAAA
                                    CAC     AAA_
GAM2057  ADARB1   3'  TCCACCAGTCCCTGGAACCC  9976        AG       A
                                  TCCACCA  CCCTGGAA TCT
                                  |||||||  |||||||| |||
                                  AGGTGGT  GGGACCTT GGG
                                     CA       _
GAM2057  GARP     3'  CCTGCCGAGCTCTGGAGCCCT  24307    A_  A   C     AAT
                                  CC  CC AGC CTGGA   CTCT
                                  ||  || ||| |||||   ||||
                                  GG  GG TCG GACCT   GGGA
                                   AC  C   A    C__
GAM2057  HLA-DMB  3'  TCCACCAAAGTTTATTTCTCT  13382         CCCTGGAAA
                                  TCCACCAAG       TCTCT
                                  |||||||||       |||||
                                  AGGTGGTTT       AGAGA
                                       CAAATAA__
GAM2057  LPIN2    3'  AAACCCTGGAAGCTCTA     31202          AT
                                  AAGCCCTGGAA  CTCTA
                                  ||||||||||  |||||
                                  TTTGGGACCTT  GAGAT
                                        C_
GAM2057  MANBA    3'  CCACCAAGAAATCTCT      25386       AGCCCT
                                  CCACCA     GGAAATCTCT
                                  ||||||     ||||||||||
                                  GGTGGT     TCTTTAGAGA
                                    _______
GAM2057  MAPK14   3'  TCCACCATGGAGGAAATCTCT  40017        AGCCCT
                                  TCCACCA     GGAAATCTCT
                                  |||||||     ||||||||||
                                  AGGTGGT     CCTTTAGAGA
                                      ACCT__
GAM2057  NAPB     3'  CCAGCCCTGACCAAGATTTCTA 43173     A      AA___  C
                                  CCA GCCCTGG    AT TCTA
                                  ||| |||||||    || ||||
                                  GGT CGGGACT    TA AGAT
                                    _      GGTTC  A
GAM2057  RXRA     3'  TCCATCAAACCCTGGCACCT   16435      C        AA
                                  TCCA CAAGCCCTGG  ATCT
                                  |||| ||||||||||  ||||
                                  AGGT GTTTGGGACC  TGGA
                                    A        G_
GAM2057  TCF8     3'  TCCGCAGAGTCCTGGAAAACT  36240     AC  _  C       T
                                  TCC  CA AG CCTGGAAA CT
                                  |||  || || |||||||| ||
```

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                                AGG  GT TC GGACCTTT GA
                                  C_  C  A      T
GAM2057  ARHGEF12  3'  TAGAGAATTACATAATTA    31644       CC
                                TAGAGAA  ACGTAATTG
                                |||||||  |||||||||
                                ATCTCTT  TGTATTAAT
                                    AA
GAM2057  DDEF1     3'  TAAAGAGTTTTGGGTC      40568       ACCAC  AA
                                TAGAGA    GT  TTGGGTC
                                ||||||    ||  |||||||
                                ATTTCT    CA  AACCCAG
                                   _____  A_
GAM2057  EGR2      3'  TAGAGAACAGTGTGGGTACA   7583        CAC  AAT    _
                                TAGAGAAC   GT   TGGGT CA
                                ||||||||   ||   ||||| ||
                                ATCTCTTG   CA   ACCCA GT
                                     T__  C__     T
GAM2057  ENPP3     3'  GAGAACCACTCGGGGGGTCA   22712        GTAATT
                                GAGAACCAC     GGGTCA
                                |||||||||     ||||||
                                CTCTTGGTG     CCCAGT
                                     AGCCC_
GAM2057  ITGB3     3'  AGAGAACCATAGCTGGGT    6837         CG  A
                                AGAGAACCA  TA TTGGGT
                                |||||||||  || ||||||
                                TCTCTTGGT  AT GACCCA
                                    __  C
GAM2057  LIF       3'  TAGAAATCATGCCAGGTCA    14151       ACCA   AA TG
                                TAGAGA    CGT  T  GGTCA
                                ||||||    |||  |  |||||
                                ATCTTT    GTA  G  CCAGT
                                   A____   C_ GT
GAM2057  MAFG      5'  TAGAGAACCAGGTGGGAGGTCA 43131          C  AATT
                                TAGAGAACCA GT    GGGTCA
                                |||||||||| ||    ||||||
                                ATCTCTTGGT CA    TCCAGT
                                     C  CCC_
GAM2057  PPARGC1   3'  TAGAGAACACATGTGGTC    29958        C    AATTG
                                TAGAGAAC ACGT    GGTC
                                |||||||| ||||    ||||
                                ATCTCTTG TGTA    CCAG
                                    _    CA____
GAM2057  PRKY      3'  TAGAGACCATGTAGGTCA     15707       A   C  AATT
                                TAGAGA CCA GT    GGGTCA
                                |||||| ||| ||    ||||||
                                ATCTCT GGT CA    TCCAGT
                                   _  A  _____
GAM2057  PSMD7     3'  CAGAGAGCTCTTGTTGGGTCA  15835       ACCACGTAA
                                TAGAGA        TTGGGTCA
                                ||||||        ||||||||
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                                GTCTCT       AACCCAGT
                                   CGAGAAC__
GAM2057  SYN3     3'  TAGATAATCGGTTCCTGGGTCA 18567     GAACCAC  AA
              A                    TAGA      GT  TTGGGTCAA
                                   ||||      ||  |||||||||
                                   ATCT      CA  GACCCAGTT
                                     ATTAGC_  AG
GAM2057  TACC1    3'  TAGAAACCACGTGAGAAAACTG 26598       A     _____
              G                    TAGAGA CCACGT    AATTGG
                                   |||||| ||||||    ||||||
                                   ATCTTT GGTGCA    TTGACC
                                      _     CTCTT
GAM2057  TRPM2    3'  TAGAGAGCTTTGGGTCA     17694       ACCAC  AA
                                   TAGAGA    GT  TTGGGTCA
                                   ||||||    ||  ||||||||
                                   ATCTCT    CG  AACCCAGT
                                      _____  A_
GAM2058  MGA      3'  AGGCTTGAATTTGTTAAT    41721      CCTG   A
                                   AGGC    GAA TTGTTAAT
                                   ||||    ||| ||||||||
                                   TCCG    CTT AACAATTA
                                     AA__   A
GAM2058  NFE2L1   3'  ATAAGCCCAGTTGTT       17329         T  AAA
                                   ATAGGCCC GG   TTGTT
                                   |||||||| ||   |||||
                                   TATTCGGG TC   AACAA
                                      _ ____
GAM2058  SCG3     3'  AACAGGGGGAAATTGTTA    29877       CCCT
                                   AATAGG    GGAAATTGTTA
                                   ||||||    ||||||||||
                                   TTGTCC    CCTTTAACAAT
                                      C___
GAM2058  SLC17A7  3'  AGGTCCTGGAAACTGCCA    33694     C
                                   AGG CCTGGAAATTGTTA
                                   ||| ||||||||||||||
                                   TCC GGACCTTTGACGGT
                                     A
GAM2058  DSCR3    3'  CGTTAAATATTTTCATCTCATT 25824          ATTA
              A                    TGTTAAATATT    GTCTCATTA
                                   ||||||||||    |||||||||
                                   GCAATTTATAA    TAGAGTAAT
                                         AAG_
GAM2059  KCND2    3'  TATGTAATAATCTTCATCATAG 29367           _    C  A
              CC                     TATGTAATAGTCT CATCA TA CC
                                   |||||||||||| ||||| || ||
                                   ATACATTATTAGA GTAGT AT GG
                                         A    _ C
GAM2059  SRD5A2   5'  CATGTAACCTCATCATTAA   40457        AGT      C
                                   TATGTAAT   CTCATCA TAA
                                   ||||||||   ||||||| |||
```

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                                GTACATTG   GAGTAGT ATT
                                   ___       A
GAM2059  TSG      3'  TATATAATTAAACACATCACT  34009         AGTCT_
                                TATGTAAT     CATCACT
                                ||||||||     |||||||
                                ATATATTA     GTAGTGA
                                     ATTTGT
GAM2059  ABCD4    3'  CAAAGGCCCCTGGAAGTTAGTG 33741     C     _    A
              G                  CAA AGGCCC TGGAA TTAGTGG
                                |||  ||||||  |||||  |||||||
                                GTT TCCGGG ACCTT AATCACC
                                  _     G    C
GAM2059  ABCD4    3'  CAAAGGCCCCTAGAAGTTAGTG 33740     C     _    A
              G                  CAA AGGCCC TGGAA TTAGTGG
                                |||  ||||||  |||||  |||||||
                                GTT TCCGGG ATCTT AATCACC
                                  _     G    C
GAM2059  CLN2     3'  CAACGGTCTTGGAAAGGAAGGC 7553       A  CCC     TTAGT
                                CAAC GG   TGGAAA     GGC
                                ||||  ||   ||||||     |||
                                GTTG CC   ACCTTT     CCG
                                  _ AGA     CCTT_
GAM2059  COG7     3'  AGCCCTGGCTCTCTTGGTGG   42654         AAA__  A
                                GGCCCTGG     TT GTGG
                                ||||||||     ||  ||||
                                TCGGGACC     AA CACC
                                     GAGAG  C
GAM2059  CRHR2    3'  TGACAGCCCTGGGATAAGG    12444    A    G     AAAT   T
                                C ACAG CCCTGG    TAG GG
                                |  ||||  ||||||    |||  ||
                                A TGTC GGGACC    ATT CC
                                 C    _      CT__   _
GAM2059  DLEC1    3'  CAGCATGCCCTGGGAAAAGT   28819     A  G      A  TT
                                CA CA GCCCTGG AA  AGT
                                ||  ||  |||||||  ||  |||
                                GT GT CGGGACC TT  TCA
                                 C  A      C  T_
GAM2059  FANCE    3'  AGCCTTTGGAAATATAGC     34894      C_      TA
                                GGCC  TGGAAAT  GTGGC
                                ||||  |||||||  |||||
                                TCGG  ACCTTTA  TATCG
                                  AA      ___
GAM2059  FGFR2    3'  CAACAAGCTCTGGGAGGCATGG 35658         C    AAATTA
                                CAACAGGC CTGG      GTGG
                                ||||||||  ||||      ||||
                                GTTGTTCG GACC      TACC
                                     A    CTCCG_
GAM2059  HCS      3'  AACAGCCACATGTGGTTAGTGG 33217       G  C____   AAA
              C                  AACAG CC    TGG   TTAGTGGC
                                |||||  ||    |||   ||||||||
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                                TTGTC GG    ACC   AATCACCG
                                  _ TGTAC   ___
GAM2059  HMGB1    3'  CAGGCAAGGTTAGTGG      13405      CCT  AAA
                                CAGGC   GG   TTAGTGG
                                |||||   ||   |||||||
                                GTCCG   CC   AATCACC
                                  TT_  ___
GAM2059  HOXC6    3'  CAGCAGGCCCAGGAGCCGG   21071    A      T   AATTAG
                                CA CAGGCCC GGA     TGG
                                || ||||||| |||     |||
                                GT GTCCGGG CCT     GCC
                                 C      T   CG____
GAM2059  JPH2     3'  CAGGTCCCGGAAACAAGC    45374      C        T
                                CAGG CCTGGAAAT AGT
                                |||| ||||||||| |||
                                GTCC GGGCCTTTG TCG
                                  A        T
GAM2059  JUP      3'  AGGCCCTGGGGGGCTTAGGGC   13768         AAA_    T
                                AGGCCCTGG    TTAG GGC
                                |||||||||    |||| |||
                                TCCGGGACC    AATC CCG
                                     CCCG   _
GAM2059  KCNJ15   5'  CAGGCTCTGGAAACACTGG    13876      C       T G
                                CAGGC CTGGAAAT A TGG
                                ||||| |||||||| | |||
                                GTCCG GACCTTTG T ACC
                                  A       _ G
GAM2059  PAX2     3'  GGCCCTGGGGAACTAGGC     19631        A_    GT
                                GGCCCTGG  AATTA  GGC
                                ||||||||  |||||  |||
                                CCGGGACC  TTGAT  CCG
                                     CC    __
GAM2059  S100A9   3'  AACAGGCCCCGGGGCCCTGG   16449           AAATTAG
                                AACAGGCCCTGG      TGG
                                ||||||||||||      |||
                                TTGTCCGGGGCC      ACC
                                      CCGGG__
GAM2059  SP100    3'  CAGGCAAAGGTTAGTGGC     17054      CCT  AAA
                                CAGGC   GG   TTAGTGGC
                                |||||   ||   ||||||||
                                GTCCG   CC   AATCACCG
                                  TTT  ___
GAM2059  STARD5   3'  CAACAGGGCCTGGTTTTCAGTG 36120        C     AAA
            GC                    CAACAGG CCTGG   TTAGTGGC
                                |||||||  |||||   ||||||||
                                GTTGTCC GGACC   AGTCACCG
                                    C     AAA
GAM2059  STAT6    3'  CAGCAGGCCCTGGGGGGTGAGGC 17148    A        AAATTAGT
                                CA CAGGCCCTGG       GGC
                                || ||||||||||       |||
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                                GT GTCCGGGACC       CCG
                                 C         CCCACT__
GAM2059  TRPC1    5'  TGACAGCCCCAAGTTGGTGGC  17683   A   G   T  AAA  A
                                C ACAG CCC GG   TT GTGGC
                                | |||| ||| ||   || |||||
                                A TGTC GGG TC   AA CACCG
                                 C   G   T ___  C
GAM2060  BACH2    3'  CGTGGCTGGGGCCAACACGG  34786    CA  ACAA  AA_
                                CG  GC   TG   CCAACACGG
                                ||  ||   ||   |||||||||
                                GC  CG   AC   GGTTGTGCC
                                 AC  ____  CCC
GAM2060  DXS1283E 5'  AGCACAATGCAGCCCCGG    43350         AA__  AACA
                                AGCACAATG   CC   CGG
                                |||||||||   ||   |||
                                TCGTGTTAC   GG   GCC
                                     GTCG  ____
GAM2060  FGF5     3'  GCAGCACACCAGCAG      37589        AATGA   A  C
                                GCAGCAC    ACCA CA G
                                |||||||    |||| || |
                                CGTCGTG    TGGT GT C
                                    _____   C  A
GAM2060  NCL      3'  CAGTCAAAACCAACACG     41051     _  CAAT
                                CAG CA   GAACCAACACG
                                ||| ||   ||||||||||
                                GTC GT   TTTGGTTGTGC
                                  A  ____
GAM2060  NEO1     3'  CACAGCACAAAGACACG     14750          T  ACCAA
                                CGCAGCACAA GA    CACG
                                |||||||||| ||    ||||
                                GTGTCGTGTT CT    GTGC
                                     T  _____
GAM2060  PPT1     3'  GCAGCACCAACACG       41552       ACAATGA
                                GCAGC      ACCAACACG
                                |||||      |||||||||
                                CGTCG      TGGTTGTGC
                                   _______
GAM2060  SLC21A3  3'  GCAGCACACCAACAG      22905        AATGA      C
                                GCAGCAC    ACCAACA G
                                |||||||    ||||||| |
                                CGTCGTG    TGGTTGT C
                                    _____      A
GAM2060  UGCG     5'  CCGCTGCGGCCGCCAACACGG  17867      A  ACAA  AA
                                CCGC GC   TG  CCAACACGG
                                |||| ||   ||  |||||||||
                                GGCG CG   GC  GGTTGTGCC
                                  A  CCG_  __
GAM2060  PLN      3'  GTTGATCATATGTCTTAGA   15405        CA___
                                GTTGATCA    TTTAGA
                                ||||||||    ||||||
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                                CAACTAGT    GAATCT
                                    ATACA
GAM2060  STAT3    3'  TCCTTATTTGCATTTAGATAAA 40232    G   ATCA
                A                    TC TTG    CATTTAGATAAAA
                                     || |||    ||||||||||||
                                     AG AAT    GTAAATCTATTTT
                                      G   AAAC
GAM2061  ABCE1    3'  TGATGTTTATTTATCAAATGTC 40505    A    A      CATC
                AA                    C ATGT TATTTATC    GTCAA
                                     | |||| ||||||||    |||||
                                     A TACA ATAAATAG    CAGTT
                                      C    A       TTTA
GAM2061  DMC1     3'  CAATGTATAGTTATCATAAATC 28198         T    CATC
                A                     CAATGTATA TTATC    GTCA
                                     ||||||||| |||||    ||||
                                     GTTACATAT AATAG    TAGT
                                           C     TATT
GAM2061  PHEMX    3'  TGATGTATATTTGACCAC    40024    A        AT
                                     C ATGTATATTT  CCAT
                                     | ||||||||||  ||||
                                     A TACATATAAA  GGTG
                                      C         CT
GAM2062  ATP11A   3'  TCTCTCTGCTGTGCATACACGT 44187    C   ATAGAA _
                                     TC CTC      TG ATACACGT
                                     || |||      || ||||||||
                                     AG GAG      AC TATGTGCA
                                      A   ACGAC_  G
GAM2062  MPHOSPH1  3'  TCATTCTCCATGATACACGTAT 32118      AGA__
                                     TCAT     ATGATACACGTAT
                                     ||||     ||||||||||||
                                     AGTA     TACTATGTGCATA
                                        AGAGG
GAM2062  STAT6    3'  CATAGTCTCATACACGTAT    17151       AATG
                                     CATAG    ATACACGTAT
                                     |||||    ||||||||||
                                     GTATC    TATGTGCATA
                                        AGAG
GAM2062  TLX1     3'  TCTCCCATAGATGCCCATGT   24347    C       A  ATA  C
                                     TC CTCATAGA TG   CA GT
                                     || |||||||| ||   || ||
                                     AG GGGTATCT AC   GT CA
                                      A       _  GG_  A
GAM2062  UBE4A    3'  TCATGGATATGATACCCGT    21977      A _      A
                                     TCAT GA ATGATAC CGT
                                     |||| || ||||||| |||
                                     AGTA CT TACTATG GCA
                                       C A      G
GAM2062  IL5RA    5'  TCTGTAGCCTGTCTACAGACGA 8163      A  AT     TT  A
                T                     TCT TA  CTGTCT  TA ACGAT
                                     ||| ||  ||||||  || |||||
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                                AGA AT  GACAGA  GT TGCTA
                                  C  CG     T_  C
GAM2063  BACH2    3'  CGTGGCTGGGGCCAACACGG  34786    CA  ACAA  AA_
                                CG  GC    TG   CCAACACGG
                                ||  ||    ||   |||||||||
                                GC  CG    AC   GGTTGTGCC
                                 AC  ____  CCC
GAM2063  DXS1283E 5'  AGCACAATGCAGCCCCGG    43350         AA__  AACA
                                AGCACAATG    CC    CGG
                                |||||||||    ||    |||
                                TCGTGTTAC    GG    GCC
                                     GTCG  ____
GAM2063  FGF5     3'  GCAGCACACCAGCAG       37589        AATGA    A  C
                                GCAGCAC     ACCA CA G
                                |||||||     |||| || |
                                CGTCGTG     TGGT GT C
                                   _____    C  A
GAM2063  FGF5     3'  GCAGCACACCAGCAG       37589        AATGA    A  C
                                GCAGCAC     ACCA CA G
                                |||||||     |||| || |
                                CGTCGTG     TGGT GT C
                                   _____    C  A
GAM2063  NCL      3'  CAGTCAAAACCAACACG     41051     _  CAAT
                                CAG CA    GAACCAACACG
                                |||  ||    ||||||||||
                                GTC GT    TTTGGTTGTGC
                                  A  ____
GAM2063  NEO1     3'  CACAGCACAAAGACACG     14750          T  ACCAA
                                CGCAGCACAA GA     CACG
                                ||||||||||  ||    ||||
                                GTGTCGTGTT CT     GTGC
                                     T  _____
GAM2063  PPT1     3'  GCAGCACCAACACG        41552       ACAATGA
                                GCAGC       ACCAACACG
                                |||||       |||||||||
                                CGTCG       TGGTTGTGC
                                  _______
GAM2063  SLC21A3  3'  GCAGCACACCAACAG       39574        AATGA      C
                                GCAGCAC     ACCAACA G
                                |||||||     ||||||| |
                                CGTCGTG     TGGTTGT C
                                   _____       A
GAM2063  UGCG     5'  CCGCTGCGGCCGCCAACACGG  17867      A  ACAA  AA
                                CCGC GC    TG  CCAACACGG
                                ||||  ||   ||  |||||||||
                                GGCG CG    GC  GGTTGTGCC
                                  A  CCG_  __
GAM2063  DAZL     3'  GCTGGGTTTAGATAAG      42776      ATCACA
                                GTTG      TTTAGATAAG
                                ||||      ||||||||||
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                                CGAC     AAATCTATTC
                                  CC____
GAM2064  ANXA9    5'  GCAGCACAGGAGCACA      18690         AT  ACCAA
                                GCAGCACA  GA    CACA
                                ||||||||  ||    ||||
                                CGTCGTGT  CT    GTGT
                                    C_  C____
GAM2064  LRP4     5'  GCAGCGCCCATTCCAACACAG  42062       ACAATGAA
                                GCAGC       CCAACACAG
                                |||||       |||||||||
                                CGTCG       GGTTGTGTC
                                  CGGGTAA_
GAM2064  NCL      3'  CAGTCAAAACCAACAC      41050     _  CAAT
                                CAG CA    GAACCAACAC
                                ||| ||    ||||||||||
                                GTC GT    TTTGGTTGTG
                                  A  ____
GAM2064  NEO1     3'  CACAGCACAAAGACAC      14749          T  ACCAA
                                CGCAGCACAA GA     CAC
                                |||||||||| ||     |||
                                GTGTCGTGTT CT     GTG
                                     T  _____
GAM2064  POMZP3   5'  CCGCAGCAGGCACGAGGTACAG 29238         CA_   ACCAAC
                                CCGCAGCA   ATGA     ACAG
                                ||||||||   ||||     ||||
                                GGCGTCGT   TGCT     TGTC
                                    CCG    CCA___
GAM2064  SLC21A3  3'  GCAGCACACCAACA       39573        AATGA
                                GCAGCAC    ACCAACA
                                |||||||    |||||||
                                CGTCGTG    TGGTTGT
                                  _____
GAM2064  SRM      5'  CCGCAGCACAACGGGACCA   17112           A_
                                CCGCAGCACAATG  ACCA
                                ||||||||||||  ||||
                                GGCGTCGTGTTGC  TGGT
                                      CC
GAM2064  USH3A    5'  GCAGGAATGAGCCAGTGCAG  38156      CAC    A   ACA
                                GCAG   AATGA CCA   CAG
                                ||||   ||||| |||   |||
                                CGTC   TTACT GGT   GTC
                                  C__    C   CAC
GAM2064  IMPG1    3'  GTTTCGCTGATTGCATTT    11457          CA
                                GTTTTGTTGAT  CATTT
                                ||||||||||  |||||
                                CAAAGCGACTA  GTAAA
                                      AC
GAM2064  MAS1     3'  TCTTCTGTATCACATTTAG   14367    G     TG
                                TC TTTTGT  ATCACATTTAG
                                || ||||||  ||||||||||
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                                AG AAGACA  TAGTGTAAATC
                                  _    __
GAM2064  RAD50    3'  CTCGTGATTACATTTAG     25065      TTTGTT   C
                                CTCGT     GAT ACATTTAG
                                |||||     ||| ||||||||
                                GAGCA     CTA TGTAAATC
                                  _______  A
GAM2064  SLC9A3R2 3'  GTTTTATTGCAATTATTTAGA  41533         ATCAC
                                GTTTTGTTG    ATTTAGA
                                |||||||||    |||||||
                                CAAAATAAC    TAAATCT
                                     GTTAA
GAM2064  TGM2     5'  GTTTTGTTTCAAGTTTAGA   21442        GA   CA
                                GTTTTGTT  TCA  TTTAGA
                                ||||||||  |||  ||||||
                                CAAAACAA  AGT  AAATCT
                                    __  TC
GAM2065  BTG3     3'  CAACATGACACCAACAC     27713      CAA  _
                                CAACA   TGA ACCAACAC
                                |||||   ||| ||||||||
                                GTTGT   ACT TGGTTGTG
                                  ____  G
GAM2065  JPH3     5'  TCCCGCAAACGGTGAAAAC   34023        C  AA   CC
                                TCCCGCAA AC  TGAA  AAC
                                |||||||| ||  ||||  |||
                                AGGGCGTT TG  ACTT  TTG
                                    _ CC   __
GAM2065  LHX3     5'  CCCCGCAATAGCCCCGAACC  31018        CACAA_
                                TCCCGCAA     TGAACC
                                ||||||||     ||||||
                                GGGGCGTT     GCTTGG
                                     ATCGGG
GAM2065  DAZL     3'  GCTGGGTTTAGATAAG      42776      ATCACA
                                GTTG     TTTAGATAAG
                                ||||     ||||||||||
                                CGAC     AAATCTATTC
                                  CC____
GAM2066  CDC7L1   3'  TACCTCATAACAGTAAAC    18603         AA   AAA
                                TACCTCATA  ACA   AAGC
                                |||||||||  |||   ||||
                                ATGGAGTAT  TGT   TTTG
                                    __  CA_
GAM2066  DLG5     3'  TACCTGTAAAACAAAGGACAGC 44463      CA       AA__
                                TACCT  TAAAACAAA   AGC
                                |||||  |||||||||   |||
                                ATGGA  ATTTTGTTT   TCG
                                  C_       CCTG
GAM2066  PDCL     3'  TACCTTGTTAAAACAAAAA   23933      CA_
                                TACCT   TAAAACAAAAA
                                |||||   ||||||||||
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                                ATGGA  ATTTTGTTTTT
                                   ACA
GAM2066 RP2     3' TCATAAATTCAAAAGCTAT  27935       ACAA
                                TCATAAA   AAAAGCTAT
                                |||||||   |||||||||
                                AGTATTT   TTTTCGATA
                                    AAG_
GAM2066 SCN1A   3' TGGTAATATAAACATGCATT  44820   A        GA
                                TG TAATATAAATAT  GCATT
                                || ||||||||||||  |||||
                                AC ATTATATTTGTA  CGTAA
                                 C         __
GAM2067 HTR1D   5' TATTAAACAAGACCGGACTATT 9265          TT  AA_
             T                   TATTAGACGAG  AC   ACTATTT
                                ||||||||||  ||   |||||||
                                ATAATTTGTTC  TG   TGATAAA
                                      __ GCC
GAM2068 NDRG2   5' TTGGCTGGATGCAGTGGG   32199       C  A   AATATA
                                TTGGCTGG AT CGG     GG
                                ||||||||  || |||     ||
                                AACCGACC TA GTC     CC
                                     _ C   AC_____
GAM2068 PLXNA2  3' TTGGCTGGCGTAGGGAGAGGA  36080        A  C   ATAT
                                TTGGCTGGC TA GGA    AGGA
                                |||||||||  || |||    ||||
                                AACCGACCG AT CCT    TCCT
                                     C  C   C___
GAM2069 WISP2   3' TGTGTAGGCAGGGAGTGGG   19311     A     AAA  C
                                TGT TAGGCG   AG GGG
                                |||  ||||||   ||  |||
                                ACA ATCCGT   TC CCC
                                  C     CCC  A
GAM2069 BAT4    5' GGTTAGGAAAGGCCCTCAG   37690        TC_
                                GGTTAGGAG   CCCTCAG
                                |||||||||   |||||||
                                CCAATCCTT   GGGAGTC
                                     TCC
GAM2069 PPP2R5A 5' GCCATCGCGGGTCCCCTC    26437    G   A_  A
                                GC GTT  GG GTCCCCTC
                                ||  |||  ||  ||||||||
                                CG TAG  CC CAGGGGAG
                                 G   CG  _
GAM2069 TAL1    5' TACGCGGTTGCCTCCTCA    17289        AGGA   C
                                TACGCGGTT    GTC CCTCA
                                |||||||||    ||| |||||
                                ATGCGCCAA    CGG GGAGT
                                     _____   A
GAM2070 CHC1L   3' AATGACTCCAAGTAAAAAGA   10420       ATAA
                                AATGATT    GAGTAAAAAGA
                                |||||||    ||||||||||
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                                TTACTGA   TTCATTTTTCT
                                   GG__
GAM2070  DMD     3'  AATGATTTAAAAATCAAAAAGA 19673       A     _
                                AATGATT TAAGAGT AAAAAGA
                                ||||||| ||||||| |||||||
                                TTACTAA ATTTTTA TTTTTCT
                                   _     G
GAM2070  GABPB1  3'  AATGACCTACAGAGTAAA   23523       ATA
                                AATGATT  AGAGTAAA
                                |||||||  ||||||||
                                TTACTGG  TCTCATTT
                                   ATG
GAM2070  HSPA8   5'  TAAATGATCATGAAACCAAAAA 27326         A  G
            GA                    TAAATGATTAT AGA TAAAAAGA
                                ||||||||||| ||| ||||||||
                                ATTTACTAGTA TTT GTTTTTCT
                                      C  G
GAM2070  ADK     3'  CATACCCTTGTACCC      27480     A    ATA
                                CATA CCTTGT  ACCC
                                |||| ||||||  ||||
                                GTAT GGAACA  TGGG
                                  G    ___
GAM2070  CAPN10  3'  CACAACCTTGTAGGTGCC   35762          TAA_
                                CATAACCTTGTA   CC
                                ||||||||||||   ||
                                GTGTTGGAACAT   GG
                                      CCAC
GAM2070  FBXL4   5'  CACAACCGCCGCAAGCCC   29132       _   TAA
                                CATAACC TTGTA  CCC
                                ||||||| |||||  |||
                                GTGTTGG GGCGT  GGG
                                   C    TC_
GAM2070  FCRH3   3'  CATACCCTGCAGCCC      38112     A     TAA
                                CATA CCTTGTA  CCC
                                |||| |||||||  |||
                                GTAT GGGACGT  GGG
                                  _     C__
GAM2070  LRP8    3'  CATACACTCACACAGACCC   37789     AC  TG  _
                                CATA  CT  TATA ACCC
                                ||||  ||  |||| ||||
                                GTAT  GA  GTGT TGGG
                                  GT  GT   C
GAM2070  PCDH12  5'  CACAACTTGTCACACCC    32450      C   ATA
                                CATAAC TTGT  ACCC
                                |||||| ||||  ||||
                                GTGTTG AACA  TGGG
                                   _  GTG
GAM2070  SMOH    3'  CATAACCTGGAACCC      24809       T TAT
                                CATAACCT G  AACCC
                                |||||||| |  |||||
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```
                                GTATTGGA C   TTGGG
                                     _ C__
GAM2071  ABH      3'  TCTCTGTTTTTGGCTTGTCTG  40742    C    CTCTA
                                TC CTGT     GTTTGTCTG
                                || ||||     |||||||||
                                AG GACA     CGAACAGAC
                                 A    AAAAC
GAM2071  CBFA2T2  3'  CCTTGTTTCTAGTTCAGTTC   22972    C  C       TCT
                                CC TGT TCTAGTTTG   GTTC
                                || ||| |||||||||   ||||
                                GG ACA AGATCAAGT   CAAG
                                 A  A       ____
GAM2071  COL4A3   3'  CTGTCTCTGGGTCATGTT    36379        AGTTT   _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC____   T
GAM2071  F7       3'  TCTCTGTCTCTGTCTCTCTCTG 33343    C       AG_   G
              TT                  TC CTGTCTCT   TTT TCTGTT
                                || ||||||||   ||| ||||||
                                AG GACAGAGA   AGA AGACAA
                                 A       CAG   G
GAM2071  HDAC4    3'  CCTGTTTCTGTCCAGTTTTGTT 25753       C____       GTC
                                CCTGT    TCTAGTTT   TGTT
                                |||||    ||||||||   ||||
                                GGACA    AGGTCAAA   ACAA
                                   AAGAC       ___
GAM2071  MEN1     5'  TGTTTGTTAGTTTGTCTGTT   39241     CTC_
                                TGT    TAGTTTGTCTGTT
                                |||    ||||||||||||
                                ACA    ATCAAACAGACAA
                                  AACA
GAM2071  NDRG1    3'  CCTGTTTTGCCTGT       40576       CTCTAG
                                CCTGT     TTTGTCTGT
                                |||||     |||||||||
                                GGACA     AAACGGACA
                                     _______
GAM2071  NKX3A    3'  TCACTGTCTCTGTTGT      26115    C       A   T
                                TC CTGTCTCT GTT GT
                                || |||||||| ||| ||
                                AG GACAGAGA CAA CA
                                 T       _   _
GAM2071  PACSIN1  3'  CTGTCTCTGCATACTTTGTT   45148         A  TTGTC_
                                CTGTCTCT GT     TGTT
                                |||||||| ||     ||||
                                GACAGAGA CG     ACAA
                                     _ TATGAA
GAM2071  PDCD2    3'  TCCCTGTCACTGGACACTTTTG 15143         T  AG_____
              T                   TCCCTGTC CT      TTTGT
                                |||||||| ||      |||||
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                                AGGGACAG GA      AAACA
                                    T  CCTGTGA
GAM2071  PDE4D    3'  TCCTTGTCTGTAATTTGT    43900     C    C
                                TCC TGTCT TAGTTTGT
                                ||| ||||| ||||||||
                                AGG ACAGA ATTAAACA
                                  A    C
GAM2071  SLC2A4   3'  TCTCTGCTCTGGTTTGTC    9800     C  T   A
                                TC CTG CTCT GTTTGTC
                                || ||| |||| |||||||
                                AG GAC GAGA CAAACAG
                                 A  _   C
GAM2072  AXIN1    3'  GCTGGAGGCAGGTGCAGTGCT  41382     AAA_  __
                                GCT   GCA  TGCAGTGCT
                                |||   |||  |||||||||
                                CGA   CGT  ACGTCACGA
                                  CCTC   CC
GAM2072  B3GALT2  5'  GCCAGAGCTAAAATGTAGTGCT 19111     A     GC   C
                                GCTA AGCTAAA  ATG AGTGCT
                                |||| |||||||  ||| ||||||
                                CGGT TCGATTT  TAC TCACGA
                                  C      __  A
GAM2072  EGFL5    5'  AGCTAAAGCTGAAGTGCT    44515        A  C
                                AGCTAAAGC TG AGTGCT
                                |||||||||| || ||||||
                                TCGATTTCG AC TCACGA
                                     _ T
GAM2072  FOXD2    5'  GCTAAAGCTCGGGCGTGC    20970        AAA  A
                                GCTAAAGCT   GC TGC
                                |||||||||   || |||
                                CGATTTCGA   CG ACG
                                     GCC  C
GAM2072  KCNAB1   5'  GCAAAGCTAATTGCACGGTGCT 41402    T      A_    CA
                                GC AAAGCTAA  GCATG  GTGCT
                                || ||||||||  |||||  |||||
                                CG TTTCGATT  CGTGC  CACGA
                                 _      AA    __
GAM2072  MSN      5'  GCTAGGACTGTCGGGCAGTGCT 41242     AA   AAAGCAT
                                GCTA  GCT     GCAGTGCT
                                ||||  |||     ||||||||
                                CGAT  TGA     CGTCACGA
                                  CC   CAGCC__
GAM2072  NAV2     3'  GCTGAGACTAAAGCAGGGATAG 41145     AAA       TGC__
            TG                    GCT   GCTAAAGCA    AGTG
                                |||   |||||||||    ||||
                                CGA   TGATTTCGT    TCAC
                                  CTC       CCCTA
GAM2072  SLC2A6   3'  GCTGTGGCTGGACAGCAGTGCT 32771     AAA   AAA   T
                                GCT   GCT   GCA GCAGTGCT
                                |||   |||   ||| ||||||||
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                                CGA  CGA  TGT CGTCACGA
                                  CAC  CC_  _
GAM2073  IDH3B   3'  GGGTGACCATGGTCCACT   27903    A  A      TT
                                GGG TGA CCATGGTCT  GCT
                                ||| ||| |||||||||  |||
                                CCC ACT GGTACCAGG  TGA
                                  _  _       __
GAM2073  SF1     3'  GGGTGGCTATGGCACCTTG   21570    A  AACC   _
                                GGG TG   ATGGT CTTTG
                                ||| ||   ||||| |||||
                                CCC AC   TACCG GGAAC
                                  _ CGA_   T
GAM2074  ASTN    3'  TGCATTGTGTGTGCACACGTGT 42955        _ TTTGT
            G                    TGCATTGTG GT    TGTGTG
                                |||||||||  ||    ||||||
                                ACGTAACAC CA    GCACAC
                                     A  CGTGT
GAM2074  PCP4    3'  TATGCGTGTGTGGATTGTGTG  26231     AT_   TTTT
                                TATGC   TGTGG   GTTGTGTG
                                |||||   |||||   ||||||||
                                ATACG   ACACC   TAACACAC
                                   CAC   _____
GAM2074  ALDH1B1  3'  TGATGTCACAGCATGTGT   8673    T   ___
                                C ATGTT   GCATGTGT
                                | |||||   ||||||||
                                A TACAG   CGTACACA
                                 C    TGT
GAM2074  ATP11A   3'  TTGTGTGCATGCATGTGT   44198    CTA  _
                                TTG   TGT TGCATGTGT
                                |||   ||| |||||||||
                                AAC   ACG ACGTACACA
                                  AC_   T
GAM2074  ATP7A    3'  TTGTAAACTTTGCATGTGT   6272     CT_  G
                                TTG   AT TTGCATGTGT
                                |||   || ||||||||||
                                AAC   TG AACGTACACA
                                  ATT  A
GAM2074  CLCN3    3'  TTGTTGTGGTGCATGTGT   12274    CTA  T
                                TTG   TG TGCATGTGT
                                |||   || |||||||||
                                AAC   AC ACGTACACA
                                  AAC  C
GAM2074  GPRK6    3'  TATTGCTGGGCACATGTGT   13273      AT  T
                                TATTGCT  GT GCATGTGT
                                |||||||  || ||||||||
                                ATAACGA  CG TGTACACA
                                     CC  _
GAM2074  SP3      3'  TTGTTATGTTTGCATATGT   44386    C    _
                                TTG TATGTT GCATGTGT
                                ||| |||||| ||||||||
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                                AAC ATACAA CGTATACA
                                  A     A
GAM2075 KAL1    5' CGGGTCGAGGGCGAGGGC    6870        TACAAA  T_
                                CGGGTCGAG     CG  GGC
                                |||||||||     ||  |||
                                GCCCAGCTC     GC  CCG
                                     CC_____  TC
GAM2075 DRIL1   3' TTCTGTTTTTCTGATG      23388          GAACA
                                TTCTGTTTTTC    GATG
                                ||||||||||     ||||
                                AAGACAAAAAG    CTAC
                                      A_____
GAM2075 PRKY    3' TCCTGTTTCTTCCAGATGT   15709         CGAA
                                TTCTGTTTTT   CAGATGT
                                ||||||||||   |||||||
                                AGGACAAAGA   GTCTACA
                                     AG__
GAM2075 SLC11A3  3' TGTTTTTCCACATACATGTAAA 31052       GA   G__
                                TGTTTTTC  ACA   ATGTAAA
                                ||||||||  |||   |||||||
                                ACAAAAAG  TGT   TACATTT
                                     G_   ATG
GAM2075 UBE2L3   3' TTCTGCTAATGAAGACAGATGT 17835       TTTCGA_
                                TTCTGTT      ACAGATGT
                                |||||||      ||||||||
                                AAGACGA      TGTCTACA
                                     TTACTTC
GAM2076 DAF     3' GTTCTATTTTCAAGAGGTGTA  8207          T   AC  A
                                GTTCTGTTTT CGA  AG TGTA
                                |||||||||| |||  || ||||
                                CAAGATAAAA GTT  TC ACAT
                                      _  C_  C
GAM2076 SLC11A3  3' GTTTTGTTTTTCCACATACATG 31050     C       GA   G__
           TAA                    GTT TGTTTTTC  ACA   ATGTAA
                                ||| ||||||||  |||   ||||||
                                CAA ACAAAAAG  TGT   TACATT
                                  A       G_   ATG
GAM2076 FGF2    3' TGTAATTGAAGAAAAACACA   12847         A     _
                                TGTAATTGAA AAAGAT CA
                                |||||||||| |||||| ||
                                ACATTAACTT TTTTTG GT
                                     C     T
GAM2077 TMEM1    3' TACATCAGTTAGTCTG      17598          ACACC  G
                                TACATCAGTTG    GT TG
                                ||||||||||     || ||
                                ATGTAGTCAAT    CA AC
                                      _____  G
GAM2077 XRCC2    3' CATCAGTCTACGTGTGT     24090         GACAC
                                CATCAGTT    CGTGTGT
                                ||||||||    |||||||
```

```
                                GTAGTCAG    GCACACA
                                    AT___
GAM2077  DISC1    3'  CAGTACTTATAGTACTGA    33029          ATTTC
                                CAGTACTTGTA    TTGA
                                ||||||||||    ||||
                                GTCATGAATAT    GACT
                                     CAT__
GAM2077  FBN1     3'  AGTACTTGTATTTGGAGAA    42047          A  CTT
                                AGTACTTGTA TTT   GAA
                                |||||||||| |||   |||
                                TCATGAACAT AAA   CTT
                                     _  CCT
GAM2077  FCMD     3'  CAGTACTTCTAATTTTCCT    27514          G    _
                                CAGTACTT TAATTT CTT
                                |||||||| |||||| |||
                                GTCATGAA ATTAAA GGA
                                    G     A
GAM2077  NEDD4    3'  ATGCTTGTAATTTCTAGAAACA 43098    A          T
                                GT CTTGTAATTTCT GAAACA
                                || ||||||||||| ||||||
                                TA GAACATTAAAGA CTTTGT
                                 C          T
GAM2077  NOV      3'  AATACTTGTACAATGAAA     14804          ATTTCT
                                AGTACTTGTA     TGAAA
                                ||||||||||     |||||
                                TTATGAACAT     ACTTT
                                     GTT___
GAM2077  PMP2     3'  AGTACTTGGTAATAAAAAGAAA 15418        _    TTCTT
           CA                     AGTACTTG TAAT     GAAACA
                                |||||||| ||||     ||||||
                                TCATGAAC ATTA     CTTTGT
                                    C    TTTTT
GAM2077  SOST     3'  CAGCACTTGTAGTTTTTCCCCC 36099          A____ TT  TG
           AA                     CAGTACTTGTA    T  CT  A
                                ||||||||||    |  ||  |
                                GTCGTGAACAT    A  GG  T
                                     CAAAA GG  GT
GAM2077  SRPX     3'  GTCATATAATTTTTTGAAACA  26710    ACT       C
                                GT   TGTAATTT TTGAAACA
                                ||   |||||||| ||||||||
                                CA   ATATTAAA AACTTTGT
                                 GT_       A
GAM2078  REV3L    5'  TGAGAGAAATCTTCCTCAGATA 16269       C    GA__    A
           TAT                    TGAGAG AATCT    TGGA TATAT
                                |||||| |||||    |||| |||||
                                ACTCTC TTAGA    GTCT ATATA
                                   T    AGGA   _
GAM2078  BCL2     3'  GTCCCATAATAATTTAAAA    8439        C   CAC
                                GTCCCA TGG   ATTTAAAA
                                |||||| |||   ||||||||
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                                CAGGGT ATT   TAAATTTT
                                   _  AT_
GAM2078 EHF     3' GTCCCTAACATTTAAAA     29117      ACTGGC
                                GTCCC     ACATTTAAAA
                                |||||     ||||||||||
                                CAGGG     TGTAAATTTT
                                  AT_____
GAM2078 MEN1    5' GTCTTGGCTCATTTAAA     39195     CCAC    A
                                GTC    TGGC CATTTAAA
                                |||    |||| ||||||||
                                CAG    ACCG GTAAATTT
                                  A___    A
GAM2078 PPARGC1  3' GTGTACTGCACATTTAAA    29955    CCC    G
                                GT   ACTG CACATTTAAA
                                ||   |||| ||||||||||
                                CA   TGAC GTGTAAATTT
                                 CA_   _
GAM2078 RBBP9    3' GTCTAAGCACATTTAAAA    43141     CCACT
                                GTC    GGCACATTTAAAA
                                |||    ||||||||||||
                                CAG    TCGTGTAAATTTT
                                  AT___
GAM2079 ARHGAP6  5' TTGCTGCAGTGTGGGGACA   30234        _ CACGC
                                TTGCTGCA TG    GACA
                                |||||||| ||    ||||
                                AACGACGT AC    CTGT
                                     C  ACCC_
GAM2079 HM13     5' TTGCTGCAGCAGGGACGC    43113        T _____
                                TTGCTGCA GC    ACGC
                                |||||||| ||    ||||
                                AACGACGT CG    TGCG
                                     _  TCCC
GAM2079 LPIN1    3' CATCACATGTGACAAACA    42633     G    C__
                                CAT CACG   GACAAACA
                                ||| ||||   ||||||||
                                GTA GTGT   CTGTTTGT
                                  _    ACA
GAM2079 NFIB     3' CTGTTGCATGCAGAGAGAACAC 24639     C       CGC  CA
                                TTG TGCATGCA   GA  AACAC
                                ||| ||||||||   ||  |||||
                                GAC ACGTACGT   CT  TTGTG
                                  A       CT_  C_
GAM2079 PCDH15   3' TTACTGCATCCACATGATAGAC 37511         G    C  CAA
             A                   TTGCTGCAT CACG GA   ACA
                                 |||||||||| |||| ||   |||
                                 AATGACGTA GTGT CT   TGT
                                      G    A  ATC
GAM2079 PIGN     3' TTGCTGCAGGTGCTCTCAACA  29556         __  ACG
                                TTGCTGCA  TGC   CGACA
                                ||||||||  |||   |||||
```

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                                AACGACGT  ACG   GTTGT
                                    CC   AGA
GAM2079  PUM2     3'  TTGCTGCAGTGACTGGGACA   31667        _  C  GC_
                                TTGCTGCA TG AC   GACA
                                |||||||| || ||   ||||
                                AACGACGT AC TG   CTGT
                                    C  _  ACC
GAM2079  SNX5     3'  TTGCTGTTGTTATAGTACAAAC 30867       CATGCACGCG
              AC                  TTGCTG        ACAAACAC
                                |||||||        ||||||||
                                AACGAC        TGTTTGTG
                                   AACAATATCA
GAM2080  HOXC11   3'  CAACGGTGTTCACTCGCCGT   41158        CCCC   _
                                CAACGGTG    TTTA TCGCCGT
                                ||||||||    |||| |||||||
                                GTTGCCAC    AAGT AGCGGCA
                                    _____   G
GAM2080  MEN1     5'  ACTGTGCCCCCGGGGCTGTA   39142    G       TTATC  C
                                AC GTGCCCCT     GC GTA
                                || |||||||||    || |||
                                TG CACGGGGG     CG CAT
                                 A       CCC__  A
GAM2080  MPO      3'  CAGCGGTGCCTTTATTATCA   7001     A      CCT_
                                CA CGGTGCC    TTATCG
                                || |||||||    ||||||
                                GT GCCACGG    AATAGT
                                 C      AAAT
GAM2080  CA3      5'  GCGAAGGGGCACCCACGC    23212      TAACA
                                GCGA    GCACCCACGC
                                ||||    ||||||||||
                                CGCT    CGTGGGTGCG
                                  TCCC_
GAM2080  CADPS    3'  GCTGATAACAGGGACACGC   42194    _      CACC
                                GC GATAACAG    CACGC
                                || |||||||||   |||||
                                CG CTATTGTC    GTGCG
                                 A       CCT_
GAM2080  CTNND2   3'  AACGATAACCCTTACGC     10631       ACAGC   __
                                AGCGATA    ACCC  ACGC
                                |||||||    ||||  ||||
                                TTGCTAT    TGGG  TGCG
                                    _____    AA
GAM2080  ITGAM    3'  AGCGGCTTACCCACGC      43508      ATAACA  __
                                AGCG     GC  ACCCACGC
                                ||||     ||  |||||||||
                                TCGC     CG  TGGGTGCG
                                  _______  AA
GAM2080  MEN1     5'  AGAGATAACAACAGACG     39143    C        CCC
                                AG GATAACAGCA   ACG
                                || ||||||||||   |||
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                                TC CTATTGTTGT   TGC
                                 T        C__
GAM2080  PX19     5'  AGCGGGCTCAGCACCCGCGC   29873     ATAA      A
                                AGCG    CAGCACCC CGC
                                ||||    |||||||| |||
                                TCGC    GTCGTGGG GCG
                                  CCGA       C
GAM2080  ST5      3'  AGCGAAACTTCATCCATGC    24040      T   AG  C   C
                                AGCGA AAC  CA CCA GC
                                ||||| |||  || ||| ||
                                TCGCT TTG  GT GGT CG
                                   _   AA  A   A
GAM2080  TSPY     3'  AGGACAATAGTACCCACGC    17701    C    C  C
                                AG GATAA AG ACCCACGC
                                || ||||| || ||||||||
                                TC CTGTT TC TGGGTGCG
                                 _    A  A
GAM2081  ANKRA2   3'  TATACAGTAAAACATAGTTA   35755        T    ATT
                                TATACAGTA AATG   TAGTTA
                                ||||||||| ||||   ||||||
                                ATATGTCAT TTGT   ATCAAT
                                      T   ___
GAM2081  BACH2    3'  TATACAGTATACTTGAGTTA   34798         A_   T
                                TATACAGTATA  TGA TTA
                                ||||||||||  ||| |||
                                ATATGTCATAT  ACT AAT
                                       GA   C
GAM2081  CAV2     3'  TATACAGTAAAATGAAACATC  10292        T    TTTA
                                TATACAGTA AATGA    GTT
                                ||||||||| |||||    |||
                                ATATGTCAT TTACT    TAG
                                      T    TTG_
GAM2081  CNTN3    3'  TATACAGTATATGCGGACCT   42485         AT__
                                TATACAGTATA    GATTT
                                ||||||||||    |||||
                                ATATGTCATAT    CTGGA
                                       ACGC
GAM2081  MYCN     3'  TATAAGTATCAAATTTAGTTA  23916     C    AAT
                                TATA AGTAT   GATTTAGTTA
                                |||| |||||   ||||||||||
                                ATAT TCATA   TTAAATCAAT
                                   _    GT_
GAM2081  MYO1E    3'  TATACAGTATATGATCCTGT   22659         A    TA
                                TATACAGTATA TGATT  GT
                                |||||||||| |||||  ||
                                ATATGTCATAT ACTAG  CA
                                       _    GA
GAM2081  PPP4R1   3'  TACAGTATGTGAAGAAGTT   23075        AA   TTT
                                TACAGTAT  TGA   AGTT
                                ||||||||  |||   ||||
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                                ATGTCATA  ACT   TCAA
                                    C_   TCT
GAM2081  ROCK2    3'  TACACAGTATAATGGTCA    42359          ATTTA
                                TATACAGTATAATG    GTTA
                                ||||||||||||||    ||||
                                ATGTGTCATATTAC    CAGT
                                                  _____
GAM2081  TNFSF11  3'  TACAGTATAAGATAACATTTAC 37454         T   TTAG_
                                TACAGTATAA GAT    TTAC
                                |||||||||| |||    ||||
                                ATGTCATATT CTA    AATG
                                      _  TTGTA
GAM2081  HS3ST3A1 3'  TTGAAAGCACTATGAAAACTGT 25811     TT___
                                TTGA    CTATGAAAACTGT
                                ||||    ||||||||||||
                                AACT    GATACTTTTGACA
                                  TTCGT
GAM2082  ADD1     3'  GGGCCCACACAAGCTTGCCT   30524    A     __ C
                                GGG CCCGCGC  GC TGCCT
                                ||| |||||||  || |||||
                                CCC GGGTGTG  CG ACGGA
                                  _     TT  A
GAM2082  ADRA2B   3'  CGGGACCGCGAGTGCCT    8648       CGC   CC
                                CGGGACC   GCG  TGCCT
                                |||||||   |||  |||||
                                GCCCTGG   CGC  ACGGA
                                    ___   TC
GAM2082  AXIN1    3'  GGGACCCCCTACCTGCCT    41386      GCGC
                                GGGACCC    GCCTGCCT
                                |||||||    ||||||||
                                CCCTGGG    TGGACGGA
                                   GGA_
GAM2082  BGN      3'  CGGGCCTTGCGCCCACCT    11816     A  CGC    TG
                                CGGG CC   GCGCC  CCT
                                |||| ||   |||||  |||
                                GCCC GG   CGCGG  GGA
                                  _  AA_    GT
GAM2082  BLK      3'  CGGGACCCAGTCTGGCT     11844        CGCGC   C
                                CGGGACCCG     CTG CT
                                |||||||||     ||| ||
                                GCCCTGGGT     GAC GA
                                     CA___   C
GAM2082  C8orf1   5'  CGGGACCCGCCCACCACGC   20273         G   _
                                CGGGACCCGC CGCC TGC
                                |||||||||| |||| |||
                                GCCCTGGGCG GTGG GCG
                                      G   T
GAM2082  CACNA1C  3'  CGGGACCCTCGCCGCCT    8750         GCG   T
                                CGGGACCC   CGCC GCCT
                                ||||||||   |||| ||||
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                                GCCCTGGG  GCGG CGGA
                                    A__   _
GAM2082  CCND1    3'  CGGTGGCGCCCGCCTGCCT   38204    GACC  G
                                CGG   CGC CGCCTGCCT
                                |||   ||| |||||||||
                                GCC   GCG GCGGACGGA
                                  ACC_  G
GAM2082  CDC34    5'  CGGGGCCGCCGCCTGCCT   20352    AC   G
                                CGGG  CCGC CGCCTGCCT
                                ||||  |||| |||||||||
                                GCCC  GGCG GCGGACGGA
                                  C_   _
GAM2082  CDH20    3'  GGACGCGCGCCTGCCT     36683    CC
                                GGAC  GCGCGCCTGCCT
                                ||||  ||||||||||||
                                CCTG  CGCGCGGACGGA

                                  __
GAM2082  CNP      5'  CGGGGCCGCCCGCC       37556    ACCC  G
                                CGGG   GC CGCCTGCC
                                ||||   || ||||||||
                                GCCC   CG GCGGGCGG

                                  ____  _
GAM2082  COL4A4   5'  GGATCCGCGCCCACCT     6402     C    G  T
                                GGA CCGCGC CC GCCT
                                ||| |||||| || ||||
                                CCT GGCGCG GG TGGA
                                  A     _  _
GAM2082  DNASE1   5'  CAGGACACGCCTGCC      23352     CCGC
                                CGGGAC   GCGCCTGCC
                                ||||||   |||||||||
                                GTCCTG   TGCGGACGG

                                  ____
GAM2082  DPH2L1   5'  CAGGACCCGGATTGCTGCCT  10724       CGCGC
                                CGGGACCCG    CTGCCT
                                |||||||||    ||||||
                                GTCCTGGGC    GACGGA
                                     CTAAC
GAM2082  DYT1     5'  GGACCCGCGCCACCCTGC    6475        G__
                                GGACCCGCGC   CCTGC
                                ||||||||||   |||||
                                CCTGGGCGCG   GGACG
                                     GTG
GAM2082  ENC1     5'  CAGGACCCGCAGAGCGTCT   18860        ___  C
                                CGGGACCCGC   GCG CT
                                ||||||||||   ||| ||
                                GTCCTGGGCG   CGC GA
                                     TCT   A
GAM2082  FASN     3'  CGGGACCCACACGCTGCCT   19935          C
                                CGGGACCCGCGCGC TGCCT
                                |||||||||||||| |||||
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                                GCCCTGGGTGTGCG ACGGA

                                          _
GAM2082  GGA3     3'  CAGGGCAGCCTGCC       39783      ACCC   C
                                CGGG    GCG GCCTGCC
                                ||||    ||| |||||||
                                GTCC    CGT CGGACGG

                                  _____  _
GAM2082  GJA4     5'  CGGGCCTCCGTCGCCTGCCT   40437      A  CG  _
                                CGGG CC  CG CGCCTGCCT
                                |||| ||  || |||||||||
                                GCCC GG  GC GCGGACGGA
                                  _ AG  A
GAM2082  GRLF1    3'  GGAGCCATTGCCTGCCT     44231     C   CGC
                                GGA CCG   GCCTGCCT
                                ||| |||   ||||||||
                                CCT GGT   CGGACGGA
                                  C   AA_
GAM2082  HAS3     5'  CGGGACCCCCCTGCC       39771        GCGCG
                                CGGGACCC    CCTGCC
                                ||||||||    ||||||
                                GCCCTGGG    GGACGG
                                    G____
GAM2082  HDAC4    3'  CGGGACCCGCCAGAGTGTGC   25760          G  CC___
                                CGGGACCCGC CG    TGC
                                |||||||||| ||    |||
                                GCCCTGGGCG GT    ACG
                                      _ CTCAC
GAM2082  HNRPA2B1 5'  CGGGACCCGGCGCTGC      36309         C   C
                                CGGGACCCG GCGC TGC
                                ||||||||| |||| |||
                                GCCCTGGGC CGCG ACG

                                      _   _
GAM2082  HNRPDL   5'  CGGGCCCCGCGCGGCCT     24172      A       CCT
                                CGGG CCCGCGCG   GCCT
                                |||| ||||||||   ||||
                                GCCC GGGCGCGC   CGGA
                                  G       ___
GAM2082  HTRA3    3'  CGCGGCCTCCTGCCTGCCT   44827    _  A  CGCGC
                                CG GG CC    GCCTGCCT
                                || || ||    ||||||||
                                GC CC GG    CGGACGGA
                                 G  _  AGGA_
GAM2082  HUNK     5'  CGCGGCCCGCGCGGCTCCT   31065    _  A       C  G
                                CG GG CCCGCGCG CT CCT
                                || || |||||||| || |||
                                GC CC GGGCGCGC GA GGA
                                 G  _       C  _
GAM2082  ITGA4    5'  CGGGACACACCTGC        9422         CCGC
                                CGGGAC   GCGCCTGC
                                ||||||   ||||||||
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                              GCCCTG   TGTGGACG
                                   ____
GAM2082 KCNN4    3' GGGACCCAGGAGTCCTGCCT  13926       CGCG_
                              GGGACCCG    CCTGCCT
                              ||||||||    |||||||
                              CCCTGGGT    GGACGGA
                                   CCTCA
GAM2082 LASS1    3' CGGGGTCCGCGCCCGCGCCC  34602     AC    G _
                              CGGG  CCGCGC CC TGCCT
                              ||||  |||||| || |||||
                              GCCC  GGCGCG GG GCGGG
                                CA     _  C
GAM2082 LMO6     3' CAGGACGGCCTGCC       26041       CCGC C
                              CGGGAC    G GCCTGCC
                              ||||||    | |||||||
                              GTCCTG    C CGGACGG
                                   _____ _
GAM2082 LYL1     5' GGGGCCCACCTCTGCCT     24580     A    GCGC
                              GGG CCCGC    CTGCCT
                              ||| |||||    ||||||
                              CCC GGGTG    GACGGA
                                C    GA__
GAM2082 MDFI     5' CGGGGCCCGCCATGCGCGCCT 24617      A    ___    CT
                              CGGG CCCGC   GCGC  GCCT
                              |||| |||||   ||||  ||||
                              GCCC GGGCG   CGCG  CGGA
                                C    GTA   __
GAM2082 MGAT4B   3' GGGGGCCGCCTGCCT      38271     ACCC  G
                              GGG    GC CGCCTGCCT
                              |||    || |||||||||
                              CCC    CG GCGGACGGA
                                C___  _
GAM2082 MMP19    3' CAGGGCAGTGCCTGCCT     35581      ACCC   C_
                              CGGG    GCG  GCCTGCCT
                              ||||    |||  ||||||||
                              GTCC    CGT  CGGACGGA
                                   ____   CA
GAM2082 MTA1L1   5' GGGGCCCGCGCAGCCGGCACCT 21892     A      _   T__
                              GGG CCCGCGC GCC   GCCT
                              ||| ||||||| |||   ||||
                              CCC GGGCGCG CGG   TGGA
                                C      T   CCG
GAM2082 NPTX1    3' CAGGACGGCCTGCC        14832       CCGC C
                              CGGGAC    G GCCTGCC
                              ||||||    | |||||||
                              GTCCTG    C CGGACGG
                                   _____ _
GAM2082 P2RY2    5' GGGGCCACGCCCAGCCT     15016     AC     G  T
                              GGG  CCGCGC CC GCCT
                              |||  |||||| || ||||
```

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                                CCC  GGTGCG GG CGGA
                                  C_     _ T
GAM2082  PARN     5'  CGGGCCCGCGCCCGCCT     15093      A    GC
                                CGGG CCCGC  GCCTGCCT
                                |||| |||||  ||||||||
                                GCCC GGGCG  CGGGCGGA
                                  _    __
GAM2082  PIK3R2   3'  CGGGACCCCGGGGGACCT    22746        G  CGCCT
                                CGGGACCC CG    GCCT
                                |||||||| ||    ||||
                                GCCCTGGG GC    TGGA
                                    _ CCCC_
GAM2082  PITPN    5'  CGCGGCCCGCCCGGCCT     26333    _ A    G  CCT
                                CG GG CCCGC CG   GCCT
                                || || ||||| ||   ||||
                                GC CC GGGCG GC   CGGA
                                 G _    G ___
GAM2082  PPP2R2B  5'  AGGATGCTGCGCCTGCCT    21325     CCC  _
                                GGGA   GC GCGCCTGCCT
                                ||||   || ||||||||||
                                TCCT   CG CGCGGACGGA
                                  A__  A
GAM2082  PPP2R5A  5'  CGGCGCCCGCCAACGCCT    26434     GA    __
                                CGG  CCCGC  GCGCCT
                                |||  |||||  ||||||
                                GCC  GGGCG  TGCGGA
                                  GC    GT
GAM2082  PROK1    3'  GGGCTCCCTACACCTGCCT   37101     A_   GC
                                GGG  CCC  GCGCCTGCCT
                                |||  |||  ||||||||||
                                CCC  GGG  TGTGGACGGA
                                  GA  A_
GAM2082  PTGER4   5'  GGACCCGCCTCCAACCTGC   9654         GC___
                                GGACCCGC    GCCTGC
                                ||||||||    ||||||
                                CCTGGGCG    TGGACG
                                    GAGGT
GAM2082  PTPN14   5'  CGGACGCCGCCTGCCT      23997     ACC  G
                                CGGG   CGC CGCCTGCCT
                                ||||   ||| |||||||||
                                GCCT   GCG GCGGACGGA
                                  ___  _
GAM2082  RGS6     3'  GGAGCGCCGCCGCCTGCCT   20190     C__   G
                                GGA   CCGC CGCCTGCCT
                                |||   |||| |||||||||
                                CCT   GGCG GCGGACGGA
                                  CGC   _
GAM2082  ROCK2    5'  CGGGCCCACCGCCTGCCT    42356     A    G
                                CGGG CCCGC CGCCTGCCT
                                |||| ||||| |||||||||
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                                GCCC GGGTG GCGGACGGA
                                  _    _
GAM2082 RPH3AL   3' GGGGGCACTGCGCCTGCCT   28104    ACC  _
                                GGG   CGC GCGCCTGCCT
                                |||   ||| ||||||||||
                                CCC   GTG CGCGGACGGA
                                  CC_   A
GAM2082 SCN4A    3' CAGGACCCAGCCTGTCT     7319        CGC    C
                                CGGGACCCG   GCCTG CT
                                |||||||||   ||||| ||
                                GTCCTGGGT   CGGAC GA
                                     ___    A
GAM2082 SLC18A3  5' CGGGACCCGCGGCTGC      16828         C  C
                                CGGGACCCGCG GC TGC
                                |||||||||| || |||
                                GCCCTGGGCGC CG ACG
                                     _ _
GAM2082 SMARCD2  5' CGGGAACCCGCCCGCGCCT   16916      _    G   CT
                                CGGGA CCCGC CGC  GCCT
                                ||||| ||||| |||  ||||
                                GCCCT GGGCG GCG  CGGA
                                   T    G  __
GAM2082 SORL1    5' CGGGACCGCGCGCGCCGC    16971       _      T
                                CGGGACC CGCGCGCC GC
                                ||||||| |||||||| ||
                                GCCCTGG GCGCGCGG CG
                                    C      _
GAM2082 SURF5    3' GGGACCCAGCACGGGGCCT   39507       _    CCT
                                GGGACCC GCGCG   GCCT
                                ||||||| |||||   ||||
                                CCCTGGG CGTGC   CGGA
                                   T    CC_
GAM2082 TAF1C    3' CGGCACCTCCAGCCTGCCT   24989     G   CG  C
                                CGG ACC  CG GCCTGCCT
                                ||| |||  || ||||||||
                                GCC TGG  GT CGGACGGA
                                  G   AG  _
GAM2082 TEM7     5' CGGACCTGCCCCCGGCCTGC  33806     A___   G  C
                                CGGG    CCC CG GCCTGC
                                ||||    ||| || ||||||
                                GCCT    GGG GC CGGACG
                                  GGAC   G  _
GAM2082 TNFRSF6B 3' GGGCCCCGCCTGCC       32360     A   GCG
                                GGG CCC   CGCCTGCC
                                ||| |||   ||||||||
                                CCC GGG   GCGGACGG
                                  _   ___
GAM2082 XRCC3    3' AGGAGGAGCCGCCTGCCT    24099      CCC  G
                                GGGA   GC CGCCTGCCT
                                ||||   || |||||||||
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                                TCCT   CG GCGGACGGA
                                  CCT  _
GAM2082  CDS1     5'  CGTCTCCACGCAGAGGCC    10396      C       A_____
                                CGTC CCACGCAG      CC
                                |||| ||||||||      ||
                                GCAG GGTGCGTC      GG
                                  A       TCCIII
GAM2082  EPM2A    5'  GTGCCCCGCAACCCCGCGGG   24972    C   A     A
                                GT CCC CGCAG CCCGCGGG
                                || ||| ||||| ||||||||
                                CA GGG GCGTT GGGCGCCC
                                 C   _    G
GAM2082  FBLN2    5'  CTCTCCTGTAAGACCCGCGGG  12801     G   CCACGC
                                CTC TCC     AGACCCGCGGG
                                ||| |||     ||||||||||
                                GAG AGG     TCTGGGCGCCC
                                  _   ACAT__
GAM2082  SIRT7    3'  TCGTTCTCCCTAGACCCGTGGG 32416      _ _   ACGC      C
                                TCGT C CCC    AGACCCG GGG
                                |||| | |||    ||||||| |||
                                AGCA G GGG    TCTGGGC CCC
                                  A A   A___      A
GAM2082  STAT5B   5'  CTCCTCCCGCCGGGGCCCGCGG 29719     G    CA  CAGA
            G                    CTC TCCC  CG    CCCGCGGG
                                ||| ||||  ||    ||||||||
                                GAG AGGG  GC    GGGCGCCC
                                  G    CG  CCC_
GAM2083  ATP11B   3'  TTATATGCACGTTTTATAAG   44313          AGCAGC
                                TTATGTGCACG      ATAAG
                                ||||||||||      |||||
                                AATATACGTGC      TATTC
                                      AAAA__
GAM2083  DTNA     3'  TGTGTATAACAGCAGCAT     37376      C___  G
                                TGTG    AC AGCAGCAT
                                ||||    || ||||||||
                                ACAC    TG TCGTCGTA
                                  ATAT  _
GAM2083  WHN      3'  TGTGCACGAGGGCTTAAG     18755          CA  A
                                TGTGCACGAG  GC TAAG
                                |||||||||  || ||||
                                ACACGTGCTC  CG ATTC
                                      C_  A
GAM2083  ATP2B4   5'  AAACAGGATGTGCATGT     43193          CACAA
                                AAGCAGGATG     ATGT
                                ||||||||||     ||||
                                TTTGTCCTAC     TACA
                                      ACG__
GAM2083  BACE     3'  AGTAGGATGCAGTGGGTAT   39950    C       CAAAT
                                AG AGGATGCA     GTAT
                                || ||||||||     ||||
```

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                              TC TCCTACGT    CATA
                               A      CACC_
GAM2083 CACNA1D  3' AACCAGGACGCAGTGTAT   8762    G      CAAA
                              AA CAGGATGCA   TGTAT
                              || |||||||||   |||||
                              TT GTCCTGCGT   ACATA
                               G      C___
GAM2083 CENTD1   3' CAGGTAGCCCCCAAATGTAT  40135    AT  A__
                              CAGG  GC   CAAATGTAT
                              ||||  ||   |||||||||
                              GTCC  CG   GTTTACATA
                                AT  GGG
GAM2083 GLP1R    3' AAGCAGGATGTATGT      13137        CACAA
                              AAGCAGGATG    ATGT
                              ||||||||||    ||||
                              TTCGTCCTAC    TACA
                                   A____
GAM2083 GLS      3' ACAGGATAAAATGTA      31373       CAC
                              GCAGGATG   AAATGTA
                              ||||||||   |||||||
                              TGTCCTAT   TTTACAT
                                   ___
GAM2083 GPR81    3' AGAAGGATGCAGTTCATGT  37187   C      CAA_
                              AG AGGATGCA    ATGT
                              || ||||||||    ||||
                              TC TCCTACGT    TACA
                               T      CAAG
GAM2083 MAPRE2   3' AAGCACCACAAATGT      30687      GGATG
                              AAGCA    CACAAATGT
                              |||||    |||||||||
                              TTCGT    GTGTTTACA
                                 G____
GAM2083 PACE4    3' GCAGAGGCCAAATGTAT     15049      AT  A
                              GCAGG  GC CAAATGTAT
                              |||||  || |||||||||
                              CGTCT  CG GTTTACATA
                                 C_  _
GAM2083 PCDHB7   3' AAGCAGGACTTTTGGTGTAT  33201        GCACAAA
                              AAGCAGGAT      TGTAT
                              |||||||||      |||||
                              TTCGTCCTG      ACATA
                                   AAAACC_
GAM2083 RAD50    5' GGATCGTGTACAAATGTAT   39437    ___  C
                              GGA   TG ACAAATGTAT
                              |||   || ||||||||||
                              CCT   AC TGTTTACATA
                                AGC  A
GAM2083 RUNX3    3' AAACAGGTTACAGACAGGTGT 20315       A  __  AA
                              AAGCAGG TGC  ACA  TGT
                              ||||||| |||  |||  |||
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                                TTTGTCC ATG  TGT  ACA
                                    A   TC   CC
GAM2083  SLC6A12  3'  AAGCAGGATGGCAAATG     16795          CA
                                AAGCAGGATG  CAAATG
                                ||||||||||  ||||||
                                TTCGTCCTAC  GTTTAC
                                     C_
GAM2083  SLC7A6   3'  AAGAGGATGCAGCCTGATGT   19582     C       CAA__
                                AAG AGGATGCA     ATGT
                                ||| ||||||||     ||||
                                TTC TCCTACGT     TACA
                                  _      CGGAC
GAM2083  SRP14    3'  AAGCAGGAAATGTA        17115         TGCACA
                                AAGCAGGA     AATGTA
                                ||||||||     ||||||
                                TTCGTCCT     TTACAT
                                     _______
GAM2083  TAL1     5'  AAGAGGATGCACACCCG     17275     C         AA
                                AAG AGGATGCACA  TG
                                ||| ||||||||||  ||
                                TTC TCCTACGTGT  GC
                                  _        GG
GAM2083  TEM5     3'  GCTGGACGGAAATGTAT     37234     A     CAC
                                GC GGATG   AAATGTAT
                                || |||||   ||||||||
                                CG CCTGC   TTTACATA
                                 A    C__
GAM2083  TPX1     5'  AGCAGGATGAAATAT       17664          CAC
                                AGCAGGATG   AAATGT
                                |||||||||   ||||||
                                TCGTCCTAC   TTTATA
                                     ____
GAM2083  USP5     3'  AGAGGATGCACAAAGC      18501     C          T
                                AG AGGATGCACAAA GT
                                || ||||||||||| ||
                                TC TCCTACGTGTTT CG
                                  _         _
GAM2083  ZNF36    3'  AAGCAGGATGTTGGCCAAA   45286          CA___
                                AAGCAGGATG     CAAA
                                ||||||||||     ||||
                                TTCGTCCTAC     GTTT
                                     AACCG
GAM2084  ALDH3B2  3'  TGTGCAGTGGAGTGATG     8686      TA       GT
                                TGT  CAGTGGAG  GTG
                                |||  ||||||||  |||
                                ACA  GTCACCTC  TAC
                                  C_       AC
GAM2084  ARHD     3'  TGTTGCAGTGGAGTTCGGC   31025      A       GTG
                                TGTT CAGTGGAG   TGGT
                                |||| ||||||||   ||||
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                                ACAA GTCACCTC   GCCG
                                  C       AA_
GAM2084  ARHG     5'  TGCTGTAGTGGAGGCAGTG   11688      AC       _
                                TGTT  AGTGGAGGT GTG
                                ||||  ||||||||| |||
                                ACGA  TCACCTCCG CAC
                                  CA        T
GAM2084  KIF5C    3'  TGTTACATGGACTATAGTAC   21168       G    GG
                                TGTTACA TGGA  TGTGGTAC
                                ||||||| ||||  ||||||||
                                ACAATGT ACCT  ATATCATG
                                    _   G_
GAM2084  LY64     3'  TGCTGTAGTGGGGGTGGGT   24571      AC    A   T
                                TGTT  AGTGG GGTG GGT
                                ||||  ||||| |||| |||
                                ACGA  TCACC CCAC CCA
                                  CA    C   _
GAM2084  PARK2    3'  TTACAGTGGAGCCAAATG    30382         G ___
                                TTACAGTGGAG T  GTG
                                |||||||||||  |  |||
                                AATGTCACCTC G  TAC
                                      G TT
GAM2084  PML      3'  TGTGACAGTGGAGGCAGGGC   37746     T         T
                                TGT ACAGTGGAGGTG GGT
                                ||| ||||||||||| |||
                                ACA TGTCACCTCCGT CCG
                                  C          C
GAM2084  PRY      5'  TGTCTGTTTCTGGTGTGGT    41258     ACA  GGA_
                                TGTT   GT    GGTGTGGT
                                ||||   ||    ||||||||
                                ACAG   CA    CCACACCA
                                  A__  AAGA
GAM2084  PTPRA    3'  TTACAGTGCATGGTGGTAC    38920        GAGGT
                                TTACAGTG    GTGGTAC
                                ||||||||    |||||||
                                AATGTCAC    CACCATG
                                     GTAC_
GAM2084  SOX10    3'  GTTGTAGTGGAGGAGGAC    28013     AC       TGT  T
                                GTT  AGTGGAGG   GG AC
                                |||  ||||||||   || ||
                                CAA  TCACCTCC   CC TG
                                  CA       T__  _
GAM2084  ZNF10    3'  TGTTGTATGTGGGCATGGT    31745     ACA   GA
                                TGTT   GTG  GGTGTGGT
                                ||||   |||  ||||||||
                                ACAA   TAC  CCGTACCA
                                  CA_   AC
GAM2084  ACTB     3'  AACCAAAACAAAACAAAAAAA  9922          TGTTT
                                AGCCAAAACAA    TAAAAAAA
                                ||||||||||    ||||||||
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                                TTGGTTTTGTT    GTTTTTTT
                                      TT___
GAM2084  ANKH     3'  ACCAAAACAAAACAAAAAA   38309         TGTTT
                                GCCAAAACAA    TAAAAAA
                                ||||||||||    |||||||
                                TGGTTTTGTT    GTTTTTT
                                     TT___
GAM2084  DXYS155E  3'  AGCAAAACAGCTTCTTAAAAAA 22942    C     ATG
            A                    AGC AAAACA   TTTTAAAAAAA
                                ||| ||||||   ||||||||||||
                                TCG TTTTGT   AGAATTTTTTT
                                  _     CGA
GAM2084  EIF4E    3'  AGCAAAGACAATGCTGTAAAAA 12691    C  A      T
                                AGC AA ACAATGTT TAAAAA
                                ||| || |||||||| ||||||
                                TCG TT TGTTACGA ATTTTT
                                  T  C       C
GAM2084  ENTPD3   3'  AGCCAAGGGATGCCTCAA    10348      AACA
                                AGCCAA    ATGTTTTAA
                                ||||||    |||||||||
                                TCGGTT    TACGGAGTT
                                   CCC_
GAM2084  IDS      3'  AGCCGTAACTGTTTTAAAAA   25957     AA   AA
                                AGCC  AAC  TGTTTTAAAAA
                                ||||  |||  ||||||||||
                                TCGG  TTG  ACAAAATTTTT
                                  CA  __
GAM2084  MAD2L1   3'  ACCAAAACATCTGATTTA    14309        A_  T
                                GCCAAAACA  TG TTTA
                                |||||||||  || ||||
                                TGGTTTTGT  AC AAAT
                                     AG  T
GAM2084  MTMR8    3'  AGTCCAAAACTATTTTAAA   31748    _     AA
                                AG CCAAAAC  TGTTTTAAA
                                || |||||||  |||||||||
                                TC GGTTTTG  ATAAAATTT
                                 A      __
GAM2084  PDCL     3'  AACCAAAAAGTTTTAAAAAAA  23930        CAAT
                                AGCCAAAA    GTTTTAAAAAAA
                                ||||||||    ||||||||||||
                                TTGGTTTT    CAAAATTTTTTT
                                     T___
GAM2084  PIGA     3'  GCCAAAAAATGCCCAGAAAA   33832       C      TA
                                GCCAAAA AATGTTT  AAAA
                                ||||||| |||||||  ||||
                                CGGTTTT TTACGGG  TTTT
                                   _      TC
GAM2084  PRPSAP2  3'  GCCAAAACACAAAGTTTTAGAA 15737         AT__     A
            AAA                   GCCAAAACA    GTTTTA AAAAA
                                ||||||||||    |||||| |||||
```

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                                CGGTTTTGT   CAAAAT TTTTT
                                     GTTT    C
GAM2084  PTPRO    5'  AGCAAAGACAAAGTTTTAAAAA 36220    C  A   T
              AA                   AGC AA ACAA GTTTTAAAAAAA
                                   ||| || |||| ||||||||||||
                                   TCG TT TGTT CAAAATTTTTTT
                                     T  C   T
GAM2084  SORBS1   3'  CCAAAATAATGAAATTAAAAA  31704      C   TT_
                                   CCAAAA AATG   TTAAAAA
                                   |||||| ||||   |||||||
                                   GGTTTT TTAC   AATTTTT
                                      A   TTT
GAM2084  SULT1C1  3'  AGCAAGACCCTATTTTAAAAAA 9837     C  A  AA
              A                    AGC AA AC  TGTTTTAAAAAAA
                                   ||| || ||  ||||||||||||
                                   TCG TT TG  ATAAAATTTTTTT
                                    _  C  GG
GAM2084  WHSC1L1  3'  AGCCAAAACAATAGTGCAAAAA 32818           TTT
                                   AGCCAAAACAATG   TAAAAA
                                   ||||||||||||   ||||||
                                   TCGGTTTTGTTAT   GTTTTT
                                          CAC
GAM2084  ZNF264   3'  AGCAAAACAATGTCCAAAAA   18265    C        TT
                                   AGC AAAACAATGTT  AAAA
                                   ||| ||||||||||  ||||
                                   TCG TTTTGTTACAG  TTTT
                                    _         GT
GAM2085  DOC1     5'  CGCTGCGAGCCGACTGTG    40480        A  _ _
                                   CGCTGCGAG CG C GTG
                                   ||||||||| || | |||
                                   GCGACGCTC GC G CAC
                                        G  T A
GAM2085  HNRPDL   5'  CCGCCGCGCGCACGCGTG    24171        AG_
                                   CCGCTGCG   ACGCGTG
                                   ||||||||   |||||||
                                   GGCGGCGC   TGCGCAC
                                        GCG
GAM2085  KCNS3    5'  CGCGTGGGCGGACGCGTG    13933     T___   A
                                   CGC    GCG GACGCGTG
                                   |||    ||| ||||||||
                                   GCG    CGC CTGCGCAC
                                     CACC   _
GAM2085  MUS81    5'  CCGCTGCGCAGCGGCAGTG    36060        _  AC  _
                                   CCGCTGCG AG  GC GTG
                                   |||||||| ||  || |||
                                   GGCGACGC TC  CG CAC
                                        G  GC  T
GAM2085  NCOR2    3'  CCGCTGCGGCAACGATGTG   26730        A_   C_
                                   CCGCTGCG  GACG  GTG
                                   ||||||||  ||||  |||
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                                GGCGACGC  TTGC  CAC
                                    CG    TA
GAM2086  CLOCK    3'  CAGTAAGAATCATAAA      22214       TTTTT
                                CAGTA    GGAATCATAAA
                                |||||    ||||||||||
                                GTCAT    TCTTAGTATTT
                                  _____
GAM2086  DIAPH2   3'  CAGTATTTTCTAACATAA    28670         GGAAT
                                CAGTATTTTT    CATAA
                                ||||||||||    |||||
                                GTCATAAAAG    GTATT
                                    ATT__
GAM2086  GOCAP1   3'  CAGTATTTTTCTCATAAAAA  35547         GGAA
                                CAGTATTTTT   TCATAAAAA
                                ||||||||||   |||||||||
                                GTCATAAAAA   AGTATTTTT
                                    G___
GAM2086  MTRR     3'  TCATATTTCCCAGCATCATAAA 14686     GTA   TG A
             AA                   TCA   TTTT  G ATCATAAAAA
                                |||   ||||  | ||||||||||
                                AGT   AAGG  C TAGTATTTTT
                                  ATA    GT G
GAM2086  SLC38A2  3'  AGTATTTTTGGTACAAAAA   33271         AATC
                                AGTATTTTTGG    ATAAAAA
                                ||||||||||    |||||||
                                TCATAAAAACC    TGTTTTT
                                    A___
GAM2086  TGFBR2   3'  TCAGTATTTTTAGGAACTACA  17482          _    C
                                TCAGTATTTTT GGAAT ATA
                                |||||||||| ||||| |||
                                AGTCATAAAAA CCTTG TGT
                                    T    A
GAM2087  AXIN1    3'  TGCCGGGGGATGGGGGGGGGTC 41395         CA  A  A
                                TGCTGGGGGA  GG GG GGGTT
                                ||||||||||  || || |||||
                                ACGGCCCCCT  CC CC CCCAG
                                    AC  _  C
GAM2087  BCL2L10  5'  TGCTGGGGGGCCGGGCC     33790         ACAG AGGA
                                TGCTGGGGG    G    GGGTT
                                |||||||||    |    |||||
                                ACGACCCCC    C    CCCGG
                                    ____ GG__
GAM2087  CD68     3'  TGCTGGGGGGGGGGGGGGGC   40785         ACA  A  A
                                TGCTGGGGG   GG GG GGGT
                                |||||||||   || || ||||
                                ACGACCCCC   CC CC CCCG
                                    CCC  _  _
GAM2087  CDKN1A   3'  GCTGGGGGGCAGGGGGC     38510         A    AGGA
                                GCTGGGGG CAGG    GGGT
                                |||||||| ||||    ||||
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                                CGACCCCC GTCC   CCCG
                                     C   ____
GAM2087  CNTFR    3'  TGCTGGGGGGAGGGGG     12304        ACAG   A
                                TGCTGGGGG   GAGG GGG
                                |||||||||   |||| |||
                                ACGACCCCC   CTCC CCC
                                     ____   _
GAM2087  DNAI2    5'  TGCTGGGGGGCAGAGGGA    35748        A  GA
                                TGCTGGGGG CAG  GGA
                                ||||||||| |||  |||
                                ACGACCCCC GTC  CCT
                                     C  TC
GAM2087  DNMT3L   5'  GCTGGGGGATTGGGGTT     30057        CA  AGGAG
                                GCTGGGGGA  GG    GGTT
                                |||||||||  ||    ||||
                                CGACCCCCT  CC    CCAA
                                     AA _____
GAM2087  GADD45B  3'  TGCTGGGGGGGAGGGGGTT   31829        ACA    A
                                TGCTGGGGG   GGAGG GGGTT
                                |||||||||   ||||| |||||
                                ACGACCCCC   CCTCC CCCAA
                                     ___    _
GAM2087  MAP4     3'  TGTGGGGGGCGGGAGACAATGT 36278    C     ACA    AGG_
           C                     TG TGGGGG   GGAGG   GTT
                                || ||||||   |||||   |||
                                AC ACCCCC   CCTCT   CAG
                                 _     CGC    GTTA
GAM2087  MIC2     3'  CTGGGGGACGGGGGGGT     14503        A  A  A
                                CTGGGGGAC GG GG GGGT
                                ||||||||| || || ||||
                                GACCCCCTG CC CC CCCA
                                     _  _  _
GAM2087  MNT      3'  TGTTGAGGGGATGGGAGGA   33734    C _    CA
                                TG TG GGGGA  GGAGGA
                                || || |||||  ||||||
                                AC AC CCCCT  CCTCCT
                                 A  T    AC
GAM2087  PIAS3    3'  TGTTGGGGGACAGCGAAG    25914    C        _
                                TG TGGGGGACAG GAGG
                                || ||||||||| ||||
                                AC ACCCCCTGTC CTTC
                                 A        G
GAM2087  PRG3     3'  TGGGGGACGGGAGGGAGC    37253        A    A
                                TGGGGGAC GGAGG GGGT
                                |||||||| ||||| ||||
                                ACCCCCTG CCTCC CTCG
                                     C    _
GAM2087  SF3A2    3'  TGCTGGGGGGAGGGAGCAGCTTC 28404         CA   GA  G
                                TGCTGGGGGA  GGAG  GG TTC
                                |||||||||  ||||  || |||
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                                ACGACCCCCT  CCTC  TC AAG
                                      C_   G_  G
GAM2087  TFE3     3'  TGCTGGGGGAAGGCTTCCAGTT 27176         C   AGGAG
                                TGCTGGGGGA AGG    GGTT
                                |||||||||| |||    ||||
                                ACGACCCCCT TCC    TCAA
                                      _  GAAGG
GAM2087  TWIST    3'  TGCTGAGGGGGTGGGGGGCTC  7872         ACA  A  A
                                TGCTGGGGG   GG GG GGGTTC
                                |||||||||   || || ||||||
                                ACGACTCCC   CC CC CCCGAG
                                      ___  A  C
GAM2088  CNGB3    3'  TAAACAGCTATACATGTAGGTT 33308        CCCG  T  AC
                                TAAACAGC    AT TG  AGGTT
                                ||||||||    || ||  |||||
                                ATTTGTCG    TG AC  TCCAA
                                     ATA_  T  A_
GAM2088  EFNA1    3'  GCCCCAAGACAGGTT      20702        TTT
                                GCCCCGA   GACAGGTT
                                |||||||   ||||||||
                                CGGGGTT   CTGTCCAA
                                     ___
GAM2088  STAU     5'  TAAACAGCTTTCAGTGCAGGTT 32697        CCCGATT  A
                                TAAACAGC      TG CAGGTT
                                ||||||||      || ||||||
                                ATTTGTCG      AC GTCCAA
                                     AAAGTC_ _
GAM2088  DRG2     3'  GTTTGGGTGTTTGTGTG     10788    CGG
                                GT   GGGTGTTTGTGTG
                                ||   ||||||||||||
                                CA   CCCACAAACACAC
                                 AA_
GAM2088  GAGED2   5'  GTGGTTCTGTGTTTGTGTG   39417    C  GG__
                                GT GG    GTGTTTGTGTG
                                || ||    ||||||||||
                                CA CC    CACAAACACAC
                                 _ AAGA
GAM2089  SPTBN4   3'  TGCAGATCGGGGCTGGGGGCT  36091    T  A        TTTAT
                                TG CA ATCGGGGCTG     GCT
                                || || ||||||||||     |||
                                AC GT TAGCCCCGAC     CGA
                                 _ C         CCC__
GAM2089  ANK3     3'  AAATACCCCCGACTGGG     10091     C        GTGAA
                                AAA ACCCCCGAC     GGG
                                ||| |||||||||     |||
                                TTT TGGGGGCTG     CCC
                                  A       A____
GAM2089  CACNA2D2 3'  CAAACACCTGCGGCGTCCCGCT 25703         CC  A   GAAGG
                                CAAACACC  CG CGT     GCT
                                ||||||||  || |||     |||
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                                GTTTGTGG  GC GCA    CGA
                                    AC  C   GGG__
GAM2089  CDH6     3'  AAACACCCCTATGTAG     22319        CGAC   A
                                AAACACCCC   GTG AG
                                |||||||||   ||| ||
                                TTTGTGGGG   TAC TC
                                    A___   A
GAM2089  PIGR     3'  CACCCCTGGTGAAAAG     43697       CGAC
                                CACCCC   GTGAAGGG
                                ||||||   ||||||||
                                GTGGGG   CACTTTTC
                                   AC__
GAM2089  PLA2G2D  3'  CAAACACCACCTCTGAGGGCT  29630        C  GACG   A
                                CAAACACC CC   TGA GGGCT
                                |||||||| ||   ||| |||||
                                GTTTGTGG GG   ACT CCCGA
                                    T  AG__  _
GAM2089  RCE1     3'  AAACACCCCTTTCAAAAGGGGC 23066        CGA  T  A
            T                    AAACACCCC   CG GA GGGCT
                                |||||||||   || || |||||
                                TTTGTGGGG   GT TT CCCGA
                                    AAA  T  C
GAM2089  TMSB4Y   5'  CACATGCCTCTGCAAGAAGGGC 20086     CC_  GA__  T
            T                    CAC   CC    CG GAAGGGCT
                                |||   ||    || ||||||||
                                GTG   GG    GT CTTCCCGA
                                  TAC  AGAC  T
GAM2089  ZNF174   3'  CAAACACCTTCCGTGTGAA   18358       C_   AC
                                CAAACACC  CCG  GTGAA
                                ||||||||  |||  |||||
                                GTTTGTGG  GGC  CACTT
                                    AA   A_
GAM2090  SPTBN4   3'  TGCAGATCGGGGCTGGGGGCT  36091    T  A       ATTTAT
                                TG CA ATCGGGGCT     GCT
                                || || |||||||||     |||
                                AC GT TAGCCCCGA     CGA
                                 _  C       CCCC__
GAM2090  ADAMTS13 3'  ACGACCATCCTCCAGGAGGG   40025    _   C_  GA  T  A
                                AC ACC  CC  CA GA GGG
                                || |||  ||  || || |||
                                TG TGG  GG  GT CT CCC
                                 C   TA  AG  C  _
GAM2090  ANK3     3'  AAATACCCCCGACTGGGG    10092     C       A  AA
                                AAA ACCCCCGAC TG  GGG
                                ||| |||||||| ||  |||
                                TTT TGGGGGCTG AC  CCC
                                  A       _ __
GAM2090  ATP6V1A1 3'  CACAAACATTCCTGATTTATAC 11779        CC  C  C__   AA
            TGGG                   CACAAACA  CC GA   ATG  GGG
                                |||||||  || ||   |||  |||
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                                GTGTTTGT  GG CT   TAT  CCC
                                     AA  A  AAA   GA
GAM2090  DAB2     3'  CAAAACAGTATGATATGAAGGG 10642    C    CCCCC  C
                                A AAACA    GA ATGAAGGG
                                | |||||    || ||||||||
                                G TTTGT    CT TACTTCCC
                                 T    CATA_  A
GAM2090  ENDOG    5'  CACAAACACTGCCAAG     20758        CC   ACATGA
                                CACAAACAC  CCG     AG
                                |||||||||  |||     ||
                                GTGTTTGTG  GGT     TC
                                     AC  _______
GAM2090  GNAO1    3'  CACAAACATCCCCACATG    44938        C    G
                                CACAAACA CCCC ACATG
                                |||||||| |||| |||||
                                GTGTTTGT GGGG TGTAC
                                     A   _
GAM2090  GRN      3'  CACAAACACCCCTGTGGATAGG 13291           CGACAT  _
              G                  CACAAACACCCC     GA AGGG
                                ||||||||||||     || ||||
                                GTGTTTGTGGGG     CT TCCC
                                      ACAC__  A
GAM2090  LPIN2    3'  ACAAACACACTCGAG      31204        CCCCG  A   A
                                ACAAACAC    AC TGA G
                                ||||||||    || ||| |
                                TGTTTGTG    TG GCT C
                                     ______  A   _
GAM2090  MPG      5'  CACAAACACCCTGACACA    14618          CC
                                CACAAACACCC  GACATG
                                ||||||||||  ||||||
                                GTGTTTGTGGG  CTGTGT
                                      A_
GAM2090  PAX3     3'  ACACCGCGCATGAAGGG     30326      CC  A
                                ACACC  CG CATGAAGGG
                                |||||  || |||||||||
                                TGTGG  GC GTACTTCCC
                                   C_  _
GAM2090  RAB36    3'  CAAACATATCCTGGAGGCCCGA 22232       C__  CC  CA__
             AGGG                  CAAACA   CC  GA   TGAAGGG
                                ||||||   ||  ||   |||||||
                                GTTTGT   GG  CT   GCTTCCC
                                    ATA  AC  CCGG
GAM2090  RAD54B   3'  ACAAACACTTTTGAAAG     39581        CCCCGACA
                                ACAAACAC       TGAAGG
                                ||||||||       ||||||
                                TGTTTGTG       ACTTTC
                                     AAA_____
GAM2090  RCE1     3'  AAACACCCCTTTCAAAAGGG   23065         CGA  T
                                AAACACCCC   CA GAAGGG
                                |||||||||   || ||||||
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                                TTTGTGGGG  GT TTTCCC
                                     AAA  _
GAM2090  SFRS1    3'  CACAAACACCCCCAACAT    27958
                                CACAAACACCCCCGACAT
                                ||||||||||||||||||
                                GTGTTTGTGGGGGTTGTA

GAM2090  SPON2    3'  CACAGGAGCCCCCGACAC    29711      AACA
                                CACA   CCCCCGACAT
                                ||||   ||||||||||
                                GTGT   GGGGGCTGTG
                                  CCTC
GAM2090  USF2     3'  CACACACACCCCCAAAGG    17893      A        CATGA
                                CACA ACACCCCCGA    AGG
                                |||| ||||||||||    |||
                                GTGT TGTGGGGGTT    TCC
                                  G        _____
GAM2091  ADAM12   5'  GCCCGGGGACTAGGAAGAGCG  18473        _ CAA   C  A
                                GCCCGGGG C   GAA AG TG
                                |||||||| |   ||| || ||
                                CGGGCCCC G   CTT TC GC
                                     T ATC   C  _
GAM2091  BCAT2    3'  GCTGGGGGCCAAGATGCCTGGG 10162    CC        ACAGAT
           TC                    GC  GGGGCCAAGA     GGTC
                                ||  ||||||||||     ||||
                                CG  CCCCGGTTCT     CCAG
                                 AC         ACGGAC
GAM2091  DUSP1    5'  CGGGGCCAAGGGCAGGGC    20654         AA   AT
                                CGGGGCCAAG  CAG  GGT
                                ||||||||||  |||  |||
                                GCCCCGGTTC  GTC  CCG
                                     CC   __
GAM2091  EDN2     3'  GGGACCAAGGCCCCGGTC    12647         AACAGA
                                GGGGCCAAG     TGGTC
                                |||||||||     |||||
                                CCCTGGTTC     GCCAG
                                     CGGG__
GAM2091  ENIGMA   3'  GCTCGGGCCAGGAGCCAGGGT  41635    C   G   A  A_   AT
                                GC CGGG CCA GA  CAG  GGT
                                || |||| ||| ||  |||  |||
                                CG GCCC GGT CT  GTC  CCA
                                 A   _  C  CG   __
GAM2091  FMOD     3'  GGAGCCAAGAACGTAGTC    12930           AGA
                                GGGGCCAAGAAC   TGGTC
                                ||||||||||||  |||||
                                CCTCGGTTCTTG   ATCAG
                                       C__
GAM2091  GALNT2   3'  CCGGGGCCGAGGCCGGTGGTC  21003         A  AACAGA
                                CCGGGGCC AG     TGGTC
                                |||||||| ||     |||||
```

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                                GGCCCCGG TC     ACCAG
                                     C  CGGCC_
GAM2091  HS3ST3B1  5'  GCTCGGGGCCAGGAGGACG   25797    C       A  ACA
                                GC CGGGGCCA GA   GATG
                                || |||||||| ||   ||||
                                CG GCCCCGGT CT   CTGC
                                 A       C  C__
GAM2091  KIF5C     5'  CCGGGGCCGGGAACGAC     21149         AA    A
                                CCGGGGCC  GAAC GAT
                                ||||||||  |||| |||
                                GGCCCCGG  CTTG CTG
                                     CC    _
GAM2091  NCOR2     3'  GCCCGGGGCGGGAGTCTTAGT  26735         CAA  ACAGA
                                GCCCGGGGC   GA    TGGT
                                |||||||||   ||    ||||
                                CGGGCCCCG   CT    ATCA
                                     CC_  CAGA_
GAM2091  NUCB1     3'  GCTGGGGGCCAAGAGG      26155    CC        ACAGAT
                                GC  GGGGCCAAGA     GG
                                ||  ||||||||||     ||
                                CG  CCCCGGTTCT     CC
                                 AC         _______
GAM2091  OTX1      5'  GCCCGGGGCCAGGAGCGGT   30988          A  ACA A
                                GCCCGGGGCCA GA   G TGGT
                                |||||||||||  ||   | ||||
                                CGGGCCCCGGT CT   C GCCA
                                      C  ___ _
GAM2091  PRKY      3'  GCTGGGGGCAAGGCAGATGGT  15700    CC    C   AA
                                GC  GGGGC AAG  CAGATGGT
                                ||  ||||| |||  ||||||||
                                CG  CCCCG TTC  GTCTACCA
                                 AC     _   C_
GAM2091  PTPRN     3'  GCCCGGGGCTGAGAAGCAG    15980         CA   _
                                GCCCGGGGC  AGAA CAG
                                |||||||||  |||| |||
                                CGGGCCCCG  TCTT GTC
                                     AC   C
GAM2091  SMG1      5'  GCCCGGGGCTGAGGAGGAAGC  31509         CA  AAC  AT
                                GCCCGGGGC  AG   AG  GGT
                                |||||||||  ||   ||  |||
                                CGGGCCCCG  TC   TC  TCG
                                     AC  C__  CT
GAM2091  TP53BP1   5'  GCCCGGGGCAAGGACAG     24939         C   A
                                GCCCGGGGC AAG ACAG
                                ||||||||| ||| ||||
                                CGGGCCCCG TTC TGTC
                                     _  C
GAM2091  VGF       3'  GCCCGGGGACAGGGGC      17991         CCAAGA   AT
                                GCCCGGGG     ACAG  GGT
                                ||||||||     ||||  |||
```

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                                CGGGCCCC    TGTC  CCG
                                    _______   C_
GAM2091  CACNA1C   3'  GAGCCGGCGGCCCCGGCCCGG  8753     AGTTT
                                GAGC    CGGCCCCGGCCCGG
                                ||||    ||||||||||||||
                                CTCG    GCCGGGGCCGGGCC
                                  GCC__
GAM2091  CDK5R2    5'  GCCTAGCCCCGGCCCGG    19473     C
                                GTTT GGCCCCGGCCCGG
                                |||| ||||||||||||
                                CGGA TCGGGGCCGGGCC
                                  _
GAM2091  CSF2      3'  GAGCAGCTCCCCGGCTG    8897        TCGG     CC
                                GAGCAGTT   CCCCGGC  G
                                ||||||||   |||||||  |
                                CTCGTCGA   GGGGCCG  C
                                    _____     AA
GAM2091  EPO       5'  GCGGTGGCCCCGGTCCGG   9033    A  TTC      C
                                GC GT   GGCCCCGG CCGG
                                || ||   |||||||| ||||
                                CG CA   CCGGGGCC GGCC
                                 C ___       A
GAM2091  GCN5L2    3'  TGAGCAGTTCTGGTCCTCAG   40813        TC  _  C
                                TGAGCAGTT  GG CC CGG
                                |||||||||  || || |||
                                ACTCGTCAA  CC GG GTC
                                     GA  A  A
GAM2091  MIC1      5'  TGCGCGGTGGAGCCCGGCCCGG 30031    A  A  TTC    C
                                TG GC GT   GGCCC GGCCCGG
                                || || ||   ||||| |||||||
                                AC CG CA   TCGGG CCGGGCC
                                 G  C  CC_    _
GAM2091  SOX4      3'  AGAGTGGGTCCCCGGCCCG   16974    C   TTC  _
                                AG AGT   GG CCCCGGCCCG
                                || |||   || ||||||||||
                                TC TCA   CC GGGGCCGGGC
                                 _   C__  A
GAM2091  XT3       5'  CGGCGCGCTCGGCTCCGGCTCG 33664    A  A_  T   C    C
           G                     TG GC  GTT CGGC CCGGC CGG
                                || ||  ||| |||| ||||| |||
                                GC CG  CGA GCCG GGCCG GCC
                                 _ CG   _    A    A
GAM2092  FOXD2     5'  CTTCGCCGCCGCTCCTGC    20962          GA  C
                                CTTCGCCGCCGC  CC GC
                                ||||||||||||  || ||
                                GAAGCGGCGGCG  GG CG
                                      A_  A
GAM2092  JUN       5'  CTTTGCTGCTGCAGCCGC    13741     C  C  C   AC
                                CTT GC GC GCG  CCGC
                                ||| || || |||  ||||
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                                GAA CG CG CGT  GGCG
                                  A  A  A   C_
GAM2092  MYO1E    5'  TACTCGCCGCTCGCCGC     22658      T     _  GACC
                                TACT CGCCGC CGC    CGC
                                |||| |||||| |||    |||
                                ATGA GCGGCG GCG    GCG
                                  _     A  _____
GAM2092  PKD1     5'  CTGCGCGGCCGCGACCTGC   7136     T  C        C
                                CT CGC GCCGCGACC GC
                                || ||| |||||||| ||
                                GA GCG CGGCGCTGG CG
                                 C  C        A
GAM2092  REV3L    5'  TTCGCCGCCGCCGCCA      16271           GACC
                                TTCGCCGCCGC    CGCCA
                                ||||||||||    |||||
                                AAGCGGCGGCG    GCGGT

                                      _____
GAM2092  RGS19IP1 5'  CTCCGCCGCCGCCGCCGC    41695           GAC
                                CTTCGCCGCCGC   CCGC
                                ||||||||||||   ||||
                                GAGGCGGCGGCG   GGCG
                                       GC_
GAM2092  UBE3A    5'  TTCGCTGCCGCCACCGC     39287      C    G  C
                                TTCGC GCCGC ACC GC
                                ||||| ||||| ||| ||
                                AAGCG CGGCG TGG CG
                                   A    G  _
GAM2092  ABCG5    3'  GTGCTCTGTAGCAGTGGTGC  35330        A   CTCGC
                                GTGCTCTG TAGT    GTGC
                                |||||||| ||||    ||||
                                CACGAGAC ATCG    CACG
                                     _   TCAC_
GAM2092  ATP11A   3'  GTGCTCTGGTAGCCTGGGC   44179        A    C_
                                GTGCTCTG TAGTCT  GC
                                |||||||| ||||||  ||
                                CACGAGAC ATCGGA  CG
                                     C     CC
GAM2092  ATP8A2   3'  GTATTCTGATAGGTACC     45263     C      TCTCGC
                                GTG TCTGATAG     GTGCC
                                ||| ||||||||     |||||
                                CAT AGACTATC     CATGG
                                  A      _______
GAM2092  BDKRB1   5'  GTTTTCTGATAGTGAGAGCTGC 8736     GC       CTC_  G
                                GT  TCTGATAGT    GC TGC
                                ||  |||||||||    || |||
                                CA  AGACTATCA    CG ACG
                                 AA        CTCT  _
GAM2092  MST1R    3'  GTGCTTTAATAGTCATTTGT   14667      C       TCGC
                                GTGCT TGATAGTC    GT
                                |||||  ||||||||    ||
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                                CACGA ATTATCAG   CA
                                  A       TAAA
GAM2092  NOV     3'  GTGCTCTGTAGGTGTGC     14812         A   TCTCGC
                                GTGCTCTG TAG     GTGC
                                |||||||| |||     ||||
                                CACGAGAC ATC     CACG
                                    _   CA____
GAM2092  PARK2   3'  GTGCTCTGGTATTTGTGTCATC 30374         A  GTCTCG_   G
             C                   GTGCTCTG TA      CGT CC
                                 |||||||| ||      ||| ||
                                 CACGAGAC AT      GTA GG
                                     C  AAACACA   _
GAM2092  SMCX    5'  GTGCTCTGAGAGTCTCAGGC   20074         T      C
                                GTGCTCTGA AGTCTCG GT
                                ||||||||| ||||||| ||
                                CACGAGACT TCAGAGT CG
                                     C      C
GAM2093  BRCA1   3'  TCTAATACCTGCCTCAGAATTT 28647    CG         ___    C
             CCT                   TC  AATACCTGTC   GAAT TCCT
                                   ||  ||||||||||   |||| ||||
                                   AG  TTATGGACGG   CTTA AGGA
                                    A_        AGT    A
GAM2093  CD1D    5'  GAATACCTCTTGAATAAATTCC 44298         GTC    C___
             T                    GAATACCT   GAAT    TCCT
                                  ||||||||   ||||    ||||
                                  CTTATGGA   CTTA    AGGA
                                       GAA    TTTA
GAM2093  HOXA7   3'  TCTGAATACCTGTTCTGCCC   27890    C        CGAA   _
                                  TC GAATACCTGT    TCT CCT
                                  || ||||||||||    ||| |||
                                  AG CTTATGGACA    AGA GGG
                                   A         _____   C
GAM2093  NFE2L1  3'  GAATATTGGGAATCTCCT    17330      CC  TC
                                  GAATA  TG  GAATCTCCT
                                  |||||  ||  |||||||||
                                  CTTAT  AC  CTTAGAGGA
                                     A_  C_
GAM2093  PRKACG  3'  CTCCAAATATCTGGGCTTCCT  15600         C   TCGAATC
                                  CTCCGAATA CTG      TCCT
                                  |||||||| |||      ||||
                                  GAGGTTTAT GAC      AGGA
                                       A   CCGA___
GAM2093  GEMIN5  3'  TCTTTGGCTTTAATCTGAT   44845         GGCTCC    C
                                  TCTTTGGTT     AATC GAT
                                  |||||||||     |||| |||
                                  AGAAACCGA     TTAG CTA
                                       AA_____    A
GAM2094  ACCN2   3'  GCACCCAGAAGGAGGA      33445        CGC
                                  GCACCC   GAAGGAGGA
                                  ||||||   |||||||||
```

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                                CGTGGG  CTTCCTCCT
                                   T__
GAM2094  ADM     3'  AAGCCCCCAGAAGGAGG     10026     A    C
                                AAGC CCCCG GAAGGAGG
                                |||| ||||| ||||||||
                                TTCG GGGGT CTTCCTCC
                                  _    _
GAM2094  ADRA2B  3'  AAGCACCCACCTGGGGGGA   8644        C  GAA  A
                                AAGCACCC GC   GG GGA
                                |||||||| ||   || |||
                                TTCGTGGG TG   CC CCT
                                     _ GAC  C
GAM2094  ASC     5'  AGCCGCCGACCAGGAGGA    29937     AC  C  GA
                                AGC  CC GC  AGGAGGA
                                |||  || ||  |||||||
                                TCG  GG TG  TCCTCCT
                                  GC  C  G_
GAM2094  AXIN1   3'  GCCCTCAGAAAGGAGGA     41378    A  C  C
                                GC CC CG GAAGGAGGA
                                || || || |||||||||
                                CG GG GT TTTCCTCCT
                                 _ A  C
GAM2094  BCL2    3'  AAGCCCCCGCGGAAGGAGG   8515      A     _
                                AAGC CCCCGCG AAGGAGG
                                |||| ||||||| |||||||
                                TTCG GGGGCGC TTCCTCC
                                  _      C
GAM2094  CA7     3'  AGCACCCCCCCAGGGAGGA    41194       G  AA
                                AGCACCCC CG  GGAGGA
                                |||||||| ||  ||||||
                                TCGTGGGG GT  CCTCCT
                                     G  C_
GAM2094  CARD15  3'  AAACACCGGAAAGGAGG     35257       CCGC
                                AAGCACC    GAAGGAGG
                                |||||||    ||||||||
                                TTTGTGG    TTTCCTCC
                                    CC__
GAM2094  CBL     5'  AAGCAGGGCGTGAAGGAGG   23277      CCC  C
                                AAGCA   CG GAAGGAGG
                                |||||   || ||||||||
                                TTCGT   GC CTTCCTCC
                                   CCC  A
GAM2094  CSNK1G2 3'  GCACCCCACTGGGGA      10614        GAA  A
                                GCACCCCGC   GG GGA
                                |||||||||   || |||
                                CGTGGGGTG   CC CCT
                                     A__  _
GAM2094  ELL     3'  AGACCCTGCCCAAGGAGGA   27204    C   C  G_
                                AG ACCC GC  AAGGAGGA
                                || |||| ||  ||||||||
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                                TC TGGG CG  TTCCTCCT
                                 _   A  GG
GAM2094  HDAC5    3'  AGACCAAGAGGAAGGAGGA   24190    C   CCGC_
                                AG ACC    GAAGGAGGA
                                || |||    |||||||||
                                TC TGG    CTTCCTCCT
                                 _  TTCTC
GAM2094  HNF4A    3'  AGCAGCAGAAGGAGGA      7841       CCCC  _
                                AGCA   GC GAAGGAGGA
                                ||||   || |||||||||
                                TCGT   CG CTTCCTCCT
                                  ____  T
GAM2094  HOXA3    3'  AAGCATCCCCAGAGGA      36189       _   GCGAA
                                AAGCA CCCC    GGAGGA
                                ||||| ||||    ||||||
                                TTCGT GGGG    TCTCCT
                                   A  _____
GAM2094  IRS1     5'  GCAGCTGAAGGAGGA       24423     CCCC  _
                                GCA   GC GAAGGAGGA
                                |||   || |||||||||
                                CGT   CG CTTCCTCCT
                                 _____  A
GAM2094  ITPKB    3'  AAGCACAGGAGGAGGA      13640       CCCGC  A
                                AAGCAC    GA GGAGGA
                                ||||||    || ||||||
                                TTCGTG    CT CCTCCT
                                   TC___  _
GAM2094  ITPR3    3'  AACTACCCACAAGGAGGA    13683     AC    G
                                AGC  CCCGC AAGGAGGA
                                |||  ||||| ||||||||
                                TTG  GGGTG TTCCTCCT
                                  AT    _
GAM2094  KLRG1    3'  AGCTCAGAAGGAGGA       25152     ACCC  C
                                AGC   CG GAAGGAGGA
                                |||   || |||||||||
                                TCG   GT CTTCCTCCT
                                  A___  _
GAM2094  LTBP3    3'  AAACACCCTCTGGGAGGA    34338         CGCGAA
                                AAGCACCC     GGAGGA
                                ||||||||     ||||||
                                TTTGTGGG     CCTCCT
                                    AGAC__
GAM2094  MEN1     5'  AAGCACCCCAATGAGGA     39140          CGAAG
                                AAGCACCCCG    GAGGA
                                ||||||||||    |||||
                                TTCGTGGGGT    CTCCT
                                      TA___
GAM2094  MYO6     3'  AAGACACTGCAAAGGAGGA   22662     _  CCC
                                AAG CAC   GCGAAGGAGGA
                                ||| |||   ||||||||||
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                                TTC GTG   CGTTTCCTCCT
                                  T   A__
GAM2094  NPC1     5'  AGCACCCCGCGCAGGAGGA   7076           A
                                AGCACCCCGCG AGGAGGA
                                |||||||||| |||||||
                                TCGTGGGGCGC TCCTCCT
                                      G
GAM2094  NPR1     5'  AGCGCTTCGTGAAGAAGGA   44574     ACCC  C
                                AGC    CG GAAGGAGGA
                                |||    || |||||||||
                                TCG    GC CTTCTTCCT
                                  CGAA  A
GAM2094  NR1I2    3'  AAGCAGCTCGGAAGAGGAGG   35097      CCC  C  __
                                AAGCA   CG GA  AGGAGG
                                |||||   || ||  ||||||
                                TTCGT   GC CT  TCCTCC
                                   CGA  _  TC
GAM2094  OSM      3'  AAACACGGAAAGGAGGA     33909       CCC C
                                AAGCAC   G GAAGGAGGA
                                ||||||   | |||||||||
                                TTTGTG   C TTTCCTCCT
                                   ___ C
GAM2094  OXTR     3'  AAGCCACCCCAAGGAGG     9516      _     CGA
                                AAGC ACCCCG   AGGAGG
                                |||| ||||||   ||||||
                                TTCG TGGGGT   TCCTCC
                                  G     ___
GAM2094  PCDHA2   3'  AAGCACATTGGAAAAAAGGAGG 33138       CCCGC___
              A                  AAGCAC       GAAGGAGGA
                                ||||||       |||||||||
                                TTCGTG       TTTCCTCCT
                                   TAACCTTT
GAM2094  PNUTL1   3'  AGCAGGCAAAGGAGG       15426      CCCC
                                AGCA    GCGAAGGAGG
                                ||||    ||||||||||
                                TCGT    CGTTTCCTCC
                                  C___
GAM2094  PRV1     3'  AAGCACCCCAGGAGG       43871         GCGA
                                AAGCACCCC    AGGAGG
                                |||||||||    ||||||
                                TTCGTGGGG    TCCTCC
                                      ____
GAM2094  RASGRP1  3'  AAGTACCCCCAAAAAGGA    25069     C    G    G
                                AAG ACCCC CGAAG AGGA
                                ||| ||||| ||||| ||||
                                TTC TGGGG GTTTT TCCT
                                  A    _    _
GAM2094  RUNX1    3'  AACACAGGAAAAGGAGGA    12002       CCCGC
                                AGCAC    GAAGGAGGA
                                |||||    |||||||||
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                                TTGTG    TTTCCTCCT
                                  TCCT_
GAM2094 S100A12  3' AAGACCCTCATTGAGGA    24736    C   CG  AAG
                                AAG ACCC  CG   GAGGA
                                ||| ||||  ||   |||||
                                TTC TGGG  GT   CTCCT
                                  _   A_  AA_
GAM2094 SERPINE1 3' AGCACCCCTGTACTGGGGAGG 8281        ___ GAA
                                AGCACCCC   GC   GGAGG
                                ||||||||   ||   |||||
                                TCGTGGGG   TG   CCTCC
                                    ACA  ACC
GAM2094 SLC1A5   3' AGCACCCCCAGCAGG      24743        G GA  G
                                AGCACCCC C  AG AGG
                                |||||||| |  || |||
                                TCGTGGGG G  TC TCC
                                    _ __  G
GAM2094 SLC2A8   3' AGCATGACAGGAAGGAGG    31026     CCC  C
                                AGCA   CG GAAGGAGG
                                ||||   || ||||||||
                                TCGT   GT CTTCCTCC
                                  ACT  C
GAM2094 TACC1    3' AAGACCCCAAAGAGG       26586     C     CGA
                                AAG ACCCCG   AGGAGG
                                ||| ||||||   ||||||
                                TTC TGGGGT   TTCTCC
                                  _    ____
GAM2094 WASF3    3' AAGCATTACCAAAGGGGA    27375      CCCCG     A
                                AAGCA    CGAAGG GGA
                                |||||    |||||| |||
                                TTCGT    GTTTCC CCT
                                  AATG_    _
GAM2094 WEE1     3' AGCATTCCAAAGGAGG      18078      CC  GC
                                AGCA  CC  GAAGGAGG
                                ||||  ||  ||||||||
                                TCGT  GG  TTTCCTCC
                                  AA  __
GAM2094 ZNF215   5' AGCCCCCGCGACCTGGA     29915     A       AGGA
                                AGC CCCCGCGA    GGA
                                ||| ||||||||    |||
                                TCG GGGGCGCT    CCT
                                  _       GGA_
GAM2094 ZNF26    3' AAGCACCCCAGAGAGG      43789          C  AG
                                AAGCACCCCG GA  GAGG
                                |||||||||| ||  ||||
                                TTCGTGGGGT CT  CTCC
                                      _ __
GAM2095 DUT      3' TGATCATAAAAAAAAGTAAAAA 12626           _____       A
             ATGCA                  TGATCGTAAAAA    TAAAAAAT CA
                                ||||||||||||    |||||||| ||
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                                ACTAGTATTTTT   ATTTTTTA GT
                                      TTTC      C
GAM2095  NOTCH2   3'  GTATTGGAAAATAAAAAATACA 35911    ____
             A                   GTA   AAAATAAAAAATACAA
                                 |||   ||||||||||||||||
                                 CAT   TTTTATTTTTTATGTT
                                   AACC
GAM2096  ABCC5    3'  GGAGGCGGCAGAGGGGGCTGTC 25024           A  ___
             GG                   GGAGGCGGCAGAGG GGC  CGG
                                  |||||||||||||| |||  |||
                                  CCTCCGCCGTCTCC CCG  GCC
                                          C  ACA
GAM2096  ACHE     3'  AGAGGGGACAGGAGGGGGAG  8558      C   GA   CC
                                  GGAGG GGCA  GGAGG  GGAG
                                  ||||| ||||  |||||  ||||
                                  TCTCC CTGT  CCTCC  CCTC
                                     C   __    C_
GAM2096  ACTN2    5'  GGCGGGCGGCGGGCGCGG   9949    A_    AGAGGA  _
                                  GG  GGCGGC    GGC CGG
                                  ||  ||||||    ||| |||
                                  CC  CCGCCG    CCG GCC
                                   GC    C_____  C
GAM2096  AF5Q31   5'  GGAGGCGGCGGGGGTTCCGGAG 30856        AGA  A  __
                                  GGAGGCGGC   GG GG  CCGGAG
                                  |||||||||   || ||  ||||||
                                  CCTCCGCCG   CC CC  GGCCTC
                                        C__  _  AA
GAM2096  AGRN     3'  GGGGTGTGGCAGAGGGATACGG 44256    A  C__      A  C_
                                  GG GG   GGCAGAGG GG  CGG
                                  || ||   |||||||| ||  |||
                                  CC CC   CCGTCTCC CT  GCC
                                   _  ACA       _  AT
GAM2096  AKT1     3'  AGGAGGCGTGGAGGGGCC    23136       GCA   A
                                  AGGAGGCG   GAGG GGCC
                                  ||||||||   |||| ||||
                                  TCCTCCGC   CTCC CCGG
                                       AC_   _
GAM2096  ALPP     3'  AGGAGGTGGGGAGCAGGA    42866      C  CAGA   G C
                                  AGGAGG GG    GGAG C GGA
                                  |||||| ||    |||| | |||
                                  TCCTCC CC    CCTC G CCT
                                     A  ____   _ T
GAM2096  AP2B1    5'  GGTGGCGGCGGGAGCCGGAG   10490    A     AGA  AG
                                  GG GGCGGC   GG  GCCGGAG
                                  || ||||||   ||  |||||||
                                  CC CCGCCG   CC  CGGCCTC
                                   A     ___  CT
GAM2096  AR       5'  AGGAGGTGGAGAGAGAGTGGG  6227       C  C   _  GCC
                                  AGGAGG GG AGAG GAG   GG
                                  |||||| || |||| |||   ||
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                                TCCTCC CC TCTC CTC   CC
                                   A  _   T  AC_
GAM2096 ATP5J    5' GGAGGCGGGAGGGGGGTTGG  11770        CA   A  CC_
                                GGAGGCGG  GAGG GG   GG
                                ||||||||  |||| ||   ||
                                CCTCCGCC  CTCC CC   CC
                                    __    C  CAA
GAM2096 ATP6V0D1 5' GGGAGCGGCGGGACCGGA    21725    AG    AGA  A
                                GG  GCGGC   GG GGCCGGA
                                ||  |||||   || |||||||
                                CC  CGCCG   CC CTGGCCT
                                 CT    ___  _
GAM2096 B4GALT6  5' GGAGGCGCGGAGGCCGA     40851        G AGA
                                GGAGGCG C   GGAGGCCGG
                                ||||||| |   |||||||||
                                CCTCCGC G   CCTCCGGCT
                                   _ ___
GAM2096 BACE2    5' AGAAGGCGGAGGCCGG      29049        GGCAGA
                                AGGAGGC     GGAGGCCGG
                                |||||||     |||||||||
                                TCTTCCG     CCTCCGGCC
                                   _______
GAM2096 BACH2    5' GAAGGGGCGAGGGGAGGCCGG 34787      C   _  A
                                GGAGG GGC AG GGAGGCCGG
                                ||||| ||| || |||||||||
                                CTTCC CCG TC CCTCCGGCC
                                   _  C  C
GAM2096 BARHL1   3' GGAGCCGGCAGAGGCTGGGG  33467     G       A_  CC
                                GGAG CGGCAGAGG  GG  GG
                                ||||  |||||||||  ||  ||
                                CCTC GCCGTCTCC  CC  CC
                                  G       GA  __
GAM2096 BCL7A    5' GGAGACGGAGGCTGG       34216       GGCAGA     C
                                GGAGGC     GGAGGC GG
                                ||||||     |||||| ||
                                CCTCTG     CCTCCG CC
                                   _______     A
GAM2096 BTG1     5' AGGAGGCGGCAGGAGAGA    11906           AG
                                AGGAGGCGGCAG  GAGG
                                ||||||||||||  ||||
                                TCCTCCGCCGTC  CTCT
                                      CT
GAM2096 CABC1    5' GGAGGAGGCCTGGCCGG     33685      C   AGAGGA
                                GGAGG GGC     GGCCGG
                                ||||| |||     ||||||
                                CCTCC CCG     CCGGCC
                                   T  GA____
GAM2096 CACNG7   3' AGGAGGAGGCAGGGGGAG    36684       C    A_
                                AGGAGG GGCAG  GGAG
                                |||||| |||||  ||||
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                                TCCTCC CCGTC  CCTC
                                   T    CC
GAM2096  CAPG     3'  AGGCAGGTGGTGGGGGGCAGG  11960     _  C  CAGA  A   C
                                AGG AGG GG    GG GGC GG
                                ||| ||| ||    || ||| ||
                                TCC TCC CC    CC CCG CC
                                  G   A  ACC_  _   T
GAM2096  CAPON    5'  GGAGGGCGGCAGGGGAGG    41924       _     A
                                GGAGG CGGCAG GGAGG
                                ||||| |||||| |||||
                                CCTCC GCCGTC CCTCC
                                   C     C
GAM2096  CAPON    5'  AGGAGGTGGCGGCGGGAGCGGG 41918       C   AGA  AG  C
                                AGGAGG GGC   GG  GC GG
                                |||||| |||   ||  || ||
                                TCCTCC CCG   CC  CG CC
                                    A   CCG  CT  C
GAM2096  CBFA2T2  3'  AGGAGGCAGATGGGGTCGG   22966         CAGA  A  C
                                AGGAGGCGG    GG GG CGG
                                |||||||||    || || |||
                                TCCTCCGTC    CC CC GCC
                                      TA__  _  A
GAM2096  CD34     3'  AGGAGGGGGTAGGGGAAGGG   12110       C  C  A    CC
                                AGGAGG GG AG GGAGG  GG
                                |||||| || || |||||  ||
                                TCCTCC CC TC CCTTC  CC
                                   C  A  C    __
GAM2096  CD7      3'  AGGGGTGTGGCAGGGTGGGG   26002     A  C__    A  A  CC
                                AGG GG   GGCAG GG GG  GG
                                ||| ||   ||||| || ||  ||
                                TCC CC   CCGTC CC CC  CC
                                  _  ACA    _  A  __
GAM2096  CD97     5'  AGGAGCGGCAGGGGAAAGA   38522      G     A   GCC
                                AGGAG CGGCAG GGAG   GGA
                                ||||| |||||| ||||   |||
                                TCCTC GCCGTC CCTT   TCT
                                   _     C   ____
GAM2096  CELSR1   3'  GGAGGCGGTGAGGGG       30654        CA   AGGCC
                                GGAGGCGG  GAGG    GG
                                ||||||||  ||||    ||
                                CCTCCGCC  CTCC    CC
                                    A_   ______
GAM2096  CEP2     5'  GGGGGCGGCAGAGCGCGG    28443    A        GAG  C
                                GG GGCGGCAGAG   GC GG
                                || ||||||||||   || ||
                                CC CCGCCGTCTC   CG CC
                                 C         G__  _
GAM2096  CHIC2    5'  GAGGCGGCGGAGGCTGAG    29052        AGA     CG
                                GAGGCGGC   GGAGGC  GAG
                                ||||||||   ||||||  |||
```

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                                CTCCGCCG  CCTCCG  CTC
                                   ___     A_
GAM2096  CLASP1   3'  GGAGGCAGCAGCTTGGAG   42242          A__
                                GGAGGCGGCAG  GGAG
                                ||||||||||  ||||
                                CCTCCGTCGTC  CCTC
                                    GAA
GAM2096  CLC      3'  GGAGGTGGGGAGGAGAC    29898      C  CA
                                GGAGG GG  GAGGAGGC
                                ||||| ||  ||||||||
                                CCTCC CC  CTCCTCTG
                                  A  C_
GAM2096  CLDN3    5'  GGAGACGAGGGGCCGG     10568       GGCA   A
                                GGAGGC   GAGG GGCCGG
                                ||||||   |||| ||||||
                                CCTCTG   CTCC CCGGCC
                                   ____   _
GAM2096  COL6A2   3'  AGGAGGCGTGGGGGCAGTGAG  12333        GCAGA  A  CG_
                                AGGAGGCG    GG GGC  GAG
                                ||||||||    || |||  |||
                                TCCTCCGC    CC CCG  CTC
                                    AC___  _  TCA
GAM2096  CSK      5'  AGGGGGCGGGAGGGAGTCGG  20458    A    C  A   GC
                                AGG GGCGG AG GGAG  CGG
                                ||| ||||| || ||||  |||
                                TCC CCGCC TC CCTC  GCC
                                  C    C  _   A_
GAM2096  CXCL16   5'  AGGAGACGGCGGCCGG     35193         AGAGGA
                                AGGAGGCGGC    GGCCGG
                                ||||||||||    ||||||
                                TCCTCTGCCG    CCGGCC
                                   _______
GAM2096  DDX26    5'  AGGAGATGGTAGAGGTGGA   29085     GC  C    AGGCC
                                AGGAG  GG AGAGG    GGA
                                |||||  || |||||    |||
                                TCCTC  CC TCTCC    CCT
                                   TA  A    A____
GAM2096  DES      5'  GGCAGGCGGCCGGCCGGA   43569   _     AGAGGA
                                GG AGGCGGC    GGCCGGA
                                || |||||||    |||||||
                                CC TCCGCCG    CCGGCCT
                                 G     G_____
GAM2096  DLG4     3'  AGGGGTGGGAGGGAGGCCGG  10701    A  C  C  A
                                AGG GG GG AG GGAGGCCGG
                                ||| || || || |||||||||
                                TCC CC CC TC CCTCCGGCC
                                  _  A  C  _
GAM2096  DPYSL3   3'  AGAGGCAATATGAGGAGGTTGG 10760       CA_     CC
                                GGAGGCGG  GAGGAGG  GG
                                ||||||||  |||||||  ||
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                                TCTCCGTT  CTCCTCC  CC
                                    ATA     AA
GAM2096  DUSP4    5'  GGAGGCGGCGAAGGCGCCTGCG 38421        AG  AG  ___
             G                   GGAGGCGGC  AGG  GCC  GG
                                 |||||||||  |||  |||  ||
                                 CCTCCGCCG  TCC  CGG  CC
                                     CT  G_  ACG
GAM2096  EIF4G1   3'  AGGGGTGGTACAGGGGCTGG  22407    A  C  CAG  A  C
                                 AGG GG GG  AGG GGC GG
                                 ||| || ||  ||| ||| ||
                                 TCC CC CC  TCC CCG CC
                                   _ A ATG  _  A
GAM2096  ELL      3'  AGGAGGCAGTGGGCTTCCTGG  27205       CAGA  AGG  _
                                 AGGAGGCGG   GG  CC GG
                                 |||||||||   ||  || ||
                                 TCCTCCGTC   CC  GG CC
                                     AC__  GAA  A
GAM2096  ESR1     3'  GGAGGCGGTAGGGAACGG   6530       C  A   GC
                                 GGAGGCGG AG GGAG  CGG
                                 |||||||| || ||||  |||
                                 CCTCCGCC TC CCTT  GCC
                                     A  _   __
GAM2096  FAAH     5'  AGGAGGCGGCGGGGGGGCGGAG  11044        AGA  A   C
                                 AGGAGGCGGC  GG GGC GGAG
                                 ||||||||||  || ||| ||||
                                 TCCTCCGCCG  CC CCG CCTC
                                     CC_  _  _
GAM2096  FASN     3'  GGAGGCGGCGGGTGGGTGG   19939        AGA  A  CC
                                 GGAGGCGGC  GG GG  GG
                                 |||||||||  || ||  ||
                                 CCTCCGCCG  CC CC  CC
                                     C__  A  CA
GAM2096  FGD1     3'  AGGAGGCAGGGCTGGGTCGG  20897        CAGA  A__  C
                                 AGGAGGCGG   GG  GG CGG
                                 |||||||||   ||  || |||
                                 TCCTCCGTC   CC  CC GCC
                                     ____  GAC  A
GAM2096  FGFR4    3'  GGAGGTGTGGGGAAAGGGG   35655      C___  C    A
                                 GGAGG   GG AGAGG GG
                                 |||||   || ||||| ||
                                 CCTCC   CC TTTCC CC
                                   ACAC  C    _
GAM2096  FHIT     5'  GGAGCGCGGGGCCGGA     12872     _   CAGAGGA
                                 GGAG GCGG     GGCCGGA
                                 |||| ||||     |||||||
                                 CCTC CGCC     CCGGCCT
                                   G  ________
GAM2096  FKBP2    3'  AGAAGGTGGTGGGGTATGCTGG 38386      C  CAGA  AG_  C
             AG                   AGGAGG GG   GG  GC GGAG
                                  ||||||  ||   ||  || ||||
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                                TCTTCC CC    CC   CG CCTC
                                   A  ACC_  ATA  A
GAM2096  FPGS     3'  AGGAGGCAGGCGGGGTGTTGG  22425        _   AGA  A  CC__
                                AGGAGGC GGC   GG GG    GG
                                ||||||| |||   || ||    ||
                                TCCTCCG CCG   CC CC    CC
                                   T   ___  _  ACAA
GAM2096  FSTL3    3'  GGGGGCTGGAGGAGGCTGGAG  25222    A   GGCA       C
                                GG GGC    GAGGAGGC GGAG
                                || |||    |||||||| ||||
                                CC CCG    CTCCTCCG CCTC
                                 C   AC__       A
GAM2096  GABPB1   5'  AGGAGGTGGTGCGGGGACCCGA 23525       C  CAGA  A    G
            G                    AGGAGG GG    GG GGCC GAG
                                ||||||  ||    || |||| |||
                                TCCTCC CC    CC CTGG CTC
                                   A  ACG_  C    G
GAM2096  GARS     5'  GGAGGCGGCGGCGGGCAAGGAG 13059         AGA  A_   C_
                                GGAGGCGGC   GG  GGC  GGAG
                                |||||||||   ||  |||  ||||
                                CCTCCGCCG   CC  CCG  CCTC
                                     ___  GC   TT
GAM2096  GAS1     5'  GGGAGCGGCGGACGCGGA    13070    AG    AGA   G  C
                                GG  GCGGC   GGA GC GGA
                                ||  |||||   ||| || |||
                                CC  CGCCG   CCT CG CCT
                                 CT    ____   G  _
GAM2096  GLRX2    5'  AGGATGGTGGCAGACATGCTGG 32002      _  C     GGAG  C
                                AGGA GG GGCAGA    GC GG
                                ||||  || ||||||    || ||
                                TCCT CC CCGTCT    CG CC
                                  A  A     GTA_  A
GAM2096  GLTSCR1  3'  AGCAGGCGGCAGGGAAGGA   31831    G       A    GCC
                                AG AGGCGGCAG GGAG   GGA
                                || |||||||| ||||   |||
                                TC TCCGCCGTC CCTT   CCT
                                 G       _   ___
GAM2096  GNA15    5'  AGGAGGTGGGGAGGCCAG    40898       C  CAGA
                                AGGAGG GG    GGAGGCCGG
                                ||||||  ||    |||||||||
                                TCCTCC CC    CCTCCGGTC
                                   A  _____
GAM2096  GPC1     3'  AGGAGGCGGGGAGGAAG     13232         CA
                                AGGAGGCGG  GAGGAGG
                                |||||||||  |||||||
                                TCCTCCGCC  CTCCTTC
                                     C_
GAM2096  GPC3     5'  GGAGAGTGGCAGCCGGA     21022      _ C   GAGGAG
                                GGAG G GGCA     GCCGGA
                                |||| | ||||     ||||||
```

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                                CCTC C CCGT     CGGCCT
                                  T A   _______
GAM2096  GRB14    5'  GAGGCGGCGGGGGAGGGGAG  21036        AGA    CC
                                GAGGCGGC   GGAGG  GGAG
                                ||||||||   |||||  ||||
                                CTCCGCCG   CCTCC  CCTC
                                     CCC    __
GAM2096  GRB14    5'  AGGGGGCGGAGGAGGAGG    21028     A    CA
                                AGG GGCGG  GAGGAGG
                                |||  |||||  |||||||
                                TCC CCGCC  CTCCTCC
                                  C    TC
GAM2096  GRIN2A   5'  GGGGGCGGCTATCCCAGCCGGA 9112     A     AGAGGA
              G                  GG GGCGGC     GGCCGGAG
                                || ||||||     ||||||||
                                CC CCGCCG     TCGGCCTC
                                 C     ATAGGG
GAM2096  HIF1A    5'  AGCGGGCGGCAATCGCCGG   11346    GA      AGGAG
                                AG  GGCGGCAG    GCCGG
                                ||  |||||||     |||||
                                TC  CCGCCGTT    CGGCC
                                 GC       AG___
GAM2096  HK1      5'  GGGGCGGCAGGCGTGGGG    37918    A      A___  A
                                GG GGCGGCAG    GG GG
                                || ||||||||    || ||
                                CC CCGCCGTC    CC CC
                                 _       CGCA  _
GAM2096  HNF4A    3'  GGAGGCAGCAGAGGTGGGG   7842             A  CC
                                GGAGGCGGCAGAGG GG  GG
                                ||||||||||||||  ||  ||
                                CCTCCGTCGTCTCC CC  CC
                                         A  __
GAM2096  HOXB5    3'  GGCGGCGGCAGAGCGGGG    13449    A       GA  CC
                                GG GGCGGCAGAG  GG  GG
                                ||  ||||||||||  ||  ||
                                CC CCGCCGTCTC  CC  CC
                                 G         G_  __
GAM2096  HOXD3    3'  GGAGGCGGCGGCAGGGCAAGAG 27899          AGA  A   C
                                GGAGGCGGC   GG GGC GGAG
                                |||||||||   ||  |||  ||||
                                CCTCCGCCG   TC CCG TCTC
                                      CCG  _   T
GAM2096  HRB      5'  AGGAGGCCGGCAGGGCCGG   21081        _    AGGA
                                AGGAGGC GGCAG    GGCCGG
                                |||||||  |||||    ||||||
                                TCCTCCG CCGTC    CCGGCC
                                    G    _____
GAM2096  HS3ST3A1 5'  GGAGGCAGCGGCCGG       25807          AGAGGA
                                GGAGGCGGC     GGCCGG
                                |||||||||     ||||||
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                                CCTCCGTCG     CCGGCC
                                          ______
GAM2096  IL2RB    3'  GGAGGGAAGGAGGAGGCTGG  9385       C  CA      C
                                GGAGG GG  GAGGAGGC GG
                                ||||| ||  |||||||| ||
                                CCTCC CT  CTCCTCCG CC
                                  _ TC       A
GAM2096  IL6R     5'  AGGGGTGGCAGGGGCGGG    8166     A  C    GA  A   C
                                AGG GG GGCA  GG GGC GG
                                ||| || ||||  || ||| ||
                                TCC CC CCGT  CC CCG CC
                                  _ A   __ _  C
GAM2096  ILF1     5'  AGGAGGCGTGGGGGGG      21102        GCAGA  A  CC
                                AGGAGGCG    GG GG  GG
                                ||||||||    || ||  ||
                                TCCTCCGC    CC CC  CC
                                    AC___  _ __
GAM2096  INS      3'  AGGAGGCGGCGGGTGGGG    6818          AGA  A  CC
                                AGGAGGCGGC   GG GG  GG
                                ||||||||||   || ||  ||
                                TCCTCCGCCG   CC CC  CC
                                     C__  A  __
GAM2096  ITGBL1   5'  GGAGGCGGCAGGAGGGA     21986         GA    CCG
                                GGAGGCGGCA  GGAGG   GA
                                ||||||||||  |||||   ||
                                CCTCCGCCGT  CCTCC   CT
                                          __    ___
GAM2096  JAM2     5'  AGGAGCGCAGGAGGCCGG    34538       _  GGCAG
                                AGGAG GC    AGGAGGCCGG
                                ||||| ||    ||||||||||
                                TCCTC CG    TCCTCCGGCC
                                  G  ______
GAM2096  KCNK4    5'  AGGTGGGTGGCAGAGGAGCCGG 32487     A_  C        G
              AG                  AGG  GG GGCAGAGGAG CCGGAG
                                ||| || ||||||||| ||||||
                                TCC  CC CCGTCTCCTC GGCCTC
                                  AC  A        _
GAM2096  LAMB1    5'  GGACGCGGCAGAGGAGTGGAG  14066     G          GCC
                                GGA GCGGCAGAGGAG   GGAG
                                ||| ||||||||||||   ||||
                                CCT CGCCGTCTCCTC   CCTC
                                  G          A__
GAM2096  LBX1     3'  GGAGTGGCAGAGGAGGTCCCAG 27286      GC         __
                                GGAG  GGCAGAGGAGG  CCGG
                                ||||  ||||||||||  ||||
                                CCTC  CCGTCTCCTCC  GGTC
                                  A_         AG
GAM2096  LCN1     3'  GGGGGTGGTAGGAAGGGG    42020    A  C  C  A    CC
                                GG GG GG AG GGAGG  GG
                                || || || || |||||  ||
```

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                                CC CC CC TC CTTCC  CC
                                 C  A  A  _    __
GAM2096  LFG     3'  AGGAGGTGGAGGAGGGTGG   44131       C  CAG     CC
                                AGGAGG GG   AGGAGG  GG
                                ||||||  ||   ||||||  ||
                                TCCTCC CC   TCCTCC  CC
                                   A  ___     CA
GAM2096  LIMK1   5'  GGAGGCGGGGGCGG        14169         CAGAG A   C
                                GGAGGCGG    G GGC GG
                                ||||||||    | ||| ||
                                CCTCCGCC    C CCG CC
                                      _____ _  _
GAM2096  LRP1    5'  AGGAGGCGGGGAGGGGGGGTGG 14203          CA   A  CC_
                                AGGAGGCGG  GAGG GG   GG
                                |||||||||  ||||  ||   ||
                                TCCTCCGCC  CTCC CC   CC
                                     C_   C  CCA
GAM2096  LRP1    5'  AGGAGGCGGGGAGGGG      14202         CAGA    CC
                                AGGAGGCGG   GGAGG  GG
                                |||||||||   |||||  ||
                                TCCTCCGCC   CCTCC  CC
                                      ____    __
GAM2096  LRP1    5'  AGGGGGGGTGGGGGGCGTGG   14205     A  C  CAGA  A   C_
                                AGG GG GG   GG GGC  GG
                                ||| || ||   || |||  ||
                                TCC CC CC   CC CCG  CC
                                 _ _  CACC  _   CA
GAM2096  LSP1    3'  GGGGGCGGCAAGCAGCGGG   14240    A      G  GA   C
                                GG GGCGGCA AG  GGC GG
                                || ||||||| ||  ||| ||
                                CC CCGCCGT TC  TCG CC
                                 C      _ G_   C
GAM2096  LSP1    3'  AGGAGGTGGCAGCGGATGG   14236       C    A   _
                                AGGAGG GGCAG GGA GG
                                |||||| ||||| ||| ||
                                TCCTCC CCGTC CCT CC
                                   A    G   A
GAM2096  MAFF    3'  GGAGGGAGCTGAGGCCGGAG   29515      C   AGAG
                                GGAGG GGC   GAGGCCGGAG
                                ||||| |||   ||||||||||
                                CCTCC TCG   CTCCGGCCTC
                                  C   A___
GAM2096  MEN1    3'  AGGAGGCGGCAGGGGAGGCGGG 39147           A     C
                                AGGAGGCGGCAG GGAGGC GG
                                |||||||||||| |||||| ||
                                TCCTCCGCCGTC CCTCCG CC
                                       C     C
GAM2096  MLLT2   3'  GGGGGCGGCAGGAGCGG    25503    A     GA   GC
                                GG GGCGGCA  GGAG  CGG
                                || |||||||  ||||  |||
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                                CC CCGCCGT  CCTC  GCC
                                 C      __   __
GAM2096  MMP14    3'  AGGAGGCTGCGGGGAGGGG   22630       G  AGA    CC
                                AGGAGGC GC   GGAGG  GG
                                ||||||| ||   |||||  ||
                                TCCTCCG CG   CCTCC  CC
                                   A  CC_    __
GAM2096  MN1      5'  GAGGCGGCAGGCGCCGGGGGCT 14581          A____  A   C
            GGAG                   GAGGCGGCAG    GG GGC GGAG
                                |||||||||     || ||| ||||
                                CTCCGCCGTC    CC CCG CCTC
                                     CGCGG  C   A
GAM2096  MPDU1    3'  GGAAGCAGGGAGGCTGGA    22178        CAGA     C
                                GGAGGCGG    GGAGGC GGA
                                ||||||||    |||||| |||
                                CCTTCGTC    CCTCCG CCT
                                    ____     A
GAM2096  MSL3L1   5'  GGAGGCGGTGCGCCGTGGCCGG 38587        CAGAGGA_
                                GGAGGCGG       GGCCGG
                                ||||||||       ||||||
                                CCTCCGCC       CCGGCC
                                     ACGCGGCA
GAM2096  NCK2     3'  GGAGGCGAGTGTGGGGCCGG   44305        CAGA  A
                                GGAGGCGG    GG GGCCGG
                                ||||||||    || ||||||
                                CCTCCGCT    CC CCGGCC
                                     CACA  _
GAM2096  NF1      5'  GGGGCGTTGGCAAGGAGGCTGG 7060     A  ___   G      C
                                GG GGC   GGCA AGGAGGC GG
                                || |||   |||| ||||||| ||
                                CC CCG   CCGT TCCTCCG CC
                                  _  CAA   _      A
GAM2096  NFKB1    5'  AAGAGGCGGCGGCAGGCCGGAG 19648          AGA  _
                                AGGAGGCGGC   GG AGGCCGGAG
                                ||||||||||   || |||||||||
                                TTCTCCGCCG   CC TCCGGCCTC
                                     ___  G
GAM2096  NPEPPS   5'  GGAGGAGGCGGAGGGCCGA   26717      C   A    AG
                                GGAGG GGC GAGG  GCCGG
                                ||||| ||| ||||  |||||
                                CCTCC CCG CTCC  CGGCT
                                   T   C   __
GAM2096  OTP      3'  GGAGGCGGCGGGCGAGGGG   36996        A___    A
                                GGAGGCGGC    GAGG GG
                                |||||||||    |||| ||
                                CCTCCGCCG    CTCC CC
                                     CCCG   _
GAM2096  OXCT     5'  AGGAGGAGGCTGCGGGTTGGAG 7744        C   AGA  AGGCC
                                AGGAGG GGC   GG    GGAG
                                |||||| |||   ||    ||||
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                                TCCTCC CCG   CC    CCTC
                                   T  ACG  CAA__
GAM2096  P2RY1    5'  AGGAGGCGGCGAGAGGGC    15003          A   GA
                                AGGAGGCGGC GAG  GGC
                                |||||||||| |||  |||
                                TCCTCCGCCG CTC  CCG
                                      _  TC
GAM2096  PAX2     3'  AGGGGCGGCAGGCGGGGCTGG  19618     A       A_ A   C
                                AGG GGCGGCAG  GG GGC GG
                                ||| ||||||||  || ||| ||
                                TCC CCGCCGTC  CC CCG CC
                                  _      CG  _  A
GAM2096  PAX5     3'  GGATGAGCAGGAGGCTGG    32514     GGC    GA     C
                                GGA   GGCA  GGAGGC GG
                                |||   ||||  |||||| ||
                                CCT   TCGT  CCTCCG CC
                                  AC_   __     A
GAM2096  PCTK1    5'  AGGATGCGGCGCCAAGCCGGAG 37463      G    AGAGG
                                AGGA GCGGC    AGGCCGGAG
                                |||| |||||    |||||||||
                                TCCT CGCCG    TTCGGCCTC
                                  A    CGG__
GAM2096  PDE4A    3'  AGGAGGAGGTGGTCGG      26243       CGGCAG   A  C
                                AGGAGG     AGG GG CGG
                                ||||||     ||| || |||
                                TCCTCC     TCC CC GCC
                                   _______  A  A
GAM2096  PDE4A    3'  AGGAGGTGGTCGGGGGGAGCAGG 26244       C  CAGA  AG  C
                                AGGAGG GG    GG  GC GG
                                |||||| ||    ||  || ||
                                TCCTCC CC    CC  CG CC
                                   A  AGCC  CT  T
GAM2096  PDGFB    5'  GGAGGCAGCGGGGGGAGGCTGCG 15185          AGA     __
            G                    GGAGGCGGC   GGAGGC  CGG
                                |||||||||   ||||||  |||
                                CCTCCGTCG   CCTCCG  GCC
                                      CCC     AC
GAM2096  PFN1     5'  GGAGGCGGAGAGCTCGG     22718         C   GGAG  _
                                GGAGGCGG AGA    GC CGG
                                |||||||| |||    || |||
                                CCTCCGCC TCT    CG GCC
                                   _  _____  A
GAM2096  PGAM1    3'  GGAGGGGCAGAGGGACAAG    44058       C       A   C
                                GGAGG GGCAGAGG GGC GG
                                ||||| |||||||| ||| ||
                                CCTCC CCGTCTCC CTG TC
                                   _       _  T
GAM2096  PHKG2    5'  AGGGGGCAGGCAGAGGAGCCAG 7128      A  _        G
                                AGG GGC GGCAGAGGAG CCGG
                                ||| ||| |||||||||| ||||
```

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                                TCC CCG CCGTCTCCTC GGTC
                                  C  T       _
GAM2096  PIK3R3   5'  AGGAAGGCAAAAAAGGGGGCTG 41435     _    C    A  C
                GAG                  AGGA GGCGG AGAGG GGC GGAG
                                |||| ||||| ||||| ||| ||||
                                TCCT CCGTT TTTCC CCG CCTC
                                  T   T   C  A
GAM2096  PKP1     5'  GGAGGCGGGTGGCGCGCGGCCG 7151        CAGAGGA__
                G                  GGAGGCGG       GGCCGG
                                |||||||||       ||||||
                                CCTCCGCC       CCGGCC
                                     CACCGCGCG
GAM2096  PLA2G10  5'  GGAGGGTGGCAGAGGTGG    18674      C_      A
                                GGAGG  GGCAGAGG GG
                                |||||  |||||||| ||
                                CCTCC  CCGTCTCC CC
                                   CA      A
GAM2096  PLOD3    5'  GGAGGCGGGGGAGGGGCGG   9893       CA   A  C
                                GGAGGCGG  GAGG GGC GG
                                ||||||||  |||| ||| ||
                                CCTCCGCC  CTCC CCG CC
                                     CC   _  _
GAM2096  PLTP     3'  AGGGGCTGAGAGGGGTTGG   26346    A  GGC   A  CC
                                AGG GGC   AGAGG GG  GG
                                ||| |||   ||||| ||  ||
                                TCC CCG   TCTCC CC  CC
                                  _  AC_    _  AA
GAM2096  POMC     3'  GGAGGCGGCAGCAGGGCAGG  9603         A  A   C
                                GGAGGCGGCAG GG GGC GG
                                |||||||||| || ||| ||
                                CCTCCGCCGTC TC CCG CC
                                       G  _   T
GAM2096  PPP1R11  3'  AGAGGGAAGGAGGGGGCTGGAG 45507      C  CA   A  C
                                GGAGG GG  GAGG GGC GGAG
                                ||||| ||  |||| ||| ||||
                                TCTCC CT  CTCC CCG CCTC
                                   _ TC   C  A
GAM2096  PPP2R5A  5'  AGGAGGCGGGGGAGA      26431        CAGA
                                AGGAGGCGG   GGAGG
                                |||||||||   |||||
                                TCCTCCGCC   CCTCT
                                     C____
GAM2096  PTGIS    3'  AGGAGGCGGCAGTGGGG     9670          A  A
                                AGGAGGCGGCAG GG GG
                                |||||||||||| || ||
                                TCCTCCGCCGTC CC CC
                                       A  _
GAM2096  PTMS     5'  GGAGGCGGGGTCCCGG      15889        CAGA  AGG
                                GGAGGCGG   GG  CCGG
                                ||||||||   ||  ||||
```

```
                                CCTCCGCC   CC  GGCC
                                    ____ AG_
GAM2096 PTMS    5' AAGAGGCGGCAGAGGCGCGCGG 15878           AG _
                                AGGAGGCGGCAGAGG GC CGG
                                ||||||||||||||| || |||
                                TTCTCCGCCGTCTCC CG GCC
                                      G_ C
GAM2096 PTPN6   5' AGGGGGCGCAGGGAATGAGGAG 38703    A  G  A  GCC
                                AGG GGCG CAG GGAG  GGAG
                                ||| |||| ||| ||||  ||||
                                TCC CCGC GTC CCTT  CCTC
                                  C  _  _  ACT
GAM2096 PTPRS   3' GGAGGGGCAGAGGCATCCGG  39304     C     AGG
                                GGAGG GGCAGAGG  CCGG
                                ||||| ||||||||  ||||
                                CCTCC CCGTCTCC  GGCC
                                   _     GTA
GAM2096 RAD1    5' GGAGGCGGCACAGACCTGGAG 15994       GAGG  _
                                GGAGGCGGCA   AGGCC GGAG
                                ||||||||||   ||||| ||||
                                CCTCCGCCGT   TCTGG CCTC
                                     G___    A
GAM2096 RAD23B  5' GAAGGCGGTGGGGGTGGG   16138       CAGA A CC
                                GGAGGCGG   GG GG  GG
                                ||||||||   || ||  ||
                                CTTCCGCC   CC CC  CC
                                    AC__ _ AC
GAM2096 RAX     5' GGAGGCGGGAGGGCGCTTTGGA 30245      CA  AG  C__
          G                     GGAGGCGG  GAGG  GC  GGAG
                                ||||||||  ||||  ||  ||||
                                CCTCCGCC  CTCC  CG  CCTC
                                    __   CG  AAA
GAM2096 RFX2    3' AGGAGGCGCCGGCCGG     8446        GCAGAGGA
                                AGGAGGCG      GGCCGG
                                ||||||||      ||||||
                                TCCTCCGC      CCGGCC
                                    GG_____
GAM2096 ROR2    3' GGAGGCAGCAGAAATGGAG   21263         ___
                                GGAGGCGGCAGA  GGAG
                                ||||||||||||  ||||
                                CCTCCGTCGTCT  CCTC
                                      TTA
GAM2096 RXRA    3' GGAGGGCGGCGGGGAGGAG   16430     _  A__
                                GGAGG CGGC  GAGGAG
                                ||||| ||||  ||||||
                                CCTCC GCCG  CTCCTC
                                  C   CCC
GAM2096 S100A10 5' GGAGGCGGCGCGGGAGCGGG  40395       AGA AG C
                                GGAGGCGGC  GG  GC GG
                                |||||||||  ||  || ||
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                                CCTCCGCCG  CC  CG CC
                                     CG_  CT  C
GAM2096 SIX3    3' AGGAGGCGGAGGGGAAGGA  24016        CAG  A  CC
                                AGGAGGCGG  AGG GG  GGA
                                |||||||||  ||| ||  |||
                                TCCTCCGCC  TCC CC  CCT
                                     ___  _ TT
GAM2096 SLC29A1  3' AGGAGGCGCAGGGGAGAATGGA 22412       G  A   CC
           G                     AGGAGGCG CAG GGAGG  GGAG
                                |||||||| ||| |||||  ||||
                                TCCTCCGC GTC CCTCT  CCTC
                                     _  C    TA
GAM2096 SLC5A5   5' GGAAGCGGCGAGAGGGGCCGG  7827         _   A
                                GGAGGCGGC AGAGG GGCCGG
                                ||||||||| ||||| ||||||
                                CCTTCGCCG TCTCC CCGGCC
                                     C   _
GAM2096 SMG1    5' AGGAGGCGGCGGCGG      31501         AGAGGA  C
                                AGGAGGCGGC    GGC GG
                                ||||||||||    ||| ||
                                TCCTCCGCCG    CCG CC
                                      _______  _
GAM2096 SMG1    5' AGGCGGCGGCGGAGGGCGG  31503    A    AGA   C
                                AGG GGCGGC  GGAGG CGG
                                ||| ||||||  ||||| |||
                                TCC CCGCCG  CCTCC GCC
                                  G    ___    C
GAM2096 SMT3H1   5' GGAGGCGGCGCGGGGGAA   40998       AGA  A  CC
                                GGAGGCGGC  GG GG  GGA
                                |||||||||  || ||  |||
                                CCTCCGCCG  CC CC  CTT
                                     CG_  _  __
GAM2096 SOX12    3' AGGGGGGTGTGGGGAGGCCGGA 28025    A  C  CAGA_
           G                     AGG GG GG    GGAGGCCGGAG
                                ||| || ||    ||||||||||
                                TCC CC CC    CCTCCGGCCTC
                                  _  _  ACACC
GAM2096 SREBF1   3' AGGGGTGCTGAGGCCGG    45368    A  CG  AGAG
                                AGG GG  GC   GAGGCCGG
                                ||| ||  ||   ||||||||
                                TCC CC  CG   CTCCGGCC
                                  _  A_  A___
GAM2096 STAU    5' AGGAGGCGGGCGCCGCCGGGCC 32689        _ AGAGGA_
           GG                     AGGAGGCGG C      GGCCGG
                                |||||||||  |      ||||||
                                TCCTCCGCC G      CCGGCC
                                     C CGGCGGC
GAM2096 STX1A    3' AGGGGTTGCTCCTGGGGCCGGA 21408    A  CG  AGA_  A
           G                     AGG GG  GC   GG GGCCGGAG
                                ||| ||  ||   || ||||||||
```

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                                TCC CC  CG    CC CCGGCCTC
                                  _ AA  AGGA  _
GAM2096  SUPT6H   3'  AGGAGGGGCAGGGAGGGA    41284       C     A    CCG
                                AGGAGG GGCAG GGAGG   GA
                                |||||| ||||| |||||   ||
                                TCCTCC CCGTC CCTCC   CT
                                   _    _    ____
GAM2096  TBP      3'  AGGGGGTGGGGGAGGCAAGG   42111     A  C  CAGA     C_
                                AGG GG GG    GGAGGC  GG
                                ||| || ||    ||||||  ||
                                TCC CC CC    CCTCCG  CC
                                  C  A  C___     TT
GAM2096  TCIRG1   5'  AGGAGGAGGCGGGGCCAG    25836       C   AGA  A
                                AGGAGG GGC   GG GGCCGG
                                |||||| |||   || ||||||
                                TCCTCC CCG   CC CCGGTC
                                   T  ____ _
GAM2096  TGFB1    3'  AGGAGGAGGCAGAGAGGGA    8533        C      G   CCG
                                AGGAGG GGCAGAG AGG   GA
                                |||||| ||||||| |||   ||
                                TCCTCC CCGTCTC TCC   CT
                                   T      _  ____
GAM2096  TLR9     3'  GGAGGCGAGCAGGGGAGG     32661         _    A
                                GGAGGCG GCAG GGAGG
                                ||||||| |||| |||||
                                CCTCCGC CGTC CCTCC
                                    T   C
GAM2096  UBE2A    5'  AGGAGGCCGAAGAGGCTGGAG  17784        GGCA       C
                                AGGAGGC    GAGGAGGC GGAG
                                |||||||    |||||||| ||||
                                TCCTCCG    CTTCTCCG CCTC
                                   G___       A
GAM2096  UBE2V1   3'  GGAGGCGGGAGGGTAAAGGGAG 35347         CA    AGGCC_
                                GGAGGCGG  GAGG     GGAG
                                ||||||||  ||||     ||||
                                CCTCCGCC  CTCC     CCTC
                                    __    CATTTC
GAM2096  UBE2V1   3'  GGAGGCGGGAGGGTAAGGGG   35348        CA   ___   CC
                                GGAGGCGG  GAGG   AGG  GG
                                ||||||||  ||||   |||  ||
                                CCTCCGCC  CTCC   TCC  CC
                                    __    CAT   __
GAM2096  USP14    5'  GGAGGCGGCGGCGCAGGA    23115         AGA  AG  C
                                GGAGGCGGC   GG  GC GGA
                                |||||||||   ||  || |||
                                CCTCCGCCG   CC  CG CCT
                                    ____ G_  T
GAM2096  VASP     3'  AGGGGATGGCAGAGGGG     17913     A  C_       A
                                AGG GG  GGCAGAGG GG
                                ||| ||  |||||||| ||
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                                TCC CC  CCGTCTCC CC
                                  _  TA      _
GAM2096  VDR      3'  GGAGGTGGCAGAGGAGGGG   7522       C         CC
                                GGAGG GGCAGAGGAGG  GG
                                ||||| ||||||||||  ||
                                CCTCC CCGTCTCCTCC  CC
                                   A         __
GAM2096  WDR1     5'  AGTGGGCGGTCCGAGGCCGG  32748    GA    CAGAG
                                AG  GGCGG    GAGGCCGG
                                ||  |||||    ||||||||
                                TC  CCGCC    CTCCGGCC
                                 AC    AGG__
GAM2096  WNT5A    5'  GGGGGGTGGAGGATGGGG    18123    A  C  CA    _  CC
                                GG GG GG  GAGGA GG  GG
                                || || ||  ||||| ||  ||
                                CC CC CC  CTCCT CC  CC
                                 _ _  AC    A  __
GAM2096  YY1      5'  AGGAGGCGGCCGGCCG      18164          AGAGGA
                                AGGAGGCGGC     GGCCG
                                ||||||||||     |||||
                                TCCTCCGCCG     CCGGC
                                     G_____
GAM2096  ZNF16    3'  GGAAGTGGCAGAGGCTGA    28085      C       AGGCCG
                                GGAGG GGCAGAGG     GA
                                ||||| ||||||||     ||
                                CCTTC CCGTCTCC     CT
                                   A       GA____
GAM2096  ZNF274   5'  AGGGGCGGCAGGCGAAGCCGG  32246     A       AG
                                AGG GGCGGCAG  GAGGCCGG
                                ||| ||||||||  ||||||||
                                TCC CCGCCGTC  CTTCGGCC
                                  _       CG
GAM2096  ZNFN2A1  5'  GGGGGCCGCAGGGCGCCAG   41363    A   G    A  AG
                                GG GGC GCAG GG  GCCGG
                                || ||| |||| ||  |||||
                                CC CCG CGTC CC  CGGTC
                                 C   G    _  G_
GAM2097  B3GALT5  3'  GAAACTTGGGTTGTG       37681         CC   CGCC
                                GAAACTTG  GGT    GTG
                                ||||||||  |||    |||
                                CTTTGAAC  CCA    CAC
                                     __   A___
GAM2097  SOCS4    3'  TGGAAATTTGTGGCTGC     38923        C   CC   C
                                TGGAAA TTG  GGT GC
                                ||||||  |||  ||| ||
                                ACCTTT AAC  CCG CG
                                   A  A_   A
GAM2098  COG7     3'  GGACATGATGTACTGCCC    42658         C__  _
                                GGACATGA   GC GCCC
                                ||||||||   || ||||
```

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                              CCTGTACT  TG CGGG
                                   ACA  A
GAM2098 KITLG    3' GGTACATGCAGTCTGAGACACG 19646    _    A  CGCCCA
             T                  GG ACATG CG     AGACACGT
                              || ||||| ||     ||||||||
                              CC TGTAC GT     TCTGTGCA
                               A    _  CAGAC_
GAM2099 SDHD     3' TATTATATAACATTTTAT    16532
                              TATTATATAATATTTTAT
                              ||||||||||||||||||
                              ATAATATATTGTAAAATA

GAM2100 ADAM11   3' CTCCTGTAAATGTCAAAAC   14388         AGA_
                              TTCCTGTAAA   AAAAC
                              ||||||||||   |||||
                              GAGGACATTT   TTTTG
                                    ACAG
GAM2100 KRT1     3' TCTCCACAAAAGAAAAAC    25939    _ TG
                              TC C  TAAAAGAAAAAC
                              || |  ||||||||||||
                              AG G  GTTTTCTTTTTG
                               A GT
GAM2100 OTOF     3' CTCCAAGAAAAGAAAAAC    22057     TGT
                              TTCC   AAAAGAAAAAC
                              ||||   ||||||||||
                              GAGG   TTTTCTTTTTG
                                TTC
GAM2100 TNFSF4   3' TCCCTGTATACAAGAAAA    17753        A__
                              TTCCTGTA   AAGAAAA
                              ||||||||   |||||||
                              AGGGACAT   TTCTTTT
                                   ATG
GAM2100 ATP8B2   3' TTTCTTGTTTTTGGTTCCAC  42225        CTAC    AA
                              TTTCTTGT   TGGTT  CAT
                              ||||||||   |||||  |||
                              AAAGAACA   ACCAA  GTG
                                   AAA_    G_
GAM2100 INMT     3' TTCCTTGTCCTTAACATA    27685         ACTGG
                              TTTCTTGTCT    TTAACATA
                              ||||||||||    ||||||||
                              AAGGAACAGG    AATTGTAT
                                             _____
GAM2100 VEGF     3' TTTCTTGTTTGGTTTGAACATA 17977        CTAC    __
             T                  TTTCTTGT   TGGTT  AACATAT
                              ||||||||   |||||  |||||||
                              AAAGAACA   ACCAA  TTGTATA
                                   A___    AC
GAM2101 BAZ2A    3' CTTTTCTACAGCTGCAC     30307       GATT
                              TTTTTT   TAGCTGCAC
                              ||||||   |||||||||
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                                GAAAAG   GTCGACGTG
                                   AT__
GAM2101  CARD15   3'  TTTTTTAAAGCTGCA      35263        TTT
                                TTTTTTGA   AGCTGCA
                                ||||||||   |||||||
                                AAAAAATT   TCGACGT
                                    ___
GAM2101  CUGBP1   5'  TTCTTTGAGCAGCGGCTGCACC 27279        TTTA__
                                TTTTTTGA     GCTGCACC
                                ||||||||     ||||||||
                                AAGAAACT     CGACGTGG
                                     CGTCGC
GAM2101  GGT1     5'  TTTTGGGCTGCACCC      23575      ATTTA
                                TTTTG    GCTGCACCC
                                |||||    |||||||||
                                AAAAC    CGACGTGGG
                                   C_____
GAM2101  RRM2     5'  TTCCCATTGGCTGCGCC     9764      G   TA    A
                                TTTT ATT  GCTGC CC
                                |||| |||  ||||| ||
                                AAGG TAA  CGACG GG
                                  G   C_    C
GAM2101  CIT      5'  TCTGCTCCTCGTGCTCTAGACT 43057    C       AC  G
                                TC GCTCTTCGT  CT TAGACT
                                || |||||||||  || ||||||
                                AG CGAGGAGCA  GA ATCTGA
                                 A        C_  G
GAM2101  MSF      3'  GCTCTTCAGCTGTGGACT    44733        TAC    A
                                GCTCTTCG   CTGT GACT
                                ||||||||   |||| ||||
                                CGAGAAGT   GACA CTGA
                                     C__    C
GAM2102  AS3      3'  TTCAGCAGTCCCATTTTGTGCA 31981     G    T    C
              T                  TTC AGTA TTCCA TTTGTGCAT
                                 ||| |||| ||||| |||||||||
                                 AAG TCGT AGGGT AAACACGTA
                                   _   C    A
GAM2102  GNB1     3'  GAGCATTTCTACAGCA      13204         C  TTTGT
                                GAGTATTTC AC     GCA
                                |||||||||  ||    |||
                                CTCGTAAAG TG     CGT
                                     A  T_____
GAM2102  ICAM1    3'  TTCAGTATTTCCCAGTTGTA   43438     G       ACT
                                TTC AGTATTTCC   TTGTG
                                ||| |||||||||   |||||
                                AAG TCATAAAGG   AACAT
                                  _       GTC
GAM2103  BACH2    3'  AGAGGAATGTTGGAACCTG   34769        CATC    G
                                AGAGGAAT    GGAA CTG
                                ||||||||    |||| |||
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                                TCTCCTTA   CCTT GAC
                                     CAA_   G
GAM2103 DIAPH2   3' AAAGGAATTATCTGTGGGCT  28663       C  GGAA_
                                AGAGGAAT ATC    GCT
                                |||||||| |||    |||
                                TTTCCTTA TAG    CGA
                                     A  ACACC
GAM2103 ELAC2    3' AGGGAATCACTTTGCTG    32850   A     CGGAA
                                AG GGAATCAT    GCTG
                                || ||||||||    ||||
                                TC CCTTAGTG    CGAC
                                 _      AAA__
GAM2103 KCNE1L   3' AAGGCAACTGGAAGCTGGACT 29370    AATC  C      A
                                GAGG   AT GGAAGCTG ACT
                                ||||   || |||||||| |||
                                TTCC   TG CCTTCGAC TGA
                                  GT__  A      C
GAM2103 PRKY     3' AGAGGGAGTGGGGCTGAACT  15684     AATCATC  AA
                                AGAGG     GG  GCTGAACT
                                |||||      ||  |||||||||
                                TCTCC     CC  CGACTTGA
                                   CTCA___  C_
GAM2103 PTTG1IP  3' AGAGCGGCTGGAAGCTGGACT 20279    GAATCATC      A
                                AGAG      GGAAGCTG ACT
                                ||||      |||||||| |||
                                TCTC      CCTTCGAC TGA
                                  GCCGA___       C
GAM2103 RAD23A   3' GAGGACAGGAAGCTGGACT   22794     ATCATC      A
                                GAGGA     GGAAGCTG ACT
                                |||||     |||||||| |||
                                CTCCT     CCTTCGAC TGA
                                   GT____       C
GAM2103 SLC9A3R1 3' GAGGAACCAGCTGAA      43249       TCGGAA
                                GAGGAATCA     GCTGAA
                                |||||||||     ||||||
                                CTCCTTGGT     CGACTT
                                          _______
GAM2103 TEM8     3' AGAGGAATTAGTGGGAGCC   38172       CATC  A
                                AGAGGAAT   GG AGCT
                                ||||||||   || ||||
                                TCTCCTTA   CC TCGG
                                     ATCA  C
GAM2103 TRPM6    3' AGAGGCAATCATTGGCAAACT 32781     _    C  _
                                AGAGG AATCAT GG AAGCT
                                ||||| |||||| || |||||
                                TCTCC TTAGTA CC TTTGA
                                   G     A  G
GAM2103 ETF1     3' TTTGGTATACTTTTTTCCATCG 21835       C____   _
                                TTTGGTATAC    TCCA CG
                                ||||||||||    |||| ||
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                                AAACCATATG    AGGT GC
                                     AAAAA   A
GAM2103 FGA     3' CCTTGGTATATCTTTACAA  34838        C  CC
                                CTTTGGTATA CT  ACGA
                                |||||||||| ||  ||||
                                GGAACCATAT GA  TGTT
                                     A  AA
GAM2104 AK1     3' GAGACGGAGTCTTGCTCTGT  7875    AA     CAA  AG
                                GA  ACGGAGTC  CT  TGT
                                ||  ||||||||  ||  |||
                                CT  TGCCTCAG  GA  ACA
                                 C_     AAC  G_
GAM2104 DAPP1   3' ACGGAGTCTGACTCTGT    30811       CA   AG
                                ACGGAGTC  ACT  TGT
                                ||||||||  |||  |||
                                TGCCTCAG  TGA  ACA
                                    AC   G_
GAM2104 DFFA    3' GAGACGGAGTCTCGCTCTGT  20581   AA     CAA  AG
                                GA  ACGGAGTC  CT  TGT
                                ||  ||||||||  ||  |||
                                CT  TGCCTCAG  GA  ACA
                                 C_     AGC  G_
GAM2104 DMC1    3' GAGACGGAGTCTCACTCTGT  28199   AA     CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_     AG   G_
GAM2104 GRAF    3' GAGACGGAGTCTGGCTCTGT  31446   AA     CAA  AG
                                GA  ACGGAGTC  CT  TGT
                                ||  ||||||||  ||  |||
                                CT  TGCCTCAG  GA  ACA
                                 C_     ACC  G_
GAM2104 IL1R1   3' GAGACGGAGTCTTGCTCTGT  9358    AA     CAA  AG
                                GA  ACGGAGTC  CT  TGT
                                ||  ||||||||  ||  |||
                                CT  TGCCTCAG  GA  ACA
                                 C_     AAC  G_
GAM2104 ITGAL   3' GAGACGGAGTCTCGCTGTGT  13618   AA     CAA  A
                                GA  ACGGAGTC  CT GTGT
                                ||  ||||||||  || ||||
                                CT  TGCCTCAG  GA CACA
                                 C_     AGC  _
GAM2104 LDLR    3' GAGACGGAGTCTCGCTCTGT  8026    AA     CAA  AG
                                GA  ACGGAGTC  CT  TGT
                                ||  ||||||||  ||  |||
                                CT  TGCCTCAG  GA  ACA
                                 C_     AGC  G_
GAM2104 OGG1    5' GAGACGGAGTCTCACTCTGT  32564   AA     CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
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                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2104  PSMB2    3'  GAGACGGAGTCTCACTCTGT  15818    AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2104  RAB7L1   3'  GAGACGGAGTCCTTCTCTGT  19434    AA      AA   AG
                                GA  ACGGAGTCC  CT  TGT
                                ||  |||||||||  ||  |||
                                CT  TGCCTCAGG  GA  ACA
                                 C_      AA   G_
GAM2104  SLC26A4  3'  GAGACGGAGTCTTGCTCTGT  7762     AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AAC  G_
GAM2104  SLC2A3   3'  GAGACGGAGTCTCGCCCTGT  27977    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GG  ACA
                                 C_      AGC  G_
GAM2104  TEM7     3'  GAGACGGAGTCTCGCTCTGT  33809    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2104  VHL      3'  GAGACGGAGTCTCACTCTGT  8108     AA      CA   AG
                                GA  ACGGAGTC  ACT  TGT
                                ||  ||||||||  |||  |||
                                CT  TGCCTCAG  TGA  ACA
                                 C_      AG   G_
GAM2104  WRB      3'  TCGAGGACGGTGTTCACTAGT  21546     AA   A  CCA
                                TCGA  ACGG GT   ACTAGT
                                ||||  |||| ||   ||||||
                                AGCT  TGCC CA   TGATCA
                                  CC    A  AG_
GAM2104  ZNF91    3'  GAGACGGAGTCTCGCTCTGT  18316    AA      CAA  AG
                                GA  ACGGAGTC   CT  TGT
                                ||  ||||||||   ||  |||
                                CT  TGCCTCAG   GA  ACA
                                 C_      AGC  G_
GAM2104  ABCD4    3'  TTCATCAAGCACTGCG      33752       TG CGC
                                TTCGT  G   GCACTGCG
                                |||||  |   ||||||||
                                AAGTA  T   CGTGACGC
                                   GT ___
GAM2104  FGFR1    5'  TTCCTCCGCGCGCTGCG     35792     G  G     AC
                                TTC TT GCGCGC  TGCG
                                |||  ||  ||||||  ||||
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                                AAG AG CGCGCG  ACGC
                                  G  G     __
GAM2104  MATN2    3'  TTGGGGCTCTGCACTGCG    14373      C  ___
                                TTGG GC   GCACTGCG
                                |||| ||   ||||||||
                                AACC CG   CGTGACGC
                                  C  AGA
GAM2104  NR1H2    3'  TTCAAGGTGCACTGCG      43121      TT  CGC
                                TTCG  GG   GCACTGCG
                                ||||  ||   ||||||||
                                AAGT  CC   CGTGACGC
                                  T_  A__
GAM2104  PELO     5'  CTCCCGGCGCGCTGCG      31982     G        AC
                                TTC TTGGCGCGC  TGCG
                                ||| |||||||||  ||||
                                GAG GGCCGCGCG  ACGC
                                  _       __
GAM2104  PTPN2    5'  GCGGCGCATGCGCGCTGCG    15915    T    ____  A
                                GT GGCGC    GC CTGCG
                                || |||||    || |||||
                                CG CCGCG    CG GACGC
                                 _     TACG  C
GAM2105  FADD     3'  TGTAGAATTGCAGGACCCA    19247         AC  T    A
                                TGTAGAATT  CG GGATC CA
                                |||||||||  || ||||| ||
                                ACATCTTAA  GT CCTGG GT
                                     C_  _    _
GAM2105  PPAT     3'  TGTAGAATTACTAAACTGTCAC 15486          CGTGGA_
              A                  TGTAGAATTAC      TCACA
                                 ||||||||||||      |||||
                                 ACATCTTAATG      AGTGT
                                       ATTTGAC
GAM2105  ARNTL    3'  CAAAATATACAATTAATGCAAG 10131          CTTT__
                                 CAAAATATAT     TGCAAG
                                 ||||||||||     ||||||
                                 GTTTTATATG     ACGTTC
                                       TTAATT
GAM2105  DSCR2    3'  CAAAATATATCCCCCAAAAG   18987           TT C
                                 CAAAATATATCTT  G AAG
                                 ||||||||||||  | |||
                                 GTTTTATATAGGG  T TTC
                                        GG T
GAM2105  ERBB2    3'  CAAAATATATTTGCAAA     20817          CTT
                                 CAAAATATAT   TTGCAAG
                                 ||||||||||   |||||||
                                 GTTTTATATA   AACGTTT
                                              ___
GAM2105  FBP1     3'  CAAAATATATCTTAACA     7999             TT
                                 CAAAATATATCTT  GCA
                                 ||||||||||||  |||
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                                GTTTTATATAGAA  TGT
                                       T_
GAM2105  GORASP1   3'  CAAAAGATATCCTCCCACAAG  36703      T     _ TG
                                CAAAA ATATCTT T  CAAG
                                ||||| ||||||| |  ||||
                                GTTTT TATAGGA G  GTTC
                                   C      G GT
GAM2105  MLLT2     3'  CAAAATATTCTTGCAAG     25493        ATC
                                CAAAATAT   TTTTGCAAG
                                ||||||||   |||||||||
                                GTTTTATA   AGAACGTTC
                                    ___
GAM2105  PCTK1     5'  CAAACGGGACTTTTGCAAG   37465      ATATAT
                                CAAA     CTTTTGCAAG
                                ||||     ||||||||||
                                GTTT     GAAAACGTTC
                                  GCCCT_
GAM2105  SNCAIP    3'  CAAAATGAATCTTTTACA    45502       AT
                                CAAAAT  ATCTTTTGCA
                                ||||||  ||||||||||
                                GTTTTA  TAGAAAATGT
                                   CT
GAM2105  TEX15     3'  TGAAACATATCAGAAGCAAG  36328   A       TTTT
                                C AAATATATC    GCAAG
                                | |||||||||    |||||
                                A TTTGTATAG    CGTTC
                                 C        TCTT
GAM2106  MATN3     3'  CAAGCATTAATACAGA      14374         TTCGT
                                CAAGTATTAA     TACAGA
                                ||||||||||     ||||||
                                GTTCGTAATT     ATGTCT
                                      _____
GAM2106  TRPS1     3'  TACTGCTTTAGTATAATAATA  30466       CC  AAT
                                TACTGCT  AG   TAATAATA
                                |||||||  ||   ||||||||
                                ATGACGA  TC   ATTATTAT
                                    AA  AT_
GAM2107  ACCN2     3'  TACAGCACCAGGGCCGCA    33454          TTCT  A
                                TACAGCACCAGG    CC CA
                                ||||||||||||    || ||
                                ATGTCGTGGTCC    GG GT
                                       C___  C
GAM2107  ACVR1B    3'  GCACTGAGTTCTCCACAC    33759      CA
                                GCAC  GGTTCTCCACAC
                                ||||  ||||||||||||
                                CGTG  TCAAGAGGTGTG
                                  AC
GAM2107  ADAMTS4   5'  GCACCAAGTCCTCCACAC    23008
                                GCACCAGGTTCTCCACAC
                                ||||||||||||||||||
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                                CGTGGTTCAGGAGGTGTG

GAM2107 AF3P21   3' TACAGCACATAGGAAAATACAC 32403       C_  TTCTC_
                                TACAGCAC AGG    CAC
                                |||||||| |||    |||
                                ATGTCGTG TCC    GTG
                                    TA  TTTTAT
GAM2107 AK3      3' CACAGCACCAATACTACAC   30178        GTT  C
                                TACAGCACCAG  CT CAC
                                ||||||||||  || |||
                                GTGTCGTGGTT  GA GTG
                                      AT_  T
GAM2107 C18orf1  3' TACAGCACAGAGCCACCGCAC 41227       C  TT T  A
                                TACAGCAC AGG  C CC CAC
                                |||||||| |||  | || |||
                                ATGTCGTG TCT  G GG GTG
                                    _  CG T  C
GAM2107 C18orf1  3' TAAGCCCTTCTCCAC      41226   C   A  AGG
                                A AGC CC   TTCTCCAC
                                | ||| ||   ||||||||
                                A TCG GG   AAGAGGTG
                                 T  _ ___
GAM2107 CLK2     3' GCAGCCTATACTCCACAC    41277    _ AG  T
                                GCA CC  GT CTCCACAC
                                ||| ||  || ||||||||
                                CGT GG  TA GAGGTGTG
                                  C  A_  T
GAM2107 CNTNAP2  3' TACACACCAGGTGCCA     30492     G      TCT
                                TACA CACCAGGT   CCA
                                |||| ||||||||   |||
                                ATGT GTGGTCCA   GGT
                                  _      C__
GAM2107 CTLA4    3' CAGCACAATTCCAC       23327       CA   TC
                                CAGCAC  GGT  TCCAC
                                ||||||  |||  |||||
                                GTCGTG  TTA  AGGTG
                                   __   __
GAM2107 DDX11    3' CAGCGCTCTGGACTCCACAC  36170     ACCA_  TT
                                CAGC    GG  CTCCACAC
                                ||||    ||  ||||||||
                                GTCG    CC  GAGGTGTG
                                  CGAGA  T_
GAM2107 DDX11    3' CAGCACTCTGGACTCCACAC  36169      CA_  TT
                                CAGCAC   GG  CTCCACAC
                                ||||||   ||  ||||||||
                                GTCGTG   CC  GAGGTGTG
                                   AGA  T_
GAM2107 DGCR2    3' CAGCACCACAGAACTGCA    23086        _  TT  C
                                CAGCACCA GG  CT CA
                                |||||||| ||  || ||
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                                GTCGTGGT TC  GA GT
                                     G  TT  C
GAM2107  DUOX2    3'  TAAGCATCACAGCTTCTGCAC  30449   C   C__  G   C
                                A AGCA   CAG TTCT CAC
                                | ||||   ||| |||| |||
                                A TCGT   GTC AAGA GTG
                                 T   AGT   G   C
GAM2107  DVL1     3'  TACAGCACAGACAC       40415        C   TTCTC
                                TACAGCAC AGG    CAC
                                |||||||| |||    |||
                                ATGTCGTG TCT    GTG
                                   _  _____
GAM2107  EPHA3    3'  TACACACCAAAACTGCAC    23441     G     TT  C
                                TACA CACCAGG  CT CAC
                                |||| |||||||  || |||
                                ATGT GTGGTTT  GA GTG
                                  _     T_  C
GAM2107  EPHB2    3'  GCGCCTCCCCCTCCACAC    32672    A  AGG
                                GC CC   TTCTCCACAC
                                || ||   ||||||||||
                                CG GG   GGGAGGTGTG
                                 C  AGG
GAM2107  EXTL1    3'  CACAGCGTTCACCCTCCACA   20863       ACCAG TT
                                TACAGC    G  CTCCACA
                                ||||||    |  |||||||
                                GTGTCG    T  GAGGTGT
                                   CAAG_ GG
GAM2107  FLOT2    3'  TACAGCACTCGATTCTGTAC   20984        CA    CC
                                TACAGCAC  GGTTCT  AC
                                ||||||||  ||||||  ||
                                ATGTCGTG  CTAAGA  TG
                                     AG    CA
GAM2107  GRB10    5'  GCACCGCTTGGACTCCACAC   23657      A___  TT
                                GCACC   GG  CTCCACAC
                                |||||   ||  ||||||||
                                CGTGG   CC  GAGGTGTG
                                  CGAA  T_
GAM2107  GRM4     3'  CAGCACCAAGCCAC       9156          TTCT
                                CAGCACCAGG   CCAC
                                ||||||||||   ||||
                                GTCGTGGTTC   GGTG
                                    _____
GAM2107  GSK3B    5'  CAGCATTAAGTTCTCCCAC   13302      CC       A
                                CAGCA  AGGTTCTCC CAC
                                |||||  ||||||||| |||
                                GTCGT  TTCAAGAGG GTG
                                  AA       _
GAM2107  HIF1A    5'  TAAGCGCTGGCTCCCTCCACAC 11351   C   ACCA  __
                                A AGC   GGT  TCTCCACAC
                                | |||   |||  |||||||||
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                                A TCG   CCG  GGAGGTGTG
                                 T  CGA_  AG
GAM2107  IFNA4    3'  ACACCAAGCTTCTTCACAC   34334         _  C
                                GCACCAGGTT CT CACAC
                                |||||||||| || |||||
                                TGTGGTTCGA GA GTGTG
                                     A  A
GAM2107  IL6R     3'  CAGCCGCTTCTCCACAC     8167      ACCAGG
                                CAGC     TTCTCCACAC
                                ||||     ||||||||||
                                GTCG     AAGAGGTGTG
                                  GCG___
GAM2107  ITGA1    3'  TACAGCACAGGGTAACCA    41852        CA   TCT
                                TACAGCAC  GGT   CCA
                                ||||||||  |||   |||
                                ATGTCGTG  CCA   GGT
                                     TC   TT_
GAM2107  LDHB     5'  ACAGCACCTCCACA       14113        AGGTTC
                                ACAGCACC     TCCACA
                                ||||||||     ||||||
                                TGTCGTGG     AGGTGT
                                     _______
GAM2107  MAP1B    5'  CACAGCACTGAAATTCTCTACA 25390        C_      C
                                TACAGCAC  AGGTTCTC ACA
                                ||||||||  |||||||| |||
                                GTGTCGTG  TTTAAGAG TGT
                                     AC       A
GAM2107  MECP2    3'  TACAGTGTCCAGATACAC    22609      CA_     TCTC
                                TACAG   CCAGGT   CAC
                                |||||   ||||||   |||
                                ATGTC   GGTCTA   GTG
                                   ACA     T___
GAM2107  NOC4     3'  CAGCACCAGCACTCCAC     25865        GTT
                                CAGCACCAG   CTCCAC
                                |||||||||   ||||||
                                GTCGTGGTC   GAGGTG
                                     GT_
GAM2107  OLR1     3'  TGAGCAAGTTCTCCA       14943    C   CCA
                                A AGCA   GGTTCTCCA
                                | ||||   |||||||||
                                A TCGT   TCAAGAGGT
                                 C   ___
GAM2107  OSCAR    3'  TACAGCACAGGGCAC       39310        C   TTCTC
                                TACAGCAC AGG    CAC
                                |||||||| |||    |||
                                ATGTCGTG TCC    GTG
                                     _  C_____
GAM2107  PCDHA11  5'  TACAGTACCAGATTCTTCA   36579      C        C
                                TACAG ACCAGGTTCT CA
                                ||||| |||||||||| ||
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                                ATGTC TGGTCTAAGA GT
                                   A         A
GAM2107  PHLDA3   3'  CAGCGCCTCCTCCACAC     29610      A  AGG
                                CAGC CC   TTCTCCACAC
                                |||| ||   ||||||||||
                                GTCG GG   AGGAGGTGTG
                                  C  ___
GAM2107  PIK3C2B  3'  TACAGCCCACCCCACA      15294       A   GGTT
                                TACAGC CCA    CTCCACA
                                |||||| |||    |||||||
                                ATGTCG GGT    GGGGTGT
                                   _  _____
GAM2107  PIK3R3   3'  ACGGCACCAAAGTCACA     41431    A      _  TCTC
                                AC GCACCAG GT    CACA
                                || ||||||| ||    ||||
                                TG CGTGGTT CA    GTGT
                                 C      T  _____
GAM2107  RXRA     3'  TACAGCACATACATGTTTACAC 16434         ___  G   CTC
                                TACAGCAC   CA GTT   CAC
                                ||||||||   || |||   |||
                                ATGTCGTG   GT CAA   GTG
                                     TAT  A   AT_
GAM2107  SLC12A2  5'  CAGCACGCCCTCCACAC     9823        CAG
                                CAGCAC   GTTCTCCACAC
                                ||||||   ||||||||||||
                                GTCGTG   CGGGAGGTGTG
                                   ___
GAM2107  SLC17A1  3'  GCAAGTGCTCTGTTTCACAC  22904     CC  _    C___
                                GCA  AG GTTCT    CACAC
                                |||  || |||||    |||||
                                CGT  TC CGAGA    GTGTG
                                  __  A    CAAA
GAM2107  STK19    3'  ACAGCACCATTTTACAC     20084         GG  CTC
                                ACAGCACCA  TT   CAC
                                |||||||||  ||   |||
                                TGTCGTGGT  AA   GTG
                                     AA  T__
GAM2107  TARDBP   3'  CACCACCAAGTCTCTGCAC   28905    G      _  C
                                CA CACCAGGT TCT CAC
                                || |||||||| ||| |||
                                GT GTGGTTCA AGA GTG
                                 G      G   C
GAM2107  TPM1     3'  AGCACCAATCCACA       7482          GTTC
                                AGCACCAG    TCCACA
                                ||||||||    ||||||
                                TCGTGGTT    AGGTGT
                                   _____
GAM2107  TRIM9    3'  TACACACCAGGGGCACA     38138      G      TTCTC
                                TACA CACCAGG    CACA
                                |||| |||||||    ||||
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                                ATGT GTGGTCC    GTGT
                                  _     CC___
GAM2107  ADRBK1   3'  TCGGGGAAGGGGCGGGAG    11541          GA
                                TCGGGGAAGGGG  GGAG
                                ||||||||||||  ||||
                                AGCCCCTTCCCC  CCTC
                                      GC
GAM2107  BACH2    3'  GGGAAGGGGACAGGGAGGGTT  34795         _  A  A
                                GGGAAGGGGG AGG GA GGTT
                                |||||||||| ||| || ||||
                                CCCTTCCCCT TCC CT CCAA
                                      G  _  C
GAM2107  BTG2     3'  AGGGAAGGGGGAGGGGAGGGTT 27616           A  A
                                GGGGAAGGGGGAGG GA GGTT
                                |||||||||||||| || ||||
                                TCCCTTCCCCCTCC CT CCAA
                                      C  C
GAM2107  CLN2     3'  GGGGAGGGAGGAGGAAAAA   7556       A
                                GGGGA GGGGGAGGAGAAG
                                ||||| ||||||||||||
                                CCCCT CCTCCTCCTTTTT
                                   C
GAM2107  HM13     3'  CCGGGGAGGGGGGAAGCTGGGG 43108        A       AGAA_
            GTT                   TCGGGGA GGGGGAGG    GGTT
                                ||||||| ||||||||    ||||
                                GGCCCCT CCCCCTTC    CCAA
                                   C       GACCC
GAM2107  KCNC4    5'  CGGGGGAGGGGGAGGAGA    22528      A
                                CGGGG AGGGGGAGGAGA
                                ||||| ||||||||||
                                GCCCC TCCCCCTCCTCT
                                   C
GAM2107  MN1      5'  GGGGAGGGAAGGGGGT      14587      AG      AGAA
                                GGGGA  GGGGAGG   GGT
                                |||||  |||||||   |||
                                CCCCT  CCCTTCC   CCA
                                   __      C___
GAM2107  NPTX1    3'  GGGGAGGGGGAGAGGGAAA   14841      A   _   A
                                GGGGA GGGG GAGG GAAG
                                ||||| |||| |||| ||||
                                CCCCT CCCC CTCC CTTT
                                   C   T   _
GAM2107  OPHN1    3'  TCGGGGGAGGGGGGAGGGA   14973       AA_      A
                                TCGGGG   GGGGGAGG GA
                                ||||||   |||||||| ||
                                AGCCCC   CCCCCTCC CT
                                   CTC      _
GAM2107  RAD21    5'  TCGGGGGAGGGGGGTGGGGA   26530       A     A  A
                                TCGGGG AGGGGG GG GA
                                |||||| |||||| || ||
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                                AGCCCC TCCCCC CC CT
                                   C     A  C
GAM2107  RBMX     3'  GGGGAAGGGAAAGGGGAGGTT  42810        GG   A  A
                                GGGGAAGGG  AGG GA GGTT
                                |||||||||  ||| || ||||
                                CCCCTTCCC  TCC CT CCAA
                                     TT   C  _
GAM2107  SHC1     3'  GGGGAAGGGGCATCAGGTT   16704         GAGGAGA
                                GGGGAAGGGG      AGGTT
                                ||||||||||      |||||
                                CCCCTTCCCC      TCCAA
                                     GTAG___
GAM2107  SOX12    3'  TCGGGGAAGGGGTGGGGGTT  28060          GA  AGAA
                                TCGGGGAAGGGG  GG    GGTT
                                ||||||||||||  ||    ||||
                                AGCCCCTTCCCC  CC    CCAA
                                      AC  ____
GAM2107  SPARC    3'  GGGGAAACACGAAGGGGAGG  17067       _______
                                GGGGAA     GGGGGGAGG
                                ||||||     ||||||||
                                CCCCTT     TCCCCTCC
                                   TGTGCT
GAM2107  TBX6     3'  GGGGAAGGGAGCGGGAGGTT  38859          A  A  A
                                GGGGAAGGGGG GG GA GGTT
                                |||||||||||| || || ||||
                                CCCCTTCCCTC CC CT CCAA
                                      G  _  _
GAM2107  TEM8     3'  GGGGAGAGGCTGGGGGGTT   38185      A    GA  AGAA
                                GGGGA GGGG  GG    GGTT
                                |||||  ||||  ||    ||||
                                CCCCT CTCC  CC    CCAA
                                   _    GA  CC__
GAM2108  ADAM19   3'  GGAGGAGGGTGGGAGGAGC   37771        C  G
                                GGAGGAG GG GGGAGGAGC
                                |||||||  || |||||||||
                                CCTCCTC CC CCCTCCTCG
                                     _  A
GAM2108  ADH5     5'  GGGGCGGGGCGTGGGGGGGGC  8581      A  A  _    A  A
                                GGGG GG GCG GGGGG GG GC
                                ||||  ||  |||  |||||  ||  ||
                                CCCC CC CGC CCCCC CC CG
                                   G  C   A    _  _
GAM2108  AIPL1    3'  GGGGAGACAGGGAGGG      40819        GA       A
                                GGGGAG  GCGGGGGG GG
                                ||||||  ||||||||  ||
                                CCCCTC  TGTCCCTC CC
                                     __       _
GAM2108  ANK1     3'  GGGAGGAGCGTCACCAGGGAG  33870          G____
                                GGGAGGAGCG    GGGGAG
                                ||||||||||    ||||||
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                                CCCTCCTCGC    TCCCTC
                                      AGTGG
GAM2108 ANK1    3' GGGGAGGATGGAGGGGGGC  33871       GC    A A
                                GGGGAGGA  GGGGGG GG GC
                                ||||||||  |||||| || ||
                                CCCCTCCT  CCTCCC CC CG
                                    A_    _ _
GAM2108 ANKH    5' GGCGAGGGGCGACGGGGG   38320   G   A   G   A
                                GG GAGG GCGG GGG GG
                                || |||| |||| ||| ||
                                CC CTCC CGCT CCC CC
                                 G   C   G  _
GAM2108 ANP32A  3' GGGGGGAGAGGGGATATGG  26707    A   C   GA_
                                GGGG GGAG GGGGG  GG
                                |||| |||| |||||  ||
                                CCCC CCTC CCCCT  CC
                                  _   T    ATA
GAM2108 AOC2    3' GGGGTGGGAATCTGGGGAG  41818    A_   CGG
                                GGGG  GGAG  GGGGAG
                                ||||  ||||  ||||||
                                CCCC  CCTT  CCCCTC
                                  AC   AGA
GAM2108 AR      5' GGGGGGCGGGTGGGGAGAAG  6242    A A   __
                                GGG GG GCGGG  GGGAGGAG
                                ||| || |||||  ||||||||
                                CCC CC CGCCC  CCCTCTTC
                                  _ _    AC
GAM2108 AR      5' GGGGAGGGGGGGAAGG     6240       AGC
                                GGGGAGG  GGGGGGAGG
                                |||||||  |||||||||
                                CCCCTCC  CCCCCTTCC
                                   ___
GAM2108 ARHC    5' GGGAGAGGGGTGGGAG     23173     GAGC   GA
                                GGGAG   GGGGG  GGAG
                                |||||   |||||  ||||
                                CCCTC   TCCCC  CCTC
                                  ____    AC
GAM2108 ARHGDIA 3' GGGGAGGGCTGAGGAGG    20212      A GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCCCTCC CG  CTCCTCC
                                   _ A_
GAM2108 ARHGDIA 3' GGGGAGGGGCTGGGGGGG   20213      A G   A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCCC CC
                                    C A   _
GAM2108 ARHGDIA 3' GGGGATGGGGCGGGGGAGG  20214     _ A    G
                                GGGGA GG GCGGGGG AGG
                                ||||| || ||||||| |||
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                                CCCCT CC CGCCCCC TCC
                                  A  C      _
GAM2108 ARL2     3' GGGGTGGAGGAGGGGGAG    11692      A    C
                                GGGG GGAG GGGGGGAG
                                |||| |||| ||||||||
                                CCCC CCTC TCCCCCTC
                                  A   C
GAM2108 ARVCF    3' GGGGGGAGTGGGGTGGGGGGGC 11708      A    C   _ A A
                                GGGG GGAG GGGG GG GG GC
                                |||| |||| |||| || || ||
                                CCCC CCTC CCCC CC CC CG
                                  _   A   A C  C
GAM2108 ASGR1    5' GGAGGGGAGCGGGCAGGG    11713      A       G  A
                                GGGG GGAGCGGG GG GG
                                |||| |||||||| || ||
                                CCTC CCTCGCCC TC CC
                                  C       G  _
GAM2108 ATP4A    3' GGGAGGGGAGTGGGCAGG    8719        AGC  _   G
                                GGGAGG   GG GGG AGG
                                ||||||   || ||| |||
                                CCCTCC   TC CCC TCC
                                   CC_  A   G
GAM2108 ATP6V0D1 3' GGGAGGGAGCTGAGGAG    21726     GA    GG
                                GGG  GGAGC  GGGGAG
                                |||  |||||  ||||||
                                CCC  CCTCG  CTCCTC
                                  TC    A_
GAM2108 B3GAT1   5' GGAGAGGGGCGGCCACGGG   38300        A   G___
                                GGGGAGG GCGG   GGG
                                ||||||| ||||   |||
                                CCTCTCC CGCC   CCC
                                   C   GGTG
GAM2108 B3GAT1   3' GGGGAGGTGCGCTGGAG     38302        A  GGG
                                GGGGAGG GCG  GGAG
                                ||||||| |||  ||||
                                CCCCTCC CGC  CCTC
                                   A  GA_
GAM2108 BAZ1B    5' GGGGTGGGGTGGGGGAAGG   37094      A  AGC
                                GGGG GG  GGGGGGAGG
                                |||| ||  |||||||||
                                CCCC CC  CCCCCTTCC
                                  A  CCA
GAM2108 BAZ1B    3' GGGGGGGTGGGAGGAG      37092      AGGAGC  _
                                GGGG     GGG GGGAGGAG
                                ||||     ||| ||||||||
                                CCCC     CCC CCCTCCTC
                                  _______  A
GAM2108 BCL11A   3' GGGGAGTGGTGAAAAAGGGG  39717       ____  CG
                                GGGGAG   GAG  GGGGG
                                ||||||   |||  |||||
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                                CCCCTC   CTT  TCCCC
                                   ACCA  TT
GAM2108  BIN1    5'  GGGGAGGGGCCGGGCCTCAGG  40301       A  G  GG__
                                GGGGAGG GC GGG   AGG
                                ||||||| || |||   |||
                                CCCCTCC CG CCC   TCC
                                   C  G  GGAG
GAM2108  BIN1    5'  AGGGAGGGAGAGGGGAGGGGC  40293       AGC       A
                                GGGGAGG  GGGGGGAGG GC
                                |||||||  ||||||||| ||
                                TCCCTCC  CTCCCCTCC CG
                                   CT_       C
GAM2108  BMP1    3'  AGGGAGGAGTGGGGGAG    25968         CG
                                GGGGAGGAG  GGGGGAG
                                |||||||||  |||||||
                                TCCCTCCTC  CCCCCTC
                                     A_
GAM2108  C1QG    3'  GGGGAGGGGGTGCAGTGGGG  41688       A___   _
                                GGGGAGG   GCGG GGGG
                                |||||||   |||| ||||
                                CCCCTCC   CGTC CCCC
                                   CCCA   A
GAM2108  CA12    3'  GGGAGGAAAATGGAGGAG    10247       CG_
                                GGGAGGAG  GGGGGAG
                                ||||||||  |||||||
                                CCCTCCTT  CCTCCTC
                                     TTA
GAM2108  CACNA1B  3'  GGGGAGGAGGGGGAGGGAGGGG 8743         C  _    A
            C                    GGGGAGGAG GGG GGGAGG GC
                                ||||||||| ||| |||||| ||
                                CCCCTCCTC CCC CCCTCC CG
                                     C  T    C
GAM2108  CACNA1B  3'  AGGGAGGGGCCACAGGAGC   8741       A  GGGGGG
                                GGGGAGG GC    AGGAGC
                                ||||||| ||    ||||||
                                TCCCTCC CG    TCCTCG
                                   C  GTG___
GAM2108  CACNA2D2 5'  GGGGAGGGGGGGGCAG      25720       AGC    G
                                GGGGAGG  GGGGG AG
                                |||||||  ||||| ||
                                CCCCTCC  CCCCC TC
                                   ___    G
GAM2108  CACNG7   3'  GAGGAGGAGGCAGGGGGAG   36689        _
                                GGGGAGGAG CGGGGGGAG
                                |||||||||  |||||||||
                                CTCCTCCTC GTCCCCCTC
                                     C
GAM2108  CACNG7   3'  GGGGAGGAGTCATTTGGGAG  36690        _  GG_
                                GGGGAGGAG CG  GGGAG
                                |||||||||  ||  |||||
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                                CCCCTCCTC GT   CCCTC
                                     A  AAA
GAM2108  CALM3    3'  GGGGTGGGGTGGGGAGG     23242      A  AGC  _
                                GGGG GG   GG GGGGAGG
                                |||| ||   || |||||||
                                CCCC CC   CC CCCCTCC
                                  A ___  A
GAM2108  CALR     3'  GGGGAGGGGGTGGGGGAGA   41773        AGCG
                                GGGGAGG    GGGGGAGG
                                |||||||    ||||||||
                                CCCCTCC    CCCCCTCT
                                    CCCA
GAM2108  CALR     3'  GGGGAGAAAGGGAGGGG     41772         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTCTTT CCCTCC CC

                                      _     _
GAM2108  CAPON    5'  GGGGAGCGGTGGGGCTTGC   41930    A     _   AGGA
                                GG GGAGCGG GGGG   GC
                                || ||||||| ||||   ||
                                CC CCTCGCC CCCC   CG
                                 _     A   GAA_
GAM2108  CAPON    5'  GGGGAGGGGAGACTGGAGC   41934        AGC    GA
                                GGGGAGG   GGGGG  GGAGC
                                |||||||   |||||  |||||
                                CCCCTCC   CCTCT  CCTCG
                                    ___    GA
GAM2108  CAPON    5'  GGGGAGGAGGTGGCGGCGGGAG 41932         CG  G  A_
              C                  GGGGAGGAG  GG GG  GGAGC
                                |||||||||  || ||  |||||
                                CCCCTCCTC  CC CC  CCTCG
                                     CA  G  GC
GAM2108  CARPX    5'  GGGGGGAAGGGGGGAG      33578      A   C
                                GGGG GGAG GGGGGGAG
                                |||| |||| ||||||||
                                CCCC CCTT CCCCCCTC

                                  _   _
GAM2108  CD74     3'  GGGTGGGACATGGGGGAGGGGC 20339     GA   GCG       A
                                GGG  GGA   GGGGGAGG GC
                                |||  |||   |||||||| ||
                                CCC  CCT   CCCCCTCC CG
                                  AC   GTA       C
GAM2108  CDC42    3'  GGGAGGGGGAAGGGGGGGGC   12158       AGC_     A  A
                                GGGAGG    GGGGGG GG GC
                                ||||||    |||||| || ||
                                CCCTCC    TCCCCC CC CG
                                   CCCT     _  _
GAM2108  CENTD2   5'  GGGGAGGGTGGACAGGGG    31600        A___
                                GGGGAGG    GCGGGGG
                                |||||||    |||||||
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                                CCCCTCC    TGTCCCC
                                    CACC
GAM2108  CHST6    3'  GGGGAGGGGGAGGGG       34681        AGC      A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCTCC CC
                                   ___     _
GAM2108  CKM      3'  GGGCGAGGAGTGAGGGAG     12262     _     CG
                                GGG GAGGAG  GGGGGAG
                                |||  ||||||  |||||||
                                CCC CTCCTC  CTCCCTC
                                  G     A_
GAM2108  CKM      3'  GGGGGCGGGGCGAGGAG      12264      AGGA     G
                                GGGG    GCGGGG GAGGAG
                                ||||    |||||| ||||||
                                CCCC    CGCCCC CTCCTC
                                  _____     G
GAM2108  CLTB     3'  GGGGAGGAGTGGAATAGG     28226          C    GG
                                GGGGAGGAG GGGG  AGG
                                |||||||||  ||||  |||
                                CCCCTCCTC CCTT  TCC
                                     A    A_
GAM2108  CNN2     3'  GGGGAGAGAGCGTGCTGGGAG  20405        _     GG__
                                GGGGAG GAGCG    GGGAG
                                ||||||  |||||    |||||
                                CCCCTC CTCGC    CCCTC
                                    T     ACGA
GAM2108  COL1A1   3'  GGGCAGGAGCGGGCTGAGG    6377      G        GG
                                GGG AGGAGCGGG  GAGG
                                |||  |||||||||  ||||
                                CCC TCCTCGCCC  CTCC
                                  G         GA
GAM2108  COL1A1   3'  GGGGAGGCCAAGGGGGG      6379         AG       A
                                GGGGAGG  CGGGGGG GG
                                |||||||  ||||||| ||
                                CCCCTCC  GTTCCCC CC
                                    G_       _
GAM2108  CRHR2    3'  GGTGGAGGAGGACAGGGGAGC  12443     _      C  G   A
                                GG GGAGGAG GG GGG GGAGC
                                ||  |||||||  ||  |||  |||||
                                CC CCTCCTC CT TCC CCTCG
                                  A       _  G   _
GAM2108  CSH2     3'  GGAGAGGCACTGGGGAGG     35459        A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2108  CSHL1    3'  GGAGAGGCACTGGGGAGG     35456         A  GG
                                GGGGAGG GC  GGGGAGG
                                |||||||  ||  |||||||
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                                CCTCTCC TG  CCCCTCC
                                   G  A_
GAM2108 CSK      5' GGGGGGAGGGGAGGGG      20470      A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  _   _     _
GAM2108 CSNK1G2  3' GGGGCAGGAGTGGGGTAGGGC 10618      _    C   GG  A
                                GGGG AGGAG GGGG  AGG GC
                                |||| ||||| ||||  ||| ||
                                CCCC TCCTC CCCC  TCC CG
                                  G    A   A_  _
GAM2108 CYLN2    3' GGGCGAGGGGTTGGGGGAG   18060     _   AGCG
                                GGG GAGG    GGGGGAG
                                ||| ||||    |||||||
                                CCC CTCC    CCCCCTC
                                  G    CCAA
GAM2108 CYP21A2  3' GGGGGGAGGGGAGGGG      7984       A   C     A
                                GGGG GGAG GGGGGG GG
                                |||| |||| |||||| ||
                                CCCC CCTC CCCTCC CC
                                  _   _     _
GAM2108 DACH     5' GGGGTGGGGCGGGGAGGG    38874      A A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCTC CC
                                  A C       _
GAM2108 DBH      3' GGAGGAGGGGGAGGAG      8970         GCG
                                GGAGGA   GGGGGAGGAG
                                ||||||   ||||||||||
                                CCTCCT   CCCCCTCCTC
                                   ___
GAM2108 DBN1     3' GGGGAGGGGGTCCCAGGGAGC 38940         AGC   G___  A
                                GGGGAGG   GGG    GG GGAGC
                                |||||||   |||    || |||||
                                CCCCTCC   CCC    TC CCTCG
                                   ___   AGGG  _
GAM2108 DES      3' GGGGAGGGCGTGGGGAGG    43573        A   G
                                GGGGAGG GCG GGGGAGG
                                ||||||| ||| |||||||
                                CCCCTCC CGC CCCCTCC
                                   _   A
GAM2108 DLG4     3' AGGGAGGCCGGGGGGAG     10700        AG
                                GGGGAGG  CGGGGGGAG
                                |||||||  |||||||||
                                TCCCTCC  GCCCCCCTC
                                   G_
GAM2108 DNASE1L1 3' GAGGAGGATGGAAGGGAGG   27496         GC
                                GGGGAGGA  GGGGGGAGG
                                ||||||||  |||||||||
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                                CTCCTCCT  CTTCCCTCC
                                     AC
GAM2108  DNMT3L   5'  GGGGAGGGGCGGGGGCGGGGC  30069        A      GA  A
                                GGGGAGG GCGGGGG  GG GC
                                ||||||| |||||||  || ||
                                CCCCTCC CGCCCCC  CC CG
                                    C      G_  C
GAM2108  DNMT3L   5'  GGGAGGGGCGAGGAG       30063      GGAGC    G
                                GGGA    GGGG GAGGAG
                                ||||    |||| ||||||
                                CCCT    CCCC CTCCTC
                                  _____   G
GAM2108  DNMT3L   5'  GGGGGCGGGGAGGGG       30071      AGGA       A  A
                                GGGG   GCGGGGGG GG G
                                ||||   |||||||| || |
                                CCCC   CGCCCCTC CC C
                                  _____       _ _
GAM2108  DNMT3L   5'  GGGCGAGGAGCTGCGGGGGG   30066     _      ___
                                GGG GAGGAGC   GGGGGG
                                ||| |||||||   ||||||
                                CCC CTCCTCG   CCCCCC
                                  G      ACG
GAM2108  DVL3     3'  GGGTGGGAGCGGAATGGAGC   20687     GA       GGA
                                GGG  GGAGCGGGG   GGAGC
                                |||  |||||||||   |||||
                                CCC  CCTCGCCTT   CCTCG
                                  AC        A__
GAM2108  DYRK3    5'  GGGGAGAGGCGCCAGTTGGGGG 18719       GA  _______
                                GGGGAG  GCG     GGGGG
                                ||||||  |||     |||||
                                CCCCTC  CGC     CCCCC
                                    TC   GGTCAA
GAM2108  EFNB1    3'  AGGGGGGCGAGGGAGGGGC   20708      A  A      GA  A
                                GGGG GG GCGGGGG  GG GC
                                |||| || |||||||  || ||
                                TCCC CC CGCTCCC  CC CG
                                  _ _      TC  _
GAM2108  EHD2     3'  GGGAAGGGGCTGCGGAGGG   31135        A___
                                GGGGAGG   GCGGGGGG
                                |||||||   ||||||||
                                CCCTTCC   CGCCTCCC
                                    CCGA
GAM2108  EPS15    5'  GGGGAGGAGGCGGAGGGAG   12746         _
                                GGGGAGGAG CGGGGGGAG
                                ||||||||| |||||||||
                                CCCCTCCTC GCCTCCCTC
                                     C
GAM2108  ESRRA    3'  GGGGAGGAGAGGGCGTGGG   20836         C  ___
                                GGGGAGGAG GGG   GGG
                                ||||||||| |||   |||
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                                CCCCTCCTC CCC   CCC
                                     T  GCA
GAM2108  ESRRA    3'  GAGGAGGAGCGAAGGGGG    20830            A
                                GGGGAGGAGCGGGGGG GG
                                |||||||||||||||| ||
                                CTCCTCCTCGCTTCCC CC
                                                _
GAM2108  F2RL3    3'  GGGGAGGCGGGGCTGGAGGAGC 19523       GA    __
                                GGGGAG  GCGGGG  GGAGGAGC
                                ||||||  ||||||  ||||||||
                                CCCCTC  CGCCCC  CCTCCTCG
                                   __     GA
GAM2108  F2RL3    3'  GGGGAGGGGCGTGGCTGGGGGA 19525       A  _____
             G                   GGGGAGG GCG    GGGGGGAG
                                |||||||  |||    |||||||
                                CCCCTCC CGC    CCCCCTC
                                    C  ACCGA
GAM2108  FBXL11   3'  GGGGAGGAGGGGCACAGGGC  29437        C  GGG  A
                                GGGGAGGAG GGG  AGG GC
                                |||||||||  |||  ||| ||
                                CCCCTCCTC CCC  TCC CG
                                     _  GTG  _
GAM2108  FBXL11   3'  GGGGCGGGGTGGGGGGAAGAG  29439     A  AGC
                                GGGG GG  GGGGGGAGGAG
                                ||||  ||  ||||||||||
                                CCCC CC  CCCCCCTTCTC
                                  G  CCA
GAM2108  FGFR4    3'  GGGGAGGTGTGGGGAAAGG   35656       AGC   GG
                                GGGGAGG  GGGG  AGG
                                |||||||  ||||  |||
                                CCCCTCC  CCCC  TCC
                                    ACA   TT
GAM2108  FKBP10   3'  GGGGAGGAAGGCAGAGGG   34959        __
                                GGGGAGGA  GCGGGGGG
                                ||||||||  ||||||||
                                CCCCTCCT  CGTCTCCC
                                     TC
GAM2108  FLT1     5'  GGGGAGGAGCCGAGAGGAG   12912         _
                                GGGGAGGAGC GGGGGGAG
                                |||||||||| ||||||||
                                CCCCTCCTCG CTCTCCTC
                                      G
GAM2108  FMNL     5'  GGGGAGGGGAGGCCGGG    25307       AGC   GA  A
                                GGGGAGG  GGGGG  GG G
                                |||||||  |||||  || |
                                CCCCTCC  CCTCC  CC C
                                   ____   GG  _
GAM2108  FOS      5'  GGGCGAGGGGCCGAGGGG   23518    _   A  _
                                GGG GAGG GC GGGGGG
                                ||| |||| || ||||||
```

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                                CCC CTCC CG CTCCCC
                                  G   C G
GAM2108 FOXD2   5' GGGGAGGGGGCGGGGGACTGAG 20971       A_     AG
                                GGGGAGG GCGGGGGG GAG
                                ||||||| |||||||| |||
                                CCCCTCC CGCCCCCT CTC
                                    CC      GA
GAM2108 FOXG1B  5' GGGGGGGCGGCGGGCGG    23512     A A   G   A
                                GGGG GG GCGG GGG GG
                                |||| || |||| ||| ||
                                CCCC CC CGCC CCC CC
                                  _ _   G   G
GAM2108 FXR2    5' GAGGAGGAGCCGGAGGGGGAGC 22161         _     A
                                GGGGAGGAGC GGGGGG GGAGC
                                |||||||||| |||||| |||||
                                CTCCTCCTCG CCTCCC CCTCG
                                      G     _
GAM2108 FXYD1   3' GGGAAGGGGCGGCGGAGGGGGC 34864       A   G  GA  A
                                GGGGAGG GCGG GG  GG GC
                                ||||||| |||| ||  || ||
                                CCCTTCC CGCC CC  CC CG
                                    C   G  TC  C
GAM2108 FZD7    3' GGGTGGGAAAGGTGGGGAGGGG 18635    GA   C _     A
            C                    GGG  GGAG GG GGGGAGG GC
                                ||| |||| || ||||||| ||
                                CCC  CCTT CC CCCCTCC CG
                                  AC   T A     C
GAM2108 GAS1    5' GGGGAGCGGCGGACGCGGAGC  13072    A     G  A__
                                GG GGAGCGG GGG   GGAGC
                                || ||||||| |||   |||||
                                CC CCTCGCC CCT   CCTCG
                                 _     G  GCG
GAM2108 GATA2   5' GGGGAGGGGAGGGACTCGG   13089       AGC     ___
                                GGGGAGG   GGGGGGA   GG
                                |||||||   |||||||   ||
                                CCCCTCC   CCTCCCT   CC
                                    ___     GAG
GAM2108 GDF2    5' GGGGAGGAGCTGGGAAGGAGC  32128         GG
                                GGGGAGGAGC  GGGGAGGAGC
                                ||||||||||  ||||||||||
                                CCCCTCCTCG  CCCTTCCTCG
                                      A_
GAM2108 GDF2    5' GGGAAGGAGCGGGCCGG    32125          GGGA
                                GGGGAGGAGCGGG   GG
                                ||||||||||||    ||
                                CCCTTCCTCGCCC   CC
                                       GG__
GAM2108 GH1     3' GGAGAGGCACTGGGGAGG   8012        A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
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                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2108  GH2      3'  GGAGAGGCACTGGGGAGG    35433        A  GG
                                GGGGAGG GC  GGGGAGG
                                ||||||| ||  |||||||
                                CCTCTCC TG  CCCCTCC
                                    G  A_
GAM2108  GNA15    3'  GGGCAGGAGTACCCTGGGGGGG  40906     G    C_____
                                GGG AGGAG     GGGGGGG
                                ||| |||||     ||||||
                                CCC TCCTC     CCCCCC
                                  G    ATGGGA
GAM2108  GPR30    3'  GGGGAGGAGCTGGGTGACAGG  11315          _  _ G
                                GGGGAGGAGC GGG GG AGG
                                |||||||||| ||| || |||
                                CCCCTCCTCG CCC CT TCC
                                      A  A  G
GAM2108  GRB14    5'  GGGGAGAGGGGAGGAGC     21049       GAGCG
                                GGGGAG    GGGGGAGGAGC
                                ||||||    ||||||||||
                                CCCCTC    TCCCCTCCTCG
                                  _____
GAM2108  GRM7     5'  GGGGGAATCCGGGGAGGGGC   9188       A  G_     A  A
                                GGGG GGA  CGGGGGG GG GC
                                |||| |||  ||||||| || ||
                                CCCC CTT  GCCCCTC CC CG
                                  _  AG     _ _
GAM2108  HOXB2    5'  GGGGAGGGGGCTGCTGGGGGGG 13435        A_ ____     A
            G                    GGGGAGG  GC   GGGGGG GG
                                ||||||| ||   |||||| ||
                                CCCCTCC  CG   CCCCCC CC
                                    CC  ACGA    _
GAM2108  HOXC10   3'  GAGGAGGGGCGGGGAGAGGAA  41488        A
                                GGGGAGG GCGGGGGGAGGAG
                                ||||||| |||||||||||||
                                CTCCTCC CGCCCCTCTCCTT
                                    C
GAM2108  HOXC13   3'  GGGGAGGCAGTGGGGCAAAGGC 40669        _ C   G   A
                                GGGGAGG AG GGGG GAGG GC
                                ||||||| || |||| |||| ||
                                CCCCTCC TC CCCC TTTC CG
                                    G A   G   _
GAM2108  HOXD4    3'  GGGGTGGAGTGGGGGAGAA   31177     A   CG
                                GGGG GGAG  GGGGGAGGA
                                |||| ||||  |||||||||
                                CCCC CCTC  CCCCCTCTT
                                  A   A_
GAM2108  HPCA     3'  GGGGAGGGGTCGGGCCTTGGG  13426       AG_   ____
                                GGGGAGG   CGGG   GGG
                                |||||||   ||||   |||
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                                CCCCTCC  GCCC   CCC
                                   CCA   GGAA
GAM2108 HPSE    5' GGGGAGGAGCGCCCGGGGAGGA 27417         G__
            GC                   GGGGAGGAGCG  GGGGAGGAGC
                                ||||||||||  |||||||||
                                CCCCTCCTCGC  CCCCTCCTCG
                                   GGG
GAM2108 HPSE    5' GGGAGGCCTGGGGAGGAGC   27415      AGCGG
                                GGGAGG   GGGGAGGAGC
                                ||||||   ||||||||||
                                CCCTCC   CCCCTCCTCG
                                  GGA__
GAM2108 HPSE    5' GGGGAGGAGCGCCCGGGGAG  27416         G__
                                GGGGAGGAGCG  GGGGAG
                                ||||||||||  ||||||
                                CCCCTCCTCGC  CCCCTC
                                   GGG
GAM2108 HR      5' GGGGAGGGCCGGGCCGGGGC  32930       A G  GGA A
                                GGGGAGG GC GGG  GG GC
                                ||||||| || |||  || ||
                                CCCCTCC CG CCC  CC CG
                                   _ G  GG_ C
GAM2108 HRMT1L2  3' GGAGAGGAAGGGGGAG     11360       GC
                                GGGGAGGA  GGGGGGAG
                                ||||||||  ||||||||
                                CCTCTCCT  TCCCCCTC
                                   __
GAM2108 HRY     3' GGAGGAGGGGTGGCCTGAGC  24355       C  G AG_
                                GGAGGAG GGG GG  GAGC
                                ||||||| ||| ||  ||||
                                CCTCCTC CCC CC  CTCG
                                   _  A GGA
GAM2108 IFI35   5' GGGGAGGGGAGTAGGAG    41776       AGC  GG
                                GGGGAGG  GGGG AGGAG
                                |||||||  ||||  |||||
                                CCCCTCC  CCTC  TCCTC
                                   ____  A_
GAM2108 IGF2    5' GGGGGGGACGGGAGGGAGC   8314      A AG     AG
                                GGGG GG  CGGGGGG  GAGC
                                |||| ||  |||||||  ||||
                                CCCC CC  GCCCTCC  CTCG
                                  _ CT     __
GAM2108 IGFBP2  3' GGAGAGGGGCGGGGGGGCAGGGG 8261        A      _  A
            C                    GGGGAGG GCGGGGGG AGG GC
                                ||||||| |||||||| ||| ||
                                CCTCTCC CGCCCCCC TCC CG
                                   C      G  C
GAM2108 IKBKG   5' GGAGGAGGAGGGAGGAG    18881       GC
                                GGAGGA  GGGGGGAGGAG
                                ||||||  ||||||||||
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                                CCTCCT  CCTCCCTCCTC
                                  __
GAM2108 ILF1     5'  GGGGAGGAGGCGTGGGGGGGGG 21117         _ _    A  A
              GC                   GGGGAGGAG CG GGGGG GG GC
                                   ||||||||| || ||||| || ||
                                   CCCCTCCTC GC CCCCC CC CG
                                        C  A    C  C
GAM2108 IMPDH1   3'  GGGGAGCGGCCTGAGGAGC   9413     A      GGG
                                   GG GGAGCGG   GAGGAGC
                                   || |||||||   |||||||
                                   CC CCTCGCC   CTCCTCG
                                    _     GGA
GAM2108 INSR     3'  GGGGGCGGGTGGGGGGAAC   43379      AGGA    _  A
                                   GGGG   GCGGG GGG GGAGC
                                   ||||   ||||| ||| |||||
                                   CCCC   CGCCC CCC CCTTG
                                     ____    A  C
GAM2108 IRS2     5'  GGGCGAGGGGCGGAGGGGG   40711     _   A      A
                                   GGG GAGG GCGGGGGG GG
                                   ||| |||| |||||||| ||
                                   CCC CTCC CGCCTCCC CC
                                     G   C      _
GAM2108 JAG2     3'  GAGGAGGGGCGGCCGGGG    13719        A   __
                                   GGGGAGG GCGG  GGGG
                                   ||||||| ||||  ||||
                                   CTCCTCC CGCC  CCCC
                                       C   GG
GAM2108 JUND     3'  GGGGAGGGGGGGACGG      23808        AGC    GA
                                   GGGGAGG   GGGGG  GG
                                   |||||||   |||||  ||
                                   CCCCTCC   CCCCC  CC
                                       ___    TG
GAM2108 KCNC3    5'  GGGGCGGGGCGGGAGGGG    22513      A  A       A
                                   GGGG GG GCGGGGGG GG
                                   |||| || |||||||| ||
                                   CCCC CC CGCCCTCC CC
                                     G  C      _
GAM2108 KCNC3    5'  GGGAGGGGCGGGGACGCAGGGG 22510        A      G__   A
              C                     GGGAGG GCGGGGG   AGG GC
                                    |||||| |||||||   ||| ||
                                    CCCTCC CGCCCCT   TCC CG
                                       C      GCG   C
GAM2108 KCNC3    5'  GAGGAGGGGCGGGGCGGGG   22504        A     _  A
                                   GGGGAGG GCGGGG GG GG
                                   ||||||| |||||| || ||
                                   CTCCTCC CGCCCC CC CC
                                       C     G  _
GAM2108 KCNK3    3'  GGGGATGAGGAAGGGGAG    13909      G   CG
                                   GGGGA GAG  GGGGGAG
                                   ||||| |||  |||||||
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                                CCCCT CTC  TCCCCTC
                                  A   CT
GAM2108  KCNMB4   5'  GGGGAGTGGGCGGCGAGGGGGA 30950       GA_   _   A
                GC                  GGGGAG   GCGG GGGG GGAGC
                                    ||||||   |||| |||| |||||
                                    CCCCTC   CGCC CTCC CCTCG
                                       ACC   G   C
GAM2108  KCNN4    5'  GGGGAGGGGCAGGGGAGG    13927       A     G
                                    GGGGAGG GCGGGGG AGG
                                    ||||||| ||||||| |||
                                    CCCCTCC CGTCCCC TCC
                                       C     _
GAM2108  KCNQ2    5'  GGGGCGGAGCGCGGGGGG    41511     A    G   A
                                    GGGG GGAGCG GGGG GG
                                    |||| |||||| |||| ||
                                    CCCC CCTCGC CCCC CC
                                      G     G   _
GAM2108  KIAA0442 5'  GGGGAGGAGGGACGGGGAGC   31792         C   G  A
                                    GGGGAGGAG GGG GG GGAGC
                                    ||||||||| ||| || |||||
                                    CCCCTCCTC CCT CC CCTCG
                                         _   G  _
GAM2108  KIFC3    3'  GGAGAGGGGCGGGGAGGG    24462       A      A
                                    GGGGAGG GCGGGGGG GG
                                    ||||||| |||||||| ||
                                    CCTCTCC CGCCCCTC CC
                                       C      _
GAM2108  KLF8     3'  GGGGGGATGGGAAGG      28536     A   GCGG
                                    GGGG GGA    GGGGAGG
                                    |||| |||    |||||||
                                    CCCC CCT    CCCTTCC
                                      _   A___
GAM2108  KRT8     3'  GGGGTAGGCTGGGAGGGG    14007     _   AGC     A
                                    GGGG AGG   GGGGGG GG
                                    |||| |||   |||||| ||
                                    CCCC TCC   CCCTCC CC
                                      A   GA_     _
GAM2108  LIMK1    3'  GGGGGGCAGTTTGGGGGG    32535     A  _  C__
                                    GGGG GG AG   GGGGGG
                                    |||| || ||   ||||||
                                    CCCC CC TC   CCCCCC
                                      _  G  AAA
GAM2108  LRP1     3'  GGGAAGGGCTGGCTGGGGAGGG 14218       A  _  __      A
                GC                  GGGGAGG GC GG  GGGGAGG GC
                                    ||||||| || ||  ||||||| ||
                                    CCCTTCC CG CC  CCCCTCC CG
                                       _  A  GA      C
GAM2108  LRP1     5'  GGGGAGGGGGGGGTGGGGGGC   14222       AGC   _   A  A
                                    GGGGAGG   GGG GGG GG GC
                                    |||||||   ||| ||| || ||
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                                CCCCTCC   CCC CCC CC CG
                                    CC_   A  _ _
GAM2108 LRP6     5'  GGGGGAGGCGAGGAG      14232      AGGAGC    G
                                GGGG     GGGG GAGGAG
                                ||||     |||| ||||||
                                CCCC     CTCC CTCCTC
                                  _______   G
GAM2108 LY9      3'  GGGTGAGAAGGAGGGGGAGGGG 43469     _     C       A
              C                   GGG GAGGAG GGGGGGAGG GC
                                ||| |||||| ||||||||| ||
                                CCC CTCTTC TCCCCCTCC CG
                                  A     C        C
GAM2108 MAF      5'  GGAGAGGGAGGGGGGGAG     23835        AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCTCTCC   CCCCCCTC
                                    CT_
GAM2108 MAML1    3'  GGGAGGGAGGAGGAGGAGC   31292       AGC
                                GGGAGG   GGGGGGAGGAGC
                                ||||||   ||||||||||||
                                CCCTCC   TCCTCCTCCTCG
                                   C__
GAM2108 MAN2A1   5'  GGGGAGGCGCGGGTTCGG    14335        A    GGGA
                                GGGGAGG GCGGG   GG
                                ||||||| |||||   ||
                                CCCCTCC CGCCC   CC
                                    G    AAG_
GAM2108 MAP1A    3'  GGGAAGCGTGGGGAGGAGC   14345    A     G
                                GG GGAGCG GGGGAGGAGC
                                || |||||| ||||||||||
                                CC CTTCGC CCCCTCCTCG
                                 _     A
GAM2108 MAT1A    3'  GGGGAGGGAGGGGGAG      44905       AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCCCTCC   TCCCCCTC
                                    C__
GAM2108 MBD3     3'  GGGGAGGAGCTGGCCTCGAGC  19421         GG  GGAG
                                GGGGAGGAGC  GG   GAGC
                                ||||||||||  ||   ||||
                                CCCCTCCTCG  CC   CTCG
                                      A_  GGAG
GAM2108 MECP2    3'  GGGGAGGTGGGGGGAG      22605       AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCCCTCC   CCCCCCTC
                                    A__
GAM2108 MECP2    3'  GGGGGGAGCTGGGGGAG     22607     A    G
                                GGGG GGAGC GGGGGAG
                                |||| ||||| |||||||
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                                CCCC CCTCG CCCCCTC
                                  _    A
GAM2108 MECP2    3' GGGAAGGGGACTGGGGGAG   22602       A_ G
                                GGGGAGG  GC GGGGGAG
                                |||||||  || |||||||
                                CCCTTCC  TG CCCCCTC
                                    CC  A
GAM2108 MFAP4    3' GGGGAGCAAGGAGGAG     42910    A     GG
                                GG GGAGCG  GGGAGGAG
                                || ||||||  ||||||||
                                CC CCTCGT  TCCTCCTC
                                 _    __
GAM2108 MGMT     5' GGGGCGGCGGGGGGGG     14492     AGGA      A
                                GGGG   GCGGGGGG GG
                                ||||   |||||||| ||
                                CCCC   CGCCCCCC CC
                                  GC__      _
GAM2108 MIC2     5' GGGGGCGGGTGAGGGGAGC   14507     AGGA   _  A
                                GGGG   GCGGG GGG GGAGC
                                ||||   ||||| ||| |||||
                                CCCC   CGCCC CTC CCTCG
                                  _____   A  C
GAM2108 MMP2     3' GGGAAGGGGCGCCTGGGAGGAG 21199       A  GG_
                                GGGGAGG GCG  GGGAGGAG
                                ||||||| |||  ||||||||
                                CCCTTCC CGC  CCCTCCTC
                                    C  GGA
GAM2108 MNT      3' GGGCAGGCTGAGGGGAGGGGC  33720    G  AGC      A
                                GGG AGG  GGGGGGAGG GC
                                ||| |||  |||||||| ||
                                CCC TCC  CTCCCCTCC CG
                                  G  GA_      C
GAM2108 MPP2     3' GGGGAGGGGTGGCAGGGGG   40800       A___
                                GGGGAGG   GCGGGGGG
                                |||||||   ||||||||
                                CCCCTCC   CGTCCCCC
                                    CCAC
GAM2108 MSL3L1   5' GGGGAGGGCGGGCGGGGGC   38591       A   G A A
                                GGGGAGG GCGGG GG GG GC
                                ||||||| ||||| || || ||
                                CCCCTCC CGCCC CC CC CG
                                   _    G _ _
GAM2108 MSN      3' GGGGAGAGGAGGGGAG     41244      G  C
                                GGGGAG AG GGGGGGAG
                                |||||| || ||||||||
                                CCCCTC TC CTCCCCTC
                                   _ _
GAM2108 MUCDHL   3' GGGGGAGAGGGTGGAGGGGC  34941    A  C  G   A
                                GGG GGAG GGG GGAGG GC
                                ||| |||| ||| ||||| ||
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                                CCC CCTC CCC CCTCC CG
                                  _   T  A    C
GAM2108 MVK     3' AGGGAGGGGCGACAAGGGG   41337       A  ___
                                GGGGAGG GCG   GGGGG
                                ||||||| |||   |||||
                                TCCCTCC CGC   TCCCC
                                    C   TGT
GAM2108 NCALD   3' GGGGAAGAGAGGGGAG     36768        CG
                                GGGGAGGAG  GGGGGAG
                                |||||||||  |||||||
                                CCCCTTCTC  TCCCCTC
                                     __
GAM2108 NCOA6IP  5' GGGAAGGGGCGGGACCACGGGC 36051       A     GGA_ A
                                GGGGAGG GCGGGG   GG GC
                                ||||||| ||||||   || ||
                                CCCTTCC CGCCCT   CC CG
                                    C     GGTG _
GAM2108 NEUD4   3' GGGGAGAATTGAGGAGC    21623        GCGGGGG
                                GGGGAGGA      GAGGAGC
                                ||||||||      |||||||
                                CCCCTCTT      CTCCTCG
                                    AA_____
GAM2108 NEUROD2  3' GGGGAGGGGTGCCTCCAGGGAG 26067       A__  GG__
                                GGGGAGG   GC   GGGGAG
                                |||||||   ||   ||||||
                                CCCCTCC   CG   TCCCTC
                                    CCA  GAGG
GAM2108 NEUROD2  5' GGGGAGGGGAGGGGGGGAGGGG 26065      __   C       A_
           GC                   GGGGA  GGAG GGGGGGAGG  GC
                                |||||  |||| |||||||||  ||
                                CCCCT  CCTC CCCCCCTCC  CG
                                  CC   _       CC
GAM2108 NFATC4   5' GGGTGGGAGGGGGGAG     21247     GA   GC
                                GGG  GGA  GGGGGGAG
                                |||  |||  ||||||||
                                CCC  CCT  CCCCCCTC
                                  AC  __
GAM2108 NGFR    3' GGGGGGCAAGAGGGG      14788     A  A      A
                                GGG GG GCGGGGGG GG
                                ||| || |||||||| ||
                                CCC CC CGTTCTCC CC
                                    _ _      _
GAM2108 NGFR    3' GGGGAGGATGGGGGAG     14787        GCG
                                GGGGAGGA   GGGGGAG
                                ||||||||   |||||||
                                CCCCTCCT   CCCCCTC
                                    A__
GAM2108 NPC2    5' GGGGCGGGCCCGGGGAGGAGC  26965     A  A  GG
                                GGGG GG GC  GGGGAGGAGC
                                |||| || ||  ||||||||||
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                                CCCC CC CG  CCCCTCCTCG
                                  G  _  GG
GAM2108  NRXN1    5'  GGGGAGCGGGCGGCGCGGAG  39846    A      G  A__
                                GG GGAGCGGG GG   GGAG
                                || |||||||| ||   ||||
                                CC CCTCGCCC CC   CCTC
                                 _       G  GCG
GAM2108  NT5M     5'  GGGGAGCGGGGCGGGGAGC   33654    A       _  A
                                GG GGAGCGGGG GG GGAGC
                                || ||||||||| || |||||
                                CC CCTCGCCCC CC CCTCG
                                 _       G  _
GAM2108  NTE      3'  GGGGAGGGGCTGGTCAAG    27459       A  G  GG
                                GGGGAGG GC GG  GAG
                                ||||||| || ||  |||
                                CCCCTCC CG CC  TTC
                                    C  A  AG
GAM2108  NTSR1    3'  GGGGAGGGGTGGGGAGGAG   14890       AGC  _
                                GGGGAGG   GG GGGGAGGAG
                                |||||||   || |||||||||
                                CCCCTCC   CC CCCCTCCTC
                                   ___  A
GAM2108  NTSR1    3'  GGGGAGGAGTTGGGGACAGG  14889        CG    _
                                GGGGAGGAG  GGGGG AGG
                                |||||||||  ||||| |||
                                CCCCTCCTC  CCCCT TCC
                                     AA    G
GAM2108  OGG1     3'  GGGGAGGAGGGTACACTGGGG  32567        C  _______
                                GGGGAGGAG GG     GGGG
                                |||||||||  ||     ||||
                                CCCCTCCTC CC     CCCC
                                   _  ATGTGA
GAM2108  OLR1     3'  GGGGAGGAGTCATCAGGAGGAG 14942         _  GG
                C                GGGGAGGAG CG  GGGAGGAGC
                                |||||||||  ||  |||||||||
                                CCCCTCCTC GT  TCCTCCTCG
                                     A  AG
GAM2108  OTOF     3'  GGGGCAGGGGTGGGAAGA    22064      AGG  C  _
                                GGGG   AG GGG GGGAGGA
                                ||||   ||  ||| |||||||
                                CCCC   TC CCC CCCTTCT
                                  G__  _   A
GAM2108  OTP      3'  GGGGAGGCGGCGGGCGAGGG  36999        A_    G GA
                                GGGGAGG  GCGGG G  GG
                                |||||||  ||||| |  ||
                                CCCCTCC  CGCCC C  CC
                                    GC    G TC
GAM2108  OTP      3'  GGGGCGGAGCGGGCCGGG    37000      A       __
                                GGGG GGAGCGGG  GGG
                                |||| ||||||||  |||
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                                CCCC CCTCGCCC  CCC
                                  G       GG
GAM2108  PACSIN1   5'  GGGGAGGAGGGGGCTGG     45161         C    GGA
                                GGGGAGGAG GGGG   GG
                                ||||||||| ||||   ||
                                CCCCTCCTC CCCC   CC
                                     _   GA_
GAM2108  PACSIN1   3'  GGGGAGGAGTGACGGGAG    45162         C  G
                                GGGGAGGAG GG GGGAG
                                ||||||||| || |||||
                                CCCCTCCTC CT CCCTC
                                     A  G
GAM2108  PACSIN1   3'  GGGGAGGGGCGGCAGTGGGGAG 45164        A   ____
            GAG                    GGGGAGG GCGG    GGGGAGGAG
                                ||||||| ||||    |||||||||
                                CCCCTCC CGCC    CCCCTCCTC
                                    C    GTCA
GAM2108  PAFAH1B1  5'  GGGGGAGGGGAGGGGAG     7715      A    C     A
                                GGG GGAG GGGGGG GGAG
                                ||| |||| |||||| ||||
                                CCC CCTC CCCTCC CCTC
                                  _   _     _
GAM2108  PAG       3'  GGGGAGGACTGGCGAG      32957         G GG  G
                                GGGGAGGA C  GG GAG
                                |||||||| |  || |||
                                CCCCTCCT G  CC CTC
                                     _ A_  G
GAM2108  PAX2      3'  GGGAGGGGATGGGAGGAG    19632        AGC  _
                                GGGAGG   GGG GGGAGGAG
                                ||||||   ||| ||||||||
                                CCCTCC   CCT CCCTCCTC
                                   ___   A
GAM2108  PAX2      3'  GGGGCGGGGCGGAGGGGGAG  19637      A  A      A
                                GGGG GG GCGGGGGG GGAG
                                |||| || |||||||| ||||
                                CCCC CC CGCCTCCC CCTC
                                  G  C       _
GAM2108  PBX2      3'  GGGGAAGGGAAAGTGGGGGAG  15106       __    CG_
                                GGGGA  GGAG   GGGGGAG
                                |||||  ||||   |||||||
                                CCCCT  CCTT   CCCCCTC
                                   TC    TCA
GAM2108  PCBD      3'  GGGGAGTGGTGGGAGG      7100         GAGC  G
                                GGGGAG    GG GGGAGG
                                ||||||    || ||||||
                                CCCCTC    CC CCCTCC
                                   A___   A
GAM2108  PCTK3     3'  GGGGAGGAGGGTAGAG      43783         C  GG
                                GGGGAGGAG GG  GGAG
                                ||||||||| ||  ||||
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                                CCCCTCCTC CC  TCTC
                                     _ A_
GAM2108  PDE4A    3'  AGGGGAGTGAGGGGAGGAG   26246     A   C
                                GGG GGAG GGGGGGAGGAG
                                ||| |||| ||||||||||
                                TCC CCTC CTCCCCTCCTC
                                  _   A
GAM2108  PDE4A    3'  GGGGCGGGGGGGCGGGGGG    26269     A  A__
                                GGGG GG   GCGGGGGG
                                |||| ||   ||||||||
                                CCCC CC   CGCCCCCC
                                  G  CCC
GAM2108  PDE4A    3'  GGGGGGCGGGGGGGGTGAG    26274     A  A       AG
                                GGG GG GCGGGGGG  GAG
                                ||| || ||||||||  |||
                                CCC CC CGCCCCCC  CTC
                                  _ _       CA
GAM2108  PDE4A    3'  GGGGAGGAGTGGAGGGGAA   26266         C     A
                                GGGGAGGAG GGGGGG GGA
                                ||||||||| |||||| |||
                                CCCCTCCTC CCTCCC CTT
                                     A     _
GAM2108  PDE4A    3'  GGGGGTGAGTGGATCAGAGC   26276      AG   C   GGGA
                                GGGG  GAG GGG    GGAGC
                                ||||  ||| |||    |||||
                                CCCC  CTC CCT    TCTCG
                                  CA   A   AG__
GAM2108  PDE4A    3'  GGGGAGGAGGGAGAGAGGGGGC 26265         C        A_
                                GGGGAGGAG GGGGGGAGG  GC
                                ||||||||| |||||||||  ||
                                CCCCTCCTC CCTCTCTCC  CG
                                     _        CC
GAM2108  PDE4A    3'  GGGGGGCAGTGGGGGAAGG   26272      A  _  C
                                GGGG GG AG GGGGGGAGG
                                |||| || || |||||||||
                                CCCC CC TC CCCCCTTCC
                                  _  G  A
GAM2108  PEX14    3'  GGAGAGGGGGCTGGGGAGGGGC 41872         A_  GG      A
                                GGGGAGG  GC  GGGGAGG GC
                                |||||||  ||  ||||||| ||
                                CCTCTCC  CG  CCCCTCC CG
                                    CC  A_      C
GAM2108  PFKM     5'  GGGAAAGGGGGGAGG       41179        AGC
                                GGGAGG   GGGGGGAGG
                                ||||||   |||||||||
                                CCCTTT   CCCCCCTCC
                                     ___
GAM2108  PHF1     3'  GGGAAGGATGGGAGGGG     35871         GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
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                                CCCTTCCT  CCCTCC CC
                                   A_     _
GAM2108  PIP5K1A   3'  GAGGAGGAGTTTAAAGAGGAGC 18653         CGG
                                GGGGAGGAG   GGGGAGGAGC
                                |||||||||   ||||||||||
                                CTCCTCCTC   TTTCTCCTCG
                                    AAA
GAM2108  PLCB2     3'  GGGGAGGGGAGGGCCCTCAGC  21321       AGC     AGG__
                                GGGGAGG   GGGGGG    AGC
                                |||||||   ||||||    |||
                                CCCCTCC   CCTCCC    TCG
                                   ___     GGGAG
GAM2108  PLEK      3'  GGGGAGGAGGAATGCAGGAG   15390        C   GGG
                                GGGGAGGAG GGG   AGGAG
                                |||||||||| |||   |||||
                                CCCCTCCTC CTT   TCCTC
                                    _   ACG
GAM2108  PLOD3     5'  GGGAGGCGGGGGAGGGGC    9894        AGCG       A
                                GGGAGG    GGGGGAGG GC
                                ||||||    |||||||| ||
                                CCCTCC    CCCCCTCC CG
                                   G___       C
GAM2108  PML       3'  GGCGAGGAGTGGGCTGGCGAGG 37755    G     C   __  _
            AG                    GG GAGGAG GGG  GG GAGGAG
                                || |||||| |||  || ||||||
                                CC CTCCTC CCC  CC CTCCTC
                                 G     A   GA  G
GAM2108  PMP22     3'  GGGAAGGGGCGACATGGAG    7162         A    GG_
                                GGGGAGG GCGG   GGAG
                                |||||||| ||||   ||||
                                CCCTTCC CGCT   CCTC
                                   C    GTA
GAM2108  POLA      3'  GGGGAGGGGAGCTTGGGGAGGG 32616       __     GG      A
            GC                    GGGGA  GGAGC  GGGGAGG GC
                                |||||  |||||  ||||||| ||
                                CCCCT  CCTCG  CCCCTCC CG
                                   CC     AA      C
GAM2108  POMZP3    5'  GGGGAGGGCGGTGTGGAG    29245        A   GG_
                                GGGGAGG GCGG   GGAG
                                ||||||| ||||   ||||
                                CCCCTCC CGCC   CCTC
                                   _    ACA
GAM2108  PPGB      3'  GGGAGAGGCTGGGAGGGG    7175        GA  _     A
                                GGGAG  GC GGGGGG GG
                                |||||  || |||||| ||
                                CCCTC  CG CCCTCC CC
                                   TC  A     _
GAM2108  PPP2R4    3'  AGGGAGGGGATGGGGAGGGGC  41326        AGCGG      A
                                GGGGAGG    GGGGAGG GC
                                |||||||    ||||||| ||
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                                TCCCTCC    CCCCTCC CG
                                   CCTA_     C
GAM2108 PPT2    5' GGGAAGGGCGGGCTGCTTGGG 39922       A    _______
                                GGGGAGG GCGGG     GGG
                                ||||||| |||||     |||
                                CCCTTCC CGCCC     CCC
                                   _    GACGAA
GAM2108 PRDM16  3' GGGGAGGATGCTGAGGAG   35245       _ GG
                                GGGGAGGA GC  GGGGAG
                                |||||||| ||  ||||||
                                CCCCTCCT CG  CTCCTC
                                    A  A_
GAM2108 PRKACG  3' GGGCGGGGGGGTGAGGGAGC   15601    A      A___
                                GG GCGGGGGGG    GGAGC
                                || ||||||||    |||||
                                CC CGCCCCCC    CCTCG
                                 _      ACTC
GAM2108 PRKCABP 3' GGGGAGGGAGGGTGGAGGGGC 29672       AGC   _    A
                                GGGGAGG   GGGG GGAGG GC
                                |||||||   |||| ||||| ||
                                CCCCTCC   TCCC CCTCC CG
                                   C__    A    C
GAM2108 PRKCL1  5' AGGGAGGGGCGGCCAGAGGAGC 41701       A    GG
                                GGGGAGG GCGG  GGAGGAGC
                                ||||||| ||||  ||||||||
                                TCCCTCC CGCC  TCTCCTCG
                                   C    GG
GAM2108 PROC    3' GGGGGGGGGCGGGGGGGG    7194      A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  C  C      _
GAM2108 PROK1   3' GGGGAGGGGAGGGGGAA    37103       AGC     A
                                GGGGAGG   GGGGGG GGAG
                                |||||||   |||||| ||||
                                CCCCTCC   CCTCCC CCTT
                                   ___    _
GAM2108 PSAP    3' GGGGAGGTGGGGGAG      42969       AGCG
                                GGGGAGG   GGGGGAG
                                |||||||   |||||||
                                CCCCTCC   CCCCCTC
                                   A___
GAM2108 PTGFRN  3' GGGGTGGGGTGGGGAG     42593     AGGAGC   _ A
                                GGGG     GGGG GG GGAG
                                ||||     |||| || ||||
                                CCCC     CCCC CC CCTC
                                  A_____   A  _
GAM2108 PTK2B   3' GGGTAGGGGTGGGGAGAGGGC 19923     G  AGC       A
                                GGG AGG   GGGGGGAGG GC
                                ||| |||   |||||||| ||
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                                CCC TCC   CCCCTCTCC CG
                                  A   CCA       _
GAM2108  PTK2B    3'  GGGGAGAGAAAGAGGAGGAG   19922       G  CG
                                GGGGAG AG  GGGGGAGGAG
                                |||||| ||  ||||||||||
                                CCCCTC TC  TCTCCTCCTC
                                   _  TT
GAM2108  PTMS     3'  AGGGAGGGGAGGGGGG      15881        AGC     A  A
                                GGGGAGG   GGGGGG GG G
                                |||||||   |||||| || |
                                TCCCTCC   CCTCCC CC C
                                   ___     _ _
GAM2108  PTPRG    5'  GGGGAGAGGCAGGGGGAG    15939       GA
                                GGGGAG  GCGGGGGGAG
                                ||||||  ||||||||||
                                CCCCTC  CGTCCCCCTC
                                    TC
GAM2108  PTPRZ1   5'  GGAGAGGGAGGGGGAG      15986       AGC
                                GGGGAGG   GGGGGGAG
                                |||||||   ||||||||
                                CCTCTCC   TCCCCCTC
                                    C__
GAM2108  RAB13    5'  GGGGAGGGGTGGGGAG      16116       AGC  _
                                GGGGAGG   GG GGGGAG
                                |||||||   || ||||||
                                CCCCTCC   CC CCCCTC
                                   ___  A
GAM2108  RAB13    5'  GGGGGAGCCGGGGGAGG     16118     A    G
                                GGG GGAGC GGGGGAGG
                                ||| ||||| ||||||||
                                CCC CCTCG CCCCCTCC
                                  _    G
GAM2108  RAB3A    3'  GGGGGGGGGGGGGTCCCAGG   16076      A  AGC     _____
                                GGGG GG   GGGGGG    AGG
                                |||| ||   ||||||    |||
                                CCCC CC   CCCCCC    TCC
                                  _ ___      AGGG
GAM2108  RAB5C    3'  GGGGAGGAAGTGGGAAGAGC   40807         CGGG
                                GGGGAGGAG    GGGAGGAGC
                                |||||||||    |||||||||
                                CCCCTCCTT    CCCTTCTCG
                                    CA__
GAM2108  RAB7     3'  AGGGAGGGGAAAGGGGGGG    21575       AGC_     A
                                GGGGAGG    GGGGGG GG
                                |||||||    |||||| ||
                                TCCCTCC    TCCCCC CC
                                    CCTT     _
GAM2108  RABL2A   3'  GGGGAGGGGGTGGGGAAGG    30197       AGCG
                                GGGGAGG    GGGGGAGG
                                |||||||    ||||||||
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                                CCCCTCC   CCCCTTCC
                                    CCCA
GAM2108  RABL2B   3'  GGGGAGGGGGTGGGGAAGG   28204       AGCG
                                GGGGAGG   GGGGGAGG
                                |||||||   ||||||||
                                CCCCTCC   CCCCTTCC
                                    CCCA
GAM2108  RARA     3'  GAGGAGGAGAACTGGGGGG   9709        C___
                                GGGGAGGAG   GGGGGG
                                |||||||||   ||||||
                                CTCCTCCTC   CCCCCC
                                     TTGA
GAM2108  RARB     5'  GGGGAGGAAGTGGAGATGGGGG 32060       _ C ____   A
             G                   GGGGAGGA G GG   GGGG GG
                                |||||||| | ||   |||| ||
                                CCCCTCCT C CC   CCCC CC
                                    T A  TCTA   _
GAM2108  RCE1     3'  GGGGGGTGGGGAGAGG    23069     A  AGC
                                GGGG GG   GGGGGGAGG
                                |||| ||   |||||||||
                                CCCC CC   CCCCTCTCC
                                  _ A__
GAM2108  RCV1     5'  GGAGGAGGGGCCCAGGAGC   16220       C   GGG
                                GGAGGAG GGG   AGGAGC
                                ||||||| |||   ||||||
                                CCTCCTC CCC   TCCTCG
                                    _   GGG
GAM2108  RCV1     3'  AGGGAGGGGTGGGACCGGGC   16218       AGC _   A_ A
                                GGGGAGG   GG GGGG  GG GC
                                |||||||   || ||||  || ||
                                TCCCTCC   CC CCCT  CC CG
                                    ___ A   GG  _
GAM2108  RERE     5'  GGGGAGGCGACGCGGAGGG   29031       A___
                                GGGGAGG   GCGGGGGG
                                |||||||   ||||||||
                                CCCCTCC   CGCCTCCC
                                    GCTG
GAM2108  REST     5'  GGGGAGAGGTGGGGGAGG    24710      G  CG
                                GGGGAG AG  GGGGGAGG
                                ||||||  ||  ||||||||
                                CCCCTC TC  CCCCCTCC
                                    _  CA
GAM2108  RNPEPL1  3'  GGGAGAGCCCAGGGGAGGGGC  32885      G  G_      A
                                GGGAG AGC  GGGGGAGG GC
                                |||||  |||  |||||||| ||
                                CCCTC TCG  TCCCCTCC CG
                                   _  GG      C
GAM2108  RPA1     3'  GGGGATGGGGGGGGGG      16370      _ AGC     A
                                GGGGA GG   GGGGGG GG
                                |||||  ||   ||||||  ||
```

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                                CCCCT CC   CCCCCC CC
                                  A ____     _
GAM2108  RTN4     5'  GGGGAGGACTGAGAGGGG    42493         GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CTCTCC CC
                                    GA     _
GAM2108  RXRB     3'  GGGGGGGCGGCGGGAAG     35042      A  A   G
                                GGGG GG GCGG GGGAGG
                                |||| || |||| ||||||
                                CCCC CC CGCC CCCTTC
                                  _ _   G
GAM2108  SALL1    3'  GGGGCGGGGTGGGGGGCAAGGA 16461      A  AGC     __
              G                  GGGG GG   GGGGGG  AGGAG
                                ||||  ||   ||||||  |||||
                                CCCC CC   CCCCCC  TCCTC
                                  G  CCA     GT
GAM2108  SALL1    3'  GGGGCGGGGCGGGGTGGGGGGC 16459      A  A     _  A  A
                                GGGG GG GCGGGG GG GG GC
                                |||| || |||||| || || ||
                                CCCC CC CGCCCC CC CC CG
                                  G  C     A  _  C
GAM2108  SCN4A    3'  GGGGAGGAGAGGGGAG      7327          CG
                                GGGGAGGAG  GGGGGAG
                                |||||||||  |||||||
                                CCCCTCCTC  TCCCCTC
                                                __
GAM2108  SDC1     3'  GGGCAGGAGCGACCAGAGGGGC 16508     G       GG     A
                                GGG AGGAGCGG  GGAGG GC
                                |||  ||||||||  ||||| ||
                                CCC TCCTCGCT  TCTCC CG
                                  G       GG     C
GAM2108  SET7     5'  GAGGAGGAGGAAGAGGAGGAGC 36156          CG
                                GGGGAGGAG  GGGGGAGGAGC
                                |||||||||  ||||||||||
                                CTCCTCCTC  TCTCCTCCTCG
                                     CT
GAM2108  SH3GL1   3'  GGGGCGGGGCGGGGACACGG   16674      A  A      GA_
                                GGGG GG GCGGGGG   GG
                                |||| || |||||||   ||
                                CCCC CC CGCCCCT   CC
                                  G  C      GTG
GAM2108  SIAT8E   5'  GGGGAGGGGGAGGGG       40836         AGC     A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
                                CCCCTCC   CCCTCC CC
                                               ___     _
GAM2108  SIX6     3'  GGGGTGGGGCGGGAAACGG    28902      A  A     GG A
                                GGGG GG GCGGG  G GG
                                |||| || |||||  | ||
```

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                                CCCC CC CGCCC  T CC
                                  A  C    TT G
GAM2108  SLC6A8   5'  GGGGCGGCGGTCAGGCGGGGGG 24780     A  A_______
                                GGGG GG      GCGGGGGG
                                |||| ||      ||||||||
                                CCCC CC      CGCCCCCC
                                  G  GCCAGTC
GAM2108  SLC7A8   3'  GGGGAGGGGCAGGAAAGAGGGC 29293       A  _  GG    A
                                GGGGAGG GC GG  GGAGG GC
                                ||||||| || ||  ||||| ||
                                CCCCTCC CG CC  TCTCC CG
                                    C  T  TT    _
GAM2108  SLC9A1   3'  GGGGAGGAGCTGTGCTGGGG  43237         GG____
                                GGGGAGGAGC     GGGG
                                ||||||||||     ||||
                                CCCCTCCTCG     CCCC
                                      ACACGA
GAM2108  SLC9A1   3'  GGGAGGCGGCAGGGGAGGAGC  43235      A_     G
                                GGGAGG  GCGGGGG AGGAGC
                                ||||||  ||||||| ||||||
                                CCCTCC  CGTCCCC TCCTCG
                                   GC     _
GAM2108  SLC9A3R2 3'  GGGGAGGGGAAGGGGGGGGG  41530       ___ C     A
                                GGGGAGG   AG GGGGGG GG
                                |||||||   || |||||| ||
                                CCCCTCC   TC CCCCCC CC
                                    CCT  _    _
GAM2108  SLIT3    5'  GGGGAGCGGGCGGCGGAG    16873    A      G  A
                                GG GGAGCGGG GG GGAG
                                || |||||||| || ||||
                                CC CCTCGCCC CC CCTC
                                  _      G  G
GAM2108  SMG1     3'  GGGGAGGAGTAGGGAACGA   31510        CG     G
                                GGGGAGGAG  GGGGGA GA
                                |||||||||  |||||| ||
                                CCCCTCCTC  TCCCTT CT
                                     A_     G
GAM2108  SNRP70   3'  GGGGAGGGGATGACAGCAAGGG 44215       ________
              G                  GGGGAGG      AGCGGGGGGG
                                 |||||||      |||||||||
                                 CCCCTCC      TCGTTCCCC
                                    CCTACTG
GAM2108  SOX11    3'  GGGGGGCCGGGGGAGG      17029     A  A  G
                                GGG GG GC GGGGGAGG
                                ||| || || ||||||||
                                CCC CC CG CCCCCTCC
                                  _  _  G
GAM2108  SOX12    3'  GGGGTGGGCCCCAGCGGAGGG  28050      A  _____
                                GGGG GG    AGCGGGGGGG
                                |||| ||    |||||||||
```

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                                CCCC CC    TCGCCTCCC
                                  A  CGGGG
GAM2108  SOX12    3'  GAGGGGGCGACGTGGGGAGGGG 28040     A  A   ___      A
              C                   GGGG GG GCGG   GGGGAGG GC
                                  |||| || ||||   ||||||| ||
                                  CTCC CC CGCT   CCCCTCC CG
                                    _ _   GCA      C
GAM2108  SOX13    3'  GGGGAGGGGAGGGCAGG     25014        AGC     _
                                  GGGGAGG   GGGGGG AGG
                                  |||||||   |||||| |||
                                  CCCCTCC   CCTCCC TCC
                                      ___      G
GAM2108  SPI1     3'  GGGGAGGGGCGGGTGACGGAGC 17081         A     G GA
                                  GGGGAGG GCGGG G  GGAGC
                                  ||||||| ||||| |  |||||
                                  CCCCTCC CGCCC C  CCTCG
                                      C     A TG
GAM2108  SPTB     3'  GGGGAGGAGTGGAGGAGG    7383          CG
                                  GGGGAGGAG  GGGGGAGG
                                  |||||||||  ||||||||
                                  CCCCTCCTC  CCTCCTCC
                                       A_
GAM2108  SQSTM1   3'  AGGGAGGGGTCAGGAG      19375       GGAGC    GG
                                  GGGGA    GGGG  AGGAG
                                  |||||    ||||  |||||
                                  TCCCT    CCCC  TCCTC
                                     _____   AG
GAM2108  SRD5A1   5'  GAGGAGGGGCGGCTACCGGAGG 9826         A    GG___     A
              GGC                    GGGGAGG GCGG     GGAGG GC
                                  ||||||| ||||     ||||| ||
                                  CTCCTCC CGCC     CCTCC CG
                                      C    GATGG     C
GAM2108  SREBF2   3'  GGTGGAGGGGTGGGCTGAGC   21406    A    C   _   AG
                                  GG GGAG GGG GGG  GAGC
                                  || |||| ||| |||  ||||
                                  CC CCTC CCC CCC  CTCG
                                   A    _   A   GA
GAM2108  SSRP1    5'  GGGGGGACGCGGGGGGGG     17129      A   _       A
                                  GGGG GGA GCGGGGGG GG
                                  |||| ||| |||||||| ||
                                  CCCC CCT CGCCCCCC CC
                                     _   G       _
GAM2108  SYN2     3'  GGGGGGAGGAGAGGAG      39465      A    C
                                  GGGG GGAG GGGGGGAG
                                  |||| |||| ||||||||
                                  CCCC CCTC CTCTCCTC
                                     _    _
GAM2108  SYNGR1   3'  GGGGACAGATGGGGAGGGGC   21764       _   GC      A  A
                                  GGGGA GGA  GGGGGG GG GC
                                  ||||| |||  |||||| || ||
```

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                                CCCCT TCT  CCCCTC CC CG
                                  G  A_    _ _
GAM2108  TAF1C    3'  AGGGAGGAAAGAAAGGGGGGAG 24988        C____
                                GGGGAGGAG    GGGGGGAG
                                |||||||||    ||||||||
                                TCCCTCCTT    CCCCCCTC
                                    TCTTT
GAM2108  TAGLN    3'  GGGGAGGGCCGGGCTCAGGGC  40618       A  G   GG_  A
                                GGGGAGG GC GGG   AGG GC
                                ||||||| || |||   ||| ||
                                CCCCTCC CG CCC   TCC CG
                                   _ G   GAG  _
GAM2108  TBR1     3'  GGGGAAGAGCTGTGAGGGG   27313         ___
                                GGGGAGGAGC   GGGGGG
                                ||||||||||   ||||||
                                CCCCTTCTCG   CTCCCC
                                     ACA
GAM2108  TFAP2A   3'  GGTGAGGCGTGGGAGGGGC   17398    GA  A   GG     A
                                GG  GG GCG  GGGAGG GC
                                ||  || |||  |||||| ||
                                CC  TC CGC  CCCTCC CG
                                 AC  _  A_     C
GAM2108  TFAP4    3'  GGGAAGGGGGGAGGGGGGC    17412       AGC     A  A
                                GGGGAGG   GGGGGG GG GC
                                |||||||   |||||| || ||
                                CCCTTCC   CCTCCC CC CG
                                   C__     _ _
GAM2108  TFAP4    3'  GAGGAGGGCTGGGGGGG     17411       A  G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CTCCTCC CG CCCCC CC
                                   _  A    _
GAM2108  TFE3     3'  GGGAAGGGGTGGGGCCTGGC   27168       AGC  _   AGGA
                                GGGGAGG   GG GGGG   GC
                                |||||||   || ||||   ||
                                CCCTTCC   CC CCCC   CG
                                   ___  A   GGAC
GAM2108  TGFB1    3'  GGGGCGGGGCGGGGTGGGG   8546      A  A    _  A
                                GGGG GG GCGGGG GG GG
                                |||| || |||||| || ||
                                CCCC CC CGCCCC CC CC
                                  G  C     A  _
GAM2108  TGFB1    3'  GGGGCGGGGTGGGGCCGGGC  8548      A  AGC  _   A_  A
                                GGGG GG   GG GGGG  GG GC
                                ||||  ||   || ||||  || ||
                                CCCC CC   CC CCCC  CC CG
                                  G  ___  A   GG  _
GAM2108  THY1     3'  GGTGGAGGCAGGGAGGGGC   26628   _   GA      A  A
                                GG GGAG  GCGGGGGG GG GC
                                || ||||  |||||||| || ||
```

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                                CC CCTC  CGTCCCTC CC CG
                                 A   __      _ _
GAM2108  TIMP3    3'  AGGGAGGAGGCTGGAGGAG   7441          _ G
                                GGGGAGGAG C GGGGGAG
                                ||||||||| | |||||||
                                TCCCTCCTC G CCTCCTC
                                    C A
GAM2108  TLX1     5'  GGGGAGGGGAGGGAGAGAG   24343        AGC      _
                                GGGGAGG   GGGGGGAG GAG
                                |||||||   |||||||| |||
                                CCCCTCC   CCTCCCTC CTC
                                   ___       T
GAM2108  TMEPAI   5'  GGGGCGGCCGGGGGGGG    33615     A  AG     A
                                GGGG GG  CGGGGGG GG
                                |||| ||  ||||||| ||
                                CCCC CC  GCCCCCC CC
                                  G  G_     _
GAM2108  TNFRSF11A 3'  GGGGGGAGTCGGGGGGAGGAAG 19277     A   _        _
              C                  GGGG GGAG CGGGGGGAGGA GC
                                 |||| |||| |||||||||| ||
                                 CCCC CCTC GCCCCCCTCCT CG
                                   _   A         T
GAM2108  TNFSF5   3'  GGGGGGGGGGGGGGGG     6330      A  AGC     A
                                GGGG GG   GGGGGG GG
                                |||| ||   |||||| ||
                                CCCC CC   CCCCCC CC
                                  _ CC_     _
GAM2108  TSLP     5'  GGGGAGGAAGGTCAGGGAGGAG 39699         C  __
              C                  GGGGAGGAG GG  GGGGAGGAGC
                                 ||||||||| ||  ||||||||||
                                 CCCCTCCTT CC  TCCCTCCTCG
                                     _ AG
GAM2108  TSLP     5'  AGGGAGGAGCGGGGAACACAAG 37499             AG_
                                GGGGAGGAGCGGGGGGG   GAG
                                |||||||||||||||   |||
                                TCCCTCCTCGCCCCTT   TTC
                                        GTG
GAM2108  TULP1    3'  GGGGAGGAGGGGGGCACAGC   17730        GC     AGG
                                GGGGAGGA  GGGGGG   AGC
                                |||||||  ||||||   |||
                                CCCCTCCT  CCCCCC   TCG
                                   __      GTG
GAM2108  UCP3     3'  GGGGGGGGGTGGGGAAGAG    17854      A  AGC  _
                                GGGG GG   GG GGGGAGGAG
                                |||| ||   || |||||||||
                                CCCC CC   CC CCCCTTCTC
                                  _ C__  A
GAM2108  UGCG     5'  GGGGTGGGGACGGAAGGGG    17878      A_  AG      A
                                GGGG  GG  CGGGGGG GG
                                ||||  ||  ||||||| ||
```

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                                CCCC  CC  GCCTTCC CC
                                  AC  CT      _
GAM2108  UNC5C    5'  GGGGAGGGGAGGGGGA      19010        AGC     A
                                GGGGAGG   GGGGGG GGA
                                |||||||   |||||| |||
                                CCCCTCC   CCTCCC CCT
                                    ____     _
GAM2108  UNRIP    5'  AGGGAGGGGTGAGGGAGG    28420        AGCG
                                GGGGAGG   GGGGGAGG
                                |||||||   ||||||||
                                TCCCTCC   CTCCCTCC
                                    CCA_
GAM2108  VAT1     3'  GGGGAGGGGCAGGGGAGAGC  26850        A      GA
                                GGGGAGG GCGGGGG  GGAGC
                                ||||||| |||||||  |||||
                                CCCCTCC CGTCCCC  TCTCG
                                    C      __
GAM2108  VDR      3'  GGGGAGGTGGCAGAGGAGGGGC 7524         A_      GA  A
                                GGGGAGG  GCGGGGG  GG GC
                                |||||||  |||||||  || ||
                                CCCCTCC  CGTCTCC  CC CG
                                    AC      TC  _
GAM2108  VEGF     5'  GGGGAGGAGGTGGTAACTGGGG 17960         CG  GG A_  A
              C                  GGGGAGGAG  GG  G  GG GC
                                |||||||||  ||  |  || ||
                                CCCCTCCTC  CC  T  CC CG
                                     CA  AT GA  C
GAM2108  VIPR1    3'  GGGAAGGGGCGGGAGGGG    21512        A       A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCTTCC CGCCCTCC CC
                                    C      _
GAM2108  VIPR2    3'  GGGGAGGAACAGCCGAGGGGC  18023          GGG    A
                                GGGGAGGAGCGG   GAGG GC
                                ||||||||||||   |||| ||
                                CCCCTCCTTGTC   CTCC CG
                                       GG_    C
GAM2108  WNT5A    5'  GGGCAGGGGGTGGGGGG     18122     G   AGC   _   A  A
                                GGG AGG   GGG GGG GG G
                                ||| |||   ||| ||| || |
                                CCC TCC   CCC CCC CC C
                                  G   ____   A   _  _
GAM2108  WNT7A    5'  GGGAGGAGGGAGGGAGGAGC   21528        C
                                GGGAGGAG GGGGGGAGGAGC
                                |||||||| ||||||||||||
                                CCCTCCTC CCTCCCTCCTCG
                                    _
GAM2108  WSX1     5'  AGGGGGAGTGGGGAGG      22113      A   CGG
                                GGGG GGAG   GGGGAGG
                                |||| ||||   |||||||
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                                TCCC CCTC   CCCCTCC
                                  _   A__
GAM2108 WT1     5' GGGCGGGAAGTGGGGGAG    35971     GA   CG
                                GGG  GGAG  GGGGGAG
                                |||  ||||  |||||||
                                CCC  CCTT  CCCCCTC
                                  GC    CA
GAM2108 YWHAE    3' GGGGAGGAGTGAGGGGAAGGAG 27599          C _
                                GGGGAGGAG G GGGGGAGGAG
                                ||||||||| | ||||||||||
                                CCCCTCCTC C CCCCTTCCTC
                                     A T
GAM2108 ZNF278   5' GGGGAGGAGAAGGAGGGG    36805         C     A
                                GGGGAGGAG GGGGGG GG
                                |||||||| |||||| ||
                                CCCCTCCTC TCCTCC CC
                                     T     _
GAM2108 ABL1     3' GGTGGGAGCGGGGCTGGCGGG  23126    GA       GGAGGA
                                GG  GGAGCGGGG     GCGGG
                                ||  |||||||||     |||||
                                CC  CCTCGCCCC     CGCCC
                                 AC        GAC___
GAM2108 ARVCF    3' GGGGGAGTGGGGTGGGGGGGCA 11707     A    C    _  A  A
             GG                   GGG GGAG GGGG GG GG GCGGG
                                ||| |||| |||| || || |||||
                                CCC CCTC CCCC CC CC CGTCC
                                  _   A    A  C  C
GAM2108 ARVCF    3' GGTAGGATGGGGGGGAGTGG   11709    G   GC      GAGC
                                GG AGGA  GGGGGGGAG   GG
                                || ||||  ||||||||   ||
                                CC TCCT  CCCCCCTC   CC
                                 A   A_       A____
GAM2108 ATBF1    5' GGGCGGGGCGGGGGGCCTTCGG 27852     A  A       AGGAG
             G                    GGG GG GCGGGGGGG    CGGG
                                ||| || ||||||||    ||||
                                CCC CC CGCCCCCC    GCCC
                                  G  C       GGAA_
GAM2108 BCL11B   5' GGGGGAGCCGGGGGAGG    39751    A    G
                                GGG GGAGC GGGGGAGG
                                ||| ||||| ||||||||
                                CCC CCTCG CCCCCTCC
                                  _    G
GAM2108 BCR      5' GGGAGGGCCGGGGGGAGG    34640       AG
                                GGGAGG  CGGGGGGAGG
                                ||||||  ||||||||||
                                CCCTCC  GCCCCCCTCC
                                   CG
GAM2108 BMP1     3' GGGAGGAGTGGGGGAGCTAAGG 25984         C    _ AG   C
             G                    GGGAGGAG GGGGG G  GAG GG
                                |||||||| ||||| |  ||| ||
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                                CCCTCCTC CCCCC C  TTC CC
                                    A    T GA  _
GAM2108 BSN     3' GGGTGGGGTGGGGAGGGGTGGG 18411    A  AGC  _     AGC
                                GGG GG   GG GGGGAGG   GGG
                                ||| ||   || |||||||   |||
                                CCC CC   CC CCCCTCC   CCC
                                  A ___  A      CCA
GAM2108 C1orf6  5' GAGGAGGAGGAGGGGCGG    33527       C     A  A
                                GAGGAG GGGGGG GG GCGG
                                |||||| |||||| || ||||
                                CTCCTC CTCCTC CC CGCC
                                   _     _ _
GAM2108 CACNG7  3' GGGGGAGCTCCGAGGGGCGGG 36691    A    GGGGG   A
                                GGG GGAGC    GAGG GCGGG
                                ||| |||||    |||| |||||
                                CCC CCTCG    CTCC CGCCC
                                  _    AGG__   C
GAM2108 CAPON   5' GGGAGGAGGTGGCGGCGGGAGC 41927        CG  G  A_
            GGG                   GGGAGGAG  GG GG  GGAGCGGG
                                |||||||  || ||  ||||||||
                                CCCTCCTC  CC CC  CCTCGCCC
                                    CA  G  GC
GAM2108 CDC25B  5' GGCGAGGGGTGGGGGGGG    34843   _   AGC     A
                                GG GAGG   GGGGGG GG
                                || ||||   |||||| ||
                                CC CTCC   CCCCCC CC
                                 G   CCA    _
GAM2108 CDC25B  5' GGGAGGCAGCGGGCGAGGGGTG 34855       _     G GA  AGC
            GG                    GGGAGG AGCGGG G  GG   GGG
                                |||||| |||||| |  ||   |||
                                CCCTCC TCGCCC C  CC   CCC
                                   G     G TC  CA_
GAM2108 CEP2    5' GAGGGGCGGGGGGGCGG    28436     A      AGGA
                                GAGG GCGGGGGG   GCGG
                                |||| ||||||||   ||||
                                CTCC CGCCCCCC   CGCC
                                  C      _____
GAM2108 CIAO1   5' GGGGGAGGTGGGGGCG     43685    A   CG   GAGGA
                                GGG GGAG  GGGG    GCG
                                ||| ||||  ||||    |||
                                CCC CCTC  CCCC    CGC
                                  _   CA   ______
GAM2108 COL1A1  3' GGGCAGGAGCGGGCTGAGGGTG 6378     _       GG   AGC
            GG                    GGG AGGAGCGGG  GAGG   GGG
                                ||| |||||||||  ||||   |||
                                CCC TCCTCGCCC  CTCC   CCC
                                  G       GA   CA_
GAM2108 CSNK1G2 3' GGGCAGGAGTGGGGTAGGGCGG 10617    _   C   GG   A
            G                     GGG AGGAG GGGG  AGG GCGGG
                                ||| ||||| ||||  ||| |||||
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                                CCC TCCTC CCCC  TCC CGCCC
                                  G    A   A_  _
GAM2108 DES     3' GGGAGGGCGTGGGGAGGTGGG 43571       A  G     AGC
                                GGGAGG GCG GGGGAGG  GGG
                                |||||| ||| |||||||  |||
                                CCCTCC CGC CCCCTCC  CCC
                                   _  A     A__
GAM2108 DLX2    3' GGGAGGGCGGGCAGGCGGG   20594       A    G  AGGA
                                GGGAGG GCGGG GG   GCGGG
                                |||||| ||||| ||   |||||
                                CCCTCC CGCCC TC   CGCCC
                                   _    G  ____
GAM2108 DNMT3L  5' GGGAGGGGCGGGGGCGG    30064       A    GGAGGA
                                GGGAGG GCGGGG    GCGG
                                |||||| ||||||     ||||
                                CCCTCC CGCCCC    CGCC
                                   C    _______
GAM2108 DNMT3L  5' GGGGGCGGGGAGGGGCGGG   30073    A A      A A
                                GG GG GCGGGGGG GG GCGGG
                                || || |||||||| || |||||
                                CC CC CGCCCCTC CC CGCCC
                                 _ _      _ _
GAM2108 ED1     5' GGGAGGAGGAGGGGCGG    10821        C    GAGGA
                                GGGAGGAG GGGGG   GCGG
                                |||||||| |||||    ||||
                                CCCTCCTC CTCCC    CGCC
                                   _    _____
GAM2108 EGLN1   5' GGGAGGGCCGGGGGGAGG    35172       AG
                                GGGAGG  CGGGGGGAGG
                                ||||||  ||||||||||
                                CCCTCC  GCCCCCCTCC
                                   CG
GAM2108 EGLN1   5' GGGAGGGCCGAGGGGCGGG   35171       A  G    AGGA
                                GGGAGG GC GGGGG   GCGGG
                                |||||| || |||||   |||||
                                CCCTCC CG CTCCC   CGCCC
                                   _ G   ____
GAM2108 EMX2    5' GGGGGTGGGGGGAAG      44692     A  AGC
                                GGG GG   GGGGGGAGG
                                ||| ||   |||||||||
                                CCC CC   CCCCCCTTC
                                  _ A__
GAM2108 ERBB2   5' GAGGGGTGGGGGCCGG     20819     C  _  A  AG
                                GAG GGG GGG GG  CGG
                                ||| ||| ||| ||  |||
                                CTC CCC CCC CC  GCC
                                  _  A  _ G_
GAM2108 F2RL3   3' GGGGGGCGGGGCCGAACGGG  19527     A  A     GGAG
                                GGG GG GCGGGG   GAGCGGG
                                ||| || ||||||   |||||||
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                                CCC CC CGCCCC   CTTGCCC
                                  _ _    GG__
GAM2108  FACL4   5'  GGAGGGGCGGGCGGAGCGGG  35681     C  _  A
                                GGAG GGG GGG GGAGCGGG
                                |||| ||| ||| ||||||||
                                CCTC CCC CCC CCTCGCCC
                                  _  G  G
GAM2108  FBXL11  3'  GGGCGGGGTGGGGGGAAGAG  29436    A  AGC
                                GGG GG  GGGGGGGAGGAG
                                ||| ||  ||||||||||
                                CCC CC  CCCCCCTTCTC
                                 G  CCA
GAM2108  FCN2    3'  GGGAGGAGTGTGGGGGTGG   31892       CG_   A
                                GGGAGGAG  GGGGG GG
                                ||||||||  ||||| ||
                                CCCTCCTC  CCCCC CC
                                     ACA   A
GAM2108  FE65L2  3'  GGGAGGGGCAGGGGACCTCCTG 39321      A      AGGAGC
            GG                    GGGAGG GCGGGGGG    GGG
                                ||||||| ||||||||     |||
                                CCCTCC CGTCCCCT     CCC
                                   C       GGAGGA
GAM2108  FHIT    3'  GGGAGAGGCGGGGGGGCGG   12874      GA      AGGA
                                GGGAG  GCGGGGGG   GCGG
                                |||||  ||||||||   ||||
                                CCCTC  CGCCCCCC   CGCC
                                  TC      _____
GAM2108  FMNL    5'  GGGAGAGGCGGGGCCTGTGGG  25304     GA    GGAGGAGC
                                GGGAG  GCGGGG      GGG
                                |||||  ||||||      |||
                                CCCTC  CGCCCC      CCC
                                  TC     GGACA___
GAM2108  FNTB    3'  GGGAGGAGTGAGGCAGGTGGG  13005       CG   G  AGC
                                GGGAGGAG  GGGG AGG  GGG
                                ||||||||  |||| |||  |||
                                CCCTCCTC  CTCC TCC  CCC
                                     A_   G  A__
GAM2108  FXR2    5'  GGGAGCCGCGGGGGGCGGG   22163     GA     GAGGA
                                GGGAG  GCGGGGG    GCGGG
                                |||||  |||||||    |||||
                                CCCTC  CGCCCCC    CGCCC
                                  GG     ______
GAM2108  GDF2    5'  GGGAGGAGCTGGGAAGGAGCGG 32126        GG
            G                    GGGAGGAGC  GGGGAGGAGCGGG
                                |||||||||  ||||||||||||
                                CCCTCCTCG  CCCTTCCTCGCCC
                                     A_
GAM2108  GRB14   5'  GGGAGGAGCGGCCGGTGG    21046         GG  A
                                GGGAGGAGCGG  GG GG
                                ||||||||||  || ||
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                                CCCTCCTCGCC  CC CC
                                      GG  A
GAM2108  GRM6     5'  GGGGAGACAGAGGGGCGGG   9174     A   _      AGGA
                                GG GGAG CGGGGGG    GCGGG
                                || |||| |||||||    |||||
                                CC CCTC GTCTCCC    CGCCC
                                 _   T      ____
GAM2108  GTF2IRD1  5'  GAGAGGAGCGGAGAGCGG    32257          GGGGA
                                GGGAGGAGCGG    GGAGCGG
                                ||||||||||     |||||||
                                CTCTCCTCGCC    TCTCGCC
                                               _____
GAM2108  HD       3'  GGGGGAGGCGGGAGGCGG    13356     A   _     GAGGA
                                GGG GGAG CGGGGG    GCGG
                                ||| |||| ||||||     ||||
                                CCC CCTC GCCCTC    CGCC
                                 _   C     _____
GAM2108  HOXC4    3'  GGGAGGGTGGGGGCATGGGGTG 31154       AGC    GA_ AGC
            GG                   GGGAGG   GGGGG   GG   GGG
                                ||||||   |||||   ||   |||
                                CCCTCC   CCCCC   CC   CCC
                                   CA_    GTA  CCA
GAM2108  HS2ST1   5'  GCGGGGGGCGGGGAGCGG    29333        A__
                                GCGGGGGG   GGAGCGG
                                ||||||||   |||||||
                                CGCCCCCC   CCTCGCC
                                     GCC
GAM2108  HYOU1    3'  GGGGGTGGGGTGAGGGGTGGG  40635    A  AGC    G    AGC
                                GGG GG   GGGG GAGG   GGG
                                ||| ||   |||| ||||   |||
                                CCC CC   CCCC CTCC   CCC
                                  _ A__    A    CCA
GAM2108  ICAM5    3'  GCGGGGAGAGGGGAGCGG    40861         __
                                GCGGGGGGA  GGAGCGG
                                |||||||||  |||||||
                                CGCCCCTCT  CCTCGCC
                                      CC
GAM2108  IGFBP2   3'  GAGAGGGGCGGGGGGCAGG   8257        A      _
                                GGGAGG GCGGGGGG AGG
                                |||||| |||||||| |||
                                CTCTCC CGCCCCCC TCC
                                   C       G
GAM2108  JAM2     5'  GGCGAGGAGCTGGGGGCGG   34544   _     GG    AGGA
                                GG GAGGAGC  GGGG    GCGG
                                || |||||||  ||||    ||||
                                CC CTCCTCG  CCCC    CGCC
                                 G      A_   _____
GAM2108  JUNB     3'  GGGAGGGCAGGGGGCGG     13758       A      GAGGA
                                GGGAGG GCGGGGG    GCGG
                                |||||| |||||||     ||||
```

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                                CCCTCC CGTCCCC    CGCC
                                  _    _____
GAM2108  KCNC3    5'  GGGGGGCGGGGCGGGAGGGGCG 22518    A  A    __    A
                GG                  GGG GG GCGGGG  GGAGG GCGGG
                                    ||| || ||||||  ||||| |||||
                                    CCC CC CGCCCC  CCTCC CGCCC
                                     _ _     GC    C
GAM2108  KCNC3    3'  AGGAGCAGTGGGGGGGGGGTGG 22489      G  C    A  AGC
                G                    GGGAG AG GGGGGG GG   GGG
                                    ||||| || |||||| ||   |||
                                    TCCTC TC CCCCCC CC   CCC
                                      G  A     _  CCA
GAM2108  KCNC3    5'  GGGAGGAGGGGCGGGGCGG   22509        C  _  AGGA
                                    GGGAGGAG GGG GGG    GCGG
                                    |||||||| ||| |||    ||||
                                    CCCTCCTC CCC CCC    CGCC
                                       _  G  ____
GAM2108  KCNC3    5'  GGGAGGGGCGGGGACGCAGGGG 22512       A     G__  A
                CGGG                  GGGAGG GCGGGGG   AGG GCGGG
                                    |||||| |||||||   ||| |||||
                                    CCCTCC CGCCCCT   TCC CGCCC
                                       C      GCG   C
GAM2108  KCNC3    3'  GGGGGGGGGTGGGGGGGGAGGG  22521    A  AGC    A   C
                                    GGG GG   GGGGGG GGAG GG
                                    ||| ||   |||||| |||| ||
                                    CCC CC   CCCCCC CCTC CC
                                     C  CCA     _   _
GAM2108  KCNF1    3'  GGGAGGGTTGGGGGGACACAGG 13836       AGC      GGA
                                    GGGAGG   GGGGGGA   GCGGG
                                    ||||||   |||||||   |||||
                                    CCCTCC   CCCCCCT   TGTCC
                                       CAA      G__
GAM2108  KCNJ3    5'  GGGGGCGGGGGGAGGAAAGGG  13849    A  A          C
                                    GG GG GCGGGGGGAGGAG GGG
                                    || || ||||||||||||| |||
                                    CC CC CGCCCCCCTCCTT CCC
                                     _ _           T
GAM2108  KCNK3    3'  GGGATGAGGAAGGGGAGTGGG  13908     G   CG      GAGC
                                    GGGA GAG  GGGGGAG    GGG
                                    |||| |||  |||||||    |||
                                    CCCT CTC  TCCCCTC    CCC
                                      A  CT      A___
GAM2108  KLK13    5'  GGGAGGGGAGGGCAGGGCGGG  31812       AGC     _  A
                                    GGGAGG   GGGGGG AGG GCGGG
                                    ||||||   |||||| ||| |||||
                                    CCCTCC   CCTCCC TCC CGCCC
                                       ___      G  _
GAM2108  KPNB1    5'  GGGAGGGTGGGGTGGGGGGCGG 13973       AGC  _  A  A
                G                    GGGAGG   GGG GGG GG GCGGG
                                    ||||||   ||| ||| || |||||
```

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                                CCCTCC   CCC CCC CC CGCCC
                                   CAC   A   _ _
GAM2108 LAG3     5' GGGGGCAGTGGTGGGGGGTGGG 14046     A _ C _   A AGC
                                GGG GG AG GG GGGG GG   GGG
                                ||| || || || |||| ||   |||
                                CCC CC TC CC CCCC CC   CCC
                                  _ G A A   _ A__
GAM2108 LASS2    5' GGGAGGGGAGGGCGGGGCGGG 42681       AGC     A A
                                GGGAGG   GGGGGG GG GCGGG
                                ||||||   |||||| || |||||
                                CCCTCC   CCTCCC CC CGCCC
                                   ___     G  C
GAM2108 LMO2     5' GGGGGCGGCGGCCTAGGGGCGG 24547    A A   G  G__   A
            G                    GG GG GCGG GG   AGG GCGGG
                                || || |||| ||   ||| |||||
                                CC CC CGCC CC   TCC CGCCC
                                 _ _   G  GGA   C
GAM2108 LRP1     5' GGGAGGAGGCGGGGAGGGGGGG 14219         _      A AGC
                                GGGAGGAG CGGGGGG GG   GGG
                                |||||||| ||||||| ||   |||
                                CCCTCCTC GCCCCTC CC   CCC
                                     C      _ C__
GAM2108 MADD     5' GGGGAGTGGGGGGGGCGTGG   39068    A   C     AGGA  _
                                GG GGAG GGGGGG    GCG GG
                                || |||| ||||||    ||| ||
                                CC CCTC CCCCCC    CGC CC
                                 _   A     _____   A
GAM2108 MAP3K10  5' GGGAGGGGCCGGGGGCTGCGGG 42756       A  G    AGGA
                                GGGAGG GC GGGGG    GCGGG
                                |||||| || |||||    |||||
                                CCCTCC CG CCCCC    CGCCC
                                   C  G    GA__
GAM2108 MAP3K13  3' GGGATGAGTCTGGGGGTGG   21796     G   CG_    A
                                GGGA GAG   GGGGG GG
                                |||| |||   ||||| ||
                                CCCT CTC   CCCCC CC
                                  A  AGA    A
GAM2108 MECP2    3' GGGGGAGGTGGGGGGAGCTGGG 22606     A   CGG   A    _
                                GGG GGAG   GGGG GGAGC GGG
                                ||| ||||   |||| ||||| |||
                                CCC CCTC   CCCC CCTCG CCC
                                  _   CA_   _    A
GAM2108 MGMT     5' GGGGGGGCGGGGGGGGG      14494     A A      A
                                GGG GG GCGGGGGG GG
                                ||| || |||||||| ||
                                CCC CC CGCCCCCC CC
                                  _ C       _
GAM2108 MGMT     5' GGGCGGCGGGGGGGGGCGG    14491    A   _   A A
                                GG GCGG GGGG GG GCGG
                                || |||| |||| || ||||
```

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                                CC CGCC CCCC CC CGCC
                                 _   G   _ C
GAM2108 MKPX     5' AGGAGGAGCGGCGGGGCGGG  33633          G  AGGA
                                GGGAGGAGCGG GGG   GCGGG
                                |||||||||| |||   |||||
                                TCCTCCTCGCC CCC   CGCCC
                                      G  ____
GAM2108 MSL3L1   5' GGGAGGGCGGGCGGGGGCGGG 38589       A   G A A
                                GGGAGG GCGGG GG GG GCGGG
                                |||||| ||||| || || |||||
                                CCCTCC CGCCC CC CC CGCCC
                                   _   G _ _
GAM2108 MXI1     5' GAGCACGGGGGAGGGGCGGG  39020      _      A
                                GAGCG GGGGGAGG GCGGG
                                ||||| |||||||| |||||
                                CTCGT CCCCCTCC CGCCC
                                  G      C
GAM2108 NCALD    3' GGGAAGAGAGGGGAGTGG    36767       C     A
                                GGGAGGAG GGGGGG GG
                                |||||||| |||||| ||
                                CCCTTCTC CCCCTC CC
                                     T     A
GAM2108 NEUROD2  5' GGGAGGGGAGGGGGGGAGG   26063     __   C
                                GGGA  GGAG GGGGGGAGG
                                ||||  |||| |||||||||
                                CCCT  CCTC CCCCCCTCC
                                  CC   _
GAM2108 NPR1     5' GGAAGGAGCAGGAGCGG     44583         GGGGGG
                                GGGAGGAGC     AGGAGCGG
                                |||||||||     ||||||||
                                CCTTCCTCG     TCCTCGCC
                                      _______
GAM2108 NRXN1    5' GGAGCGGGCGGCGCGGAGTGGG 39844        G  A__   C
                                GGAGCGGG GG   GGAG GGG
                                |||||||| ||   |||| |||
                                CCTCGCCC CC   CCTC CCC
                                     G  GCG   A
GAM2108 NTSR1    3' GAGGAGATGGGGGAGGGGTGGG 14881       CG       AGC
                                GAGGAG  GGGGGAGG   GGG
                                ||||||  ||||||||   |||
                                CTCCTC  CCCCCTCC   CCC
                                   TA       CCA
GAM2108 NTSR1    3' GGGAGGGGTGGGGAGGAGTTGG 14887       AGC  _       C_
            G                    GGGAGG   GG GGGGAGGAG  GGG
                                ||||||   || |||||||||  |||
                                CCCTCC   CC CCCCTCCTC  CCC
                                   ___ A        AA
GAM2108 PACSIN1  3' GGGAGGGGCGGCAGTGGG    45157       A   G  GA
                                GGGAGG GCGG GG  GG
                                |||||| |||| ||  ||
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                                CCCTCC CGCC TC  CC
                                   C   G  AC
GAM2108  PACSIN1   3'  GGGAGAGTGGGGGGCCAGGG  45156      G  C     AGG  C
                                GGGAG AG GGGGGG  AG GG
                                ||||| || ||||||  || ||
                                CCCTC TC CCCCCC  TC CC
                                  _ A     GG_ _
GAM2108  PAFAH1B1  5'  GGGGGAGGGGAGGGGAGCGGG  7718     A   C     A
                                GGG GGAG GGGGGG GGAGCGGG
                                ||| |||| |||||| ||||||||
                                CCC CCTC CCCTCC CCTCGCCC
                                  _   _    _
GAM2108  PAX2      3'  GGGAGGGGCGGCAGGCGG    19634       A   G  GAGGA
                                GGGAGG GCGG GG    GCGG
                                |||||| |||| ||    ||||
                                CCCTCC CGCC TC    CGCC
                                   C   G  _____
GAM2108  PAX9      3'  GGAGGGCAGGAGGGGTGG    26207      A      A  AGC
                                GGAGG GCGGGGGG GG  GG
                                ||||| |||||||| ||  ||
                                CCTCC CGTCCTCC CC  CC
                                  _      _ A__
GAM2108  PCBP1     5'  GGAGCGAGCGGGAGCGG     26221        G  AG
                                GGAGCGGG GG  GAGCGG
                                |||||||| ||  ||||||
                                CCTCGCTC CC  CTCGCC
                                    G  __
GAM2108  PCTK3     3'  GGGAGGAGTGGAGGGTGG    43781        C     A
                                GGGAGGAG GGGGGG GG
                                |||||||| |||||| ||
                                CCCTCCTC CCTCCC CC
                                    A     A
GAM2108  PDE4A     3'  GGGAGGAGTGGAGGGGAACAGG 26264        CG    A
                                GGGAGGAG  GGGGG GGAGCGGG
                                ||||||||  ||||| ||||||||
                                CCCTCCTC  CCTCC CCTTGTCC
                                    A_    _
GAM2108  PLOD3     5'  GGGAGGGGCGGCGGCTCGG   9896       A   G  GAGGAG
                                GGGAGG GCGG GG    CGG
                                |||||| |||| ||    |||
                                CCCTCC CGCC CC    GCC
                                   C   G  GA____
GAM2108  PRKCA     3'  GGGAGGGCTGGGGGCTGG    15625      A  G   AGGAGC
                                GGGAGG GC GGGGG    GG
                                |||||| || |||||    ||
                                CCCTCC CG CCCCC    CC
                                   _ A    GA____
GAM2108  PROC      3'  GGGGGGGGCGGGGGGGG    7193     A  A      A
                                GGG GG GCGGGGGG GG
                                ||| || |||||||| ||
```

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                                CCC CC CGCCCCCC CC
                                  C  C       _
GAM2108  PTN      5'  GGGAGGGATGAGAGGAGCGGG  44389        AGC GG
                                GGGAGG  G  GGGAGGAGCGGG
                                ||||||  |  ||||||||||||
                                CCCTCC  C  CTCTCCTCGCCC
                                   ___ TA
GAM2108  PXN      3'  GGGAGGATGGAGAGTGG     16029        GC     A
                                GGGAGGA  GGGGGG GG
                                |||||||  ||||||  ||
                                CCCTCCT  CCTCTC CC
                                    A_     A
GAM2108  RAB13    5'  GGGGGAGCCGGGGGAGGGGTGG 16119     A    G       AGC
              G                  GGG GGAGC GGGGGAGG   GGG
                                |||  |||||  ||||||||   |||
                                CCC CCTCG CCCCCTCC   CCC
                                  _    G       CCA
GAM2108  RAB3A    3'  GGGGGGGGGGGGGGTCCCAGG   16075     A  AGC     A  AG_
                                GGG GG   GGGGGG GG   CGGG
                                |||  ||   ||||||  ||   ||||
                                CCC CC   CCCCCC CC   GTCC
                                  _  ___     _  AGG
GAM2108  RELN     5'  GGAGCGGGCCTGGGAGCGGG   45357         GGGA
                                GGAGCGGG    GGAGCGGG
                                ||||||||    ||||||||
                                CCTCGCCC    CCTCGCCC
                                     GGAC
GAM2108  RFX1     3'  GGGTGGGGCGGGGGGACCCTGG 16296     A  A        GGAGC
                                GGG GG GCGGGGGGGA     GG
                                |||  ||  |||||||||     ||
                                CCC CC CGCCCCCCT     CC
                                  A  C        GGGA_
GAM2108  RNH      5'  GGGGAGGGGTGGGTGGGGTGGG 40609    A    C   _   A  AGC
                                GG GGAG GGG GGG GG   GGG
                                ||  ||||  |||  |||  ||   |||
                                CC CCTC CCC CCC CC   CCC
                                  _   _   A   A  CCA
GAM2108  RXRB     3'  GGGGGGGCGGCGGGAAGCTGGG 35043     A  A    G     AGC
                                GGG GG GCGG GGGAGG   GGG
                                |||  ||  ||||  ||||||   |||
                                CCC CC CGCC CCCTTC   CCC
                                  _  C    G     GA_
GAM2108  RYR1     5'  GGGAGGGCTGGGGGCG      8069        A  GG    AGGA
                                GGGAGG GC  GGGG    GCG
                                ||||||  ||  ||||    |||
                                CCCTCC CG  CCCC    CGC
                                   _  A_    _____
GAM2108  S100A10  5'  GGGAGGCGGCGCGGGAGCGGG  40396       A_   G   GAGG
                                GGGAGG  GCG GGG    AGCGGG
                                ||||||  |||  |||    ||||||
```

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                                CCCTCC  CGC CCC    TCGCCC
                                   GC   G  ____
GAM2108  SALL1    3'  GGAAGGGGCGGGGCGGGGTGGG 16458       A     _  A  AGC
                                GGGAGG GCGGGG GG GG   GGG
                                |||||| |||||| || ||   |||
                                CCTTCC CGCCCC CC CC   CCC
                                   C     G  _  A__
GAM2108  SCA2     5'  GGGAGGGACACGTGAGGAGCGG 16477       AG  GGGG
              G                  GGGAGG  CG   GAGGAGCGGG
                                |||||| ||   ||||||||||
                                CCCTCC  GT   CTCCTCGCCC
                                   CT  GCA_
GAM2108  SCRT1    3'  GGGAGGGGAGGGGGCTCGGG   36367       AGC     A  AG
                                GGGAGG   GGGGGG GG  CGGG
                                ||||||   |||||| ||  ||||
                                CCCTCC   CCTCCC CC  GCCC
                                   ___     _  GA
GAM2108  SLC22A5  3'  AGGGGAGTGGGGAAAGGGGTGG 16857     A   C    GG   AGC
              G                  GGG GGAG GGGG  AGG   GGG
                                ||| |||| ||||  |||   |||
                                TCC CCTC CCCC  TCC   CCC
                                  _   A   TT   CCA
GAM2108  SLC9A1   3'  GGGAGGAGCTGTGCTGGGGTGG 43234         GG____   A
                                GGGAGGAGC     GGGG GG
                                |||||||||     |||| ||
                                CCCTCCTCG     CCCC CC
                                      ACACGA   A
GAM2108  SMARCC1  3'  GAGAGGGGTGGTAAGAGGAGTG 16901       AGC  GG     C
              GG                   GGGAGG   GG  GGAGGAG GGG
                                ||||||   ||  ||||||| |||
                                CTCTCC   CC  TCTCCTC CCC
                                   CCA  AT      A
GAM2108  SNAI1    3'  AGGGGAGTGGGGTCCCCTGAGT 25607     A   C   GGAG__  C
              GGG                  GGG GGAG GGGG     GAG GGG
                                ||| |||| ||||     ||| |||
                                TCC CCTC CCCC     CTC CCC
                                  _   A   AGGGGA   A
GAM2108  SOLH     3'  GGGGGGCGGGGGGCCCATGGG  24833     A  A      AGGAGC
                                GGG GG GCGGGGGGG     GGG
                                ||| || ||||||||     |||
                                CCC CC CGCCCCCC     CCC
                                  _  _       GGGTA_
GAM2108  SPI1     3'  GGAGTGGGGGGGAGGGGCGGG   17078      C        A
                                GGAG GGGGGGAGG GCGGG
                                |||| ||||||||| |||||
                                CCTC CCCCCCTCC CGCCC
                                  A        C
GAM2108  SPTB     3'  GGGAGGATGGAGGGCG      7382         GCGGGG    A
                                GGGAGGA     GGAGG GCG
                                |||||||     ||||| |||
```

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                                CCCTCCT     CCTCC CGC
                                   A_____   _
GAM2108 SSRP1    5' GGGGGGCGCGGGGAGGGGGATG 17130     A A    _ A  GC
           GG                    GGG GG GCGGGG GG GGA  GGG
                                 ||| || |||||| || |||  |||
                                 CCC CC CGCCCC CC CCT  CCC
                                   C G     T C   A_
GAM2108 SYNGR1   3' GAGAGGGGACAGATGGGGAGGG 21758       A_   __     A
           GCGGG                   GGGAGG  GCGG  GGGGAGG GCGGG
                                 ||||||  ||||  ||||||| |||||
                                 CTCTCC  TGTC  CCCCTCC CGCCC
                                    CC    TA      C
GAM2108 TACSTD1  5' GGGAGGGCGTGCGCCGGGAGTG 14302       A  GGGGGA_   C
           GG                    GGGAGG GCG      GGAG GGG
                                 |||||| |||      |||| |||
                                 CCCTCC CGC      CCTC CCC
                                    _  ACGCGGC    A
GAM2108 TBL1X    5' GGGAGAGGGCGGGACAGCGGG  24891      G  C  G    GG
                                 GGGAG AG GG GGGA  AGCGGG
                                 ||||| || || ||||  ||||||
                                 CCCTC TC CC CCCT  TCGCCC
                                   _ _ G   G_
GAM2108 TBXA2R   3' GGGAGGAGTTGGGGGGTCCCCGG 9858         CG     AGGAG
           G                     GGGAGGAG  GGGGG    CGGG
                                 ||||||||  |||||    ||||
                                 CCCTCCTC  CCCCC    GCCC
                                      AA    AGGG_
GAM2108 TCF3     3' GGGGGGACGGGGGGGGCTCAGG  43324     A  AG      AG AG
                                 GGG GG  CGGGGGGG  G  CGGG
                                 ||| ||  |||||||  |  ||||
                                 CCC CC  GCCCCCC  C  GTCC
                                   _  CT      __ GA
GAM2108 TFAP2A   3' GGTGAGGCGTGGGAGGGGCGGG 17400    GA  A   GG     A
                                 GG  GG GCG  GGGAGG GCGGG
                                 ||  || |||  |||||| |||||
                                 CC  TC CGC  CCCTCC CGCCC
                                  AC  _   A_     C
GAM2108 TFAP4    5' GGGAGGCGGGCATGGGAGGGGC 17413       GA    ___     A
           GGG                     GGGAG  GCGGG   GGGAGG GCGGG
                                 |||||  |||||   |||||| |||||
                                 CCCTC  CGCCC   CCCTCC CGCCC
                                    __    GTA     C
GAM2108 TFAP4    5' GGGAGGGGCGGGAGGGAGG   17414       A    _
                                 GGGAGG GCGGG GGGAGG
                                 |||||| ||||| ||||||
                                 CCCTCC CGCCC CCCTCC
                                    C     T
GAM2108 TFE3     3' GGGAGGGTGGGGGAAAAGGCGG 27169       AGCG        _
           G                     GGGAGG    GGGGGAGGAG CGGG
                                 ||||||    |||||||||| ||||
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                                CCCTCC   CCCCCTTTTC GCCC
                                   CA__       C
GAM2108 TGIF    5' GGAGGGGCCAGGAGCGG    17501    GC   GG
                                GGA  GGGG  AGGAGCGG
                                |||  ||||  ||||||||
                                CCT  CCCC  TCCTCGCC
                                  __   GG
GAM2108 TNFRSF11A 3' GGGGGAGTCGGGGGGAGG   19275    A   _
                                GGG GGAG CGGGGGGAGG
                                ||| |||| ||||||||||
                                CCC CCTC GCCCCCCTCC
                                  _   A
GAM2108 TNFRSF12  3' GGGCGAGCAGGGGTGGG    19126    AG       GA
                                GGG  GAGCGGGGG  GG
                                |||  |||||||||  ||
                                CCC  CTCGTCCCC  CC
                                  G_       AC
GAM2108 TNFSF5   3' GGGGGGGGGGGGGGG       6328     A  AGC     A  AGC
                                GGG GG   GGGGGG GG   G
                                ||| ||   |||||| ||   |
                                CCC CC   CCCCCC CC   C
                                  _ ___     _ ___
GAM2108 TNFSF5   3' GGGGGGGGGGGGGGGGTTTCGG  6331     A  AGC     A  AG_
                                GGG GG   GGGGGG GG   CGG
                                ||| ||   |||||| ||   |||
                                CCC CC   CCCCCC CC   GCC
                                  _ CC_     _  AAA
GAM2108 TSLP    5' GGGAGGAAGGTCAGGGAGGAGC 39698        C __
            GGG                   GGGAGGAG GG  GGGGAGGAGCGGG
                                ||||||||  ||  ||||||||||||||
                                CCCTCCTT CC  TCCCTCCTCGCCC
                                    _ AG
GAM2108 UBE2V1   3' GGGAGGGTGGGAGGCG      35349       AGCGGG    GA
                                GGGAGG     GGGAG  GCG
                                ||||||     |||||  |||
                                CCCTCC     CCCTC  CGC
                                   CA____    __
GAM2108 WNT5A    5' GGAAGGGCAGGGGGTGG     18121       A      A
                                GGGAGG GCGGGGGG GG
                                |||||| ||||||||  ||
                                CCTTCC CGTCCCCC CC
                                   _       A
GAM2108 WT1      5' GGGAGGGCGGGAAGTGG     35965       A      A
                                GGGAGG GCGGGGGG GG
                                |||||| ||||||||  ||
                                CCCTCC CGCCCTTC CC
                                   _       A
GAM2108 XRCC1    5' GGGAGAGTGGGAGGGAGCGGG  26669      G  CG    A
                                GGGAG AG  GGGGG GGAGCGGG
                                |||||  ||  ||||| ||||||||
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                                CCCTC TC  CCCTC CCTCGCCC
                                  _ A_    _
GAM2108  YWHAE    3'  GGGAGGAGTGAGGGGAAG    27597        C
                                GGGAGGAG GGGGGGAGG
                                |||||||| |||||||||
                                CCCTCCTC CTCCCCTTC
                                    A
GAM2109  ANK1     5'  GACACCGAATGGCCC       33860         AACG
                                GACGCCGAA   GGCCC
                                |||||||||   |||||
                                CTGTGGCTT   CCGGG
                                    A___
GAM2109  ARIH1    5'  GACGCCGAGGCCCC        25089         AAACG
                                GACGCCGA    GGCCCC
                                ||||||||    ||||||
                                CTGCGGCT    CCGGGG
                                            _____
GAM2109  BARHL1   3'  GCCGGGCAGGGCCCCCTCC   33466      AAAAC      _
                                GCCG    GGGCCCCC CC
                                ||||    |||||||| ||
                                CGGC    CCCGGGGG GG
                                  CCGT_      A
GAM2109  CD1D     5'  AGACCCCGGCAGCCCTCC    44293     G  AAAACG    C
                                AGAC CCG    GGCCC CC
                                |||| |||    ||||| ||
                                TCTG GGC    TCGGG GG
                                  G  CG____    A
GAM2109  DAAM2    3'  AGAGGCTGGAACAGACCCTTCC 45170    C  CGAA       CC
           C                     AGA GC   AACGGGCCC  CCC
                                ||| ||   |||||||||  |||
                                TCT CG   TTGTCTGGG  GGG
                                 C  ACC_       AA
GAM2109  EPAS1    5'  AGACGCCGAGCACCTGGGCTCC 11000        AA __   C
           C                     AGACGCCGA  AC  GGGC CCC
                                |||||||||  ||  |||| |||
                                TCTGCGGCT  TG  CCCG GGG
                                     CG  GA   A
GAM2109  GCN5L1   5'  ACGCCGGGCCCCCTCC     11243      GAAAAC      _
                                ACGCC     GGGCCCCC CC
                                |||||     |||||||| ||
                                TGCGG     CCCGGGGG GG
                                  _______      A
GAM2109  GNA11    5'  CGACCGAGGGAGCCCCCC    44040   _   AAAC
                                CG CCGA   GGGCCCCCC
                                || ||||   |||||||||
                                GC GGCT   CTCGGGGGG
                                 T   CC__
GAM2109  HDAC4    3'  AGACGCCGAGGCAGATCC    25744        AAA  GC
                                AGACGCCGA  CGG  CC
                                |||||||||  |||  ||
```

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                              TCTGCGGCT  GTC  GG
                                   CC_  TA
GAM2109  HOXB3    5'  ACGCCGGACCCCCC       13438      GAAAAC
                              ACGCC     GGGCCCCCC
                              |||||     |||||||||
                              TGCGG     CCTGGGGGG
                                 _______
GAM2109  INHBB    5'  AGGCGCTGGAGCCCCCC     13541    A  CGAAAAC
                              AG CGC      GGGCCCCCC
                              || |||      |||||||||
                              TC GCG      CTCGGGGGG
                               C  AC_____
GAM2109  MADH6    5'  GCCGAGGTCGCCCCCCC     24600      AAAC __
                              GCCGA   GG  GCCCCCCC
                              |||||   ||  ||||||||
                              CGGCT   CC  CGGGGGGG
                                 _____ AG
GAM2109  MAGEA8   5'  AGACCCTGAGCCCGCTTCCC  23844     G  GAAAAC     C___
                              AGAC CC     GGGCCC   CCC
                              |||| ||     ||||||   |||
                              TCTG GG     CTCGGG   GGG
                                _ A_____     CGAA
GAM2109  MAP3K10  5'  GATGCAGAGGGCGGGCCCC   42755    C  C  AAA
                              GA GC GA   CGGGCCCC
                              || || ||   ||||||||
                              CT CG CT   GCCCGGGG
                               A  T  CCC
GAM2109  MSX1     5'  AGAGCCGGGCCCCCC       14668     C   GAAAAC
                              AGA GCC     GGGCCCCCC
                              ||| |||     |||||||||
                              TCT CGG     CCCGGGGGG
                                _  _______
GAM2109  NFRKB    5'  AGACGCCGAGGCTTCCGCGCCC 26091          AAA___  G
              CC                AGACGCCGA     CG GCCCCC
                              |||||||||     || ||||||
                              TCTGCGGCT     GC CGGGGG
                                   CCGAAG  G
GAM2109  NGFR     3'  GCCAGGCGGGCCCCCCCC    14778      AAAA
                              GCCG   CGGGCCCCCCCC
                              ||||   ||||||||||||
                              CGGT   GCCCGGGGGGGG
                                CC__
GAM2109  RAB7L1   3'  AGATGCCCAGACCCCTCC     19429     C   GAAAA      C
                              AGA GCC     CGGGCCCC CC
                              ||| |||     |||||||| ||
                              TCT CGG     GTCTGGGG GG
                                A  _____       A
GAM2109  RASAL1   3'  CGCTGAAGAGGGCCCCC     21654     C   AAC
                              CGC GAA   GGGCCCCC
                              ||| |||   ||||||||
```

```
                                GCG CTT   CCCGGGGG
                                  A   CT_
GAM2109  RELN     5'  GCCTGGGAGCGGGCCCCCGCC  45356     GAAAA_       _
                                GCC     CGGGCCCCC CC
                                |||     ||||||||| ||
                                CGG     GCCCGGGGG GG
                                  ACCCTC        C
GAM2109  SNX9     3'  AGACGCCGGGGTGCTGGGTGCC 32147         AAAAC___ _    C
              CTCC                  AGACGCCG       GG GCCC CC
                                |||||||||       || |||| ||
                                TCTGCGGC       CC CGGG GG
                                    CCCACGAC  A    A
GAM2109  THBD     5'  GACGCCGATGGCGACAGCCTCT 7425         AAA __    CCC
              CC                    GACGCCGA   CG  GGCC   CC
                                |||||||||   ||  ||||   ||
                                CTGCGGCT   GC  TCGG   GG
                                    ACC  TG    AGA
GAM2109  VANGL2   3'  GCCTGAGAACCAAGCCCCCTCC 43459     _ AAA_       _
                                GCC GA    CGGGCCCCC CC
                                ||| ||    ||||||||| ||
                                CGG CT    GTTCGGGGG GG
                                  A  CTTG        A
GAM2109  ABL1     3'  AGGAGTGGGGGAGGGGAAGGG  28701       CG       AGC
                                AGGAG  GGGGGAGG   GGGGGG
                                |||||  ||||||||   ||||||
                                TCCTC  CCCCCTCC   CTTCCC
                                   A_       C__
GAM2109  ADH5     5'  GGGGGGCGGGGCGTGGGG    8582        A  A   _
                                GGGGGG GG GCG GGGG
                                |||||| || ||| ||||
                                CCCCCC CC CGC CCCC
                                   G  C   A
GAM2109  ADRB1    5'  GGAGGCCGGGGGGCGGGGG    8657       _ G    GAGGA
                                GGAG C GGGG    GCGGGGG
                                |||| | ||||    |||||||
                                CCTC G CCCC    CGCCCCC
                                  C G   ______
GAM2109  ALMS1    5'  AGGAGGGGGGGAGGGAGGG   31528       C        AGC
                                AGGAG GGGGGGAGG   GGGGG
                                |||||  |||||||||   |||||
                                TCCTC CCCCCCTCC   CTCCC
                                   _       ____
GAM2109  ANP32A   3'  AGGGGGGGGGGAGAGGGG    26706     AGC     A    C
                                AGG   GGGGGG GGAG GGGG
                                |||   |||||| |||| ||||
                                TCC   CCCCCC CCTC CCCC
                                  ____     _    T
GAM2109  AR       5'  GGAGGGGGGGAAGGCAGGGTGG 6235       C        A     _
                                GGAG GGGGGGAGG GCGGGG GG
                                |||| ||||||||| |||||| ||
```

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                                CCTC CCCCCCTTC CGTCCC CC
                                  _       _     A
GAM2109 AR      5' AGGGTGGGGGGAGGCGGGG   6229     AGC      GA
                                AGG   GGGGGGAG  GCGGGG
                                |||   ||||||||  ||||||
                                TCC   CCCCCCTC  CGCCCC
                                  CA_       __
GAM2109 AR      5' GGGGCGGGGGGGGCGGGTGGG  6241     A      AGGA    _
                                GG GCGGGGGGG    GCGGG GGG
                                || ||||||||    ||||| |||
                                CC CGCCCCCC    CGCCC CCC
                                 C       _____     A
GAM2109 ARHGEF1  3' GGGGTGGGGGGTGGAGGGG    21735    AGCG    A   C
                                GG    GGGGG GGAG GGG
                                ||    ||||| |||| |||
                                CC    CCCCC CCTC CCC
                                 CCA_    A   _
GAM2109 ARVCF    3' AGGATGGGGGGGAGTGGGGTGGG 11698     GC       GAGC__
            GGG                   AGGA  GGGGGGGAG     GGGGGGG
                                ||||  ||||||||      ||||||
                                TCCT  CCCCCCTC      CCCCCC
                                  A_       ACCCCA
GAM2109 ARVCF    3' GGAGTGGGGTGGGGGGGGCAGG  11705      C   _  A  A
                                GGAG GGGG GG GG GCGGG
                                |||| |||| || || |||||
                                CCTC CCCC CC CC CGTCC
                                  A   A  C  C
GAM2109 ATBF1    5' GGGGCGGGCGGGGCGGGGGG   27854    A    _   AGGA
                                GG GCGGG GGG    GCGGGGGGG
                                || ||||| |||    |||||||||
                                CC CGCCC CCC    CGCCCCCC
                                 C    G  _____
GAM2109 ATP2B3   3' GGGGGACGGGGGGCGGGGG    34975      GA  A_
                                GGGGG  GG  GCGGGGG
                                |||||  ||  |||||||
                                CCCCC  CC  CGCCCCC
                                   TG  CC
GAM2109 B4GALT1  3' GGGGTGGGGGGGAGGACG     11285    AGC        G
                                GG   GGGGGGAGGA CG
                                ||   ||||||||||  ||
                                CC   CCCCCCTCCT GC
                                 CCA        _
GAM2109 BACE     3' AGGAGCGGGGAGGGGAAGAACA 39948          ____
            GG                    AGGAGCGGGG   GGAGGAGCGGG
                                ||||||||||   ||||||||||||
                                TCCTCGCCCC   CCTTCTTGTCC
                                      TCC
GAM2109 BACH2    3' AGGGGTGGGTGGGAGGAAGG   34773     AGC  _      C
                                AGG   GGG GGGAGGAG GG
                                |||   ||| ||||||||  ||
```

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                                TCC   CCC CCCTCCTT CC
                                  CCA   A       _
GAM2109 BACH2    5' AGGGGCGAGGGGAGGCCGGGGG 34772     A         AG
              G                    AGG GCGGGGGGAGG  CGGGGGG
                                ||| |||||||||||  |||||||
                                TCC CGCTCCCCTCC  GCCCCCC
                                  C          G_
GAM2109 BARHL1   3' GGGGCGCGGGGAGAGGGG    33472    A  G     GAGC
                                GG GCG GGGGAG    GGGGG
                                || ||| ||||||    |||||
                                CC CGC CCCCTC    TCCCC
                                 C  G     _____
GAM2109 BCL11B   5' GGAGCCGGGGGGAGGGGG     39750      G       AGC
                                GGAGC GGGGGGAGG   GGG
                                ||||| ||||||||   |||
                                CCTCG CCCCCTCC   CCC
                                   G       ____
GAM2109 BMP1     3' AGGAGTGGGGGAGCTAAGGGG  25967      CG      GAGC
                                AGGAG  GGGGGAG    GGGGG
                                |||||  |||||||    |||||
                                TCCTC  CCCCCTC    TCCCC
                                   A_      GAT_
GAM2109 BSN      3' AGGGGTGGGGTGGGGAGGGG   18390     AGC   _  A   C
                                AGG   GGGG GG GGAG GGG
                                |||   |||| || |||| |||
                                TCC   CCCC CC CCTC CCC
                                  CCA   A  _   _
GAM2109 CACNA1S  5' AGGAGTGGGGGGGCAGGAG    6300       C     GAGGA
                                AGGAG GGGGG    GCGGGGG
                                ||||| |||||    |||||||
                                TCCTC CCCCC    CGTCCTC
                                   A    ______
GAM2109 CALM3    3' GGGGTGGGGGGGTGGGGTGGGG  23241    AGC     A  AGCG
                                GG   GGGGGG GG    GGGG
                                ||   |||||| ||    ||||
                                CC   CCCCCC CC    CCCC
                                 CCA     A  CCA_
GAM2109 CALM3    3' GAAGCAGGGGGGTGGGGG     23234          AGGAGC
                                GGAGCGGGGGGG     GGGGG
                                ||||||||||      |||||
                                CTTCGTCCCCC     CCCCC
                                      A_____
GAM2109 CBFA2T3  3' AGGAGTGGAGGGAGGGTGGG   23259      C       AGCG
                                AGGAG GGGGGGAGG    GGG
                                ||||| |||||||||    |||
                                TCCTC CCTCCCTCC    CCC
                                   A       CA__
GAM2109 CDC25B   5' GAGGGGTGGGGGGGGGGGG    34849     C   _   A  AGC
                                GAG GGG GGG GG   GGGGG
                                ||| ||| ||| ||   |||||
```

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                                CTC CCC CCC CC   CCCCC
                                  _  A  _ C__
GAM2109 CDC25B   5' GGATGCGGGGAGGGCGGGGGG 34852    _ GG     A
                                GGA GC  GGGGAGG GCGGGGGG
                                ||| ||  ||||||| ||||||||
                                CCT CG  CCCCTCC CGCCCCCC
                                  A __     _
GAM2109 CDC25B   5' AGGCAGCGGGCGAGGGGTGGGG 34845    _    G GA  AGC
             GG                   AGG AGCGGG G  GG   GGGGGG
                                ||| |||||| |  ||   ||||||
                                TCC TCGCCC C  CC   CCCCCC
                                  G     G TC  CA_
GAM2109 CEP2     5' GGAGCGAGGGGCGGGGG     28441          GAGGA
                                GGAGCGGGGG    GCGGGGG
                                ||||||||||    |||||||
                                CCTCGCTCCC    CGCCCCC
                                              _____
GAM2109 CHST1    3' GGAGTGGGGTGAGCTGGGGG   18911     C   GGAG   _
                                GGAG GGGG    GAGC GGGGG
                                |||| ||||    |||| |||||
                                CCTC CCCC    CTCG CCCCC
                                  A   A___    A
GAM2109 CKM      3' GGGGCGGGGCGAGGAGTGAGGG 12263    A     G     C
                                GG GCGGGG GAGGAG GGGGG
                                || |||||| |||||| |||||
                                CC CGCCCC CTCCTC CTCCC
                                 C     G     A
GAM2109 CLCN6    3' AGGGGCGGGGAGAGGGGACAAA 34713     A         A_
             G                   AGG GCGGGGGGGAGG  GCGGGG
                                ||| ||||||||||  ||||||
                                TCC CGCCCCTCTCC  TGTTTC
                                  C         CC
GAM2109 CLTC     5' GGAGGGGGGAGGCTGGG     22152     GC       AGCG
                                GGA  GGGGGGAGG    GGG
                                |||  |||||||||   |||
                                CCT  CCCCCCTCC    CCC
                                  __        GA__
GAM2109 COL15A1  3' GGGGTTGGGGGAGGAGAG    12357    AGCG        C
                                GG    GGGGGAGGAG GG
                                ||    ||||||||||| ||
                                CC    CCCCCTCCTC TC
                                 CCAA         _
GAM2109 COL1A1   3' AGGAGTGGAGGGGAGGCCAAGG 6361       C  _      AGC_
             GGGG                   AGGAG GG GGGGAGG    GGGGGG
                                ||||| || |||||||    ||||||
                                TCCTC CC CCCCTCC    CCCCCC
                                   A  T      GGTT
GAM2109 COL5A3   3' AGGGGCAGGGGGAGGGGA    31849     A         AGC
                                AGG GCGGGGGGGAGG   GGG
                                ||| ||||||||||   |||
```

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                                TCC CGTCCCCCTCC  CCT
                                  C        ___
GAM2109 CSK     5' GGGGCGGGAGGGAGTCGGGGGG 20469    A      AG  _
                                GG GCGGGGGG  GAG CGGGGGG
                                || ||||||||  ||| |||||||
                                CC CGCCCTCC  CTC GCCCCCC
                                 C       __  A
GAM2109 CYLN2   3' GGAGGGGGGCCGGGG      18057     C    GAGGAG
                                GGAG GGGGG     CGGGG
                                |||| |||||     |||||
                                CCTC CCCCC     GCCCC
                                  _    G_____
GAM2109 DACH    5' GGGGTGGGGGTGGGGCGGGG  38876    AGC    GA  A
                                GG   GGGGG  GG GCGGGG
                                ||   |||||  || ||||||
                                CC   CCCCC  CC CGCCCC
                                 CCA    AC  _
GAM2109 DNMT3L  5' GGGGCGGGGAGGGGCGGGGG  30070    A      A  A
                                GG GCGGGGGG GG GCGGGGG
                                || |||||||| || |||||||
                                CC CGCCCCTC CC CGCCCCC
                                 C       _ _
GAM2109 EGLN1   5' GGGGCGGAGGGAGGGCCGGG  35175    A        A  G
                                GG GCGGGGGGAGG GC GGG
                                || |||||||||| || |||
                                CC CGCCTCCCTCC CG CCC
                                 C         _ G
GAM2109 EGLN1   5' AGGGCCGGGGGGGAGGGCCGAGG 35159     AG        AG
           GG                     AGG  CGGGGGGAGG  CGGGGGG
                                ||| ||||||||||  |||||||
                                TCC  GCCCCCCTCC  GCTCCCC
                                  CG         CG
GAM2109 EGR3    5' GGAGGGGGGAGGGAAGAAGGG  40552     C    GA   CG
                                GGAG GGGGG  GGAG  GGGG
                                |||| |||||  ||||  ||||
                                CCTC CCCCC  CCTT  TCCC
                                  _    TC    CT
GAM2109 EGR3    3' AGGAGTGGGAGGGCAGGGG   40537      CGGG     A
                                AGGAG    GGGAGG GCGGGGG
                                |||||    |||||| |||||||
                                TCCTC    CCCTCC CGTCCCC
                                  A___     _
GAM2109 EMX2    5' GGGTGGGGGGAAGGAAAGG   44694    AGC        C
                                GG   GGGGGGAGGAG GG
                                ||   ||||||||||| ||
                                CC   CCCCCTTCCTT CC
                                 CAC         T
GAM2109 ENG     3' GGAGCGGGGGCAGGGGCGGAGG 6501          G   A
                                GGAGCGGGGG AGG GCGGGGG
                                |||||||||| ||| |||||||
```

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                                CCTCGCCCCC TCC CGCCTCC
                                      G  C
GAM2109 ENTPD2   3' AGGGGTTGGGGGAGGGATGGGG 10332    AGCG      AGCG
                                AGG   GGGGGAGG   GGGG
                                |||   ||||||||   ||||
                                TCC   CCCCCTCC   CCCC
                                  CCAA      CTA_
GAM2109 FACL4    5' AGGGGCGGGCGGAGCGGGGG  35675   C  _  A
                                AG GGG GGG GGAGCGGGGG
                                || ||| ||| ||||||||||
                                TC CCC CCC CCTCGCCCCC
                                 _  G  G
GAM2109 FHL2     5' GGGCGTGGGGCGCGGGGG   11115   A  G   AGGA
                                GG GCG GGGG   GCGGGGG
                                || ||| ||||   |||||||
                                CC CGC CCCC   CGCCCCC
                                 _  A   G___
GAM2109 FKBP2    5' AGCAGCGGGGGGAGGGGG   20925   G        AGC
                                AG AGCGGGGGGAGG  GGG
                                || ||||||||||||  |||
                                TC TCGCCCCCCTCC  CCC
                                 G         ___
GAM2109 GNB1     3' AGGAGTGCGGGGGGGCGGGGCGG 13197     __      A  A
           GGGG                   AGGA  GCGGGGGG GG GCGGGGGG
                                |||| |||||||| || ||||||||
                                TCCT  CGCCCCCC CC CGCCCCCC
                                  CA      G  C
GAM2109 GPC1     3' GGAGCTGGGGGGGAGGGCTAGG  13252      _      A  G
                                GGAGC GGGGGGAGG GC GGG
                                ||||| ||||||||| || |||
                                CCTCG CCCCCCTCC CG TCC
                                   A       _ A
GAM2109 GTF2IRD1 5' GGCGCGGGGGGGGGAATCGG   32262    A      A   _
                                GG GCGGGGGG GGAG CGG
                                || |||||||| |||| |||
                                CC CGCCCCCC CCTT GCC
                                 G      _   A
GAM2109 HBA1     3' AGGGGCTGGGGGGGAGGCCCAAG 8150     A  _      AG
           GGG                    AGG GC GGGGGGGAGG  CGGGGGG
                                ||| || |||||||||  |||||||
                                TCC CG CCCCCCTCC  GTTCCCC
                                  C  A       GG
GAM2109 HOXB9    3' GGAGCAGGGGGGAGGAACGG   35844
                                GGAGCGGGGGGGAGGAGCGG
                                |||||||||||||||||||
                                CCTCGTCCCCCTCCTTGCC

GAM2109 HOXC10   3' AGGGGCGGGGAGAGGAAGG   41485    A          C
                                AGG GCGGGGGGGAGGAG GG
                                ||| ||||||||||||| ||
```

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                                TCC CGCCCCTCTCCTT CC
                                  C          _
GAM2109  HOXC6    3'  GGGGCGGGGGGTGGGGGCG    21076    A      GA  A
                                GG GCGGGGGG  GG GCG
                                || |||||||  || |||
                                CC CGCCCCC  CC CGC
                                 C      AC  C
GAM2109  HYOU1    3'  GGGTGGGGTGAGGGGTGGG   40639     _  AG   C  _
                                GGG GGG  GAG GGG GGG
                                ||| |||  ||| ||| |||
                                CCC CCC  CTC CCC CCC
                                  A  CA  _  A
GAM2109  IGFBP2   3'  AGGGGCGGGGGGGCAGGGG    8253      A      GAGGA
                                AGG GCGGGGGG    GCGGGGGG
                                ||| |||||||    |||||||
                                TCC CGCCCCCC    CGTCCCC
                                  C     ______
GAM2109  INS      3'  AGGAGGCGGCGGGTGGGGG   6819       _  G   AGGAGC
                                AGGAG CGG GGG     GGGGGG
                                ||||| ||| |||     ||||||
                                TCCTC GCC CCC     CCCCC
                                   C  G  A_____
GAM2109  ITGA3    3'  GGGCCGGGGGCGGGGG      24265    A  G    GAGGA
                                GG GC GGGG    GCGGGGGG
                                || || ||||    |||||||
                                CC CG CCCC    CGCCCCC
                                 _  G   _____
GAM2109  ITGB4    5'  GGCGCGGGGGGTTGGGGG    6845     A      AGGAGC
                                GG GCGGGGGGG     GGGGG
                                || ||||||||     |||||
                                CC CGCCCCCC     CCCCC
                                 G       AA____
GAM2109  JUP      3'  AGGGGCGGGGAGGGGGTGTCAG 13769     A       A  AG__
              G                  AGG GCGGGGGGG GG    CGGG
                                ||| ||||||| ||    ||||
                                TCC CGCCCCTC CC    GTCC
                                  C       C  CACA
GAM2109  KCNC3    3'  AGGAGCAGTGGGGGGGGGGTGG 22490       ___      A  AGC
              GGGG                 AGGAGC   GGGGGG GG   GGGGGG
                                ||||||   |||||| ||   ||||||
                                TCCTCG   CCCCCC CC   CCCCCC
                                   TCA     _  CCA
GAM2109  KCNC3    5'  AGGGGCGGGGACACGGGGG   22494     A      GAGGA
                                AGG GCGGGGG    GCGGGGG
                                ||| |||||||    |||||||
                                TCC CGCCCCT    TGCCCCC
                                  C      G____
GAM2109  KCNC3    3'  GGGGTGGGGGGGGGAGGG    22523    AGC     A   C
                                GG   GGGGGG GGAG GG
                                ||   |||||| |||| ||
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                                CC   CCCCCC CCTC CC
                                 CCA     _   _
GAM2109  KCNJ3    5'  AGGAGGTGGGGGCGGGGG    13844      CG    GAGGA
                                AGGAG  GGGG    GCGGGGG
                                |||||  ||||    |||||||
                                TCCTC  CCCC    CGCCCCC
                                  CA   _____
GAM2109  KCNJ3    5'  GGGGCGGGGGGAGGAAAGGGGG 13848    A          C
                                GG GCGGGGGGAGGAG GGGGG
                                || ||||||||||||| |||||
                                CC CGCCCCCCTCCTT CCCCC
                                 C          T
GAM2109  KPNB1    5'  GGAGGGTGGGGTGGGGG     13971      C  _   AGGAGC
                                GGAG GG GGGG     GGGGG
                                |||| || ||||     |||||
                                CCTC CC CCCC     CCCCC
                                  _ A   A_____
GAM2109  LAG3     5'  GGCAGTGGTGGGGGGTGGGGGG 14044    _ C  _   A  AGC
                                GG AG GG GGGG GG   GGGGGG
                                || || || |||| ||   ||||||
                                CC TC CC CCCC CC   CCCCCC
                                 G  A  A   _  A__
GAM2109  LDB1     5'  GGGCCGGCCTGGGGGGCGGGGG 19343    A  G  ___   A  A
           G                     GG GC GG   GGG GG GCGGGGGG
                                || || ||   ||| || ||||||||
                                CC CG CC   CCC CC CGCCCCCC
                                 _  G  GGA   _  _
GAM2109  LRP1     5'  AGGAGGCGGGGAGGGGGGGTGG 14204      _      A  AGC_
           GGGG                    AGGAG CGGGGGG GG    GGGGGG
                                ||||| ||||||| ||    ||||||
                                TCCTC GCCCCTC CC    CCCCCC
                                  C      C  CCCA
GAM2109  MADD     5'  GCGCGGGGAGTGGGGGG     39066     G     GAGC
                                GCG GGGGAG    GGGGGG
                                ||| ||||||    ||||||
                                CGC CCCCTC    CCCCCC
                                  G     A___
GAM2109  MECP2    3'  GGAGTGGGGGAGGTGGGGGG   22599      CG       AGC
                                GGAG  GGGGGAGG   GGGGGG
                                ||||  ||||||||   ||||||
                                CCTC  CCCCCTCC   CCCCCC
                                  A_       A__
GAM2109  MECP2    3'  GGAGGTGGGGGGGAGCTGGGGG  22598      CGG   A   _
                                GGAG   GGGG GGAGC GGGGG
                                ||||   |||| ||||| |||||
                                CCTC   CCCC CCTCG CCCCC
                                  CA_   _    A
GAM2109  MGAT5    5'  AGGGGTGGGGAGGAGAGAGGGG 14469     AGC  _       C
                                AGG   GG GGGGAGGAG GGGGGG
                                |||   || |||||||| ||||||
```

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                                TCC   CC CCCCTCCTC CTCCCC
                                  ___ A       T
GAM2109 MGMT     5' AGGGGCGGCGGGGGGGGCGGGG 14486     A   _   A A
             GG                    AGG GCGG GGGG GG GCGGGGGG
                                |||  |||| |||| || ||||||||
                                TCC CGCC CCCC CC CGCCCCCC
                                  C   G   _ C
GAM2109 MSI1     3' AGGGGCGGGTGGGGATGGGGG  14635     A    G A  GC
                                AGG GCGGG GG GGA  GGGGG
                                |||  ||||| || |||  |||||
                                TCC CGCCC CC CCT  CCCCC
                                  C    A _  A_
GAM2109 NEUROD2  5' GGAGGGGGGGAGGGGG      26062      C       AGC
                                GGAG GGGGGGAGG   GGG
                                ||||  |||||||||   |||
                                CCTC CCCCCCTCC   CCC

                                  _       ___
GAM2109 NFIA     5' GGGGTGTGGGGGAGGGGG    43220      ___ A   C
                                GGGG   GG GGAG GGGG
                                ||||   ||  |||| ||||
                                CCCC   CC CCTC CCCC
                                  ACA  C   _
GAM2109 NOTCH3   3' GGTGAGGGGAGTGGGGGG    7738     _   A   C
                                GG GGGG GGAG GGGGGG
                                ||  |||| |||| ||||||
                                CC CTCC CCTC CCCCCC
                                 A   _   A
GAM2109 NPAS1    5' AGGAGCTGGGGGGGGGGG    40869       _     AGGAGC
                                AGGAGC GGGGGG     GGGGG
                                ||||||  ||||||      |||||
                                TCCTCG CCCCCC     CCCCC
                                   A     _______
GAM2109 NRXN1    5' GGGCTGGGGTGCGGCGGGGGG  39845    A  G    GAGGA
                                GG GC GGGG     GCGGGGGG
                                ||  ||  ||||     ||||||||
                                CC CG CCCC     CGCCCCCC
                                 _  A   ACGC_
GAM2109 NT5M     5' GGAGCGGGGCGGGGAGCGCAGG 33652          _ A     G
             G                    GGAGCGGGG GG GGAGCG GGGG
                                |||||||||  ||  ||||||  ||||
                                CCTCGCCCC CC CCTCGC TCCC
                                     G  _     G
GAM2109 NTSR1    3' AGGGGTGGGGAGGAGTTGGGG  14876     AGC  _       CG
                                AGG   GG GGGGAGGAG  GGGG
                                |||   ||  |||||||||  ||||
                                TCC   CC CCCCTCCTC  CCCC
                                  ___ A       AA
GAM2109 PCBD     3' GGAGTGGTGGGAGGGTAAGGG  7099       C  G     AGC
                                GGAG GG GGGAGG   GGGGG
                                ||||  ||  ||||||   |||||
```

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                                CCTC CC CCCTCC   TTCCC
                                  A A     CA_
GAM2109  PDE4A    3'  GGGGCGGGGGGGGTGAGTGG   26270    A      AG   C
                                GG GCGGGGGGG  GAG GG
                                || ||||||||  ||| ||
                                CC CGCCCCCC  CTC CC
                                 C       CA   A
GAM2109  PDE4A    3'  GGAGTGAGGGGAGGAGTGG   26261     C        C
                                GGAG GGGGGGAGGAG GG
                                |||| ||||||||||| ||
                                CCTC CTCCCCTCCTC CC
                                  A         A
GAM2109  PDE4A    3'  AGAAGTGGGGCGGGGGGCGGGG 26242      C   _ A A
              GG                  AGGAG GGGG GG GG GCGGGGGG
                                ||||| |||| || || ||||||||
                                TCTTC CCCC CC CC CGCCCCCC
                                  A   G _ C
GAM2109  PGR      5'  GGGGCGGGGGAGGGCGG    9570    A     G   A
                                GG GCGGGGG AGG GCGG
                                || ||||||| ||| ||||
                                CC CGCCCCC TCC CGCC
                                 C     _  _
GAM2109  PNUTL1   3'  GGGGCGGGGGAAGGGCAAGGG  15435   A        A
                                GG GCGGGGGGAGG GCGGGGG
                                || |||||||||| |||||||
                                CC CGCCCCCTTCC CGTTCCC
                                 C         _
GAM2109  POMZP3   5'  AGGAGTGGGGAGAGAGGGG   29237     C      GAGC
                                AGGAG GGGGGGAG   GGGGG
                                ||||| ||||||||   |||||
                                TCCTC CCCCTCTC   TCCCC
                                  A      ____
GAM2109  PROC     3'  GCAGGGGGGGGGGGCGGGGGG  7190        A  A_
                                GCGGGGGG GG  GCGGGGGG
                                |||||||| ||  ||||||||
                                CGTCCCCC CC  CGCCCCCC
                                     C  CC
GAM2109  RAB13    5'  GGAGCCGGGGGAGGGGTGGGG  16115     G      AGCG
                                GGAGC GGGGGAGG   GGGG
                                ||||| ||||||||   ||||
                                CCTCG CCCCCTCC   CCCC
                                  G       CCA_
GAM2109  RAB3A    3'  GGGCGGGGGGGGGGG      16073    A      AGGAGC
                                GG GCGGGGGG    GGGGG
                                || ||||||||    |||||
                                CC CGCCCCCC    CCCCC
                                 _     _______
GAM2109  RANBP3   3'  GGAGGGGGGTTTGGGGG    28779     C    GAGGAGC
                                GGAG GGGGG     GGGGG
                                |||| |||||     |||||
```

```
                                CCTC CCCCC      CCCCC
                                  _    AAA____
GAM2109  RFX1     3'  GGGGCGGGTGGGGCGGGG    16294    A    _  AGGA
                                GG GCGGG GGG    GCGGGG
                                || ||||| |||    ||||||
                                CC CGCCC CCC    CGCCCC
                                 C    A  ____
GAM2109  RFX1     3'  GGGGCGGGTGGGGCGGGGGG   16295    A    _  AGGA
                                GG GCGGG GGG    GCGGGGGG
                                || ||||| |||    ||||||||
                                CC CGCCC CCC    CGCCCCCC
                                 C    A  ____
GAM2109  RNH      5'  AGGGGTGGGTGGGGTGGGG   40600    C  _  A  AGCG
                                AG GGG GGG GG    GGGG
                                || ||| ||| ||    ||||
                                TC CCC CCC CC    CCCC
                                 _  A  A  CCA_
GAM2109  RNMT     3'  GGCCGGGGGGAGGGGGG     19151    AG        AGC
                                GG  CGGGGGGAGG   GGGG
                                ||  ||||||||||   ||||
                                CC  GCCCCCCTCC   CCCC
                                 G_         ___
GAM2109  RPA1     3'  GGATGGGGGGGGGGG       16368     GC     AGGAGC   _
                                GGA  GGGGGG     GGGG G
                                |||  ||||||     |||| |
                                CCT  CCCCCC     CCCC C
                                  A_     _______    A
GAM2109  SALL1    3'  AGGGGCGGGGCGGGGTGGGGGG 16453     A     _  A  AGC
                                AGG GCGGGG GG GG   GGGGGG
                                ||| |||||| || ||   ||||||
                                TCC CGCCCC CC CC   CCCCCC
                                  C     G  _  A__
GAM2109  SEPN1    3'  GGGGTGGGGAGAGAACTGGGGG 42434    AGC  _     _   _
                                GG   GG GGGGAG GAGC GGGGG
                                ||   || |||||| |||| |||||
                                CC   CC CCCCTC CTTG CCCCC
                                 ___  A     T    A
GAM2109  SERPINE1 3'  AGGGGCGCGGGGGGGCGCGGGGG 8282      A   G    A  A
            G                    AGG GCG GGGG GG GCGGGGGG
                                ||| ||| |||| || ||||||||
                                TCC CGC CCCC CC CGCCCCCC
                                  C   G    _  G
GAM2109  SH3GL1   3'  AGGGGCGGGGCGGGGACACGGG 16665     A     _  A  _
                                AGG GCGGGG GG GGA GCGGG
                                ||| |||||| || ||| |||||
                                TCC CGCCCC CC CCT TGCCC
                                  C     G  _  G
GAM2109  SIAT8E   5'  AGGGACGGGGGGGAGGGGG    40832     AG        AGC
                                AGG  CGGGGGGAGG   GGG
                                |||  ||||||||||   |||
```

```
                                TCC  GCCCCCCTCC   CCC
                                  CT         ___
GAM2109  SIT      3'  GGAGCGGGGGTGGGGAGG    30899          GA  AGC
                                GGAGCGGGGG  GG   GGGGG
                                ||||||||||  ||   |||||
                                CCTCGCCCCC  CC   CCTCC
                                     A_  ___
GAM2109  SIX3     3'  AGGAGTGGGGGAGGAGGGG   24017      CG        C
                                AGGAG  GGGGGAGGAG GGG
                                |||||  |||||||||| |||
                                TCCTC  CCCCCTCCTC CCC
                                  A_         _
GAM2109  SLC6A8   5'  GGGGCGGCGGTCAGGCGGGGGG 24780    A    G  GA  A
                                GG GCGG GG  GG GCGGGGGG
                                || |||| ||  || ||||||||
                                CC CGCC CC  TC CGCCCCCC
                                 C    G  AG  _
GAM2109  SLC9A3R2 5'  AGGGGCGCGGGGGAGCTCGGGG 41523     A  _      GAG
            G                    AGG GCG GGGGGAG   CGGGGG
                                ||| ||| |||||||   ||||||
                                TCC CGC CCCCCTC   GCCCCC
                                  C   G      GA_
GAM2109  SMT3H1   3'  GGAGTGGGGTGGGAGGGG    41000      C    GGA    C
                                GGAG GGGG   GGAG GGG
                                |||| ||||   |||| |||
                                CCTC CCCC   CCTC CCC
                                  A    AC_   _
GAM2109  SOLH     3'  GGAGGGGAAGGAGGGGGGCGGG 24831      C        A__
            GGG                    GGAG GGGGGGAGG   GCGGGGGG
                                |||| |||||||||   ||||||||
                                CCTC CCTTCCTCC   CGCCCCCC
                                  C        CCC
GAM2109  SORCS3   5'  GGAGTGGGGAGGGGGCGG    31422      C     A  A
                                GGAG GGGGGG GG GCGG
                                |||| |||||| || ||||
                                CCTC CCCCTC CC CGCC
                                  A     _  C
GAM2109  SOX10    3'  GGGGCAGGGGCTGGGCGGGGGG 28010    A      GA  A
                                GG GCGGGGG  GG GCGGGGGG
                                || |||||||  || ||||||||
                                CC CGTCCCC  CC CGCCCCCC
                                 C      GA  _
GAM2109  SOX10    5'  GGGAGGGAGGGGCGGGGG    28008    _     A
                                GGG GGGAGG GCGGGGG
                                ||| |||||| |||||||
                                CCC CCCTCC CGCCCCC
                                  T     C
GAM2109  SOX11    3'  GGGGCCGGGGGAGGGGTGG   17027    A  G      AGC  G
                                GG GC GGGGGAGG   GG GG
                                || || ||||||||   || ||
```

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                                CC CG CCCCCTCC   CC CC
                                 C  G       ___  A
GAM2109  SOX12    3'  GGGGTGTGGGGAGGCCGGAGGG 28053    AGCGG      AG
                                GG    GGGGAGG  CGGGGGG
                                ||    |||||||  |||||||
                                CC    CCCCTCC  GCCTCCC
                                 CCACA      G_
GAM2109  SP4      5'  GGGGGTGGGGGGCGAGGG     17050      GA  A     _
                                GGGGG  GG GCGGGG G
                                |||||  || |||||| |
                                CCCCC  CC CGCTCC C
                                   AC  C     G
GAM2109  SPI1     3'  GGAGTGGGGGGGAGGGGCGGG   17078      C        A
                                GGAG GGGGGGAGG GCGGG
                                |||| ||||||||| |||||
                                CCTC CCCCCCTCC CGCCC
                                   A        C
GAM2109  SPI1     3'  GGGGGCCTGGAGTGGGGG    17082      GA_   C
                                GGGGG   GGAG GGGGG
                                |||||   |||| |||||
                                CCCCC   CCTC CCCCC
                                   GGA    A
GAM2109  SSRP1    5'  GGCGCGGGGAGGGGGATGGGGG 17127    A     _  A   GC
              G                  GG GCGGGG GG GGA  GGGGGG
                                || |||||| || |||  ||||||
                                CC CGCCCC CC CCT  CCCCCC
                                 G     T  C   A_
GAM2109  SSRP1    5'  GGACGCGGGGGGGGGCGCGGGG  17126     _       A  A
                                GGA GCGGGGGG GG GCGGGG
                                ||| |||||||| || ||||||
                                CCT CGCCCCCC CC CGCCCC
                                  G       _  G
GAM2109  STIM1    3'  GGAGTGGTGGGAGGGAGG    41129      C  G     AGC
                                GGAG GG GGGAGG   GGGG
                                |||| || ||||||   ||||
                                CCTC CC CCCTCC   CTCC
                                   A  A     ___
GAM2109  TAGLN    3'  AGGAGCTGGGGGAGGGCCGGG  40616       G       A  G
                                AGGAGC GGGGGAGG GC GGG
                                |||||| |||||||| || |||
                                TCCTCG CCCCCTCC CG CCC
                                   A       _  G
GAM2109  TBP      3'  GGGGTGGGGGAGGCAAGGG   42112    AGCG      GA
                                GG   GGGGGAG  GCGGGGG
                                ||   |||||||  |||||||
                                CC   CCCCCTC  CGTTCCC
                                 CCA_      __
GAM2109  TCF3     3'  GGGGGGGGGGGGGGACGGGGGG  43327    AGC     A  AG
                                GG   GGGGGG GG  CGGGGGG
                                ||   |||||| ||  |||||||
```

```
                                CC   CCCCCC CC  GCCCCCC
                                 CC_     _ CT
GAM2109  TNFRSF11A 3'  GGAGTCGGGGGGAGGAAGCTGG 19274      _        _ G
              G                   GGAG CGGGGGGAGGA GC GGG
                                  |||| |||||||||| || |||
                                  CCTC GCCCCCCTCCT CG CCC
                                    A         T  A
GAM2109  TNFSF5   3'  GGTGGCGGGGGGGGGGG     6332     A_      AGGAGC
                                  GG  GCGGGGGG     GGGGG
                                  ||  ||||||||     |||||
                                  CC  CGCCCCCC     CCCCC
                                   AC       _______
GAM2109  TNFSF5   3'  GGGGGGGGGGGGGGG       6329        A  AGC
                                  GGGGGG GG   GGGGGG
                                  |||||| ||   ||||||
                                  CCCCCC CC   CCCCCC
                                     _ C__
GAM2109  WNT5A    5'  AGGGCAGGGGGTGGGGG     18110     A       AGGAGC
                                  AGG GCGGGGGG     GGGGG
                                  ||| ||||||||     |||||
                                  TCC CGTCCCCC     CCCCC
                                    _       A_____
GAM2109  YY1      5'  GGGCGGGGGGAGAGGGGG     18179     A         AGC
                                  GG GCGGGGGGAGG   GGGGG
                                  || ||||||||||   |||||
                                  CC CGCCCCCCTCT   CCCCC
                                   _        ____
GAM2109  ZIC3     5'  GGAGGGGGTGTTGGCGGGGGG  18251      C    GGAGGA
                                  GGAG GGGG     GCGGGGGG
                                  |||| ||||     ||||||||
                                  CCTC CCCC     CGCCCCCC
                                    _    ACAAC_
GAM2110  ACTN2    5'  CGGGCGGCGGGCGCGGGG     9942          TGCGC    C
                                  CGGGCGGCG    GCGCG GG
                                  |||||||||    ||||| ||
                                  GCCCGCCGC    CGCGC CC
                                       C_____     C
GAM2110  ATOX1    5'  GGCGGTGTGGCGGCGGTGTGGC 19724      C   C   C   C___
              G                   GGCGG GTG GCG GCG    GGCG
                                  ||||| ||| ||| |||    ||||
                                  CCGCC CAC CGC CGC    CCGC
                                    A   _   _   CACA
GAM2110  B3GNT4   5'  CGGGCGGCGGCGGCGGCG    42455         T   C   C
                                  CGGGCGGCG GCG GCG GCG
                                  ||||||||| ||| ||| |||
                                  GCCCGCCGC CGC CGC CGC
                                          _   _   _
GAM2110  BCL11A   5'  CGGGCGGCGGCGGCGGCG    39709         T   C   C
                                  CGGGCGGCG GCG GCG GCG
                                  ||||||||| ||| ||| |||
```

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                                GCCCGCCGC CGC CGC CGC
                                      _  _  _
GAM2110 BDNF     5'  CGGGCGGGTGCGCCCGGGCGCG 40594        C     G __
              GCG                    CGGGCGG GTGCGC C  GCGCGGCG
                                |||||||  ||||||  |  ||||||||
                                GCCCGCC CACGCG G  CGCGCCGC
                                   _     G CC
GAM2110 CACNA1A  5'  CGGGCGGCGGCGGCTCGGC    35730         T   CGC  G
                                CGGGCGGCG GCG   GC CGGC
                                |||||||||  |||   ||  ||||
                                GCCCGCCGC CGC   CG GCCG
                                   _  ____  A
GAM2110 CAPON    5'  GGGCGCGGCGACGCGTGGCG   41929      G  T   C     C
                                GGGCG CG GCG GCGCG GGCG
                                |||||  ||  |||  |||||  ||||
                                CCCGC GC CGC TGCGC CCGC
                                   _  _  _     A
GAM2110 CDK2AP1  5'  CGGGCGGCGGGCGCGCCGGGCG 21597          T     ____
              CGGCG                  CGGGCGGCG GCGCGC   GCGCGGCG
                                |||||||||  ||||||   ||||||||
                                GCCCGCCGC CGCGCG   CGCGCCGC
                                     C     GCC
GAM2110 COPEB    5'  GGGCGGCGAGGCGCGCGG    44431         TGCGC
                                GGGCGGCG    GCGCGCGG
                                ||||||||    ||||||||
                                CCCGCCGC    CGCGCGCC
                                     TC____
GAM2110 DVL3     5'  GGCGGCGGCGCGCGGCG     20685        T      C
                                GGCGGCG GCGCGCG GCG
                                |||||||  |||||||  |||
                                CCGCCGC CGCGCGC CGC
                                   _      _
GAM2110 EGR3     3'  GGCGCGCGTGCGTGCGGCG   40553         C   C
                                GGCGTGCG GCG GCGGCG
                                ||||||||  |||  ||||||
                                CCGCGCGC CGC CGCCGC
                                     A   A
GAM2110 EXT1     5'  GGGTGGCGGCGGCGGCG     6550      C    T   C   C
                                GGG GGCG GCG GCG GCG
                                |||  ||||  |||  |||  |||
                                CCC CCGC CGC CGC CGC
                                  A   _  _  _
GAM2110 FASN     5'  CGGGCGGCGGTGCGGGCGGCG  19936         _    C   C
                                CGGGCGGCG TGCG GCG GCG
                                |||||||||  ||||  |||  |||
                                GCCCGCCGC ACGC CGC CGC
                                     C   C  _
GAM2110 FTH1     5'  GGCGGCGGTGGCTGCGCGGCG  42790         _  C  GC
                                GGCGGCG TG GC  GCGCGGCG
                                |||||||  ||  ||  ||||||||
```

```
                                CCGCCGC AC CG  CGCGCCGC
                                    C  _  A_
GAM2110  HDAC4    5'  CGGGCGGCGGCGGGGACGG   25764        T  CGCGC
                                CGGGCGGCG GCG    GCGG
                                ||||||||| |||    ||||
                                GCCCGCCGC CGC    TGCC
                                     _  CCC__
GAM2110  HDAC4    5'  CGGGCGGCGGCGGCGGCG    25763        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _  _  _
GAM2110  HDAC5    5'  CGGGCGGCGGCGGCAGCAGCGG 40165        T  C  _  _
              CG                  CGGGCGGCG GCG GC GC GCGGCG
                                ||||||||| ||| || || ||||||
                                GCCCGCCGC CGC CG CG CGCCGC
                                     _  _  T  T
GAM2110  JAG2     5'  GGGCGGCGGGCGTGCAGGGGCG 13732        T  C  C__
              GCG                   GGGCGGCG GCG GCG   GCGGCG
                                ||||||||| ||| |||   ||||||
                                CCCGCCGC CGC CGT   CGCCGC
                                     C  A  CCC
GAM2110  KIF3B    5'  CGGGCGGCGGCGGCGGCG    22034        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _  _  _
GAM2110  LATS2    5'  CGGGCGGCGGCGGTGGCG    31021        T  CGC
                                CGGGCGGCG GCG   GCG
                                ||||||||| |||   |||
                                GCCCGCCGC CGC   CGC
                                     _  CAC
GAM2110  LEF1     5'  CGGGGGCGTCTGCGCGGCG   32206     C    GC    C
                                CGGG GGCGT  GCGCG GCG
                                |||| |||||  ||||| |||
                                GCCC CCGCA  CGCGC CGC
                                  _    GA    _
GAM2110  MAML1    5'  CGGAGCGGGCTCGCGCGCGGCG 31282     _   CGT  G
                                CGG GCGG   GC CGCGCGCGGCG
                                ||| ||||   || ||||||||||
                                GCC CGCC   CG GCGCGCGCCGC
                                  T   ___  A
GAM2110  MSL3L1   5'  GGGCGGGCGGAGCGCGCGCGG  38590       C  C_
                                GGGCGG GTG  GCGCGCGCGG
                                |||||| |||  ||||||||||
                                CCCGCC CGC  CGCGCGCGCC
                                   _  CT
GAM2110  NFATC1   5'  AGGGGCGTGTGCGCGCGTGGCG 26069     C     C     C
                                GGG GGCGTG GCGCGCG GGCG
                                ||| |||||| ||||||| ||||
```

```
                                TCC CCGCAC CGCGCGC CCGC
                                  _     A      A
GAM2110 NFKB1    5' CGGGCGGCTGCGGCCTCGGCG 19652        G   C  GCG
                                CGGGCGGC TGCG GC   CGGCG
                                |||||||| |||| ||   |||||
                                GCCCGCCG ACGC CG   GCCGC
                                     _   _ GA_
GAM2110 NR2F2    5' CGGGCGGCGGCGGGGCGGC   34233         T  CGCGC
                                CGGGCGGCG GCG    GCGGC
                                ||||||||| |||    |||||
                                GCCCGCCGC CGC    CGCCG
                                     _  CC___
GAM2110 ODC1     5' CGGGCGGCGGCGGCGGCG    14915         T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                     _  _  _
GAM2110 OPTN     5' CGGGCGGCGGCGGTGGCG    35067         T  CGC
                                CGGGCGGCG GCG   GCG
                                ||||||||| |||   |||
                                GCCCGCCGC CGC   CGC
                                     _  CAC
GAM2110 PDGFB    5' GGCTGCTCCGCGCGCGCGGCG 15188     G GTG
                                GGC GC   CGCGCGCGCGGCG
                                ||| ||   |||||||||||||
                                CCG CG   GCGCGCGCGCCGC
                                  A  AG_
GAM2110 POMZP3   5' GGGCGGTGTGGAGCGCGGCG  29244       C  CGCGC
                                GGGCGG GTG    GCGCGGCG
                                |||||| |||    ||||||||
                                CCCGCC CAC    CGCGCCGC
                                   A  CT___
GAM2110 PTGER3   5' CGGGCGGCGGCGGAGGTCGGCG 9646         T  CGCGCG
                                CGGGCGGCG GCG     CGGCG
                                ||||||||| |||     |||||
                                GCCCGCCGC CGC     GCCGC
                                     _  CTCCA_
GAM2110 PTMA     5' GGCGGCGGAGGAGGCGCGCGGC 15872       TGCGC_
            G                    GGCGGCG     GCGCGCGGCG
                                 |||||||     ||||||||||
                                 CCGCCGC     CGCGCGCCGC
                                    CTCCTC
GAM2110 PTPN18   5' CGGCCCCGCGCGCGCGGC    30766     GTG
                                CGGC   CGCGCGCGCGGC
                                ||||   ||||||||||||
                                GCCG   GCGCGCGCGCCG
                                  GG_
GAM2110 PYGL     5' GGGCGGCGGGCTGCGCGGCG  16057        TGC  GC
                                GGGCGGCG   GC  GCGCGGCG
                                ||||||||   ||  ||||||||
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                                CCCGCCGC  CG  CGCGCCGC
                                    C__  A_
GAM2110  SLC6A8   5'  CGGGCGGCGGCGGCTGCGGCG  24762        T  C  GC
                                CGGGCGGCG GCG GC  GCGGCG
                                ||||||||| ||| ||  ||||||
                                GCCCGCCGC CGC CG  CGCCGC
                                    _  _ A_
GAM2110  SLC6A8   5'  CGGGCGGCGGCGGCGGCG    24761        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                    _  _  _
GAM2110  SORCS3   5'  CGGGGGGTGTGCGCGCGCCGGC 31417     C  C       G
            G                    CGGG GG GTGCGCGCGC CGGCG
                                |||| || |||||||||| |||||
                                GCCC CC CACGCGCGCG GCCGC
                                  C  A       _
GAM2110  TLE1     5'  CGGCGATCCGCGTGCGCGGCG  22918      _ G   C
                                CGGCG T CGCG GCGCGGCG
                                ||||| | |||| ||||||||
                                GCCGC A GCGC CGCGCCGC
                                   T G   A
GAM2110  USF2     3'  GGGCGGCGGCGGCTGCGTGG   17904       T  C  _  C
                                GGGCGGCG GCG GC GCG GG
                                |||||||| ||| || ||| ||
                                CCCGCCGC CGC CG CGC CC
                                    _  _ A  A
GAM2110  VGF      3'  GGGCGCCGGCGCGCGCGCGCGG 17995      G  _
            CG                    GGGCG CG TGCGCGCGCGCGGCG
                                ||||| || ||||||||||||||
                                CCCGC GC GCGCGCGCGCGCCGC
                                   G  C
GAM2110  VIM      5'  GGGCGGCGGCGGTGGCG     45226        T  CGC
                                GGGCGGCG GCG   GCG
                                |||||||| |||   |||
                                CCCGCCGC CGC   CGC
                                    _  CAC
GAM2110  ZNF219   5'  CGGGCGGCGGGCCGGCGGC   32326         TGC  G  C
                                CGGGCGGCG   GC CG GCGGC
                                |||||||||   || || |||||
                                GCCCGCCGC   CG GC CGCCG
                                    C__  _  _
GAM2110  ZNF219   5'  CGGGCGGCGGCGGCGGCG    32325        T  C  C
                                CGGGCGGCG GCG GCG GCG
                                ||||||||| ||| ||| |||
                                GCCCGCCGC CGC CGC CGC
                                    _  _  _
GAM2110  ZNF219   5'  CGGGCGGCGGCGGAGCGGGCGG 32324        T  C_  C
            CG                    CGGGCGGCG GCG  GCG GCGGCG
                                ||||||||| |||  ||| ||||||
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                                GCCCGCCGC CGC  CGC CGCCGC
                                     _  CT   C
GAM2110 ABCC3    5' GCAAGGAAGGCGAGCGCGGTC 33422     AA       G
                                GCAA  AAGGCGGGCG CGGTC
                                |||| |||||||||| |||||
                                CGTT  TTCCGCTCGC GCCAG
                                  CC       _
GAM2110 ALAS1    5' GCGGCGAAGGAGGCGGGCA   8662     _ A  AA
                                GCG C AA  AGGCGGGCG
                                ||| | ||  |||||||||
                                CGC G TT  TCCGCCCGT
                                  C C  CC
GAM2110 CERD4    3' GCAGCAAGAGAGGTGGGGTGGT 28949    _   AAA   CG  C  C
            C                    GC GCAA   AGG  GG GG GGTC
                                || ||||   |||  || || ||||
                                CG CGTT   TCC  CC CC CCAG
                                 T   CTC   A_ _ A
GAM2110 DACH     5' GCGCAAGAGGGGCGAGCA    38871       AAAA
                                GCGCAA   GGCGGGCG
                                ||||||   ||||||||
                                CGCGTT   CCGCTCGT
                                   CTCC
GAM2110 GLUD1    5' GCGGAGGGGAGGTGCGTGATGG 23589     CAAAAAA  C  _  GC__
            TC                    GCG      GG GG GCG   GGTC
                                |||      || || |||   ||||
                                CGC      CC CC CGC   CCAG
                                  CTCC___  T  A   ACTA
GAM2110 GP1BB    3' GCGGAGGAGGCGGGGACCGGTC 7626     CAAAAA     C  _
                                GCG     AGGCGGG GGC GGTC
                                |||     ||||||| ||| ||||
                                CGC     TCCGCCC CTG CCAG
                                  CTCC__      _  G
GAM2110 HR       5' GCGCGGGCGGTGGCGG     32922     AAAAAA    GC
                                GCGC     GGCGG  GGCGG
                                ||||     |||||  |||||
                                CGCG     CCGCC  CCGCC
                                  C_____     A_
GAM2110 INS      3' GCAGGAGGCGGCGG       6821     AAAAA  C
                                GCA    GG GGGCGGCGG
                                |||    || |||||||||
                                CGT    CC TCCGCCGCC
                                  _____  _
GAM2110 JMJ      5' GCAAAAAAATATCCTGGTGGT  22484        GCGGGC  C
                                GCAAAAAAG     GG GGT
                                |||||||||     || |||
                                CGTTTTTTT     CC CCA
                                     ATAGGA  A
GAM2110 MAP4K2   5' GCGCGGGGCGGGGCGGGCG   21353     AAAAAA     _  _
                                GCGC     GGCGGG CGG CG
                                ||||     |||||| ||| ||
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                                CGCG     CCGCCC GCC GC
                                  CC____     C  C
GAM2110  MAPK8IP1  5'  GCGCGGAGGAGGCGGCGGC   24157     AAAAA  C
                                GCGC    AGG GGGCGGCGGT
                                ||||    ||| ||||||||||
                                CGCG    TCC TCCGCCGCCG
                                  CC___  _
GAM2110  MEN1      3'  GCGGCAGGGGAGGCGGGTGG  39186    _ AAAA     C
                                GCG CA   AGGCGGG GG
                                ||| ||   ||||||| ||
                                CGC GT   TCCGCCC CC
                                  C  CCCC     A
GAM2110  MGAT2     5'  GCACGGAAGGGGCGGGCGGGC  14448     AAAAAA      _
                                GCGC     GGCGGGCGG C
                                ||||     ||||||||| |
                                CGTG     CCGCCCGCC G
                                  CCTTCC       C
GAM2110  NRXN1     5'  GCGCAGGGGAGCGGGCGGCG   39842     AAAAA
                                GCGCA    GGCGGGCGGCG
                                |||||    ||||||||||
                                CGCGT    TCGCCCGCCGC
                                   CCCC_
GAM2110  RFNG      3'  GCGGCAGAGAGGGCGGCG    44773    _ AAAA  C
                                GCG CA   AGG GGGCGGCG
                                ||| ||   ||| ||||||||
                                CGC GT   TCT CCCGCCGC
                                  C  C___  _
GAM2110  SLC6A5    5'  GCAAAGCAAGGTGCCCTTGGT  20108     AAAA     CG _____
                                GCAA   GGCGGG  GC   GGT
                                ||||   ||||||  ||   |||
                                CGTT   TCGTTC  CG   CCA
                                  _____     CA  GGAA
GAM2110  SLIT3     5'  GCGCGGGGAGCGCGGGCGGC   16870     AAAAA  _
                                GCGC    AG GCGGGCGGC
                                ||||    || |||||||||
                                CGCG    TC CGCCCGCCG
                                  CCCC_  G
GAM2110  TAPBP     3'  GCACAAGAGGGACGCGCGGCGG 17303       AAAA   G
              TC                  GCGCAA   GGCG GCGGCGGTC
                                  ||||||   |||| |||||||||
                                  CGTGTT   CTGC CGCCGCCAG
                                     CTCC   G
GAM2110  TCN2      3'  GCACAGGAGGTGGCAGCAGGGT 7405       AAAA  CG    __
              C                   GCGCA   AGG  GGCGGC  GGTC
                                  |||||   |||  ||||||  ||||
                                  CGTGT   TCC  CCGTCG  CCAG
                                    CC__   A_     TC
GAM2110  TFDP1     5'  GCGCGGAGAGGCGCGG      28279      AAAAAA  C _   G
                                GCGC     GG G GGCG CGG
                                ||||     || | |||| |||
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                                CGCG     CC C CCGC GCC
                                  _______ T T   _
GAM2110 TJP1    5' GCGCAGAGACAGGCGGGGCC  17545      AAAA       C
                                GCGCA    AGGCGGGCGG GGTC
                                |||||    |||||||||| ||||
                                CGCGT    TCTGTCCGCC CCGG
                                  C___         _
GAM2111 ADCY8   5' GGGGCGGAGCTGGGGGCGG   10014     A    G    A
                                GGGG GGAGC GGGGG GG
                                |||| ||||| ||||| ||
                                CCCC CCTCG CCCCC CC
                                  G    A    G
GAM2111 AQP5    5' GGGGGGGCAGGGGGCGG     11636     A A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGTCCCCC CC
                                  _ _      G
GAM2111 AR      5' GGGGGGCGGGTGGGGAGAAGGG 6244     A A    __      C
                                GGG GG GCGGG  GGGAGGAG GG
                                ||| || |||||  |||||||| ||
                                CCC CC CGCCC  CCCTCTTC CC
                                  _ _    AC       _
GAM2111 ARHG    5' GGGGGAGCTGGGGGCGG     11686    A    G    A
                                GGG GGAGC GGGGG GG
                                ||| ||||| ||||| ||
                                CCC CCTCG CCCCC CC
                                  _    A    G
GAM2111 ARHGDIA 3' GGGGAGGGGCTGGGGGGG    20213       A G    A
                                GGGGAGG GC GGGGG GG
                                ||||||| || ||||| ||
                                CCCCTCC CG CCCCC CC
                                    C A    _
GAM2111 B3GAT1  5' GGAGAGGGGCGGCCACGGGCGG 38301       A   GGGGA A
                                GGGGAGG GCGG    GG GCGG
                                ||||||| ||||    || ||||
                                CCTCTCC CGCC    CC CGCC
                                    C   GGTG_ _
GAM2111 BSN     3' GGGGTGGGGTGGGGAGG     18408     A AGC _
                                GGGG GG   GG GGGGAGG
                                |||| ||   || |||||||
                                CCCC CC   CC CCCCTCC
                                  A ___ A
GAM2111 C1orf6  5' GAGGAGGAGGAGGGGCGG    33527        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CTCCTCCTC CTCCCC CC
                                      _    G
GAM2111 C1QG    3' GGGGAGGGGGTGCAGTGGGGGT 41689       A___  __    A
            GG                  GGGGAGG   GCG  GGGGG GG
                                |||||||   |||  ||||| ||
```

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                                CCCCTCC   CGT  CCCCC CC
                                    CCCA  CA    A
GAM2111  CACNA2D2  5'  GGGGAGGGGGGGGCAG      25720       AGC    G
                                GGGGAGG   GGGGG AG
                                |||||||   ||||| ||
                                CCCCTCC   CCCCC TC
                                    ___    G
GAM2111  CACNG6   5'  GGGCGGGAGCGAGGAGCG    36698    A     _
                                GG GCGGGGG GAGGAGCG
                                || ||||||| ||||||||
                                CC CGCCCTC CTCCTCGC
                                 _     G
GAM2111  CALM3    3'  GGGGTGGGGTGGGGAGG     23242     A  AGC  _
                                GGGG GG   GG GGGGAGG
                                |||| ||   || |||||||
                                CCCC CC   CC CCCCTCC
                                  A ___  A
GAM2111  CALR     3'  GGGGAGGGGGTGGGGGAGAGTG 41774       AGCG     G  C
            G                    GGGGAGG    GGGGGAG AG GG
                                |||||||    ||||||| || ||
                                CCCCTCC    CCCCCTC TC CC
                                    CCCA      _ A
GAM2111  CAPON    5'  GGGGAGCGGTGGGGCTTGCGG  41931    A     _   AGGA
                                GG GGAGCGG GGGG    GCGG
                                || ||||||| ||||    ||||
                                CC CCTCGCC CCCC    CGCC
                                 _     A   GAA_
GAM2111  CAPON    5'  GGGGAGGAGGTGGCGGCGGGAG 41933        CG  G  A_
            CGG                   GGGGAGGAG  GG GG  GGAGCGG
                                |||||||||  || ||  |||||||
                                CCCCTCCTC  CC CC  CCTCGCC
                                     CA  G  GC
GAM2111  CDC25B   5'  GGGCGAGGGGTGGGGGGGG   34856    _   AGC     A
                                GGG GAGG   GGGGGG GG
                                ||| ||||   |||||| ||
                                CCC CTCC   CCCCCC CC
                                  G   CCA    _
GAM2111  CDC25B   5'  GGGCGAGGGGTGGGGGGGG   34856    _   AGC     A
                                GGG GAGG   GGGGGG GG
                                ||| ||||   |||||| ||
                                CCC CTCC   CCCCCC CC
                                  G   CCA    _
GAM2111  COL11A2  3'  GGGGAGGACAGGGGTGG     38778       G     GA
                                GGGGAGGA CGGGGG  GG
                                |||||||| ||||||  ||
                                CCCCTCCT GTCCCC  CC
                                    _     A_
GAM2111  COL11A2  3'  GGGGAGGACAGGGGTGG     38778       G     GA
                                GGGGAGGA CGGGGG  GG
                                |||||||| ||||||  ||
```

```
                                CCCCTCCT GTCCCC  CC
                                    _     A_
GAM2111  COL1A1   3'  GGGCAGGAGCGGGCTGAGG   6377     G       GG
                                GGG AGGAGCGGG  GAGG
                                ||| |||||||||  ||||
                                CCC TCCTCGCCC  CTCC
                                  G        GA
GAM2111  CSNK1G2  3'  GGGGCAGGAGTGGGGTAGGGCG 10619     _    C   GG   A
           G                     GGGG AGGAG GGGG  AGG GCGG
                                |||| ||||| ||||  ||| ||||
                                CCCC TCCTC CCCC  TCC CGCC
                                  G    A   A_  _
GAM2111  CST1     3'  GGGTGGGAGTGGGTGGTGG   12495     GA   C  G  A
                                GGG  GGAG GGG GG GG
                                |||  |||| ||| || ||
                                CCC  CCTC CCC CC CC
                                  AC   A  A  A
GAM2111  CTRL     3'  GGAGGAGGGGTGGGGGCCCCGG 12523       C  _  A  AG_
                                GGAGGAG GGG GGG GG   CGG
                                ||||||| ||| ||| ||   |||
                                CCTCCTC CCC CCC CC   GCC
                                    _  A  _ GGG
GAM2111  DES      3'  GGGGAGGGCGTGGGGAGG    43573       A  G
                                GGGGAGG GCG GGGGAGG
                                ||||||| ||| |||||||
                                CCCCTCC CGC CCCCTCC
                                    _  A
GAM2111  DLX2     3'  GGGGAGGGCGGGCAGGCG    20595       A    G  AGGA
                                GGGGAGG GCGGG GG    GCG
                                ||||||| ||||| ||    |||
                                CCCCTCC CGCCC TC    CGC
                                    _    G  ____
GAM2111  DNMT3L   5'  GGGGAGGGGCGGGGGCGG    30068       A     GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                    C      G_
GAM2111  DNMT3L   5'  GGGGGCGGGGAGGGGCG     30072     AGGA      A  A
                                GGGG   GCGGGGGG GG GCG
                                ||||   |||||||| || |||
                                CCCC   CGCCCCTC CC CGC
                                     ____      _ _
GAM2111  ED1      5'  AGGGAGGAGGAGGGGCGG    10819        C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                TCCCTCCTC CTCCCC CC
                                    _    G
GAM2111  EGFL5    3'  GGGGGGGGCAGGGGGCGG    44531     A  A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
```

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                                CCCC CC CGTCCCCC CC
                                  _ C       G
GAM2111  EGLN1    5'  GGGGAGGGCCGAGGGGCGG   35174        A  G    AGGA
                                GGGGAGG GC GGGGG   GCGG
                                ||||||| || |||||   ||||
                                CCCCTCC CG CTCCC   CGCC
                                   _ G   _____
GAM2111  EIF4G1   3'  GGGGAGGAGAGGGACACCTGGC 22409         C   GGAGGA
           GG                    GGGGAGGAG GGGG     GCGG
                                ||||||||| ||||     ||||
                                CCCCTCCTC CCCT     CGCC
                                     T   GTGGAC
GAM2111  EMX2     5'  GGGTGGGGGGTGGGGGGAAG   44695     GA  AGC
                                GGG  GG   GGGGGGGAGG
                                |||  ||   |||||||||
                                CCC  CC   CCCCCCTTC
                                  AC  CCA
GAM2111  EPS15    5'  GGGGAGGAGGCGGAGGGAGCGG 12747          _       GGA
                                GGGGAGGAG CGGGGGGA   GCGG
                                |||||||| ||||||||   ||||
                                CCCCTCCTC GCCTCCCT   CGCC
                                     C      ___
GAM2111  F2RL3    3'  GGGGAGGGGCGTGGCTGGGGGA 19526        A  _ __  A   C
           GTGG                   GGGGAGG GCG GG  GGG GGAG GG
                                ||||||| ||| ||  ||| |||| ||
                                CCCCTCC CGC CC  CCC CCTC CC
                                   C  A  GA  _   A
GAM2111  F2RL3    3'  GGGGAGGCGGGGCTGGAGGAGC 19524       GA    __
           GG                    GGGGAG  GCGGGG  GGAGGAGCGG
                                ||||||  ||||||  ||||||||||
                                CCCCTC  CGCCCC  CCTCCTCGCC
                                   __     GA
GAM2111  FBXL11   3'  GGGGCGGGGTGGGGGGAAG   29438     A  AGC
                                GGGG GG   GGGGGGGAGG
                                |||| ||   |||||||||
                                CCCC CC   CCCCCCTTC
                                  G  CCA
GAM2111  FCN2     3'  GGGAGGAGTGTGGGGGTGG   31892        CG_    A
                                GGGAGGAG   GGGGG GG
                                ||||||||   ||||| ||
                                CCCTCCTC   CCCCC CC
                                     ACA    A
GAM2111  FHIT     3'  GGGGAGAGGCGGGGGGGCG   12875       GA      AGGA
                                GGGGAG  GCGGGGGG   GCG
                                ||||||  ||||||||   |||
                                CCCCTC  CGCCCCCC   CGC
                                   TC      _____
GAM2111  FOS      5'  GGGCGAGGGGCCGAGGGGCGG  23519    _   A  G    AGGA
                                GGG GAGG GC GGGGG   GCGG
                                ||| |||| || |||||   ||||
```

```
                                CCC CTCC CG CTCCC    CGCC
                                  G   C G    ____
GAM2111  FOXG1B   5'  GGGGGGGCGGCGGGCGG     23512      A A   G   A
                                GGGG GG GCGG GGG GG
                                |||| || |||| ||| ||
                                CCCC CC CGCC CCC CC
                                  _ _   G  G
GAM2111  FXR2     5'  GGGGAGCCGCGGGGGGCGG   22166       GA      A
                                GGGGAG  GCGGGGGG GG
                                ||||||  |||||||| ||
                                CCCCTC  CGCCCCCC CC
                                   GG       G
GAM2111  FXYD1    3'  GGGAAGGGGCGGCGGAGGGGGC 34865        A   G  GA  A
           GG                     GGGGAGG GCGG GG  GG GCGG
                                |||||||  |||| ||  || ||||
                                CCCTTCC CGCC CC  CC CGCC
                                    C   G  TC  C
GAM2111  FXYD1    3'  GGGAAGGGGCGGCGGAGGGGGC 34865        A   G  GA  A
           GG                     GGGGAGG GCGG GG  GG GCGG
                                |||||||  |||| ||  || ||||
                                CCCTTCC CGCC CC  CC CGCC
                                    C   G  TC  C
GAM2111  GAP43    3'  GGGGAGGGTGGGGATGTGG   13048        AGC    GA_
                                GGGGAGG  GGGGG  GG
                                |||||||  |||||  ||
                                CCCCTCC  CCCCT  CC
                                    CA_    ACA
GAM2111  GDF2     5'  GGGGAGGAGCTGGGAAGGAGCG 32129          GG
           G                     GGGGAGGAGC  GGGGAGGAGCGG
                                ||||||||||  ||||||||||||
                                CCCCTCCTCG  CCCTTCCTCGCC
                                     A_
GAM2111  GNA15    3'  GGGCAGGAGTACCCTGGGGGGC 40907     G    C_____     A
           GG                     GGG AGGAG     GGGGGG GG
                                ||| |||||     |||||| ||
                                CCC TCCTC     CCCCCC CC
                                  G    ATGGGA     G
GAM2111  GRB14    5'  GGGGAGGAGCGGCCGGTGG   21051          GG  A
                                GGGGAGGAGCGG  GG GG
                                ||||||||||||  || ||
                                CCCCTCCTCGCC  CC CC
                                      GG  A
GAM2111  GRB14    5'  GGGGAGAGGGGAGGAGCGG   21050       GAGCG
                                GGGGAG    GGGGGAGGAGCGG
                                ||||||    ||||||||||||
                                CCCCTC    TCCCCTCCTCGCC
                                          _____
GAM2111  GRB7     3'  GGAGAGGGGTCAGGAGG     23640      C   GG    C
                                GGAG GGGG  AGGAG G
                                |||| ||||  ||||| |
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```
                                CCTC CCCC  TCCTC C
                                  T   AG    A
GAM2111  GTF2IRD1  5'  GGAGAGGAGCGGAGAGCGG   32261            A
                                GGGGAGGAGCGGGGGG GG
                                |||||||||||||||| ||
                                CCTCTCCTCGCCTCTC CC
                                       G
GAM2111  HNRPDL   5'  GAGGAGGGGCGGGGGCTGG   24174       A     GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CTCCTCC CGCCCCC  CC
                                    C      GA
GAM2111  HOXC4    3'  GGGGAGGGTGGGGGCATGG   31155       AGC    GA_
                                GGGGAGG   GGGGG   GG
                                |||||||   |||||   ||
                                CCCCTCC   CCCCC   CC
                                    CA_    GTA
GAM2111  HYOU1    3'  GGGGTGGGGTGAGGGGTGG   40638     A  AGC     A
                                GGGG GG   GGGGGG GG
                                ||||  ||   |||||| ||
                                CCCC CC   CTCCCC CC
                                  A  CCA     A
GAM2111  IGFBP2   3'  GGAGAGGGGCGGGGGGGCAGG   8260        A      _
                                GGGGAGG GCGGGGGGG AGG
                                ||||||| |||||||| |||
                                CCTCTCC CGCCCCCCC TCC
                                    C       G
GAM2111  INSR     3'  GGGGGCGGGTGGGGGGAACG   43380      AGGA    _  A
                                GGGG   GCGGG GGG GGAGCG
                                ||||   ||||| ||| ||||||
                                CCCC   CGCCC CCC CCTTGC
                                  ____    A  C
GAM2111  ITGA6    5'  GGAGGGGAGCGGGGACCTGCAG 6832      A        GAGG_
            CGG                   GGGG GGAGCGGGGG    AGCGG
                                |||| ||||||||||    |||||
                                CCTC CCTCGCCCCT    TCGCC
                                  C        GGACG
GAM2111  JAM2     5'  GGGCGAGGAGCTGGGGGCGG   34546    _     G    A
                                GGG GAGGAGC GGGGG GG
                                ||| ||||||| ||||| ||
                                CCC CTCCTCG CCCCC CC
                                  G      A    G
GAM2111  JUNB     3'  GGGGAGGGCAGGGGGCGG    13760       A      A
                                GGGGAGG GCGGGGGG GG
                                ||||||| |||||||| ||
                                CCCCTCC CGTCCCCC CC
                                    _      G
GAM2111  KCNC3    5'  GGGGGGCGGGGCGGGAGGGGCG 22517    A  A    __    A
            G                   GGG GG GCGGGG  GGAGG GCGG
                                ||| || ||||||  ||||| ||||
```

```
                                CCC CC CGCCCC  CCTCC CGCC
                                  _ _     GC     C
GAM2111  KCNC3    3'  GGGGGGGGGGTGGGGGGGG    22520      A  AGC     A
                                GGGG GG   GGGGGG GG
                                |||| ||   |||||| ||
                                CCCC CC   CCCCCC CC
                                  C  CCA     _
GAM2111  KCNC3    5'  GGGAGGGGCGGGGACGCAGGGG 22511       A      G__   A
             CGG                   GGGAGG GCGGGGG   AGG GCGG
                                |||||| |||||||   ||| ||||
                                CCCTCC CGCCCCT   TCC CGCC
                                   C      GCG   C
GAM2111  KCNC3    3'  GGGAAGGGGCGGGGGGGACCG  22508        A       AG  G
                                GGGGAGG GCGGGGGG  GA CG
                                ||||||| ||||||||  || ||
                                CCCTTCC CGCCCCCC  CT GC
                                    C       __  G
GAM2111  KCNF1    3'  GGGGAGGGTTGGGGGGACACAG 13837        AGC      GGA
                                GGGGAGG   GGGGGGA   GCGG
                                |||||||   |||||||   ||||
                                CCCCTCC   CCCCCCT   TGTC
                                    CAA      G__
GAM2111  KCNK3    3'  GGGGATGAGGAAGGGGAG    13909      G   CG
                                GGGGA GAG  GGGGGAG
                                ||||| |||  |||||||
                                CCCCT CTC  TCCCCTC
                                   A   CT
GAM2111  KCNQ2    5'  GGGGCGGAGCGCGGGGGGCGG  41512      A     _    AGGA
                                GGGG GGAGCG GGGGG    GCGG
                                |||| |||||| |||||    ||||
                                CCCC CCTCGC CCCCC    CGCC
                                  G     G    _____
GAM2111  LASS1    3'  GGAGGGGGTGGAGGGGCG    34609      C   _    A
                                GGAG GGGG GGAGG GCG
                                |||| |||| ||||| |||
                                CCTC CCCC CCTCC CGC
                                  _   A    C
GAM2111  LBX1     3'  GGGGAGGAGGCGGGAGTGG    27288          _     GA
                                GGGGAGGAG CGGGGG  GG
                                |||||||| ||||||  ||
                                CCCCTCCTC GCCCTC  CC
                                     C     A_
GAM2111  LRP1     5'  GGCGGGGAGGGGGGGGTGG    14217    _ A   C     A
                                GG GG GGAG GGGGGG GG
                                || || |||| |||||| ||
                                CC CC CCTC CCCCCC CC
                                 G  _   _     A
GAM2111  LRP1     5'  GGAGGGGGGGGTGGGGGGCG    14216      C     A__  A
                                GGAG GGGGGG   GG GCG
                                |||| ||||||   || |||
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```
                                CCTC CCCCCC   CC CGC
                                  _     ACC  C
GAM2111  LSP1     3'  GGGGAGGGCGGGGGCGG     14239        A      GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGCCCCC  CC
                                   _      G_
GAM2111  MAP3K10  5'  GGGGAGGGGCCGGGGGCTGCGG 42758        A  G    AGGA
                                GGGGAGG GC GGGGG    GCGG
                                ||||||| || |||||    ||||
                                CCCCTCC CG CCCCC    CGCC
                                    C  G    GA__
GAM2111  MGMT     5'  GGGGGGGGCGGGGGGGG     14495      A  A       A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  _ C       _
GAM2111  MGMT     5'  GGGGCGGCGGGGGGGGCG     14493      AGGA       A GA
                                GGGG   GCGGGGGG G  GCG
                                ||||   |||||||| |  |||
                                CCCC   CGCCCCCC C  CGC
                                  GC__       _ __
GAM2111  MIC2     5'  GGGGGCGGGTGAGGGGAGCGG  14508      AGGA    _   A
                                GGGG   GCGGG GGG GGAGCGG
                                ||||   ||||| ||| |||||||
                                CCCC   CGCCC CTC CCTCGCC
                                  ____    A   C
GAM2111  MKPX     5'  GAGGAGGAGCGGCGGGGCGG   33638           _    A
                                GGGGAGGAGCGG GGGG GG
                                |||||||||||| |||| ||
                                CTCCTCCTCGCC CCCC CC
                                      G   G
GAM2111  MNT      3'  GGGGAGGGGCAGCGGGTGG    33721        A    G   A
                                GGGGAGG GCGG GGG GG
                                ||||||| |||| ||| ||
                                CCCCTCC CGTC CCC CC
                                   C   G   A
GAM2111  MSL3L1   5'  GGCGGGGGCGGGGAGGCG    38588    _ A  A       AGGA
                                GG GG GG GCGGGGGG   GCG
                                || || || ||||||||   |||
                                CC CC CC CGCCCCTC   CGC
                                 G  _ _      ____
GAM2111  MSL3L1   5'  GGGGAGGGCGGGCGGGGGCGG  38592        A    G  A  A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                   _    G  _  _
GAM2111  MSL3L1   5'  GGGGAGGGCGGGCGGGGGCGG  38600        A    G  A  A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
```

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                                CCCCTCC CGCCC CC CC CGCC
                                   _    G _ _
GAM2111 MSL3L1   5' GGCGGGGGGCGGGGAGGCG    38599    _ A A      AGGA
                                GG GG GG GCGGGGGGG    GCG
                                || || || ||||||||    |||
                                CC CC CC CGCCCCTC    CGC
                                 G _ _      _____
GAM2111 MSL3L1   5' GGCGGGGGGCGGGGAGGCG    38588    _ A A      AGGA
                                GG GG GG GCGGGGGGG    GCG
                                || || || ||||||||    |||
                                CC CC CC CGCCCCTC    CGC
                                 G _ _      _____
GAM2111 MSL3L1   5' GGGGAGGGGCGGGCGGGGGGCGG 38592       A    G A A
                                GGGGAGG GCGGG GG GG GCGG
                                ||||||| ||||| || || ||||
                                CCCCTCC CGCCC CC CC CGCC
                                   _    G _ _
GAM2111 NAGA     5' GGAGGGGCGGGGCTGCG     7040       A     GGAGGA
                                GGAGG GCGGGG     GCG
                                ||||| ||||||     |||
                                CCTCC CGCCCC     CGC
                                   C     GA____
GAM2111 NCALD    3' GGGGAAGAGAGGGGAGTGG   36769         C     A
                                GGGGAGGAG GGGGGG GG
                                ||||||||| |||||| ||
                                CCCCTTCTC CCCCTC CC
                                     T     A
GAM2111 NCOA6IP  5' GGGAAGGGGCGGGACCACGGGC 36052       A     GGA_ A
           GG                    GGGGAGG GCGGGG    GG GCGG
                                ||||||| ||||||    || ||||
                                CCCTTCC CGCCCT    CC CGCC
                                   C     GGTG _
GAM2111 NEUROD2  5' GGGGAGGGGAGGGGGGGAGG  26064      __    C
                                GGGGA  GGAG GGGGGGAGG
                                |||||  |||| |||||||||
                                CCCCT  CCTC CCCCCCTCC
                                   CC   _
GAM2111 NFIA     5' GGGGGGAGGGGGTGTGG     43219      A   C   GGA
                                GGGG GGAG GGGG   GG
                                |||| |||| ||||   ||
                                CCCC CCTC CCCC   CC
                                  _   _    ACA
GAM2111 NGFR     3' GGGAAGGGGTGGGGGTCTGG  14784       AGC    GA_
                                GGGGAGG   GGGGG   GG
                                |||||||   |||||   ||
                                CCCTTCC   CCCCC   CC
                                    CCA    AGA
GAM2111 NPR1     5' GGGAAGGAGCAGGAGC      44585          GGGGGG
                                GGGGAGGAGC     AGGAGC
                                ||||||||||     ||||||
```

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                                CCCTTCCTCG     TCCTCG
                                       ______
GAM2111  NRXN1    5'  GGGGAGCGGGCGGCGCGGAGTG 39847    A      G  A__   C
             G                   GG GGAGCGGG GG   GGAG GG
                                 || |||||||| ||   |||| ||
                                 CC CCTCGCCC CC   CCTC CC
                                  _      G  GCG    A
GAM2111  NTSR1    3'  GGGGAGGGGTGGGGAGGAG   14890       AGC  _
                                 GGGGAGG   GG GGGGAGGAG
                                 |||||||   || |||||||||
                                 CCCCTCC   CC CCCCTCCTC
                                     ___  A
GAM2111  PACSIN1  3'  GGGGAGGGGCGGCAGTGG    45163       A   G  GA
                                 GGGGAGG GCGG GG  GG
                                 ||||||| |||| ||  ||
                                 CCCCTCC CGCC TC  CC
                                     C   G  A_
GAM2111  PAFAH1B1 5'  GGGGGAGGGGAGGGGAGCG   7717     A   C     A
                                 GGG GGAG GGGGGG GGAGCG
                                 ||| |||| |||||| ||||||
                                 CCC CCTC CCCTCC CCTCGC
                                   _   _    _
GAM2111  PAX2     3'  GGGAGGGGATGGGAGGAGTGG  19633       AGC  _      C
                                 GGGAGG   GGG GGGAGGAG GG
                                 ||||||   ||| |||||||| ||
                                 CCCTCC   CCT CCCTCCTC CC
                                     ___  A       A
GAM2111  PAX2     3'  GGGGAGGGGCGGCAGGCGG   19636       A   G   A
                                 GGGGAGG GCGG GGG GG
                                 ||||||| |||| ||| ||
                                 CCCCTCC CGCC TCC CC
                                     C   G   G
GAM2111  PAX2     3'  GGGGAGGGGCGGCAGGCGG   19636       A   G   A
                                 GGGGAGG GCGG GGG GG
                                 ||||||| |||| ||| ||
                                 CCCCTCC CGCC TCC CC
                                     C   G   G
GAM2111  PAX2     3'  GGGAGGGGATGGGAGGAGTGG  19633       AGC  _      C
                                 GGGAGG   GGG GGGAGGAG GG
                                 ||||||   ||| |||||||| ||
                                 CCCTCC   CCT CCCTCCTC CC
                                     ___  A       A
GAM2111  PCTK3    3'  GGGGAGGAGTGGAGGGTGG   43784        C     A
                                 GGGGAGGAG GGGGGG GG
                                 ||||||||| |||||| ||
                                 CCCCTCCTC CCTCCC CC
                                      A     A
GAM2111  PDE4A    3'  AGGGGAGTGAGGGGAGGAGTGG 26247    A   C        C
                                 GGG GGAG GGGGGGAGGAG GG
                                 ||| |||| |||||||||| ||
```

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                                TCC CCTC CTCCCCTCCTC CC
                                  _   A         A
GAM2111  PDE4A    3'  GGGGGGCGGGGGGGGTGAGTGG  26275    A  A      AG   C
                                GGG GG GCGGGGGGG  GAG GG
                                ||| || ||||||||  ||| ||
                                CCC CC CGCCCCCC  CTC CC
                                  _ _      CA   A
GAM2111  PDE4A    3'  GGGGAGGAGTGGAGGGGAACAG 26267          CG     A
                                GGGGAGGAG  GGGGG GGAGCGG
                                |||||||||  ||||| |||||||
                                CCCCTCCTC  CCTCC CCTTGTC
                                     A_    _
GAM2111  PLOD3    5'  GGGAGGCGGGGGAGGGGCGG   9895        AGCG       A
                                GGGAGG    GGGGGAGG GCGG
                                ||||||    |||||||| ||||
                                CCCTCC    CCCCCTCC CGCC
                                   G___       C
GAM2111  PLOD3    5'  GGGGAGGGGCGGCGGCTCGG   9897         A    G  GA_
                                GGGGAGG GCGG GG   GG
                                ||||||| |||| ||   ||
                                CCCCTCC CGCC CC   CC
                                    C    G  GAG
GAM2111  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 37732    G     C  __ _     C
           AGTGG                  GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA  G     A
GAM2111  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 37732    G     C  __ _     C
           AGTGG                  GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA  G     A
GAM2111  PML      3'  GGCGAGGAGTGGGCTGGCGAGG 37756    G     C  __ _     C
           AGTGG                  GG GAGGAG GGG  GG GAGGAG GG
                                || |||||| |||  || |||||| ||
                                CC CTCCTC CCC  CC CTCCTC CC
                                 G     A  GA  G     A
GAM2111  PPP2R1A  3'  GGGGAGGACGGGAGGTGG    30600         G      A
                                GGGGAGGA CGGGGGG GG
                                |||||||| ||||||| ||
                                CCCCTCCT GCCCTCC CC
                                    _      A
GAM2111  PRDM16   3'  GGGGAGGATGCTGAGGAGTGG  35246          _ _     A
                                GGGGAGGA GC GGGGGG GG
                                |||||||| || |||||| ||
                                CCCCTCCT CG CTCCTC CC
                                    A  A     A
GAM2111  PRDM2    3'  GGGGAGAGAGGGGTGG      31973         AGC      A
                                GGGGAGG   GGGGGG GG
                                |||||||   |||||| ||
```

```
                                CCCCTCT  CTCCCC CC
                                   ___     A
GAM2111  PRKCA    3'  GGGGAGGGCTGGGGGCTGG   15626       A _    GA
                                GGGGAGG GC GGGGG  GG
                                ||||||| || |||||  ||
                                CCCCTCC CG CCCCC  CC
                                   _ A    GA
GAM2111  PROC     3'  GGGGGGGGGCGGGGGGGG    7194      A A      A
                                GGGG GG GCGGGGGG GG
                                |||| || |||||||| ||
                                CCCC CC CGCCCCCC CC
                                  C  C      _
GAM2111  PRODH    3'  GGCGGGGGCGGGGGGTGCTGG  32279    _ A A      AGGA _
                                GG GG GG GCGGGGGG   GC GG
                                || || || ||||||||   || ||
                                CC CC CC CGCCCCCC   CG CC
                                 G _ _      A___  A
GAM2111  PRX      3'  GGGGAGGAGCGGCGGCGG    34131          G  GA
                                GGGGAGGAGCGG GG  GG
                                |||||||||||| ||  ||
                                CCCCTCCTCGCC CC  CC
                                      G  G_
GAM2111  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   39036    A   C     A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _     _
GAM2111  PTPRF    3'  GGCGGAGGAGAGGGGAGCG   39036    A   C     A
                                GG GGAG GGGGGG GGAGCG
                                || |||| |||||| ||||||
                                CC CCTC CTCTCC CCTCGC
                                 G   _     _
GAM2111  PTPRG    5'  GGGGAGAGGCAGGGGGAGCGG  15940       GA       GGA
                                GGGGAG  GCGGGGGGA   GCGG
                                ||||||  |||||||||   ||||
                                CCCCTC  CGTCCCCCT   CGCC
                                   TC        ___
GAM2111  PXN      3'  GGGGAGGATGGAGAGTGG    16030        GC     A
                                GGGGAGGA  GGGGGG GG
                                ||||||||  |||||| ||
                                CCCCTCCT  CCTCTC CC
                                    A_     A
GAM2111  RAB13    5'  GGGGAGGGGTGGGGAGCGC   16117        AGC _    GA
                                GGGGAGG   GG GGGGAG  GC
                                |||||||   || ||||||  ||
                                CCCCTCC   CC CCCCTC  CG
                                   ___ A     G_
GAM2111  RAB13    5'  GGGGGAGCCGGGGGAGG     16118     A    G
                                GGG GGAGC GGGGGAGG
                                ||| ||||| ||||||||
```

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                                CCC CCTCG CCCCCTCC
                                  _    G
GAM2111  RAB3A    3'  GGGGGGGGGGGGGGGTCCCAG  16074     A  AGC     A  AG_
                                GGGG GG   GGGGGG GG   CGG
                                |||| ||   |||||| ||   |||
                                CCCC CC   CCCCCC CC   GTC
                                  _ ___     _ AGG
GAM2111  RANBP3   3'  GGGAGGGGGGTTTGGGGGGCGG 28762       AGC  ___  A  A
                                GGGAGG   GGG   GGG GG GCGG
                                ||||||   |||   ||| || ||||
                                CCCTCC   CCC   CCC CC CGCC
                                   C__   AAA  _ _
GAM2111  REST     5'  GGGGAGAGGTGGGGGAGG    24710       G  CG
                                GGGGAG AG  GGGGGAGG
                                ||||||| ||  ||||||||
                                CCCCTC TC  CCCCCTCC
                                   _ CA
GAM2111  RHCG     3'  GGGGAGGGCAGGGGTGG     32243       A      GA
                                GGGGAGG GCGGGGG  GG
                                ||||||| |||||||  ||
                                CCCCTCC CGTCCCC  CC
                                   _      A_
GAM2111  RNH      5'  GGGGAGGGGTGGGTGGGGTGG  16361       AGC_ _   A
                                GGGGAGG    GG GGGG GG
                                |||||||    || |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM2111  RNH      5'  GGGGAGGGGTGGGTGGGGTGG  40608       AGC_ _   A
                                GGGGAGG    GG GGGG GG
                                |||||||    || |||| ||
                                CCCCTCC    CC CCCC CC
                                    CCAC  A    A
GAM2111  RPA1     3'  GGGGATGGGGGGGGGGTGG    16371      _ AGC     A
                                GGGGA GG   GGGGGG GG
                                ||||| ||   |||||| ||
                                CCCCT CC   CCCCCC CC
                                   A  CC_     A
GAM2111  SALL1    3'  GGGGCGGGGTGGGGGGCAAGG  16460     A  AGC     __
                                GGGG GG   GGGGGG  AGG
                                |||| ||   ||||||  |||
                                CCCC CC   CCCCCC  TCC
                                  G  CCA     GT
GAM2111  SCRT1    3'  GGGGAGGGGAGGGGGCTCGG   36370       AGC     A  AG
                                GGGGAGG   GGGGGG GG  CGG
                                |||||||   |||||| ||  |||
                                CCCCTCC   CCTCCC CC  GCC
                                    ___     _ GA
GAM2111  SF1      5'  GGGGCGGGCCGGGGGCGG    21568      A  A  G    A
                                GGGG GG GC GGGGG GG
                                |||| || || ||||| ||
```

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                                CCCC CC CG CCCCC CC
                                  G _ G    G
GAM2111  SIAT8E   5'  GGGGAGGGGGAGGGGCG    40837      GGAGCG      A
                                GGGGA     GGGGGGAGG GCG
                                |||||     |||||||| |||
                                CCCCT     CCCCCTCC CGC
                                  _______       C
GAM2111  SLC9A1   3'  GGGGAGGAGCTGTGCTGGGGTG 43238          GG____    A
            G                    GGGGAGGAGC     GGGG GG
                                ||||||||||     |||| ||
                                CCCCTCCTCG     CCCC CC
                                      ACACGA    A
GAM2111  SLC9A3R2  5'  GGGGGAGCTCGGGGGCGG    41532     A    G_    A
                                GGG GGAGC  GGGGG GG
                                ||| |||||  ||||| ||
                                CCC CCTCG  CCCCC CC
                                  _    AG    G
GAM2111  SMG1     3'  GGGGAGGAGTAGGGAACGATGG 31511         CG     G  GC
                                GGGGAGGAG  GGGGGA GA  GG
                                |||||||||  ||||||  ||  ||
                                CCCCTCCTC  TCCCTT CT  CC
                                     A_     G  A_
GAM2111  SOX11    3'  GGGGGGCCGGGGGGAGG      17029     A  A  G
                                GGG GG GC GGGGGGAGG
                                ||| || || ||||||||
                                CCC CC CG CCCCCTCC
                                  _ _  G
GAM2111  SOX12    3'  GGGGTGGGCCCCAGCGGAGGGG 28051      A  A  G__  G    A
            CGG                    GGGG GG GC   GG GGAGG GCGG
                                |||| || ||   || ||||| ||||
                                CCCC CC CG   TC CCTCC CGCC
                                  A  _  GGG  G    C
GAM2111  SOX12    3'  GGGGAGGCCGGAGGGGCG    28049        AG      AGGA
                                GGGGAGG  CGGGGGG    GCG
                                |||||||  |||||||    |||
                                CCCCTCC  GCCTCCC    CGC
                                    G_      _____
GAM2111  SOX12    3'  GGGAAGGGGTGGGGGTTGG    28048        AGC     GA
                                GGGGAGG   GGGGG  GG
                                |||||||   |||||  ||
                                CCCTTCC   CCCCC  CC
                                    CCA     AA
GAM2111  SPI1     3'  GGGGAGGGGCGGGTGACGG    17080        A     G GA
                                GGGGAGG GCGGG G  GG
                                ||||||| ||||| |  ||
                                CCCCTCC CGCCC C  CC
                                    C     A TG
GAM2111  SPI1     3'  GGAGTGGGGGGGAGGGGCGG    17077      C        A
                                GGAG GGGGGGAGG GCGG
                                |||| |||||||| ||||
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                                CCTC CCCCCCTCC CGCC
                                  A       C
GAM2111 SPTB    3' GGGGAGGATGGAGGGCGG   7384        GC    A
                                GGGGAGGA GGGGGG GG
                                |||||||| |||||| ||
                                CCCCTCCT CCTCCC CC
                                    A_    G
GAM2111 SRD5A1  5' GAGGAGGGGCGGCTACCGGAGG 9827       A   GG___   A
          GGCGG                  GGGGAGG GCGG   GGAGG GCGG
                                ||||||| ||||   ||||| ||||
                                CTCCTCC CGCC   CCTCC CGCC
                                    C   GATGG   C
GAM2111 SYNGR1  3' GGGGACAGATGGGGAGGGGCGG 21765     _  GC    A A
                                GGGGA GGA GGGGGG GG GCGG
                                ||||| ||| |||||| || ||||
                                CCCCT TCT CCCCTC CC CGCC
                                  G  A_    _ _
GAM2111 TCF3    3' GGGGGGGACGGGGGGGCTCAGG 43325     A AG     ____
                                GGGG GG CGGGGGG   AGG
                                |||| || ||||||   |||
                                CCCC CC GCCCCCC   TCC
                                  _ CT     CGAG
GAM2111 TFAP2A  3' GGTGAGGCGTGGGAGGGGCGG 17399   GA A  GG    A
                                GG GG GCG GGGAGG GCGG
                                || || ||| |||||| ||||
                                CC TC CGC CCCTCC CGCC
                                 AC _  A_    C
GAM2111 TNFRSF11A 3' GGGGGGAGTCGGGGGGAGG   19276    A  _
                                GGGG GGAG CGGGGGGAGG
                                |||| |||| ||||||||||
                                CCCC CCTC GCCCCCCTCC
                                  _   A
GAM2111 TNFSF5  3' GGGGGGGGGGGGGGGTTTCGG 6331     A AGC    A AG_
                                GGGG GG  GGGGGG GG  CGG
                                |||| ||  |||||| ||  |||
                                CCCC CC  CCCCCC CC  GCC
                                  _ C__    _ AAA
GAM2111 TNFSF5  3' GGGGGGGGGGGGGGG     6329     A AGC    A
                                GGGG GG  GGGGGG GG
                                |||| ||  |||||| ||
                                CCCC CC  CCCCCC CC
                                  _ C__    _
GAM2111 TSLP    5' GGGGAGGAAGGTCAGGGAGGAG 39700       C __
          CGG                  GGGGAGGAG GG  GGGGAGGAGCGG
                                ||||||||| ||  ||||||||||||
                                CCCCTCCTT CC  TCCCTCCTCGCC
                                    _ AG
GAM2111 TULP1   3' GGGGAGGAGGGGGGCACAGCGG 17731       GC    AGG
                                GGGGAGGA GGGGGG  AGCGG
                                |||||||| ||||||  |||||
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                                CCCCTCCT  CCCCCC   TCGCC
                                    __      GTG
GAM2111  UGCG     5'  GGGGGGTGGGGACGGAAGGGGC 17877      A  AGC  __     A
              GG                  GGGG GG   GGG  GGGAGG GCGG
                                ||||  ||   |||  |||||| ||||
                                CCCC CC   CCC  CCTTCC CGCC
                                  _  AC_   TG     C
GAM2111  VAT1     3'  GGGGAGGGGCAGGGGAGAGCGG 26851        A      GA
                                GGGGAGG GCGGGGG  GGAGCGG
                                |||||||  |||||||  |||||||
                                CCCCTCC CGTCCCC  TCTCGCC
                                    C      __
GAM2111  WSX1     5'  AGGGGGAGTGGGGAGGCG    22114      A   C     AGGA
                                GGGG GGAG GGGGGG    GCG
                                ||||  ||||  ||||||    |||
                                TCCC CCTC CCCCTC    CGC
                                  _    A     _____
GAM2111  YWHAE    3'  GGGGAGGAGTGAGGGGAAG    27598         C
                                GGGGAGGAG GGGGGGAGG
                                |||||||||  |||||||||
                                CCCCTCCTC CTCCCCTTC
                                     A
GAM2111  ABR      5'  GCGGGCGGGAGCCGGGGGAGG  35011       G  AG    G
                                GCGGG GG  GAGC GGGGGAGG
                                |||||  ||  ||||  ||||||||
                                CGCCC CC  CTCG CCCCCTCC
                                   G  __    G
GAM2111  AGL      5'  CGGGGGGAGGGGACGGGG    8488           A_
                                CGGGGGGAGG  GCGGGG
                                ||||||||||  ||||||
                                GCCCCCCTCC  TGCCCC
                                      CC
GAM2111  ANP32A   3'  AGGGGGGGGGGAGAGGGG    26706    C     A    C
                                AG GGGGGG GGAG GGGG
                                ||  ||||||  ||||  ||||
                                TC CCCCCC CCTC CCCC
                                  _     C    T
GAM2111  AP2M1    3'  GGGGGAGGGAGCGGCACCTGG  19822       GA      GG___
                                GGGGG  GGAGCGG    GG
                                |||||  |||||||    ||
                                CCCCC  CCTCGCC    CC
                                   TC      GTGGA
GAM2111  AR       5'  GCGGGGGGGCGGGTGGG     6233          AGGA    _
                                GCGGGGGG   GCGGG GGG
                                ||||||||   |||||  |||
                                CGCCCCCC   CGCCC CCC
                                     _____     A
GAM2111  ARIH1    5'  GCGGCGGGGAGGGCGCGGAGG  25091      _      A_
                                GCGG GGGGAGG  GCGGGGG
                                ||||  |||||||  |||||||
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                                CGCC CCCCTCC  CGCCTCC
                                  G      CG
GAM2111  ARSD     3'  GCGGTGGGGCCTGGGGGGAGG  28928      _   AGGAGC
                                GCGG GGGG     GGGGGGAGG
                                |||| ||||     |||||||||
                                CGCC CCCC     CCCCCCTCC
                                  A   GGA___
GAM2111  ARVCF    3'  AGTGGGGTGGGGGGGGCAGGAGG 11699    C   _ A A
                                AG GGGG GG GG GCGGGGGG
                                || |||| || || ||||||||
                                TC CCCC CC CC CGTCCTCC
                                 A   A C  C
GAM2111  ASNS     5'  GCGGGGTGAGAGGGGAG     11716       G   GAGCG
                                GCGGGG GAG    GGGGGAG
                                |||||| |||    |||||||
                                CGCCCC CTC    TCCCCTC
                                   A  _____
GAM2111  ATRX     3'  AGTGGGGGAGAGGGGCGTGG   7934     C    _   A   G
                                AG GGGGG GAGG GCG GG
                                || ||||| |||| ||| ||
                                TC CCCCC CTCC CGC CC
                                 A    T   C   A
GAM2111  ATRX     3'  AGTGGGGGAGAGGGGCGTGG   39603    C    _   A   G
                                AG GGGGG GAGG GCG GG
                                || ||||| |||| ||| ||
                                TC CCCCC CTCC CGC CC
                                 A    T   C   A
GAM2111  AXIN1    3'  GCCGGGGGATGGGGGGGGG   41379    G    _ AGC
                                GC GGGGGA GG   GGGGGG
                                || |||||| ||   ||||||
                                CG CCCCCT CC   CCCCCC
                                 G     A  C__
GAM2111  AXL      5'  AGCGGGGGAGGGGGA       11789         AGGAGC    G
                                AGCGGGGGGG     GGGGG A
                                |||||||||      ||||| |
                                TCGCCCCCT      CCCCC T
                                    _______    G
GAM2111  AXL      5'  AGCGGGGGAGGGGGA       34879         AGGAGC    G
                                AGCGGGGGGG     GGGGG A
                                |||||||||      ||||| |
                                TCGCCCCCT      CCCCC T
                                    _______    G
GAM2111  B3GAT1   3'  GCGGGGAGCTCTGGGGAGG   33004        AGGAGCGG
                                GCGGGGGG       GGGGAGG
                                ||||||||       |||||||
                                CGCCCCTC       CCCCTCC
                                    GAGA____
GAM2111  B3GAT1   3'  GCGGGGAGCTCTGGGGAGG   33004        AGGAGCGG
                                GCGGGGGG       GGGGAGG
                                ||||||||       |||||||
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                                CGCCCCTC      CCCCTCC
                                    GAGA____
GAM2111 B4GALT1  3' GAAAGAAGGGGGTGGGGGGAGG 11282   GG    AGC_
                                G GGGAGG   GGGGGGAGG
                                | ||||||   |||||||||
                                C TCTTCC   CCCCCCTCC
                                 TT    CCCA
GAM2111 BACE2    5' GCGGCGGGGAGGACGGGAGG  39991    _     G
                                GCGG GGGGAGGA CGGGGGG
                                |||| |||||||| |||||||
                                CGCC CCCCTCCT GCCCTCC
                                  G      _
GAM2111 BACE2    5' GCGGCGGGGAGGACGGGAGG  39991    _     G
                                GCGG GGGGAGGA CGGGGGG
                                |||| |||||||| |||||||
                                CGCC CCCCTCCT GCCCTCC
                                  G      _
GAM2111 BACE2    5' GCGGCGGGGAGGACGGGAGG  39991    _     G
                                GCGG GGGGAGGA CGGGGGG
                                |||| |||||||| |||||||
                                CGCC CCCCTCCT GCCCTCC
                                  G      _
GAM2111 BACH2    5' GCGAGGGGAGGCCGGGGGG   34792        AG
                                GCGGGGGGAGG  CGGGGGG
                                ||||||||||  |||||||
                                CGCTCCCCTCC  GCCCCCC
                                      G_
GAM2111 BAZ1B    5' GGGGTGGGGGAAGGGAGG    37093    _ A   C
                                GGGG GG GGAG GGGGGG
                                |||| || |||| ||||||
                                CCCC CC CCTT CCCTCC
                                  A  C   _
GAM2111 BCL11B   5' GGGGGGAGCCGGGGGAGG    39753    A    G
                                GGGG GGAGC GGGGGAGG
                                |||| ||||| ||||||||
                                CCCC CCTCG CCCCCTCC
                                  _    G
GAM2111 BCL11B   5' GGGGGGAGCCGGGGGAGG    39753    A    G
                                GGGG GGAGC GGGGGAGG
                                |||| ||||| ||||||||
                                CCCC CCTCG CCCCCTCC
                                  _    G
GAM2111 BRAF     5' GCGGGGAGGGGGCCGGGAGG  20262      A  AG
                                GCGGGGGG GG  CGGGGGG
                                |||||||| ||  |||||||
                                CGCCCCTC CC  GCCCTCC
                                     C  CG
GAM2111 BRF1     3' AGCGGGGAGGGGGGTCTGGAGG 11325      A  AGC   G__
                                AGCGGGGGG GG   GGG   GGAGG
                                ||||||||| ||   |||   |||||
```

```
                                TCGCCCCTC CC   CCC   CCTCC
                                    _ ___  AGA
GAM2111  CALM3    3'  GGTGGGGAGGTGGTGGGGGG  23244    _     AGC_
                                GG GGGGAGG   GGGGGG
                                || |||||||   ||||||
                                CC CCCCTCC   CCCCCC
                                 A      ACCA
GAM2111  CALM3    3'  GGGGGGTGGGGTGGGGAGG   23236      A  AGC  _
                                GGGGGG GG   GG GGGGAGG
                                |||||| ||   || |||||||
                                CCCCCC CC   CC CCCCTCC
                                   A ___ A
GAM2111  CALR     3'  GCGGGGAGGGGGTGGGGG    41770       A  AGCG
                                GCGGGGGG GG   GGGGG
                                |||||||| ||   |||||
                                CGCCCCTC CC   CCCCC
                                    _ CCA_
GAM2111  CD34     3'  AGTGGGGGCAGGGGTGGG    12111    C    G   AGC  _
                                AG GGGGG AGG   GG GGG
                                || ||||| |||   || |||
                                TC CCCCC TCC   CC CCC
                                 A    G   ___ A
GAM2111  CDC25B   5'  GGGGGGGGGGGGGAAGGAGG   34857      A  AGC
                                GGGGGG GG   GGGGGGAGG
                                |||||| ||   |||||||||
                                CCCCCC CC   CCTTCCTCC
                                   _ CC_
GAM2111  CDC25B   5'  GGGGGGGGGGGGGAAGGAGG   34857      A  AGC
                                GGGGGG GG   GGGGGGAGG
                                |||||| ||   |||||||||
                                CCCCCC CC   CCTTCCTCC
                                   _ CC_
GAM2111  CDC25B   5'  GCAGCGGGCGAGGGGTGGGGGG 34850     _  _   AGC    A
            GG                   GCGG GGG GAGG   GGGGGG GG
                                |||| ||| ||||   |||||| ||
                                CGTC CCC CTCC   CCCCCC CC
                                  G  G   CCA    _
GAM2111  CDC25B   5'  GCAGCGGGCGAGGGGTGGGGGG 34850     _  _   AGC    A
            GG                   GCGG GGG GAGG   GGGGGG GG
                                |||| ||| ||||   |||||| ||
                                CGTC CCC CTCC   CCCCCC CC
                                  G  G   CCA    _
GAM2111  CKM      3'  GCGGGGCGAGGAGTGAGG    12260      G    C
                                GCGGGG GAGGAG GGGG
                                |||||| |||||| ||||
                                CGCCCC CTCCTC CTCC
                                   G    A
GAM2111  COL1A1   3'  AGTGGAGGGGAGGCCAAGGGGG 6364    C  _     AGC_
            G                    AG GG GGGGAGG   GGGGGG
                                || || |||||||   ||||||
```

```
                                TC CC CCCCTCC    CCCCCC
                                 A  T      GGTT
GAM2111  CSK      5'  GCGGGGGAAGGGGGCGGGAGG  20464          A_
                                GCGGGGGGAGG  GCGGGGGG
                                ||||||||||  ||||||||
                                CGCCCCCTTCC  CGCCCTCC
                                      CC
GAM2111  CSK      5'  GCGGGAGGGAGTCGGGGGGAGG 20462         AG  _
                                GCGGGGGG  GAG CGGGGGGAGG
                                ||||||||  ||| ||||||||||
                                CGCCCTCC  CTC GCCCCCCTCC
                                     __  A
GAM2111  DACH     5'  GGGGGTGGGGCGGGGAG     38873       GA  A
                                GGGGG  GG GCGGGGGG
                                |||||  || ||||||||
                                CCCCC  CC CGCCCCTC
                                   AC  _
GAM2111  DLG4     3'  GGGAGGGAGGCCGGGGGG    10707     _     AG
                                GGG GGGAGG  CGGGGGG
                                |||  ||||||  |||||||
                                CCC CCCTCC  GCCCCCC
                                  T     G_
GAM2111  DRPLA    3'  GGGGGGAGGGTGGGGG      12591          AGCG
                                GGGGGGAGG   GGGGG
                                |||||||||   |||||
                                CCCCCCTCC   CCCCC
                                      CA__
GAM2111  EGFL3    5'  GCGGGCGGGAGGGGGCGAGG  41707       _     AGCG  G
                                GCGGG GGGAGG   GGG GAGG
                                |||||  ||||||   |||  ||||
                                CGCCC CCCTCC   CCC CTCC
                                   G     _____  G
GAM2111  EGLN1    5'  GCGGAGGGAGGGCCGGGAGG  35169          AG
                                GCGGGGGGAGG  CGGGGGG
                                ||||||||||  |||||||
                                CGCCTCCCTCC  GCCCTCC
                                      CG
GAM2111  ELAVL3   3'  GGGGGCAGGAGGATGGGG    10886       G    C  _
                                GGGGG AGGAG GG GGGG
                                |||||  |||||  ||  ||||
                                CCCCC  TCCTC CT CCCC
                                   G    _  A
GAM2111  ENG      3'  AGCGGGGGCAGGGGCGGAGG  6490          G  A
                                AGCGGGGG AGG GCGGGGG
                                ||||||||  |||  |||||||
                                TCGCCCCC TCC CGCCTCC
                                     G  C
GAM2111  EPHA8    3'  GGGGTGGGGTGGGGAG      33898       A  AGC  _
                                GGGG GG   GG GGGGAG
                                ||||  ||   ||  ||||||
```

```
                                CCCC CC   CC CCCCTC
                                  A ___ A
GAM2111  FAAH    5'  GCGGGGGGCGGAGCGGGGG   11057       A
                                GCGGGGGG GGAGCGGGGG
                                |||||||| ||||||||||
                                CGCCCCCC CCTCGCCCCC
                                    G
GAM2111  FBXL11  3'  GCGGGGTGGGGGGAAGAG    29431      GGA  AGC
                                GCGGGG  GG  GGGGGGAG
                                ||||||  ||  ||||||||
                                CGCCCC  CC  CCCTTCTC
                                  AC_ ___
GAM2111  FBXL11  3'  GCGGGGCGGGGTGGGGGG    29430      _  A  AGC
                                GCGGGG GG GG  GGGGGG
                                |||||| || ||  ||||||
                                CGCCCC CC CC  CCCCCC
                                  G _ A__
GAM2111  FE65L2  3'  AGCAGGGGGAGGGGCAGGGG  39315         A
                                AGCGGGGGGAGG GCGGGGG
                                |||||||||||| |||||||
                                TCGTCCCCCTCC CGTCCCC
                                      C
GAM2111  FE65L2  3'  AGCAGGGGGAGGGGCAGGGG  39315         A
                                AGCGGGGGGAGG GCGGGGG
                                |||||||||||| |||||||
                                TCGTCCCCCTCC CGTCCCC
                                      C
GAM2111  FGFR1   5'  GGAGGCGGGGCGGGGGGAG   31946      A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
                                CCTCC CC CGCCCCCCTC
                                  G  C
GAM2111  FGFR1   5'  GGAGGCGGGGCGGGGGGAG   31946      A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
                                CCTCC CC CGCCCCCCTC
                                  G  C
GAM2111  FGFR1   5'  GGAGGCGGGGCGGGGGGAG   31946      A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
                                CCTCC CC CGCCCCCCTC
                                  G  C
GAM2111  FGFR1   5'  GGAGGCGGGGCGGGGGGAG   31946      A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
                                CCTCC CC CGCCCCCCTC
                                  G  C
GAM2111  FGFR1   5'  GGAGGCGGGGCGGGGGGAG   31946      A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
```

```
                                CCTCC CC CGCCCCCCTC
                                   G  C
GAM2111  FGFR1    5'  GGAGGCGGGGCGGGGGGAG   31946      A  A
                                GGGGG GG GCGGGGGGAG
                                ||||| || ||||||||||
                                CCTCC CC CGCCCCCCTC
                                   G  C
GAM2111  FKBP2    5'  AGCGGGGGGAGGGGGTCAGGGG 38388          AGCG_
            AGG                    AGCGGGGGGAGG    GGGGGAGG
                                ||||||||||||    ||||||||
                                TCGCCCCCCTCC    TCCCCTCC
                                      CCCAG
GAM2111  FOXD2    5'  GCGGGGAGGGGGGCGGGGG    20969        A  A
                                GCGGGGGGG GG GCGGGGGG
                                |||||||| || |||||||
                                CGCCCCTC CC CGCCCCC
                                    _  C
GAM2111  FZD7     3'  GCGGGAGGGGGGCAGGGGAGG   18633        A  A     G
                                GCGGGGGGG GG GCGGGGG AGG
                                |||||||| || ||||||| |||
                                CGCCCTCC CC CGTCCCC TCC
                                    _ _     _
GAM2111  GABRB3   5'  GCGGAGGGGGGAGGGGAGG    34874        A   C
                                GCGGGGGGG GGAG GGGGGG
                                |||||||| |||| ||||||
                                CGCCTCCC CCTC CCCTCC
                                    _   _
GAM2111  GPC1     3'  AGTGGGAGGAGGCGGGGAG   13235    C      GA
                                AG GGGGGGAG  GCGGGGGG
                                || ||||||||  ||||||||
                                TC CCCTCCTC  CGCCCCTC
                                 A      __
GAM2111  GRB14    5'  GCGGGGGAGGGGAGGGGG    21043       GA  AGC
                                GCGGGGG  GG   GGGGGG
                                |||||||  ||   ||||||
                                CGCCCCC  CC   TCCCCC
                                    TC  C__
GAM2111  GRB14    5'  GCGGCGGGGGAGGGGAGG    21042     G   A   C
                                GCGG GGG GGAG GGGGGG
                                |||| ||| |||| ||||||
                                CGCC CCC CCTC CCCTCC
                                  G  _   _
GAM2111  GTF2IRD1 5'  GCGGGGAGGGGGCGCGGGGGGG 32260        A  A_      A
            G                   GCGGGGGG GG  GCGGGGGG GG
                                |||||||| ||  |||||||| ||
                                CGCCCCTC CC  CGCCCCCC CC
                                    C  CG       _
GAM2111  HIP12    3'  GGTGGGGGGGAGCAGGAGG    42405    _   A
                                GG GGGG GGAGCGGGGGG
                                || |||| ||||||||||
```

```
                                CC CCCC CCTCGTCCTCC
                                 A   _
GAM2111  HIP2     3'  GGGGGGGGTGAAGGGGG     23769        A  AGC
                                GGGGGG GG   GGGGGG
                                |||||| ||   ||||||
                                CCCCCC CC   TCCCCC
                                   _  ACT
GAM2111  HLX1     5'  GCGGGCGGGGGAGCCAGG    34989       _  A    G
                                GCGGG GGG GGAGC GGG
                                ||||| ||| ||||| |||
                                CGCCC CCC CCTCG TCC
                                   G   _    G
GAM2111  HOXB2    5'  GGGGGAGGGGGCTGCTGGGGGG 13436         A_ _____     A
              GG                  GGGGGAGG  GC    GGGGGG GG
                                |||||||  ||    |||||| ||
                                CCCCCTCC  CG    CCCCCC CC
                                     CC  ACGA     _
GAM2111  HOXC6    3'  GCGGGGGTGGGGGGCGTCGAAGG 21074        GA  A   GGG
                                GCGGGGG  GG GCG   GGAGG
                                |||||||  || |||   |||||
                                CGCCCCC  CC CGC   CTTCC
                                    AC  C   AG_
GAM2111  HYOU1    3'  GGTGGGGTGAGGGGTGGG    40640    _   AG   C   _
                                GG GGGG  GAG GGG GGG
                                || ||||  ||| ||| |||
                                CC CCCC  CTC CCC CCC
                                 A   A_  _  A
GAM2111  IGF2     5'  AGGGGGGGAGGGAGTCGGAGG  8309     C       _ _
                                AG GGGGGGAGG AG CGGGGG
                                || |||||||| || ||||||
                                TC CCCCCCTCC TC GCCTCC
                                 _       C  A
GAM2111  IGFBP2   3'  GCGGGGGGCAGGGGCGCCAGG  8259         _  A   GG
                                GCGGGGGG AGG GCG  GGG
                                |||||||| ||| |||  |||
                                CGCCCCCC TCC CGC  TCC
                                    G   C   GG
GAM2111  IHPK2    5'  GCGGGGAGATGGGGGAG     41590         GGAGCG
                                GCGGGGGGA     GGGGGAG
                                |||||||||     |||||||
                                CGCCCCTCT     CCCCCTC
                                    A_____
GAM2111  ILF1     5'  GGCGGGAGGAGGGGAGGAG   21114    G       C
                                GG GGGAGGAG GGGGGGAG
                                || |||||||| ||||||||
                                CC CCCTCCTC CCCTCCTC
                                 G       _
GAM2111  KCNC3    3'  AGTGGGGGGGGGGGTGGGGGGGG 22495    C     A  AGC     A
                                AG GGGGGG GG   GGGGGG GG
                                || |||||| ||   |||||| ||
```

```
                                TC CCCCCC CC   CCCCCC CC
                                 A     _ CCA     _
GAM2111  KCNJ3    5'  GGAGGTGGGGGGCGGGGGGAGG  13847      GA  A
                                GGGGG  GG GCGGGGGGAGG
                                |||||  || ||||||||||
                                CCTCC  CC CGCCCCCCTCC
                                   AC  C
GAM2111  KCNJ3    5'  GCGGGGGGAGGAAAGGGGG   13846           C
                                GCGGGGGGAGGAG GGGGG
                                |||||||||||| |||||
                                CGCCCCCCTCCTT CCCCC
                                        T
GAM2111  KCNN4    5'  GCGGGGAGGGGCAGGGGAGG  13925        A  A      G
                                GCGGGGGG GG GCGGGGG AGG
                                |||||||| || ||||||| |||
                                CGCCCCTC CC CGTCCCC TCC
                                   _ _     _
GAM2111  KPNB1    5'  GCGGGGGAGGGACCCTGGGGG  13969       GA   GCG_
                                GCGGGGG  GGA   GGGGG
                                |||||||  |||   |||||
                                CGCCCCC  CCT   CCCCC
                                    TC   GGGA
GAM2111  LAG3     5'  AGTGGTGGGGGGGTGGGGGG   14042    C  _   A  AGC
                                AG GG GGGG GG   GGGGGG
                                || || |||| ||   ||||||
                                TC CC CCCC CC   CCCCCC
                                 A  A   _  A__
GAM2111  LRP1     5'  GCGGGGAGGGGGGGGTGGGGGG  14212        A  AGC_
                                GCGGGGGGG GG   GGGGGG
                                |||||||| ||   ||||||
                                CGCCCCTC CC   CCCCCC
                                    C  CCCA
GAM2111  LU       3'  GCGGGGTGAGGGGGGGG     24563       G   AGC
                                GCGGGG GAGG   GGGGGG
                                |||||| ||||   ||||||
                                CGCCCC CTCC   CCCCCC
                                   A   ____
GAM2111  MAP3K7IP1 3'  GGTGGGAGGAGGGGTGGG    25933    G      C  _
                                GG GGGAGGAG GGG GGG
                                || |||||||| ||| |||
                                CC CCCTCCTC CCC CCC
                                 A       _  A
GAM2111  MAX      5'  GCGGCGGGGAGGGGAAGGGG  40363     _     AGC
                                GCGG GGGGAGG   GGGGGG
                                |||| |||||||   ||||||
                                CGCC CCCCTCC   TTCCCC
                                  G      CC_
GAM2111  MAX      5'  GCGGCGGGGAGGGGAAGGGG  40363     _     AGC
                                GCGG GGGGAGG   GGGGGG
                                |||| |||||||   ||||||
```

```
                                CGCC CCCCTCC  TTCCCC
                                  G     CC_
GAM2111  MAX     5' GCGGCGGGGAGGGGAAGGGG  40363    _    AGC
                                GCGG GGGGAGG  GGGGGG
                                |||| |||||||  ||||||
                                CGCC CCCCTCC  TTCCCC
                                  G     CC_
GAM2111  MAX     5' GCGGCGGGGAGGGGAAGGGG  40363    _    AGC
                                GCGG GGGGAGG  GGGGGG
                                |||| |||||||  ||||||
                                CGCC CCCCTCC  TTCCCC
                                  G     CC_
GAM2111  MDM4    5' GGTGGGGGGAGGGGTGGCAG  14395   _  A  C  _ G
                                GG GGGG GGAG GGG GG AG
                                || |||| |||| ||| || ||
                                CC CCCC CCTC CCC CC TC
                                 A  _  _  A G
GAM2111  MDS1    3' GCTTCGGGTGGGGGGAGG   22563   GGG  AGGAGC
                                GC  GGG    GGGGGGAGG
                                ||  |||    |||||||||
                                CG  CCC    CCCCCCTCC
                                 AAG  A_____
GAM2111  MGMT    5' GCGGCGGGGGGGGCGGGGGGGG 14489    _  A A     A
                                GCGG GGGG GG GCGGGGGG GG
                                |||| |||| || |||||||| ||
                                CGCC CCCC CC CGCCCCCC CC
                                  G  _ C      _
GAM2111  MKPX    5' GCGGGGCGGGCGGGGAG    33640      GGA  A
                                GCGGGG  GG GCGGGGGG
                                ||||||  || ||||||||
                                CGCCCC  CC CGCCCCTC
                                   G__ _
GAM2111  MSL3L1  5' GCGGGCGGGGGCGGGGAG   38598     G  A  A
                                GCGGG GG GG GCGGGGGG
                                ||||| || || ||||||||
                                CGCCC CC CC CGCCCCTC
                                  G  _  _
GAM2111  MSL3L1  5' GCGGGCGGGGGCGGGGAG   38586     G  A  A
                                GCGGG GG GG GCGGGGGG
                                ||||| || || ||||||||
                                CGCCC CC CC CGCCCCTC
                                  G  _  _
GAM2111  MSL3L1  5' GCGGGCGGGGGCGGGGAG   38586     G  A  A
                                GCGGG GG GG GCGGGGGG
                                ||||| || || ||||||||
                                CGCCC CC CC CGCCCCTC
                                  G  _  _
GAM2111  MUC4    5' AGTGGCGGGAGGGATGGGAGG 39662   C  G    AGC
                                AG GG GGGAGG  GGGGGG
                                || || ||||||  ||||||
```

```
                                TC CC CCCTCC   CCCTCC
                                 A  G     CTA
GAM2111  MUC4     5'  AGTGGCGGGAGGGATGGGAGG  39662    C  G     AGC
                                AG GG GGGAGG   GGGGGG
                                || || ||||||   ||||||
                                TC CC CCCTCC   CCCTCC
                                 A  G     CTA
GAM2111  NCOR2    3'  GCGGAGGGAGGGCGCGGGGG   26739          A_
                                GCGGGGGGAGG  GCGGGGG
                                ||||||||||  |||||||
                                CGCCTCCCTCC  CGCCCCC
                                      CG
GAM2111  NDST2    5'  GCGGGGGGAGGAAGGGAGG    18879           C
                                GCGGGGGGAGGAG GGGGGG
                                |||||||||||| ||||||
                                CGCCCCCCTCCTT CCCTCC

                                          _
GAM2111  NFATC4   5'  GGGGGGAGTTCAGGAGG     21246        GAG
                                GGGGGGAG   CGGGGGG
                                ||||||||   |||||||
                                CCCCCCTC   GTCCTCC
                                     AA_
GAM2111  NHLH1    5'  GGTGGGAGGGGGAGG       24656    G     AGC
                                GG GGGAGG   GGGGGG
                                || ||||||   ||||||
                                CC CCCTCC   CCCTCC
                                 A     ____
GAM2111  NHLH1    5'  AGGGGGAGGAAGGGGGAGG   24648          GC
                                GGGGGGAGGA  GGGGGGAGG
                                ||||||||||  |||||||||
                                TCCCCCTCCT  TCCCCCTCC

                                          __
GAM2111  NOTCH3   3'  GGTGGGGTGGGGAGGA      7739     _    A  AGCG
                                GG GGGG GG    GGGGGA
                                || |||| ||    ||||||
                                CC CCCC CC    CCTCCT
                                 A    A _____
GAM2111  NPDC1    5'  AGCGGGGGAGGACGCAGGAGG  31724          G   _
                                AGCGGGGG AGGA GCGGGGGG
                                |||||||| |||| ||||||||
                                TCGCCCCC TCCT CGTCCTCC
                                     _    G
GAM2111  NRGN     3'  GCGGGGGGGGAGGGCGGG    26128          A    C  G
                                GCGGGGGG GGAG GG GGG
                                |||||||| |||| || |||
                                CGCCCCCC CCTC CC CCC
                                     _    _  G
GAM2111  NT5M     5'  AGCGGGGCGGGGAGCGCAGG  33643          _  A     G
                                AGCGGGG GG GGAGCG GGG
                                ||||||| || |||||| |||
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                                TCGCCCC CC CCTCGC TCC
                                   G _    G
GAM2111 PABPC4   5' GGGGCCCGAGCGGGGGGAG  19229     AG_
                                GGGG  GAGCGGGGGGAG
                                ||||  ||||||||||||
                                CCCC  CTCGCCCCCCTC
                                  GGG
GAM2111 PAFAH1B1 5' GCGGGGGAGGGGGA      7711        GAGGAGC
                                GCGGGGG     GGGGGGA
                                |||||||     |||||||
                                CGCCCCC     TCCCCCT
                                   ________
GAM2111 PAPOLA   5' GCGGGAGGGAGGGGGGGG   37206     _    AGC
                                GCGGG GGGAGG  GGGGGG
                                ||||| ||||||  ||||||
                                CGCCC CCCTCC  CCCCCC
                                  T    ___
GAM2111 PAX2     3' GCGGGGCGGGGCGGAGGGGGAG 19630      _ A  AGC
           G                     GCGGGG GG GG  GGGGGGAGG
                                 |||||| || ||  |||||||||
                                 CGCCCC CC CC  TCCCCCTCC
                                    G _ GCC
GAM2111 PAX2     3' GCGGGGCGGGGCGGAGGGGGAG 19630      _ A  AGC
           G                     GCGGGG GG GG  GGGGGGAGG
                                 |||||| || ||  |||||||||
                                 CGCCCC CC CC  TCCCCCTCC
                                    G _ GCC
GAM2111 PAX7     5' GGGGTGGAGGTTGGGGGGAGG  30334     _    AGC
                                GGGG GGAGG  GGGGGGAGG
                                |||| |||||  |||||||||
                                CCCC CCTCC  CCCCCCTCC
                                  A    AA_
GAM2111 PAX7     5' GGGGTGGAGGTTGGGGGGAGG  30334     _    AGC
                                GGGG GGAGG  GGGGGGAGG
                                |||| |||||  |||||||||
                                CCCC CCTCC  CCCCCCTCC
                                  A    AA_
GAM2111 PCBP1    5' GCGGGGGGAGGGGAGGTGTAGG 26220          AGC    G__
                                GCGGGGGGAGG  GGGGG  AGG
                                ||||||||||  |||||  |||
                                CGCCCCCCTCC  CCTCC  TCC
                                      ___    ACA
GAM2111 PCBP1    5' GGCGGCTGGCGGGGGGAG    26222    G  AGGA
                                GG GG   GCGGGGGGAG
                                || ||   ||||||||||
                                CC CC   CGCCCCCCTC
                                 G  GAC_
GAM2111 PCDHGA1  3' AGTGGGGTGGGGAGGAGG    36728    C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
```

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                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA10 3' AGTGGGGTGGGGAGGAGG   36869   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA11 3' AGTGGGGTGGGGAGGAGG   36878   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA11 3' AGTGGGGTGGGGAGGAGG   36878   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA12 3' AGTGGGGTGGGGAGGAGG   36887   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA2  3' AGTGGGGTGGGGAGGAGG   33154   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA3  3' AGTGGGGTGGGGAGGAGG   33158   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA4  3' AGTGGGGTGGGGAGGAGG   36819   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA5  3' AGTGGGGTGGGGAGGAGG   36827   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA6  3' AGTGGGGTGGGGAGGAGG   36835   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA7  3' AGTGGGGTGGGGAGGAGG   36843   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
```

```
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA8 3' AGTGGGGTGGGGAGGAGG   36852   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGA9 3' AGTGGGGTGGGGAGGAGG   33170   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB1 3' AGTGGGGTGGGGAGGAGG   36896   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB2 3' AGTGGGGTGGGGAGGAGG   36905   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB3 3' AGTGGGGTGGGGAGGAGG   36914   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB4 3' AGTGGGGTGGGGAGGAGG   36923   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB5 3' AGTGGGGTGGGGAGGAGG   36932   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB6 3' AGTGGGGTGGGGAGGAGG   36939   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGB7 3' AGTGGGGTGGGGAGGAGG   36946   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGC3 3' AGTGGGGTGGGGAGGAGG   37047   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
```

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                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGC3  3' AGTGGGGTGGGGAGGAGG   37055   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGC4  3' AGTGGGGTGGGGAGGAGG   37069   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PCDHGC5  3' AGTGGGGTGGGGAGGAGG   33181   C   _ A   C
                                AG GGGG GG GGAG GGGG
                                || |||| || |||| ||||
                                TC CCCC CC CCTC CTCC
                                 A   A _   _
GAM2111 PDE4A    3' GGGGGCAGGGGGAAAGG    26271     G  AGCG  GG
                                GGGGG AGG   GGG  AGG
                                ||||| |||   |||  |||
                                CCCCC TCC   CCC  TCC
                                   G  ____  TT
GAM2111 PDE4A    3' AGTGGGGCGGGGGGCGGGGGG 26251   C   _ A A
                                AG GGGG GG GG GCGGGGGG
                                || |||| || || ||||||||
                                TC CCCC CC CC CGCCCCCC
                                 A   G _ C
GAM2111 PDE4A    3' GCGGGGGGGTGAGTGGATCAG 26258       AG  C  G_
                                GCGGGGGG  GAG GGG  GG
                                ||||||||  ||| |||  ||
                                CGCCCCCC  CTC CCT  TC
                                     CA  A  AG
GAM2111 PDE4A    3' AGTGGGGGAAGGTGAGGGGAGG 26252   C      AGC
                                AG GGGGGGAGG  GGGGGGAGG
                                || |||||||||  |||||||||
                                TC CCCCCTTCC  CTCCCCTCC
                                 A       A__
GAM2111 PDE4A    3' AGTGAGGGGAGGAGTGGAGG  26250   C       C
                                AG GGGGGGAGGAG GGGGG
                                || ||||||||||| |||||
                                TC CTCCCCTCCTC CCTCC
                                 A         A
GAM2111 PFN1     5' GGCTGGCGGGCGGGGGGAG   22719   GG A A
                                GG  GG GG GCGGGGGGAG
                                ||  || || ||||||||||
                                CC  CC CC CGCCCCCCTC
                                 GA  G  _
GAM2111 PLOD3    5' GCGGGGGAGGGGCGGCGG    9892       GA A   G
                                GCGGGGG  GG GCGG GG
                                |||||||  || |||| ||
```

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                                CGCCCCC  CC CGCC CC
                                    TC  _   G
GAM2111  PNUTL1   3'  GCGGGGGAAGGGCAAGGGAGG  15433          A     G
                                GCGGGGGGAGG GCGGGGG AGG
                                |||||||||| ||||||| |||
                                CGCCCCCTTCC CGTTCCC TCC
                                        _     _
GAM2111  PPT2     5'  GCGGGGGGAAGGGTGAG     39921         GGAGC   G
                                GCGGGGGGA    GGGG GAG
                                |||||||||    |||| |||
                                CGCCCCCCT    TCCC CTC
                                     _____   A
GAM2111  PPT2     5'  GCGGGGGGAAGGGTGAG     39921         GGAGC   G
                                GCGGGGGGA    GGGG GAG
                                |||||||||    |||| |||
                                CGCCCCCCT    TCCC CTC
                                     _____   A
GAM2111  PROC     3'  GCAGGGGGGGGGGGCGGGGGGG 7191         A  A_      A
              G                  GCGGGGGG GG  GCGGGGGG GG
                                 |||||||| ||  |||||||| ||
                                 CGTCCCCC CC  CGCCCCCC CC
                                     C  CC      _
GAM2111  PRODH    3'  GCGGGGGCGGGGGGGTGCTGGAG 32278        GA  AGC   ____
              G                  GCGGGGG  GG   GGGG   GGAGG
                                 |||||||  ||   ||||   |||||
                                 CGCCCCC  CC   CCCC   CCTCC
                                     G_  ____   ACGA
GAM2111  PTPRA    3'  AGTGGTGGGGATGGGGGGAG   38905    C  _    GGAGCG
                                AG GG GGGGA     GGGGGAG
                                || || |||||     |||||||
                                TC CC CCCCT     CCCCCTC
                                 A  A    A_____
GAM2111  PTPRA    3'  AGTGGTGGGGATGGGGGGAG   38905    C  _    GGAGCG
                                AG GG GGGGA     GGGGGAG
                                || || |||||     |||||||
                                TC CC CCCCT     CCCCCTC
                                 A  A    A_____
GAM2111  PTPRA    3'  AGTGGTGGGGATGGGGGGAG   38905    C  _    GGAGCG
                                AG GG GGGGA     GGGGGAG
                                || || |||||     |||||||
                                TC CC CCCCT     CCCCCTC
                                 A  A    A_____
GAM2111  RAB13    5'  AGCCGGGGGAGGGGTGGGG   16111     G      AGC  _
                                AGC GGGGGAGG   GG GGGG
                                ||| ||||||||   || ||||
                                TCG CCCCCTCC   CC CCCC
                                  G       ___  A
GAM2111  RAB3A    3'  GCGGGGGGGGGGGTTCAGGAGG  16067        A  AG_
                                GCGGGGGG GG   CGGGGGG
                                |||||||| ||   |||||||
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                                CGCCCCCC CC   GTCCTCC
                                    C  CAA
GAM2111  RAB3A    3'  GCGGGGGGGGGGGGGGG      16065        A  AGC
                                GCGGGGGG GG   GGGGGG
                                |||||||| ||   ||||||
                                CGCCCCCC CC   CCCCCC
                                   _  ___
GAM2111  RCE1     3'  GGGGGGTGGGGAGAG       23068       AGGAGC
                                GGGGGG     GGGGGGAG
                                ||||||     ||||||||
                                CCCCCC     CCCCTCTC
                                   A_____
GAM2111  RFX1     3'  GCGGGTGGGGCGGGGAG     16291       _  AGGA
                                GCGGG GGG    GCGGGGGG
                                ||||| |||    ||||||||
                                CGCCC CCC    CGCCCCTC
                                  A  _____
GAM2111  RPA1     3'  AGCGGGGATGGGGGGGGG    16366        GA  AGC
                                AGCGGGGG  GG   GGGGGG
                                ||||||||  ||   ||||||
                                TCGCCCCT  CC   CCCCCC
                                    AC  ___
GAM2111  RREB1    5'  GGGGGGGGTGAGGGGGAGG   16400       A  AGC
                                GGGGGG GG   GGGGGGAGG
                                |||||| ||   |||||||||
                                CCCCCC CC   TCCCCCTCC
                                   _  AC_
GAM2111  SALL1    3'  GCGGGGTGGGGGGGCAAGG    16456       _  A  A
                                GCGGGG GG GG GCGGGG
                                |||||| || || ||||||
                                CGCCCC CC CC CGTTCC
                                   A  _  C
GAM2111  SALL1    3'  GCGGGGCGGGGTGGGGGG     16455       _  A  AGC
                                GCGGGG GG GG   GGGGGG
                                |||||| || ||   ||||||
                                CGCCCC CC CC   CCCCCC
                                   G  _  A__
GAM2111  SLC21A3  3'  GGTGGGGGAAGGGGGGAG    39577    G   A   C
                                GG GGG GGAG GGGGGGAG
                                || ||| |||| ||||||||
                                CC CCC CCTT CCCCCCTC
                                 A  _   _
GAM2111  SMG1     3'  AGTGGTGGGGAGGAGTAGG    31504    C  _       CG
                                AG GG GGGGAGGAG  GG
                                || || |||||||||  ||
                                TC CC CCCCTCCTC  CC
                                 A  A        AT
GAM2111  SMOH     3'  AGCGAGGGGAGGGGGTTAGAGG 24807           AGC  GG
                                AGCGGGGGGAGG   GG  GGAGG
                                ||||||||||||   ||  |||||
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                                TCGCTCCCCTCC  CC  TCTCC
                                      C__  AA
GAM2111  SOX11    3'  GCCGGGGGAGGGGTGGTGG   17022    G      AGC  _  _
                                GC GGGGGAGG  GG GG GG
                                || ||||||||  || || ||
                                CG CCCCCTCC  CC CC CC
                                 G      ___  A  A
GAM2111  SOX11    3'  AGTCGGGGGGCCGGGGGAG   17002   _    GAGGA  G
                                AG CGGGGG    GC GGGGGAG
                                || ||||||    || |||||||
                                TC GCCCCC    CG CCCCCTC
                                 A     _____  G
GAM2111  SOX4     3'  AGGGGGGGAGGGGTGCGCTGGG 16975    C       A__  GG
                                AG GGGGGGAGG  GCG  GGG
                                || |||||||||  |||  |||
                                TC CCCCCCTCC  CGC  CCC
                                 _       CCA  GA
GAM2111  SPI1     3'  AGTGGGGGGAGGGGCGGG    17073    C       A
                                AG GGGGGGAGG GCGGG
                                || ||||||||| |||||
                                TC CCCCCCTCC CGCCC
                                 A       C
GAM2111  SPI1     3'  GGGGGCCTGGAGTGGGGGGAGG 17083      GA_   C
                                GGGGG  GGAG GGGGGGAGG
                                |||||  |||| |||||||||
                                CCCCC  CCTC CCCCCCTCC
                                   GGA   A
GAM2111  SPTBN2   3'  GGGGGTGGGGAGGGAG     28072      A  AGC
                                GGGGG GG  GGGGGGAG
                                ||||| ||  ||||||||
                                CCCCC CC  CCTCCCTC
                                   A  ___
GAM2111  SPTBN2   3'  GCGGGGGTGGGAGAGGGGG   28070       GA   C
                                GCGGGGG  GGAG GGGGG
                                |||||||  |||| |||||
                                CGCCCCC  CCTC CCCCC
                                    AC   T
GAM2111  SRD5A1   5'  GGCGGCGGCGCGGGGGGAG   9829    G  A  A
                                GG GG GG GCGGGGGGAG
                                || || || ||||||||||
                                CC CC CC CGCCCCCCTC
                                 G  G  G
GAM2111  SSRP1    5'  GCTGGGGGGACGCGGGGGGGG  17125   _     GGA      A
                                GC GGGGGGA  GCGGGGGG GG
                                || |||||||  |||||||| ||
                                CG CCCCCCT  CGCCCCCC CC
                                 A     G__      _
GAM2111  SSRP1    5'  GCGGGGAGGGGGATGGGGGG  17123      _  A  GC
                                GCGGGG GG GGA  GGGGGG
                                |||||| || |||  ||||||
```

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                                CGCCCC CC CCT  CCCCCC
                                   T  C   A_
GAM2111  SSRP1    5'  GCGGGGGGGGGCGCGGGGAG   17124        A  A
                                GCGGGGGG GG GCGGGGGG
                                |||||||| || ||||||||
                                CGCCCCCC CC CGCCCCTC
                                     _  G
GAM2111  SYT5     3'  GGTGGAAGGTGGGGGGAG    17242    G     AGC
                                GG GGGAGG   GGGGGGAG
                                || ||||||   ||||||||
                                CC CCTTCC   CCCCCCTC
                                 A     A__
GAM2111  TCF3     3'  GGGGGGGGGGGACGGGGGG    43326       A  AG
                                GGGGGG GG  CGGGGGG
                                |||||| ||  |||||||
                                CCCCCC CC  GCCCCCC
                                   C  CT
GAM2111  TNFRSF11A 3'  GGGGGGGGGGAGTCGGGGGGAGG 19278       A   _
                                GGGGGG GGAG CGGGGGGAGG
                                |||||| |||| ||||||||||
                                CCCCCC CCTC GCCCCCCTCC
                                   C   A
GAM2111  TNFSF5   3'  GCGGGGGGGGGGGGGGGGG   6327         A  AGC     A
                                GCGGGGGG GG   GGGGGG GG
                                |||||||| ||   |||||| ||
                                CGCCCCCC CC   CCCCCC CC
                                     _  C__     _
GAM2111  TNFSF5   3'  GAGGGTGGCGGGGGGG      6325       GAGGA      A
                                GGGGG    GCGGGGGG G
                                |||||    |||||||| |
                                CTCCC    CGCCCCCC C
                                   AC___       _
GAM2111  TULP1    3'  GCGCGGGGAGGAGGGGGG    17728     G       C
                                GCG GGGGAGGAG GGGGG
                                ||| |||||||| |||||
                                CGC CCCCTCCTC CCCCC
                                  G       _
GAM2111  UNC5C    5'  CGGGGGGAGGGGAGGGGG    19007          AGC
                                CGGGGGGAGG   GGGGGG
                                ||||||||||   ||||||
                                GCCCCCCTCC   TCCCCC
                                     CC_
GAM2111  VDR      3'  AGCGGGGCCTGCAGTGGGGGGA 7510         GGAGG  C
            GG                    AGCGGGG    AG GGGGGGAGG
                                |||||||    || |||||||||
                                TCGCCCC    TC CCCCCCTCC
                                   GGACG  A
GAM2111  VDR      3'  AGTGGGGGGAGGTGCAGG    7512     C       A
                                AG GGGGGGAGG GCGGG
                                || |||||||| |||||
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                                TC CCCCCCTCC CGTCC
                                 A       A
GAM2111 WNT7A   5' AGCGGGAGGAGGGAGGGAG  21521          AGCG
                                AGCGGGGGGAGG   GGGGGAG
                                ||||||||||||  |||||||
                                TCGCCCTCCTCC   CTCCCTC
                                      ____
GAM2111 YY1     5' AGCGGGCGGGGGGGAGAGGGGG 18163      _  A   C
                                AGCGGG GGG GGAG GGGGG
                                |||||| ||| |||| |||||
                                TCGCCC CCC CCTC CCCCC
                                   G   C   T
GAM2111 ZIC3    5' GCGGGGGGAGGAGGAGG    18248          C
                                GCGGGGGGAGGAG GGGG
                                |||||||||||| ||||
                                CGCCCCCCTCCTC CTCC
                                      _
GAM2111 ZIC3    5' GGGGGTGTTGGCGGGGGGAGG 18253     GAGGA
                                GGGGG   GCGGGGGGAGG
                                |||||   ||||||||||
                                CCCCC   CGCCCCCCTCC
                                   ACAAC
GAM2111 ZNF216  5' AGTGGGAGGAGGGAAGCGAGGG 25651   C      __      A
          GGG                    AG GGGGGGAGG  AGCGGGGGG GG
                                || |||||||  |||||||| ||
                                TC CCCTCCTCC  TCGCTCCCC CC
                                 A       CT      _
GAM2112 ABCC1   5' CACCGGGCGGCGGGTGAT   33397         CCTTA
                                CACCGGGCGGC   GTGAT
                                ||||||||||   |||||
                                GTGGCCCGCCG   CACTA
                                      CC___
GAM2112 ADAMTS13 3' TGGCACTGGGTGTCCAACAGGA 40039   A  C  CGG  CT  T
          T                     TG CAC GGG  CC  TAG GAT
                                || ||| |||  ||  ||| |||
                                AC GTG CCC  GG  GTC CTA
                                 C  A  ACA  TT  _
GAM2112 GOLGA4  5' CATACTGCTTTCTTAGTGAT  41055   G  G  C__
                                CG GC GC  CTTAGTGAT
                                || || ||  |||||||||
                                GT TG CG  GAATCACTA
                                 A  A  AAA
GAM2112 WTAP    3' GAGTCCAACTTTTAGTGA   22227    __   CC
                                GGG  CGGC  TTAGTGA
                                |||  ||||  |||||||
                                CTC  GTTG  AATCACT
                                  AG   AA
GAM2112 BAT4    5' ACTTGAGGGCTCGGGCGT   37688   C        G
                                AC TGAGGGTTCGGG GT
                                || ||||||||||| ||
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                                TG ACTCCCGAGCCC CA
                                 A          G
GAM2112 COL1A1   3' CCACTTGGGTGTTTGAGCAT  6367      C A _  C  G
                                CCAC TG GG GTT GGG GT
                                |||| || || ||| ||| ||
                                GGTG AC CC CAA CTC TA
                                  A _ A  A  G
GAM2112 FOXD2    5' CCATTTAGGAAAGGGTAC    20955    CCTG   TTC
                                CCA   AGGG  GGGGGTAC
                                |||   ||||  ||||||||
                                GGT   TCCT  TTCCCATG
                                 AAA_  ___
GAM2112 GNGT2    3' CCCTCTGGGGTCTTGGGGTA  36483    AC  A   CG
                                CC  CTG GGGTT  GGGGTA
                                ||  ||| |||||  ||||||
                                GG  GAC CCCAG  CCCCAT
                                 GA  _    AA
GAM2112 MMP19    3' ACCTGAGGGAGTGGTA      35577       TTC  G
                                ACCTGAGGG   GG GGTA
                                |||||||||   || ||||
                                TGGACTCCC   TC CCAT
                                     ___ A
GAM2112 MNT      3' ACCTCTGGGGGTTTGGGGGT  33700    AC  A   C
                                ACC  CTG GGGTT GGGGGT
                                |||  ||| ||||| ||||||
                                TGG  GAC CCCAA CCCCCA
                                 A_  C    A
GAM2112 MUCDHL   3' CCACCTGAAGATGGGGTGC   34929         TC  _
                                CCACCTGAGGGT  GGGG GT
                                ||||||||||||  |||| ||
                                GGTGGACTTCTA  CCCC CG
                                      __   A
GAM2112 RING1    3' CTGGCTGGGCTGGGGGTACT  16333    A__   C
                                CTG   GGGTT GGGGGTACT
                                |||   ||||| |||||||||
                                GAC   CCCGA CCCCCATGA
                                 CGA   _
GAM2113 HELZ     3' TCTATAGATGAAGTCCAAC   31370       TTAATAAA
                                TCTATAGAT      TCCAAC
                                |||||||||      ||||||
                                AGATATCTA      AGGTTG
                                    CTTC____
GAM2113 PACE4    3' CAGAATAAATCCAACT     39686     TTTA
                                TAGA   ATAAATCCAACT
                                ||||   ||||||||||||
                                GTCT   TATTTAGGTTGA
                                  ____
GAM2114 ACR      3' GGAGTGAAGGGCTCACTGGG  9918    A     ____  CC
                                A AGTGAAGG   AC  GGG
                                | ||||||||   ||  |||
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                                C TCACTTCC    TG  CCC
                                 C       CGAG  A_
GAM2114  ATP1A1    5'  AAGTGGAGGGAGCTAGGG    8690       A   ACCC    CAA
                                AAGTG AGG    GGGC   GG
                                ||||| |||    ||||   ||
                                TTCAC TCC    CTCG   CC
                                   C  _____    ATC
GAM2114  C14orf1   3'  AAGGAAGAAGATGGCCAAGG   28409     T     CCCG
                                AAG GAAGGA    GGCCAAGG
                                ||| ||||||    ||||||||
                                TTC CTTCTT    CCGGTTCC
                                  _     CTA_
GAM2114  C20orf1   3'  AGTGAAGACCCATATAAAAGGC 29054        G    GGCC_
                                AGTGAAG ACCCG     AAGGC
                                ||||||| |||||     |||||
                                TCACTTC TGGGT     TTCCG
                                    _     ATATT
GAM2114  CACNB1    3'  AAGTGAAGGGGCTCAGGG    8773          ACCCG   _  A
                                AAGTGAAGG     GGC CA GG
                                |||||||||     ||| || ||
                                TTCACTTCC     CCG GT CC
                                      _____   A  C
GAM2114  COL6A1    3'  GTGGGGAACCCAGGTGAGGC   12331      AA        CCA
                                GTG  GGACCCGGG   AGGC
                                |||  |||||||||   ||||
                                CAC  CTTGGGTCC   TCCG
                                  CC        AC_
GAM2114  CPLX2     5'  GAGGGCGCCCGGGCCGAGG    27397    A  A_       A
                                GA GG  CCCGGGCC AGG
                                || ||  |||||||| |||
                                CT CC  GGGCCCGG TCC
                                 C  GC       C
GAM2114  CYLN2     3'  GTGGAGGCTGCAGGGCCAAGGC 18061     A   ACCC_
                                GTG AGG     GGGCCAAGGC
                                ||| |||     ||||||||||
                                CAC TCC     CCCGGTTCCG
                                  C   GACGT
GAM2114  DCTN1     3'  AGTGGGGGAACCCGGGTCAAGG 35698      AA  _     C
                                AGTG  GGA CCCGGG CAAGG
                                ||||  ||| |||||| |||||
                                TCAC  CCT GGGCCC GTTCC
                                  CC   T     A
GAM2114  DDX6      3'  AGGAAAGAGGGCCAAGG     20542    T     CCC
                                AG GAAGGA   GGGCCAAGG
                                || ||||||   |||||||||
                                TC CTTTCT   CCCGGTTCC
                                 _    ____
GAM2114  DOK1      3'  GGAGTAAGGATCCAGGC     10723    A    A   C
                                A AGTGA GGA CCGGGC
                                | ||||| ||| ||||||
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                                C TCATT CCT GGTCCG
                                 C    _  A
GAM2114  EGR1    3'  GTGAAGAACTTGGACATGGC  12665       CC   CAA
                                GTGAAGGAC  GGGC  GGC
                                |||||||||  ||||  |||
                                CACTTCTTG  CCTG  CCG
                                     AA   TA_
GAM2114  EMP1    5'  GAAGGACCCGCCTCCCGAGG  10895       GG_  A_
                                GAAGGACCCG  CC  AGG
                                ||||||||||  ||  |||
                                CTTCCTGGGC  GG  TCC
                                     GGA  GC
GAM2114  FOSB    3'  GTGAGGGGCCAAGG      27545     A  ACCCG
                                GTGA GG    GGCCAAGG
                                |||| ||    ||||||||
                                CACT CC    CCGGTTCC
                                  _ _____
GAM2114  FPGS    3'  AGGAAGGAGAGACCAAGGC  22424   T    CCC
                                AG GAAGGA  GGGCCAAGGC
                                || ||||||  ||||||||||
                                TC CTTCCT  TCTGGTTCCG
                                 _    C__
GAM2114  G6PT1   3'  AAAGTGAAAGGTTCAGGGC  11157       ACCC_
                                AAAGTGAAGG    GGGC
                                |||||||||    ||||
                                TTTCACTTTC    CCCG
                                     CAAGT
GAM2114  GRB2    3'  AAAGTGAGAGGGTCACAGG  13285      _  ACC_
                                AAAGTGA AGG   CGGG
                                ||||||| |||   ||||
                                TTTCACT TCC   GTCC
                                   C  CAGT
GAM2114  HAS3    3'  ATGAAGGAAAGCACCAGGG  39767       CCC _   A
                                GTGAAGGA  GG GCCA GG
                                ||||||||  || |||| ||
                                TACTTCCT  TC TGGT CC
                                     T__ G   C
GAM2114  HAS3    5'  GAAGGGGGCGCCAAGGC    39773     ACCC _
                                GAAGG   GG GCCAAGGC
                                |||||   || ||||||||
                                CTTCC   CC CGGTTCCG
                                  C___  G
GAM2114  IFNGR1  3'  AAAGTGAAGTGGCTACAAAGG 43541       GACCCGG  C
                                AAAGTGAAG     GC AAGG
                                |||||||||     || ||||
                                TTTCACTTC     TG TTCC
                                     ACCGA__  T
GAM2114  IL12RB2 3'  AGTGAAGGATGTAATTTTAAGG 11422       CCCGGGCC_
            C                    AGTGAAGGA       AAGGC
                                |||||||||       |||||
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                                TCACTTCCT       TTCCG
                                     ACATTAAAA
GAM2114  IL1R1    3'  AAAGGAGGAGGAAGGGTCGAGG 9348      T  A   CCC_   CCA
             C                    AAAG GA GGA    GGG   AGGC
                                  |||| || |||    |||   ||||
                                  TTTC CT CCT    CCC   TCCG
                                    _ _   CCTT   AGC
GAM2114  LPIN2    3'  AAAGGAGGGATCCCAGGC    31203      T  A  _
                                  AAAG GA GGA CCCGGGC
                                  |||| || ||| |||||||
                                  TTTC CT CCT GGGTCCG
                                    _ C   A
GAM2114  LZTS1    3'  AAATGAAGGAACTGAGGGCTGA 34257          _ CC_    CA
             GGC                    AAGTGAAGGA C   GGGC  AGGC
                                  |||||||||| |   ||||  ||||
                                  TTTACTTCCT G   CCCG  TCCG
                                       T ACT    AC
GAM2114  MAPK8IP1  3'  GTGACAGGACCAAGATGGGGC  24161      _     C_____
                                  GTGA AGGACC     GGGC
                                  |||| ||||||     ||||
                                  CACT TCCTGG     CCCG
                                    G     TTCTAC
GAM2114  MASP1    3'  AGGAAGGATTAGGCCAAGGC   40094    T     CCC
                                  AG GAAGGA   GGGCCAAGGC
                                  || ||||||   ||||||||||
                                  TC CTTCCT   TCCGGTTCCG
                                    _     AA_
GAM2114  MSF      3'  AAAGTGAAGCATCTCAAGG   44717        GACC  GGC
                                  AAAGTGAAG   CG   CAAGG
                                  |||||||||   ||   |||||
                                  TTTCACTTC   GT   GTTCC
                                       _____  AGA
GAM2114  MUC3B    3'  TGGAGGATCCGAGAGAGGC   45348    A   C    CCA
                                  TG AGGA CCGGG   AGGC
                                  || |||| |||||   ||||
                                  AC TCCT GGCTC   TCCG
                                   C    A    TC_
GAM2114  MUC5B    3'  AGGGAGGGGCAAGGCCAAGG   42496    T  A  ACCC
                                  AG GA GG    GGGCCAAGG
                                  || || ||    |||||||||
                                  TC CT CC    TCCGGTTCC
                                   C  C  CGT_
GAM2114  MYH7     5'  ATGAGGAAAGGGGCCAAGGC   7024      A   CCC
                                  GTGA GGA   GGGCCAAGGC
                                  |||| |||   ||||||||||
                                  TACT CCT   CCCGGTTCCG
                                    _   TTC
GAM2114  NGFR     3'  AAGTGAAGGGGCCACACGGGC  14773         A_  ___
                                  AAGTGAAGG  CC   CGGGC
                                  |||||||||  ||   |||||
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                                TTCACTTCC  GG   GCCCG
                                     CC  TGT
GAM2114  PACE4    5'  AAGTAAAGGGCCTGCGGG    15044         A  __
                                AAGTGAAGG CC  CGGG
                                ||||||||| ||  ||||
                                TTCATTTCC GG  GCCC
                                     C  AC
GAM2114  PPP1R8   5'  GCGTAAGTTCGGGCCAAGGC   15512    _  GACC
                                GTG AAG   CGGGCCAAGGC
                                ||| |||   ||||||||||
                                CGC TTC   GCCCGGTTCCG
                                  A  AA__
GAM2114  PRG2     5'  ATGAAGGAGGCCCTGAGGC   15559       CCCG   A__
                                GTGAAGGA   GGCC   AGGC
                                ||||||||   ||||   ||||
                                TACTTCCT   CCGG   TCCG
                                     _____   GAC
GAM2114  PTHR2    3'  AGTGAAGACCTGAGGTGC    22783       G  C__  _____
                                AGTGAAG ACC   GG   GC
                                ||||||| |||   ||   ||
                                TCACTTC TGG   CC   CG
                                     _  ACT  AIII
GAM2114  PYGO2    5'  GGAGTGGGGGACCCGGGTTAGC 41951   A   AA       CCAA
                                A AGTG  GGACCCGGG   GGC
                                | ||||  |||||||||   |||
                                C TCAC  CCTGGGCCC   TCG
                                 C   CC       AA__
GAM2114  SCN4A    3'  AAAGGAGGGGCGACAGGG    7313       CCC   __ A
                                GAAGGA   GGGC  CA GG
                                ||||||   ||||  || ||
                                TTTCCT   CCCG  GT CC
                                   C__   CT  C
GAM2114  SELL     3'  AAGTGGTGGGGTTGAGGGAGGC 8507       AA  ACCC__  CCA
                                AAGTG  GG     GGG   AGGC
                                |||||  ||     |||   ||||
                                TTCAC  CC     CCC   TCCG
                                   CA  CCAACT  ___
GAM2114  SEZ6L    5'  AGGTAAGGACCCAAAGGGC   34419    TG      ___
                                AG  AAGGACCC   GGGC
                                ||  ||||||||   ||||
                                TC  TTCCTGGG   CCCG
                                 CA       TTT
GAM2114  SYNGR1   3'  AAAGGGGTCTTGGGCCAAGG   21748      ACCC__
                                GAAGG     GGGCCAAGG
                                |||||     |||||||||
                                TTTCC     CCCGGTTCC
                                   CCAGAA
GAM2114  TGFB3    3'  AGGAGGGACCCAGAGGG     17456    T  A       CCAA
                                AG GA GGACCCGGG    GG
                                || || |||||||||    ||
```

```
                                TC CT CCTGGGTCT   CC
                                 _ C       C___
GAM2114  TNFAIP1  3'  GGAGTGAAGGCCTTCAGG   34480   A     A __
                                A AGTGAAGG CC  CGGG
                                | |||||||| ||  ||||
                                C TCACTTCC GG  GTCC
                                 C       _  AA
GAM2114  TSNAX    5'  TGAAGGACCTGGAGCGCCTTG  25633        C _______  CAAG
                                TGAAGGACC GG     GC   G
                                ||||||||| ||     ||   |
                                ACTTCCTGG CC     CG   C
                                      A  TCGIII  GAAC
GAM2114  VDAC1    3'  GTTAGGGAACCAAGG      17931    GA   ACCC
                                GT  AGG   GGGCCAAGG
                                ||  |||   |||||||||
                                CA  TCC   CTTGGTTCC
                                 A_  _____
GAM2114  NPTX1    5'  CTCGGCTGGGGCTCGGCTC   14837     CC  CATCTA
                                CTCG  GT     CTCGGCTC
                                ||||  ||     ||||||||
                                GAGC  CG     GAGCCGAG
                                  __  ACCCC_
GAM2114  NR2F2    5'  GTTTCTCTCGGCTCAG     34240    CA   A
                                GT  TCT CTCGGCTCAG
                                ||  ||| ||||||||||
                                CA  AGA GAGCCGAGTC
                                 A_  _
GAM2114  RPP30    5'  GCTTTCATCTACCACCAG    26936    CG       CG  T
                                GC  TCATCTACT  GC CAG
                                ||  |||||||||  || |||
                                CG  AGTAGATGG  TG GTC
                                 AA       __  _
GAM2114  SLC12A4  3'  CTCAGCTGTCTCCATTCGGCTC 22895    _ C   A    C
            AG                    CTC GC GTC TCTA TCGGCTCAG
                                ||| || ||| |||| |||||||||
                                GAG CG CAG AGGT AGCCGAGTC
                                  T  A   _    A
GAM2114  TLX1     5'  CTCGCTGCGCTCGGCTC     24334      C  CATCTA
                                CTCGC GT     CTCGGCTC
                                |||||  ||     ||||||||
                                GAGCG CG     GAGCCGAG
                                   A  C_____
GAM2114  USP11    5'  CTCGCCGTTTTCTATCTGG   21631        CA   _  C
                                CTCGCCGT  TCTA CT GG
                                ||||||||  |||| || ||
                                GAGCGGCA  AGAT GA CC
                                     AA   A  _
GAM2114  VEGF     5'  CTCGCGGCTCCGCTCGGCTC  17952      C  CA  TA
                                CTCGC GT  TC  CTCGGCTC
                                |||||  ||  ||  ||||||||
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                                GAGCG CG  AG  GAGCCGAG
                                   C __ GC
GAM2115 ELAVL2   5' TAAAAGAAGCAAATAAAA    20745          CCTAT
                                TAAAAGAGGCA    AATAAAA
                                ||||||||||    |||||||
                                ATTTTCTTCGT    TTATTTT
                                      _____
GAM2115 ELF3     3' GAGGCACCAGATAAAA      20753        TATA
                                GAGGCACC    ATAAAA
                                ||||||||    ||||||
                                CTCCGTGG    TATTTT
                                     TC__
GAM2115 IL18R1   3' AAAGCAAGTATAATAAAA    19293       CC
                                GAGGCA  TATAATAAAA
                                ||||||  ||||||||||
                                TTTCGT  ATATTATTTT
                                    TC
GAM2115 PLAG1    3' AAAGTAGGCACTAAAATAAAAA 15340     _     C  T
                                AAAG AGGCAC TA AATAAAAA
                                |||| |||||| || ||||||||
                                TTTC TCCGTG AT TTATTTTT
                                  A     _ T
GAM2115 PSMD9    3' TAAAAGAGACAAAAAATAAAA  15846          CCTAT
                                TAAAAGAGGCA    AATAAAA
                                ||||||||||    |||||||
                                ATTTTCTCTGT    TTATTTT
                                      TTT__
GAM2115 SLC20A2  3' GAAGCACACCATTAAAAA    27573        _   AA
                                GAGGCAC CTAT  TAAAAA
                                ||||||| ||||  ||||||
                                CTTCGTG GGTA  ATTTTT
                                    T   __
GAM2115 SLC7A8   5' TAAAAAAGGCAAGCAGATAAAA 29296          CCTATA
                                TAAAAGAGGCA     ATAAAA
                                ||||||||||     ||||||
                                ATTTTTTCCGT     TATTTT
                                      TCGTC_
GAM2115 STAU2    3' TGAGAGGGTTACCTATAA    30806   A    C__
                                A AGAGG   ACCTATAA
                                | |||||   ||||||||
                                A TCTCC   TGGATATT
                                 C    CAA
GAM2115 TRPC5    3' AAAAAGGCAAATAATAA     29761        CCT
                                AAAGAGGCA  ATAATAA
                                |||||||||  |||||||
                                TTTTTCCGT  TATTATT
                                     T__
GAM2116 MJD      3' CATCTTTCAAAAGAATTG    36186     GTAA
                                CATC   TCAAAAGAATTG
                                ||||   ||||||||||||
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                                GTAG   AGTTTTCTTAAC
                                  AA__
GAM2116 SOX11    3' AACATCTCTGCCCAAAAGAGTT 16998      GTAA_      A
            G                   AACATC    TCAAAAGA TTG
                                ||||||    |||||||| |||
                                TTGTAG    GGTTTTCT AAC
                                   AGACG       C
GAM2116 OAT      3' ATATATTCAAAAAAAAAGTTTT 7085         T_
            TG                   ATATATTTA  AAAAAAGTTTTTG
                                |||||||||  ||||||||||||
                                TATATAAGT  TTTTTTCAAAAAC
                                     TT
GAM2117 CLOCK    3' CAGTAAGAATCATAAA      22214      TTTTT
                                CAGTA    GGAATCATAAA
                                |||||    ||||||||||
                                GTCAT    TCTTAGTATTT
                                  _____
GAM2117 DIAPH2   3' CAGTATTTTCTAACATAA    28670         GGAAT
                                CAGTATTTTT    CATAA
                                ||||||||||    |||||
                                GTCATAAAAG    GTATT
                                     ATT__
GAM2117 GOCAP1   3' CAGTATTTTTCTCATAAAAA   35547         GGAA
                                CAGTATTTTT    TCATAAAAA
                                ||||||||||   |||||||||
                                GTCATAAAAA    AGTATTTTT
                                     G___
GAM2117 MTRR     3' TCATATTTCCCAGCATCATAAA 35840    GTA    TG A
            AA                   TCA   TTTT  G ATCATAAAAA
                                |||   ||||  | ||||||||||
                                AGT   AAGG  C TAGTATTTTT
                                  ATA    GT G
GAM2117 MTRR     3' TCATATTTCCCAGCATCATAAA 35840    GTA    TG A
            AA                   TCA   TTTT  G ATCATAAAAA
                                |||   ||||  | ||||||||||
                                AGT   AAGG  C TAGTATTTTT
                                  ATA    GT G
GAM2117 SLC38A2  3' AGTATTTTTGGTACAAAAA   33271         AATC
                                AGTATTTTTGG    ATAAAAA
                                ||||||||||    |||||||
                                TCATAAAAACC    TGTTTTT
                                     A___
GAM2117 TGFBR2   3' TCAGTATTTTTAGGAACTACA  17482          _    C
                                TCAGTATTTTT GGAAT ATA
                                |||||||||| ||||| |||
                                AGTCATAAAAA CCTTG TGT
                                     T    A
GAM2117 FMR2     3' TAATTTAAAAATTTAAAAAGT  12977          _
                                TAATTTAAAA TTTAAAAAGT
                                |||||||||| ||||||||||
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                                ATTAAATTTT AAATTTTTCA
                                      T
GAM2117  PARG     3'  CTAATTTAAAAAGAAAAAAGTA 18855          TTT
                                CTAATTTAAAA   AAAAAGTA
                                ||||||||||   ||||||||
                                GATTAAATTTT   TTTTTCAT
                                   TCT
GAM2118  ADAMTS1  3'  CTGCTTTTTTTCCATTGT    28112        CC    GAG
                                CTGCTTTT  TCCA   GT
                                ||||||||  ||||   ||
                                GACGAAAA  AGGT   CA
                                    AA    AA_
GAM2118  CA14     5'  TCTGCTTTTCTTGCTGTCT   29062         CTCCAGAG
                                TCTGCTTTTC       GTCT
                                ||||||||||       ||||
                                AGACGAAAAG       CAGA
                                    AACGA___
GAM2118  CCR9     3'  TCTGCTTTTGCGGTCT      36299         CCTCCAGA
                                TCTGCTTTT       GGTCT
                                |||||||||       |||||
                                AGACGAAAA       CCAGA
                                    CG_____
GAM2118  CSNK1D   3'  TCTGCTTTTCTTCCCAGCCCCG 12469          C   AG  G
            T                    TCTGCTTTTC TCC  AG TCTGT
                                ||||||||||  |||  ||  |||||
                                AGACGAAAAG AGG  TC GGGCA
                                    A   G_  G
GAM2118  EFNA1    3'  TGCTTTTCCTTCAGTCAGT    20705          C   A_
                                TGCTTTTCCT CAG  GGT
                                ||||||||||  |||  |||
                                ACGAAAAGGA GTC  TCA
                                    A   AG
GAM2118  FBXW7    3'  TCTTCTTTTCCTTCTTAGTCTG 37970     G       CCAGA
            T                    TCT CTTTTCCT     GGTCTGT
                                |||  ||||||||     |||||||
                                AGA GAAAAGGA     TCAGACA
                                  A       AGAA_
GAM2118  FUT4     3'  TCTGCTTTATTTTCACATCTGT 13017         TCCTC  GAG
                                TCTGCTTT    CA   GTCTGT
                                ||||||||    ||   ||||||
                                AGACGAAA    GT   TAGACA
                                    TAAAA  G__
GAM2118  IFIT4    3'  TCTGTTTTCCTCCTCT      43371      C       AGAGG
                                TCTG TTTTCCTCC     TCT
                                ||||  |||||||||     |||
                                AGAC AAAAGGAGG     AGA
                                  _       _____
GAM2118  LAMC1    3'  TGCTTCTCTTTAAACTCTGT   14096         CTCCA   G
                                TGCTTTTC    GAG TCTGT
                                ||||||||    ||| |||||
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                                ACGAAGAG    TTT AGACA
                                    AAA__   G
GAM2118 POU2F2   3' CCTGGACCTCCAGGGGTCTGT 15460     CTTTT     A
                                TCTG    CCTCCAG GGTCTGT
                                ||||    ||||||| |||||||
                                GGAC    GGAGGTC CCAGACA
                                  CT___     C
GAM2118 PPP1R12B 5' TCTGCTTCTTGAAGGTCTG   36981       CCTCCA
                                TCTGCTTTT    GAGGTCTG
                                |||||||||    ||||||||
                                AGACGAAGA    TTCCAGAC
                                    AC____
GAM2118 PPP2R5E  3' TGTTTTTTCCCAGAGGC    26482    C   CC
                                TG TTTT  TCCAGAGGT
                                || ||||  |||||||||
                                AC AAAA  GGGTCTCCG
                                 _   AA
GAM2118 PTMA     3' TCTTTTTTCCTCCCCT     15877    GC      AGAGG
                                TCT  TTTTCCTCC    TCT
                                |||  |||||||||    |||
                                AGA  AAAAGGAGG    GGA
                                 A_       _____
GAM2118 PTPN22   3' TGCTTTTCTTTTAAAAGC   31985       CTCC
                                TGCTTTTC   AGAGGT
                                ||||||||   ||||||
                                ACGAAAAG   TTTTCG
                                    AAAA
GAM2118 SLC4A1   3' TCTGCTTTTCCTTGGAAGGT  7358          CCA
                                TCTGCTTTTCCT  GAGGT
                                ||||||||||||  |||||
                                AGACGAAAAGGA  TTCCA
                                      ACC
GAM2118 SNX6     3' TGCTTTTCTTCAGAAAT    34567       CTC
                                TGCTTTTC  CAGAGGT
                                ||||||||  |||||||
                                ACGAAAAG  GTCTTTA
                                    AA_
GAM2118 SPAG11   3' TCTCTTTTCCTTCTTCATCTGT 38480    G      CCAGAG
                                TCT CTTTTCCT     GTCTGT
                                ||| ||||||||     ||||||
                                AGA GAAAAGGA     TAGACA
                                 _       AGAAG_
GAM2118 SPON1    3' TCTGTTTTTCCCCAGGAACT  41670     C     T   A GT
                                TCTG TTTTCC CCAG G  CT
                                |||| |||||| |||| |  ||
                                AGAC AAAAGG GGTC C  GA
                                  A     _   _ TT
GAM2118 TRIM14   3' TCTGCTTTCTTTCAGGACCT  37709       CCTC   A GT
                                TCTGCTTTT   CAG G  CT
                                |||||||||   ||| |  ||
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                                AGACGAAAG   GTC C  GA
                                     AAA_   _ TG
GAM2118 WBSCR14  3' TCTGCTCAGGAACAGAGGTCTG 37288       TTCCTC
             T                    TCTGCTT     CAGAGGTCTGT
                                  |||||||     ||||||||||
                                  AGACGAG     GTCTCCAGACA
                                      TCCTT_
GAM2118 ZNF261   3' TGCCTTGGGAGGTCTG     22995       TCCTCCA
                                  TGCTTT      GAGGTCTG
                                  ||||||      ||||||||
                                  ACGGAA      CTCCAGAC
                                     CC_____
GAM2118 CD83     3' CTCAGCAATAAATGCCTTTGGA 20136     AG     CAGA
                                  CTCA  AATAAG   CCTTTGGA
                                  ||||  ||||||   ||||||||
                                  GAGT  TTATTT   GGAAACCT
                                    CG     AC__
GAM2118 CSNK1G2  3' CTCGAGAAAACGGCCTTTGGA  10613    A   TA  AGA
                                  CTC AGAA  AGC   CCTTTGGA
                                  ||| ||||  |||   ||||||||
                                  GAG TCTT  TTG   GGAAACCT
                                    C    __   CC_
GAM2118 DAPP1    3' CTAAGAGTGAGCAGACCT    30815    C   ATA
                                  CT AAGA   AGCAGACCT
                                  || ||||   |||||||||
                                  GA TTCT   TCGTCTGGA
                                   _    CAC
GAM2118 KCNA5    3' AAAAATAGGCGACCCTTGG    40679       A  A
                                  AAGAATA GC GACCTTTGG
                                  ||||||| || |||||||||
                                  TTTTTAT CG CTGGGAACC
                                     C  _
GAM2118 PTPN1    3' CTCAAGAAGAGTGTTGACTTGG 15901        TAAGCA_  CT
             A                    CTCAAGAA      GAC  TTGGA
                                  ||||||||      |||  |||||
                                  GAGTTCTT      CTG  AACCT
                                       CTCACAA   __
GAM2118 RAB6A    3' CTCAAGAATAATTTTG      16103          GCAGACC
                                  CTCAAGAATAA      TTTG
                                  ||||||||||       ||||
                                  GAGTTCTTATT      AAAC
                                        A_______
GAM2118 SERPINA3 3' CCAAGGATAAGCAGACAGG   41456      A       CTTT
                                  TCAAG ATAAGCAGAC    GG
                                  ||||| ||||||||||    ||
                                  GGTTC TATTCGTCTG    CC
                                    C        T___
GAM2118 SEZ6L    3' TCAAGGCCCCCAGGGCCTTTGG 34425      AATAAG  A_
             A                    TCAAG     CAG  CCTTTGGA
                                  |||||     |||  ||||||||
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                                AGTTC     GTC  GGAAACCT
                                   CGGGG_   CC
GAM2118  SHC1     3'  CTCAAGAATAAGCAATGG    16698            ACCTT
                                CTCAAGAATAAGCAG    TGG
                                |||||||||||||||    |||
                                GAGTTCTTATTCGTT    ACC
                                                  _____
GAM2119  CD1D     5'  CCCTTTCCGCTGGGTGCCAGC  44297      GC  GG      A
                                CCCT  TC  GCTGGGT CCAGC
                                ||||  ||  ||||||| |||||
                                GGGA  AG  CGACCCA GGTCG
                                  A_  G_      C
GAM2119  CENPA    5'  CCTGCTCGGGCTGCCGGGT    12231           ___
                                CCTGCTCGGGCT   GGGT
                                ||||||||||||   ||||
                                GGACGAGCCCGA   CCCA
                                       CGG
GAM2119  CRABP2   3'  ACCCTGCTCTGGGCTGGTTTGG 12426         _      GTACCA
            GGC                    ACCCTGCTC GGGCTGG     GC
                                |||||||||  |||||||     ||
                                TGGGACGAG CCCGACC     CG
                                     A      AAACCC
GAM2119  CRY2     3'  CCCTGGCTGGGTGTCAGC    43580      GCTCG       AC
                                CCCT    GGCTGGGT  CAGC
                                ||||    ||||||||  ||||
                                GGGA    CCGACCCA  GTCG
                                  _____       CA
GAM2119  DUOX1    5'  ACCCTGCTTTGGCCCAGC    32651        CG    G
                                ACCCTGCT  GGCT GGT
                                ||||||||  |||| |||
                                TGGGACGA  CCGG TCG
                                     AA    G
GAM2119  HMG20A   3'  CCTTGCTGGGGCTGGGAC    32868    C    C       T
                                CC TGCT GGGCTGGG AC
                                || |||| |||||||| ||
                                GG ACGA CCCGACCC TG
                                 A    C       _
GAM2119  HUNK     5'  CCCTGCTCGGGCGCGCGGG    31061           ___
                                CCCTGCTCGGGC   TGGG
                                ||||||||||||   ||||
                                GGGACGAGCCCG   GCCC
                                       CGC
GAM2119  KIF5A    5'  ACTCTTCTTGGGCTGCAGGGGT 22546    C  G  C    ____
                                AC CT CT GGGCT    GGGT
                                || || || |||||    ||||
                                TG GA GA CCCGA    CCCA
                                 A  A  A    CGTC
GAM2119  LASS1    3'  CCCGGCTCGGGCGCTCAG    34594     T       TGG  AC
                                CCC GCTCGGGC   GT  CAG
                                ||| ||||||||   ||  |||
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                                GGG CGAGCCCG   CG  GTC
                                  C       ___  A_
GAM2119  MEN1     5'  CCGCTTTAGCTGGGTATCAG   39170      CG       C
                                CTGCT  GGCTGGGTA CAG
                                |||||  ||||||||| |||
                                GGCGA  TCGACCCAT GTC
                                   AA        A
GAM2119  MYLK2    3'  CCCTGTCTGGGGAGGTGCTAGC 37519      _ C   CT    ACC
                                CCCTG CT GGG  GGGT   AGC
                                ||||| || |||  ||||   |||
                                GGGAC GA CCC  TCCA   TCG
                                   A  C   __    CGA
GAM2119  SCN4A    3'  GCTCGGGCCTGGGTGTCAG    7322         _    AC
                                GCTCGGGC TGGGT  CAG
                                |||||||| |||||  |||
                                CGAGCCCG ACCCA  GTC
                                     G    CA
GAM2119  SDS      3'  ACCCTGCTCTGGGTACC     27765         GGGC
                                ACCCTGCTC    TGGGTACC
                                |||||||||    ||||||||
                                TGGGACGAG    ACCCATGG
                                             ____
GAM2119  SIAH2    5'  CCTGCTCGGGCTGCGGGC     22862          __
                                CCTGCTCGGGCT  GGGT
                                ||||||||||||  ||||
                                GGACGAGCCCGA  CCCG
                                      CG
GAM2119  SKP2     5'  CTGCTCGGGCCCCCAG      37209          GGGTA
                                CTGCTCGGGCT    CCAG
                                ||||||||||     ||||
                                GACGAGCCCGG    GGTC
                                      G____
GAM2119  SLC25A19 3'  ACCCCGCTTGGGGCAGCTGGC  34709        C_   TG__
                                ACCCTGCT  GGGC    GGT
                                ||||||||  ||||    |||
                                TGGGGCGA  CCCG    CCG
                                     AC    TCGA
GAM2119  SOX12    3'  CCTGCTGTGGGTGCCAG     28034       CGGGC    A
                                CCTGCT    TGGGT CCAG
                                ||||||    ||||| ||||
                                GGACGA    ACCCA GGTC
                                   C____     C
GAM2119  TRAP100  3'  ACTCTCCTCAGGTGCCAG    31347    C  G     C  GGTA
                                AC CT CTCGGG TG    CCAG
                                || || |||||| ||    ||||
                                TG GA GAGTCC AC    GGTC
                                 A  G     _ _____
GAM2119  YY1      5'  ACTCTGCTCGGGCCCGGC    18161    C         G
                                AC CTGCTCGGGCT GGT
                                || ||||||||||| |||
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                                TG GACGAGCCCGG CCG
                                 A         G
GAM2119 LEP      3'  CTCACGTAATGCTCTGGGTA   6914            ___
                                CTCGCGTAATGCT   GGTA
                                ||||||||||||   ||||
                                GAGTGCATTACGA   CCAT
                                      GAC
GAM2120 CENPF    3'  TGTGCACATTTTCCTTAAAAAC 32284        CC    GC_  TT
              AC                   TGTGCACA  TTTCC   GG  CAC
                                ||||||||  |||||   ||  |||
                                ACACGTGT  AAAGG   TT  GTG
                                     A_    AAT  TT
GAM2120 LPIN2    3'  TGGCACACCTTTCCCTGGT   31224    T         GC
                                TG GCACACCTTTCC  GGT
                                || ||||||||||||  |||
                                AC CGTGTGGAAAGG  CCA
                                 _          GA
GAM2120 DDX15    3'  TAAACTGCAAAACAT       10678           AGG
                                TAAACTGCGAA   GCGT
                                ||||||||||   ||||
                                ATTTGACGTTT   TGTA
                                          ___
GAM2121 CNTN3    3'  TATCAAAAGTCTGAAGTATG   42486      TAGTTCG
                                TATC      TTGAAGTATG
                                ||||      |||||||||
                                ATAG      GACTTCATAC
                                  TTTTCA_
GAM2121 MAT2A    3'  TATCTGGTACCAAAGTGTGCAA 25405       A  TCG TG    A
                                TATCT GT   T  AAGT TGCAA
                                ||||| ||   |  |||| |||||
                                ATAGA CA   G  TTCA ACGTT
                                   C  T__ GT    C
GAM2121 NRL      3'  TATCTAGTTGTTGGATAT    26136         C    AA
                                TATCTAGTT GTTG  GTAT
                                |||||||| ||||  ||||
                                ATAGATCAA CAAC  TATA
                                      _   C_
GAM2121 NRIP1    3'  CTGTAAGATGCAGCAGAGAATA 40961     C     A  T  T
                                TTG AAGAT CG GT AGAGAATA
                                ||| ||||| || || ||||||||
                                GAC TTCTA GT CG TCTCTTAT
                                  A    C  _  _
GAM2121 SMARCA3  3'  TTGGAAGATACGTGAAAAT   40058     C       GTTA
                                TTG AAGATACGT    GAGAAT
                                ||| |||||||||    ||||||
                                AAC TTCTATGCA    CTTTTA
                                  C       _____
GAM2121 SOX12    3'  TTGCAAGATGTTTATTAGGAAT 28064         ACG     A
              A                    TTGCAAGAT   TGTTAG GAATA
                                |||||||||   |||||| |||||
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                                AACGTTCTA  ATAATC CTTAT
                                     CAA    _
GAM2121  ZNF264   3'  TTGTAAAATACGTGTGAGAGA  18278    C        T
                                TTG AAGATACGTGT AGAGA
                                ||| |||||||||| |||||
                                AAC TTTTATGCACA TCTCT
                                  A         C
GAM2122  BRCA2    3'  CCCTTTTTTTTTTTTCTTCGTAA 6292      GCG_
            A                    CCCT   TTTTTTCTTCGTAAA
                                ||||   ||||||||||||||
                                GGGA   AAAAAAGAAGCATTT
                                  AAAA
GAM2122  CLOCK    3'  ACCCCTTCTTTTTTCTTTGTA  22213      GCG       C
                                ACCCT  TTTTTTCTT GTA
                                |||||  ||||||||| |||
                                TGGGG  AAAAAAGAA CAT
                                   AAG       A
GAM2122  MAD2L1   3'  TGGTTTTCTCCATGTAAAA   14312    C       TC
                                TG GTTTTTTCT  GTAAAA
                                || |||||||||  ||||||
                                AC CAAAAGAGG  CATTTT
                                 _       TA
GAM2122  NRXN2    3'  TGCGTTTCCTCTTCGTAA    31493
                                TGCGTTTTTTCTTCGTAA
                                ||||||||||||||||||
                                ACGCAAAGGAGAAGCATT

GAM2122  PPP1R12A 3'  TGCGCTTTTTTTTCCTTAAAA  14729         C  G_
                                TGCGTTTTTT TTC  TAAAA
                                |||||||||| |||  |||||
                                ACGCGAAAAA AAG  ATTTT
                                      A  GA
GAM2122  ST7      3'  ACCCTGCATTTTTTCTTTTTAA 30262             CG
            A                    ACCCTGCGTTTTTTCTT  TAAA
                                ||||||||||||||||  ||||
                                TGGGACGTAAAAAAGAA  ATTT
                                          AA
GAM2122  TNS      3'  ACTCCTGCTGGGGTCTTTGTA  35462    _    GTTTTT   C
                                AC CCTGC     TCTT GTA
                                || |||||     |||| |||
                                TG GGACG     AGAA CAT
                                 A    ACCCC_   A
GAM2122  USP6     5'  CCTTGTTAGTTTCTTCGTA   45029     GC  T_
                                CCT  GTT  TTTCTTCGTA
                                |||  |||  ||||||||||
                                GGA  CAA  AAAGAAGCAT
                                  A_  TC
GAM2122  STK6     3'  CCTGTGAAGACACCATGCCTA  18774    GC_     T   A
                                CC   GAAGATG CTGT CCTA
                                ||   ||||||| |||| ||||
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                                GG   CTTCTGT GGTA GGAT
                                 ACA      _   C
GAM2123  NFIA     3'  CACCATATGAGAAATTAC    43207         T_
                                CACTATGTG  AAATTAC
                                |||||||||  |||||||
                                GTGGTATAC  TTTAATG
                                     TC
GAM2123  CLC      3'  GTTAATCTCATCTCTTTTTGTG 29901    CAA__    A_
              TA                  GT    TCGTC  TTTTTGTGTA
                                ||    |||||  ||||||||||
                                CA    AGTAG  AAAAACACAT
                                 ATTAG    AG
GAM2123  TBX22    3'  GTCATTGTCAATGTGTAA    32624     ATC    TTTT
                                GTCA   GTCA    TGTGTAA
                                ||||   ||||    |||||||
                                CAGT   CAGT    ACACATT
                                  AA_    T___
GAM2124  KRTHA8   3'  AAGAGGCTGTGTTGCCACA    27667     A     CTA
                                AAGA GCTGTG   CTATA
                                |||| ||||||   |||||
                                TTCT CGACAC   GGTGT
                                  C     AAC
GAM2124  TAF1C    3'  AAGAAACTACTACTGTATTTTG 24987         GT     A
                                AAGAAGCT  GCTACT TATTTTG
                                ||||||||  |||||| |||||||
                                TTCTTTGA  TGATGA ATAAAAC
                                     __      C
GAM2124  TEM5     3'  GAAGCTGGTTTGACATTTTG   37233        TGCTACT
                                GAAGCTG      ATATTTTG
                                |||||||      ||||||||
                                CTTCGAC      TGTAAAAC
                                   CAAAC__
GAM2124  AARS     3'  CAACAGCAATGCGGGGTT    11486      TG   TCA  A
                                CAACA  GTA   GC GGGTT
                                |||||  |||   || |||||
                                GTTGT  CGT   CG CCCAA
                                   __   TA_  C
GAM2124  ACVR1B   3'  AACAATGAAACAGCAGGGTT   33754      _   TAT
                                AACA TGG   CAGCAGGGTT
                                |||| |||   ||||||||||
                                TTGT ACT   GTCGTCCCAA
                                  T   TT_
GAM2124  ADAMTS1  3'  CATATTCCCAAAGCAGGGTT   28110      GTA   __
                                CATG   TCA  GCAGGGTT
                                ||||   |||  ||||||||
                                GTAT   GGT  CGTCCCAA
                                  AAG   TT
GAM2124  AP2B1    3'  CAACTGGTATGAAACAGGGTT  10480      A     C_
                                CAAC TGGTAT  AGCAGGGTT
                                |||| ||||||  |||||||||
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                                GTTG ACCATA  TTGTCCCAA
                                  _     CT
GAM2124 BAP1    3' CAACATGGTGGCATGT     21642        ATCA  GG
                                CAACATGGT   GCA  GT
                                |||||||||   |||  ||
                                GTTGTACCA   CGT  CA
                                     C___   A_
GAM2124 BSN     3' CATGGTGGCAGGGTT      18395       ATCA
                                CATGGT   GCAGGGTT
                                ||||||   ||||||||
                                GTACCA   CGTCCCAA
                                   C___
GAM2124 CBFA2T2 3' CAAGTCTGAACAGCAGGGTT 22968   T   AT___
                                A GGT    CAGCAGGGTT
                                | |||    ||||||||||
                                G TCA    GTCGTCCCAA
                                 T  GACTT
GAM2124 CLC     3' CAAAGTGGGAGCAGGGTT   29893    CA   TATC
                                CAA  TGG   AGCAGGGTT
                                |||  |||   |||||||||
                                GTT  ACC   TCGTCCCAA
                                  TC  C___
GAM2124 DIRC1   3' AACATGATATAGGT       38123        CAGCA
                                AACATGGTAT    GGGT
                                ||||||||||    ||||
                                TTGTACTATA    TCCA
                                              _____
GAM2124 DRD3    3' TGGTATAGATCACAGGGTT   38016      CA___
                                TGGTAT    GCAGGGTT
                                ||||||    ||||||||
                                ACCATA    TGTCCCAA
                                   TCTAG
GAM2124 FRAP1   3' CAACATGGTGTCTAGACA    22437        A  _  _
                                CAACATGGT TC AG CA
                                ||||||||| || || ||
                                GTTGTACCA AG TC GT
                                     C  A  T
GAM2124 GSS     3' TGACAGGAGTGGGGCAGGGTT 6759    A   T  TATCA_
                                C ACA GG     GCAGGGTT
                                | ||| ||     ||||||||
                                A TGT CC     CGTCCCAA
                                 C   _  TCACCC
GAM2124 HMGN1   3' CAACATGGTAATAGAAG    22448        TC  C
                                CAACATGGTA  AG AGG
                                ||||||||||  || |||
                                GTTGTACCAT  TC TTC
                                      TA  _
GAM2124 IGF1    3' TGACATGGTATTTGGGGCC   8355    A      CAGCA
                                C ACATGGTAT    GGGTT
                                | |||||||||    |||||
```

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                                A TGTACCATA    CCCGG
                                 C       AAC__
GAM2124 IRAK1    3' TGGCATGGAGGCAGGGTT   11476      CA__
                                TGGTAT   GCAGGGTT
                                ||||||   ||||||||
                                ACCGTA   CGTCCCAA
                                   CCTC
GAM2124 ITPKB    3' CATGTATGCAGGCAGGGTT  13643     G  _  _
                                CATG TAT CAG CAGGGTT
                                |||| ||| ||| |||||||
                                GTAC ATA GTC GTCCCAA
                                  _  C  C
GAM2124 LEP      3' CAAAGTGCAAGCAGGGTT   6910     T  ATC
                                CA GGT  AGCAGGGTT
                                || |||  |||||||||
                                GT TCA  TCGTCCCAA
                                 T  CGT
GAM2124 LZTR1    3' CAGCATAGAGCAGGGTT    27632    A    TATC
                                CA CATGG   AGCAGGGTT
                                || |||||   |||||||||
                                GT GTATC   TCGTCCCAA
                                 C   ____
GAM2124 MAPRE2   3' CATGGTGCAGAGCC       30689      ATCA
                                CATGGT   GCAGGGTT
                                ||||||   ||||||||
                                GTACCA   CGTCTCGG
                                   ____
GAM2124 NKX3A    3' TGACAGATTGGAGCAGGGTT  26117   A  T  ATC
                                C ACA GGT  AGCAGGGTT
                                | ||| |||  |||||||||
                                A TGT CTA  TCGTCCCAA
                                 C  _  ACC
GAM2124 NOTCH2   3' CAACAGACACGCAGGGTT   35905     T GT  CA
                                CAACA G  AT  GCAGGGTT
                                ||||| |  ||  ||||||||
                                GTTGT C  TG  CGTCCCAA
                                   _ TG  __
GAM2124 PDGFRB   3' CAACCTGCAATGCAGGGTT  42333    ATG  TCA
                                CAAC   GTA  GCAGGGTT
                                ||||   |||  ||||||||
                                GTTG   CGT  CGTCCCAA
                                  GA_  TA_
GAM2124 PIM1     3' ACAGTTCCATGGCAGGGTT   44961     A  __
                                ATGGT TCA  GCAGGGTT
                                ||||| |||  ||||||||
                                TGTCA GGT  CGTCCCAA
                                   A  AC
GAM2124 PRKAB1   5' CGGCTGAGTCGGCAGGGTT   26503     A___  A
                                TGGT   TC GCAGGGTT
                                ||||   || ||||||||
```

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                                GCCG   AG CGTCCCAA
                                  ACTC  C
GAM2124 RARB    5' TGGCAGACGAAGCAGGGTT   32064      TC___
                                TGGTA    AGCAGGGTT
                                |||||    |||||||||
                                ACCGT    TCGTCCCAA
                                   CTGCT
GAM2124 SCD     3' ACACTGTGTTCAGCAGGGTT  22816     G  A_
                                ACAT GT  TCAGCAGGGTT
                                |||| ||  ||||||||||
                                TGTG CA  AGTCGTCCCAA
                                  A  CA
GAM2124 SCNN1A  3' TAATGGTGTCTGAGCAGGGTT 9783    C    A __
                                A ATGGT TC  AGCAGGGTT
                                | ||||| ||  |||||||||
                                A TACCA AG  TCGTCCCAA
                                 T    C  AC
GAM2124 TCF7L2  3' AACAAAGCAGCGGGGTT    36247     T  TAT   A
                                AACA GG   CAGC GGGTT
                                |||| ||   |||| |||||
                                TTGT TC   GTCG CCCAA
                                  T ____   C
GAM2124 TPTE    3' AACATGTGGCAGGGTT     30020       GTATCA
                                AACATG     GCAGGGTT
                                ||||||     ||||||||
                                TTGTAC     CGTCCCAA
                                   AC_____
GAM2124 TRAP240 3' CAATGAAAAATAGCAGGGTT  23056   _  TATC_
                                CA TGG     AGCAGGGTT
                                || |||     |||||||||
                                GT ACT     TCGTCCCAA
                                 T   TTTTA
GAM2125 FCMD    3' CTGTATTAGGTTGGGTTAGAAG 27517         C_  T  C
                                CTGTATTAG  TG GT AGAAG
                                |||||||||  || || |||||
                                GACATAATC  AC CA TCTTC
                                      CA  C  A
GAM2125 LDHB    5' TGTCTGTGTGTGGTCAGAA   14126    C   ATTAGC   _
                                TG CTGT     TGTG TCAGAA
                                || ||||     |||| ||||||
                                AC GACA     ACAC AGTCTT
                                 A   C______   C
GAM2125 CCKBR   3' AGGCCTGATGGTATT       8811       ATAG  A
                                AGGCT    GA TGGTATT
                                |||||    || |||||||
                                TCCGG    CT ACCATAA
                                   A___  _
GAM2125 CIT     3' CAGGAGCTATGGGATGGTATT 43043     __    A   A
                                CAG  GCTAT GGA TGGTATT
                                |||  ||||| ||| |||||||
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                                GTC  CGATA CCT ACCATAA
                                  CT    C  _
GAM2125  CNTNAP2  3'  AACAGCTGGTCACCATGGTATT 30479      G  ATAGGA_
                                AACAG CT      ATGGTATT
                                ||||| ||      ||||||||
                                TTGTC GA      TACCATAA
                                  _  CCAGTGG
GAM2125  MS4A2    3'  AACAGGTTAGTAGGAAATCAC  34978      C  _     TGG
                                AACAGG TA TAGGAA   TAT
                                |||||| || ||||||   |||
                                TTGTCC AT ATCCTT   GTG
                                   A  C     TA_
GAM2125  PAX4     3'  GGCAGGATGGTATT       26198     TAT    A
                                GGC   AGGA TGGTATT
                                |||   |||| |||||||
                                CCG   TCCT ACCATAA
                                  ____   _
GAM2125  PCMT1    3'  AACAAGCTGTGATGGT      23937        ATAG  A
                                AACAGGCT    GA TGGT
                                ||||||||    || ||||
                                TTGTTCGA    CT ACCA
                                     CA__  _
GAM2125  PIK3C2B  3'  AGGGGTAGAAAATGGTATT    15289     CTA     _
                                AGG   TAGGAA TGGTATT
                                |||   |||||| |||||||
                                TCC   ATCTTT ACCATAA
                                  CC_     T
GAM2125  PMX1     3'  GACTAAATGGTATT       35510       TAGG
                                GGCTA    AATGGTATT
                                |||||    |||||||||
                                CTGAT    TTACCATAA
                                   _____
GAM2125  PPP1R12B 3'  AGTTGTGAAGGAATGGTATT   36965    GCTAT_
                                AG      AGGAATGGTATT
                                ||      ||||||||||||
                                TC      TCCTTACCATAA
                                 AACACT
GAM2125  PSEN1    3'  AACAGGCTATGGTTGTGT    6169           A  AATG
                                AACAGGCTAT GG    GT
                                |||||||||| ||    ||
                                TTGTCCGATA CC    CA
                                      _  AACA
GAM2125  RAB23    3'  AACAAGGTTATAGAAATG    32216      _  C
                                AACA GG TATAGGAATG
                                |||| || ||||||||||
                                TTGT CC ATATCTTTAC
                                  T  A
GAM2125  TEM8     3'  AGGTCCTAATGATGGTATT   32856     _  A   GA
                                AGG CT TAG  ATGGTATT
                                ||| || |||  ||||||||
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                                TCC GG ATT  TACCATAA
                                  A  _   AC
GAM2125  TUFT1    3'  AGGCTATAGAACTTTGGTATT  33506          A__
                                AGGCTATAGGA   TGGTATT
                                ||||||||||   |||||||
                                TCCGATATCTT   ACCATAA
                                      GAA
GAM2126  ACADL    3'  ACCTTATATTGGAAAACTAG   11495        C   ___
                                ACCTTATA TGGA   CTAG
                                |||||||| ||||   ||||
                                TGGAATAT ACCT   GATC
                                     A    TTT
GAM2126  CALU     3'  TACCCTATATTGGGGCTAA    10262        C  A_
                                TACCTTATA TGG  CTAG
                                ||||||||| |||  ||||
                                ATGGGATAT ACC  GATT
                                      A   CC
GAM2126  D10S170  3'  CTTATACTGGGTGAAATG    24133         ACT_
                                CTTATACTGG    AGTG
                                ||||||||||    ||||
                                GAATATGACC    TTAC
                                      CACT
GAM2126  IDH3A    3'  CTTATACTGGTACTGC      24374         AC  G
                                CTTATACTGG  TA TGC
                                |||||||||  || |||
                                GAATATGACC  AT ACG
                                      __  G
GAM2126  TP63     3'  CCTCGCTTTGGCTAGTGCCAA  18996     ATAC   A
                                CCTT    TGG CTAGTGCCAA
                                ||||    ||| ||||||||||
                                GGAG    ACC GATCACGGTT
                                  CGAA   _
GAM2126  EMP1     5'  GTGTGTAATTTTGCGGTG    10897         GAT  _
                                GTGTGTAATTT   TG GGTG
                                ||||||||||   || ||||
                                CACACATTAAA   AC CCAC
                                      ___  G
GAM2126  VHL      3'  GTAGTGTGTAATTTTTTATAGT 8115           GATTG
              G                  GTAGTGTGTAATTT    GGTG
                                 ||||||||||||||    ||||
                                 CATCACACATTAAA    TCAC
                                       AAATA
GAM2127  ATP6V0C  3'  AGGGGGTGGGGCGCCGG     44554     AA       GGCG
                                AGG  GTGGGGCGC    TGG
                                |||  |||||||||    |||
                                TCC  CACCCCGCG    GCC
                                  CC        _____
GAM2127  ATRX     3'  TGGGGGAGAGGGGCGTGG    39614    A  A  T     C
                                TG GG AG GGGGCG GG
                                || || || |||||| ||
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                                AC CC TC CCCCGC CC
                                 C  C  T     A
GAM2127  BTAF1    5'  GGGAGCGGCCGGTGCGGCGTGG 43668    A    __  C
                G                GG AGTGG  GG GCGGCGTGGG
                                 || |||||  || ||||||||||
                                 CC TCGCC  CC CGCCGCACCC
                                  C    GG  A
GAM2127  CCND1    3'  GAGGGGTGGGGCGGGGTGGG  38207     AA      C  C
                                 GAGG  GTGGGGCG GG GTGGG
                                 ||||  |||||||| || |||||
                                 CTCC  CACCCCGC CC CACCC
                                   C_       _ _
GAM2127  DMPK     3'  TGAGGAGGGGGGCGCGG     20624       A T
                                 TGAGGA G GGGGCGCGG
                                 |||||| | |||||||||
                                 ACTCCT C CCCCGCGCC
                                     _ C
GAM2127  DSC2     5'  GAGGAGGTGGGGCGCGCG    22392      A        G
                                 GAGGA GTGGGGCGCG CG
                                 ||||| ||||||||||  ||
                                 CTCCT CACCCCGCGC GC
                                    C        _
GAM2127  EPHX1    3'  TGAGGGGGTGAGCGTG      6519       AAGT   GCGC
                                 TGAGG   GGG   GGCGTG
                                 |||||   |||   ||||||
                                 ACTCC   CCC   TCGCAC
                                    _____  AC__
GAM2127  GAN      3'  TGAGAAGTGGGGTAAAGTGGG  35152     G      CGCGGC
                                 TGAG AAGTGGGG     GTGGG
                                 |||| ||||||||     |||||
                                 ACTC TTCACCCC     CACCC
                                   _       ATTT__
GAM2127  GARP     3'  TGGAGAAGTGGGGCTG      24320    AG       GCGGCG
                                 TG  GAAGTGGGGC     TG
                                 ||  ||||||||||     ||
                                 AC  CTTCACCCCG     AC
                                  CT        _______
GAM2127  ITGA11   3'  TGAGGGAGGCCTTGGCGTGGG  29206      AAGT    GC_
                                 TGAGG   GGGGC   GGCGTGGG
                                 |||||   |||||   ||||||||
                                 ACTCC   CTCCG   CCGCACCC
                                    _____    GAA
GAM2127  NOTCH3   3'  TGAGGGAGGTGGGGTGG     7741       AA_     CGCGGCG
                                 TGAGG   GTGGGG     TGG
                                 |||||   ||||||      |||
                                 ACTCC   CACCCC     ACC
                                    CTC     ________
GAM2127  OGDH     3'  GAGGAGGGCGGTGGTGTGGG  45012      AGTG    C_  C
                                 GAGGA   GGGCG  GG GTGGG
                                 |||||   |||||  || |||||
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                                CTCCT   CCCGC  CC CACCC
                                  _____    CA  A
GAM2127  RCE1    3'  TGGGGGGTGGGGGGGTGG    23071    A  AA     CGCG C
                                TG GG  GTGGGG   G GTGG
                                || ||  ||||||   | ||||
                                AC CC  CACCCC   C CACC
                                 _  CC     _____ _
GAM2127  SPTAN1  5'  CGGGGGGTGAGGGGCGTGGG  17101    A  AA     CGC
                                TG GG  GTGGGG   GGCGTGGG
                                || ||  ||||||   ||||||||
                                GC CC  CACTCC   CCGCACCC
                                 _  CC     ____
GAM2127  WNT7A   5'  GAGGAGCGAGCGCGGCGTGGG  21526      A    G
                                GAGGA GTGGG CGCGGCGTGGG
                                ||||| ||||| ||||||||||
                                CTCCT CGCTC GCGCCGCACCC

                                  _    _
GAM2127  CHRNB1  3'  TTTTAGACGCAGGTACA     41313          CATTT
                                TTTTAGACGC    TACA
                                ||||||||||    ||||
                                AAAATCTGCG    ATGT
                                      TCC__
GAM2127  DTNB    3'  TTTTAGGCCATTTTACA     37611       AC
                                TTTTAG  GCCATTTTACA
                                ||||||  ||||||||||
                                AAAATC  CGGTAAAATGT

                                  __
GAM2127  FHL1    3'  TTCAAATGCCATTTTACA     11101       C
                                TTTAGA GCCATTTTACA
                                |||||| ||||||||||
                                AAGTTT CGGTAAAATGT
                                   A
GAM2127  NYX     3'  GTTTTAAACGCCTCCTA     35446           A
                                GTTTTAGACGCC TTTTA
                                |||||||||||| |||||
                                CAAAATTTGCGG AGGAT

                                  _
GAM2127  PTPN2   3'  ATTTTAGACAGCCATTTACA   15909         _      T
                                GTTTTAGAC GCCATTT ACA
                                ||||||||| ||||||| |||
                                TAAAATCTG CGGTAAA TGT
                                      T     _
GAM2127  RAI2    3'  GTTTTAAATGCCTTTTTA    34746        C   A
                                GTTTTAGA GCC TTTTA
                                |||||||| ||| |||||
                                CAAAATTT CGG AAAAT
                                     A   A
GAM2127  RPP30   3'  GTTTTAGAGCCCTTACA     26938        C   AT
                                GTTTTAGA GCC  TTTACA
                                |||||||| |||  ||||||
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                                CAAAATCT CGG  GAATGT
                                      _  __
GAM2128 CNTN3    3'  TAGTGCTTTATGGTGATA    42484         CTAAAA
                                TAGTGCTTTA     GATA
                                ||||||||||     ||||
                                ATCACGAAAT     CTAT
                                     ACCA__
GAM2128 GPR85    3'  TAATGCTTTTACAGATAATA  33262         ACTAAA
                                TAGTGCTTT     AGATAATA
                                |||||||||     ||||||||
                                ATTACGAAA     TCTATTAT
                                     ATG___
GAM2128 LEPR     5'  GCCCCACTGAAGGATAAT    14133         A  A
                                GCTTTACT AA GATAAT
                                |||||||| || ||||||
                                CGGGGTGA TT CTATTA
                                     C  C
GAM2128 TUBG1    3'  CAGTGCTTTATTAAAGAT    41820         CTA
                                TAGTGCTTTA   AAAGAT
                                ||||||||||   ||||||
                                GTCACGAAAT   TTTCTA
                                     AA_
GAM2128 CELSR2   3'  GAAGGGTGTGAAGCCCTGGCT  10848      CA_   T   T
                                GAAGG   TGAA CCTT GGCT
                                |||||   |||| |||| ||||
                                CTTCC   ACTT GGGA CCGA
                                   CAC   C   _
GAM2128 ESR1     3'  AGGCATGAATTAAC       6524          CCTT
                                AGGCATGAAT    TGGC
                                ||||||||||    ||||
                                TCCGTACTTA    ATTG
                                      _____
GAM2128 IRTA2    3'  GAAGCATGAAAAGCCATGG   36339     G     TC_  T
                                GAAG CATGAA   CT TGG
                                |||| ||||||   || |||
                                CTTC GTACTT   GG ACC
                                   _     TTC  T
GAM2128 LIFR     3'  ACATGAGAATTCTTTGGCT    14158       __  C
                                GCATGA  AT CTTTGGCT
                                ||||||  || ||||||||
                                TGTACT  TA GAAACCGA
                                    CT  A
GAM2128 MASP1    3'  GAAGGATCCTTTGGCT      40098      CATGA
                                GAAGG    ATCCTTTGGCT
                                |||||    ||||||||||
                                CTTCC    TAGGAAACCGA
                                      _____
GAM2128 PLA2G4C  3'  GAAGGCATTGGTCTGAACT   43859        GAATCC    _
                                GAAGGCAT     TTTGG CT
                                ||||||||     ||||| ||
```

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                                CTTCCGTA     AGACT GA
                                    ACC___     T
GAM2128  PTGIS    3'  AAGGGACTCCTTTGG       9668       CAT  A
                                AAGG   GA TCCTTTGG
                                ||||   || ||||||||
                                TTCC   CT AGGAAACC
                                  ___  G
GAM2128  PTPRA    5'  TAGAAGGCATCGGC        38915         TGAATCCT
                                TAGAAGGCA       TTGGC
                                |||||||||       |||||
                                ATCTTCCGT       AGCCG

                                _________
GAM2128  RANBP9   3'  AGAAGGCAGGATTTTTGG    24245         T  ATCC
                                AGAAGGCA GA    TTTGG
                                |||||||| ||    |||||
                                TCTTCCGT CT    AAACC
                                    C  AA__
GAM2128  SFPQ     3'  TAGAAGCATGAATGGC      22859       G     TCCTT
                                TAGAAG CATGAA     TGGC
                                |||||| |||||||     ||||
                                ATCTTC GTACTT     ACCG

                                  _    ______
GAM2128  TP63     3'  AAGGGTGCCTCGCTTTGGCT   18989      CA  AA  _
                                AAGG  TG  TC CTTTGGCT
                                ||||  ||  || ||||||||
                                TTCC  AC  AG GAAACCGA
                                  C_  GG  C
GAM2129  CHES1    3'  ACGTTGACATCCCTGCG     23281         AT    GA
                                ACGTTGACG  TCTC  TGCG
                                |||||||||  ||||  ||||
                                TGCAACTGT  AGGG  ACGC

                                    __   __
GAM2129  HYAL3    5'  CAACGTTGGCCCCCAGCGGTGC 18644         ACGA   __  A
            GG                    TAACGTTG    TTCT  CG TGCGG
                                |||||||||    ||||  || |||||
                                GTTGCAAC    GGGG  GC ACGCC
                                    CG__    TC  C
GAM2130  SLC14A1  3'  CCAAGAATATCAATAAATAC   31964      A        TCT
                                TCAA AATATCAATA   AATAC
                                |||| ||||||||||   |||||
                                GGTT TTATAGTTAT   TTATG
                                  C        ___
GAM2130  PDK4     3'  TATATCAAAAATATATCT     15206           TCAA
                                TGTATCAAAAATA    TATCT
                                ||||||||||||||   |||||
                                ATATAGTTTTTAT    ATAGA

                                    _____
GAM2130  SDC1     3'  TGTGCAAAAACAAGTCGATATC 16514     AT       __  A
            TA                    TGT  CAAAAATA  TC ATATCTA
                                |||  ||||||||  || |||||||
```

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                                ACA  GTTTTTGT  AG TATAGAT
                                  C_       TC  C
GAM2130  VAPB     3'  TGTACCAAGGCCTACCAAT   21877        AAA_
                                TGTATCAA    TATCAAT
                                ||||||||    |||||||
                                ACATGGTT    ATGGTTA
                                     CCGG
GAM2131  ZNF10    3'  TGATATGTTCAAATGCCCAAT  31744         A   A_
                                TGATATGTT AAAT  TCAAT
                                ||||||||| ||||  |||||
                                ACTATACAA TTTA  GGTTA
                                     G   CG
GAM2131  ZNF10    3'  TGATATGTTCAAATGCCCAAT  31744         A   A_
                                TGATATGTT AAAT  TCAAT
                                ||||||||| ||||  |||||
                                ACTATACAA TTTA  GGTTA
                                     G   CG
GAM2132  ACTN2    3'  TGATGAACCAGTCAGTACT    9953         A   TTTTT
                                TGATGAAC AGTT    TACT
                                |||||||| ||||    ||||
                                ACTACTTG TCAG    ATGA
                                     G   TC___
GAM2132  CXCL6    3'  TATGATGCATGGTCTTTTTT   16490        AACAA
                                TATGATG    GTTTTTTTT
                                |||||||    |||||||||
                                ATACTAC    CAGAAAAAA
                                    GTAC_
GAM2132  PDGFB    3'  TATGATGAGCAGGTCCCTT    15193         A  A
                                TATGATGA CA GTTTTTT
                                |||||||| || |||||||
                                ATACTACT GT CAGGGAA
                                     C  C
GAM2132  RNF12    5'  TGATGAACAAGTGGAAAATACT 32041           TTTTTT
                                TGATGAACAAGT     TACT
                                ||||||||||||     ||||
                                ACTACTTGTTCA     ATGA
                                      CCTTTT
GAM2132  C14orf1  3'  AGAAAAGAAATTAAAGA     28410       GTT
                                AGAAA   AGAAATTAAAGA
                                |||||   ||||||||||||
                                TCTTT   TCTTTAATTTCT
                                   ____
GAM2132  CDC42    3'  AAAGAAGTTAGAAATTA      12154        A
                                AAAGAA GTTAGAAATTA
                                |||||| ||||||||||
                                TTTCTT CAATCTTTAAT
                                   _
GAM2132  CLNS1A   3'  TAAAAGGCTGGAAATTAAAG   10529       AAA  A
                                TAAAAG   GTT GAAATTAAAG
                                ||||||   ||| ||||||||||
```

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                                ATTTTC  CGA CTTTAATTTC
                                   ___  C
GAM2132 ENTPD3   3' AAGAAAGTCTTAGTTAAAGA  10347        AGAAA
                                AAGAAAGTT    TTAAAGA
                                |||||||||    |||||||
                                TTCTTTCAG    AATTTCT
                                     AATC_
GAM2132 FNTB     3' AAGAAAGATAGAAACCCCCAGA 12998       T      AA_
                                AAGAAAG TAGAAATT  AGA
                                ||||||| ||||||||  |||
                                TTCTTTC ATCTTTGG  TCT
                                     T      GGG
GAM2132 GABRP    3' AGGAAGCTAAGAAATTAAAGA  30555    A    _
                                AG AAGTTA GAAATTAAAGA
                                || |||||| ||||||||||
                                TC TTCGAT CTTTAATTTCT
                                 C    T
GAM2132 MYLK     3' AAAGAAAGTTAAAAATTCCTAA 38164            ___
             AGA                   AAAGAAAGTTAGAAAT  TAAAGA
                                |||||||||||||||  ||||||
                                TTTCTTTCAATTTTTA  ATTTCT
                                       AGG
GAM2132 PABPC1   3' AAAGAATTACAAAATTAAAGA  15021      AGTTA
                                AAAGAA    GAAATTAAAGA
                                ||||||    ||||||||||
                                TTTCTT    TTTTAATTTCT
                                   AATG_
GAM2132 POU3F2   3' TAAAAGAACAATCAGAAGTTAG 24673       _      A  A
             AGA                   TAAAAGAA AGTTAGAA TTA AGA
                                |||||||| |||||||| ||| |||
                                ATTTTCTT TTAGTCTT AAT TCT
                                     G      C  C
GAM2132 PTPRC    3' TAAAAGAGAGTAGAAACC    38968       A  T
                                TAAAAGA AGT AGAAATT
                                ||||||| ||| |||||||
                                ATTTTCT TCA TCTTTGG
                                     C  _
GAM2132 SMCY     3' CAAAAGAAATGAAATTAAAGA  21637        GTTA
                                TAAAAGAAA   GAAATTAAAGA
                                |||||||||   ||||||||||
                                GTTTTCTTT   CTTTAATTTCT
                                      A___
GAM2132 TAF15    3' AGAAGGTTGGAAACTAAAG   40182     A  A
                                AGAA GTT GAAATTAAAG
                                |||| ||| ||||||||||
                                TCTT CAA CTTTGATTTC
                                  C  C
GAM2133 B4GALT2  3' CCAGCATAGGGAAGCCGGAAGC 36138        AAACTT TA
                                CCAGTATAG     T  GAAGC
                                |||||||||     |  |||||
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                                GGTCGTATC     G  CTTCG
                                     CCTTC_ GC
GAM2133  CALB1    3'  ACCAGTATAGGATATTCTAG  22307         AAAC
                                ACCAGTATAG    TTTTAG
                                ||||||||||    ||||||
                                TGGTCATATC    AAGATC
                                     CTAT
GAM2133  CALB1    3'  CAGTATAGAAACAA       22309          TTTTAG
                                CAGTATAGAAAC     AA
                                ||||||||||||     ||
                                GTCATATCTTTG     TT
                                          ______
GAM2133  HS2ST1   3'  AGTTAGGAGCTTTTAGAAG   29321     A   AAA
                                AGT TAG   CTTTTAGAAG
                                ||| |||   ||||||||||
                                TCA ATC   GAAAATCTTC
                                  _   CTC
GAM2133  KPNA1    3'  ACCAGTATCACATTTAGGAG  44315       AGAA  T    A
                                ACCAGTAT    AC TTTAG AG
                                ||||||||    || ||||| ||
                                TGGTCATA    TG AAATC TC
                                     G___  T    C
GAM2133  SLC21A3  3'  ACAGAAAATTTTTAGAAG    39569       C_
                                ATAGAAA  TTTTAGAAG
                                |||||||  |||||||||
                                TGTCTTT  AAAATCTTC
                                     TA
GAM2133  SLC4A7   3'  ACCAGTAACATTTAGAAG    18817       TAGAA  T
                                ACCAGTA     AC TTTAGAAG
                                |||||||     || |||||||||
                                TGGTCAT     TG AAATCTTC
                                     _____  T
GAM2133  SMARCC1  3'  CAGTGTGGAGGCCCTCAGAGGC 16900      ATA  AA      A
                                CAGT   GA  CTTTTAGA GC
                                ||||   ||  |||||||| ||
                                GTCA   CT  GGGAGTCT CG
                                  CAC  CC       C
GAM2133  CALCA    3'  CATCTGAAGTTTGAGACATCCT 11938        AC  _     AG
            CTG                  CATCTGAA  TTG GACATT  TTG
                                ||||||||  ||| ||||||  |||
                                GTAGACTT  AAC CTGTAG  GAC
                                     CA   T     GA
GAM2133  RAB6A    3'  CATCTGAAGATTGAAAGTT    16101        AC    CATT
                                CATCTGAA  TTGGA    AGTT
                                ||||||||  |||||    ||||
                                GTAGACTT  AACTT    TCAA
                                     CT    _____
GAM2134  CENTD2   3'  TATATTATCAAAAAGTCCCCAA 31604         A        TG
                                TATATTAT AAAAAGTTTT  A
                                |||||||| ||||||||||  |
```

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                                ATATAATA TTTTTCAGGG  T
                                    G        GT
GAM2134  MJD     3'  CATCTTTCAAAAGAATTG    36186     GTAA
                                CATC   TCAAAAGAATTG
                                ||||   ||||||||||||
                                GTAG   AGTTTTCTTAAC
                                  AA__
GAM2134  SOX11    3'  AACATCTCTGCCCAAAAGAGTT 16998       GTAA_      A
             G                   AACATC    TCAAAAGA TTG
                                ||||||    |||||||| |||
                                TTGTAG    GGTTTTCT AAC
                                   AGACG       C
GAM2135  CD244    3'  GCTGTTTCTTCTTCCCCTG   32297     CATC       A
                                GCT   TCTTCTTC CTTG
                                |||   |||||||| ||||
                                CGA   AGAAGAAG GGAC
                                  CAA_       G
GAM2135  GRIN2B   3'  AAGCTCATTTCTCTTAACT   9118         C   T   C
                                AAGCTCAT TCT CTT ACT
                                |||||||| ||| ||| |||
                                TTCGAGTA AGA GAA TGA
                                    A   _   T
GAM2135  NR2E1    3'  AAGCTCTTCTCTTTTTGACATG 17570       A     C  C  T
                                AAGCTC TCTCTT TT AC TG
                                |||||| |||||| || || ||
                                TTCGAG AGAGAA AA TG AC
                                   A     A  C  T
GAM2135  PCMT1    3'  AAGCTCATCTCTATTTTC    23938          TC_
                                AAGCTCATCTCT   TTC
                                ||||||||||||   |||
                                TTCGAGTAGAGA   AAG
                                       TAA
GAM2135  ADAMTS5  3'  TAGTAAGAGAAGCAGAG     28184        AT   T
                                TAGTAAGA  AGC AGAG
                                ||||||||  ||| ||||
                                ATCATTCT  TCG TCTC
                                    CT   _
GAM2135  ASPH     3'  CTAGTAAGAGCACTGAG     37135         ATA   A
                                TTAGTAAGA   GCT GAG
                                |||||||||   ||| |||
                                GATCATTCT   TGA CTC
                                   CG_   _
GAM2135  CDR2     3'  TTAGTAGTAGAGCTAGAG    44023       AGAAT
                                TTAGTA    AGCTAGAG
                                ||||||    ||||||||
                                AATCAT    TCGATCTC
                                   CATC_
GAM2135  EIF1A    3'  TAGTAAGAGTAGATTAGAG   44810         A   C_
                                TAGTAAGA TAG  TAGAG
                                |||||||| |||  |||||
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                                ATCATTCT ATC  ATCTC
                                    C   TA
GAM2135  EML1     3'  TTACTAAGAATATACCAG    40726     G       _
                                TTA TAAGAATA GCTAG
                                ||| |||||||| |||||
                                AAT ATTCTTAT TGGTC
                                  G       A
GAM2135  EXO1     5'  TAGTAAGAATGGCTGAG     25699          A   A
                                TAGTAAGAAT GCT GAG
                                |||||||||| ||| |||
                                ATCATTCTTA CGA CTC
                                      C   _
GAM2135  GALNT1   3'  CTAGTGAAAAGCTAGAG     33838       AA   T
                                TTAGT  GAA AGCTAGAG
                                |||||  ||| ||||||||
                                GATCA  CTT TCGATCTC
                                  __   T
GAM2135  JUN      3'  TAGTAAGAAGCACTGAG     13748         TA   A
                                TAGTAAGAA  GCT GAG
                                |||||||||  ||| |||
                                ATCATTCTT  TGA CTC
                                    CG   _
GAM2135  PPP1R3C  3'  TCATCAAGGATAGCTAGAG   23991     G    A
                                TTA TAAG ATAGCTAGAG
                                ||| |||| ||||||||||
                                AGT GTTC TATCGATCTC
                                  A    C
GAM2135  RFXAP    3'  CTAGTAAGAATAAACTAAAG   8052            _
                                TTAGTAAGAATAG CTAGAG
                                |||||||||||||| ||||||
                                GATCATTCTTATT GATTTC
                                       T
GAM2135  SLC20A1  5'  TTAGTAAGAGAACTACTGAG  40454         AT    __
                                TTAGTAAGA  AGCTA  GAG
                                |||||||||  |||||  |||
                                AATCATTCT  TTGAT  CTC
                                    C_    GA
GAM2135  TMEPAI   3'  TCAGTAAGGCACTAGAG     33621         AATA
                                TTAGTAAG    GCTAGAG
                                ||||||||    |||||||
                                AGTCATTC    TGATCTC
                                    CG__
GAM2136  COX10    3'  GAGAATCAATGAATTGTACA   10550           _
                                GAGAATCAATGA TTGTATA
                                |||||||||||| |||||||
                                CTCTTAGTTACT AACATGT
                                       T
GAM2136  MSR1     3'  GAATTAATGATTGAATGAA    39817      C       TAT
                                GAAT AATGATTG   ATGAA
                                |||| ||||||||   |||||
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                                CTTA TTACTAAC   TACTT
                                  A       T__
GAM2136  THPO     3'  GAGAATCAGTGAGTTGCA    7852         A  _
                                GAGAATCA TGA TTGTA
                                |||||||| ||| |||||
                                CTCTTAGT ACT AACGT
                                     C   C
GAM2136  TRPM8    3'  GAGAATCAATTGGAAATGAAC  35858          GATTGTAT
                                GAGAATCAAT       ATGAAC
                                ||||||||||       ||||||
                                CTCTTAGTTA       TACTTG
                                      ACCTT___
GAM2137  SLC2A2   3'  TTTAGAAGAACCTTGTTATAA  7352           ATA
                                TTTAGAAGAATT   TTGTTATAA
                                ||||||||||||   |||||||||
                                AAATCTTCTTGG   AACAATATT
                                               ___
GAM2138  CYP1B1   3'  ACTTTTTTAATAGCCTATTTGA 6441         TCT_  _   A
              GA                  ACTTTTTT   GCC ATTT AGA
                                |||||||    ||| |||| |||
                                TGAAAAAA   CGG TAAA TCT
                                     TTAT  A   C
GAM2138  MAP4K5   3'  TTTTCCTGTCATTTGAGA    27306        C    A
                                TTTTTCTG CATTT AGA
                                |||||||| ||||| |||
                                AAAAGGAC GTAAA TCT
                                     A    C
GAM2138  PPARBP   3'  TAACTTTCTTTCTGGCAC    21932           C
                                TAACTTTTTTTCTG CAT
                                |||||||||||||| |||
                                ATTGAAAGAAAGAC GTG
                                       C
GAM2139  ABR      3'  GGAGGAAATGAAAGAACA    35012        C_
                                GGAGGAAA  GAAGAATG
                                ||||||||  ||||||||
                                CCTCCTTT  TTTCTTGT
                                     AC
GAM2139  BAZ1B    3'  ACGGAGGAAGCAGAGGCCACA  37083         ACGA  AT  A
                                ACGGAGGAA    AGA  GC ACA
                                |||||||||    |||  || |||
                                TGCCTCCTT    TCT  CG TGT
                                     CG__   C_  G
GAM2139  CEP1     5'  GGGGAAAAAAATGCA      28138    A  AAC
                                GG GGA   GAAGAATGCA
                                || |||   ||||||||||
                                CC CCT   TTTTTTACGT
                                 _  ____
GAM2139  COL5A3   3'  ACGGAGGAGTGAGGAGGCA   31848         AAC  A  AT
                                ACGGAGGA   GA GA  GCA
                                ||||||||   || ||  |||
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                                TGCCTCCT  CT CT  CGT
                                    CA_  C  C_
GAM2139  CTSK    3'  GGAAGAAATGGAAGAGCA   7576        C_   AT
                                GGAGGAAA  GAAGA  GCA
                                ||||||||  |||||  |||
                                CCTTCTTT  CTTCT  CGT
                                    AC   __
GAM2139  CYB561  3'  CGGAGAAACGAGAAGCA    12542      G    A  T
                                CGGAG AAACGA GAA GCA
                                ||||| |||||| ||| |||
                                GCCTC TTTGCT CTT CGT
                                  _    _  _
GAM2139  DSP     5'  CGGAGAAAGCGGAGGGGGC   20643       A  A  AAT
                                CGGAGGAA CG AG  GC
                                |||||||| || ||  ||
                                GCCTCTTT GC TC  CG
                                    C  C  CCC
GAM2139  FANCG   5'  GGAGGAAACGAGTCAGCA   21558         AGAAT
                                GGAGGAAACGA   GCA
                                ||||||||||    |||
                                CCTCCTTTGCT   CGT
                                     CAGT_
GAM2139  GALC    3'  GAGGAAACGACTACAACA   6674         AGAA
                                GAGGAAACGA   TGCAACA
                                ||||||||||   |||||||
                                CTCCTTTGCT   ATGTTGT
                                     G___
GAM2139  INSR    3'  GGGGGGAACGAAAAAACA   43381   A  A      T
                                GG GG AACGAAGAA GCA
                                || || ||||||||| |||
                                CC CC TTGCTTTTT TGT
                                 C  C       _
GAM2139  LDOC1   3'  ACGGAGAAATGAAGAGAGAGAG 29487        AC   AT____
           CA                    ACGGAGGAA  GAAGA    GCA
                                |||||||||  |||||    |||
                                TGCCTCTTT  CTTCT    CGT
                                    A_    CTCTCT
GAM2139  MAP3K4  3'  ACGGAGGAGACAGAGGC    25428       A  A  AAT
                                ACGGAGGA ACG AG  GC
                                |||||||| ||| ||  ||
                                TGCCTCCT TGT TC  CG
                                    C  C  ___
GAM2139  MAPK14  3'  GGAGGAAATCTCTGCAACA   40013       CGAAGAA
                                GGAGGAAA     TGCAACA
                                ||||||||     |||||||
                                CCTCCTTT     ACGTTGT
                                    AGAG___
GAM2139  MECP2   3'  ACGGAGGAAGGGAAAGAA   22568        AC_
                                ACGGAGGAA  GAAGAA
                                |||||||||  ||||||
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                                TGCCTCCTT  TTTCTT
                                     CCC
GAM2139  POU4F1   3'  GGAGGAAAGAGAGC       26392        C  A  AT
                                GGAGGAAA GA GA  GC
                                |||||||| || ||  ||
                                CCTCCTTT CT CT  CG
                                     _  _  __
GAM2139  PTPRG    5'  CGGAGGAAACGGAGGAAAACA  15933          AA_  T
                                CGGAGGAAACG  GAA GCA
                                ||||||||||  ||| |||
                                GCCTCCTTTGC  CTT TGT
                                      CTC  T
GAM2139  SLC7A6   3'  ACGGAGGGGAGAAGTGACA   19585       AAAC   AAT
                                ACGGAGG   GAAG  GCA
                                |||||||   ||||  |||
                                TGCCTCC   CTTC  TGT
                                    CCT_   AC_
GAM2139  TAZ      5'  GGAGGAAACGGGAAGGC     31769         AA  T
                                GGAGGAAACG  GAA GC
                                ||||||||||  ||| ||
                                CCTCCTTTGC  CTT CG
                                     C_  C
GAM2139  TRIM9    3'  GGAGGAAATTAATTTCTACA  31574        CG  GAA_
                                GGAGGAAA  AA   TGCA
                                ||||||||  ||   ||||
                                CCTCCTTT  TT   ATGT
                                     AA  AAAG
GAM2139  UBE2L3   3'  ACGGAGGAAGTGGAGAGCA   17822         ACGA  AT
                                ACGGAGGAA   AGA  GCA
                                |||||||||   |||  |||
                                TGCCTCCTT   TCT  CGT
                                     CACC  __
GAM2139  ZNF239   5'  GGAGGAAAGCTCATGTAACA  24977        CGAAGA  C
                                GGAGGAAA     ATG AACA
                                ||||||||     ||| ||||
                                CCTCCTTT     TAC TTGT
                                     CGAG__  A
GAM2139  ZNF278   5'  CGGAGGAAACAAAAGGC     36789           AAT
                                CGGAGGAAACGAAG  GC
                                ||||||||||||||  ||
                                GCCTCCTTTGTTTT  CG
                                       C__
GAM2139  IER5     3'  TAGCCGCTTCCTTCTCCAC   32422
                                TAGCCGCTTCCTTTTCCAT
                                ||||||||||||||||||
                                ATCGGCGAAGGAAGAGGTG

GAM2139  IGF1     3'  GCTCCTTTCTATGAAAT     8341      T     CC
                                GCT CCTTTT  ATGAAAT
                                ||| ||||||  |||||||
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                                CGA GGAAAG  TACTTTA
                                  _     A_
GAM2139  OPA1     3'  TAGCCTTTTCCTTGGGAGAAAT 39272      GC     TTCCAT
                                TAGCC  TTCCTT     GAAAT
                                |||||  ||||||     |||||
                                ATCGG  AAGGAA     CTTTA
                                   AA     CCCT__
GAM2139  SPARC    3'  AGCAGCTTTTTCATGAAA    17064     C   CCT   C
                                AGC GCTT   TTTC ATGAAA
                                ||| ||||   |||| ||||||
                                TCG CGAA   AAAG TACTTT
                                 T   ___   _
GAM2139  ZNF6     5'  ACTGCTTCCTTTATATGA    35089    C       TCC
                                GC GCTTCCTTT   ATGA
                                || |||||||||   ||||
                                TG CGAAGGAAA   TACT
                                 A        TA_
GAM2140  COL19A1  3'  TGTTTTGATGGTGGCTTCT   12390       CT    GC
                                TGTTTTGA  GTGGT  CT
                                ||||||||  |||||  ||
                                ACAAAACT  CACCG  GA
                                     AC    AA
GAM2140  CRYGS    3'  TGTTTTATTGATGATGCCTA  32756       ACT
                                TGTTTTG   GTGGTGCCTA
                                |||||||   ||||||||||
                                ACAAAAT   TACTACGGAT
                                     AAC
GAM2140  ORC3L    3'  TGTTTTGATACATGCCT     29607       CTGTG
                                TGTTTTGA    GTGCCT
                                ||||||||    ||||||
                                ACAAAACT    TACGGA
                                     ATG__
GAM2140  PROCR    3'  TATTTTGATTGTGGATGACT   26918       C    _  C
                                TGTTTTGA TGTGG TG CT
                                |||||||| ||||| || ||
                                ATAAAACT ACACC AC GA
                                     A    T  T
GAM2140  IL6R     5'  CCGCAGAGGCGGACAGGCTAAT 8171        CAAA   TTA
                                CCGCAGAG   ACG   TAAT
                                ||||||||   |||  ||||
                                GGCGTCTC   TGT   ATTA
                                     CGCC   CCG
GAM2140  MBP      3'  CGCAGAGCAACATGAAGCTA  44886        AAC___
                                CGCAGAGCAA     GTTA
                                ||||||||||     ||||
                                GCGTCTCGTT     CGAT
                                      GTACTT
GAM2140  NOS1     3'  GCAGAGCAAGGTGAGTCATA  8375         AAC__
                                GCAGAGCAA    GTTATA
                                |||||||||    ||||||
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                                CGTCTCGTT    CAGTAT
                                     CCACT
GAM2140  SLC4A10   3'  CCATGGAGCAAAACTTACAGTA 35192    CA       G    A
              G                   CCG  GAGCAAAAC TTATA TAG
                                  |||  ||||||||| ||||| |||
                                  GGT  CTCGTTTTG AATGT ATC
                                    AC       _    C
GAM2140  TMOD      3'  GCAGAGCACAGGTCATCAATAG 17600        AAAC    _
                                  GCAGAGCA    GTTAT AATAG
                                  ||||||||    ||||| |||||
                                  CGTCTCGT    CAGTA TTATC
                                       GTC_    G
GAM2141  FDX1      3'  TCTGTTATAGGCAGAGATT    41268        CGA  TG   A
                                  TCTGTTAT   AG  GGA GATT
                                  ||||||||   ||  ||| ||||
                                  AGACAATA   TC  TCT CTAA
                                       ___  CG   _
GAM2141  MECP2     3'  TGTTTTGAAGTGGGAACAT    22624      ATC        G
                                  TGTT   GAAGTGGGAA AT
                                  ||||   |||||||||| ||
                                  ACAA   CTTCACCCTT TA
                                    AA_        G
GAM2141  EVA1      3'  TTAAAAACTGAAAATATCA    25132         T
                                  TTAAAAACT AAAATATTA
                                  |||||||||| |||||||||
                                  AATTTTTGA TTTTATAGT
                                       C
GAM2142  TACSTD1   5'  CGTCGGGAGGACAGCGACG    14298    _  CAC
                                  CG CG   AGGACAGCGACG
                                  || ||   ||||||||||||
                                  GC GC   TCCTGTCGCTGC
                                   A  CC_
GAM2142  ATP1A1    3'  ACTGAAGTACACAAAGAGG    8691        A     CGC
                                  ACTGAA TACGCG   GAGG
                                  |||||| ||||||   ||||
                                  TGACTT ATGTGT   CTCC
                                     C     TT_
GAM2142  EGLN3     5'  GAAGCCGAGGCGCGGGGAGCG  35207     ATA  C_    A   A
                                  GAA   CG  GCGCG GGA CG
                                  |||   ||  ||||| ||| ||
                                  CTT   GC  CGCGC CCT GC
                                    CG_  TC     C   C
GAM2142  MADD      5'  ACCGGGCGCGCGCGGGGA    39061      AAATA       A
                                  ACTG    CGCGCGCG GGA
                                  ||||    |||||||| |||
                                  TGGC    GCGCGCGC CCT
                                    CC___       C
GAM2142  MTMR1     3'  TGAAATACAGTGCAACAGA    43160         CGC    _
                                  TGAAATACG   GCGA GGA
                                  |||||||||   |||| |||
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                                ACTTTATGT   CGTT TCT
                                     CA_   G
GAM2142  RPA3     5'  ACTGAAACTGTGCGCCCCGCGG 16379        AC_   ___   A
              G                   ACTGAAAT   GCGC   GCG GG
                                  ||||||||   ||||   ||| ||
                                  TGACTTTG   CGCG   CGC CC
                                     ACA   GGG   _
GAM2143  ACO1     3'  CACCCGACCTATCCATG     13581        GCACC
                                  CACCCGAC    ATCCATG
                                  ||||||||    |||||||
                                  GTGGGCTG    TAGGTAC
                                     GA___
GAM2143  AIRE     5'  CCCGGCCCACCCACG      8530      AC  A
                                  CCCG  GC CCATCCATG
                                  ||||  || |||||||||
                                  GGGC  CG GGTGGGTGC
                                    __  _
GAM2143  ANXA8    3'  CACCCAACCTGCGTCCATG   11572        __  ACCA
                                  CACCCGAC  GC   TCCATG
                                  ||||||||  ||   ||||||
                                  GTGGGTTG  CG   AGGTAC
                                     GA  C___
GAM2143  BCL11A   3'  CCCTATGACAGCCATCCATG   39707     GAC_   _
                                  CCC   GCA CCATCCATG
                                  |||   ||| |||||||||
                                  GGG   TGT GGTAGGTAC
                                    ATAC   C
GAM2143  CD244    3'  CCCTCCACCCATTCATG     32295     GA   A    C
                                  CCC  CGC CCAT CATG
                                  |||  ||| |||| ||||
                                  GGG  GTG GGTA GTAC
                                    AG   _    A
GAM2143  GNAS     3'  CACCCACGTCAAACATG     38654      G   CAC  TC
                                  CACCC ACG   CA  CATG
                                  ||||| |||   ||  ||||
                                  GTGGG TGC   GT  GTAC
                                     _   A__  TT
GAM2143  GPLD1    3'  CCTCCAGCTCCATCCATG    45113    GA _  A
                                  CC  C GC CCATCCATG
                                  ||  | || |||||||||
                                  GG  G CG GGTAGGTAC
                                   AG T  A
GAM2143  HMGB3    3'  CACCCATGGCCACTTCATG   23777       ACGCA    C_
                                  CACCCG    CCAT  CATG
                                  ||||||    ||||  ||||
                                  GTGGGT    GGTG  GTAC
                                     ACC__    AA
GAM2143  MYOM2    3'  CACCCATGTGCCCACACC    19556       AC_  A    _
                                  CACCCG   GC CCAT CC
                                  ||||||   || |||| ||
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                                GTGGGT  CG GGTG GG
                                   ACA  _   T
GAM2143 YWHAG   3' CACCCGACCCCCAACTCATG  29790       GCA  TC_
                                CACCCGAC  CCA  CATG
                                ||||||||  |||  ||||
                                GTGGGCTG  GGT  GTAC
                                    GG_  TGA
GAM2143 GOCAP1  3' TGGAATAATGTGGGGTTTGTGA 35549        C  CAC  CGC__
            C                    TGGAATGATG GG  GG   GAC
                                ||||||||||  ||  ||   |||
                                ACCTTATTAC CC  CC   CTG
                                     A  ___  AAACA
GAM2143 RPA3    5' GGAATGATACGTGGTGTGGC  16381         GCAC__
                                GGAATGATGCG    GGC
                                ||||||||||     |||
                                CCTTACTATGC    CCG
                                      ACCACA
GAM2143 TBL2    3' GGCCAGGCGGCACGGCGCG  37410   AATGAT
                                GG    GCGGCACGGCGCG
                                ||    ||||||||||||
                                CC    CGCCGTGCCGCGC
                                 GGTC__
GAM2144 ADAMTS5 3' TGACAAGGGGGAGACAGT   28186       A  T   T
                                TGACAAGG GG GATG GT
                                |||||||| || |||| ||
                                ACTGTTCC CC CTGT CA
                                     C  T   _
GAM2144 BACE    3' TGATAGGGAGGTAATGAACT  29047    CAA       TGT
                                TGA  GGAGGTGATG  GACT
                                |||  ||||||||||  ||||
                                ACT  CCTCCATTAC  TTGA
                                  ATC       ___
GAM2144 CBFB    3' AAGGAGGTGCCAAATGACT   35630       ATGT
                                AAGGAGGTG   GTGACT
                                |||||||||   ||||||
                                TTCCTCCAC   TACTGA
                                     GGTT
GAM2144 CHST6   3' TGCAGGGAGGATGTGACT   34685   A  A   TGAT
                                TG CA GGAGG   GTGTGACT
                                || || |||||   ||||||||
                                AC GT CCTCC   TACACTGA
                                 _  C    ____
GAM2144 CPT2    3' TGATGAGGAAGTGATGGTAGCT 6432     CA       T  A
                                TGA  AGGAGGTGATG GTG CT
                                |||  |||||||||| ||| ||
                                ACT  TCCTTCACTAC CAT GA
                                  AC         _  C
GAM2144 PYCR1   5' TGAAGGGGATGATGTGTGGCT  43128   C   A       A
                                A AAGG GGTGATGTGTG CT
                                | |||| |||||||||| ||
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                                A TTCC CTACTACACAC GA
                                 C   C        C
GAM2144  BAZ2A    5'  TCCCTGAGCCTCAAG      30315         ACCA   CCC
                                TCCCTGAGCC   TCA   AG
                                ||||||||||   |||   ||
                                AGGGACTCGG   AGT   TC
                                     _____   ___
GAM2144  C5R1     3'  TCCCTCGGTCACCCAG      11924       _ AGCCACCA
                                TCCCT G      TCACCCAG
                                ||||| |      ||||||||
                                AGGGA C      AGTGGGTC
                                   G C_______
GAM2144  DDEF2    3'  CTGAGCCATCATCCCAGA     19318        C   CA
                                CTGAGCCA CAT  CCCAGA
                                |||||||| |||  ||||||
                                GACTCGGT GTA  GGGTCT
                                     A  __
GAM2144  EDG8     3'  TCCCTGACCACCATCAC      44208        G
                                TCCCTGA CCACCATCAC
                                ||||||| ||||||||||
                                AGGGACT GGTGGTAGTG
                                     _
GAM2144  IL1R1    3'  CTTGGTCATCATCACCCCCAC  9357     GAGC  C       AG
                                CT   CA CATCACCC  AC
                                ||   || ||||||||  ||
                                GA   GT GTAGTGGG  TG
                                 ACCA  A       GG
GAM2144  IL2RB    3'  TCCCTGAGCTGCAGAGGAGAC  9394          CAC  TCACCC
                                TCCCTGAGC   CA     AGAC
                                |||||||||   ||     ||||
                                AGGGACTCG   GT     TCTG
                                     AC_  CTCC__
GAM2144  LFG      3'  CCTGGGCCCAGCCCCACCCAG  44133     A   A__  A
                                CCTG GCC   CC TCACCCAG
                                |||| |||   || ||||||||
                                GGAC CGG   GG GGTGGGTC
                                  C   GTC  _
GAM2144  LPIN2    3'  TCCCTGAGCCGTCACCC      31220          ACCA
                                TCCCTGAGCC   TCACCC
                                ||||||||||   ||||||
                                AGGGACTCGG   AGTGGG
                                     C___
GAM2144  MADH1    5'  TCCCCGAGCCTCGGCCC      25341         ACCA  A_
                                TCCCTGAGCC   TC  CCC
                                ||||||||||   ||  |||
                                AGGGGCTCGG   AG  GGG
                                     _____  CC
GAM2144  NDST2    3'  TCTATGAGCCACTGTCCGA    18880    CC       CATCAC  A
                                TC  TGAGCCAC     CC GA
                                ||  ||||||||     || ||
```

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                                AG  ACTCGGTG     GG CT
                                 AT       ACA___ _
GAM2144  ORC2L    3'  TCCCTGAGCACACTGTTCA   26195        _  CA_
                                TCCCTGAGC CAC   TCA
                                ||||||||| |||   |||
                                AGGGACTCG GTG   AGT
                                      T   ACA
GAM2144  PPP2R2B  3'  TCCCTAGCCAAATTCTCAG   21337     G    CCA  ACC
                                TCCCT AGCCA   TC   CAG
                                ||||| |||||   ||   |||
                                AGGGA TCGGT   AG   GTC
                                   _    TTA  A__
GAM2144  PSMB8    3'  TCCCTGAGTCGGCCAAGA    45548       CCACCA  A_  C
                                TCCCTGAG     TC  CC AGA
                                ||||||||     ||  || |||
                                AGGGACTC     AG  GG TCT
                                     _______  CC  T
GAM2144  PTPN1    3'  CCTAAAGGACCGTCACCCAG   15900      CC   A
                                CCTGAG  ACC TCACCCAG
                                ||||||  ||| ||||||||
                                GGATTT  TGG AGTGGGTC
                                    CC   C
GAM2144  RXRA     3'  CCTGAGCCCCTCTCTCTCCAG  16421       A  A_  AC_
                                CCTGAGCC CC  TC   CCAG
                                ||||||| ||  ||   ||||
                                GGACTCGG GG  AG   GGTC
                                     _  AG  AGA
GAM2144  SCGB2A1  3'  CCTCTGAGCCAAACGCC     14441    _      CCATC  _
                                CC CTGAGCCA     AC CC
                                || ||||||||     || ||
                                GG GACTCGGT     TG GG
                                 A       T____  C
GAM2144  TMPRSS2  3'  CTGGCCACCATCCAG       24935     A       CAC
                                CTG GCCACCAT   CCAG
                                ||| ||||||||   ||||
                                GAC CGGTGGTA   GGTC
                                   _      ___
GAM2144  TSSC3    3'  TCACTGAGCCACAGCCGGA   17704    C       CATCAC  A
                                TC CTGAGCCAC     CC GA
                                || |||||||||     || ||
                                AG GACTCGGTG     GG CT
                                 T       TC____  C
GAM2144  YWHAB    5'  CCTAAGCCCACTACTCAG    18186       AC   C  C
                                CCTGAGCC  CAT AC CAG
                                ||||||||  ||| || |||
                                GGATTCGG  GTG TG GTC
                                     __   A  A
GAM2145  ABCB9    3'  TGAGGCCCCTCCAGACC     33359        G   TA
                                TGAGGCCCTT TAG  ACC
                                |||||||||| |||  |||
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                                ACTCCGGGGA GTC  TGG
                                      G  __
GAM2145  ABL1    3'  TGGGCCCTTGCAGACC     28720    A        TA
                                TG GGCCCTTGTAG  ACC
                                || ||||||||||  |||
                                AC CCGGGAACGTC  TGG
                                 _        __
GAM2145  AGRN    3'  TGAGCTCCTCTCGATAGC    44258     G_ _   _
                                TGAG  CC CTTG TAGT
                                ||||  || |||| ||||
                                ACTC  GG GAGC ATCG
                                  GA  A   T
GAM2145  ANPEP   3'  GAGGCCCTGCACCAGCC     10096       T  G  A
                                GAGGCCCT GTA TA CC
                                |||||||| ||| || ||
                                CTCCGGGA CGT GT GG
                                     _  G  C
GAM2145  ATP2B3  3'  TGGGTCCTTGCAAATGCC    34977    A  C      TAA
                                TG GG CCTTGTAG   CC
                                || || ||||||||   ||
                                AC CC GGAACGTT   GG
                                 _ A       TAC
GAM2145  CML66   5'  GAGGCCCTAGCAACC       42816       TGT
                                GAGGCCCT   AGTAACC
                                ||||||||   |||||||
                                CTCCGGGA   TCGTTGG
                                     ____
GAM2145  DGCR2   3'  TGGGCCCCCAGTGACC     23102    A     TG   A
                                TG GGCCCT  TAGT ACC
                                || ||||||  |||| |||
                                AC CCGGGG  GTCA TGG
                                 _     __   C
GAM2145  EGFL5   5'  TGAAGCCCCTGATAACC     44540         TA
                                TGAGGCCCTTG  GTAACC
                                ||||||||||  ||||||
                                ACTTCGGGGAC  TATTGG
                                     __
GAM2145  EGR3    3'  TGCAGGTCCTTGGCGCGGCC  40561    _  C    TA  AA
                                TG AGG CCTTG  GT  CC
                                || ||| |||||  ||  ||
                                AC TCC GGAAC  CG  GG
                                  G   A    CG  CC
GAM2145  EPHB3   3'  TGGGCCCTGTGGAACC     20789    A     T  AGT
                                TG GGCCCT GT   AACC
                                || |||||| ||   ||||
                                AC CCGGGA CA   TTGG
                                 _     _ CC_
GAM2145  EPHB4   3'  TGGGCCCCTGTTTCAAC     20794    A       AG
                                TG GGCCCTTGT  TAAC
                                || |||||||||  ||||
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                                AC CCGGGGACA  GTTG
                                 _       AA
GAM2145  EXTL1    5'  TGAGGCCCATCGAGACC     20874         _  T  TA
                                TGAGGCCC TTG AG  ACC
                                |||||||| ||| ||  |||
                                ACTCCGGG AGC TC  TGG
                                     T  _  __
GAM2145  FACL3    3'  TGATGCCTACAGTAAC      20884     G   CT
                                TGA GCC  TGTAGTAAC
                                ||| |||  |||||||||
                                ACT CGG  ATGTCATTG
                                  A  __
GAM2145  GNAZ     3'  TGGGCTTGTAGTGACC      13189    A   CC      A
                                TG GGC  TTGTAGT ACC
                                || |||  ||||||| |||
                                AC CCG  AACATCA TGG
                                 _  __      C
GAM2145  HOXC6    3'  TGAGGCCCTGGAGCAGAGGCC  21078         T__    TAA
                                TGAGGCCCT   GTAG   CC
                                |||||||||   ||||   ||
                                ACTCCGGGA   CGTC   GG
                                     CCT    TCC
GAM2145  IHPK1    3'  TGAGACCCTGAGCGGACC     45496         T T   A_
                                TGAGGCCCT G AGT  ACC
                                ||||||||| | |||  |||
                                ACTCTGGGA C TCG  TGG
                                     _ _  CC
GAM2145  IL6R     3'  TGAGGTCCTGCAACC       8188       C   TGTA
                                TGAGG CCT    GTAACC
                                ||||| |||    ||||||
                                ACTCC GGA    CGTTGG
                                  A  _____
GAM2145  LENG4    5'  TGAGTCCTTTAGCAACC     35891      GC    G
                                TGAG  CCTT TAGTAACC
                                ||||  |||| ||||||||
                                ACTC  GGAA ATCGTTGG
                                  A_   _
GAM2145  LPIN1    3'  TAAGGCCCTTTCGATAGT    42641          ___
                                TGAGGCCCTT   GTAGT
                                ||||||||||   |||||
                                ATTCCGGGAA   TATCA
                                     AGC
GAM2145  LTBR     3'  GACGTCCTTGCAGGTGACC   14255     __       TA_
                                GGC  CCTTGTAG   ACC
                                |||  ||||||||   |||
                                CTG  GGAACGTC   TGG
                                  CA       CAC
GAM2145  MCL1     3'  TGGGGCCCCTAAAAACC     35003     A       TAGT
                                TG GGCCCTTG    AACC
                                || ||||||||    ||||
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                                AC CCGGGGAT    TTGG
                                 C       TT__
GAM2145  MTNR1B   3'  TGAGGCCCTTGTAGTTACC   25556            A
                                TGAGGCCCTTGTAGT ACC
                                ||||||||||||||| |||
                                ACTCCGGGAACATCA TGG
                                          A
GAM2145  PACSIN1  3'  TGGGGCCCTGAGGACC     45168    A     T T  TA
                                TG GGCCCT G AG  ACC
                                || |||||| | ||  |||
                                AC CCGGGA C TC  TGG
                                 C     _ _  C_
GAM2145  PLAU     3'  GAGGCCCCAGGAGTGACC    42879        TGT   A
                                GAGGCCCT   AGT ACC
                                ||||||||   ||| |||
                                CTCCGGGG   TCA TGG
                                     TCC   C
GAM2145  PSD      3'  GAGGCCCTCGTGGGTGGCC   15786          A_  AA
                                GAGGCCCTTGT  GT  CC
                                ||||||||||  ||  ||
                                CTCCGGGAGCA  CA  GG
                                       CC  CC
GAM2145  RFNG     3'  TGAGCCCTTGCAATGGCC    44776     G        AA
                                TGAG CCCTTGTAGT  CC
                                |||| ||||||||||  ||
                                ACTC GGGAACGTTA  GG
                                  _        CC
GAM2145  RPS6KA2  3'  TGGGGCCCTGCAACC      34469    A     TGTA
                                TG GGCCCT    GTAACC
                                || ||||||    ||||||
                                AC CCGGGA    CGTTGG
                                 C    _____
GAM2145  RUNX3    3'  TGAGACCCTAATAACC      20328         TGT
                                TGAGGCCCT   AGTAACC
                                |||||||||   |||||||
                                ACTCTGGGA   TTATTGG
                                          ___
GAM2145  SH3BP2   3'  GAGGTACCCAGTAACC      16632     __   TTGT
                                GAGG  CCC    AGTAACC
                                ||||  |||    |||||||
                                CTCC  GGG    TCATTGG
                                  AT  _____
GAM2145  SIGLEC6  3'  TGGCAGCCCTAGTAACC     40935    A_     TGT
                                TG  GGCCCT   AGTAACC
                                ||  ||||||   |||||||
                                AC  TCGGGA   TCATTGG
                                 CG     ___
GAM2145  SLC4A1   5'  TGAGCCCCCAGCATAACC    7359      G   T   G
                                TGAG CCCT GTA TAACC
                                |||| |||| ||| |||||
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                                ACTC GGGG CGT ATTGG
                                  G   T  _
GAM2145 SORBS1   3' AACCTTTTTTGTAGTAACC   31700     C___
                                GGCC   TTGTAGTAACC
                                ||||   ||||||||||
                                TTGG   AACATCATTGG
                                  AAAA
GAM2145 STK24    5' TAAGGCTTCGTCAGTAACC   18705      CC  _
                                TGAGGC  TTGT AGTAACC
                                ||||||  |||| |||||||
                                ATTCCG  AGCA TCATTGG
                                   A_   G
GAM2145 TACC1    3' TGAGCTTGAGTAAC       26605     GCC   T
                                TGAG   CTTG AGTAAC
                                ||||   |||| ||||||
                                ACTC   GAAC TCATTG
                                  ___   _
GAM2145 TAF5     3' TGAGTGCCATACAGTAAC    40061     _  CT
                                TGAG GCC  TGTAGTAAC
                                |||| |||  |||||||||
                                ACTC CGG  ATGTCATTG
                                  A  T_
GAM2145 TCP10    3' TGGGTGTCCTTGTAGTGAC   21431    A  C__      A
                                TG GG   CCTTGTAGT AC
                                || ||   |||||||| ||
                                AC CC   GGAACATCA TG
                                 _ ACA       C
GAM2145 TRIM14   3' TGAGGCCCGCCTAAC      37710       TT  AG
                                TGAGGCCC  GT  TAAC
                                ||||||||  ||  ||||
                                ACTCCGGG  CG  ATTG
                                    __  G_
GAM2145 VNN1     3' TGAGGCCCTCTCTTCTTAGC  21688        G_____
                                TGAGGCCCTT     TAGT
                                ||||||||||     ||||
                                ACTCCGGGAG     ATCG
                                     AGAAGA
GAM2145 WISP3    5' TGGGACTCTTCTAATAACC   38979    A   C   G
                                TG GGC CTT TAGTAACC
                                || ||| ||| ||||||||
                                AC CTG GAA ATTATTGG
                                 C   A   G
GAM2145 ADAMTS13 5' TGCTGCAAGCTGGGCCTTGC  40038       CAACCG
                                TGCTGCA     GGGCTTTGC
                                |||||||     |||||||||
                                ACGACGT     CCCGGAACG
                                    TCGA__
GAM2145 ADAMTS5  5' GCTGCGCGACTGGGACTT    28181      ACA  C
                                GCTGC   AC GGGGCTT
                                |||||   || |||||||
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                                CGACG   TG CCCTGAA
                                   CGC  A
GAM2145 CDH5     3'  TGCAGTGTGAGGGGCTTTGCCC 12194      CAACC_
                                TGCA     GGGGCTTTGCCC
                                ||||     ||||||||||||
                                ACGT     CCCCGAAACGGG
                                  CACACT
GAM2145 CELSR2   3'  GCTGCGTGTGGCTTTGTCC   10851      ACAACCGG     _
                                GCTGC       GGCTTTG CC
                                |||||       ||||||| ||
                                CGACG       CCGAAAC GG
                                   CACA____       A
GAM2145 COLQ     5'  TGCTGCGGAGCCTTGC      38702       ACAACC
                                TGCTGC     GGGGCTTTGC
                                ||||||     ||||||||||
                                ACGACG     CCTCGGAACG
                                             _______
GAM2145 CYP3A43  5'  TGTGCATATAGAGCTTTG    38401    C   CAACC
                                TG TGCA    GGGGCTTTG
                                || ||||    |||||||||
                                AC ACGT    TCTCGAAAC
                                 _   ATA__
GAM2145 DEDD     3'  TGCTGTAGACTTTGC       37430       CACAACCG
                                TGCTG       GGGCTTTGC
                                |||||       |||||||||
                                ACGAC       TCTGAAACG
                                   A________
GAM2145 EBAG9    5'  TGCTGCACGCCTGGGTCC    20120        AA  G  _
                                TGCTGCAC  CC GGG CT
                                ||||||||  || ||| ||
                                ACGACGTG  GG CCC GG
                                     C_  A   A
GAM2145 FLRT2    3'  TGTTGCAATGGCCTTGC     29867    C   CAACCGG
                                TG TGCA      GGCTTTGC
                                || ||||      ||||||||
                                AC ACGT      CCGGAACG
                                 A   TA_____
GAM2145 PLS1     3'  TGTTGCACAACAGTATTGC    15413    C      C  GGCT
                                TG TGCACAAC GG    TTGC
                                || |||||||| ||    ||||
                                AC ACGTGTTG TC    AACG
                                 A       _ AT__
GAM2145 S100B    3'  TGCTGGATAAGGCTTTG     26576      CACAACC
                                TGCTG      GGGGCTTTG
                                |||||      |||||||||
                                ACGAC      TTCCGAAAC
                                   CTA____
GAM2145 SORCS1   3'  TGCTGAACAGGCTTT       38105      C   ACCGG
                                TGCTG ACA    GGCTTT
                                ||||| |||    ||||||
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                                ACGAC TGT    CCGAAA
                                  T  _____
GAM2145  SPON2    5'  TGCTGCACGGCCTGGC      29715        AACCGG    T
                                TGCTGCAC     GGCTT GC
                                ||||||||     ||||| ||
                                ACGACGTG     CCGGA CG
                                     _______    C
GAM2145  TNNC2    5'  TGCTGGTGACCGGGACTC    17615      CACA
                                TGCTG   ACCGGGGCTT
                                |||||   ||||||||||
                                ACGAC   TGGCCCTGAG
                                  CAC_
GAM2145  TP53BP2  3'  TGCTACACGGGACACCTTTGCC 24063        AACC    ___
             C                   TGCTGCAC   GGGGC   TTTGCCC
                                |||||||   |||||  |||||||
                                ACGATGTG   CCCTG   AAACGGG
                                     ____    TGG
GAM2146  GHR      3'  AAGTATTCTTCACTGAGA    6711             T
                                AAGTATTCTTCACTG AGA
                                |||||||||||||| |||
                                TTCATAAGAAGTGAC TCT
                                          _
GAM2146  IDS      3'  AAGTATTCTTTGTGTATAATGT 25956         CAC   GAC
                                AAGTATTCTT   TGTA   ATGT
                                ||||||||||   ||||   ||||
                                TTCATAAGAA   ACAT   TACA
                                     AC_    AT_
GAM2146  PSMB2    3'  AAATATTTTTCACTACATG    15815       C     GTAG
                                AAGTATT TTCACT    ACATG
                                ||||||| ||||||    |||||
                                TTTATAA AAGTGA    TGTAC
                                   A     ____
GAM2146  APM1     3'  TCAGAACACAGAAAATTATCA  22018       ACTT  _
                                TCAGAA    CA AGAATTATCA
                                ||||||    || ||||||||||
                                AGTCTT    GT TTTTAATAGT
                                   GT__  C
GAM2146  EMR1     3'  TCAGAAACTCTGGAATT     12704         CAA
                                TCAGAAACTT   GAATT
                                ||||||||||   |||||
                                AGTCTTTGAG   CTTAA
                                     AC_
GAM2146  GABRA5   3'  TCAGAACAGTAAGAATTATCA  41186       ACTTC
                                TCAGAA    AAGAATTATCA
                                ||||||    ||||||||||||
                                AGTCTT    TTCTTAATAGT
                                   GTCA_
GAM2146  LANCL1   3'  TCAGAAACTGATGAATT     25856         TCAA
                                TCAGAAACT    GAATT
                                |||||||||    |||||
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                                AGTCTTTGA   CTTAA
                                     CTA_
GAM2146 NUFIP1   3' TCATGAACTTCAATAATCA   29596    GA      G
                                TCA  AACTTCAA AATTA
                                |||  |||||||| |||||
                                AGT  TTGAAGTT TTAGT
                                  AC       A
GAM2146 SLC17A5  3' TCAGTACCTGAGAATTATCA  29690     AA   CA
                                TCAG  ACTT  AGAATTATCA
                                ||||  ||||  ||||||||||
                                AGTC  TGGA  TCTTAATAGT
                                  A_   C_
GAM2146 VRK2     3' GAAACTTAAAAAATTATCA   26665       C
                                GAAACTT AAGAATTATCA
                                ||||||| ||||||||||
                                CTTTGAA TTTTTAATAGT
                                     T
GAM2147 MANBA    3' TGCTAAAGCTGAGAG       25387       AATTTT      A
                                TGTTAA     AGCTGAGA G
                                ||||||     |||||||| |
                                ACGATT     TCGACTCT C
                                   _______      C
GAM2147 RNMT     3' TGCTAAAATTTTAGCTAAG   19157
                                TGTTAAAATTTTAGCTGAG
                                ||||||||||||||||||
                                ACGATTTTAAAATCGATTC

GAM2147 BACH1    3' ATAGTTCCAGAATTTGAA    10144    A       C
                                GTG TTCCAGAATT GAA
                                ||| |||||||||| |||
                                TAT AAGGTCTTAA CTT
                                  C        A
GAM2147 DPYSL3   3' ATGAGGTGCCAGTGAATTCGAA 10761     A  ATT  __
                                ATGA GTG   CCA  GAATTCGAA
                                |||| |||   |||  |||||||||
                                TACT CAC   GGT  CTTAAGCTT
                                  C  ___  CA
GAM2147 IKBKAP   5' GATGAAGTGATTCCCACGA   43287           AGAATT
                                GATGAAGTGATTCC     CGA
                                ||||||||||||||     |||
                                CTACTTCACTAAGG     GCT
                                        GT____
GAM2147 MTCP1    5' GATGAAGTGATTGCCAAA    30579          _
                                GATGAAGTGATT CCAGA
                                |||||||||||| |||||
                                CTACTTCACTAA GGTTT
                                        C
GAM2147 NEBL     3' GATTTCCATTCCAGAATTTGAA 26902     GAAGTG        C
                                GAT     ATTCCAGAATT GAA
                                |||     |||||||||| |||
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                                CTA     TAAGGTCTTAA CTT
                                  AAGG__         A
GAM2147  NRXN3    5'  GAGGAAGAGTTGCCAGAATTCG 39942    T   TGATT
                                GA GAAG    CCAGAATTCG
                                || ||||    ||||||||||
                                CT CTTC    GGTCTTAAGC
                                 C   TCAAC
GAM2148  ADRBK1   3'  GACTGTCAGCTGGGA      11528        GGACT
                                GACTGTTA    GTTGGGA
                                ||||||||    |||||||
                                CTGACAGT    CGACCCT
                                      _____
GAM2148  ADSS     3'  AAGATTGTTGTTTTGGGAAA  43475     C   AGGACTG
                                AAGA TGTT      TTGGGAAA
                                |||| ||||      ||||||||
                                TTCT ACAA      AACCCTTT
                                  A   CAA____
GAM2148  APLP1    3'  AGGCTGCTGGGACTATCTGGGA 23162    A    A     _
             A                   AG CTGTT GGACTGT TGGGAA
                                || ||||| ||||||| ||||||
                                TC GACGA CCTGATA ACCCTT
                                 C    C      G
GAM2148  B4GALT1  3'  AGGCTTTAGGACCGAAG     11277    A  G       TT
                                AG CT TTAGGACTG  GG
                                || || |||||||||  ||
                                TC GA AATCCTGGC  TC
                                 C  _       T_
GAM2148  C5R1     3'  AAGATGTTGCCATTGGG     11917     C   AGGA
                                AAGA TGTT   CTGTTGGG
                                |||| ||||   ||||||||
                                TTCT ACAA   GGTAACCC
                                  _   C___
GAM2148  CHC1     3'  GACTGTTAGGGACAGGAAA   10425         _  TGTT
                                GACTGTTAGG AC   GGGAAA
                                |||||||||| ||   ||||||
                                CTGACAATCC TG   TCCTTT
                                      C  ____
GAM2148  CRABP2   3'  GACTGCTGACTTGGGGA     12428       AG   GTT
                                GACTGTT  GACT   GGGA
                                |||||||  ||||   ||||
                                CTGACGA  CTGA   CCCT
                                    __    AC_
GAM2148  CRTAP    3'  AACAGCCTGGGCTGTTGGGAAA 26838     T  TA  A
                                GAC GT  GG CTGTTGGGAAA
                                ||| ||  || ||||||||||
                                TTG CG  CC GACAACCCTTT
                                  T  GA  C
GAM2148  DDX26    5'  CTGGGGCTGTTGGGA       29092     TTA  A
                                CTG   GG CTGTTGGGA
                                |||   || |||||||||
```

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                                GAC   CC GACAACCCT
                                  C__  _
GAM2148  EMX2     3'  GATGTTAGGAAAGGGAA     44688    C       CTGTT
                                GA TGTTAGGA     GGGAA
                                || ||||||||     |||||
                                CT ACAATCCT     CCCTT
                                  _       TT___
GAM2148  ESRRA    3'  AGGCTCGTTGGGAGCTGATGGG 20824    A _   A   _   T
                                AG CT GTT GGA CTG TGGG
                                || || ||| ||| ||| ||||
                                TC GA CAA CCT GAC ACCC
                                 C G   C   C   T
GAM2148  GNB3     3'  AGGCTGTGAGGACTGTGGGGA  13216    A    T       T
                                AG CTGT AGGACTGT GGGA
                                || |||| |||||||| ||||
                                TC GACA TCCTGACA CCCT
                                 C    C       C
GAM2148  GRINL1A  3'  GATAGTTAGCTCTGGGGGA   43000    CT    GA   TT
                                GA  GTTAG  CTG  GGGA
                                ||  |||||  |||  ||||
                                CT  CAATC  GAC  CCCT
                                 AT     GA   C_
GAM2148  GSTM5    3'  AAGACGTTAGGAGGGGGA     9204       T      CTGTT
                                AAGAC GTTAGGA     GGGA
                                ||||| |||||||     ||||
                                TTCTG CAATCCT     CCCT
                                   _       CC___
GAM2148  HSPA1L   3'  AAGAATGTTAGGGTGGCTGGAA 45117      C       ACT
            A                    AAGA TGTTAGG   GTTGGGAA
                                |||| |||||||   ||||||||
                                TTCT ACAATCC   CGACCTTT
                                  T      CAC
GAM2148  IL27     3'  AAGCTGTTGGGAGCCAGGA   42103     A    A   CT  TG
                                AAG CTGTT GGA  GT  GGA
                                ||| ||||| |||  ||  |||
                                TTC GACAA CCT  CG  CCT
                                  _     C   __  GT
GAM2148  MAP3K9   3'  AAGACTGTGGAGGGTGGGG   41351        TA   CT  T
                                AAGACTGT  GGA  GT GGG
                                ||||||||  |||  || |||
                                TTCTGACA  CCT  CA CCC
                                     __   CC  C
GAM2148  NOLA2    3'  CTGTTAGAGCTGCCTGGGAA   45396       GA   _
                                CTGTTAG  CTGT TGGGAA
                                |||||||  |||| ||||||
                                GACAATC  GACG ACCCTT
                                    TC    G
GAM2148  OSCAR    3'  GACTGTGGGGCTGCAGGAAA   39309       TA  A    T
                                GACTGT  GG CTGT GGGAA
                                ||||||  || |||| |||||
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                                CTGACA  CC GACG CCTTT
                                   CC _   T
GAM2148 PRKACA   3' AAGACAGGTCTGTTGGG    15570      TGTT  A
                                AAGAC   AGG CTGTTGGG
                                |||||   ||| ||||||||
                                TTCTG   TCC GACAACCC
                                  _____  A
GAM2148 RAB26    3' GACTGTTGCTGGGA       30746       TAGGAC
                                GACTGT     TGTTGGGA
                                ||||||     ||||||||
                                CTGACA     ACGACCCT
                                  _______
GAM2148 SHOX     3' AAGACTGTTGGTTTGGGAAA  27813        A  ACTG
                                AAGACTGTT GG    TTGGGAAA
                                ||||||||| ||    ||||||||
                                TTCTGACAA CC    AACCCTTT
                                     _ A___
GAM2148 SLC21A9  3' AAGGCTGCTGGAGTTGGG    28556    A    A  CT
                                AAG CTGTT GGA  GTTGGG
                                ||| ||||| |||  ||||||
                                TTC GACGA CCT  CAACCC
                                  C    _  __
GAM2148 SURF5    3' AAGCTGAGGGACTGTTGGG   39497    A  TTA
                                AAG CTG   GGACTGTTGGG
                                ||| |||   ||||||||||
                                TTC GAC   CCTGACAACCC
                                  _  TC_
GAM2149 ADAM19   3' CAGTGGCTGGCTTGACCC    37764       GC   GAC
                                CAGTGGCT  GGC   GACCC
                                ||||||||  |||   |||||
                                GTCACCGA  CCG   CTGGG
                                     __  AA_
GAM2149 AKAP13   3' GTGGCTGCGCACCTAGACGGTC 28484        _ ___   AC
           C                     GTGGCTGCG GC   GACG  CC
                                |||||||| ||   ||||  ||
                                CACCGACGC TG   CTGC  GG
                                     G  GAT    CA
GAM2149 ATP1B1   5' GTGGCTGCGGCGCGCCCC    11733          A  A
                                GTGGCTGCGGCG CG CCCC
                                |||||||||||| || ||||
                                CACCGACGCCGC GC GGGG
                                     _ _
GAM2149 CLCA3    3' AATGGCTGTTACATTGATTCC  22258       CG   AC  CC
                                AGTGGCTG  GCG  GA  CC
                                ||||||||  |||  ||  ||
                                TTACCGAC  TGT  CT  GG
                                     AA   AA  AA
GAM2149 CREBL2   3' GCGGTGCTGTGCACAACTCC  10582     C  G__  G   _
                                GTGG TGC   GC ACGAC CC
                                ||||  |||   || ||||| ||
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                                CGCC ACG   CG TGTTG GG
                                  _  ACA  _    A
GAM2149  DSCR3    5'  CAGTGGCTCACGTGACC     25820        G  G  AC
                                CAGTGGCT CG CG  GACC
                                |||||||| || ||  ||||
                                GTCACCGA GT GC  CTGG
                                    _ _  A_
GAM2149  GALNT2   3'  CAGTGGCTAACTGACGA     21002         CG  _
                                CAGTGGCTG  GC GACGA
                                |||||||||  || |||||
                                GTCACCGAT  TG CTGCT
                                    __  A
GAM2149  GRIK3    3'  CAGGGCTGCGGCAGAAAC    9095      T        AC
                                CAG GGCTGCGGCG  GAC
                                ||| ||||||||||  |||
                                GTC CCGACGCCGT  TTG
                                  _         CT
GAM2149  HDAC4    5'  ACGGTGCTCCGCGGCGGCGGCC 25743    A   G_       A  A
              CC                  AC GTG  CTGCGGCG CG CCCC
                                || |||  |||||||| || ||||
                                TG CAC  GGCGCCGC GC GGGG
                                 C   GA       C  C
GAM2149  HS3ST4   3'  TACAGTGCTTGGGAGAGA    43870        GC  C  C  C
                                TACAGTG  TG GG GA GA
                                |||||||  || || || ||
                                ATGTCAC  AC CC CT CT
                                    GA  _  T  _
GAM2149  KLHL2    5'  CACCACCTGCGGCGGCGGCCCC 28524    G  G       A  A
                                CA TG CTGCGGCG CG CCCC
                                || || |||||||| || ||||
                                GT GT GACGCCGC GC GGGG
                                 G  G       C  C
GAM2149  KPNB1    5'  GTGGCGGCGGCGGCGACTCC   13977       T     A   _
                                GTGGC GCGGCG CGAC CC
                                ||||| |||||| |||| ||
                                CACCG CGCCGC GCTG GG
                                   C     C   A
GAM2149  LEF1     5'  GCGGTAGCTGGCGACTCC    32211      CT  _     GA
                                GTGG  GC GGCGAC  CC
                                ||||  || ||||||  ||
                                CGCC  CG CCGCTG  GG
                                  AT  A     A_
GAM2149  MTAP     5'  GTGGCTGTGCCAACC       14677        CG  GA
                                GTGGCTG  GC  CGACC
                                |||||||  ||  |||||
                                CACCGAC  CG  GTTGG
                                    A_  __
GAM2149  NAP1L4   5'  GCGGCAGTGGCGGCGACCC   25572       TGC   A
                                GTGGC   GGCG CGACCC
                                |||||   |||| ||||||
```

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                                CGCCG  CCGC GCTGGG
                                  TCA   C
GAM2149 NDUFB7   5' CAGTCGCTGCAGATCCC    19983     G     CGACGA
                                CAGT GCTGCGG    CCC
                                |||| |||||||    |||
                                GTCA CGACGTC    GGG
                                  G     TA____
GAM2149 NPY2R    5' CAGAGGCTGCGGGCGATGGTCC 9489     T     _  CGAC
                                CAG GGCTGCGG CGA   CC
                                ||| |||||||| |||   ||
                                GTC CCGACGCC GCT   GG
                                  T     C  ACCA
GAM2149 NR2F2    5' GCGGCGGGGCGGCGGCGGCTCC 34235     T__    A  AC_
                                GTGGC  GCGGCG CG  CC
                                |||||  |||||| ||  ||
                                CGCCG  CGCCGC GC  GG
                                  CCC    C  CGA
GAM2149 PLXNB3   3' CAGTGGCTGGCTCGGTTCC   23945       GC  GA  AC_
                                CAGTGGCT  GGC  CG  CC
                                ||||||||  |||  ||  ||
                                GTCACCGA  CCG  GC  GG
                                    __  A_  CAA
GAM2149 POU4F1   5' GCGGCGGCTGGCGGCGGCCCC  26390     T  _   A  A
                                GTGGC GC GGCG CG CCCC
                                ||||| || |||| || ||||
                                CGCCG CG CCGC GC GGGG
                                  C  A   C  C
GAM2149 PTP4A2   5' GCGGCGGCGGCGACGACTCC   38634     T       _
                                GTGGC GCGGCGACGAC CC
                                ||||| |||||||||| ||
                                CGCCG CGCCGCTGCTG GG
                                  C         A
GAM2149 PTPRA    5' GCGGCGGCGGCGGCGGCC    38914     T    A  A
                                GTGGC GCGGCG CG CC
                                ||||| |||||| || ||
                                CGCCG CGCCGC GC GG
                                  C     C  C
GAM2149 PYGB     3' CACAGTGGTGGTCAGGGTGGTG 16044       CTG_  CGACGA__
          GCCCC                  TACAGTGG   CGG      CCCC
                                |||||||   |||      ||||
                                GTGTCACC   GTC      GGGG
                                    ACCA  CCACCACC
GAM2149 PYGB     3' CAGGGCTGGCCACGACCC    16045    T  GC  G
                                CAG GGCT  GGC ACGACCC
                                ||| ||||  ||| |||||||
                                GTC CCGA  CCG TGCTGGG
                                  _   __  G
GAM2149 SGT      3' CAGGGCCGCGGCGGCCC     16609    T       ACGA
                                CAG GGCTGCGGCG   CCC
                                ||| ||||||||||   |||
```

```
                                GTC CCGGCGCCGC    GGG
                                  _       C___
GAM2149  SNRPN    5'  TACAGTGGCTGCGGCCAGCCC  35609            GA  A
                                TACAGTGGCTGCGGC  CG CCC
                                |||||||||||||||  || |||
                                ATGTCACCGACGCCG  GT GGG
                                       __  C
GAM2149  TEM7     3'  TACAGTGGCATGATTATGACCC 33812         TGCGGCGAC
              C                  TACAGTGGC        GACCCC
                                |||||||||        ||||||
                                ATGTCACCG        CTGGGG
                                     TACTAATA_
GAM2149  TWIST    3'  CAGTGGCTGATTGGCACGACC  7871          C__   G
                                CAGTGGCTG   GGC ACGACC
                                |||||||||   ||| ||||||
                                GTCACCGAC   CCG TGCTGG
                                     TAA   _
GAM2149  ABCC5    3'  TGAGGTAGGTCTCTTTACA   25027    C  A       C
                                TG GG TAGGTCTCT TACA
                                || || ||||||||| ||||
                                AC CC ATCCAGAGA ATGT
                                 T  _       A
GAM2149  ACCN2    3'  GGTGGGGGGCTATCTCTACA   33452     C  ATA   C_
                                GGTG GG   GGT  TCTCTACA
                                |||| ||   |||  ||||||||
                                CCAC CC   CCG  AGAGATGT
                                  _ ____  AT
GAM2149  GRM6     3'  TAGGTGCGATGGCTC       9176          ATA  T
                                TAGGTGCGG   GG CTC
                                |||||||||   || |||
                                ATCCACGCT   CC GAG
                                     A__  _
GAM2150  COL19A1  3'  ACAGTGTTTCTAATTGTA    12367        CCAT  GTAC
                                ACAGTGTT    TC    TGTA
                                ||||||||    ||    ||||
                                TGTCACAA    AG    ACAT
                                     _____  ATTA
GAM2150  KCNJ6    3'  TACAGTATTTAGCAGTGCTGT  13860         CCATTC  A
                                TACAGTGTT     GT CTGT
                                |||||||||     || ||||
                                ATGTCATAA     CA GACA
                                     ATCGT_  C
GAM2150  MEN1     3'  TACAATGTTCTGCTCCCTGT   39198         CA   GTA
                                TACAGTGTTC  TTC   CTGT
                                ||||||||||  |||   ||||
                                ATGTTACAAG  GAG   GACA
                                     AC   G__
GAM2150  NRIP1    5'  CAGTGTTCTTCTGGCTGT    40956         CA   GTA
                                CAGTGTTC  TTC   CTGT
                                ||||||||  |||   ||||
```

```
                                GTCACAAG  AAG   GACA
                                   __   ACC
GAM2150  PCSK1    3'  CAGTGTTCTAATGTAGTGT    7751         CATTC   C
                                CAGTGTTC     GTA TGT
                                ||||||||     ||| |||
                                GTCACAAG     CAT ACA
                                     ATTA_   C
GAM2150  UBQLN1   3'  TACAGTGTTCCTTCAGTCTGC  30280          A   _  A
                                TACAGTGTTCC TTC GT CTGT
                                |||||||||||| ||| || ||||
                                ATGTCACAAGG AAG CA GACG
                                      _   T  _
GAM2150  DPH2L2   3'  TCAAGTACGAGTTTGAGAAACC 10736     C        C  TCT
              C                  TCA GTACGAGTT GA   AATCT
                                 ||| ||||||||| ||   |||||
                                 AGT CATGCTCAA CT   TTGGG
                                   T        A  CT_
GAM2151  TLX1     3'  TGTGACCCTCTGTCTGGT    24349          C_  C
                                TGTGATCCTC  TC GGT
                                ||||||||||  || |||
                                ACACTGGGAG  AG CCA
                                     AC  A
GAM2151  CHN1     5'  GGAGGTACCTGCGAGGCA    12245          C  _  T
                                GGAGGTACC GT AG CG
                                ||||||||| || || ||
                                CCTCCATGG CG TC GT
                                     A  C  C
GAM2151  PDE4D    5'  GGAGGCACTTGTAGCTGAGTGA 43895         CC    CGT_
                                GGAGGTAC  GTAGT    TGA
                                ||||||||  |||||    |||
                                CCTCCGTG  CATCG    ACT
                                     AA     ACTC
GAM2152  CACNB1   3'  GGACAGTGGTTTTATAT     8783         ATTTATT
                                GGACAGT      TTTTATAT
                                |||||||      ||||||||
                                CCTGTCA      AAAATATA
                                   CC_____
GAM2152  YES1     3'  TGGACAGTAGTTTCAATTATAT 24121          T  A  TT
              A                  TGGACAGTA TT TT  TTATATA
                                 ||||||||| || ||  |||||||
                                 ACCTGTCAT AA AG  AATATAT
                                      C  _  TT
GAM2153  ADCY7    3'  TGGAAATAAAAATGCAT     9991           AACTC
                                TGGAAATAAAGA     GCAT
                                ||||||||||||    ||||
                                ACCTTTATTTTT     CGTA
                                      A____
GAM2153  AGTR1    3'  TGGAAATAAAAAATAACA    28925           ACTC
                                TGGAAATAAAGAA    GCA
                                ||||||||||||    |||
```

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                                ACCTTTATTTTTT   TGT
                                      AT__
GAM2153 BID     3' TGGAAATAAAGGCACCG    10180        AA  T
                                TGGAAATAAAG  AC CG
                                |||||||||||  || ||
                                ACCTTTATTTC  TG GC
                                      CG  _
GAM2153 COL19A1  3' TGGAAATAAACACA      12387        GAAACT
                                TGGAAATAAA    CGCA
                                ||||||||||    ||||
                                ACCTTTATTT    GTGT
                                      _______
GAM2153 GABRA1   3' TATGAAAATAAGGAAACT   9040          A
                                TATGGAAATAA GAAACT
                                |||||||||| ||||||
                                ATACTTTTATT CTTTGA
                                      C
GAM2154 OCRL    3' GTAGAGCCCAGAGT       11483     T   GTTG
                                GTAG AGCC   TAGAGT
                                |||| ||||   ||||||
                                CATC TCGG   GTCTCA
                                  _   _____
GAM2154 PRKCG   3' GCTGTAGAGGCTGTATGGAGT 15627   A   CC    __
                                GT GTAG  GTTGTA  GAGT
                                || ||||  ||||||  ||||
                                CG CATC  CGACAT  CTCA
                                 A   TC     AC
GAM2155 DNMT2   3' TCAAGTATTTATAGTTGGT   20632          CAC   A
                                TCAAGTATTTATA   GTTG GT
                                ||||||||||||   |||| ||
                                AGTTCATAAATAT   CAAC CA
                                      ___   _
GAM2155 EEF2    3' TCAAGTGTTATGGTTGAGT   45412      AT   ACAC
                                TCAAGT  TTAT   GTTGAGT
                                ||||||  ||||   |||||||
                                AGTTCA  AATA   CAACTCA
                                   C_   C___
GAM2155 PX19    3' CAAGTATTTATTGAG      29874         ACACGT
                                CAAGTATTTAT     TGAG
                                ||||||||||     ||||
                                GTTCATAAATA     ACTC
                                      _______
GAM2156 CROT    3' GAGCATGATTCTACTAATTTC 34497   A  CA       C
                                GA CA  ATTCTACTAA TTC
                                || ||  |||||||||| |||
                                CT GT  TAAGATGATT AAG
                                 C  AC        A
GAM2156 CX3CR1  3' TTGAGCACAATTCTCAAC   43303     A       AC
                                TTGA CACAATTCT  TAAC
                                |||| |||||||||  ||||
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                                AACT GTGTTAAGA  GTTG
                                  C       __
GAM2156 HCS      3'  CCTGAATACCACTAACTT    33228       CACAATT
                                CTTGAA      CTACTAACTT
                                ||||||      ||||||||||
                                GGACTT      GGTGATTGAA
                                   AT_____
GAM2156 TNFSF4   3'  TTCTAGTTTCAATTATCAATGT 17760          CTC   T  C
             GA                   TTTTAGTTTCAA   TTA TG GA
                                ||||||||||||   ||| || ||
                                AAGATCAAAGTT   AGT AC CT
                                      AAT   T  A
GAM2157 ATP7A    3'  TAAAACTAGATGTTTTATACAC 6263          AATC
                                TAAAACTAGGT    TATACAC
                                ||||||||||    |||||||
                                ATTTTGATCTA    ATATGTG
                                      CAAA
GAM2157 CALU     3'  TATAAAACTTGGTTTACAC    10263         A   AATC
                                TATAAAACT GGT    TATAC
                                |||||||| |||    |||||
                                ATATTTTGA CCA    ATGTG
                                     A   A___
GAM2157 EFNB2    3'  TACAAGACTAGGTAAGCT     19883       A       T
                                TATAA ACTAGGTAA CT
                                ||||| |||||||| ||
                                ATGTT TGATCCATT GA
                                   C        C
GAM2157 MPHOSPH1 3'  TATAAAACAGCAATCTATA    32117        TA
                                TATAAAAC  GGTAATCTATA
                                ||||||||  ||||||||||
                                ATATTTTG  TCGTTAGATAT
                                          __
GAM2157 POLR2J   3'  TATAAAACCTAATCTAT      26359         AGG
                                TATAAAACT   TAATCTAT
                                |||||||||   ||||||||
                                ATATTTTGG   ATTAGATA
                                          ___
GAM2157 PRPS2    3'  TAAAACTAGCTCTATACA     15733         GTAA
                                TAAAACTAG    TCTATACA
                                |||||||||    ||||||||
                                ATTTTGATC    AGATATGT
                                     G___
GAM2157 SLC2A1   3'  TATAAATATCTTGCATCTATAC 27144       ACTAG_  A
             AC                   TATAAA     GTA TCTATACAC
                                ||||||     ||| |||||||||
                                ATATTT     CGT AGATATGTG
                                   ATAGAA  _
GAM2157 STC1     3'  TACAAAACTAAATCTATA     17181         GGT
                                TATAAAACTA   AATCTATA
                                ||||||||||   ||||||||
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                                ATGTTTTGAT   TTAGATAT
                                    ___
GAM2157 TFRC     3'  TAAATCTAGGTAAGTGACAC   17432      A       TCT
                                TAAA CTAGGTAA   ATAC
                                |||| ||||||||   ||||
                                ATTT GATCCATT   TGTG
                                  A       CAC
GAM2158 ACRC     3'  TATAATACTTCTGCACATACAC 38128        C   A   C_
              A                   TATAATAC TTT CAC  ACGCA
                                |||||||| ||| |||  |||||
                                ATATTATG AGA GTG  TGTGT
                                     A   C   TA
GAM2159 ABR      3'  AGGAAGACTGAGGGGAGGC    35005         A  AAAA
                                AGGAAGATT AG    AGGC
                                ||||||||| ||    ||||
                                TCCTTCTGA TC    TCCG
                                     C  CCC_
GAM2159 ADRB3    3'  GAAGATTAGGAAGAAAAGAG   6179          ___     AG
                                GAAGATTA   AGAAAA  G
                                ||||||||   ||||||  |
                                CTTCTAAT   TCTTTT  C
                                     CCT     CT
GAM2159 ALOX15   3'  AGGAAGATAGGAAAGG      10073         TAA   AA
                                AGGAAGAT   GAA  AGG
                                ||||||||   |||  |||
                                TCCTTCTA   CTT  TCC
                                     TC_  __
GAM2159 CDC27    3'  AGGGAGATTAAAGAAAAA    10366     A      _
                                AGG AGATTAA GAAAAA
                                ||| ||||||| ||||||
                                TCC TCTAATT CTTTTT
                                  C      T
GAM2159 DDB2     5'  GGAGGATTGAGAGGCCTC    6463      A   A   AAAA
                                GGA GATT AGA    GGCCTC
                                ||| |||| |||    ||||||
                                CCT CTAA TCT    CCGGAG
                                  C    C  _____
GAM2159 HHLA1    5'  GGAGAGATTAAGCTGAAGG   25052     _       AAA
                                GGA AGATTAAG   AAGG
                                ||| ||||||||   ||||
                                CCT TCTAATTC   TTCC
                                  C       GAC
GAM2159 KCNK5    3'  GGAAGGTTAGGAAGGCCCC   19037       A   A  AAA
                                GGAAG TTA GA   AGGCCTC
                                ||||| ||| ||   |||||||
                                CCTTC AAT CT   TCCGGGG
                                   C   C  ___
GAM2159 MUTYH    5'  GGGAGAGGGGAAGGCCTC    29223    A   TTAA  AAA
                                GG AGA    GA   AGGCCTC
                                || |||    ||   |||||||
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                                CC TCT   CT  TCCGGAG
                                 C  CCC_ ___
GAM2159 NR2E1   5' AGGAAGACTGAGGAAGAAG   17572       AA_  A
                                AGGAAGATT  GAA AAG
                                |||||||||  ||| |||
                                TCCTTCTGA  CTT TTC
                                     CTC  C
GAM2159 PTK2B   3' AGGAGGAGTAAGAAAAGAG   19916    A T     AG
                                AGGA GA TAAGAAAA  G
                                |||| || ||||||||  |
                                TCCT CT ATTCTTTT  C
                                  C  C      CT
GAM2159 SGPL1   3' AGGAAGATAAGAGGAAG    45039       T   AA
                                AGGAAGAT AAGA  AAG
                                |||||||| ||||  |||
                                TCCTTCTA TTCT  TTC
                                    _   CC
GAM2159 TAF1    3' AGGAAGATTAGGAGAGG    39887        A  AAA
                                AGGAAGATTA GA  AGG
                                |||||||||| ||  |||
                                TCCTTCTAAT CT  TCC
                                     C  C__
GAM2159 TNFRSF6  5' AGGAGGATGGGAAGGAAGCCTC 6219     A  TAA  AA
          G                      AGGA GAT  GAA  AGGCCTCG
                                |||| |||  |||  ||||||||
                                TCCT CTA  CTT  TTCGGAGC
                                  C  CC_  CC
GAM2159 ZFP36L1  3' AGATCGGGAAGAAAAAGG   22279     ___
                                AGATT  AAGAAAAAGG
                                |||||  ||||||||||
                                TCTAG  TTCTTTTTCC
                                   CCC
GAM2159 BMPR1B   3' AGTACCTGTTGGCTTTCT    10200     T   _
                                AGTA CCTGT GGTTTTTT
                                |||| ||||| ||||||||
                                TCAT GGACA CCGAAAGA
                                  _    A
GAM2159 CRY2    3' GTATCTGTGTGTACTTCT    43585     C   GTTTT
                                GTATC TGTG    TTTCT
                                ||||| ||||    |||||
                                CATAG ACAC    GAAGA
                                   _   ACAT_
GAM2159 EGFL5   5' AAGATCTTGGGACTTTTCTAC  44509    T  CTG  TT
                                AAG ATC  TGG  TTTTTCTAC
                                ||| |||  |||  |||||||||
                                TTC TAG  ACC  GAAAAGATG
                                  _  A__  CT
GAM2159 NFATC1  3' TATCCTGTAACAGGTTTTTCT  26080       ____
                                TATCCTGT   GGTTTTTTT
                                ||||||||   |||||||||
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                                ATAGGACA   CCAAAAAGA
                                    TTGT
GAM2160 PPP1R12B 3' TTGTGTGGACTCTGGGTT   36987     CA    AAACT
                                TTGTG  GATTT    TGGGTT
                                ||||| |||||    ||||||
                                AACAC  CTGAG    ACCCAA
                                  AC    _____
GAM2160 TCF7L2   5' TTCTGCACGCGTGAGTTTGGGT 36253    G   GATTTAAAC
           TT                    TT TGCA       TTGGGTTT
                                || ||||       ||||||||
                                AA ACGT       AACCCAAA
                                 G   GCGCACTCA
GAM2161 SPARC    3' TCATTTTTAGCACCGTTA    17069       AATC   C
                                TCATTTTT   AGC CCGTTA
                                ||||||||   ||| ||||||
                                AGTAAAAA   TCG GGCAAT
                                    ____   T
GAM2161 FACL4    5' CAATCGGAGGGGCGGCCCAC   20886       A__   AAA
                                CAATCGGA   GTG   CCAC
                                ||||||||   |||   ||||
                                GTTAGCCT   CGC   GGTG
                                    CCC   CG_
GAM2161 SMURF1   3' TCCAGCTGGTTCCATAACCACA 45199     ATC  AAGTGA
           T                    TCCA   GG     AACCACAT
                                ||||   ||     ||||||||
                                AGGT   CC     TTGGTGTA
                                  CGA  AAGGTA
GAM2162 BMPR1B   3' ACAAGTTACCCAACGGTTT   10199     TC_    TCCG
                                ACAA   ACCCG   TGGTTT
                                ||||   |||||   ||||||
                                TGTT   TGGGT   GCCAAA
                                  CAA    T___
GAM2162 DLST     3' ACATGGTCCCCGGGGGTTT   12569    CAA  A   TCCGT
                                ACA   TC CCCG    GGTTT
                                |||   || ||||    |||||
                                TGT   AG GGGC    CCAAA
                                  ACC  _   CC___
GAM2162 GALNT2   3' CACAGTCGTCCGTGCCTT    21000     ATCACC      G
                                CACA     CGTCCGTG TTT
                                ||||     |||||||| |||
                                GTGT     GCAGGCAC GAA
                                  CA____       G
GAM2162 PTTG1IP  3' ACACAGACGCTGTCCGTGGTTT 20277      ATCACCC
                                ACACA      GTCCGTGGTTT
                                |||||      ||||||||||
                                TGTGT      CAGGCACCAAA
                                  CTGCGA_
GAM2162 SLC9A5   5' CACAATCTTGGTGGTTT     21382       ACCCGTCC
                                CACAATC       GTGGTTT
                                |||||||       |||||||
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                                GTGTTAG       CACCAAA
                                   AAC_____
GAM2162 ZNF236   5' ACACAATCCTTTGTAGTTT   28856        ACCCGTCC
                                ACACAATC      GTGGTTT
                                ||||||||      |||||||
                                TGTGTTAG      CATCAAA
                                   GAAA____
GAM2162 ARMET    5' CGCGAGCCCAGACGCGG    25664    ACA    GC
                                CG   GGCCC  AGACGCGG
                                ||   |||||  ||||||||
                                GC   TCGGG  TCTGCGCC
                                 GC_    __
GAM2162 AVP      5' CGTGGAGGCGAGACGCGG    7935     AC_   CCGC
                                CG   AGGC   AGACGCGG
                                ||   ||||   ||||||||
                                GC   TCCG   TCTGCGCC
                                 ACC   C___
GAM2162 CGTHBA   3' CACATGGGCCTTGAAGGATGCG 28959     ACA   CGCA__  C
             GC                   CACG   GGCC     GA GCGGC
                                ||||   ||||     || |||||
                                GTGT   CCGG     CT CGCCG
                                  AC_   AACTTC  A
GAM2162 COX7A1   5' GACAGCTGGGGACGCGGC    12409      G CCGCA
                                GACAG C     GACGCGGC
                                ||||| |     ||||||||
                                CTGTC G     CTGCGCCG
                                  _ ACCC_
GAM2162 FBXL3A   5' CGCGGAGGGCGCCAACGCGGC 29126    AC_   CC   A
                                CG   AGG  CGC GACGCGGC
                                ||   |||  ||| ||||||||
                                GC   TCC  GCG TTGCGCCG
                                 GCC   C_   G
GAM2162 GNA14    5' CGACGGGGCGACGCGG     20192     A  CCC  A
                                CGAC GG   GC GACGCGG
                                |||| ||   || |||||||
                                GCTG CC   CG CTGCGCC
                                  C ___  _
GAM2162 GPR30    3' CACGGCAGCTCGCACGG     11304     ACA   C   AGAC
                                CACG   GGC CGC    GCGG
                                ||||   ||| |||    ||||
                                GTGC   TCG GCG    TGCC
                                  CG_   A  ____
GAM2162 HDAC4    5' CGACAGCCGGGACGCGGC    25754      GC   CA
                                CGACAG  CCG  GACGCGGC
                                ||||||  |||  ||||||||
                                GCTGTC  GGC  CTGCGCCG
                                   __   C_
GAM2162 HLCS     5' ACGCAGAAGACGCGGC      7632      A   CCCGC
                                ACG CAGG    AGACGCGGC
                                ||| ||||    |||||||||
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                                TGC GTCT    TCTGCGCCG
                                  _  _____
GAM2162 HMGA1   3' CAGCAGGTGCAGGGTGCGGC  44160   A   CCC   AC_
                                CG CAGG  GCAG  GCGGC
                                || ||||  ||||  |||||
                                GT GTCC  CGTC  CGCCG
                                 C   A__   CCA
GAM2162 IL9R    5' CACGACAGGTTCACACAGGC  13517       CCCG  G  C
                                CACGACAGG   CA ACG GGC
                                |||||||||   || ||| |||
                                GTGCTGTCC   GT TGT CCG
                                     AA__  G  _
GAM2162 LENG4   3' ACGCAGGATGCAGACGCGGC  35876   A   CCC
                                ACG CAGG  GCAGACGCGGC
                                ||| ||||  ||||||||||
                                TGC GTCC  CGTCTGCGCCG
                                  _   TA_
GAM2162 NDUFS7  3' CGACAGGCTCCGGCGG     35902       _  CAGAC
                                CGACAGGC CCG   GCGG
                                |||||||| |||   ||||
                                GCTGTCCG GGC   CGCC
                                     A  _____
GAM2162 PACE4   5' CGACAGGCTCGCGCGG     15047       C  AGAC
                                CGACAGGC CGC   GCGG
                                |||||||| |||   ||||
                                GCTGTCCG GCG   CGCC
                                     A  ____
GAM2162 PDGFB   5' CGACAGGTGGACGCGG     15173       CCCGCA
                                CGACAGG    GACGCGG
                                |||||||    |||||||
                                GCTGTCC    CTGCGCC
                                    AC____
GAM2162 RNMT    3' ACAGCGCCTGCAGGTGTGGC  19145    _  C   ACGC
                                ACAG GCC GCAG   GGC
                                |||| ||| ||||   |||
                                TGTC CGG CGTC   CCG
                                  G  A   CACA
GAM2162 WNT1    5' CGACGGTGGGACGGGACGCGGC 24078    A__  CC  CA
                                CGAC  GG  CG  GACGCGGC
                                ||||  ||  ||  ||||||||
                                GCTG  CC  GC  CTGCGCCG
                                  CCA  CT  C_
GAM2163 ENO2    5' TCGGGACTGCAGACTCAGACGG 12716   A   C      TTA__
            TG                  TC GGAC TGCAGACTC    GTG
                                || |||| |||||||||    |||
                                AG CCTG ACGTCTGAG    CAC
                                 C   _       TCTGC
GAM2163 TCF1    3' TCAGGACCTCAGACTCCT    8091         G
                                TCAGGACCT CAGACTCTT
                                ||||||||| |||||||||
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                                AGTCCTGGA GTCTGAGGA
                                        _
GAM2163  TRIM14   3'  TCAGGACCTCAGACTCCCCAGA 37706          G        AGT
                                TCAGGACCT CAGACTCTT   GA
                                ||||||||| |||||||||   ||
                                AGTCCTGGA GTCTGAGGG   CT
                                      _       GT_
GAM2164  SHOX     3'  TATGATCGCACCAGT       27829          A AATAGA
                                TATGATCG C     GCCAGT
                                |||||||| |     ||||||
                                ATACTAGC G     TGGTCA
                                      _ _______
GAM2165  SPG4     3'  TAGATTTATGAAGAAGAAACTC 31401      C     TAT
              T                  TAGA TTTGT   GGAGAAACTCT
                                |||| |||||   ||||||||||
                                ATCT AAATA   CTTCTTTGAGA
                                  _    CTT
GAM2166  KLRG1    3'  TGCTATCTTGAAATTAATA   25156     CA    A
                                TGT  TATC TGAAATTAATA
                                |||  |||| ||||||||||
                                ACG  ATAG ACTTTAATTAT
                                  __    A
GAM2166  RCN2     3'  TGTCATATGGCACAATATTAAT 16217         __  TG A
              A                  TGTCATAT  CA  A ATTAATA
                                |||||||  ||  | |||||||
                                ACAGTATA  GT  T TAATTAT
                                     CC  GT A
GAM2167  ZNF217   3'  TTATGTTTATACAACGT     27193           ACT
                                TTATGTTTATA   CGACGT
                                ||||||||||   ||||||
                                AATACAAATAT   GTTGCA
                                      ___
GAM2168  DPP4     5'  GCGCGTCCTGCACCGCTGCTCC 12580      A      A   _  G
              G                   GCGC TCCTGCA CTGC GC TCCG
                                |||| ||||||| |||| || ||||
                                CGCG AGGACGT GGCG CG AGGC
                                  C       _    A  _
GAM2168  NR3C2    3'  GCGCATCCTGCCATGATC    9471           AAC  CGC
                                GCGCATCCTGC   TG   GTC
                                ||||||||||   ||   |||
                                CGCGTAGGACG   AC   TAG
                                      GT_  ___
GAM2168  RENT1    3'  GCGCGACCTCGGCGCGTCC    16255     AT   GCAACT
                                GCGC  CCT     GCGCGTCC
                                ||||  |||     ||||||||
                                CGCG  GGA     CGCGCAGG
                                  CT   GC____
GAM2169  APPBP2   3'  GGAACCCGGGAGGCGGA     26881        ACCA
                                GGAACCC    GAGGCGGA
                                |||||||    ||||||||
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                                CCTTGGG   CTCCGCCT
                                   CC__
GAM2169 ARCN1    3' GAACCCAGGAGGCGGA     11653       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                   C__
GAM2169 BAP1     3' GGGCCCACCAGGACAG     21647    AA      A
                                GG  CCCACCAG GGCGG
                                ||  |||||||| |||||
                                CC  GGGTGGTC CTGTC
                                 C_      _
GAM2169 CHST6    3' CCGGGCAGAGGCGGA      34676     AACCCAC
                                CCGG      CAGAGGCGGA
                                ||||      ||||||||||
                                GGCC      GTCTCCGCCT
                                  C_______
GAM2169 COL5A1   3' GGAGGTTGTTAAAAACGGAGGC 6418     ACCCACC       A
                                GGA      AGAGGCGGA GC
                                |||      ||||||||| ||
                                CCT      TTTTTGCCT CG
                                  CCAACAA       C
GAM2169 CRTAP    3' GAACCCAAGAGGCGGA     26841       CC
                                GAACCCA  AGAGGCGGA
                                |||||||  |||||||||
                                CTTGGGT  TCTCCGCCT
                                   __
GAM2169 CYP4F3   3' CCCGAACGCAGGAGGCGGA  9453    G   C  CCA
                                CC GAAC CA   GAGGCGGA
                                || |||| ||   ||||||||
                                GG CTTG GT   CTCCGCCT
                                 G   C  C__
GAM2169 DFFB     3' GAACCTGAGAGGCGGA     44599     CACC
                                GAACC    AGAGGCGGA
                                |||||    |||||||||
                                CTTGG    TCTCCGCCT
                                   AC__
GAM2169 DSCR1L2  3' CCAGAGCCCACCAGGGCAG  30281      A      A
                                CCGGA CCCACCAG GGCGG
                                ||||| |||||||| |||||
                                GGTCT GGGTGGTC CCGTC
                                   C      _
GAM2169 EGFL4    3' CGGAAGGCGGGAGGTGGGAGC 41566      CCCACCA   C  A
                                CGGAA      GAGG GG AGC
                                |||||      |||| || |||
                                GCCTT      CTCC CC TCG
                                   CCGCC__    A  C
GAM2169 EPB72    3' GAACCCAGGAGGCGGA     19899       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
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                                CTTGGGT  CTCCGCCT
                                   C__
GAM2169  FBXW1B   5'  CGGAGGCGGGCAGAGGCGGAGG 37989     ACCCAC       A
             C                   CGGA     CAGAGGCGGA GC
                                ||||     |||||||||| ||
                                GCCT     GTCTCCGCCT CG
                                  CCGCCC        C
GAM2169  FUT1     3'  GAACACAGGAGGCGGAAG    6633      C  CCA
                                GAAC CA   GAGGCGGAAG
                                |||| ||   ||||||||||
                                CTTG GT   CTCCGCCTTC
                                  T  C__
GAM2169  GAS11    3'  GGAGCCGCCGCAGAAG      11216     AC  A  AGAG
                                GGA  CC CC    GCGGAAG
                                |||  || ||    |||||||
                                CCT  GG GG    CGTCTTC
                                  C_  C  _____
GAM2169  GATA3    5'  CCGGAACCCGCGCGGGGAGGGA 13093         ACCAGA  C_
             AG                   CCGGAACCC     GG  GGAAG
                                |||||||||     ||  |||||
                                GGCCTTGGG     CC  CCTTC
                                     CGCGCC  TC
GAM2169  GM2A     3'  GAACCCAGGAGGCGGA      42688       CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                   C__
GAM2169  GRAF     3'  GAACCCGGGAGGCGGA      31445       ACCA
                                GAACCC    GAGGCGGA
                                ||||||    ||||||||
                                CTTGGG    CTCCGCCT
                                   CC__
GAM2169  HLCS     5'  GGAACCCAGTAGGCAGA      7641        CCAG
                                GGAACCCA    AGGCGGA
                                ||||||||    |||||||
                                CCTTGGGT    TCCGTCT
                                     CA__
GAM2169  HTR1E    5'  CCGCGAACCCGGGAGGCGGA   9270      _     ACCA
                                CCG GAACCC    GAGGCGGA
                                ||| ||||||    ||||||||
                                GGC CTTGGG    CTCCGCCT
                                  G     CC__
GAM2169  ITGAM    3'  GAACCCGGGAGGCGGA      43514       ACCA
                                GAACCC    GAGGCGGA
                                ||||||    ||||||||
                                CTTGGG    CTCCGCCT
                                   CC__
GAM2169  LILRA3   3'  GAACCCGAGAGGCGGA      45463       ACC
                                GAACCC   AGAGGCGGA
                                ||||||   |||||||||
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                              CTTGGG  TCTCCGCCT
                                 C__
GAM2169 MAFF    3' CCAGGCCCAACCAGAGGTGGGG 29511     AA C      C AA
           GC                  CCGG  CC ACCAGAGG GG  GC
                               ||||  || |||||||| ||  ||
                               GGTC  GG TGGTCTCC CC  CG
                                 CG  T       A  CC
GAM2169 MHC2TA  3' GAACCCAAGAGGCGGA     6982        CC
                               GAACCCA  AGAGGCGGA
                               |||||||  |||||||||
                               CTTGGGT  TCTCCGCCT
                                  __
GAM2169 MRPL23  5' CCGGGGTCCGCGAGGCGGAGGA 34454     AAC  ACCA      __
           GC                  CCGG   CC   GAGGCGGA  AGC
                               ||||   ||   ||||||||  |||
                               GGCC   GG   CTCCGCCT  TCG
                                 CCA  CG__       CC
GAM2169 NDUFB3  5' CCGGAGCCAACCGGAAACGGA  14743      A  C   A
                               CCGGA CC ACC GAGGCGGA
                               ||||| || ||| ||||||||
                               GGCCT GG TGG CTTTGCCT
                                 C  T   C
GAM2169 PABPC4  5' CGGAAACGGGAGGCGGGGGC   19222      CCC  CA     AA
                               CGGAA   AC  GAGGCGG  GC
                               |||||   ||  |||||||  ||
                               GCCTT   TG  CTCCGCC  CG
                                  ___ CC      CC
GAM2169 PK428   5' CCGCGCACAGAGGCGGAG    18799     GAACC   C       A
                               CCG    CAC AGAGGCGGA G
                               |||    ||| ||||||||| |
                               GGC    GTG TCTCCGCCT C
                                 GC___  _       C
GAM2169 PRKACA  3' CCAGGATGGGGGAGGCGGAAGC 15576     AACCCACCA
                               CCGG        GAGGCGGAAGC
                               ||||        ||||||||||
                               GGTC        CTCCGCCTTCG
                                 CTACCCC__
GAM2169 PTGES   3' GAACCCGGGAGGCGGAGGC   22181       ACCA       A
                               GAACCC   GAGGCGGA GC
                               ||||||   |||||||| ||
                               CTTGGG   CTCCGCCT CG
                                  CC__       C
GAM2169 RFNG    3' CCGCAGCCCACCAGGGGC    44767     GAA       A
                               CCG   CCCACCAG GGC
                               |||   |||||||| |||
                               GGC   GGGTGGTC CCG
                                 GTC       C
GAM2169 SEDL    3' CCTGAACCTGGGAGGCGGA   31004    G    CACCA
                               CC GAACC    GAGGCGGA
                               || |||||    ||||||||
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                                GG CTTGG     CTCCGCCT
                                 A     ACC__
GAM2169  SIRT6     3'  CCGGAACCGCACCAGAGGC   32417         _
                                CCGGAACC CACCAGAGGC
                                |||||||| ||||||||||
                                GGCCTTGG GTGGTCTCCG
                                     C
GAM2169  SKIV2L    5'  CCGGAACGGGCGGAA       27971        CCACCAGA
                                CCGGAAC       GGCGGAA
                                |||||||       |||||||
                                GGCCTTG       CCGCCTT
                                    C_______
GAM2169  SULT2B1   5'  GAACCCAGGAGGCGGA      21418        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2169  TAL1      5'  CCGGAAAGGGGCGGAAG     17281        CCCACC  A
                                CCGGAA     AG GGCGGAAG
                                ||||||     || ||||||||
                                GGCCTT     TC CCGCCTTC
                                   _______  C
GAM2169  TAPBP     3'  GAACCCAGGAGGCGGA      17300        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2169  TBXA2R    3'  GAACCCGGGAGGCGGA      9853         ACCA
                                GAACCC    GAGGCGGA
                                ||||||    ||||||||
                                CTTGGG    CTCCGCCT
                                   CC__
GAM2169  TCOF1     3'  CGGGATCAGCCAGAGACCGAGC 7409      AACC  _      G  A
                                CGG    CA CCAGAGGC GA GC
                                |||    || |||||||| || ||
                                GCC    GT GGTCTCTG CT CG
                                  CTA_  C       G  _
GAM2169  TFG       5'  GGAAGAACAGAGGCGGGAGC   25873      CCCAC        A
                                GGAA     CAGAGGCGG AGC
                                ||||     ||||||||| |||
                                CCTT     GTCTCCGCC TCG
                                  CTT__        C
GAM2169  TNFRSF10B 3'  GAACCCAGGAGGCGGA      19285        CCA
                                GAACCCA   GAGGCGGA
                                |||||||   ||||||||
                                CTTGGGT   CTCCGCCT
                                    C__
GAM2169  TRPV1     3'  GGAATCCAGGAGGCGGA     38796      C   CCA
                                GGAA CCA   GAGGCGGA
                                |||| |||   ||||||||
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                                CCTT GGT   CTCCGCCT
                                  A  C__
GAM2169  TRPV4    5'  CCGGCCAGGGGCGGGG      41345      AACCCA   A    AA
                                CCGG     CCAG GGCGG  G
                                ||||     |||| |||||  |
                                GGCC     GGTC CCGCC  C
                                  _______   C    CC
GAM2169  UBE2A    5'  GGAGAAGGGGAGGCGGAAGC   17786     ACCCACCA
                                GGA      GAGGCGGAAGC
                                |||      ||||||||||
                                CCT      CTCCGCCTTCG
                                 CTTCCC__
GAM2169  VENTX2   3'  GAACCCAGGAGGCGGA      30915       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                    C__
GAM2169  VHL      3'  GGACCAGAGGCTGGA       8113      ACCCA      _
                                GGA    CCAGAGGC GGA
                                |||    |||||||| |||
                                CCT    GGTCTCCG CCT
                                 _____       A
GAM2169  WHSC1    3'  GGAACCAAGGAGGCGGA     39404       CACCA
                                GGAACC    GAGGCGGA
                                ||||||    ||||||||
                                CCTTGG    CTCCGCCT
                                   TTC__
GAM2169  WWOX     3'  CCGAGGCCCACCAAGGGGG   39110      AA      A  C
                                CCGG  CCCACCAG GG GG
                                ||||  |||||||| || ||
                                GGCT  GGGTGGTT CC CC
                                  CC       C  _
GAM2169  ZNF264   3'  GAACCCAGGAGGCGGA      18271       CCA
                                GAACCCA  GAGGCGGA
                                |||||||  ||||||||
                                CTTGGGT  CTCCGCCT
                                    C__
GAM2169  ZNF42    5'  CAGGGCCTGGAGAAGGCGGAAG 18290     AA  CACCA
             C                   CGG  CC    GAGGCGGAAGC
                                 |||  ||    ||||||||||
                                 GTC  GG    TTCCGCCTTCG
                                   CC  ACCTC
GAM2170  ATP10C   5'  TAGGTTATCATCACTCGC    35982        TGATGA   C
                                TAGGTTATT     CAC CGC
                                |||||||||     ||| |||
                                ATCCAATAG     GTG GCG
                                     TA____   A
GAM2170  CX3CR1   3'  AAGTTCTGATGACATTTGCAG  43289      TA        CCC
                                AGGT  TTTGATGACA   GCAG
                                ||||  ||||||||||   ||||
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                                TTCA  AGACTACTGT   CGTC
                                  __         AAA
GAM2170  TRPM1    3'  TAGGCTATTTGGTGGCCCTCAG 14540          A  ACA   G
                                TAGGTTATTTG TG   CCC CAG
                                |||||||||||  ||   |||  |||
                                ATCCGATAAAC AC   GGG GTC
                                      C  C__   A
GAM2171  ABCB10   3'  TTCATAGTCTCTGAGTTT    28990      TG
                                TTTAT  AGTCTCTGAGTTT
                                |||||  ||||||||||||||
                                AAGTA  TCAGAGACTCAAA
                                  __
GAM2171  ABCD3    3'  TTTATAGGATATCTGAGTTT   16022      T_  GTC
                                TTTAT  GA   TCTGAGTTT
                                |||||  ||   |||||||||
                                AAATA  CT   AGACTCAAA
                                   TC  AT_
GAM2171  ADCY4    3'  TCTCTTTATTGAGGTTCT    40204    C        TC
                                TC CTTTATTGAG  TCT
                                || ||||||||||  |||
                                AG GAAATAACTC  AGA
                                 A         CA
GAM2171  PDX1     3'  CCTTTATTAGTTAGAGTTT    18488        G   CTCT
                                CCTTTATT AGT    GAGTTT
                                |||||||| |||    ||||||
                                GGAAATAA TCA    CTCAAA
                                     _  AT__
GAM2171  PSMB7    3'  TTTATTGAGTTGAGTTT     15825          CTC
                                TTTATTGAGT   TGAGTTT
                                ||||||||||   |||||||
                                AAATAACTCA   ACTCAAA
                                       ___
GAM2171  UCP3     3'  TTTATTGAGTCATAATAATTT  17861           TCTG_
                                TTTATTGAGTC    AGTTT
                                ||||||||||     |||||
                                AAATAACTCAG    TTAAA
                                      TATTA
GAM2172  MMP13    3'  CTGTGTGAAGAAGGGCACATA  14553    A  _  CT
                                CT TGT AAG  GGGGGCACATA
                                || ||| |||  ||||||||||
                                GA ACA TTC  TTCCCGTGTAT
                                 C  C  __
GAM2172  XK       3'  GACTGGTAAGTACTGGCACATA 34361      AT    C  GG
                                GACT  GTAAG TG  GGCACATA
                                ||||  ||||| ||  ||||||||
                                CTGA  CATTC AT  CCGTGTAT
                                  C_    _ GA
GAM2173  DAG1     3'  ACTTGGCGTGAGCCAGGGC   20516    C   ATAA  T   C
                                AC TGGC    GG GCC GGGC
                                || ||||    || ||| ||||
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                                TG ACCG    CT CGG CCCG
                                 A    CA__  _   T
GAM2173  EGLN2    5'  TACCTGGCCTAAGGAAGGGC   38834        A     TGCCC
                                TACCTGGC TAAGG     GGGC
                                |||||||| |||||     ||||
                                ATGGACCG ATTCC     CCCG
                                    G     TT___
GAM2173  EMD      5'  CCTGGCGGCGGCCCGGGC     6488        ATAA   _
                                CCTGGC    GGTG CCCGGGC
                                ||||||    |||| |||||||
                                GGACCG    CCGC GGGCCCG
                                   _____    C
GAM2173  GPR4     5'  CTGGCACAGGGTGGA       40882         A   GCCC
                                CTGGCATA GGT    GGG
                                |||||||| |||    |||
                                GACCGTGT CCA    CCT
                                    C   _____
GAM2173  KCNQ2    5'  CCTGGCGGGAGGCGCCCCGGG  41507       ATA      _
                                CCTGGC   AGGTGCCC GGG
                                ||||||   |||||||| |||
                                GGACCG   TCCGCGGG CCC
                                   CCC       G
GAM2173  LAD1     3'  CCTGGCATGAGGGAGG      24488         A   TGCCC
                                CCTGGCAT AGG     GGG
                                |||||||| |||     |||
                                GGACCGTA TCC     TCC
                                    C   C_____
GAM2173  MAGEC1   5'  CCTGGCACTGCCTGGG      24165         AAGG    C
                                CCTGGCAT    TGCC GGG
                                ||||||||    |||| |||
                                GGACCGTG    ACGG CCC
                                   _____    A
GAM2173  PPID     5'  TACCTAGTGGCCGCCCGGGC   44617        CATAA  _
                                TACCTGG     GGT GCCCGGGC
                                |||||||     ||| ||||||||
                                ATGGATC     CCG CGGGCCCG
                                    A_____   G
GAM2173  RANBP3   3'  CCTGGTGTGCAGCCGGGC     28777      CATAAG   __
                                CCTGG     GTGC  CCGGGC
                                |||||     ||||  ||||||
                                GGACC     CACG  GGCCCG
                                   A______    TC
GAM2173  VENTX2   3'  CCTGTTGGGGTGCCCGGG     30914      GCATAA
                                CCTG     GGTGCCCGGG
                                ||||     ||||||||||
                                GGAC     CCACGGGCCC
                                  AACC__
GAM2173  VIPR2    3'  CCCGACACGGTGCTCGGGC    18006         AA    C
                                CCTGGCAT  GGTGC CGGGC
                                ||||||||  ||||| |||||
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                                GGGCTGTG  CCACG GCCCG
                                   __     A
GAM2174  ANGPT4   3'  TCACAGACGGAGGGGAG     31987        TA    ACAT
                                TCACAGAC  AGGG    GAG
                                ||||||||  ||||    |||
                                AGTGTCTG  TCCC    CTC
                                    CC    ____
GAM2174  HTR1E    3'  TATCACAGATAAGACCAGAGG  9272         C     GA  T
                                TATCACAGA TAAGG  CA GAGG
                                |||||||||  |||||  || ||||
                                ATAGTGTCT ATTCT  GT CTCC
                                   _     G_  _
GAM2174  NT5C2    3'  TATCACAGATAAGAAGGAG   29234        C     ACAT
                                TATCACAGA TAAGGG   GAG
                                |||||||||  ||||||   |||
                                ATAGTGTCT ATTCTT   CTC
                                   _     C___
GAM2174  ROCK2    3'  TCACAGACTAATACTGAGG   42365          GGGACA
                                TCACAGACTAA     TGAGG
                                ||||||||||      |||||
                                AGTGTCTGATT     ACTCC
                                    ATG___
GAM2175  GPM6A    3'  TATAACACATGGGAAGTG    23615        GAAAA   ATA
                                TATAACACA    GGAA   TG
                                |||||||||    ||||   ||
                                ATATTGTGT    CCTT   AC
                                    AC___    C__
GAM2177  CENTD2   3'  GTTGGGCCAAGAGGTCT     31602         AC   ATA
                                GTTGGGCCAA  AGG   TCT
                                ||||||||||  |||   |||
                                CAACCCGGTT  TCC   AGA
                                    C_    ___
GAM2177  CLCN7    3'  GCTGGGCCAGGTGTCCTCTG  10519         AACA  ATA__
                                GTTGGGCCA   GG    TCTG
                                |||||||||   ||    ||||
                                CGACCCGGT   CC    AGAC
                                    ____  ACAGG
GAM2177  KCNH3    3'  GTTGGGCCGAACAGCAGAT   42088         A    __
                                GTTGGGCC AACAG  GAT
                                ||||||||  |||||  |||
                                CAACCCGG TTGTC  CTA
                                    C     GT
GAM2177  ORC5L    3'  GCTGGGCCAGCACCTG      14980         AACAG A
                                GTTGGGCCA    G TATCTG
                                |||||||||    | ||||||
                                CGACCCGGT    C GTGGAC
                                    _____ _
GAM2177  PRV1     3'  GTTGGGCCACACAGCCCTG   43877         A   GATA
                                GTTGGGCCA ACAG   TCTG
                                |||||||||  ||||   ||||
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                                CAACCCGGT TGTC    GGAC
                                     G    G___
GAM2178  ABCD2     3'  TAACATACTTCATGCAGTATAA 23151         ATAA__     C
                CA                    TAACATAT      CAGTA AACA
                                      |||||||||      ||||| ||||
                                      ATTGTATG      GTCAT TTGT
                                           AAGTAC     A
GAM2178  BARD1     3'  TGAACATTAAAAACAGTACAA  7869      T     ATAT
                                      TG AACAT    AACAGTACAA
                                      || |||||    ||||||||||
                                      AC TTGTA    TTGTCATGTT
                                       _     ATTT
GAM2178  EML1      3'  TGTGTCATATATTGTACAACA  40725     AA       AACA
                                      TGT  CATATAT    GTACAACA
                                      |||  |||||||    ||||||||
                                      ACA  GTATATA    CATGTTGT
                                        CA       A___
GAM2178  F11       5'  TGTAACATTCTCTCTCAGTACA 6554          ATATAA_
                                      TGTAACAT       CAGTACA
                                      |||||||||      |||||||
                                      ACATTGTA       GTCATGT
                                           AGAGAGA
GAM2178  FBXL3A    3'  TAACATATACTTTACAGTA    29130          A__
                                      TAACATATAT   ACAGTA
                                      ||||||||||   ||||||
                                      ATTGTATATG   TGTCAT
                                           AAA
GAM2178  GOLGA5    3'  TGTAACATGTACAAAGTA     23049         A     C
                                      TGTAACAT TATAA AGTA
                                      |||||||| ||||| ||||
                                      ACATTGTA ATGTT TCAT
                                           C     _
GAM2178  MEN1      5'  TGTAACATAGCAATACAAC    39239         TATAA
                                      TGTAACATA     CAGTACAAC
                                      |||||||||     |||||||||
                                      ACATTGTAT     GTTATGTTG
                                           C____
GAM2178  RNF6      3'  GTAACATATATATAGCA      25578           AC
                                      GTAACATATATA  AGTA
                                      ||||||||||||  ||||
                                      CATTGTATATAT  TCGT
                                             A_
GAM2178  SLC25A14  3'  TGTAACACATATAGCAATA    19537            A
                                      TGTAACATATATA CAGTA
                                      |||||||||||||| |||||
                                      ACATTGTGTATAT GTTAT
                                             C
GAM2178  TRHDE     3'  TGTAACACATATTCACACACAA 30116           A_   G
                CA                    TGTAACATATAT  ACA TACAACA
                                      ||||||||||||  ||| |||||||
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                                ACATTGTGTATA  TGT GTGTTGT
                                      AG  _
GAM2179 ABR     3' TGGAGGAAGACTGAGGGG    35019     CAC       A
                                TGG   AAGACTGA GGG
                                |||   |||||||| |||
                                ACC   TTCTGACT CCC
                                  TCC       C
GAM2179 ARHC    3' TGCCACTAAAGAAGGG      23175    G   A   CT
                                TG CAC AGA  GAAGGG
                                || ||| |||  ||||||
                                AC GTG TTT  CTTCCC
                                 G   A  __
GAM2179 ARHC    5' TGGCAGGCTGAAGGG       23176       CAA A
                                TGGCA   G CTGAAGGG
                                |||||   | ||||||||
                                ACCGT   C GACTTCCC
                                   ___ C
GAM2179 ATP5B   5' GGCAGCGACGCTGAAGGG    40650      CAA  __
                                GGCA   GAC  TGAAGGG
                                ||||   |||  |||||||
                                CCGT   CTG  ACTTCCC
                                  CG_   CG
GAM2179 CCND2   3' TGGCCAAAAGAGGGG       12054      A    CT  A
                                TGGC CAAGA  GA GGG
                                |||| |||||  || |||
                                ACCG GTTTT  CT CCC
                                  _    __ C
GAM2179 CDK5R2  3' TGGATAAAACCGAGGGG     19478     CAC       A
                                TGG   AAGACTGA GGG
                                |||   |||||||| |||
                                ACC   TTTTGGCT CCC
                                  TA_       C
GAM2179 CRI1    3' TGGCACAAAACTATTTGG    30736           AAG
                                TGGCACAAGACTG   GG
                                ||||||||||||   ||
                                ACCGTGTTTTGAT   CC
                                      AAA
GAM2179 CYLN2   3' TGGCAAGACCAGGAAGGG    18068      CA   __
                                TGGCA  AGACT  GAAGGG
                                |||||  |||||  ||||||
                                ACCGT  TCTGG  CTTCCC
                                   __    TC
GAM2179 DLX4    3' TGGCAAGACCAAGGG       12578      CA    G
                                TGGCA  AGACT AAGGG
                                |||||  ||||| |||||
                                ACCGT  TCTGG TTCCC
                                   __   _
GAM2179 EDNRA   3' TGGCACAACTGCGGGG      42005        AG   AA
                                TGGCACA  ACTG  GGG
                                |||||||  ||||  |||
```

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                                ACCGTGT  TGAC  CCC
                                   __    GC
GAM2179  ERCC3    3'  TGGCCAACGCTGGAGGG     6522       A   GA   A
                                TGGC CAA  CTG AGGG
                                |||| |||  ||| ||||
                                ACCG GTT  GAC TCCC
                                  _  GC   C
GAM2179  FGF12    3'  TGCCACAAGACAGGG       34301     G       TGA
                                TG CACAAGAC   AGGG
                                || ||||||||   ||||
                                AC GTGTTCTG   TCCC
                                 G      ___
GAM2179  FLOT1    3'  TGGCAAGGAGAGATGAGGGG  25135      CA_   C_   A
                                TGGCA   AGA  TGA GGG
                                |||||   |||  ||| |||
                                ACCGT   TCT  ACT CCC
                                   TCC   CT   C
GAM2179  FLOT2    3'  TGGCACAAGGGCTCTGGGG   20985        A___   AA
                                TGGCACAAG   CTG  GGG
                                |||||||||   |||  |||
                                ACCGTGTTC   GAC  CCC
                                     CCGA   __
GAM2179  GCKR     3'  TGGCACAAGTCCCCTTGGG   11242        A_  GAA
                                TGGCACAAG  CT   GGG
                                |||||||||  ||   |||
                                ACCGTGTTC  GG   CCC
                                     AG  GAA
GAM2179  GNB1     3'  TGCCACAAAACAGGG       13213     G       TGA
                                TG CACAAGAC   AGGG
                                || ||||||||   ||||
                                AC GTGTTTTG   TCCC
                                 G      ___
GAM2179  GPRK7    5'  AGCACAAGAGGGCTGGAGGG  40178         ___   A
                                GGCACAAGA   CTG AGGG
                                |||||||||   ||| ||||
                                TCGTGTTCT   GAC TCCC
                                     CCC   C
GAM2179  GRM8     3'  TAGCACAACCCAGGG       9191        AG   GA
                                TGGCACA  ACT  AGGG
                                |||||||  |||  ||||
                                ATCGTGT  TGG  TCCC
                                   __   G_
GAM2179  KCNS3    5'  TGGCCAAAAAGAAGGG      13938      A    CT
                                TGGC CAAGA  GAAGGG
                                |||| |||||  ||||||
                                ACCG GTTTT  CTTCCC
                                  _    T_
GAM2179  KIF3C    3'  TGTCAAAGCTGAAGGG      13959     G  C   A
                                TG CA AAG CTGAAGGG
                                || || ||| ||||||||
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                                AC GT TTC GACTTCCC
                                 A  _  _
GAM2179  LYAAT1   5'  TGGCACAAGATAGGG      38530         CTGA
                                TGGCACAAGA   AGGG
                                ||||||||||   ||||
                                ACCGTGTTCT   TCCC
                                     A___
GAM2179  MAL      3'  TGGCACAAGATGGGG      35337         C  AA
                                TGGCACAAGA TG  GGG
                                |||||||||| ||  |||
                                ACCGTGTTCT AC  CCC
                                      _ __
GAM2179  MAP4     3'  TGGGGCAAGACCAAAGCAGGG 36277     CA     TG ___
                                TGG  CAAGAC  A   AGGG
                                |||  ||||||  |   ||||
                                ACC  GTTCTG  T   TCCC
                                  CC     GT TCG
GAM2179  MFAP2    3'  TGGCCACAGGCTGAAGGA    32708     ACA  A
                                TGGC   AG CTGAAGGG
                                ||||   || ||||||||
                                ACCG   TC GACTTCCT
                                  GTG  C
GAM2179  MLH3     3'  TGAAGAAGACTGAAGGG     30782     CAC
                                TGG   AAGACTGAAGGG
                                |||   ||||||||||||
                                ACT   TTCTGACTTCCC
                                  TC_
GAM2179  OTX1     3'  TGGCACAAAAATGGGGG     31002         C  AA
                                TGGCACAAGA TG  GGG
                                |||||||||| ||  |||
                                ACCGTGTTTT AC  CCC
                                      T  C_
GAM2179  PAK1     3'  TGGCACAATGAGGCTGGGG   15087        _  __  AA
                                TGGCACAA GA  CTG  GGG
                                |||||||| ||  |||  |||
                                ACCGTGTT CT  GAC  CCC
                                     A  CC  __
GAM2179  PARK2    3'  TGGACAAACTGAAAGG      30380     C   A
                                TGG ACA GACTGAAGGG
                                ||| ||| ||||||||||
                                ACC TGT TTGACTTTCC
                                  _  _
GAM2179  PDGFB    3'  TGGAGCAGACTGAAGGG     15199     CACA
                                TGG   AGACTGAAGGG
                                |||   ||||||||||||
                                ACC   TCTGACTTCCC
                                  TCG_
GAM2179  PHLDA3   3'  TGGCACAAAGCCAGGG      29615        GA  GA
                                TGGCACAA  CT  AGGG
                                ||||||||  ||  ||||
```

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                                ACCGTGTT  GG  TCCC
                                    TC  __
GAM2179  PML      3'  TGGGGCAAGACCAGGG      37757     CA      GA
                                TGG  CAAGACT  AGGG
                                |||  |||||||  ||||
                                ACC  GTTCTGG  TCCC
                                  CC      __
GAM2179  PNUTL2   3'  TGGCAGTAGCTGAAGGG     38651       CA  A
                                TGGCA  AG CTGAAGGG
                                |||||  || ||||||||
                                ACCGT  TC GACTTCCC
                                   CA  _
GAM2179  PPP1R14B 3'  TGGAAAACTGAGGGG       39796     CAC       A
                                TGG   AAGACTGA GGG
                                |||   |||||||| |||
                                ACC   TTTTGACT CCC
                                  ___       C
GAM2179  PPP2R4   3'  TGGACGGGAGTGAAGGG     41333     C  AA  C
                                TGG AC  GA TGAAGGG
                                ||| ||  || |||||||
                                ACC TG  CT ACTTCCC
                                  _  CC  C
GAM2179  RARG     3'  TGGCACAAGGACGGG       9731          ACT  A
                                TGGCACAAG   GA GGG
                                |||||||||   || |||
                                ACCGTGTTC   CT CCC
                                      ___  G
GAM2179  RPL10    5'  TGGCACACCGAAGGG       25675       AAG
                                TGGCAC   ACTGAAGGG
                                ||||||   |||||||||
                                ACCGTG   TGGCTTCCC
                                     ___
GAM2179  RRAS2    3'  TAGCTAAAACTGAAGGG     29310      AC
                                TGGC  AAGACTGAAGGG
                                ||||  ||||||||||||
                                ATCG  TTTTGACTTCCC
                                  A_
GAM2179  SLC19A1  3'  TGGCACAAGTGTGGG       16852         AC  AA
                                TGGCACAAG  TG  GGG
                                |||||||||  ||  |||
                                ACCGTGTTC  AC  CCC
                                      __  A_
GAM2179  TPT1     5'  TGGCGACTGAAGGG        17662      ACAA
                                TGGC   GACTGAAGGG
                                ||||   ||||||||||
                                ACCG   CTGACTTCCC
                                     ____
GAM2179  TRIM9    3'  TAGCCAAGACTGAAGGG     31579      A
                                TGGC CAAGACTGAAGGG
                                |||| ||||||||||||
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                                ATCG GTTCTGACTTCCC
                                   _
GAM2179 WBSCR1   3' TGGCTCTGAACTGAAGGG   35273     ACAA
                                TGGC   GACTGAAGGG
                                ||||   ||||||||||
                                ACCG   TTGACTTCCC
                                  AGAC
GAM2179 ZNF261   3' TGGCTCACTGAAGGG      22996     A AAG
                                TGGC C  ACTGAAGGG
                                |||| |  |||||||||
                                ACCG G  TGACTTCCC
                                  A ___
GAM2180 SURF5    3' TGCAAAAAAGTGGCGGT    39510    C      A  A
                                TGC GAGGAAGT GC GT
                                ||| |||||||| || ||
                                ACG TTTTTTCA CG CA
                                  _      C  C
GAM2181 CLTC     3' TGGAATCATGGTGCTC     22155        CACGCAGA
                                TGGAATCGT      TGCTC
                                |||||||||      |||||
                                ACCTTAGTA      ACGAG
                                     CC_______
GAM2181 FMOD     3' TGGTGTTCACATGCAGATGCT 12934    AATCG   __
                                TGG    TCAC  GCAGATGCT
                                |||    ||||  |||||||||
                                ACC    AGTG  CGTCTACGA
                                  ACA__   TA
GAM2181 GNL1     5' GGCCGCCGCAGATGTTCTC   45130    AA   CA     C
                                GG  TCGT  CGCAGATG TCTC
                                ||  ||||  |||||||| ||||
                                CC  GGCG  GCGTCTAC AGAG
                                 __   __      A
GAM2181 SRRM1    3' GGCCTTTTCACGCAGGTGCT  25189    AATCG      A
                                GG    TCACGCAG TGCT
                                ||    |||||||| ||||
                                CC    AGTGCGTC ACGA
                                 GGAAA       C
GAM2182 DGKI     3' TCTGACAGACATTTCTGACTAG 21787    A      GCC
            A                    TCT ATAGATA   CTGACTAGA
                                |||  |||||||   |||||||||
                                AGA TGTCTGT   GACTGATCT
                                  C      AAA
GAM2182 IFNA21   3' CAATAGATAGATAATTAGA   13481         CCC   C
                                TAATAGATAG   TGA TAGA
                                ||||||||||   ||| ||||
                                GTTATCTATC   ATT ATCT
                                      T__   A
GAM2183 CHD2     3' ACAGAATACAAGTGAGCTGTGA 10436     T      CATTTTA
                                ACAG ATACAAGT      TGA
                                |||| ||||||||      |||
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                                TGTC TATGTTCA      ACT
                                  T       CTCGAC_
GAM2183  HS2ST1   3'  ACAGTAAGCAAGTCATCT    29320       TA
                                ACAGTA  CAAGTCATTT
                                ||||||  ||||||||||
                                TGTCAT  GTTCAGTAGA
                                   TC
GAM2183  PBX3     3'  ACAATGTACATTACATTTTATG 26210      A    AGT
             AA                   ACAGT TACA   CATTTTATGAA
                                |||||  ||||   ||||||||||
                                TGTTA ATGT   GTAAAATACTT
                                  C    AAT
GAM2183  PIGN     3'  GTAAAGGGTCATTTTATG    29548     TACAA
                                GTA    GTCATTTTATG
                                |||    ||||||||||
                                CAT    CAGTAAAATAC
                                  TTCC_
GAM2184  ACR      3'  GGCTCACTGGGTCTGTTGA   9919     AA       CGC
                                GG  CACTGGGTC   TGA
                                ||  |||||||||   |||
                                CC  GTGACCCAG   ACT
                                 GA        ACA
GAM2184  ADAM12   3'  GGAACACCGGGAAAGTGAAA   18475          TCCGC
                                GGAACACTGGG     TGAAA
                                ||||||||||     |||||
                                CCTTGTGGCCC     ACTTT
                                       TTTC_
GAM2184  ADD2     3'  AAGGAGCACTGGACTG      32719       A     GTCC
                                AAGGA CACTGG    GCTG
                                |||||  ||||||    ||||
                                TTCCT GTGACC    TGAC
                                  C     _____
GAM2184  DNMT3L   5'  GGAGGACTGGGCCATGGAA   30058     AC     T   CT
                                GGA  ACTGGG CCG  GAA
                                |||  |||||| |||  |||
                                CCT  TGACCC GGT  CTT
                                  CC      _   AC
GAM2184  HCK      3'  TGAGGAAACTGTGGCTGAA   40942   A    C   GGTCC
                                C AGGAA ACTG     GCTGAA
                                | |||||  ||||     ||||||
                                A TCCTT TGAC     CGACTT
                                 C     _    AC____
GAM2184  IGFBP4   3'  AGGGGACGCTGAGTCCCTG   11394     A_  A       G
                                AGG  AC CTGGGTCC CTG
                                |||  ||  ||||||||  |||
                                TCC  TG GACTCAGG GAC
                                  CC  C       _
GAM2184  JAM3     3'  CAGGGAGCACTGAGCCACTG   37261    A   A      T
                                CA GGA CACTGGG CCGCTG
                                ||  |||  |||||||  ||||||
```

```
                                GT CCT GTGACTC GGTGAC
                                 C  C     _
GAM2184 LEF1    5' AAGGGCACTGGGCGGCGA   32200     AA      CC  T
                                AAGG  CACTGGGT  GC GA
                                ||||  ||||||||  || ||
                                TTCC  GTGACCCG  CG CT
                                  C_      C_ _
GAM2184 MEIS2   3' TGAGGAACACGTGCTGA    33546   A      TGG  CC
                                C AGGAACAC   GT  GCTGA
                                | ||||||||   ||  |||||
                                A TCCTTGTG   CA  CGACT
                                 C      ___  __
GAM2184 MKPX    3' CAAGGGCTATTTCCCAAGCTG 33635      AACA   GG  ___
                                CAAGG   CTG  TCC   GCTG
                                |||||   |||  |||   ||||
                                GTTCC   GAT  AGG   CGAC
                                   C___   AA   GTT
GAM2184 MN1     5' CAAGTCCGATTGGGTCTGCTG  14571     GAACAC     C
                                CAAG     TGGGTC GCTG
                                ||||     |||||| ||||
                                GTTC     ACCCAG CGAC
                                  AGGCTA     A
GAM2184 OGDH    3' GGACACTGCAGAGACTGAA   45013     A    _  TCC
                                GGA CACTG GG   GCTGAA
                                ||| ||||| ||   ||||||
                                CCT GTGAC TC   TGACTT
                                  _    G  TC_
GAM2184 OSM     3' GGAACTTGGGGCTGA      33914      AC    TCC
                                GGAAC  TGGG   GCTGA
                                |||||  ||||   |||||
                                CCTTG  ACCC   CGACT
                                   A_   ___
GAM2184 PON1    3' AAGAACACTGGGTCCTCGGAA  7776             GCT
                                AGGAACACTGGGTCC   GAA
                                ||||||||||||||   |||
                                TTCTTGTGACCCAGG   CTT
                                         AGC
GAM2184 PTHLH   3' TGAGAGCACCCCGCTGA     15855   A  A    GGGT
                                A GGA CACT    CCGCTGA
                                | ||| ||||    |||||||
                                A TCT GTGG    GGCGACT
                                 C  C   ____
GAM2184 ST5     3' CAGAGAGCACTGGCAGAGCTG  24042    AG  A     GTCC
                                CA  GA CACTGG    GCTG
                                ||  || ||||||    ||||
                                GT  CT GTGACC    CGAC
                                 CT  C     GTCT
GAM2184 TRPM2   3' TGAGGGGCACTGGGTCCACCAA 17698   A   AA         TG
             A                   C AGG  CACTGGGTCCGC  AA
                                | |||  ||||||||||||  ||
```

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                                A TCC  GTGACCCAGGTG  TT
                                 C   CC          GT
GAM2185  WHSC1    3'  CTAATTACAGTCAATTTGACA  39403     TTGAT_  A
                                CTA     GT CAATTTGACA
                                |||     || ||||||||||
                                GAT     CA GTTAAACTGT
                                  TAATGT  _
GAM2185  ZFP36L1  3'  TATTGATGTGCAGTGAC     22294          A  ATT
                                TATTGATGT CA   TGAC
                                ||||||||| ||   ||||
                                ATAACTACA GT   ACTG
                                      C  C__
GAM2186  CARPX    5'  GACGATAGCCCCCCGCCGGGCT 33570    G    TGA        A
                G                GA GATA   CCCCCGCCG GCTG
                                || ||||   ||||||||| ||||
                                CT CTAT   GGGGGCGGC CGAC
                                 G   CG_       C
GAM2186  DUSP7    5'  GGCGCCCGCCTCCCGCCGAGCT 42275    ATA_  A  _
                G                GG    TG CC CCCGCCGAGCTG
                                ||    || || ||||||||||||
                                CC    GC GG GGGCGGCTCGAC
                                 GCGG  _  A
GAM2186  GADD45G  3'  AGACCAAGGTCCCCGCCGGGCT 27460      ATGAC_       A
                G                GGAT     CCCCGCCG GCTG
                                ||||     |||||||| ||||
                                TCTG     GGGGCGGC CGAC
                                  GTTCCA       C
GAM2186  SLC6A6   3'  GAGGATACGACTCAAAAGCTG  16788          CCCCGCC
                                GAGGATATGAC      GAGCTG
                                ||||||||||       ||||||
                                CTCCTATGCTG      TTCGAC
                                      AGTT___
GAM2187  ADCY7    3'  CAGCATTTGTGAGGGGGCGGG  9982          C  TTGTAA
                                CAGCATTTG TG     CGGG
                                ||||||||| ||     ||||
                                GTCGTAAAC AC     GCCC
                                      _  TCCCCC
GAM2187  ASTN     3'  CAGCATTTGCCACAGG      42941          GTTGTA
                                CAGCATTTGCT     ACGGG
                                ||||||||||      |||||
                                GTCGTAAACGG     TGTCC
                                                _____
GAM2187  CUL5     3'  TACAGTATTTGCTGCTGT    18493       C
                                TACAG ATTTGCTGTTGT
                                ||||| ||||||||||||
                                ATGTC TAAACGACGACA
                                   A
GAM2187  MPV17    3'  GCATTTGCTGGGATATGGG   43262          TT   AC
                                GCATTTGCTG  GTA  GGG
                                |||||||||  |||  |||
```

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                                CGTAAACGAC  TAT  CCC
                                      CC   A_
GAM2187  RAI14    3'  CAGCATTTCTGTGCGG     31799        G    TGTAA
                                CAGCATTT CTGT    CGG
                                |||||||| ||||    |||
                                GTCGTAAA GACA    GCC
                                     _   C____
GAM2187  SLC7A5   3'  GCACTTGCTTGTTGTGGTGGG  18546         _    AAC
                                GCATTTGCT GTTGT   GGG
                                ||||||||| |||||   |||
                                CGTGAACGA CAACA   CCC
                                      A    CCA
GAM2189  JAM3     3'  AATACTCTTAATTATTGATATT 37258        GATTGA
                                AATACTC     TATTGATATT
                                |||||||     ||||||||||
                                TTATGAG     ATAACTATAA
                                     AATTA_
GAM2189  PBX3     3'  TTGAGGTTTAGTGTATATT    26217      TAA
                                TTGA   TTAGTGTATATT
                                ||||   ||||||||||||
                                AACT   AATCACATATAA
                                  CCA
GAM2190  KERA     3'  TACGGTATCTGCATAAGTA    28156     AA
                                TAC  TATCTGTATAAGTA
                                |||  ||||||||||||||
                                ATG  ATAGACGTATTCAT
                                  CC
GAM2190  MTMR1    3'  TACAATACTGTACCAGT      43159        T     A
                                TACAATA CTGTAT AGT
                                ||||||| |||||| |||
                                ATGTTAT GACATG TCA
                                     _     G
GAM2191  ITGA5    3'  CCTCTGTCCCTGGATCTGAG   41496       GTTAGA  A_
                                TCTCTG     CC  GATCTGAG
                                ||||||     ||  ||||||||
                                GGAGAC     GG  CTAGACTC
                                    AG____  AC
GAM2191  SCD      3'  CTCTTGATCAGATCTGAG     22825      _  TAGAC
                                CTCT GGT    CAGATCTGAG
                                |||| |||    ||||||||||
                                GAGA CTA    GTCTAGACTC
                                  A  _____
GAM2191  SF3B3    3'  TCTGGTTAGATTCTAGAGC    29681          CCAGA  _
                                TCTGGTTAGA    TCT GAGC
                                ||||||||||    ||| ||||
                                AGACCAATCT    AGA CTCG
                                      A____   T
GAM2191  SLC22A11 3'  TCTCTGGTTGGCGTGGCTGAG  32965         AGACCAGAT
                                TCTCTGGTT       CTGAG
                                |||||||||       |||||
```

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                                AGAGACCAA       GACTC
                                     CCGCACC__
GAM2191  SLC4A4   3'  TCTGGTTAACAACTCTGAGC   19065        AC   A
                                TCTGGTTAG  CAG TCTGAGC
                                |||||||||  ||| |||||||
                                AGACCAATT  GTT AGACTCG
                                     __  G
GAM2191  ZNF180   3'  TCTCTGATTCAGGTCTGAG   29936        AGAC   A
                                TCTCTGGTT   CAG TCTGAG
                                |||||||||   ||| ||||||
                                AGAGACTAA   GTC AGACTC
                                     ____  C
GAM2191  AKAP13   3'  CAACTAGAGCACTG       28470        AACC
                                TAACTAGGG   CACTG
                                |||||||||   |||||
                                GTTGATCTC   GTGAC

                                     ____
GAM2191  DNAH11   3'  CTAGAAAATCCTCACTGC    19096     GG  _  _
                                CTAG  AA CC CACTGC
                                ||||  || || ||||||
                                GATC  TT GG GTGACG
                                  TT  A  A
GAM2191  FGFR2    3'  TAACTAGGTGAATACTG     35667        _  CCC
                                TAACTAGG GAA   ACTG
                                |||||||| |||   ||||
                                ATTGATCC CTT   TGAC
                                     A  A__
GAM2191  GTF2E2   3'  TAACAGGGAACATCACATTGC  13318     T     C_  __
                                TAAC AGGGAAC  CAC  TGC
                                |||| |||||||  |||  |||
                                ATTG TCCCTTG  GTG  ACG
                                  _     TA  TA
GAM2191  ILK      3'  CAACCAGAGGCCTGCTGC    21122        AA  CA
                                TAACTAGGG  CC  CTGC
                                |||||||||  ||  ||||
                                GTTGGTCTC  GG  GACG
                                     C_  AC
GAM2191  KIF3B    3'  AACAGGCCCACTGC       22027     T  GAA
                                AAC AGG   CCCACTGC
                                ||| |||   ||||||||
                                TTG TCC   GGGTGACG
                                  _  ___
GAM2191  MAP1B    3'  ACTAAAGAATGCCTACTGC   25389        __  C
                                ACTAGGGAA  CC ACTGC
                                |||||||||  || |||||
                                TGATTTCTT  GG TGACG
                                     AC  A
GAM2191  MLH3     3'  CAACTAGGGGAATCATCTGC  30778        AACC  _
                                TAACTAGGG   CA CTGC
                                |||||||||   || ||||
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                                GTTGATCCC   GT GACG
                                     CTTA  A
GAM2191  MYO1A    5'  AACTAGGGTATAACTTCACTG  23919        ___  C_
                                AACTAGGG   AAC  CACTG
                                ||||||||   |||  |||||
                                TTGATCCC   TTG  GTGAC
                                    ATA   AA
GAM2191  POMZP3   3'  GAAGGCAAAGCCCACTGC    29241   T  G  __
                                C AGG AA  CCCACTGC
                                | ||| ||  ||||||||
                                C TCC TT  GGGTGACG
                                 T   G  TC
GAM2191  TRPM2    5'  CAACCAGGCCTGCTGC     17687        GAA  CA
                                TAACTAGG   CC  CTGC
                                ||||||||   ||  ||||
                                GTTGGTCC   GG  GACG
                                    ___  AC
GAM2191  UTY      3'  TAACTAAGGAAAATTCTGC   28314          CCCA
                                TAACTAGGGAA    CTGC
                                ||||||||||    ||||
                                ATTGATTCCTT    GACG
                                      TTAA
GAM2191  YWHAZ    3'  CAACTAAGGAGAGATTTGCTGC 18201          ACCCA___
                                TAACTAGGGA       CTGC
                                ||||||||||       ||||
                                GTTGATTCCT       GACG
                                     CTCTAAAC
GAM2191  ZP3A     3'  GAAGGCAAAGCCCACTGC    28385   T  G  __
                                C AGG AA  CCCACTGC
                                | ||| ||  ||||||||
                                C TCC TT  GGGTGACG
                                 T   G  TC
GAM2192  ARHGEF7  3'  AGTCTGTCAGCCAGCAAGTT   19359    _  C    AGA
                                AG CTG CAGTT   AGCAAGTT
                                || ||| |||||   ||||||||
                                TC GAC GTCGG   TCGTTCAA
                                 A   A    ___
GAM2192  CSN1     5'  AAGTCTGGAGAGAAGCAAGTT  12459     _  CC  TT
                                AAG CTG  AG  AGAAGCAAGTT
                                |||  |||  ||  ||||||||||
                                TTC GAC  TC  TCTTCGTTCAA
                                  A   C_  __
GAM2192  FGF1     3'  AACTGGGCATTTAGAAGCAAGT 37565      C_  G
              T                  AGCTG  CA TTAGAAGCAAGTT
                                 |||||  ||  ||||||||||||
                                 TTGAC  GT AATCTTCGTTCAA
                                    CC  A
GAM2192  MBL2     3'  AAGTTGCCAGTTCTGCATAAGT 6957      C       AGAA  __
              T                  AAG TGCCAGTT    GCA  AGTT
                                 |||  ||||||||    |||  ||||
```

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                                TTC ACGGTCAA   CGT  TCAA
                                  A       GA__   AT
GAM2192  NBS1     3'  AAGCAGCCAGAACTTGGAAGTA 42984      T    TTA___   C
              AGTTA                   AAGC GCCAG     GAAG AAGTTA
                                |||| |||||     |||| ||||||
                                TTCG CGGTC     CTTC TTCAAT
                                  T    TTGAAC    A
GAM2192  SLC7A7   5'  AAGCTGTCCCAGAGCAAGTTA  19574       _ AGT    A
                                AAGCTG CC   TAGA GCAAGTTA
                                |||||| ||   |||| ||||||||
                                TTCGAC GG   GTCT CGTTCAAT
                                  A ___   _
GAM2192  YWHAH    3'  AAGCTGATGGAAAGGAGCAAGT 18191       CCAGTT  A
              T                    AAGCTG     AG AGCAAGTT
                                ||||||     || ||||||||
                                TTCGAC     TC TCGTTCAA
                                   TACCTT  C
GAM2192  CAMLG    3'  TTGCTTGCTTAAAACATACTT  11956            ACCT
                                TTGCTTGCTTAAAG   CTT
                                ||||||||||||||   |||
                                AACGAACGAATTTT   GAA
                                       GTAT
GAM2192  DGKA     5'  CGTTGCTTGGACCTC      10645    C      CTTAAA
                                CG TTGCTTG     GACCTC
                                || |||||||     ||||||
                                GC AACGAAC     CTGGAG
                                _     _______
GAM2192  GNRH1    5'  GCTGGCTTGCCTTTAGTTTCTT 9077      T       AA  ACC
                                GCT GCTTGCTT  AG   TCTT
                                ||| ||||||||  ||   ||||
                                CGA CGAACGGA  TC   AGAA
                                  C       AA  AA_
GAM2192  GSN      3'  TGCTCGCTCTAAGGCCTCT   6757          A   A
                                TGCTTGCTT AAG CCTCT
                                ||||||||| ||| |||||
                                ACGAGCGAG TTC GGAGA
                                     A   C
GAM2192  IL15RA   3'  CGCTTCCTTGCACCTC      13530       G    TTAAAG
                                CGCTT CTTGC     ACCTC
                                ||||| |||||     |||||
                                GCGAA GAACG     TGGAG
                                   G    _______
GAM2192  IRTA2    3'  GCTTGCTGCTGTCCTTCT    36342        T   TAAAGA  _
                                GCTTGCT GCT     CCT CT
                                ||||||| |||     ||| ||
                                CGAACGA CGA     GGA GA
                                    _  CA____   A
GAM2192  KIF3C    3'  CGCTTGCTTTCGTTATGACCTC 13950         GCTTAAA
              TT                   CGCTTGCTT      GACCTCTT
                                |||||||||      ||||||||
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                                GCGAACGAA      CTGGAGAA
                                     AGCAATA
GAM2192  KIFAP3   5'  CGCTTGCTCTGCACCTCT    31405        _  TTAAAG
                                CGCTTGCT TGC     ACCTCT
                                |||||||| |||     ||||||
                                GCGAACGA ACG     TGGAGA
                                    G  _______
GAM2192  MEST     3'  TTGATGGCCAGGACCTCTT    43082     CTT   TAAA
                                TTG   GCT    GACCTCTT
                                |||   |||    ||||||||
                                AAC   CGG    CTGGAGAA
                                  TAC   TC__
GAM2192  MPZ      3'  TTGGTTGTTTAAAAACCATTTC 8040      C   C       ___
              TT                  TTG TTG TTAAAGACC   TCTT
                                ||| ||| |||||||||   ||||
                                AAC AAC AATTTTTGG   AGAA
                                  C   A        TAA
GAM2192  SOX9     3'  TTGCTTGCCTTTTACCTCTT   7377           AAAG
                                TTGCTTGCTT    ACCTCTT
                                ||||||||||    |||||||
                                AACGAACGGA    TGGAGAA
                                     AAA_
GAM2192  TRIM9    5'  GCTTTCTTGCTTTCCT      31573      G      AAAGA
                                GCTT CTTGCTT     CCT
                                |||| |||||||     |||
                                CGAA GAACGAA     GGA
                                  A      A____
GAM2193  CYP1B1   3'  GGTCACATAATTTAAAGCT    6451     A    AAAC
                                GG TATA    AATTTAAAGCT
                                || ||||    ||||||||||
                                CC GTGT    TTAAATTTCGA
                                 A    A___
GAM2193  FBXW1B   3'  TAGGATGAAAAGTGGTCAAAGC 37993        AT   ACAAT
              T                  TAGGAT  AAA     TTAAAGCT
                                ||||||  |||     ||||||||
                                ATCCTA  TTT     AGTTTCGA
                                   CT   CACC_
GAM2193  LIMD1    3'  TAGGATACAAAGCACACATTAG 30635           A  AT__   A
             AGCT                  TAGGATATAAA CA    TTA AGCT
                                |||||||||| ||    ||| ||||
                                ATCCTATGTTT GT    AAT TCGA
                                      C  GTGT   C
GAM2193  PSMC2    3'  TAGGATTCCAATTTAAAG    15832       ATAAAA
                                TAGGAT     CAATTTAAAG
                                ||||||     ||||||||||
                                ATCCTA     GTTAAATTTC
                                   AG____
GAM2194  CRADD    3'  ATGACATGAGATATATATATG  19175        ATTTTA
                                ATGGCAT     ATATATATG
                                |||||||     |||||||||
```

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                                TACTGTA     TATATATAC
                                    CTCTA_
GAM2194  ELOVL4   3'  GGTATATTTCCACATATGA   35541    C      AA
                                GG ATATTTT  TATATATGA
                                || |||||||  |||||||||
                                CC TATAAAG  GTGTATACT
                                 A     __
GAM2194  GRINL1A  3'  AATGACATGAACGTTTATATAT 42993        ATTTTAA
                G                AATGGCAT      TATATATG
                                ||||||||      ||||||||
                                TTACTGTA      ATATATAC
                                    CTTGCAA
GAM2195  EHF      3'  GCAACAATGTTCACCT      29115         CCTAACA
                                GCAACAGT      TTCACCT
                                ||||||||      |||||||
                                CGTTGTTA      AAGTGGA
                                    C_______
GAM2195  GTF2H1   3'  GCAACAGTCTCCCT       23688         CTAACAT  A
                                GCAACAGTC     TC CCT
                                |||||||||      || |||
                                CGTTGTCAG     AG GGA
                                      ________ _
GAM2195  KCNS2    3'  GCAACCCAACAACGTTCACCTC 42827      CAGT      ___
                                GCAA   CCTAACA   TTCACCTC
                                ||||   |||||||  ||||||||
                                CGTT   GGGTTGT   AAGTGGAG
                                  _____      TGC
GAM2195  LILRB4   3'  TGCTGACAGTTTTCTTTCACCT 27782     A_    CCTAACA
                C                TGC  ACAGT      TTCACCTC
                                |||  |||||      ||||||||
                                ACG  TGTCA      AAGTGGAG
                                  AC    AAAGA__
GAM2195  PKD2     3'  GCATAGTATTTAACATTCATCT 41073     AC   CC_       C
                                GCA  AGT   TAACATTCA CT
                                |||  |||   ||||||||| ||
                                CGT  TCA   ATTGTAAGT GA
                                  A_   TAA       A
GAM2195  SLC6A8   3'  ACATCTGGCATTCACCT     24752     G  CTAA
                                ACA TC    CATTCACCT
                                ||| ||    |||||||||
                                TGT AG    GTAAGTGGA
                                  _  ACC_
GAM2195  ADH1B    3'  GCCATCCCATCTCTACACT    43741           __
                                GCCATCCCGTCTC  CGCT
                                ||||||||||||  ||||
                                CGGTAGGGTAGAG  GTGA
                                        AT
GAM2195  METTL1   3'  TTCGCCACTTGTGCTTTGT   35709        CCC  CTCC   C_
                                TTCGCCAT   GT   GCT  GT
                                ||||||||   ||   |||  ||
```

```
                                AAGCGGTG  CA   CGA  CA
                                   AA_  ____  AA
GAM2195 UBTF    5' TTCGCCATCTCGGGCTTTGTC 30620       C  TCTCC  C_
                                TTCGCCATC CG   GCT  GTC
                                ||||||||| ||   |||  |||
                                AAGCGGTAG GC   CGA  CAG
                                     A  C____  AA
GAM2196 GAC1    5' TGGAGGTTTGTATACCGCTGTA 26798      _______   TT_
            TCT                 TGGAGGT    TCGCT  TCT
                                |||||||     |||||  |||
                                ACCTCCA     GGCGA  AGA
                                   AACATAT    CAT
GAM2196 CLOCK   3' GTCGCTACCAAGTCTACT   22218      TTC_  C
                                GTCGCTG   GTC TACT
                                |||||||   ||| ||||
                                CAGCGAT   CAG ATGA
                                   GGTT  _
GAM2196 CRAT    5' GTCGGTGGGTCCTTGCTA   19668    C  TTC   A_
                                GTCG TG  GTCCT  CTA
                                |||| ||  |||||  |||
                                CAGC AC  CAGGA  GAT
                                  C  C__   AC
GAM2196 DSP     5' GTCGCTGCTCGCTACC     20645        TC
                                GTCGCTGTTCG  CTACT
                                ||||||||||  |||||
                                CAGCGACGAGC  GATGG
                                         __
GAM2196 GNRH1   5' AAAGTAGCTCCTACTA     9072      C  TGTTCG
                                AAAGT GC    TCCTACTA
                                ||||| ||    ||||||||
                                TTTCA CG    AGGATGAT
                                  T  _______
GAM2196 IL1R1   3' AAAGTTGGTGTTCACCCA   9349      CGC    T
                                AAAGT  TGTTCG CCTA
                                |||||  |||||| ||||
                                TTTCA  ACAAGT GGGT
                                   ACC    _
GAM2197 KHK     3' TGAGGCAGATTGCGTTAAGTGC 27056    AAA     GT_ AC
                                TGA  AGATTGCG  AG  GC
                                |||  ||||||||  ||  ||
                                ACT  TCTAACGC  TC  CG
                                  CCG      AAT  A_
GAM2198 ANKTM1  3' TGATTTTCCACCCTTTCTGT  28808    G  TG  C_
                                TGAT TTT  TCC  TCTGT
                                |||| |||  |||  |||||
                                ACTA AAG  GGG  AGACA
                                  A  GT  AA
GAM2198 DXF68S1E 3' TGATGTTCCATTTTGTCTT  41039       TG CCCTC
                                TGATGTTT  T   TGTCTT
                                ||||||||  |   ||||||
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                                ACTACAAG  A    ACAGAA
                                    GT AA___
GAM2198  PTEN    3'  ATGGTGTTTTATCCCTCT    7202     A
                                ATG TGTTTTGTCCCTCT
                                ||| ||||||||||||||
                                TAC ACAAAATAGGGAGA
                                  C
GAM2198  SS18    3'  ATGACGCCCCTTCTGT     24839     GTTTT    _
                                ATGAT    GTCCCT CTGT
                                |||||    |||||| ||||
                                TACTG    CGGGGA GACA
                                  _____    A
GAM2198  STAR    3'  ATGAGTTTTGTCTTTTTCC   7386     T      CCTCTG
                                ATGA GTTTTGTC     TCT
                                |||| ||||||||     |||
                                TACT CAAAACAG     AGG
                                  _      AAAA__
GAM2198  WBSCR1  3'  ATGTGTTTTGTTCTTTATCTTA 35265    A      CC  C
                                ATG TGTTTTGT  CT TGTCTTA
                                ||| ||||||||  || |||||||
                                TAC ACAAAACA  GA ATAGAAT
                                  _      A_  A
GAM2199  AGA     3'  CTGAGAAAGCACGCGCACAACT 6185         __  T  ATGT
           TC                    CTGAGAAA  AC CG   ACTTC
                                |||||||  || ||   |||||
                                GACTCTTT  TG GC   TGAAG
                                    CG  C  GTGT
GAM2199  ASIC4   3'  ACTGAGAAGGCTCCCTTC   33062        AA   GATGTA
                                ACTGAGAA  CTC     CTTC
                                ||||||||  |||     ||||
                                TGACTCTT  GAG     GAAG
                                    CC   G_____
GAM2199  BTG2    3'  TGGGAAACTCGAGGTCTT   27623    A   A    T  A
                                TG GAAA CTCGA GT CTT
                                || |||| ||||| || |||
                                AC CTTT GAGCT CA GAA
                                 C   _    C  _
GAM2199  DPH2L2  3'  ACTGAGAAACTGAGC      10732         A  C  T
                                ACTGAGAAA CT GA GT
                                ||||||||| || || ||
                                TGACTCTTT GA CT CG
                                      _ _ _
GAM2199  MASP1   3'  TGAGAAAGTGGACACTTCC   40109       ACTC   GT
                                TGAGAAA   GAT  ACTTCC
                                |||||||   |||  ||||||
                                ACTCTTT   CTG  TGAAGG
                                    CAC_  ___
GAM2199  NPY2R   5'  CTGAGAAAATTCCACAACTTCC 9494         C  G   T
                                CTGAGAAAA TC ATG ACTTCC
                                ||||||||| || ||| ||||||
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                                GACTCTTTT AG TGT TGAAGG
                                     A  G  _
GAM2199  NPY2R    3'  CTGAGAAAATTCCACAACTTCC 9494          C  G   T
                                CTGAGAAAA TC ATG ACTTCC
                                ||||||||| || ||| ||||||
                                GACTCTTTT AG TGT TGAAGG
                                     A  G  _
GAM2199  PEX10    3'  ACTGAGAGTGTTCTAACTTC  15216        AAAC  GATGT
                                ACTGAGA   TC    ACTTC
                                |||||||   ||    |||||
                                TGACTCT   AG    TGAAG
                                    CACA  AT___
GAM2199  PIK3CG   3'  ACTGAAAAGACTAACTCG    15300         ____
                                ACTGAGAA   AACTCG
                                ||||||||   ||||||
                                TGACTTTT   TTGAGC
                                     CTGA
GAM2199  SLC7A6   3'  ACTGAGAAACTGAGC       19586         A  C  T
                                ACTGAGAAA CT GA GT
                                ||||||||| || || ||
                                TGACTCTTT GA CT CG
                                          _  _  _
GAM2199  SPON1    3'  ACTGAGAAAATGTCCTT     41667         AACTC    A
                                ACTGAGAA    GATGT CTT
                                ||||||||    ||||| |||
                                TGACTCTT    TTACA GAA
                                     _____    G
GAM2199  TACC1    3'  TGAGAAAACTGGGCTTC     26604          CGAT TA
                                TGAGAAAACT   G  CTTC
                                ||||||||||   |  ||||
                                ACTCTTTTGA   C  GAAG
                                     ____ CC
GAM2199  TRPS1    3'  TAAGAAAAATGTATTTC     30465        ACTC     C
                                TGAGAAA   GATGTA TTC
                                |||||||   |||||| |||
                                ATTCTTT   TTACAT AAG
                                     ____     A
GAM2199  WNT5A    3'  TGAGAAAAAGAAAATGTATTTC 18138         CTC_     C
                                TGAGAAAA   GATGTA TTC
                                ||||||||   |||||| |||
                                ACTCTTTT   TTACAT AAG
                                     TCTT     A
GAM2200  DSC3     3'  TTTTCTTTTATACATTCAAAAT 35957          TAT
           TT                    TTTTCTTTTAT   TTCAAAATTT
                                ||||||||||   ||||||||||
                                AAAAGAAAATA   AAGTTTTAAA
                                      TGT
GAM2200  DSC3     3'  TTTCTTCTATTATTTTAAAATT 35955            C
           T                     TTTCTTTTATTATTT AAAATTT
                                ||||||||||||||| |||||||
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                                AAAGAAGATAATAAA TTTTAAA
                                       A
GAM2201  BCL9     5'  ACACTTGGTACGGCCCAGGCAT 20234        CA____    CA
                T                ATACTTGG     CTAG  GCATT
                                 ||||||||     ||||  |||||
                                 TGTGAACC     GGTC  CGTAA
                                     ATGCCG   __
GAM2201  ESR1     3'  TTGGAACATGGCAGCATT    6542       C  TA_
                                 TTGG AC   GCAGCATT
                                 |||| ||   ||||||||
                                 AACC TG   CGTCGTAA
                                   T  TAC
GAM2201  INPP5D   3'  ACAGCACTTGGCACATCA    44417     A        TAG
                                 ACA TACTTGGCAC   CA
                                 ||| ||||||||||   ||
                                 TGT GTGAACCGTG   GT
                                   C         TA_
GAM2201  SH3BP2   3'  ACAAAACTGTTGCTAGCAGCAT 16622      T   T GCA
                T                ACAA ACT G   CTAGCAGCATT
                                 |||| ||| |   ||||||||||
                                 TGTT TGA C   GATCGTCGTAA
                                   T   _ AAC
GAM2202  DISC1    3'  CACTGTGTTACTGAGTACC    33028      A       __
                                 TACT TGTTACTGA  ACC
                                 |||| |||||||||  |||
                                 GTGA ACAATGACT  TGG
                                   C        CA
GAM2202  SRGAP1   3'  TGTTTAAAGGAACCTAGGTG   43613     ACT__
                                 TGTT    GAACCTAGGTG
                                 ||||    ||||||||||
                                 ACAA    CTTGGATCCAC
                                   ATTTC
GAM2202  VPS41    3'  CTAATGTTATTCCCAGGTG    38762     _    CTGAA
                                 CTA TGTTA    CCTAGGTG
                                 ||| |||||    ||||||||
                                 GAT ACAAT    GGGTCCAC
                                   T    AA___
GAM2202  BAZ2A    3'  TGGTAAGCTGGTGATGGT    30317        CA    A
                                 TGGTAAGC  GTGGT GT
                                 ||||||||  ||||| ||
                                 ACCATTCG  CACTA CA
                                     AC    C
GAM2202  GRAF     3'  TGGTGGGTTAGAGGCAGGCAAG 31459      AAGCC  T    TA
                G                 TGGT    AG GGTAG  AAGG
                                  ||||    || |||||  ||||
                                  ACCA    TC CCGTC  TTCC
                                    CCCAA  T    CG
GAM2202  PACE     3'  TGGTGGCCAGTGGTGGTGGAGG 15043      AA       A  AA
                                  TGGT  GCCAGTGGT GT  AGG
                                  ||||  |||||||| ||  |||
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                                ACCA  CGGTCACCA CA  TCC
                                  C_       C  CC
GAM2202  SALL2    3'  GGCTTGGAGTGGTAGTGGAGGT 41900     AAGCC       AA
                                GGT    AGTGGTAGT  AGGT
                                |||    |||||||||  ||||
                                CCG    TCACCATCA  TCCA
                                  AACC_       CC
GAM2203  ADAM12   3'  AGTAGACAGAGCACCATAGCA  18466        AA    ___
                                AGTAGACA  GAGCAC   AGCA
                                ||||||||  ||||||   ||||
                                TCATCTGT  CTCGTG   TCGT
                                     __     GTA
GAM2203  CEACAM1  3'  TACAGGTAGACAACCCTGACAG 11833     CA      AGAGC
                                TAC  GTAGACAA    ACAG
                                |||  ||||||||    ||||
                                ATG  CATCTGTT    TGTC
                                  TC       GGGAC
GAM2203  CLASP2   3'  CCAGTATATGCACAACA     42077       GACAAAGA
                                CCAGTA       GCACAGCA
                                ||||||       ||||||||
                                GGTCAT       CGTGTTGT
                                   ATA_____
GAM2203  CSNK2A1  3'  TACCAGCTATGGAGCACAGCA  12480        AGACAAA
                                TACCAGT      GAGCACAGCA
                                |||||||      ||||||||||
                                ATGGTCG      CTCGTGTCGT
                                    ATAC___
GAM2203  FMR2     3'  TACCAGCAGGTAATTACCAG   12979         ACA  GA  A
                                TACCAGTAG   AA  GC CAG
                                |||||||||   ||  || |||
                                ATGGTCGTC   TT  TG GTC
                                     CA_  AA  _
GAM2203  GNA11    5'  CCAGTGGGCAAAGCACAGC    44031       AGACAA
                                CCAGT     AGAGCACAGC
                                |||||     ||||||||||
                                GGTCA     TTTCGTGTCG
                                   CCCG__
GAM2203  GPR56    3'  CAGTAGACAAACATTTACAGCA 24996          GAGC_
                                CAGTAGACAAA     ACAGCA
                                ||||||||||     ||||||
                                GTCATCTGTTT     TGTCGT
                                      GTAAA
GAM2203  LIG4     5'  TAGATGAAGAGCACAGCA    14165      CA
                                TAGA  AAGAGCACAGCA
                                ||||  ||||||||||||
                                ATCT  TTCTCGTGTCGT
                                  AC
GAM2203  LILRA3   3'  CCAGCAGACAGTCCAGATGGCA 45462          A___  __
                                CCAGTAGACA    AGA  GCA
                                ||||||||||    |||  |||
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                                GGTCGTCTGT   TCT  CGT
                                     CAGG   AC
GAM2203  LNK      3'  CAGTAGACAAGCCAGC      24195        AAG   A
                                CAGTAGACA   AGC CAGC
                                |||||||||   ||| ||||
                                GTCATCTGT   TCG GTCG
                                     ___   _
GAM2203  MAN2A2   3'  CCATAGACAAGGACCTGCA   25943     G      A AG ACA
                                CCA TAGACAA G  C   GCA
                                ||| ||||||| |  |   |||
                                GGT ATCTGTT C  G   CGT
                                  _      _ CT GA_
GAM2203  NCALD    3'  GCATTCAAAGAGCACGGCA   36764     GA         A
                                GTA  CAAAGAGCAC GCA
                                |||  |||||||||| |||
                                CGT  GTTTCTCGTG CGT
                                  AA         C
GAM2203  PNUTL2   3'  CCTAGTAGACAGGAAGGCA   38648    _       __   A
                                CC AGTAGACA  AAG GCA
                                || ||||||||  ||| |||
                                GG TCATCTGT  TTC CGT
                                 A       CC  _
GAM2203  PRKWNK3  3'  TACTAGTAGACAGAAC      41538     C       AA
                                TAC AGTAGACA  GAGC
                                ||| ||||||||  ||||
                                ATG TCATCTGT  CTTG
                                  A       __
GAM2204  CENTD2   5'  GGTGGGTCTGAGGC        40131         TAAGA  A
                                GGTGGGTCT    GA GGT
                                |||||||||    || |||
                                CCACCCAGA    CT CCG
                                     ______  _
GAM2204  GRIK5    3'  AGTGGGTCTTAAGAGCCATT   13295            AAG
                                GGTGGGTCTTAAGAG   GTT
                                ||||||||||||||   |||
                                TCACCCAGAATTCTC   TAA
                                       GG_
GAM2204  PCDHA1   3'  AGTTGGTTAGAGAAGGTT    36395     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2204  PCDHA10  3'  AGTTGGTTAGAGAAGGTT    33134     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2204  PCDHA11  3'  AGTTGGTTAGAGAAGGTT    36575     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
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                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA12 3' AGTTGGTTAGAGAAGGTT   36595   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA13 3' AGTTGGTTAGAGAAGGTT   36603   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA2  3' AGTTGGTTAGAGAAGGTT   36466   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA3  3' AGTTGGTTAGAGAAGGTT   36474   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA4  3' AGTTGGTTAGAGAAGGTT   36488   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA5  3' AGTTGGTTAGAGAAGGTT   33145   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA6  3' AGTTGGTTAGAGAAGGTT   36510   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA7  3' AGTTGGTTAGAGAAGGTT   36518   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA8  3' AGTTGGTTAGAGAAGGTT   36528   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
                                TCA CCA   TCTCTTCCAA
                                  A  A___
GAM2204 PCDHA9  3' AGTTGGTTAGAGAAGGTT   36539   G  CTTA
                                GGT GGT   AGAGAAGGTT
                                ||| |||   ||||||||||
```

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                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2204  PCDHAC1   3'  AGTTGGTTAGAGAAGGTT    36618     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2204  PCDHAC2   3'  AGTTGGTTAGAGAAGGTT    36629     G   CTTA
                                GGT GGT    AGAGAAGGTT
                                ||| |||    ||||||||||
                                TCA CCA    TCTCTTCCAA
                                  A   A___
GAM2205  GGCX      3'  TGACTGGCTGCTTCTACATCTG 9063         GTACATAGC    C
              C                   TGACTGGC        CATC GC
                                  ||||||||        |||| ||
                                  ACTGACCG        GTAG CG
                                       ACGAAGAT_    A
GAM2206  HDAC4     3'  ATGCATTGCTGACATGC     25747          _   CT
                                ATGCATTGCT ACA  TGC
                                |||||||||| |||  |||
                                TACGTAACGA TGT  ACG
                                      C   __
GAM2206  SLC23A1   5'  CGCTGAGTTACATTTGCTTATG 44053     ATTGC    C
              C                   TGC     TACA TTGCTTATGC
                                  |||     |||| ||||||||||
                                  GCG     ATGT AACGAATACG
                                    ACTCA    A
GAM2206  UBE4A     3'  GCTACACACTTGCTTGTGC    21973     AT   T        A
                                GC  TGC ACACTTGCTT TGC
                                ||  ||| |||||||||| |||
                                CG  ATG TGTGAACGAA ACG
                                  __   _         C
GAM2206  DCC       3'  AACTGCTTCAGGATCTTCC    23344         T  AT  ACA
                                AACTGCTT CA  GA   TTCC
                                |||||||| ||  ||   ||||
                                TTGACGAA GT  CT   AAGG
                                     _  C_  AG_
GAM2206  DRD3      5'  CTGCTTTCGAATGTATCC     38013         _    AACAT
                                CTGCTTTC AATG     TCC
                                |||||||| ||||     |||
                                GACGAAAG TTAC     AGG
                                     C    AT___
GAM2206  EGFL5     3'  TGTTTCAGAAACATTCCCT    44544     C     AT
                                TG TTTCA  GAACATTCCCT
                                || |||||  ||||||||||
                                AC AAAGT  TTTGTAAGGGA
                                  _    C_
GAM2206  EIF2B5    3'  AACTGCTCTCTGCTGTTCCCT  41534          AA  AACA
                                AACTGCTTTC  TG    TTCCCT
                                ||||||||||  ||    ||||||
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                                TTGACGAGAG AC   AAGGGA
                                     __ GAC_
GAM2206 HNF4G   5' CTGCTTTCGCTGGTGCTCC  19974       AA AACA
                                CTGCTTTC TG   TTCC
                                |||||||| ||   ||||
                                GACGAAAG AC   GAGG
                                    CG CAC_
GAM2206 NOTCH2  3' ACAGCTTTCACATTCCC    35904   T    AATGA
                                AC GCTTTC   ACATTCCC
                                || ||||||   ||||||||
                                TG CGAAAG   TGTAAGGG
                                 T   _____
GAM2206 SURF5   3' GCTTTCAAGGCCATTCCCT  39506       TGAA
                                GCTTTCAA   CATTCCCT
                                ||||||||   ||||||||
                                CGAAAGTT   GTAAGGGA
                                    CCG_
GAM2207 GCH1    3' CTTATCAAGGCACAGAGAGT  6701    CG_  A
                                CT  CAG GCACAGAGAGT
                                ||  ||| ||||||||||
                                GA  GTT CGTGTCTCTCA
                                 ATA  C
GAM2207 SREBF1  5' TCCACTCGCAGAGCACAG   45373
                                TTCACTCGCAGAGCACAG
                                ||||||||||||||||||
                                AGGTGAGCGTCTCGTGTC

GAM2207 STAU    3' ACTCGCAGGGCTACCAGGT  32688       A _ AG A
                                ACTCGCAG GC AC  AG GT
                                |||||||| || ||  || ||
                                TGAGCGTC CG TG  TC CA
                                    C A G_ _
GAM2208 FGF2    5' CCGGCGGCCCGGGACCTGGGGT 12835    A      CT  TCGA
                                TCG CGGCCCGGG  CT   GGT
                                ||| |||||||||  ||   |||
                                GGC GCCGGGCCC  GA   CCA
                                  C       TG  CC__
GAM2208 POMZP3  5' CGGCGGCCCGGGCTTGCCCAGG 29240   A       CT  G
            T                    CG CGGCCCGGGCT  TC AGGT
                                || ||||||||||  || ||||
                                GC GCCGGGCCCGA  GG TCCA
                                 C         AC  G
GAM2208 TACSTD2 5' TCGGGGCTCGGGCTCCGGC  14295    AC  C      TCGA
                                TCG  GGC CGGGCTCT   GGT
                                |||  ||| ||||||||   |||
                                AGC  CCG GCCCGAGG   CCG
                                  C_  A      _____
GAM2209 DLG5    5' GGAGGTGAGGTCCTCATCACA  44461    A_  TAAAA  G
                                GGA  TG    TT TTATCACA
                                |||  ||    || ||||||||
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                                CCT  AC    AG AGTAGTGT
                                  CC  TCC__  G
GAM2209  FBP1    3'  AGGAATGTAAGGTGCACA    7998          AAT  TTAT
                                AGGAATGTAA   TG   CACA
                                ||||||||||  ||   ||||
                                TCCTTACATT   AC   GTGT
                                     CC_  ____
GAM2209  NR1I2   3'  AGGAATGCTAGCCAGCTGTCA  35099        AAAATT  A
                                AGGAATGT     GTT TCA
                                ||||||||     ||| |||
                                TCCTTACG     CGA AGT
                                     ATCGGT   C
GAM2209  NR4A2   3'  AGGAATGTTGGACGGTGTTAC  26163        AAAAT__
                                AGGAATGT      TGTTAT
                                ||||||||      ||||||
                                TCCTTACA      ACAATG
                                     ACCTGCC
GAM2209  PTEN    3'  AGGATGTGAACCAGTATATCAC 7200       A  A  ATT  _
            AA                    AGGA TGT AA   GT TATCACAA
                                ||||| ||| ||   || ||||||||
                                TCCT ACA TT   CA ATAGTGTT
                                  _  C  GGT  T
GAM2209  PYGO2   3'  AGGAATGAGAATTGCTA     41945        TAA
                                AGGAATG   AATTGTTA
                                |||||||   ||||||||
                                TCCTTAC   TTAACGAT
                                     TC_
GAM2209  SHANK2  3'  GGAATGTAGAACAAGTTAC   29459        A  T_
                                GGAATGTA AAT  GTTAT
                                |||||||| |||  |||||
                                CCTTACAT TTG  CAATG
                                     C   TT
GAM2209  SNX6    3'  AGGAAGTGTGGAATCATCAC  34558       _  AAAATT
                                AGGAA TGT     GTTATCAC
                                ||||| |||     ||||||||
                                TCCTT ACA     TAGTAGTG
                                   C  CCT___
GAM2209  SYT4    3'  GGCAATGTAAAAAATCTTCACA 41659    _       TT  A
                                GG AATGTAAAA  GTT TCACA
                                || |||||||||  ||| |||||
                                CC TTACATTTT  TAG AGTGT
                                 G       T_  A
GAM2209  VBP1    3'  AGAAATGTGGAAAAAAAAATCA 17923        A_  TTGTT
            CAA                   AGGAATGT  AAA    ATCACAA
                                ||||||||  |||    |||||||
                                TCTTTACA  TTT    TAGTGTT
                                     CC   TTTTT
GAM2209  LARGE   3'  TGTGTGTGCACTGA       21869          GCAA
                                TGTGTGTGCA    TTGA
                                ||||||||||    ||||
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                                ACACACACGT   GACT
                                     ____
GAM2210 STC1    3' CGTTACTGGTTTTAAAGGCT  17176       T A      A
                                CGTTACT G TTTTAAAG CT
                                ||||||| | |||||||| ||
                                GCAATGA C AAAATTTC GA
                                    _ C      C
GAM2210 VPS41   3' AATCAGTTACTTAAAAATGAAG 38761     _       TTTTA
           ACT                    AATC GTTACTTGA    AAGACT
                                |||| |||||||||    ||||||
                                TTAG CAATGAATT    TTCTGA
                                  T       TTTAC
GAM2210 ABCG2   3' TACATTTCCAGTATAGC    22095        T   AC
                                TACATTTCC GTAT  GGC
                                ||||||||| ||||  |||
                                ATGTAAAGG CATA  TCG
                                     T   __
GAM2210 B4GALT4 3' TCTTATTTCCTGTGGCCT   19103    AC       ATAC
                                TCT  ATTTCCTGT   GGCTT
                                |||  |||||||||   |||||
                                AGA  TAAAGGACA   CCGGA
                                 A_      ____
GAM2210 EPM2A   3' TCTGTATTTCCTGTAGAACCT 24974    AC       TAC
                                TCT  ATTTCCTGTA  GGCTT
                                |||  ||||||||||  |||||
                                AGA  TAAAGGACAT  TTGGA
                                  CA       C__
GAM2210 SCN1A   3' TCTACATTTCTTGTGGTACA  44817        C  A_
                                TCTACATTTC TGT  TACG
                                |||||||||| |||  ||||
                                AGATGTAAAG ACA  ATGT
                                     A  CC
GAM2211 GYPC    3' AGTGCTCTCTCTCTCTGTCTGG 32541        A    CTA
                                AGTGCTCTC CTCTC   TCTGG
                                ||||||||| |||||   |||||
                                TCACGAGAG GAGAG   AGACC
                                     A    AC_
GAM2211 HLF     3' TAGTACTCTTACTTATCTG   13394        C  CTCC
                                TAGTGCTCT ACT   TATCTG
                                |||||||| |||   ||||||
                                ATCATGAGA TGA   ATAGAC
                                     A  ____
GAM2211 NTSR1   3' TAGAGGCCCTTTTCCTATCTGG 14893    T_   CACTC
                                TAG  GCTCT   TCCTATCTGG
                                |||  |||||   ||||||||||
                                ATC  CGGGA   AGGATAGACC
                                  TC    AA___
GAM2211 RBBP2   3' GTGAGAGGTTCTCCTATTTGG  22803    CTCTCAC      C
                                GTG      TCTCCTAT TGG
                                |||      |||||||| |||
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                                CAC      AGAGGATA ACC
                                  TCTCCA_       A
GAM2211  THY1     3'  GTGCCCTCACATCT       26631          TCTCCT
                                GTGCTCTCAC     ATCT
                                ||||||||||     ||||
                                CACGGGAGTG     TAGA
                                       _______
GAM2211  FN1      3'  TGGGTGACTTTCCTACTT    38341    A  A      C
                                TG GT GACTTTCC ATTT
                                || || |||||||| ||||
                                AC CA CTGAAAGG TGAA
                                 C  _       A
GAM2211  IRTA2    3'  TGAGCAGATTTTTTTCTTT   36349        C   CCCA
                                TGAGTAGA TTT    TTTCTTT
                                |||||||| |||    |||||||
                                ACTCGTCT AAA    AAAGAAA
                                     A  _____
GAM2211  JJAZ1    3'  GCAGTTTCCCTCTTTCCT    31690      AC     A_
                                GTAG  TTTCCC  TTTCTT
                                ||||  ||||||  ||||||
                                CGTC  AAAGGG  AAAGGA
                                  __     AG
GAM2211  OXTR     3'  TGAGTACTTCATTTCTTT    9532       AG    TCC
                                TGAGT  ACTT   CATTTCTTT
                                |||||  ||||   |||||||||
                                ACTCA  TGAA   GTAAAGAAA
                                       __   ___
GAM2211  ZNF10    3'  AGTAGCATACTCATTTCTTTT 31732       ACTTTCC
                                AGTAG      CATTTCTTTT
                                |||||      ||||||||||
                                TCATC      GTAAAGAAAA
                                   GTATGA_
GAM2212  SH3GL3   5'  CTTTATGGTGCAGCTTGA    16684      T   C   C  GC
                                CTTT TGG GCG GC  GA
                                |||| ||| ||| ||  ||
                                GAAA ACC CGT CG  CT
                                  T   A   _  AA
GAM2212  CEP2     5'  GATACTTCAGCAGGGTCCTG   27688         AA    ATA
                                GATACTTCA  CAGG   CTG
                                |||||||||  ||||   |||
                                CTATGAAGT  GTCC   GAC
                                     C_    CAG
GAM2213  PIP5K1A  3'  GTTCCTAGTCAAAGACGA    18655     A   C_
                                GTT CTG  CAAAGACGA
                                |||  |||  |||||||||
                                CAA GAT  GTTTCTGCT
                                  G   CA
GAM2214  MMP25    5'  GGGGTCCCGGGAAGTGCGC   35389    A  A   TT_
                                GG GT CTC   GAGTGCGC
                                || || |||   ||||||||
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```
                                CC CA GGG   TTCACGCG
                                 C  _   CCC
GAM2214  ODC1     3'  AGGGGCACTCTTGAGTAGCG   14912     A          _
                                AGG GTACTCTTGAGT GCG
                                ||| |||||||||||| |||
                                TCC CGTGAGAACTCA CGC
                                  C           T
GAM2214  AP1G1    3'  TCTCTTCAGCTCCTCATGC    10050      _   GAA  _
                                TCTCT CAGC   TC TGC
                                ||||| ||||   || |||
                                AGAGA GTCG   AG ACG
                                   A    AGG  T
GAM2214  FZD8     3'  TCTCCCAGGTGAAATCTG     36614        C__
                                TCTCTCAG   GAATCTG
                                ||||||||   |||||||
                                AGAGGGTC   TTTAGAC
                                     CAC
GAM2214  PIP5K1A  3'  TCTCCCAGCCCATGGCTGC    18659         GA  __
                                TCTCTCAGC  AT  CTGC
                                |||||||||  ||  ||||
                                AGAGGGTCG  TA  GACG
                                     GG  CC
GAM2214  PRDM2    5'  TCTCTCAACAATAACTGC     31975          AT_
                                TCTCTCAGCGA   CTGC
                                ||||||||||   ||||
                                AGAGAGTTGTT   GACG
                                      ATT
GAM2214  TNFAIP1  3'  TCCCTCAGATTGATTCTGC    34483        C__  A
                                TCTCTCAG   GA TCTGC
                                ||||||||   || |||||
                                AGGGAGTC   CT AGACG
                                     TAA  A
GAM2214  UFD1L    5'  TCTCCCAGCCGCCGCTGC     43826         _ AAT
                                TCTCTCAGC G   CTGC
                                ||||||||| |   ||||
                                AGAGGGTCG C   GACG
                                     G GGC
GAM2214  VAV2     3'  TCTCCCAAGAAAATCTGC     17922        C_
                                TCTCTCAG  GAATCTGC
                                ||||||||  ||||||||
                                AGAGGGTT  TTTAGACG
                                     CT
GAM2215  AGM1     3'  TTAGTGTTTAAGAAAAACA    31818          T
                                TTAGTGTTTAA AAAAATA
                                |||||||||| |||||||
                                AATCACAAATT TTTTTGT
                                      C
GAM2215  CLECSF5  3'  TTAGTGTTGTAATAAAAAATAT 29933         _       _
              G                  TTAGTGTT TAATAAAAA TATG
                                ||||||||  ||||||||| ||||
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                                AATCACAA ATTATTTTT ATAC
                                    C        T
GAM2215 IL21R    3' GTGTTTAATAAATATCTCTTGG 34756           A  A___
             G                   GTGTTTAATAAA AT    TGGG
                                 |||||||||||| ||    ||||
                                 CACAAATTATTT TA    ACCC
                                       A  GAGA
GAM2215 YES1     3' TTAGAGTTTAATACTTGGG    24122      T       AAAATA
                                 TTAG GTTTAATA     TGGG
                                 |||| ||||||||      ||||
                                 AATC CAAATTAT     ACCC
                                   T       GA____
GAM2216 C1D      3' TTACATATTAATGTACTTTTTG 26763     G        CGTA
             AA                    TTA ATATTAATGT    TTTGAA
                                 ||| ||||||||||    ||||||
                                 AAT TATAATTACA    AAACTT
                                   G         TGAA
GAM2217 DGKE     3' TATACCCATTATACTACTA    18890       AA   C
                                 TATACT  CAT TATACTACTA
                                 ||||||  ||| ||||||||||
                                 ATATGG  GTA ATATGATGAT
                                      __  _
GAM2217 TIAL1    3' CATATACTGTCCATACT     35295         AACA
                                 TATATACT    TCTATACT
                                 ||||||||    ||||||||
                                 GTATATGA    AGGTATGA
                                     C___
GAM2218 BAALC    3' TGCCAGTGGGGACATAT     36045    A   A  A
                                 TG CAG TG GGACATAT
                                 || ||| || ||||||||
                                 AC GTC AC CCTGTATA
                                  G   _  C
GAM2218 NEDD4    3' TGACAGATGAAGAAATATG    43103            C
                                 TGACAGATGAGGA ATATG
                                 |||||||||||| |||||
                                 ACTGTCTACTTCT TATAC
                                        T
GAM2219 COG4     3' CTTTATTCAGGGATCATA     31722          T_
                                 CTTTATTCAG  ATCATA
                                 ||||||||||  ||||||
                                 GAAATAAGTC  TAGTAT
                                      CC
GAM2219 CYP4F3   3' TCTTTCATTCAGTATCAT    9457       _
                                 TCTT TATTCAGTATCAT
                                 |||| ||||||||||||
                                 AGAA GTAAGTCATAGTA
                                   A
GAM2219 DSPG3    3' CAATCTCAAAGTATCAT     41173        TATTC
                                 TAATCTT     AGTATCAT
                                 |||||||     ||||||||
```

```
                                GTTAGAG    TCATAGTA
                                   TT___
GAM2220  TESK1    3'  TATTGAAATCTTTTTAAAT   26616       T
                                TATTGAA ATCTTTTTAAAT
                                ||||||| ||||||||||||
                                ATAACTT TAGAAAAATTTA
                                   _
GAM2220  UC28     3'  TCTATTAATATCTTTTTA    34694       A
                                TCTATTGA TATCTTTTTA
                                |||||||| ||||||||||
                                AGATAATT ATAGAAAAAT
                                   _
GAM2221  FH       3'  TTTTTTAAATTTTATACAT   6625        A
                                TTTTTTAAAT TTTATACAT
                                |||||||||| |||||||||
                                AAAAAATTTA AAATATGTA
                                   _
GAM2222  FMOD     3'  TATTATCATCATGCTGGTGACC 12931       ATATAATA
                                TATTATCAT      TGACC
                                |||||||||      |||||
                                ATAATAGTA      ACTGG
                                   GTACGACC
GAM2223  AKAP2    3'  CTGTACATTCTCTTGCCCCCAG 28494       _________  TCTGG
           A                     TTGTACATTC      CCT    G
                                ||||||||||      |||    |
                                GACATGTAAG      GGG    T
                                   AGAACIII  GGTCT
GAM2223  ALDH1B1  3'  TTGTACATCTCTCTGG     8675        CCC
                                TTGTACATT   TTCTGG
                                |||||||||   ||||||
                                AACATGTAG   GAGACC
                                   A__
GAM2223  CARD15   3'  TTGTACATCCTGGG       35262       CCCTT
                                TTGTACATT    CTGGG
                                |||||||||    |||||
                                AACATGTAG    GACCC
                                   _____
GAM2223  CDH13    3'  TTGTACATTTACTGAGGAGG  10375       CC  TCT
                                TTGTACATT  CT   GGGGG
                                |||||||||  ||   |||||
                                AACATGTAA  GA   CCTCC
                                   AT  CT_
GAM2223  DEC1     3'  TTGTGCATGTCTCTGAGG    32646     A   TCCC
                                TTGT CAT    TTCTGGGG
                                |||| |||    ||||||||
                                AACA GTA    GAGACTCC
                                  C   CA__
GAM2223  F7       5'  TTGACATTCCCCATGGG     33349     T       TC
                                TTG ACATTCCCT  TGGG
                                ||| |||||||||  ||||
```

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                                AAC TGTAAGGGG  ACCC
                                  _       T_
GAM2223  HCRT     3'  ATTGCCTTTTTTCTGGGGG   11344     C  ____
                                ATT CCT    TCTGGGGG
                                ||| |||    ||||||||
                                TAA GGA    AGACCCCC
                                  C   AAAA
GAM2223  KNSL1    3'  TTGTACATATTCCTTCTG    21181        TC_
                                TTGTACAT   CCTTCTG
                                ||||||||   |||||||
                                AACATGTA   GGAAGAC
                                     TAA
GAM2223  MEIS1    3'  TTGGCATTCCAGGGTGGGG   14418     TA     CTTC
                                TTG  CATTCC    TGGGG
                                |||  ||||||    |||||
                                AAC  GTAAGG    ACCCC
                                  C_     TCCC
GAM2223  PABPN1   3'  TGCATTTCCCCAGGGGGG    21612     CA     TCT
                                TGTA  TTCCCT   GGGGG
                                ||||  ||||||   |||||
                                ACGT  AAGGGG   CCCCC
                                   A_     T__
GAM2223  PDGFRA   3'  TTGTACATGCCTTTCCTTGG   26291        T  C    GG
                                TTGTACAT CC TTCT  GG
                                |||||||| || ||||  ||
                                AACATGTA GG AAGG  CC
                                     C  A    AA
GAM2223  PDGFRA   3'  TTGTGCTTTCTCTGGAGG    26292     ACA   CCT
                                TTGT   TTC   TCTGGGGG
                                ||||   |||   ||||||||
                                AACA   AAG   AGACCTCC
                                   CGA   ___
GAM2223  PYGB     3'  TGTGCAAAGTTCTGGGGG    16052     A  TTCCC
                                TGT CA     TTCTGGGGG
                                ||| ||     |||||||||
                                ACA GT     AAGACCCCC
                                  C  TTC__
GAM2223  RAD51C   3'  CTGTGCATTCCTTCTGG     38483     A     C
                                TTGT CATTCC TTCTGG
                                |||| |||||| ||||||
                                GACA GTAAGG AAGACC
                                   C     _
GAM2223  RARB     5'  TTGTACACTCGAGGGG      9718          CCTTCT
                                TTGTACATTC     GGGG
                                ||||||||||     ||||
                                AACATGTGAG     CCCC
                                      CT_____
GAM2223  SLC38A2  3'  TTGTCCATTCTCTGGAATGGG  33280     A    CCT    ___
                                TTGT CATTC   TCTGG   GGG
                                |||| |||||   |||||   |||
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                                AACA GTAAG   AGACC   CCC
                                  G    ___     TTA
GAM2223  SPOCK    3'  TTGTACATTTTCCTAAG     41747         CCC
                                TTGTACATT   TTCTGGG
                                |||||||||   |||||||
                                AACATGTAA   AGGATTC
                                     A__
GAM2223  SPRR1B   3'  GCACATTCTTTTTTGGGGG   44607        CC  C
                                GTACATTC  TT TGGGGG
                                ||||||||  || ||||||
                                CGTGTAAG  AA ACCCCC
                                     AA  A
GAM2223  TRPC5    3'  CACTCTCCTTTCTGGGGG    29766       _   _
                                CATTC CCTT CTGGGGG
                                ||||| |||| |||||||
                                GTGAG GGAA GACCCCC
                                   A    A
GAM2223  VEGF     3'  TTGCACATTCTTGGGCAGGGG  17976         CCTTCT
                                TTGTACATTC     GGGGG
                                ||||||||||     |||||
                                AACGTGTAAG     TCCCC
                                      AACCCG
GAM2223  ZNF83    5'  TGTACATTTTTCTGGG      32896         CCC
                                TGTACATT   TTCTGGG
                                ||||||||   |||||||
                                ACATGTAA   AAGACCC
                                     A__
GAM2223  SHOX     5'  TATTTACGCCTTTCCATTGG   27830           A   C
                                TATTTACGCCTTT TCAT GG
                                |||||||||||| |||| ||
                                ATAAATGCGGAAA GGTA CC
                                        _   A
GAM2224  RAD51L3  3'  GCCAGACACGCCATGCGCCGGC 39470     CA  T   ATA_   A
                                GCC  AC ACGC    CGCC GC
                                |||  || ||||    |||| ||
                                CGG  TG TGCG    GCGG CG
                                  TC  _   GTAC    C
GAM2224  CARD15   3'  CGGGGAATGGCCTGGATGG    35260    A   CT    AT
                                CG GGAA  GCTTG  ATGG
                                || ||||  |||||  ||||
                                GC CCTT  CGGAC  TACC
                                 C   AC    C_
GAM2224  PPP2R4   3'  AGGAACTGTGGCCTGGGTGG   41325       ___    ATA
                                AGGAACT   GCTTG   TGG
                                |||||||   |||||   |||
                                TCCTTGA   CGGAC   ACC
                                    CAC    CC_
GAM2225  DDX6     3'  TGCCCATTCCTGCAAAAGTT   20569    AAAAT    A
                                TG    TTCCT CAAAAGTT
                                ||    ||||| ||||||||
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                                AC     AAGGA GTTTTCAA
                                 GGGT_     C
GAM2225  GLRB     3'  TATGAAAATTCAAAAGTT     9070          TCCTA
                                TATGAAAATT     CAAAAGTT
                                ||||||||||     ||||||||
                                ATACTTTTAA     GTTTTCAA
                                      _____
GAM2225  IL1RAP   3'  ATGAAAAATACAAAAGTT     13497        TTTCC
                                ATGAAAA     TACAAAAGTT
                                |||||||     ||||||||||
                                TACTTTT     ATGTTTTCAA
                                    T____
GAM2225  RERE     3'  TATGAAGATTTCCTACAA     29034        A
                                TATGAA ATTTCCTACAA
                                |||||| ||||||||||
                                ATACTT TAAAGGATGTT
                                   C
GAM2226  ADCY7    3'  TTTGTTAGATACGTGTG      9992          A   C
                                TTTGTTAGA TAT TGTG
                                ||||||||| ||| ||||
                                AAACAATCT ATG ACAC
                                     _  C
GAM2226  CBFB     3'  TTTGTCAGAAGGCTGTG      35637          TAT
                                TTTGTTAGAA   CTGTG
                                ||||||||||   |||||
                                AAACAGTCTT   GACAC
                                     CC_
GAM2226  DRD5     3'  CTTGTCAGTGTCTGTG       9026         AATA
                                TTTGTTAG    TCTGTG
                                ||||||||    ||||||
                                GAACAGTC    AGACAC
                                     AC__
GAM2226  DUSP4    3'  TTTGCTAGGATCTGTG       38431         AAT
                                TTTGTTAG   ATCTGTG
                                ||||||||   |||||||
                                AAACGATC   TAGACAC
                                     C__
GAM2226  HIP1     3'  TTTGCTAGAGTCACACCTG    23764          ___
                                TTTGTTAGA   ATATCTG
                                |||||||||   |||||||
                                AAACGATCT   TGTGGAC
                                     CAG
GAM2226  LNPEP    3'  TTTGTCCCCATCTGTG       24559        AGAA
                                TTTGTT    TATCTGTG
                                ||||||    ||||||||
                                AAACAG    GTAGACAC
                                   GG__
GAM2226  LRP1     3'  TTTATAAGAATATCTGTG     14230        T
                                TTTGT AGAATATCTGTG
                                ||||| ||||||||||||
```

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                                AAATA TCTTATAGACAC
                                   T
GAM2226 MMP13    3' TTCGTTAGTGTCTGTG      14556        AATA
                                TTTGTTAG   TCTGTG
                                ||||||||   ||||||
                                AAGCAATC   AGACAC
                                    AC__
GAM2226 NOS1     3' TTGTTCTTTATATCTGTG    8384       AGA_
                                TTGTT   ATATCTGTG
                                |||||   |||||||||
                                AACAA   TATAGACAC
                                   GAAA
GAM2226 OGN      3' TTGTTAGAATAATAATTGTG  37459          TC___
                                TTGTTAGAATA    TGTG
                                ||||||||||    ||||
                                AACAATCTTAT    ACAC
                                      TATTA
GAM2226 OGT      5' TTTATTAGAATACTATG     18794           T
                                TTTGTTAGAATA CTGTG
                                |||||||||||| |||||
                                AAATAATCTTAT GATAC
                                          _
GAM2226 PLAG1    3' CTTGTTAGAACATTGTG     15351           C
                                TTTGTTAGAATAT TGTG
                                |||||||||||| ||||
                                GAACAATCTTGTA ACAC
                                          _
GAM2226 RIMS1    3' TTTGTTAGAAGCATCAGTG   43739         _   T
                                TTTGTTAGAA TATC GTG
                                |||||||||| |||| |||
                                AAACAATCTT GTAG CAC
                                      C   T
GAM2226 SLC2A2   3' TCTGTTTAATCATCTGTG    7350       A  A
                                TTTGTT GA TATCTGTG
                                |||||| || ||||||||
                                AGACAA TT GTAGACAC
                                    A  A
GAM2226 SMARCD1  3' TTTGTCAGTTCTGTG       40091        AATA
                                TTTGTTAG   TCTGTG
                                ||||||||   ||||||
                                AAACAGTC   AGACAC
                                    A___
GAM2226 SRGAP1   5' TTTGTTAGAATACTGTG     43615           T
                                TTTGTTAGAATA CTGTG
                                |||||||||||| |||||
                                AAACAATCTTAT GACAC
                                          _
GAM2227 ABCD1    3' CCACGGAGATGGCTAC      6193          ACTCTACA
                                TCACGGAGAT      CTAC
                                ||||||||||      ||||
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                                GGTGCCTCTA       GATG
                                     CC_______
GAM2227  ACADL    3'  TCACAGAGATGTTCTGCA    11497          AC   A
                                TCACGGAGAT  TCT CA
                                ||||||||||  ||| ||
                                AGTGTCTCTA  AGA GT
                                     CA   C
GAM2227  ADCY2    3'  TCACGGAAACGCTAC       42146        ATACTCT  A
                                TCACGGAG      AC CTAC
                                ||||||||      || ||||
                                AGTGCCTT      TG GATG
                                     ________ C
GAM2227  FPGS     3'  TCACGGAGTATGCTGGCCCCAC 22432         _  A  __ TA
               T                 TCACGGAG AT CT  C  CACT
                                ||||||||| || ||  |  ||||
                                AGTGCCTC TA GA  G  GTGA
                                     A  C  CC GG
GAM2227  LOH11CR2A 5'  TCACAGAGATACTCTTCA    31192             A
                                TCACGGAGATACTCT CA
                                |||||||||||||||| ||
                                AGTGTCTCTATGAGA GT
                                          A
GAM2227  Nrap     3'  CTGCAATTTAATTTTAAATCAG 40192          CTC___     A
               AGTT                  CTGTAATTT     AAATCA AGTT
                                |||||||||     |||||| ||||
                                GACGTTAAA     TTTAGT TCAA
                                     TTAAAA     C
GAM2227  SLC9A6   3'  ACTGTACTTCATCAAAGT    26827       A    TCAA
                                ACTGTA TTTC    ATCAAAGT
                                |||||| ||||    ||||||||
                                TGACAT GAAG    TAGTTTCA
                                  _    _____
GAM2228  ATP6V0C  3'  GCGCATGTACAAGACC      44557     AC       TCTT
                                GC  CATGTACG    AGACC
                                ||  ||||||||    |||||
                                CG  GTACATGT    TCTGG
                                 C_       _____
GAM2228  GRM1     3'  CACCAAAAGTCTTAGACCA   9131       TGTAC
                                CACCA    GTCTTAGACCA
                                |||||    ||||||||||
                                GTGGT    CAGAATCTGGT
                                   TTT__
GAM2228  MCL1     3'  GCACCATGGTTAGAC       34998         TACGTC
                                GCACCATG     TTAGAC
                                ||||||||     ||||||
                                CGTGGTAC     AATCTG
                                     C_____
GAM2228  RXRA     3'  CCGCATCATTCCTAGAC     16419       C   GTACG
                                CCGCA CAT    TCTTAGAC
                                ||||| |||    ||||||||
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                                GGCGT GTA    AGGATCTG
                                  A  _____
GAM2228  SRC     3'  CACCATGTGTGTCCTGCCA   24030       AC    AGA
                                CACCATGT  GTCTT   CCA
                                ||||||||  |||||   |||
                                GTGGTACA  CAGGA   GGT
                                    CA    C__
GAM2228  WEE1    3'  GCAAACATGTTTTAGACCA   18093    C_    ACGTC
                                GCA  CATGT    TTAGACCA
                                |||  |||||    ||||||||
                                CGT  GTACA    AATCTGGT
                                  TT    A____
GAM2229  AGL     3'  TACTATAGTACGTGGTGT    8490     C   _  C  C
                                TAC ATAG ACG GG GT
                                ||| |||| ||| || ||
                                ATG TATC TGC CC CA
                                  A   A  A  A
GAM2229  RTN1    3'  TACCATAAGTGCGGTCGACTGC 34473       AC   _  T  A
                                TACCATAG  GCGG CG AT GT
                                ||||||||  |||| || || ||
                                ATGGTATT  CGCC GC TG CG
                                    CA   A  _  A
GAM2230  CLK2    3'  TGGATGGGGTAGGGCAGGTA   41281    A      AA   C
                                TG ATGGGGTG  GCAG TA
                                || ||||||||  |||| ||
                                AC TACCCCAT  CGTC AT
                                 C       CC   C
GAM2230  DKK1    3'  TAAATGGGGTAAAGGGTTATGC 29270           CAGC
           T                     TGAATGGGGTGAAG   TATGCT
                                ||||||||||||||   ||||||
                                ATTTACCCCATTTC   ATACGA
                                      CCA_
GAM2230  ENPP3   3'  TGAATGGGTGGGGCAGGGAGCC 22714       G  AA   CTAT
                                TGAATGGG TG  GCAG   GCT
                                ||||||||  ||  ||||   |||
                                ACTTACCC AC  CGTC   CGG
                                    _  CC   CCT_
GAM2230  PCLO    3'  TGAATGGGGAGGACTCCTGCTA 45308       T_  AGCA_
           TGCT                    TGAATGGGG  GA    GCTATGCT
                                ||||||||  ||    ||||||||
                                ACTTACCCC  CT    CGATACGA
                                   TC  GAGGA
GAM2230  PRKY    3'  AAACAGGGTGGCTATG      15680         AAGCA
                                GAATGGGGTG    GCTATG
                                ||||||||||    ||||||
                                TTTGTCCCAC    CGATAC
                                      _____
GAM2230  TCF7    3'  TGAATGGGGAGGGGTGCACACT 17325       TGAAGCA  T
                                TGAATGGGG      GC ATGCT
                                |||||||||      || |||||
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                                ACTTACCCC      CG TGTGA
                                     TCCCCA_  _
GAM2230  TPP2     3'  TGAAGATTTATTGAAGCAGTTA 17654      T  GG___       C
             TGCT                    TGAA GG     TGAAGCAG TATGCT
                                ||||| ||     |||||||| ||||||
                                ACTT CT     ACTTCGTC ATACGA
                                  _ AAATA       A
GAM2230  VDAC1    3'  TAAATTCTGAAGGTAGCTATGC 17932       GGGG     C_
             T                    TGAAT    TGAAG  AGCTATGCT
                                |||||    |||||  |||||||||
                                ATTTA    ACTTC  TCGATACGA
                                   AG__     CA
GAM2230  ARF1     3'  CTGAAGGTGGGTAGGGCG    43308          CTCGCC   A
                                TTGAAGGTGG     TAG GCG
                                ||||||||||      ||| |||
                                GACTTCCACC     ATC CGC
                                      C_____   C
GAM2230  CDK10    3'  TCGGAGGTGGCTGGGGCG    38152     A       CGCCTAGA
                                TTG AGGTGGCT       GCG
                                ||| ||||||||       |||
                                AGC TCCACCGA       CGC
                                  C       CCC_____
GAM2230  STX1A    3'  TTGGAGTGGCCCACCTGGAGTG 21416     AA          A   C
             G                    TTG  GGTGGCTCGCCT GAG GG
                                |||  ||||||||||| ||| ||
                                AAC  TCACCGGGTGGA CTC CC
                                  C_          C   A
GAM2230  TUBA2    3'  CTGGGGGTGGCAGTGGAGTGG  38615     AA     TCGCCTA   C
                                TTG  GGTGGC      GAG GG
                                |||  ||||||      ||| ||
                                GAC  CCACCG      CTC CC
                                  CC     TCAC___   A
GAM2231  SART2    3'  GCTATCATTTTTTGCCATGT   30036         C_    GC
                                GTTATCATT  TTGCT  GT
                                |||||||||  |||||  ||
                                CGATAGTAA  AACGG  CA
                                     AA    TA
GAM2232  CSRP1    3'  GGGTCCTTAAGACCTGGGTT   19842           ____
                                GGGTCCTTAAGA    GGTT
                                ||||||||||||    ||||
                                CCCAGGAATTCT    CCAA
                                       GGAC
GAM2232  GRIK5    3'  GGGTCTTAAGAGCCAT      13297       C      GT
                                GGGTC TTAAGAG  TCGT
                                |||||  |||||||  ||||
                                CCCAG AATTCTC  GGTA
                                  _      ___
GAM2232  ITGA7    3'  CAGGTCCTTGGGGTCCTGT    13608          AAGA    _
                                CGGGTCCTT    GGTTC GT
                                |||||||||    |||||  ||
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                                GTCCAGGAA   CCAGG CA
                                    CC__    A
GAM2232 LIMD1   3' GGGTTTTCAGGAGGCTCA   30633     CC  A
                                GGGT  TTA GAGGTTCG
                                ||||  ||| ||||||||
                                CCCA  AGT CTCCGAGT
                                  AA  C
GAM2232 MAP3K12 3' GGGCCTTAAGACAGGGCT   26686    T     ___
                                GGG CCTTAAGA  GGTT
                                ||| ||||||||  ||||
                                CCC GGAATTCT  CCGA
                                  _     GTC
GAM2232 MOX2    3' GGATCCTTAAGGCTTTCG   42518         AGG
                                GGGTCCTTAAG  TTCG
                                ||||||||||  ||||
                                CCTAGGAATTC  AAGC
                                      CGA
GAM2232 NMI     5' CGGGTTCTCGAAACTGTC   21719     C  AA  GG  C
                                CGGGT CTT  GA  TT GTC
                                ||||| |||  ||  || |||
                                GCCCA GAG  CT  GA CAG
                                  A  __  TT  _
GAM2232 PIK3C2B 3' CGGGTCCTTGGCAGAACCCCA  15290        A__   G
                                CGGGTCCTT  AGAG TTCG
                                |||||||||  |||| ||||
                                GCCCAGGAA  TCTT GGGT
                                     CCG   G
GAM2232 SORBS1  3' GGGTTTTAAGGAAATTCA   31711     CC   _
                                GGGT  TTAAG AGGTTCG
                                ||||  ||||| |||||||
                                CCCA  AATTC TTTAAGT
                                  A_    C
GAM2232 TCF20   3' GGGTCCTTGAGGTCCTCA   42537       AA     G
                                GGGTCCTT  GAGGTTC TCA
                                ||||||||  ||||||| |||
                                CCCAGGAA  CTCCAGG AGT
                                    __    _
GAM2233 GRIA3   3' TTGAAGCAGCCACGTTTTCGG  28781       _  TG AACATC
                                TTGAAGC GT  C     TTCGG
                                ||||||| ||  |     |||||
                                AACTTCG CG  G     AAGCC
                                    T  GT CAA___
GAM2233 CLC     3' TTTCTCTTCTGGTTTA     29906         CGA
                                TTTCTCTTCTG  GTTTA
                                ||||||||||  |||||
                                AAAGAGAAGAC  CAAAT
                                     ___
GAM2233 OXTR    3' TATGTTTCTTTCTAAGATTTTA 9529         C   C  G
            T                    TATGTTTCT TTCTG GA TTTAT
                                ||||||||| ||||| || |||||
```

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                                ATACAAAGA AAGAT CT AAATA
                                      _    T  A
GAM2233  PPIG     3'  TGTTTTTCTCATGTCGAGTTTA 21993      C    C  _
              T                  TGTTT TCTT TG CGAGTTTAT
                                 ||||| |||| || |||||||||
                                 ACAAA AGAG AC GCTCAAATA
                                    A    T  A
GAM2234  ABCE1    3'  CTCTTAAAGTTTGTCA     40501     C    AC
                                 CTC TTAA  GGTTTGTCA
                                 ||| ||||  |||||||||
                                 GAG AATT  TCAAACAGT
                                   _    __
GAM2234  CNTN3    3'  TAAATTCCTTTGGTTTATCAA  42483     C     AAAC
                                 TAAA TCCTT    GGTTTGTCAA
                                 |||| |||||    ||||||||||
                                 ATTT AGGAA    CCAAATAGTT
                                   A    A___
GAM2234  EIF2S3   3'  TAAACCCCTTGGTTGT      10864         AAAC    T
                                 TAAACTCCTT    GGTT GT
                                 ||||||||||    |||| ||
                                 ATTTGGGGAA    CCAA CA
                                       ____   _
GAM2234  FBXW1B   3'  AACTCCTTGGGTGCCA      37986        AAAC  TT
                                 AACTCCTT    GG  TGTCA
                                 ||||||||    ||  |||||
                                 TTGAGGAA    CC  ACGGT
                                       _____  C_
GAM2234  HSD11B1  3'  AACTCCTTCCATTTGTCA    24358        AAACG
                                 AACTCCTT    GTTTGTCA
                                 ||||||||    ||||||||
                                 TTGAGGAA    TAAACAGT
                                      GG___
GAM2234  ID4      3'  TAAACTCCTTAAGGATCCA   11386          AC  TTTG
                                 TAAACTCCTTAA  GG    TCA
                                 ||||||||||||  ||    |||
                                 ATTTGAGGAATT  CC    GGT
                                       __  TA__
GAM2234  LPIN2    3'  TAAACTCATTAAACAATT    31217        C
                                 TAAACTC TTAAACGGTT
                                 |||||||  ||||||||||
                                 ATTTGAG AATTTGTTAA
                                      T
GAM2234  MYO6     3'  AAACTCCTTAGAATTATGTCA  22661         AACGGTT
                                 AAACTCCTTA      TGTCA
                                 ||||||||||      |||||
                                 TTTGAGGAAT      ACAGT
                                       CTTAAT_
GAM2234  TCTE1L   3'  TAAACTCCTTTATTTTGT    43374         AAACGG
                                 TAAACTCCTT     TTTGT
                                 ||||||||||     |||||
```

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                                ATTTGAGGAA     AAACA
                                    ATA___
GAM2234  TNS     3'  TCCTTAAATGGTGGTCA     35480        C   TT
                                TCCTTAAA GGT  GTCA
                                |||||||| |||  ||||
                                AGGAATTT CCA  CAGT
                                    A   C_
GAM2234  XT3     3'  AAACTCCTTAAATGGATCTA   33657          C  _
                                AAACTCCTTAAA GG TTTG
                                |||||||||||| || ||||
                                TTTGAGGAATTT CC AGAT
                                    A  T
GAM2235  CYP19   3'  TACTAAATTAGTTTGTATTACT 36306     ATT       A
                                TAT   ATTAGTTT TATTACT
                                |||   |||||||| |||||||
                                ATG   TAATCAAA ATAATGA
                                  ATT       C
GAM2235  PDCL    3'  ATATATTATTAGCTGACCATAC 23931            T  AT
            T                    ATATATTATTAGTT AT  TACT
                                |||||||||||||| ||  ||||
                                TATATAATAATCGA TG  ATGA
                                    C  GT
GAM2235  ZFP36   3'  AATATATTATAGTCTAC     18209          T
                                AATATATTAT AGTTTAT
                                |||||||||| |||||||
                                TTATATAATA TCAGATG
                                _
GAM2236  IGF1    3'  TCAGTGAGGTTCCTTTAATTC  8351         A    ___
                                TTAGTGAG TTCCT   ATTC
                                |||||||| |||||   ||||
                                AGTCACTC AAGGA   TAAG
                                    C     AAT
GAM2236  STAT6   3'  TTAGTGAGGTCCTGTTC     17162        AT    A
                                TTAGTGAG  TCCT TTC
                                |||||||  |||| |||
                                AATCACTC  AGGA AAG
                                    C_    C
GAM2236  TAPBP   3'  GTGAGATTTTATAACAAAAT   17308        CC   TC
                                GTGAGATT  TAT  CAAAAT
                                |||||||  |||  ||||||
                                CACTCTAA  ATA  GTTTTA
                                    A_   TT
GAM2236  TRIM14  3'  TAGTGAGATTCTTGTTCC    37704          CTA
                                TAGTGAGATTC   TTCC
                                ||||||||||   ||||
                                ATCACTCTAAG   AAGG
                                    AAC
GAM2236  CAST    5'  TTTTTCTCATCTGATCCTT    11985          __
                                TTTTTCTCATTT  TCCTT
                                ||||||||||  |||||
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                                AAAAAGAGTAGA  AGGAA
                                      CT
GAM2236  GDF2     3'  TTTTCCCCCTGTCTCCTT    32133        AT_
                                TTTTTCTC   TTTCCTT
                                ||||||||   |||||||
                                AAAAGGGG   AGAGGAA
                                    GAC
GAM2236  MCP      3'  TTTCTCTCATCTCTCCTT    14387          _
                                TTTTTCTCATTT TCCTT
                                |||||||||||| |||||
                                AAAGAGAGTAGA AGGAA
                                      G
GAM2236  PAPPA    5'  TTTCTCTCCCCGCTCCTT    15092        ATT_
                                TTTTTCTC    TTCCTT
                                ||||||||    ||||||
                                AAAGAGAG    GAGGAA
                                    GGGC
GAM2236  WHSC1L1  5'  TTTCTCTCATCGGGCCTT    35723          TT_
                                TTTTTCTCATT   CCTT
                                ||||||||||   ||||
                                AAAGAGAGTAG   GGAA
                                      CCC
GAM2237  AGRN     3'  GGGGTGGGGATGGGATGGGGGT 44255    AC       ACGC__    C
           GG                    GG  GGTGGGGG     GGGGG GG
                                ||  ||||||||     ||||| ||
                                CC  CCACCCCT     CCCCC CC
                                  __       ACCCTA     A
GAM2237  AQP5     5'  GGAGGTGGATGCGGCGGGGGCG 11634     C     GGAC
           G                     GGA GGTGGG    GCGGGGGCGG
                                |||  ||||||    ||||||||||
                                CCT CCACCT    CGCCCCCGCC
                                  _     ACGC
GAM2237  AR       5'  GGTGGGGGGAGGCGGGGTGG   6245         AC_     GC
                                GGTGGGGG   GCGGGG  GG
                                ||||||||   ||||||  ||
                                CCACCCCC   CGCCCC  CC
                                      CTC     A_
GAM2237  ARHGEF1  3'  GGGGTGGGGGGTGGAGGGGTGG  21736    AC       ACGC    C
                                GG  GGTGGGGG    GGGGG GG
                                ||  ||||||||    ||||| ||
                                CC  CCACCCCC    TCCCC CC
                                  __       ACC_     A
GAM2237  BMP8     5'  GGCGGCGGGGGCGGGGGCG     11882    A       GACGCG
                                GG CGGTGGGG     GGGGCG
                                || ||||||||     ||||||
                                CC GCCGCCCC     CCCCGC
                                  _       G_____
GAM2237  BTG1     5'  GGGGCGGCGTGCGGGGGCG    11910    T  G  AC_
                                GG GG GG   GCGGGGGCG
                                || || ||   |||||||||
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                                CC CC CC   CGCCCCCGC
                                 _  G  GCA
GAM2237  C5R1     3'  GGACACGGCTGGGGTGTGGGGG 11920      __   G    ACGC     C
              TGG                  GGAC  GGT GGGG    GGGGG GG
                                |||| ||| ||||   ||||| ||
                                CCTG  CCG CCCC    CCCCC CC
                                  TG   A    ACA_     A
GAM2237  CACNA1D  5'  GGCGTTGAGGCGGGGGCG    8765       GGG  C
                                GGTG   GA GCGGGGGCG
                                ||||   || |||||||||
                                CCGC   CT CGCCCCCGC
                                  AA_  C
GAM2237  CALM3    3'  GGGGTGGGGGGGTGGGGG     23240     AC       ACGCG    C
                                GG  GGTGGGGG    GGGG G
                                ||  ||||||||    |||| |
                                CC  CCACCCCC    CCCC C
                                 __       CA___    A
GAM2237  CCND3    3'  GGTGGGGGGGGGGCG       12064         ACGCG
                                GGTGGGGG    GGGGCG
                                ||||||||    ||||||
                                CCACCCCC    CCCCGC
                                            _____
GAM2237  CHAT     5'  GGCGTGTCGCAGCGCGGGGGTG 34186    A  _  _ G  GA       C
              G                  GG CG GT G GG  CGCGGGGG GG
                                || || || | ||  |||||||| ||
                                CC GC CA C TC  GCGCCCCC CC
                                 _  A  G G  __       A
GAM2237  CSNK2A1  3'  GGACGGTGGAGGAACAATGGTG 12478            C    G  C
              G                  GGACGGTGGGGGGA GCGG GG GG
                                ||||||||||||| |||| || ||
                                CCTGCCACCTCCT TGTT CC CC
                                        _    A  A
GAM2237  DACH     5'  GGGGTGGGGGGTGGGGCG     38875     AC       ACGCG
                                GG  GGTGGGGG    GGGGCG
                                ||  ||||||||    ||||||
                                CC  CCACCCCC    CCCCGC
                                 __       A____
GAM2237  DIA1     3'  GGCGTGGGGTGCGCGGGGGGCGG 28791    A  G    GA
                                GG CG TGGGG  CGCGGGGGGCGG
                                || || |||||  ||||||||||
                                CC GC ACCCC  GCGCCCCCGCC
                                 _  _    AC
GAM2237  DMPK     5'  GGAGGTGGGGAAGGGGG     20616     C       ACGC     C
                                GGA GGTGGGGG    GGGGG G
                                ||| ||||||||    ||||| |
                                CCT CCACCCCT    TCCCC C
                                  _      _____     A
GAM2237  DNMT3L   5'  GGCGTGTCCCGCGGGGGCGG   30061      GGGGA
                                GGTG    CGCGGGGGCGG
                                ||||    ||||||||||
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                                CCGC    GCGCCCCCGCC
                                  ACAGG
GAM2237  DRIL1    5'  GGTGGGCGGCGGGGGCG    23373       GGAC
                                GGTGGG   GCGGGGGCG
                                ||||||   |||||||||
                                CCACCC   CGCCCCCGC
                                   GC__
GAM2237  DRPLA    3'  GGCACGGTGGGGGGAGGGTGG  12588    _       ACGC    C
                                GG ACGGTGGGGG   GGGGG GG
                                || ||||||||||   ||||| ||
                                CC TGCCACCCCC   CTCCC CC
                                 G        ____    A
GAM2237  EGFL4    3'  GGTGGTGGGGCTGGGGGTGG   41580      _  AC _    C
                                GGTGG GGG  GC GGGGG GG
                                ||||| |||  || ||||| ||
                                CCACC CCC  CG CCCCC CC
                                   A  __ A    A
GAM2237  FBXL4    5'  GGCCTGGGTGCGGGGGCG    29134     GG   AC
                                GGT  GGG  GCGGGGGCG
                                |||  |||  |||||||||
                                CCG  CCC  CGCCCCCGC
                                  GA  A_
GAM2237  FHL2     5'  GGCGTGGGGCGCGGGGGGCGG  11114      _   A      _
                                GGTG GGGG CGCGGGGG CGG
                                |||| |||| |||||||| |||
                                CCGC CCCC GCGCCCCC GCC
                                  A   _      C
GAM2237  FMNL     5'  GGCGGTGGCGGGGG       25302    A    GGGGAC
                                GG CGGTG     GCGGGGG
                                || |||||     |||||||
                                CC GCCAC     CGCCCCC
                                 _    _______
GAM2237  G6PD     3'  GGAGGGTGGCCGTGGCGGGGGT 7606      C    GGGAC      C
            GG                    GGA GGTGG    GCGGGGG GG
                                ||| |||||    ||||||| ||
                                CCT CCACC    CGCCCCC CC
                                  C    GGCAC      A
GAM2237  GAS7     3'  GGTGGTGCGGGGGGCAG     25279      GGGAC
                                GGTGG    GCGGGGGCGG
                                |||||    ||||||||||
                                CCACC    CGCCCCCGTC
                                  A____
GAM2237  GCGR     3'  GGGGTGGGGGGGTAGGG      6695     AC      ACGCGG   C
                                GG  GGTGGGGG     GGG G
                                ||  ||||||||     ||| |
                                CC  CCACCCCC     TCC C
                                 __       CA____   A
GAM2237  GRLF1    3'  GGACGGTGGGGATGAAGCG   44230          ACGCG
                                GGACGGTGGGGG    GGGGCG
                                ||||||||||||    ||||||
```

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                                CCTGCCACCCCT    CTTCGC
                                      A____
GAM2237  HDAC4    3'  GGACGCTGGGGAGGGGCG    25774      G    GACGC
                                GGACG TGGGG    GGGGGCG
                                ||||| |||||    |||||||
                                CCTGC ACCCC    TCCCCGC
                                  G    _____
GAM2237  HOXC4    3'  GGAGGGTGGGGGGCATGGGGTGG 31153     C       A  C    GC
                                GGA GGTGGGGGG CG GGGG  GG
                                ||| |||||||| || ||||  ||
                                CCT CCACCCCC GT CCCC  CC
                                  C       _ A   A_
GAM2237  HYOU1    3'  GGGGTGGGGTGAGGGGG     40636    AC      GACGC    C
                                GG  GGTGGGG    GGGGG G
                                ||  |||||||    ||||| |
                                CC  CCACCCC    TCCCC C
                                  __      AC___    A
GAM2237  IHH      3'  GGGGTGGGGGACGCTGG     43557    AC          G
                                GG  GGTGGGGGACGC GG
                                ||  ||||||||||| ||
                                CC  CCACCCCCTGCG CC
                                  __          A
GAM2237  IL6R     5'  GGCGGTGGGCGGGCAGGCGG   8182     A     GGGAC    __
                                GG CGGTGG    GCGGG  GGCGG
                                || ||||||    |||||  |||||
                                CC GCCACC    CGCCC  CCGCC
                                  _     _____    GT
GAM2237  IRS2     5'  GGCGGAGGGGGCGCGGGCGGGG 40709    A  T    AC___
              GCGG                    GG CGG GGGGG    GCGGGGGCGG
                                || ||| |||||    ||||||||||
                                CC GCC CCCCC    CGCCCCCGCC
                                  _  T    GCGCC
GAM2237  KCNC3    5'  GGACGGGGGGCGGGGC      22505       T   GACGCG
                                GGACGG GGGG     GGGGC
                                |||||| ||||     |||||
                                CCTGCC CCCC     CCCCG
                                    _   G_____
GAM2237  KCNC3    3'  GGGGTGGGGGGCGGTGAGGCGG 22522    AC      A  CG
                                GG  GGTGGGGG CG  GGGGCGG
                                ||  |||||||| ||  |||||||
                                CC  CCACCCCC GC  CTCCGCC
                                  __       C  CA
GAM2237  KCNC3    3'  GGACGGGGTCGGGGG      22506       T  GGGACG
                                GGACGG GG     CGGGGG
                                |||||| ||     ||||||
                                CCTGCC CC     GCCCCC
                                    _ A_____
GAM2237  KPNB1    5'  GGAGGGTGGGGTGGGGGGCGG  13972     C      GACGC
                                GGA GGTGGGG    GGGGGCGG
                                ||| |||||||    ||||||||
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                                CCT CCACCCC    CCCCCGCC
                                  C      AC___
GAM2237 LHX5    5' GGGTGGTGGGGGGCGGGTGG  35323    AC      AC   _
                                GG  GGTGGGGG  GCGGG GG
                                ||  ||||||||  ||||| ||
                                CC  CCACCCCC  CGCCC CC
                                 CA       __    A
GAM2237 LHX5    3' GGCCGAGCGCGGGGGCG    35319    G   GA
                                GGT GGG  CGCGGGGGCG
                                ||| |||  ||||||||||
                                CCG CTC  GCGCCCCCGC
                                  G  __
GAM2237 LSP1    3' GGTGGGGAGGGCGGGGGCGG  14242       AC
                                GGTGGGGGG  GCGGGGGCGG
                                |||||||||  ||||||||||
                                CCACCCCT  CGCCCCCGCC
                                     CC
GAM2237 MADH6   5' GGTGGGGGGGAGGC      24604       ACGC
                                GGTGGGGGG   GGGGGC
                                |||||||||   ||||||
                                CCACCCCC   CCTCCG
                                          _____
GAM2237 MAP3K9  3' GGTGTTGGGGGACAGCGG   41358    ACGG      _
                                GG   TGGGGGAC GCGG
                                ||   |||||||| ||||
                                CC   ACCCCCTG CGCC
                                 ACA_      T
GAM2237 MEIS2   3' GGGTGGTGGGGATGGCTTGG  33543    AC      AC  GG
                                GG  GGTGGGGGG  GC  GG
                                ||  |||||||||  ||  ||
                                CC  CCACCCCT  CG  CC
                                 CA       AC  AA
GAM2237 MGMT    5' GGCGGCGGGGGGGGGC      14490    A       ACGCGG
                                GG CGGTGGGGGG     GGGC
                                || |||||||||     ||||
                                CC GCCGCCCCC     CCCG
                                  _      _______
GAM2237 MSL3L1  5' CGGTGGGGGAGGGCG      38584         CGCGG
                                CGGTGGGGGA    GGGCG
                                ||||||||||    |||||
                                GCCACCCCCT    CCCGC
                                          ______
GAM2237 MSX2    3' GGTGGGGCGGTGGGGGGCGG  42298       GACGC
                                GGTGGGGG    GGGGGCGG
                                |||||||     ||||||||
                                CCACCCC    CCCCCGCC
                                    GCCAC
GAM2237 NFIA    5' GGGTGTGGGGGAGGGGGCG   43221    ACG      CGC
                                GG  GTGGGGGA  GGGGGCG
                                ||  ||||||||  |||||||
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                                CC  CACCCCCT  CCCCCGC
                                 CA_     ___
GAM2237 NTSR1   3' AGATGGTGGGAGTGGGGGTGG 14873    C     ACGC   C
                                GGA GGTGGGGGG   GGGGG GG
                                ||| ||||||||   ||||| ||
                                TCT CCACCCTC   CCCCC CC
                                  A      A___    A
GAM2237 PAH     5' GGGTGTGGGGGACGCAGG   7095    ACG
                                GG  GTGGGGGACGCGGG
                                ||  ||||||||||||||
                                CC  CACCCCCTGCGTCC
                                 CA_
GAM2237 PAX5    3' GGATGCTGGGGGACGGTCTCAT 32515    CGG      ____ G
            GG                   GGA  TGGGGGACG   CG GG
                                |||  |||||||||   || ||
                                CCT  ACCCCCTGC   GT CC
                                  ACG       CAGA  A
GAM2237 PRDM2   3' GGAAGGTGGGGAGAGAGGGGTG 31972    C    _ CGC   C
            G                    GGA GGTGGGG GA  GGGGG GG
                                ||| ||||||| ||  ||||| ||
                                CCT CCACCCC CT  TCCCC CC
                                  T     T C__    A
GAM2237 PTBP1   3' GGACAGGACGCGGGGGCG   36721     GGTGG
                                GGAC   GGGACGCGGGGGCG
                                ||||   ||||||||||||||
                                CCTG   TCCTGCGCCCCCGC
                                  _____
GAM2237 S100A1  3' GGGGTGGGGGTGGGGG    26560   AC     ACGCG   C
                                GG  GGTGGGGG   GGGG G
                                ||  ||||||||   |||| |
                                CC  CCACCCCC   CCCC C
                                 __      A____   A
GAM2237 SH3GL1  3' GGACGGAGGGGCGGGGCG   16672      T    A GCG
                                GGACGG GGGGG C  GGGGCG
                                |||||| ||||| |  ||||||
                                CCTGCC TCCCC G  CCCCGC
                                  _   _ ___
GAM2237 TFE3    3' GGAGGGTGGGGGAAAAGGCGG 27167    C      CGC
                                GGA GGTGGGGGA  GGGGGCGG
                                ||| |||||||||  ||||||||
                                CCT CCACCCCCT  TTTCCGCC
                                  C      ___
GAM2237 YY1     5' GGCGGGGGGGAGAGGGGGCGG  18178       ACGC
                                GGTGGGGG   GGGGGCGG
                                ||||||||   ||||||||
                                CCGCCCCC   CCCCCGCC
                                     CTCT
GAM2237 YY1     5' GGCGGCGGGGGAAGGGGCGG  18176   A      CGC
                                GG CGGTGGGGGA  GGGGGCGG
                                || ||||||||||  ||||||||
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                                CC GCCGCCCCCT   TCCCCGCC
                                 _       ____
GAM2237  ZFP36L1   3'  GGTGGGGGGGGGTGGGGGGGCGG 22291        ACGC__
                                GGTGGGGG     GGGGGCGG
                                ||||||||     ||||||||
                                CCACCCCC     CCCCCGCC
                                    CCCACC
GAM2238  DDX9      3'  CTATTACAAGTAGTATCA    44795     AG   _
                                CTA  TATA GTAGTATCA
                                |||  |||| |||||||||
                                GAT  ATGT CATCATAGT
                                  A_   T
GAM2238  SYT5      5'  TCATGCTGGGAGTTGTAGTATC 17243      A  A__   ATA
               A                 TCAT CT   AGT   GTAGTATCA
                                ||||  ||   |||   |||||||||
                                AGTA GA   TCA   CATCATAGT
                                  C  CCC   A__
GAM2239  SDC4      3'  AAGGTGCAGGTGGTTCTAG    16515        A   A__
                                AAGGTGCG GTG   CTAG
                                |||||||| |||   ||||
                                TTCCACGT CAC   GATC
                                    C   CAA
GAM2240  SERPINB6  5'  TGGCAGACCTCCAAGCTTGTTG 21302       ATA  AGATGA
               T                 TGGCA   CT     CTTGTTGT
                                |||||   ||     ||||||||
                                ACCGT   GA     GAACAACA
                                   CTG  GGTTC_
GAM2240  ASNS      5'  TCCAGGTGAGGAGGGGGGCAGT 11719      A    TCT_
                                TCCA GTGA    GGGGGCAGT
                                ||||  ||||    |||||||||
                                AGGT CACT    CCCCCGTCA
                                  C    CCTC
GAM2240  KCNJ6     3'  AGTGATCTGGTATTGTGACTGC 13855          __________  GCAG
               CC                  AGTGATCTGG       GG    TC
                                ||||||||||       ||    ||
                                TCACTAGACC       CT    GG
                                     ATAACIIIA  GACG
GAM2240  KHK       3'  CAGGCTCTGGGGCAGTCA    27053    A  GA      G
                                CA GT  TCTGGGG CAGTCA
                                ||  ||  ||||||| ||||||
                                GT CG  AGACCCC GTCAGT
                                 C  __      _
GAM2240  LARS2     3'  TTCCAAGTGGCTGGCACA    31683        AT   G G
                                TTCCAAGTG  CTG G GCA
                                |||||||||  ||| | |||
                                AAGGTTCAC  GAC C TGT
                                     C_   _ G
GAM2240  MECP2     3'  TGATCTGGGCAGGGGTCA    22615         _  CA
                                TGATCTGGG GG  GTCA
                                |||||||||  ||  ||||
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                                ACTAGACCC TC  CAGT
                                     G  CC
GAM2240  MPDU1    3'  TTCTAAGGATCTGGATCCATCA 22179     C   T      GGCA
                                TTC AAG GATCTGGG    GTCA
                                ||| ||| ||||||||    ||||
                                AAG TTC CTAGACCT    TAGT
                                  A  _       AGG_
GAM2240  RAB7     5'  GTGTTGGGGGCAGTCA      21578     ATC
                                GTG   TGGGGGCAGTCA
                                |||   ||||||||||||
                                CAC   ACCCCCGTCAGT
                                  A__
GAM2240  RELA     3'  TCCACAAAGTTGGGGGCAGT   35036     AGT  TC
                                TCCA   GA  TGGGGGCAGT
                                ||||   ||  ||||||||||
                                AGGT   TT  ACCCCCGTCA
                                  GT_  CA
GAM2240  VDR      3'  TTCCAGGAGTTGGGGCAGTCA  7532       A T  TCTG
                                TTCCA G GA    GGGGCAGTCA
                                ||||| | ||    ||||||||||
                                AAGGT C CT    CCCCGTCAGT
                                   _ _  CAA_
GAM2241  KIF5C    5'  CCACGCGGCGGGCGGA      21145       ATCA   CAA
                                TCACGCG    GTG   GCGGA
                                |||||||    |||   |||||
                                GGTGCGC    CGC   CGCCT
                                    _____   C__
GAM2241  PDE4A    3'  GCAAAATCAAGCGGAAG     26257      TCAGTG
                                GCGA     CAAGCGGAAG
                                ||||     ||||||||||
                                CGTT     GTTCGCCTTC
                                  TTA___
GAM2242  ARHGAP6  5'  CTGCGGGGTGCTGGGTGTGGAG 30214          ATAGATAAA_
            AAG                   CTGCGGGGTG        AGAAG
                                ||||||||||        |||||
                                GACGCCCCAC        TCTTC
                                      GACCCACACC
GAM2242  CDC25A   3'  CTGCAGGAAAGAGGGTAAAG   12148        TGAT  ATA
                                CTGCGGGG    AG   AAAG
                                ||||||||    ||   ||||
                                GACGTCCT    TC   TTTC
                                     TTC_  CCA
GAM2242  ILK      5'  CTGTGGAGTGATCCAGGGAAG  21124     C       AGATAAAA
                                CTG GGGGTGAT       GAAG
                                ||| ||||||||       ||||
                                GAC CCTCACTA       CTTC
                                  A       GGTCC___
GAM2242  SOX12    3'  CTCCGGGGATAAAAG       28037    G    TGATAG
                                CT CGGGG     ATAAAAG
                                || |||||     |||||||
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                              GA GCCCC     TATTTTC
                               G    _______
GAM2242 UBE2B    5' GCGGGGTGGAGAAAGA      17793         AT   TAA
                              GCGGGGTG  AGA   AAGA
                              ||||||||  |||   ||||
                              CGCCCCAC  TCT   TTCT
                                  C_  ___
GAM2242 BRCA1    3' GCCTATTCTTTTTAGGTGC    28635           CGTT
                              GTCTATTCTTTTT    TGC
                              ||||||||||||    |||
                              CGGATAAGAAAAA    ACG
                                     TCC_
GAM2242 LEP      3' GTCTCTTCTTTCTCTGCCTCT  6917       A       GTT
                              GTCT TTCTTTTTC   TGCCTCT
                              |||| |||||||||   |||||||
                              CAGA AAGAAAGAG   ACGGAGA
                                G       ____
GAM2242 PDX1     3' GTCATTCTTTTCATTCATGCTT 18489     T       T   __   C
                CT                  GTC ATTCTTTT CGTT  TGC TCT
                              ||| ||||||| ||||  ||| |||
                              CAG TAAGAAAA GTAA  ACG AGA
                                _      _   GT   A
GAM2242 SOX4     3' GTCTGTCCTTTTCGTTT     16991      AT
                              GTCT  TCTTTTTCGTTT
                              ||||  ||||||||||||
                              CAGA  AGGAAAAGCAAA
                                C_
GAM2242 TBL1X    3' TTCTGTTTTTGCTTGCCT    24901      _    C
                              TTCT TTTT GTTTGCCT
                              |||| |||| ||||||||
                              AAGA AAAA CGAACGGA
                                C    A
GAM2243 PIK3R1   3' TGTGAGTGGACGTGCCTT    42863      C   A  GT
                              TGTG AGT GA  TGTGCCTT
                              |||| ||| ||  ||||||||
                              ACAC TCA CT  GCACGGAA
                                _   C  __
GAM2243 ANKTM1   3' GTACTGACATTTGCATT     28806     T       CA
                              GTG CTGACATT  CATT
                              ||| ||||||||  ||||
                              CAT GACTGTAA  GTAA
                                _       AC
GAM2243 COL6A3   3' GTAGCCGTGACATTTGCATT   38432     T  _      CA
                              GTG GTC TGACATT  CATT
                              ||| ||| |||||||  ||||
                              CAT CGG ACTGTAA  GTAA
                                _  C      AC
GAM2243 GDF5     5' GTGTGTGTTTGTATCCA     8146          C  AC
                              GTGTGTGT TG  ATTCA
                              |||||||| ||  |||||
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                                CACACACA AC  TAGGT
                                    A  A_
GAM2243  WT1     3'  GTGTGCCAGTGTTCACATT   35967       TGACA
                                GTGTGTC    TTCACATT
                                |||||||    ||||||||
                                CACACGG    AAGTGTAA
                                   TCAC_
GAM2243  ZNF124  3'  AAGTATGTGACTGTTCA     18318        T  ACA
                                AAGTGTGTG CTG   TTCA
                                ||||||||| |||   ||||
                                TTCATACAC GAC   AAGT
                                    T  ___
GAM2244  AKT1    3'  TTTCCATCTGGGCTCGAGA   23144       CATA  A_
                                TTTCCATC   GC  GAGA
                                ||||||||   ||  ||||
                                AAAGGTAG   CG  CTCT
                                    ACC_  AG
GAM2244  ATF7    5'  ATTTCATATAGCAGAG      27792      C  CC
                                GTTTC AT  ATAGCAGAG
                                ||||| ||  |||||||||
                                TAAAG TA  TATCGTCTC
                                  _  __
GAM2244  BAALC   3'  TGTTTCTATATAAAACAGAGA  36046      CATCCAT
                                TGTTTC      AGCAGAGA
                                ||||||      ||||||||
                                ACAAAG      TTGTCTCT
                                   ATATATT
GAM2244  C18orf1 3'  TGTCTCTCCAGCAGAG      41236      CA   TA
                                TGTTTC  TCCA  GCAGAG
                                ||||||  ||||  ||||||
                                ACAGAG  AGGT  CGTCTC
                                  __   __
GAM2244  CHAD    3'  TGTTTCCACGTGGCAGGGA   10419       CCATA   A
                                TGTTTCCAT    GCAG GA
                                |||||||||    |||| ||
                                ACAAAGGTG    CGTC CT
                                    CAC__   C
GAM2244  ENPP2   3'  TGTTTCCATACAGTACAG    26304       C  TA
                                TGTTTCCAT CA  GCAG
                                |||||||||  ||  ||||
                                ACAAAGGTA GT  TGTC
                                    T  CA
GAM2244  EPS15   5'  TGTTTCCATCATGCAA      12749        C  A
                                TGTTTCCATC AT GCAG
                                |||||||||| ||  ||||
                                ACAAAGGTAG TA CGTT
                                  _  _
GAM2244  FAH     3'  TGTTTCCAGAAGAGCAGAGA  6594        TCCAT
                                TGTTTCCA    AGCAGAGA
                                ||||||||    ||||||||
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                                ACAAAGGT    TCGTCTCT
                                    CTTC_
GAM2244  FGF2     3'  ATGTTTCATTCATACAGA    12829       C  C    G
                                ATGTTTC AT CATA CAGA
                                ||||||| || |||| ||||
                                TACAAAG TA GTAT GTCT
                                   _  A   _
GAM2244  H3F3B    3'  TGTTTCCTCAGCAGAG      23706       A  CAT
                                TGTTTCC TC   AGCAGAG
                                ||||||| ||   |||||||
                                ACAAAGG AG   TCGTCTC
                                   _ ___
GAM2244  IQGAP2   3'  GTTTCCATTTATCCATAG    27372        ____
                                GTTTCCA    TCCATAG
                                |||||||    |||||||
                                CAAAGGT    AGGTATC
                                    AAAT
GAM2244  LMO1     3'  ATGTTCCCATTTATATACAGA  14178         CC  _
                                ATGTTTCCAT  ATA GCAGA
                                ||||||||||  ||| |||||
                                TACAAGGGTA  TAT TGTCT
                                     AA   A
GAM2244  P23      3'  ATGTTGTTCATCATCTCAGAGA 27337      TC_   C  AG
                                ATGTT   CATC AT  CAGAGA
                                |||||   |||| ||  ||||||
                                TACAA   GTAG TA  GTCTCT
                                  CAA   _  GA
GAM2244  PIR51    3'  ATGTTTCCTCTGCCAGA     27011       A  CATAG
                                ATGTTTCC TC    CAGA
                                |||||||| ||    ||||
                                TACAAAGG AG    GTCT
                                    _  ACG__
GAM2244  POU3F4   3'  TGTTTCCTTTGTCAACAGA   7173        ATCCA
                                TGTTTCC    TAGCAGA
                                |||||||    |||||||
                                ACAAAGG    GTTGTCT
                                    AAACA
GAM2244  RAD23B   3'  TGTTGCCATGAAACAGAGA   16142     T   CCAT
                                TGTT CCAT    AGCAGAGA
                                |||| ||||    ||||||||
                                ACAA GGTA    TTGTCTCT
                                  C   CT__
GAM2244  RYR2     3'  ATGTTTCCAAGAGAGCAGAGA 9766         TCCAT
                                ATGTTTCCA    AGCAGAGA
                                |||||||||    ||||||||
                                TACAAAGGT    TCGTCTCT
                                     TCTC_
GAM2244  SFRP1    3'  TGTTTCCATTTAAAGCAGA   16580         CCAT
                                TGTTTCCAT    AGCAGA
                                |||||||||    ||||||
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                                ACAAAGGTA   TCGTCT
                                     AATT
GAM2244  TNS     5'  TGTTTCCACCCCGGGAG     35483          ATAGCA
                                TGTTTCCATCC     GAG
                                ||||||||||     |||
                                ACAAAGGTGGG     CTC
                                      GCC___
GAM2244  TRIM    3'  TGTTTCTGATGAAACAGAGA   32304       CATCCAT
                                TGTTTC      AGCAGAGA
                                ||||||      ||||||||
                                ACAAAG      TTGTCTCT
                                   ACTACT_
GAM2244  TRPC6   3'  ATGTTTCCAGGGTTCAGTGGAG 21481         TCCA_   CA
                                ATGTTTCCA    TAG  GAG
                                |||||||||    |||  |||
                                TACAAAGGT    GTC  CTC
                                     CCCAA   AC
GAM2245  AGRN    3'  TGTTTGGAAGTCACAGTAT    44262       TTTC_
                                TGTTT    TCACAGTAT
                                |||||    |||||||||
                                ACAAA    AGTGTCATA
                                   CCTTC
GAM2245  DDX11   3'  ATCATGCTCTTCTCACAGTATC 36166          T
           G                     ATCATGTTTTT CTCACAGTATCG
                                ||||||||||| ||||||||||||
                                TAGTACGAGAA GAGTGTCATAGC
                                          _
GAM2245  CAV3    3'  TCTCCCTGTGTCTGTT      37847         TTGAAC   A
                                TCTTCCTGT     GTCT TT
                                |||||||||     |||| ||
                                AGAGGGACA     CAGA AA
                                     _______   C
GAM2245  IRTA2   3'  TCTCTTGCTCCACGTCTATTTT 36348      CC    GA
                                TCTT  TGTTT  ACGTCTATTTT
                                ||||  |||||  ||||||||||||
                                AGAG  ACGAG  TGCAGATAAAA
                                  A_    G_
GAM2246  BACE    5'  GGGTCCGGGCTGTGGAGAGC   39965    C  AGAT T      A
                                GG GT    G GCTGTGGA AGC
                                || ||    | |||||||| |||
                                CC CA    C CGACACCT TCG
                                 _  GG__ C       C
GAM2246  LAMC1   3'  GGCTGGGTGTGGAGGAAAGCA  14089     GTAGA   CTGT
                                GGC    TGTG   GGAAAGCA
                                |||    ||||   ||||||||
                                CCG    ACAC   CCTTTCGT
                                  ACCC_   CT__
GAM2246  MUC3B   5'  GTGGATGTGCTGACTGTGGA   45343    A      _____
                                GT GATGTGCT    GTGGA
                                || ||||||||    |||||
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                                CA CTACACGA    CACCT
                                 C       CTGA
GAM2246  TNFAIP1   3'  GGAGTAGATGTGTGGCCAAGCA 34479    C       GCT    A_
                                GG GTAGATGT   GTGG  AAGCA
                                || ||||||||   ||||  |||||
                                CC CATCTACA   CACC  TTCGT
                                 T       ___    GG
GAM2246  TNFRSF1B  3'  GGCTGCGGCTGTGGAGGGC    9874      GTAGA   _      AA
                                GGC    TGTG CTGTGGA  GC
                                |||    |||| |||||||  ||
                                CCG    ACGC GACACCT  CG
                                  _____   C      CC
GAM2246  IGF1R     3'  AGAAGCAATGAGACCTGT    9325          AAA
                                AGGAGTAAT   ACCTGT
                                |||||||||   ||||||
                                TCTTCGTTA   TGGACA
                                     CTC
GAM2246  JPH3      3'  TCTGGAAGGAATATGCATATCT 34027    CA       ATAAAAC
              GT                  TC  GAAGGAGTA      CTGT
                                ||  |||||||||      ||||
                                AG  CTTCCTTAT      GACA
                                 AC        ACGTATA
GAM2246  PCDH12    5'  TCCAGAAGCTGCAAGAACCTGT 32452        GA    TAA
                                TCCAGAAG  GTAA   AACCTGT
                                ||||||||  ||||   |||||||
                                AGGTCTTC  CGTT   TTGGACA
                                     GA    C__
GAM2246  PDE4B     3'  TCCAGAAAGAGTCAAAAAA    15151           AAT
                                TCCAGAAGGAGT   AAAA
                                ||||||||||||   ||||
                                AGGTCTTTCTCA   TTTT
                                       GTT
GAM2246  RAB36     3'  TCCAGAAGGAATAGTCCTG    22245           ATAAAA
                                TCCAGAAGGAGTA     CCTG
                                ||||||||||||      ||||
                                AGGTCTTCCTTAT     GGAC
                                       CA____
GAM2246  RFPL2     5'  TCCATGAGGTGAAAGCCTG    27352      GA   AGTAAT   A
                                TCCA  AGG     AAA CCTG
                                ||||  |||     ||| ||||
                                AGGT  TCC     TTT GGAC
                                  AC   AC____   C
GAM2247  MBNL      3'  TGATTATATATTTATAAGA    34326      A
                                TGAT GTATATTTATAAGA
                                |||| ||||||||||||||
                                ACTA TATATAAATATTCT
                                  A
GAM2247  MMP8      3'  TATGTAAGTATTGAAATAGTA  14547           GT_
                                TATGTAAGTAT   AGTAGTA
                                ||||||||||   |||||||
```

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                                ATACATTCATA   TTATCAT
                                      ACT
GAM2247  NUFIP1   3'  TATGTAAGTCGTGCTAGTAGGT 29595         A  AG    A
                                TATGTAAGT TGT  TAGTA GT
                                ||||||||| |||  ||||| ||
                                ATACATTCA GCA  ATCAT CA
                                      _  CG    C
GAM2248  ANGPT1   3'  AAAGTATTTTTCTTAACAA   40236          GA
                                AAAGTATTTTTT  TAACAA
                                ||||||||||||  ||||||
                                TTTCATAAAAAG  ATTGTT
                                      A_
GAM2248  CCT2     3'  TAATAGAGTATCTTTCAAACAC 26959      A       TG TA
             AA                   TAATA AGTATTTTT  A  ACAA
                                ||||| |||||||||  |  ||||
                                ATTAT TCATAGAAA  T  TGTT
                                   C        GT TG
GAM2248  ITSN1    3'  TAATAAAGTATTTCTTAA    16661
                                TAATAAAGTATTTTTTGA
                                ||||||||||||||||||
                                ATTATTTCATAAAGAATT

GAM2248  UFD1L    3'  TAACAGAGTATTCTCTGAT   43823      A
                                TAATA AGTATTTTTTGAT
                                ||||| ||||||||||||
                                ATTGT TCATAAGAGACTA
                                   C
GAM2248  USH2A    5'  ATAAAGCATTTCTAAATAA   28300          T
                                ATAAAGTATTTTT GATAA
                                |||||||||||| |||||
                                TATTTCGTAAAGA TTATT
                                      T
GAM2249  AFG3L2   3'  ACATTGGCTTCTCCGGCT    45542     C       C
                                ACAT GGCTTTTCC GTT
                                |||| ||||||||| |||
                                TGTA CCGAAGAGG CGA
                                   A       C
GAM2249  NFATC1   3'  ACGTCGGCTCTGTTA      26068    A      TCCC
                                AC TCGGCTTT   GTTA
                                || ||||||||   ||||
                                TG AGCCGAGA   CAAT
                                 C      ____
GAM2249  NFRKB    5'  GGTCCTCCCTCCCGTTAT    26098    _   __
                                GG CTTT  TCCCGTTAT
                                || ||||  |||||||||
                                CC GGAG  AGGGCAATA
                                 A   GG
GAM2249  OGN      5'  AACTCTCTTTTTCCCGTT    37455    A  GGC
                                AAC TC   TTTTCCCGTT
                                ||| ||   ||||||||||
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                                TTG AG   AAAAGGGCAA
                                  _ AGA
GAM2249  SLC4A4   3'  AACATCGGTTATTCTCAT    19057        CTT   C
                                AACATCGG   TTC CGT
                                ||||||||   ||| |||
                                TTGTAGCC   AAG GTA
                                     AAT   A
GAM2250  DSC2     3'  ACAGACCCAGCCACCGATC   22391      TTA  _
                                ACGG   CA CCACCGATC
                                ||||   || |||||||||
                                TGTC   GT GGTGGCTAG
                                  TGG  C
GAM2250  ACCN2    3'  TGGGTGGGGGCTATCTCTACAG 33456        AAA   AA_  A
              CAA                  TGGGTGGG   TAT   TA AGCAA
                                ||||||||   |||   || |||||
                                ACCCACCC   ATA   AT TCGTT
                                     CCG   GAG  G
GAM2250  CACNA1G  3'  TGAGTGGGAAAGTGGGGCA   33132          TATAATAAA
                                TGGGTGGGAAA        GCA
                                ||||||||||         |||
                                ACTCACCCTTT        CGT
                                      CACCC____
GAM2250  CDK4     3'  TGGGAGGGGAATGTCATTAAGG 6336       T_    ATA  A   A
              CA                   TGGG  GGGAA   TA TAA GCA
                                ||||  |||||   || ||| |||
                                ACCC  CCCTT   GT ATT CGT
                                  TC    ACA  A   C
GAM2250  CRP      3'  TGGGTGGGGAATTAAATA    43448        A   AT
                                TGGGTGGG AAT  AATA
                                |||||||| |||  ||||
                                ACCCACCC TTA  TTAT
                                     C   AT
GAM2250  FKBP1A   3'  TGGGTGGGAATGGTGGAGGCAA 38286          ATATAATAAA
                                TGGGTGGGAA         GCAA
                                ||||||||||         ||||
                                ACCCACCCTT         CGTT
                                      ACCACCTC__
GAM2250  OAS2     3'  TGGGTGGGGGGATAAAGGCA   32555        AAATATA     _
                                TGGGTGGG      ATAAAG CA
                                ||||||||      |||||| ||
                                ACCCACCC      TATTTC GT
                                     CCC_____     C
GAM2250  OAS3     3'  TGGGTGGGAAGCAGCA      26186          ATATAATAA
                                TGGGTGGGAA        AGCA
                                ||||||||||        ||||
                                ACCCACCCTT        TCGT
                                      CG________
GAM2250  PDE4C    3'  TGGGTGGGAAAGTGAAGCA    9560           TATAATA
                                TGGGTGGGAAA      AAGCA
                                ||||||||||       |||||
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                                ACCCACCCTTT      TTCGT
                                      CAC____
GAM2250  SMAC     3'  TGAGTGGGGAGACAGGGCA   33391        AAATATA  AA
                                TGGGTGGG      ATA  GCA
                                ||||||||      |||  |||
                                ACTCACCC      TGT  CGT
                                    CTC____   CC
GAM2250  TRPC5    3'  TGGGTGAGAAAAGCAAAGCAA  29771          TATAA
                                TGGGTGGGAAA    TAAAGCAA
                                ||||||||||    ||||||||
                                ACCCACTCTTT    GTTTCGTT
                                      TC___
GAM2251  BCL7A    5'  CCAGGCAGACCACAGAG     34203     CC  C
                                CCA  CA GACCACAGAG
                                |||  || ||||||||||
                                GGT  GT CTGGTGTCTC
                                  CC  _
GAM2251  CABC1    5'  CGCACCACGCACCTTGCAGAG  33681        C   GACCA
                                CGCACCAC CAC    CAGAG
                                |||||||| |||    |||||
                                GCGTGGTG GTG    GTCTC
                                    C   GAAC_
GAM2251  CERD4    3'  CCACCCCCCACAGAG       28946       ACGA
                                CCACCC    CCACAGAG
                                ||||||    ||||||||
                                GGTGGG    GGTGTCTC
                                   G___
GAM2251  CYP21A2  3'  CACCACCCAGCCGCTGGAG   7981         CGA  ACA_
                                CACCACCCA   CC    GAG
                                |||||||||   ||    |||
                                GTGGTGGGT   GG    CTC
                                    C__  CGAC
GAM2251  DHCR7    3'  GCCCCACCCACGACTGCAGAG  10687    A        CA
                                GC CCACCCACGAC  CAGAG
                                || ||||||||||  |||||
                                CG GGTGGGTGCTG  GTCTC
                                 G         AC
GAM2251  FECH     3'  TCACACTGCCAGCCCACAGAG  6608       CAC   CGA
                                TCGCAC   CCA   CCACAGAG
                                ||||||   |||   ||||||||
                                AGTGTG   GGT   GGTGTCTC
                                   AC_   CG_
GAM2251  HPS1     3'  CTCACACCACCCTGGGACGGAG 6802           AC_   CACA
                                CTCGCACCACCC   GAC    GAG
                                ||||||||||||   |||    |||
                                GAGTGTGGTGGG   CTG    CTC
                                      ACC   C___
GAM2251  NOLA1    5'  CTCGGTTACCGTACCGCCACAG 33296     C__   ACCCA  A
            AG                  CTCG   ACC    CG CCACAGAG
                                ||||   |||    || ||||||||
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                                GAGC  TGG    GC GGTGTCTC
                                  CAA  CATG_ _
GAM2251 RAD1    5' CTCGGCCACCGTCACCACAGAG 15993     CA    CACG
                                CTCG  CCACC   ACCACAGAG
                                |||| |||||   |||||||||
                                GAGC  GGTGG   TGGTGTCTC
                                  C_    CAG_
GAM2251 TARBP2  3' GCACCACCAGCTCCTGCAGAG  39531       CACGA  A_
                                GCACCACC    CC  CAGAG
                                ||||||||    ||  |||||
                                CGTGGTGG    GG  GTCTC
                                     TCGA_  AC
GAM2251 TRPM2   3' GCACCACCACGCAG       17692        C   ACCA
                                GCACCACC ACG    CAG
                                |||||||| |||    |||
                                CGTGGTGG TGC    GTC
                                   _  ____
GAM2251 WHSC1   3' TCCATCACCAGACCCACAGAG  39382    G  C    CACGA
                                TC CA CACC    CCACAGAG
                                || || ||||    ||||||||
                                AG GT GTGG    GGTGTCTC
                                 _ A   TCTG_
GAM2251 ARHGEF7 5' TGCGGTGAGACGAGGGCC    19370      CCCCC      A
                                TGTGGT    GAGACGAG GCC
                                ||||||    |||||||| |||
                                ACGCCA    CTCTGCTC CGG
                                   _____       C
GAM2251 BCLG    3' TGTGGTCCCTGAGAAAAG    39825        CC   C
                                TGTGGTCCC  GAGA GAG
                                |||||||||  |||| |||
                                ACACCAGGG  CTCT TTC
                                     A_   T
GAM2251 CACNA2D2 3' TGTGGTCCCACTGGGGGCC   25729        CCGAG  GAGA_
                                TGTGGTCCC    AC    GCC
                                |||||||||    ||    |||
                                ACACCAGGG    TG    CGG
                                   _____ ACCCC
GAM2251 LTA     3' TGTGGTCCCCTGGGATGCC   8241         CGAGAC  GA
                                TGTGGTCCCC     GA  GCC
                                ||||||||||     ||  |||
                                ACACCAGGGG     CT  CGG
                                     ACC___  A_
GAM2251 MFGE8   3' TGTGTCCTCTGGGGTGAAAAGC 25464     G   CCCGAGAC_
           CA                    TGTG TCC       GAGAGCCA
                                |||| |||       ||||||||
                                ACAC AGG       TTTTCGGT
                                  _  AGACCCCAC
GAM2251 PTPN18  3' TGTGGTCCCCTGAGTGTCC   30774         C   ACGAGAG
                                TGTGGTCCCC GAG      CC
                                |||||||||| |||      ||
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                                ACACCAGGGG CTC      GG
                                     A   ACA____
GAM2251  RCV1     5'  GTGGTCCCCTGGCCGCAGGC   16222         CGAGA  _  A
                                GTGGTCCCC    CG AG GC
                                |||||||||    || || ||
                                CACCAGGGG    GC TC CG
                                     ACCG_  G  _
GAM2251  WWP2     3'  TGTGGTCCCACACAGGGCC   41454         CCGAG  _  A
                                TGTGGTCCC    ACG AG GCC
                                |||||||||    ||| || |||
                                ACACCAGGG    TGT TC CGG
                                     _____  G  C
GAM2252  ANK3     5'  TGGAATGGTGTTTTGTCA    10094         CTG   AA
                                TGGAATGGTG   TTG  TCA
                                ||||||||||   |||  |||
                                ACCTTACCAC   AAC  AGT
                                     AA_  __
GAM2252  IL13RA2  3'  TGGAAACTGTTGAGTCAA    8477       TGGT      A
                                TGGAA   GCTGTTGA TCAA
                                |||||   |||||||| ||||
                                ACCTT   TGACAACT AGTT
                                   ____      C
GAM2252  MX1      5'  TGGAATGGTGGCTGGATG    14690          _  T_
                                TGGAATGGTG CTG  TG
                                |||||||||| |||  ||
                                ACCTTACCAC GAC  AC
                                     C   CT
GAM2252  ABCC3    3'  CTACTGTCTGCCATGGCATCAT 33419         _  TCA
              T                  CTGCTGTCT CC   GCATCATT
                                |||||||||  ||   ||||||||
                                GATGACAGA GG   CGTAGTAA
                                     C  TAC
GAM2252  CA3      3'  TGCTGTCTATAGTCATT     23221         CCTC  CA
                                TGCTGTCT   AG  TCATT
                                ||||||||   ||  |||||
                                ACGACAGA   TC  AGTAA
                                     TA__  __
GAM2252  CACNA1D  3'  CCTGCTGTTTCCTGCAGC    8764          C   _
                                CCTGCTGT TCCT CAGC
                                |||||||| |||| ||||
                                GGACGACA AGGA GTCG
                                     A   C
GAM2252  CHRND    3'  CCTGCTGTCTCCTGGCTC    8874           CA  A
                                CCTGCTGTCTCCT  GC TC
                                ||||||||||||  || ||
                                GGACGACAGAGGA  CG AG
                                      C_  _
GAM2252  DCD      3'  CCTGCTGCTCCTGGGTATCATT 38232         T    CAGC
                                CCTGCTG CTCCT   ATCATT
                                |||||||  |||||   ||||||
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                                GGACGAC GAGGA   TAGTAA
                                   _    CCCA
GAM2252 GABRP    3' TGTTTTCTAATAAGCATCATTC 30562    CTG  CCTC
                                TG  TCT   AGCATCATTC
                                ||  |||   ||||||||||
                                AC  AGA   TCGTAGTAAG
                                 AAA  TTAT
GAM2252 GFI1     3' TGCTGTCTTCTCAGAATTC   23560       C    CA_
                                TGCTGTCT CTCAG  TC
                                |||||||| |||||  ||
                                ACGACAGA GAGTC  AG
                                     A    TTA
GAM2252 LDLR     3' CCTCTGGGAAGTGGCATCATT  8023     G  TCTCCTCA
                                CCT CTG      GCATCATT
                                ||| |||      ||||||||
                                GGA GAC      CGTAGTAA
                                  _  CCTTCAC_
GAM2252 PPP1R12B 3' CCTGCTGTTTCTCTTGGCAC  36970       C _ CA
                                CCTGCTGT TC CT  GCAT
                                |||||||| || ||  ||||
                                GGACGACA AG GA  CGTG
                                     A  A  AC
GAM2252 PTEN     5' CCTGCTTCTCCTCAGCA     7207       G
                                CCTGCT TCTCCTCAGCA
                                |||||| ||||||||||
                                GGACGA AGAGGAGTCGT
                                   _
GAM2252 RBM8A    3' CCTGTTGCCTCTAGCATCATT  23011     C     CTC
                                CCTG TGTCTC   AGCATCATT
                                |||| ||||||   |||||||||
                                GGAC ACGGAG   TCGTAGTAA
                                  A     A__
GAM2252 SMURF1   3' CCTGCTGTTTTCTGCCCAAGTT 45191       ___  C    CA
             C                   CCTGCTG   TCT CTCAG  TC
                                |||||||   ||| |||||  ||
                                GGACGAC   AGA GGGTT  AG
                                    AAA  C    CA
GAM2252 TCF20    3' TGCTGTCCTTTCCATT     42540       CC  AGCAT
                                TGCTGTCT  TC    CATT
                                ||||||||  ||    ||||
                                ACGACAGG  AG    GTAA
                                     AA  _____
GAM2252 VIPR2    3' CTGGTTGTCTCCTCAGCCCGCC 18013    C_        ATCA_
             TTC                   CTG  TGTCTCCTCAGC    TTC
                                |||  ||||||||||||    |||
                                GAC  ACAGAGGAGTCG    AAG
                                  CA         GGCGG
GAM2253 BMX      3' CTGCTCAGTCTTTACACA    11888      C  ACA
                                CTGC CA   TTTACACG
                                |||| ||   ||||||||
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                                GACG GT   AAATGTGT
                                  A  CAG
GAM2254  TPK1     3'  TGCATTCTTACTTTTGAATTT  35358    _
                                TG ATTCTTATTTTTGAATTT
                                || ||||||||||||||||||
                                AC TAAGAATGAAAACTTAAA
                                 G
GAM2255  CD3Z     3'  AGTGGTGAAATCCCC       8817         TTTTAT
                                AGTGGTG     AAATCCCC
                                |||||||     ||||||||
                                TCACCAC     TTTAGGGG
                                          _______
GAM2255  CLCN6    3'  GTGATGCCAAGATCCTCT    34720        TTATAA    C
                                GTGGTGTT     ATCC CT
                                ||||||||     |||| ||
                                CACTACGG     TAGG GA
                                     TTC___    A
GAM2255  CLN5     3'  AATGGTGTTTTCTCC       27074          ATAAA
                                AGTGGTGTTTT     TCC
                                ||||||||||     |||
                                TTACCACAAAA     AGG
                                      G____
GAM2255  PITX2    5'  GTGATATTAGATCCCC       7251         TTATAA
                                GTGGTGTT     ATCCCC
                                ||||||||     ||||||
                                CACTATAA     TAGGGG
                                     TC____
GAM2255  RAD18    3'  TAAGTGGTGCTTTTAGTTTCC  33557           ATAAA
                                TAAGTGGTGTTTT     TCC
                                ||||||||||||     |||
                                ATTCACCACGAAA     AGG
                                       ATCAA
GAM2256  APPBP2   3'  AAATGCAATGGCTCAAA     26868        GGTGCT
                                AAATGCAA     GCTCAAA
                                ||||||||     |||||||
                                TTTACGTT     CGAGTTT
                                     AC____
GAM2256  B4GALT5  3'  TAAAACGTAAGAGCAAGCTCAA 21942        C    T  T_
              AA                  TAAAATG AAGG GC  GCTCAAAA
                                ||||||| |||| ||  ||||||||
                                ATTTTGC TTCT CG  CGAGTTTT
                                    A    _  TT
GAM2256  CLN6     3'  AATGCAGGCGCTCAAA      32824        A   GCT
                                AATGCA GGT   GCTCAAA
                                ||||||| |||   |||||||
                                TTACGT CCG   CGAGTTT
                                          _   ____
GAM2256  CRIM1    3'  TAAAAGTGCTAAGGGCTG    32374        _   _    T
                                TAAAA TGC AAGG GCTG
                                ||||| ||| |||| ||||
```

```
                                ATTTT ACG TTCC CGAC
                                  C  A   _
GAM2256  CRIM1    3'  TGCAATGCTGACTGCTCAA   32386      G  __
                                TGCAA GT  GCTGCTCAA
                                ||||| ||  |||||||||
                                ACGTT CG  TGACGAGTT
                                  A  AC
GAM2256  DPYSL3   3'  CAAAATGTGCTCCCTCTGCTCA 10762       CAAGGTG_
           A                     TAAAATG       CTGCTCAA
                                |||||||       ||||||||
                                GTTTTAC       GACGAGTT
                                    ACGAGGGA
GAM2256  IL1R1    3'  TAAAATGCAGGATAATAACAAA 9366         A  TGCTGCT
                                TAAAATGCA GG      CAAA
                                ||||||||| ||      ||||
                                ATTTTACGT CC      GTTT
                                     _  TATTATT
GAM2256  KLHL3    3'  TAAAATGCAAGCACATCT    44645         G TG TG
                                TAAAATGCAA G  C  CT
                                |||||||||| |  |  ||
                                ATTTTACGTT C  G  GA
                                     _ GT TA
GAM2256  MGAT2    3'  TAAAATGTAATGCTAACTCAAA 14452       CAA     _
           A                     TAAAATG   GGTGCTG CTCAAAA
                                |||||||   ||||||| |||||||
                                ATTTTAC   TTACGAT GAGTTTT
                                    A__      T
GAM2256  NR1I2    5'  AATGTAAGGTGCTTACACA   35098      C      _  T
                                AATG AAGGTGCT GC CA
                                |||| |||||||| || ||
                                TTAC TTCCACGA TG GT
                                  A       A  T
GAM2256  PRG1     3'  AAAATGCAGGTATTTTCAA   15557        A   CTGC
                                AAAATGCA GGTG    TCAA
                                |||||||| ||||    ||||
                                TTTTACGT CCAT    AGTT
                                     _   AAA_
GAM2256  RAB26    3'  TGCAAGGTGGAGCGTGCTC   30751        ___  _
                                TGCAAGGT   GC TGCTC
                                ||||||||   || |||||
                                ACGTTCCA   CG ACGAG
                                     CCT  C
GAM2256  RPE      3'  AATGAATAACTGCTCAAAA   41639      C  GGT
                                AATG AA   GCTGCTCAAAA
                                |||| ||   ||||||||||
                                TTAC TT   TGACGAGTTTT
                                  _  AT_
GAM2256  STAT3    3'  TAAAAGTGCCCAGATTGCTCAA 40231      _  A_   GC
           A                     TAAAA TGC  AGGT  TGCTCAAA
                                ||||| |||  ||||  ||||||||
```

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                                ATTTT ACG  TCTA  ACGAGTTT
                                  C   GG   __
GAM2257  ATP11A   3'  CATGCATGTGTGCAGGAGC   44171        C    C_
                                CGTGCATG GTGC  GAGT
                                |||||||| ||||  ||||
                                GTACGTAC CACG  CTCG
                                    A    TC
GAM2257  ATP11A   3'  CATGTGTACGTGTGGGAGC   44172     CA     CC_
                                CGTG  TGCGTG   GAGT
                                ||||  ||||||   ||||
                                GTAC  ATGCAC   CTCG
                                  AC     ACC
GAM2257  ATP2B3   3'  CGTGCATGTGTGCGTGTGA   34972        C    C A
                                CGTGCATG GTGC G GTGA
                                |||||||| |||| | ||||
                                GCACGTAC CACG C CACT
                                    A   _ A
GAM2257  EHD2     3'  GTGTGTGATGTGCCTAAGTGAA 31136     CA  C_    _
             C                   GTG  TG  GTGCC GAGTGAAC
                                ||| ||  ||||| ||||||||
                                CAC  AC  CACGG TTCACTTG
                                 AC  TA    A
GAM2257  FGFRL1   3'  CGTGCATGTGTGTGTCAAG   34906        C   C__
                                CGTGCATG GTG   CGAG
                                |||||||| |||   ||||
                                GCACGTAC CAC   GTTC
                                    A   ACA
GAM2257  IHPK1    3'  ACGTGCATGTGGTCAGGAGTGA 45479         C_  GCC
                                ACGTGCATG  GT   GAGTGA
                                |||||||||  ||   ||||||
                                TGCACGTAC  CA   CTCACT
                                    AC  GTC
GAM2257  IMMT     5'  CGTGTGTGCGTGCCCGC     27752      CA       GA
                                CGTG  TGCGTGCC  GT
                                ||||  ||||||||  ||
                                GCAC  ACGCACGG  CG
                                  AC       G_
GAM2257  SLC20A2  3'  GTGTATGTGTGGCACGAGC   27578     C   C   _ _
                                GTG ATG GTG C CGAGT
                                ||| ||| ||| | |||||
                                CAC TAC CAC G GCTCG
                                  A   A   C T
GAM2257  TACC1    3'  ACATGTATGTGTGTGAGAGT   26587      C   C   CC_
                                ACGTG ATG GTG   GAGT
                                ||||| ||| |||   ||||
                                TGTAC TAC CAC   CTCA
                                  A   A   ACT
GAM2258  ADRA1A   5'  AGGGGCGCGCGGGGCTGC    37803
                                GGGGGCGCGCGGGGCTGC
                                ||||||||||||||||||
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                                TCCCCGCGCGCCCCGACG

GAM2258 ALDH3A2  5' AGGGGGCGGCGGGGTG     42912        C     C
                                AGGGGGCG GCGGGG TG
                                |||||||| |||||| ||
                                TCCCCCGC CGCCCC AC
                                        _     _
GAM2258 APBA2    3' AGGGGTGACGGCTGCCCTG   24276      GC  GCGG
                                AGGGG  GC   GGCTGCCCTG
                                |||||  ||   ||||||||||
                                TCCCC  TG   CCGACGGGAC
                                  AC  _____
GAM2258 ATP2A3   3' AGGAGGCGCGCGGGGCTG    23189
                                AGGGGGCGCGCGGGGCTG
                                ||||||||||||||||||
                                TCCTCCGCGCGCCCCGAC

GAM2258 B4GALT7  3' GGGGGTGATGAGAGGTTGTCCT 28548      CGCGC_   C  C
             G                   GGGGG     GGGG TG CCTG
                                |||||     |||| || ||||
                                CCCCC     CTCC AC GGAC
                                  ACTACT    A  A
GAM2258 BACE2    5' GGGGGCGCCGGGGTCCACCTGC 39994        G    _ TG  C
                                GGGGGCGC CGGGG C  CC TGC
                                |||||||| ||||| |  || |||
                                CCCCCGCG GCCCC G  GG ACG
                                     _    A GT  _
GAM2258 CBR1     5' GGGGCGCGCGGAACACCTGC   12038           TGC
                                GGGGCGCGCGGGGC   CCTGC
                                ||||||||||||||   |||||
                                CCCCGCGCGCCTTG   GGACG
                                        T__
GAM2258 CSNK2A2  5' GGGGGCGGCGCGGGGCGC    12490       _      T
                                GGGGGCG CGCGGGGC GC
                                ||||||| |||||||| ||
                                CCCCCGC GCGCCCCG CG
                                   C      _
GAM2258 EPB49    3' AGGGGGTGCGTGGGTGTGC    12723      C   C  _______
                                AGGGGG GCG GGG     GC
                                |||||| ||| |||     ||
                                TCCCCC CGC CCC     CG
                                  A   A   ACAIII
GAM2258 FGD1     5' GGGGCGCGCGTGTCCTG     20910         GGGC  C
                                GGGGCGCGCG    TG CCTG
                                ||||||||||    || ||||
                                CCCCGCGCGC    AC GGAC
                                      _____  A
GAM2258 IHPK1    3' AGAGGGCGTGTGGTCTGC     45480        CGCG  G
                                AGGGGGCG    GG CTGC
                                ||||||||    || ||||
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                                TCTCCCGC   CC GACG
                                    ACA_  A
GAM2258  NPR1     5'  GGGGGCGCGCAGGGCGC     44586            T
                                GGGGGCGCGCGGGGC GC
                                |||||||||||||| ||
                                CCCCCGCGCGTCCCG CG
                                                _
GAM2258  OLFM1    5'  GGGCGGCGCGCGGGCTCTGC   26776    _       G_
                                GGG GGCGCGCGGG  CTGC
                                ||| ||||||||||  ||||
                                CCC CCGCGCGCCC  GACG
                                  G        GA
GAM2258  PLOD3    5'  AGGGGGCGCTCGGGCTGC    9891          GCG
                                AGGGGGCGC   GGGCTGC
                                |||||||||   |||||||
                                TCCCCCGCG   CCCGACG
                                    AG_
GAM2258  RHEB2    5'  GGGGGTGCGTCGGGGCGAC   24720      C  _     T
                                GGGGG GCG CGGGGC GC
                                ||||| ||| |||||| ||
                                CCCCC CGC GCCCCG TG
                                   A  A     C
GAM2258  SERPINE1 3'  GGGGGCGCGGGGGGCGC     8292          C    T
                                GGGGGCGCG GGGGC GC
                                ||||||||| ||||| ||
                                CCCCCGCGC CCCCG CG
                                    C    _
GAM2258  SNRPN    5'  AGGGGGCGGCTGGCCTTGC   35607        C  G  G  _
                                AGGGGGCG GC GG CT GC
                                |||||||| || || || ||
                                TCCCCCGC CG CC GA CG
                                    _  A  G  A
GAM2258  SYN2     5'  GGGGGCGCGCGGGGCTAC    39464
                                GGGGGCGCGCGGGGCTGC
                                ||||||||||||||||||
                                CCCCCGCGCGCCCCGATG

GAM2259  CD4      3'  ACCCAAAAGTACACATT     8322        TTACT
                                ATCCA    GAAGTACACATT
                                |||||    ||||||||||||
                                TGGGT    TTTCATGTGTAA
                                    _____
GAM2259  RAD51C   3'  TCCACTTGTACACATT      38486       ACTGAA
                                TCCATT     GTACACATT
                                ||||||     |||||||||
                                AGGTGA     CATGTGTAA
                                   A_____
GAM2259  UGT2B15  3'  TCCAGCTAAAGTACGTATTAA 41067      TTA       AC
                                TCCA   CTGAAGTAC  ATTAA
                                ||||   |||||||||  |||||
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                                AGGT  GATTTCATG  TAATT
                                  C__       CA
GAM2260 ABCG5    5' CCCCAGAGTGGCTTCA     35328       CGTC  T  A
                                CCCCAGAG   TG GT TTCA
                                ||||||||   || || ||||
                                GGGGTCTC   AC CG AAGT
                                     ____ _ _
GAM2260 ARHGEF12 3' AAGTGCCTGCTATTTAGT   31631    C    G   C
                                GAG GTCTGT TATT AGT
                                ||| |||||| |||| |||
                                TTC CGGACG ATAA TCA
                                  A     _   A
GAM2260 CANX     3' GAGTGTTTATATATTCAGT   44665    C  C
                                GAG GT TGTGTATTCAGT
                                ||| || ||||||||||||
                                CTC CA ATATATAAGTCA
                                  A  A
GAM2260 HMGB1    3' CAGAGTGGTATTCAG      13404      CGTC  T
                                CAGAG   TG GTATTCAG
                                |||||   || ||||||||
                                GTCTC   AC CATAAGTC
                                     ____ _
GAM2260 HS3ST4   3' CCCCAGAGCTCTGACCTCGGT 43866        G   TGTA  A
                                CCCCAGAGC TCTG   TTC GT
                                ||||||||| ||||   ||| ||
                                GGGGTCTCG AGAC   GAG CA
                                     _   TG__  C
GAM2260 INPP5A   3' AGAGTGCGTATTCGGT     24402     CGTC       A
                                AGAG   TGTGTATTC GT
                                ||||   ||||||||| ||
                                TCTC   ACGCATAAG CA
                                  ____       C
GAM2260 LCP1     3' CCCTGGAGCATCTGTGCCGGGC 14105     CA        ATT_
           AGT                    CCC  GAGCGTCTGTGT   CAGT
                                |||  ||||||||||||   ||||
                                GGG  CTCGTAGACACG   GTCA
                                  AC         GCCC
GAM2260 MMP19    5' CAGAGCGTTTCAGC       35580        CTGTGTA
                                CAGAGCGT     TTCAGT
                                ||||||||     ||||||
                                GTCTCGCA     AAGTCG
                                     ________
GAM2260 NKX3A    3' CAGAGTTGATATTCAG     26110      CGTC  T
                                CAGAG   TG GTATTCAG
                                |||||   || ||||||||
                                GTCTC   AC TATAAGTC
                                  A___ _
GAM2260 TXNRD1   5' GCTCGCGGCTTTGTCTGGT   17771    A      GA  CCC
                                GC TCGCGGCT  TTG  GGT
                                || ||||||||  |||  |||
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                                CG AGCGCCGA  AAC   CCA
                                 _       __   AGA
GAM2261  MOG      3'  TTCAGAGTGTTCCTGAAAGT   14616        C
                                TTCAGAGT TTCCTGAAAGT
                                |||||||| ||||||||||
                                AAGTCTCA AAGGACTTTCA
                                     C
GAM2261  PTPRG    5'  TCCATGCTCCTGAAAGTT    15944      GA  CT
                                TTCA  GT  TCCTGAAAGTT
                                ||||  ||  ||||||||||
                                AGGT  CG  AGGACTTTCAA
                                  A_  __
GAM2261  EPHA3    3'  TACATGATATACTTAAGGAAGC 23442     T       CGTC  A
                                TAC TGATATACT    AG AAGC
                                ||| |||||||||    || ||||
                                ATG ACTATATGA    TC TTCG
                                  T        AT__  C
GAM2261  GRINL1A  3'  CTTGATACTAGTTAGAAAG   42997      TA    C  C
                                CTTGA  TACT GT AGAAAG
                                |||||  |||| || ||||||
                                GAACT  ATGA CA TCTTTC
                                   __    T  A
GAM2261  MCP      3'  TACTGATATATTCGATCAG   14385      T     C  _
                                TACT GATATA TCG TCAG
                                |||| |||||| ||| ||||
                                ATGA CTATAT AGC AGTC
                                  _     A   T
GAM2261  NOS1     3'  TACTTGATATTGTTTCCAG   8376          ACTCG
                                TACTTGATAT     TCAG
                                ||||||||||     ||||
                                ATGAACTATA     GGTC
                                     ACAAA
GAM2261  PRPS1    3'  TACCTGATGTGGGATGTAGAAA 15727         ATACTC_  C
              GC                  TACTTGAT      GT AGAAAGC
                                ||||||||      || |||||||
                                ATGGACTA      CA TCTTTCG
                                    CACCCTA  _
GAM2261  SLA      3'  TACTTGATGCATTCATACAG   27566        A  C   _
                                TACTTGAT TA TCGT CAG
                                |||||||| || |||| |||
                                ATGAACTA GT AGTA GTC
                                    C  A    T
GAM2261  UTY      3'  CTTGACATACTATTCTTGGAA  28312          CG  A__
                                CTTGATATACT  TC   GAA
                                ||||||||||  ||   |||
                                GAACTGTATGA  AG   CTT
                                      TA  AAC
GAM2262  GPM6A    3'  TGCATATATCAGAAAAAT    23616      C
                                TGTA ATATCAGAAGGAT
                                |||| ||||||||||||
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                                ACGT TATAGTCTTTTTA
                                  A
GAM2262  HUNK     3'  TGTATGTCAGAAAGACT     31088      CATA
                                TGTA    TCAGAAGGATT
                                ||||    ||||||||||
                                ACAT    AGTCTTTCTGA
                                  AC__
GAM2262  SLC1A3   3'  TGTATATCAGAGGATCTAT    20046      CA      A
                                TGTA  TATCAGA GGATTTAT
                                ||||  ||||||| ||||||||
                                ACAT  ATAGTCT CCTAGATA
                                  __      _
GAM2262  ABCD3    3'  CCTCCTTGTAAGCAAGACTGCA 16020          C    TACA
                                CCTCCTTGT AGTG    ACTGCA
                                ||||||||| ||||    ||||||
                                GGAGGAACA TCGT    TGACGT
                                      T    TC__
GAM2262  APOC2    3'  CCCCTTGTCCAGTCTGGCTG   7911          AGT  ACAA
                                CTCCTTGTC   GT    CTG
                                |||||||||   ||    |||
                                GGGGAACAG   CA    GAC
                                     GT_  GACC
GAM2262  CLN5     3'  TCCTGTCAGTATCTG       27088      T       ACAA
                                TCCT GTCAGTGT    CTG
                                |||| ||||||||    |||
                                AGGA CAGTCATA    GAC
                                  _      _____
GAM2262  DVL1     3'  CCTCCCTGTGGCAGCTGT    40408          __   _
                                CCTCCTTGT  CAG TGT
                                |||||||||  ||| |||
                                GGAGGGACA  GTC ACA
                                     CC   G
GAM2262  FKBP6    3'  CTACTTGTCAGTAGCTGC    44090    C        TACAA
                                CT CTTGTCAGTG     CTGC
                                || ||||||||||     ||||
                                GA GAACAGTCAT     GACG
                                 T         C_____
GAM2262  GNAT1    3'  CTCCTTGTCCCCGACTGC    6739           AG  TACA
                                CTCCTTGTC  TG    ACTGC
                                |||||||||  ||    |||||
                                GAGGAACAG  GC    TGACG
                                     GG  _____
GAM2262  MYO1D    3'  TCTTTGTTGCAAACTGC     43506    C    CAG    C
                                TC TTGT   TGTA AACTGC
                                || ||||   |||| ||||||
                                AG AACA   ACGT TTGACG
                                 A   ____   _
GAM2262  NT5M     3'  CCTCCTTGCTGATGGCTGC   33647          CA   TACAA
                                CCTCCTTGT  GTG    CTGC
                                |||||||||  |||    ||||
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                                GGAGGAACG  TAC    GACG
                                     AC   C____
GAM2262  PDCL     3'  TCCTGTTTATACAACTG     23934      T  CAG
                                TCCT GT   TGTACAACTG
                                |||| ||   ||||||||||
                                AGGA CA   ATATGTTGAC
                                  _  A__
GAM2262  PTGS1    3'  CCATCTTGTCAGAGCCAGCTG  38732    TC       T  A  A
                                CC  CTTGTCAG GT CA CTG
                                ||  |||||||| || || |||
                                GG  GAACAGTC CG GT GAC
                                 TA       T  _  C
GAM2262  SH3BP4   3'  CTTGTCAATGACTAATTGCA   30960          T  _  C
                                CTTGTCAGTG AC AA TGCA
                                |||||||||| || || ||||
                                GAACAGTTAC TG TT ACGT
                                      _  A  A
GAM2262  SPTBN2   5'  CTCCTTGTGGCCAGAGGCTGC  28069         ___   TGTACAA
                                CTCCTTGT   CAG      CTGC
                                ||||||||   |||      ||||
                                GAGGAACA   GTC      GACG
                                     CCG   TCC_____
GAM2262  TDG      3'  CTACTTGTTGACAACTGC    17354    C    CAG  T
                                CT CTTGT   TG ACAACTGC
                                || |||||   || ||||||||
                                GA GAACA   AC TGTTGACG
                                 T    ___  _
GAM2262  ZNF174   5'  CTTCTTGTCAGTTTTTTGCA   18360    C       GTACAAC
                                CT CTTGTCAGT      TGCA
                                || |||||||||      ||||
                                GA GAACAGTCA      ACGT
                                 A        AAAA___
GAM2263  ZNF216   3'  TTTATTATTTACATAATACAA  25662      CG       _
                                TTTAT  TTTACATAA GCAA
                                |||||  ||||||||| ||||
                                AAATA  AAATGTATT TGTT
                                   AT        A
GAM2264  CACNA2D3 3'  TCGTATGTTGCACCATATT    32901      ATTTA
                                TTGTG    CACCATATT
                                |||||    |||||||||
                                AGCAT    GTGGTATAA
                                   ACAAC
GAM2264  DAZ      3'  TCAGTGTGATTTACCAAAATTC 19856     AT        ACCAT
                                TCA  TGTGATTTAC    ATTC
                                |||  ||||||||||    ||||
                                AGT  ACACTAAATG    TAAG
                                 C_         GTTT_
GAM2264  DAZL     3'  TGTGATTTACCAAAATTC    42782          ACCAT
                                TGTGATTTAC    ATTC
                                ||||||||||    ||||
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                                ACACTAAATG    TAAG
                                      GTTT_
GAM2264  EYA1    3'  TCAATTGTGAATTTAAACAAT  7991          _   C  C
                                TCAATTGTGA TTTA AC AT
                                |||||||||| |||| || ||
                                AGTTAACACT AAAT TG TA
                                      T   T  T
GAM2264  HTR2C   3'  ATTGTAACACAACACTATATT  9279        TT_   C
                                ATTGTGAT   ACAC ATATT
                                ||||||||   |||| |||||
                                TAACATTG   TGTG TATAA
                                     TGT    A
GAM2265  DLG5    5'  AGCTGTGGGCCATCAGCT    44443           _
                                AGCTGTGGGTCATT GTT
                                |||||||||||||| |||
                                TCGACACCCGGTAG CGA
                                         T
GAM2265  ELK1    3'  GAAGCTGTGTGTTTTCTGT   23409        G  CA_
                                GAAGCTGTG GT   TTGT
                                ||||||||| ||   ||||
                                CTTCGACAC CA   GACA
                                     A  AAA
GAM2265  DLG5    5'  AGCTGTGGGCCATCAGCT    44443           _
                                AGCTGTGGGTCATT GTT
                                |||||||||||||| |||
                                TCGACACCCGGTAG CGA
                                         T
GAM2265  ELK1    3'  GAAGCTGTGTGTTTTCTGT   23409        G  CA_
                                GAAGCTGTG GT   TTGT
                                ||||||||| ||   ||||
                                CTTCGACAC CA   GACA
                                     A  AAA
GAM2266  ITGA6   3'  ACAGCTAACGTGATGG     6826     TTTT
                                GCA   CTAACGTGATGG
                                |||   ||||||||||||
                                TGT   GATTGCACTACC
                                  C___
GAM2266  MAPK3   3'  TCCATTTTCTAACAGTCTGG  43847   G        TGA
                                TC CATTTTCTAACG   TGG
                                || ||||||||||||   |||
                                AG GTAAAAGATTGT   ACC
                                  _         CAG
GAM2266  ITGA6   3'  ACAGCTAACGTGATGG     6826     TTTT
                                GCA   CTAACGTGATGG
                                |||   ||||||||||||
                                TGT   GATTGCACTACC
                                  C___
GAM2266  MAPK3   3'  TCCATTTTCTAACAGTCTGG  43847   G        TGA
                                TC CATTTTCTAACG   TGG
                                || ||||||||||||   |||
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                                AG GTAAAAGATTGT   ACC
                                 _         CAG
GAM2267 DIAPH2   3' TGTGTATGTGTGTTTTCAGATC 28686        ATAAC_  TCC
            GGA                  TGTGTATGT     TCA  CGGA
                                 |||||||||     |||  ||||
                                 ACACATACA     AGT  GCCT
                                     CACAAA   CTA
GAM2267 GPM6A    3' TGTTATGTATAACACATGG   23617    G       T  CCC
                                 TGT TATGTATAAC CAT  GG
                                 ||| ||||||||||| |||  ||
                                 ACA ATACATATTG GTA  CC
                                   _       T  ___
GAM2267 INHBC    3' TGTGTCAACTCATCTTGG    24401     ATGTA      CC
                                 TGTGT    TAACTCATC  GG
                                 |||||    |||||||||  ||
                                 ACACA    GTTGAGTAG  CC
                                   _____       AA
GAM2267 PCDH11X  3' TGTGTGTGTGTAGATCATC   37317     A  A  AC
                                 TGTGT TGT TA  TCATC
                                 ||||| ||| ||  |||||
                                 ACACA ACA AT  AGTAG
                                    C  C  CT
GAM2267 PCDH11Y  3' TGTGTGTGTGTAGATCATC   37359     A  A  AC
                                 TGTGT TGT TA  TCATC
                                 ||||| ||| ||  |||||
                                 ACACA ACA AT  AGTAG
                                    C  C  CT
GAM2267 EGFL5    5' AATCCCGAAACATCTGCATTG  44510    G  C   C
                                 GAT TTG AACA CTGCATTG
                                 ||| ||| |||| ||||||||
                                 TTA GGC TTGT GACGTAAC
                                   G  T   A
GAM2267 IFNA8    5' AGATGTTGTGGATGCTGCTGAG 40580       CAACAC   AT
                                 AGATGTTG     CTGC  TGAG
                                 ||||||||     ||||  ||||
                                 TCTACAAC     GACG  ACTC
                                      ACCTAC   __
GAM2267 SLC16A1  3' AAATGTCTACTATTTGCATTGA 16811       GCAACACC
            G                    AGATGTT      TGCATTGAG
                                 |||||||      |||||||||
                                 TTTACAG      ACGTAACTC
                                     ATGATAA_
GAM2267 TGFA     3' AGATGTTGGGCTGGTTGA    17438       CAACAC  CA
                                 AGATGTTG     CTG  TTGA
                                 ||||||||     |||  ||||
                                 TCTACAAC     GAC  AACT
                                      CC____   C_
GAM2268 ABR      3' TGGCTGCAGCCTACCTGCCTGG 35021      A        __ _
            ACAC                     TGGC TGCAGCCTGCT  CC GGACAC
                                 |||| ||||||||||  || ||||||
```

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                                ACCG ACGTCGGATGG  GG CCTGTG
                                  _         AC  A
GAM2268  FCAR     3'  TGTGTGCAGCCTGGCCAG    39339    GCA       CT
                                TG   TGCAGCCTG  CCGG
                                ||   |||||||||  ||||
                                AC   ACGTCGGAC  GGTC
                                 AC_       C_
GAM2268  GLI4     3'  TGGCATGCGGTGCTGGGCA   39692        AGCC    CC  A
                                TGGCATGC    TGCT  GG CA
                                ||||||||    ||||  || ||
                                ACCGTACG    ACGA  CC GT
                                     CC__    __  C
GAM2268  NCALD    3'  GGCATGCAGTCCTCTGG     36766         _  G  CC
                                GGCATGCAG CCT CT  GG
                                ||||||||| ||| ||  ||
                                CCGTACGTC GGA GA  CC
                                     A  _ __
GAM2268  ABCD3    3'  CCAACTACCACAGGGCAC     16019          CCCAA
                                CCAATTACCAC     GCAC
                                ||||||||||     ||||
                                GGTTGATGGTG     CGTG
                                      TCC__
GAM2268  ANKH     3'  ATTCTCAATTACCTGTACCGC  38312      C       ___   CCAA
                                ATTC CAATTACC   ACC    GC
                                |||| ||||||||   |||    ||
                                TAAG GTTAATGG   TGG    CG
                                  A       ACA  _____
GAM2268  BAALC    3'  TTCCCAATCCCAGGC       36047         TACCAC    A
                                TTCCCAAT     CCCA GC
                                ||||||||     |||| ||
                                AAGGGTTA     GGGT CG
                                     _______   C
GAM2268  CASP8    3'  ATTCCCAAAGCCTTAAGC    37867         TTACCA  CC
                                ATTCCCAA     CC  AAGC
                                ||||||||     ||  ||||
                                TAAGGGTT     GG  TTCG
                                     TC_____  AA
GAM2268  CASP8    3'  ATTCCCAAAGCCTTAAGCA   37868         TTACCA  CC
                                ATTCCCAA     CC  AAGCA
                                ||||||||     ||  |||||
                                TAAGGGTT     GG  TTCGT
                                     TC_____  AA
GAM2268  CYFIP1   3'  TTCCTAATTACCAAAAGCA   42460      C       CCCC
                                TTCC AATTACCA    AAGCA
                                |||| ||||||||    |||||
                                AAGG TTAATGGT    TTCGT
                                  A       T___
GAM2268  PRKG1    3'  ACTCCACCCTACCCCAAGCA  26513       CAATTA  _
                                ATTCC     CC ACCCCAAGCA
                                |||||     || ||||||||||
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                                TGAGG     GG TGGGGTTCGT
                                   TG____  A
GAM2268  RAD23B   3'  CTCCCCTCCCACCCCAAG    16136       AATTA
                                TTCCC     CCACCCCAAG
                                |||||     ||||||||||
                                GAGGG     GGTGGGGTTC
                                   GAG__
GAM2268  REGL     3'  TTCCCAATTGCCAGCA      27126          A   CCCCAA
                                TTCCCAATT CCA      GCA
                                ||||||||| |||      |||
                                AAGGGTTAA GGT      CGT
                                     C  ______
GAM2268  ZNF175   5'  ATTCCCAATCACTTCAGC    28365            CACCCCA
                                ATTCCCAATTAC       AGC
                                ||||||||||||       |||
                                TAAGGGTTAGTG       TCG
                                      AAG____
GAM2269  FLT4     3'  CACAGGGTCAGGTGCTGAAGG  12917      A AA   TTA
                                TACA G  TCA   GTGCTGAAGG
                                |||| |  |||   ||||||||||
                                GTGT C  AGT   CACGACTTCC
                                  _ CC   C__
GAM2269  HMOX1    3'  CAGGAACTGAGGATGCTGAAGG 13410    A    CATTA
                                CA GAAT     GTGCTGAAGG
                                || ||||     ||||||||||
                                GT CTTG     TACGACTTCC
                                 C    ACTCC
GAM2269  MEF2A    5'  TACGAGAATCACTTGAACCTGG 24625     A        AGTG_   A
            AGG                    TAC AGAATCATT     CTG AGG
                                ||| |||||||||     ||| |||
                                ATG TCTTAGTGA     GAC TCC
                                  C         ACTTG   C
GAM2269  OA1      3'  ACAAGAATTGTTGAGTCTGAGG 7081          CA  _   G    A
                                ACAAGAAT  TT AGT CTGA GG
                                ||||||||  || ||| |||| ||
                                TGTTCTTA  AA TCA GACT CC
                                     AC  C   _    _
GAM2269  PAX9     3'  AAGTGTCATTAGCACAAAGG   26200     AA      TG T
                                AAG  TCATTAG  C GAAGG
                                |||  |||||||  | |||||
                                TTC  AGTAATC  G TTTCC
                                  AC       GT _
GAM2269  PIM2     3'  CAAGAATCTGCAAAAG      41019         ATTAG   T
                                CAAGAATC     TGC GAAG
                                ||||||||     ||| ||||
                                GTTCTTAG     ACG TTTC
                                     _____   T
GAM2269  PRKAR1A  3'  TACTGGAGTCAGCTGAAG    15612     AA  A   TTAGT
                                TAC  GA TCA     GCTGAAG
                                |||  || |||     |||||||
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                                ATG  CT AGT    CGACTTC
                                  AC  C  _____
GAM2269  SCD     3'  AGAATTCCTGTGCTGAAGG   22818      CA  A
                                AGAAT  TT GTGCTGAAGG
                                ||||||  || ||||||||||
                                TCTTA  GA CACGACTTCC
                                  AG  _
GAM2269  SLC4A8  3'  ACAAGATGCCAAGTGCTGAGGG 22144       A_  TT      A
                                ACAAGA  TCA  AGTGCTGA GG
                                ||||||  |||  |||||||| ||
                                TGTTCT  GGT  TCACGACT CC
                                   AC  __      C
GAM2270  FACL5   3'  TAGAGACTGTTGGCAAGTTATG 42017     AG     T  TT
                                TAGA  CTGTTGG CA  GTTATG
                                ||||  ||||||| ||  ||||||
                                ATCT  GACAACC GT  CAATAC
                                  CT      _  T_
GAM2270  NCOA4   3'  TACAGAAAGACAAAATT    24136       CAATT
                                TACAGA    GACAAAATT
                                ||||||    |||||||||
                                ATGTCT    CTGTTTTAA
                                   TT___
GAM2271  IL13RA2  3'  CAATACCATGTCTCTTGATAT  8476         ATAA   A
                                TAATACCA    TCTT ATAT
                                ||||||||    |||| ||||
                                GTTATGGT    AGAA TATA
                                     ACAG   C
GAM2271  CRHR1   3'  TCATCGTGGTGAGTCAGAGGCT 20450           ATAAAT  T
                                TCATCGTGGTGA     GAG CT
                                ||||||||||||     ||| ||
                                AGTAGCACCACT     CTC GA
                                       CAGT__  C
GAM2271  IFNA17  3'  TCGTGGTGGTTATAGAAGTGAG 34623        A__  AA__
            TCT                   TCGTGGTG   ATA   TGAGTCT
                                ||||||||  |||   |||||||
                                AGCACCAC   TAT   ACTCAGA
                                     CAA   CTTC
GAM2271  IFNA4   3'  TCGTGGTGGTTATAGAAGTGAG 34337        A__  AA__
            TCT                   TCGTGGTG   ATA   TGAGTCT
                                ||||||||  |||   |||||||
                                AGCACCAC   TAT   ACTCAGA
                                     CAA   CTTC
GAM2271  LAD1    3'  CACCTGAGAGTAAATGAGT   24482     G  T  A
                                CATC TGG GA TAAATGAGT
                                |||| ||| || |||||||||
                                GTGG ACT CT ATTTACTCA
                                  _  _  C
GAM2271  LDLR    3'  TCATTTGGTGAATGAGT    8028      CG    ATAA
                                TCAT  TGGTGA   ATGAGT
                                ||||  ||||||   ||||||
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                                AGTA  ACCACT    TACTCA
                                  A_     _____
GAM2271  MTMR8    3'  GTAAATGGATAAATGAGTCT   31753      _  A
                                GTGG TG ATAAATGAGTCT
                                |||| || ||||||||||||
                                CATT AC TATTTACTCAGA
                                  T  C
GAM2271  SMT3H1   3'  TCATCGTGGTGAATGTCCTCGA 41003             AAA__
                GT                TCATCGTGGTGAAT     TGAGT
                                |||||||||||||     |||||
                                AGTAGCACCACTTA     GCTCA
                                        CAGGA
GAM2271  VDR      3'  CATCGTGGTGGGGTAGGGTCT  7515           AATAAATGA
                                CATCGTGGTG        GTCT
                                ||||||||||        ||||
                                GTAGCACCAC        CAGA
                                      CCCATCC__
GAM2272  MECP2    3'  CGTGGATAAGTGTCCTTTGG   22585          GGATA
                                CGTGGATAAG     TTTGG
                                ||||||||||     |||||
                                GCACCTATTC     AAACC
                                      ACAGG
GAM2272  ADAMTS5  3'  AACCCGTGTATGTATTTAAGTG 28171          C  TGA_   C
                ACT                 AACCCGTGTA GT    GAG GACT
                                |||||||||| ||    ||| ||||
                                TTGGGCACAT CA    TTC CTGA
                                      A  TAAA   A
GAM2272  CAPN2    3'  CCTCGTGTCCTTTGAGAGCGAC 11965    _    ACG
                T                  CC CGTGT   TTGAGAGCGACT
                                || |||||   ||||||||||||
                                GG GCACA   AACTCTCGCTGA
                                 A     GGA
GAM2272  GRIK5    3'  TGAGGATTGAGAGTGACT    13298    TAC       C
                                TG   GTTGAGAG GACT
                                ||   |||||||| ||||
                                AC   TAACTCTC CTGA
                                 TCC       A
GAM2272  HOXD4    3'  CCCCTGTTGAGAGTGA      31170     G   ACGT     C
                                CCC TGT    TGAGAG GA
                                ||| |||    |||||| ||
                                GGG ACA    ACTCTC CT
                                  G  _____      A
GAM2272  MTMR6    5'  GTGTGGACCGAGAGCGGCT    45277      AC TT      A
                                GTGT  G  GAGAGCG CT
                                ||||  |  ||||||| ||
                                CACA  T  CTCTCGC GA
                                  CC GG      C
GAM2273  LFNG     3'  ACAGACACGCCCACTGTG     45215      _  G
                                ATAG TG GCCCACTGTG
                                |||| || ||||||||||
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                                TGTC GT CGGGTGACAC
                                  T  G
GAM2273  NDUFA9   3'  TGTTTTAATAGTGGAACTGTG  22670     AC       CCC
                                TGTT  AATAGTGGG   ACTGTG
                                ||||  |||||||||   ||||||
                                ACAA  TTATCACCT   TGACAC
                                  AA        ___
GAM2273  LFNG     3'  ACAGACACGCCCACTGTG    45215     _  G
                                ATAG TG GCCCACTGTG
                                |||| || ||||||||||
                                TGTC GT CGGGTGACAC
                                  T  G
GAM2273  NDUFA9   3'  TGTTTTAATAGTGGAACTGTG  22670     AC       CCC
                                TGTT  AATAGTGGG   ACTGTG
                                ||||  |||||||||   ||||||
                                ACAA  TTATCACCT   TGACAC
                                  AA        ___
GAM2274  SMT3H1   3'  GTTGCACTTGAAGTACA     41001        CATA
                                GTTGCACT    GAAGTACA
                                ||||||||    ||||||||
                                CAACGTGA    CTTCATGT
                                    A___
GAM2274  SMT3H1   3'  GTTGCACTTGAAGTACA     41001        CATA
                                GTTGCACT    GAAGTACA
                                ||||||||    ||||||||
                                CAACGTGA    CTTCATGT
                                    A___
GAM2275  CD1A     5'  GACTGCAACAAAGAAAATCC   43407          CATC    _
                                GACTGCAACAA    GAAA CC
                                ||||||||||    |||| ||
                                CTGACGTTGTT    TTTT GG
                                      TC__    A
GAM2275  CSNK1G2  3'  AGACTGCAGCAGCCGTGCCC   10605        A  ACA   AAA
                                AGACTGCA CA   TCG   CCC
                                |||||||| ||   |||   |||
                                TCTGACGT GT   GGC   GGG
                                    C  C__   AC_
GAM2275  DAPK1    3'  TAAACTGCAATGACCATC     22362         CAA_
                                TAGACTGCAA    CATC
                                ||||||||||    ||||
                                ATTTGACGTT    GTAG
                                      ACTG
GAM2275  IQGAP1   3'  AGACTGTAACAACACAGA     42898       C       C
                                AGACTG AACAACAT GA
                                |||||| |||||||| ||
                                TCTGAC TTGTTGTG CT
                                   A       T
GAM2275  MBNL     3'  TAGCTGCAACATCCAAACC    34320     A    ACA    G
                                TAG CTGCA   ACATC AAACC
                                ||| |||||   ||||| |||||
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                                ATC GACGT   TGTAG TTTGG
                                  _    ___     G
GAM2275  TAL1     3'  GACTCAGGCTGCGAAACCC   17285     G  ACAACAT
                                GACT CA      CGAAACCC
                                |||| ||      ||||||||
                                CTGA GT      GCTTTGGG
                                  _ CCGAC__
GAM2276  DIAPH2   3'  TGTGAAAAGTTGAATAAA    28685        AC
                                TGTGAGAA  TTGAGTAAA
                                ||||||||  |||||||||
                                ACACTTTT  AACTTATTT
                                     C_
GAM2276  ITGAV    3'  TGAGGAACTGTGAATAAA    13632     A   _
                                TGAG AACT TGAGTAAA
                                |||| |||| ||||||||
                                ACTC TTGA ACTTATTT
                                  C   C
GAM2276  KIF5C    3'  TGTAGAGATCAAGTAAAAT   21166    _   AAC TG
                                TGT GAGA   T  AGTAAAAT
                                ||| ||||   |  ||||||||
                                ACA CTCT   A  TCATTTTA
                                  T   ___ GT
GAM2276  MME      3'  TATGAGAAACAGAAATAAA   28602         TT
                                TGTGAGAAAC  GAGTAAA
                                ||||||||||  |||||||
                                ATACTCTTTG  TTTATTT
                                      TC
GAM2276  NPAT     3'  GTGAGAAACTATTCCAGATGAG 42614          _________
                                GTGAGAAACT       TGAG
                                ||||||||||       ||||
                                CACTCTTTGA       ACTC
                                      TAAGGTCT
GAM2276  PKIA     3'  TGTGAGAAATTTGATTCCATA  27747         C   GTAAA
                                TGTGAGAAA TTGA    ATA
                                ||||||||| ||||    |||
                                ACACTCTTT AACT    TAT
                                     A   AAGG_
GAM2276  TM6SF1   3'  TATGAGAAGAGAGTGAAAT   35690        ACTT   A
                                TGTGAGAA   GAGT AAAT
                                ||||||||   |||| ||||
                                ATACTCTT   CTCA TTTA
                                     CT__   C
GAM2276  TNFSF4   3'  TGTGAGAAATATAGATAAA   17759        CT  AG
                                TGTGAGAAA  TG  TAAA
                                |||||||||  ||  ||||
                                ACACTCTTT  AT  ATTT
                                      AT  CT
GAM2276  TRPM6    3'  GTGAGAAAATAAAATAA     32790       AACTT
                                GTGAGA    GAGTAAAATAA
                                ||||||    ||||||||||
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                              CACTCT    TTTATTTTATT
                                    _____
GAM2276 VCAM1    3' TGTGAAAGGGAATAAAATA   9888       AACTT
                              TGTGAGA    GAGTAAAATA
                              |||||||    ||||||||||
                              ACACTTT    CTTATTTTAT
                                  CC___
GAM2276 ZNF264   3' TGTGAGAGATAAAGTAAA    18277      AACTT
                              TGTGAGA    GAGTAAA
                              |||||||    |||||||
                              ACACTCT    TTCATTT
                                  CTAT_
GAM2277 FOXF1    3' TCAAATGGTCCTTTTATA    11125        GA_
                              TTAAATGGTTC   TATA
                              ||||||||||   ||||
                              AGTTTACCAGG   ATAT
                                    AAA
GAM2278 ADAMTS4  5' CTCCTGCCAAGGTCAGAGGCAA 23005          TCT  _
             A                 CTCCTGCTAAGGTT   GAG CAAA
                              ||||||||||||||   ||| ||||
                              GAGGACGGTTCCAG   CTC GTTT
                                     T__   C
GAM2278 AP3S1    3' CTTTAAAATCACTGAGCAA   10505    GC     T
                              CT  TAAGGTT CTGAGCAA
                              ||  ||||||| ||||||||
                              GA  ATTTTAG GACTCGTT
                               A_      T
GAM2278 ARHGEF5  3' CTCTTGCAGGGTTCTG     24128    C   TA   T
                              CTC TGC  AGG TTCTG
                              ||| |||  ||| |||||
                              GAG ACG  TCC AAGAC
                                A   __   C
GAM2278 ATP2B4   5' CTGGCTAAGGCCGGGGAG    43197    _      TCT
                              CTG CTAAGGTT   GAG
                              ||| ||||||||   |||
                              GAC GATTCCGG   CTC
                                C       CCC
GAM2278 ATP6V0C  3' CTCTAGCTAAGGTTATAGA   44556    CT       TCT
                              CTC  GCTAAGGTT   GA
                              |||  |||||||||   ||
                              GAG  CGATTCCAA   CT
                                AT        TAT
GAM2278 CD244    3' CCTGTTGGGGTCTCTGAG    32296     CTAA
                              CCTG   GGTTTCTGAG
                              ||||   ||||||||||
                              GGAC   CCAGAGACTC
                                AACC
GAM2278 CLCN6    3' CTCCCGGCTTTCTGAG      34714       _ AAGGT
                              CTCCTG CT    TTCTGAG
                              |||||| ||    |||||||
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                                GAGGGC GA    AAGACTC
                                   C _____
GAM2278 COL4A4   5' CTCCCGCTTAATCTGGGCA  6400        AAGGTT   A
                                CTCCTGCT    TCTG GCA
                                ||||||||    |||| |||
                                GAGGGCGA    AGAC CGT
                                    ATT___   C
GAM2278 CRLF1    3' CTCCTGCTGAGGGTGGCTCAG 21899       A  TTT_ G
                                CTCCTGCT AGG   CT AG
                                |||||||| |||   || ||
                                GAGGACGA TCC   GA TC
                                    C  CACC  G
GAM2278 EPB41    5' CTCCTGCTGAGGTTCTTG   20765       A    TC
                                CTCCTGCT AGGTT  TG
                                |||||||| |||||  ||
                                GAGGACGA TCCAA  AC
                                    C    GA
GAM2278 GRM7     5' CTCCTGCAGGCACGGAG    9186       TA   TTCT
                                CTCCTGC  AGGT   GAG
                                |||||||  ||||   |||
                                GAGGACG  TCCG   CTC
                                   __   TGC_
GAM2278 GTF2IRD1 3' TCCTTTAGTCTTTCTGAG   32265     GCTA  G_
                                TCCT   AG  TTTCTGAG
                                ||||   ||  ||||||||
                                AGGA   TC  AAAGACTC
                                  AA__  AG
GAM2278 HCFC1    3' TCCTGTGGGGTCACTGAGCA  43398     CTAA   T
                                TCCTG   GGTT CTGAGCA
                                |||||   |||| |||||||
                                AGGAC   CCAG GACTCGT
                                   ACC_   T
GAM2278 KCNC3    5' CTCTTTCTAAGAGAGCA    22502    CTG    TTTCT
                                CTC  CTAAGG   GAGCA
                                |||  ||||||   |||||
                                GAG  GATTCT   CTCGT
                                  AAA    _____
GAM2278 LTBP2    3' CCTTGCTTCTCTGAG      7693     _  AAGG
                                CCT GCT   TTTCTGAG
                                ||| |||   ||||||||
                                GGA CGA   AGAGACTC
                                  A  _____
GAM2278 LTF      3' TCTTGCTAAGACGACAGCA  14263   C      TTTCTG
                                TC TGCTAAGG    AGCA
                                || ||||||||    ||||
                                AG ACGATTCT    TCGT
                                 A      GCTG__
GAM2278 MYO1D    3' CCTTGCTGTTTCTCTGAG   43492    _  AAGG
                                CCT GCT   TTTCTGAG
                                ||| |||   ||||||||
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                                GGA CGA    AGAGACTC
                                  A   CAA_
GAM2278 NT5M     3'  CTCTCTGCTGGGCCCTGAGC   33650     _    AA  TT
                                CTC CTGCT  GG  TCTGAGC
                                ||| |||||  ||  |||||||
                                GAG GACGA  CC  GGACTCG
                                  A    __ CG
GAM2278 P2RY2    5'  CTCCAGCATTTTTCTGGGCA   15014     T  TAAGG     A
                                CTCC GC    TTTCTG GCA
                                |||| ||    |||||| |||
                                GAGG CG    AAAGAC CGT
                                  T  TAA__     C
GAM2278 PAFAH1B3 5'  CTCCTGCAGGATGAGC      15076       TA   TTTC
                                CTCCTGC  AGG    TGAGC
                                |||||||  |||    |||||
                                GAGGACG  TCC    ACTCG
                                   __   T___
GAM2278 PFKL     3'  CTCCTGCTGGAGGGCCTGGCA  15233       A_   TT   A
                                CTCCTGCT  AGG  TCTG GCA
                                ||||||||  |||  |||| |||
                                GAGGACGA  TCC  GGAC CGT
                                    CC   C_   _
GAM2278 PLA2G4C  5'  TCCTCCTGGTCCTGAGCA    43861     G  AA    T
                                TCCT CT  GGTT CTGAGCA
                                |||| ||  |||| |||||||
                                AGGA GA  CCAG GACTCGT
                                  G  __   _
GAM2278 PPP2R5C  3'  CTGTCAAGGTAGACAGAGCAA  15522     C     TTCT_
                                CTG TAAGGT    GAGCAA
                                ||| ||||||    ||||||
                                GAC GTTCCA    CTCGTT
                                  A     TCTGT
GAM2278 RFX5     3'  TGCTGAGATTTCTGGTACAAA  7798      A       A_
                                TGCT AGGTTTCTG  GCAAA
                                |||| |||||||||  |||||
                                ACGA TCTAAAGAC  TGTTT
                                  C       CA
GAM2278 RNF28    3'  CTCCTGCTCAGGAAAGGAAG   37200       A   TTTCT
                                CTCCTGCT AGG    GAG
                                |||||||| |||    |||
                                GAGGACGA TCC    TTC
                                    G   TTTCC
GAM2278 RNF28    3'  CCCTGCTCTCTGAGCA      37198       AAGGT
                                TCCTGCT    TTCTGAGCA
                                |||||||    |||||||||
                                GGGACGA    GAGACTCGT
                                   _____
GAM2278 SFRS7    3'  CTCCTGCTGCGTGAGC      40468       AAG  TTC
                                CTCCTGCT   GT   TGAGC
                                ||||||||   ||   |||||
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                                GAGGACGA  CG  ACTCG
                                   ___  C__
GAM2278 SIT     3' CTCCTGCTAGGGTTCTTA   30897       A   TC
                                CTCCTGCTA GGTT  TG
                                ||||||||| ||||  ||
                                GAGGACGAT CCAA  AT
                                     C   GA
GAM2278 SLC22A11 3' CTCCTGTAGGGCCCGGGTAAG 32961      C A   C__
                                CTCCTG TA GGTTT  TGAG
                                |||||| || |||||  ||||
                                GAGGAC AT CCGGG  ATTC
                                   _ C    CCC
GAM2278 SLC3A2   5' CTCCTGCCACATGCACTG   14400       AG_ TT
                                CTCCTGCTA  GT  CTG
                                |||||||||  ||  |||
                                GAGGACGGT  CG  GAC
                                     GTA  T_
GAM2278 SON     3' CTCACTGAGTCTTTTCTGAGCA 38458    _  CTAAGG
             A                   CTC CTG     TTTCTGAGCAA
                                 ||| |||     ||||||||||
                                 GAG GAC     AAAGACTCGTT
                                   T  TCAGA_
GAM2278 SPO11    5' TCCCGCGCTTTCTGAGC    29709      TAAGG
                                 TCCTGC    TTTCTGAGC
                                 ||||||    |||||||||
                                 AGGGCG    AAAGACTCG
                                    CG___
GAM2278 SUFU    3' CTCCTGCTGGGCTGTGCGGCA 32085       AA   TC_ A
                                 CTCCTGCT  GGTT  TG GCA
                                 ||||||||  ||||  || |||
                                 GAGGACGA  CCGA  GC CGT
                                     C_   CAC  _
GAM2278 TNS     3' CTCCTGCTGGGGTCTTTGTAG 35474       AA    C  _
                                 CTCCTGCT  GGTTT TG AG
                                 ||||||||  ||||| || ||
                                 GAGGACGA  CCAGA AC TC
                                     CC    A  A
GAM2278 UBE2I   5' CTCCTCTAAGTGAG       17816      G    GTTTC
                                 CTCCT CTAAG    TGAG
                                 ||||| |||||    ||||
                                 GAGGA GATTC    ACTC
                                    _   _____
GAM2278 UFD1L   3' CTCCTGCTGAGGCAGTG    43822       A   TTC
                                 CTCCTGCT AGGT  TG
                                 |||||||| ||||  ||
                                 GAGGACGA TCCG  AC
                                     C   TC_
GAM2279 ERBB2   3' CTTGATGCCAGCAGAAGT   20818    CA      TGCAAA
                                 CT  ATGTCAGC    AAGT
                                 ||  ||||||||    ||||
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                                GA  TACGGTCG     TTCA
                                 AC       TC____
GAM2279  M11S1    3'  CCAATGTCATAAAAG       25327          GCTGCA
                                TCAATGTCA     AAAAG
                                |||||||||     |||||
                                GGTTACAGT     TTTTC
                                     A_____
GAM2279  PTPN11   3'  AATGCCAGTGCAAAGGTC    38750         C     AA
                                AATGTCAG TGCAAA  GTC
                                |||||||| ||||||  |||
                                TTACGGTC ACGTTT  CAG
                                     _     C_
GAM2279  SCG3     3'  CTCAATGTCTGAAAAGT     29885          AGC  CA
                                CTCAATGTC   TG  AAAAGT
                                |||||||||   ||  ||||||
                                GAGTTACAG   AC  TTTTCA

                                     ___  __
GAM2279  TCEB1L   3'  TCAATGCCAACTTTTAAAAGGT 17313            GC_   A
              C                  TCAATGTCAGCT   AAAA GTC
                                 ||||||||||||   |||| |||
                                 AGTTACGGTTGA   TTTT CAG
                                        AAA   C
GAM2279  WIF1     3'  TCAAGCCAATGCAAAAAGT   41170      T    C
                                TCAA GTCAG TGCAAAAAGT
                                |||| ||||| ||||||||||
                                AGTT CGGTT ACGTTTTTCA

                                  _    _
GAM2279  ADD1     3'  GCTGGCAGAGCCAGG       30509      ACAATT
                                GCTG     CAGAGCCAGG
                                ||||     ||||||||||
                                CGAC     GTCTCGGTCC
                                  C_____
GAM2279  BCL11A   3'  GCTGGTTTCAGAAGGGCCAGGG 39712      ACAA     ___
              C                  GCTG    TTCAGA   GCCAGGGC
                                 ||||    ||||||   ||||||||
                                 CGAC    AAGTCT   CGGTCCCG
                                   CA__      TCC
GAM2279  CARPX    3'  CAGTTGCATGGAGCCAGGGC   33567     C  A  ATTCA
                                CAG TG CA     GAGCCAGGGC
                                ||| || ||     ||||||||||
                                GTC AC GT     CTCGGTCCCG
                                  A  _  AC___
GAM2279  CD8A     3'  AGTTGAGCAGAGGCCAGGGC   12089    C   CAATT    _
                                AG TGA     CAGAG CCAGGGC
                                || |||     ||||| |||||||
                                TC ACT     GTCTC GGTCCCG
                                 A  C_____     C
GAM2279  CDH23    3'  CAGCTGATGCGGGCTGCCAGGG 38070        CAATTCAGA
              C                  CAGCTGA        GCCAGGGC
                                 |||||||        ||||||||
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                              GTCGACT      CGGTCCCG
                                 ACGCCCGA_
GAM2279 DUSP4   5' CAGCTGACAGGTCAAATGGGC 10814       AT   GCCA
                              CAGCTGACA TCAGA  GGGC
                              ||||||||| |||||  ||||
                              GTCGACTGT AGTTT  CCCG
                                   CC   A___
GAM2279 DYRK1B  5' GCGGACGCGGCAAGCCAGGGC 21779   T  AATTCA
                              GC GAC    GAGCCAGGGC
                              || |||    ||||||||||
                              CG CTG    TTCGGTCCCG
                               C  CGCCG_
GAM2279 GPRK6   3' CAGTCTGGGAAGGGCCAGGGC 13268    _  ACAATTC A
                              CAG CTG     AG GCCAGGGC
                              ||| |||     || ||||||||
                              GTC GAC     TC CGGTCCCG
                                A  CCT____ C
GAM2279 GRHPR   3' CTGACAATACCAGGG     29192       TCAGA
                              CTGACAAT   GCCAGGG
                              ||||||||   |||||||
                              GACTGTTA   TGGTCCC
                                   _____
GAM2279 HCR     3' CAGCTGGTATCCCCCAGGG  44951     ACA  AGAG
                              CAGCTG  ATTC  CCAGGG
                              ||||||  ||||  ||||||
                              GTCGAC  TAGG  GGTCCC
                                 CA_  G___
GAM2279 HHLA1   3' ACTTGGGACAAGAGCCAGGG  25049   ___  ATTC
                              GCT  GACA  AGAGCCAGGG
                              |||  ||||  ||||||||||
                              TGA  CTGT  TCTCGGTCCC
                                ACC  ____
GAM2279 HRMT1L1 3' AGCTCGCACGCTGAGCCAGGGC 42179    GA  ATTCA
                              AGCT  CA   GAGCCAGGGC
                              ||||  ||   ||||||||||
                              TCGA  GT   CTCGGTCCCG
                                GC  GCGA_
GAM2279 KIF3C   3' CAGATGAGATGAGCCAGGG  13947   C  CAATTCA
                              CAG TGA    GAGCCAGGG
                              ||| |||    |||||||||
                              GTC ACT    CTCGGTCCC
                                T  CTA____
GAM2279 MAP3K7  3' CAGTTGGCATTCAGAAC    17270   C  ACA
                              CAG TG  ATTCAGAGC
                              ||| ||  |||||||||
                              GTC AC  TAAGTCTTG
                                A  CG_
GAM2279 MSR1    3' AGCTGAAATTACAGCCAGGG  14656     C  CAG
                              AGCTGA AATT  AGCCAGGG
                              |||||| ||||  ||||||||
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                                TCGACT TTAA   TCGGTCCC
                                   _   TG_
GAM2279  PIM2     5'  CAGCTGGGGAGCCAGGG     41020       ACAATTCA
                                CAGCTG       GAGCCAGGG
                                ||||||       |||||||||
                                GTCGAC       CTCGGTCCC
                                   CC_______
GAM2279  PSMD2    3'  CAGCTGCAGTTCAGAGC     15834       A  A
                                CAGCTG CA TTCAGAGC
                                |||||| || ||||||||
                                GTCGAC GT AAGTCTCG
                                   _ C
GAM2279  RAMP3    3'  GCTGGTGCAGGAGCCAGGGC   25202     ACAATT  _
                                GCTG     CAG AGCCAGGGC
                                ||||     ||| |||||||||
                                CGAC     GTC TCGGTCCCG
                                  CAC___   C
GAM2279  SEPX1    3'  CAGTGACCAGGGCCAGGG    32266     C   AATT   A
                                CAG TGAC    CAG GCCAGGG
                                ||| ||||    ||| |||||||
                                GTC ACTG    GTC CGGTCCC
                                  _   ____  C
GAM2279  SIGLEC5  3'  GCTTGATGACAGTGCCAGGGC  19258     GACAATT   A
                                GCT      CAG GCCAGGGC
                                |||      ||| ||||||||
                                CGA      GTC CGGTCCCG
                                  ACTACT_  A
GAM2279  SLC25A1  3'  CAGCTGTGGTAGGCCAGGG   25600       ACAATTC  A
                                CAGCTG      AG GCCAGGG
                                ||||||      || |||||||
                                GTCGAC      TC CGGTCCC
                                   ACCA___  _
GAM2279  SREBF1   5'  CAGCTTATGGTAGACCAGGGC  45370      GACAATTC   G
                                CAGCT       AGA CCAGGGC
                                |||||       ||| |||||||
                                GTCGA       TCT GGTCCCG
                                   ATACCA__  _
GAM2279  STX1A    3'  CAGGTGGCAGCAGCCAGGG   21410     C  ACAATT  _
                                CAG TG     CAG AGCCAGGG
                                ||| ||     ||| ||||||||
                                GTC AC     GTC TCGGTCCC
                                  C  C_____  G
GAM2279  TARBP2   5'  CAGCCGACGAGCTAGG      39526       AATTCA   C
                                CAGCTGAC     GAGC AGG
                                ||||||||     |||| |||
                                GTCGGCTG     CTCG TCC
                                   _______   A
GAM2279  WW45     5'  CAGCGACGCCGGGCCAGGG   34815     T   AAT  AGA
                                CAGC GAC   TC   GCCAGGG
                                |||| |||   ||   |||||||
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                                GTCG CTG   GG   CGGTCCC
                                  _  C__  CC_
GAM2280  BCRP2    3'  TGACTGCAACGCTGAAAAT   41654      __   G
                                TGGC  CGG GCTGAAAAT
                                ||||  ||| |||||||||
                                ACTG  GTT CGACTTTTA
                                  AC   G
GAM2280  DAAM2    3'  TGGCCAGATGTAGAAAAT    45183        GCT_
                                TGGCCGGG    GAAAAT
                                ||||||||    ||||||
                                ACCGGTCT    CTTTTA
                                     ACAT
GAM2281  ENTPD5   3'  CTAAATCTCTAGGCTCAAGTC  10351        GCGCGC
                                CTAAATC     GGGCTCAAGTC
                                |||||||     ||||||||||
                                GATTTAG     TCCGAGTTCAG
                                    AGA___
GAM2281  SCG3     5'  GCGCGCGGGAGTCAAGTC    29889        C_
                                GCGCGCGGG  TCAAGTC
                                |||||||||  |||||||
                                CGCGCGCCC  AGTTCAG
                                     TC
GAM2281  TNFRSF10B 3'  GCCCAAACAGGGCTCAAGT   19287    G __  _
                                GC C  GC GGGCTCAAGT
                                || |  || ||||||||||
                                CG G  TG CCCGAGTTCA
                                 G TT  T
GAM2281  ACADVL   5'  ACGCCCGCGTCCTGCA      6156          CGACA
                                ACGCCCGCGTCC     GCA
                                ||||||||||||     |||
                                TGCGGGCGCAGG     CGT
                                      A____
GAM2281  BMPR1B   5'  GCCCGCGTCCCGCGAG      10204         GACA  A
                                GCCCGCGTCCC    GC GAG
                                ||||||||||    || |||
                                CGGGCGCAGGG    CG CTC
                                      ____  _
GAM2281  CLDN5    5'  CGCCCGCGCTCCCGGC      17607        _    ACA
                                CGCCCGCG TCCCG   GC
                                |||||||| |||||   ||
                                GCGGGCGC AGGGC   CG
                                    G    ___
GAM2281  COL6A2   3'  GCCCGGGCTTTAGCAGAGG   38442      C  CCCGAC
                                GCCCG GT     AGCAGAGG
                                ||||| ||     ||||||||
                                CGGGC CG     TCGTCTCC
                                  C  AAA___
GAM2281  DNM2     5'  ACGCCCGCTCCCGGCTCG    22374        G    ACA  AGA
                                ACGCCCGC TCCCG   GC   G
                                |||||||| |||||   ||   |
```

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                                TGCGGGCG AGGGC  CG  C
                                   _    ___ AG_
GAM2281 JAG2    5' CGCCCGCGCTCCCGGCA    13712        _    ACA
                                CGCCCGCG TCCCG  GCA
                                |||||||| |||||  |||
                                GCGGGCGC AGGGC  CGT
                                    G   ___
GAM2281 MAP1B   5' GCTCCTGGGACAGCAGAG   25396   G  C__
                                GC TCC  GACAGCAGAG
                                || |||  ||||||||||
                                CG AGG  CTGTCGTCTC
                                 _  ACC
GAM2281 SLC18A3 5' CGCTGGCGTCCCGCAGTGCAGA 16827    CC      A __
           GG                    CGC  GCGTCCCG CA  GCAGAGG
                                ||| |||||||| ||  |||||||
                                GCG  CGCAGGGC GT  CGTCTCC
                                  AC      _ CA
GAM2281 SUFU    3' GCCTGTGTGTGCAGCAGAGG  32090    CGC  CCCGA
                                GCC  GT   CAGCAGAGG
                                |||  ||   |||||||||
                                CGG  CA   GTCGTCTCC
                                 A__  CACAC
GAM2281 SURF6   3' ACGTGGCCCGGCAGCAGAGG  27585     __   A
                                GCGT  CCCG CAGCAGAGG
                                ||||  |||| |||||||||
                                TGCA  GGGC GTCGTCTCC
                                  CC   C
GAM2281 TMEFF2  5' CCCGCGGACGGCGGCAGCAGAG 32101      TCC__  A
           G                     CCCGCG   CG CAGCAGAGG
                                ||||||    || |||||||||
                                GGGCGC    GC GTCGTCTCC
                                   CTGCC  C
GAM2281 TRPM7   5' CCGGAGGCGGCAGCAGAGG   41616    CGTCC  A
                                CCG    CG CAGCAGAGG
                                |||    || |||||||||
                                GGC    GC GTCGTCTCC
                                  CTCC_  C
GAM2281 TRPV2   5' GCCGGCGCTGACAGCAGAGG  32026    C   CCC
                                GCC GCGT  GACAGCAGAGG
                                ||| ||||  ||||||||||
                                CGG CGCG  CTGTCGTCTCC
                                  C   A__
GAM2282 C18orf1 3' TCTATGCCATTTCTGTTAAAA 41231     AT     ATA
                                TCTAT  CATTTCT  TAAAA
                                |||||  |||||||  |||||
                                AGATA  GTAAAGA  ATTTT
                                   CG     CA_
GAM2282 IDE     3' TATAATATTTCTACATAA   22473     TC
                                TATA  ATTTCTATATAA
                                ||||  ||||||||||||
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                                ATAT  TAAAGATGTATT
                                  TA
GAM2282  CEACAM1   3'  AAATCTAGCTCTAGCCAT    11826        CA   AA
                                AAATCTAGC  TAG  TCAT
                                |||||||||  |||  ||||
                                TTTAGATCG  ATC  GGTA
                                     AG   __
GAM2282  FCRH1    3'  TCAAAATAAATAGAATCATAT  38109      TCTAGCC
                                TCAAA      ATAGAATCATAT
                                |||||      ||||||||||||
                                AGTTT      TATCTTAGTATA
                                   TATT___
GAM2282  MLLT2    3'  TCAAATCTAGCTGAGAACAC   25506         CAT    T
                                TCAAATCTAGC   AGAA CAT
                                ||||||||||   |||| |||
                                AGTTTAGATCG   TCTT GTG
                                      AC_   _
GAM2283  DTNA     3'  TTCCAATAAATGACAATTCGTT 37377         CAAAA  TT
                                TTCCAATAA     AT  TTCGTT
                                |||||||||     ||  ||||||
                                AAGGTTATT     TG  AAGCAA
                                     TAC__  TT
GAM2283  UTX      3'  TTCCAATAACACAAAATATGAG 41605          _     TTTTC
            GTT                   TTCCAATAACA AAAAT     GTT
                                |||||||||| |||||     |||
                                AAGGTTATTGT TTTTA     CAA
                                      G     TACTC
GAM2284  COX11    3'  TCCAGAGATGTTAGAGGAG    20422       CTTCAG  C
                                TCTAGAG      GT AGAGGAG
                                |||||||      || |||||||
                                AGGTCTC      CA TCTCCTC
                                    TA_____  A
GAM2284  RFX2     5'  TCTGGAGTTCGGGCCGGGAGT  8462      A   C   A    AGA
                                TCT GAG TTC GGTC   GGAGT
                                ||| ||| ||| ||||   |||||
                                AGA CTC AAG CCGG   CCTCA
                                  C   _   C    C__
GAM2284  CD97     3'  TAGCTTAAGAGGGAAG      38523         A   CACTCTA
                                TAGCTTGA AGG       AAG
                                |||||||| |||       |||
                                ATCGAATT TCC       TTC
                                     C   C_______
GAM2284  DMD      3'  GCATGAAAGAGTAAAGC     19684     T      CACTC
                                GC TGAAAGG     TAAAGC
                                || |||||||     ||||||
                                CG ACTTTCT     ATTTCG
                                 T      C_____
GAM2284  IGF1     3'  GCTTGAAAGGGATTTTAGAGCT 8342          CACTC  A
                                GCTTGAAAGG     TA AGCT
                                ||||||||||     || ||||
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                                CGAACTTTCC     AT TCGA
                                     CTAAA  C
GAM2284  SNL      3'  CAGTTTGAAAGGCAAGGGGGCT 16938     C         CTCTAAA
                                TAG TTGAAAGGCA       GCT
                                ||| ||||||||||       |||
                                GTC AACTTTCCGT       CGA
                                  A         TCCCC__
GAM2284  STK10    3'  CAGCTTGAAGGGATCTGGGGCT 25616          A  CAC   AAA
                                TAGCTTGAA GG   TCT   GCT
                                ||||||||| ||   |||   |||
                                GTCGAACTT CC   AGA   CGA
                                     C  T__   CCC
GAM2284  USP14    3'  TTGAAAGGCATTTCAACT    23120          CTCTAA
                                TTGAAAGGCA      AGCT
                                ||||||||||      ||||
                                AACTTTCCGT      TTGA
                                     AAAG__
GAM2285  CEP2     5'  CTGGCTACAGTGTGGGGGCACG 28435          CACCCAAA
                                CTGGCTACA       GGCACG
                                |||||||||       ||||||
                                GACCGATGT       CCGTGC
                                     CACACCC_
GAM2285  CLN6     3'  CTGGTTACACACCCACAC    32826      C       AAAG
                                CTGG TACACACCC    GCAC
                                |||| |||||||||    ||||
                                GACC ATGTGTGGG    TGTG
                                  A        _____
GAM2285  FAT2     3'  CCTGGCTACATACACTCTACAC 11073          C  CCAAAG
            A                    CCTGGCTACA AC      GCACG
                                ||||||||||| ||      |||||
                                GGACCGATGT TG      TGTGT
                                     A  TGAGA_
GAM2285  PYCR1    3'  CCTGGCTATGTCCCTGGC    43123         CACA   AAA
                                CCTGGCTA    CCC   GGC
                                ||||||||    |||   |||
                                GGACCGAT    GGG   CCG
                                     ACA_   A__
GAM2285  SLC35A3  3'  CTGGCTACCATCTAGCACA   29278         A  CCCAAA
                                CTGGCTAC CA      GGCACG
                                |||||||| ||      ||||||
                                GACCGATG GT      TCGTGT
                                     _  AGA___
GAM2285  TNFRSF1B 3'  TGGCTACACACACCCAC     9880           _  AAAGG
                                TGGCTACACAC CC     CAC
                                |||||||||||| ||     |||
                                ACCGATGTGTG GG     GTG
                                     T  _____
GAM2285  TRPM2    5'  CCTGGCCACATGCTTCCTCA   17690          CA___  _
                                CCTGGCTACA     CC CA
                                ||||||||||     || ||
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                                GGACCGGTGT    GG GT
                                      ACGAA  A
GAM2285  ADAR     3'  TCTTGGAGTCACAACCAAGAC  31910    CTAAA  GTGT
                                TCT    TCA   ACCAAGAC
                                |||    |||   ||||||||
                                AGA    AGT   TGGTTCTG
                                  ACCTC  GT__
GAM2285  AMPD3    3'  TCTAGGTGAAGAAACCAAGAC  7903     AATC_  TGT
                                TCTA    AG   ACCAAGAC
                                ||||    ||   ||||||||
                                AGAT    TC   TGGTTCTG
                                  CCACT  TT_
GAM2285  FGFRL1   3'  TCTTAAATATAAATACCAAGGC 34922    C    CAGT      A
             C                   TCT TAAAT   GTACCAAG CC
                                ||| |||||   |||||||| ||
                                AGA ATTTA   TATGGTTC GG
                                  _    TATT      C
GAM2285  FTH1     3'  TCTGATTCATCCCAAGACC   42793    AAA  GTGTA
                                TCT  TCA    CCAAGACC
                                |||  |||    ||||||||
                                AGA  AGT    GGTTCTGG
                                  CTA  AG___
GAM2285  KTN1     3'  TCTTTAAATCAGTAGTCTAACA 22556    C       _  AC__
             AG                   TCT TAAATCAGT GT    CAAG
                                ||| |||||||| ||   ||||
                                AGA ATTTAGTCA CA    GTTC
                                  A       T  GATT
GAM2285  PSMB8    3'  TCCCTGAGTCGGCCAAGAC   45549     AAATC  GTA
                                TCTCT    AGT  CCAAGAC
                                |||||    |||  |||||||
                                AGGGA    TCA  GGTTCTG
                                  C_____  GCC
GAM2285  ZNF135   3'  TCTCAGAATCAGTGAGAC    18333     TA      TACCA
                                TCTC  AATCAGTG    AGAC
                                ||||  ||||||||    ||||
                                AGAG  TTAGTCAC    TCTG
                                  TC      ______
GAM2286  SALL1    3'  TAAGCTTTCTTAGAACTCTAAA 16462      G     TACG
             G                    TAAGC TTCTTA    TTCTAAAG
                                ||||| ||||||    ||||||||
                                ATTCG AAGAAT    GAGATTTC
                                   A     CTT_
GAM2286  MUT      3'  TTAATTAATATATGGATTTTAT 7023      GA       C
             T                    TTAA  AATATATGGA TTTATT
                                ||||  |||||||||| ||||||
                                AATT  TTATATACCT AAATAA
                                  AA        A
GAM2286  SWAP70   3'  TAAGAGAAAAGGACTTTATT   43424      AATATAT
                                TAAGA      GGACTTTATT
                                |||||      ||||||||||
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                                ATTCT      CCTGAAATAA
                                   CTTTT__
GAM2287  BICD1    3'  TAAATGAACTGTAGCCATTT   11839          TT   G
                                TAAATGAATTGT  AGT ATTT
                                ||||||||||||  ||| ||||
                                ATTTACTTGACA  TCG TAAA
                                      __   G
GAM2287  IRAK4    3'  TGAGTTGTTTAGGAACCT    41462     A       TG
                                TGA TTGTTTAG  ATTT
                                ||| ||||||||  ||||
                                ACT AACAAATC  TGGA
                                  C       CT
GAM2287  PPP1R2   3'  AAATGAGTTTGTGATTTA    26415       ATT    A
                                AAATGA   GTTT GTGATTTA
                                ||||||   |||| ||||||||
                                TTTACT   CAAA CACTAAAT
                                   ___   _
GAM2287  RGS1     3'  TAAATGAATTATTTATTTATTT 16308            GTG
                                TAAATGAATTGTTTA   ATTT
                                ||||||||||||||   ||||
                                ATTTACTTAATAAAT   TAAA
                                         AAA
GAM2288  EPHB3    3'  AACAGACAAGTGTGAGG     20783         A    CT
                                AACAGACAA TGTGA  GG
                                |||||||| |||||  ||
                                TTGTCTGTT ACACT  CC
                                     C    __
GAM2288  EVA1     3'  TAACAGACAAATTGGC      40346          GTGAC
                                TAACAGACAAAT    TGGC
                                ||||||||||||    ||||
                                ATTGTCTGTTTA    ACCG
                                      _____
GAM2288  IFNAR1   3'  AACAGACAGGTGTGGC      8427         AAT   AC
                                AACAGACA   GTG  TGGC
                                ||||||||   |||  ||||
                                TTGTCTGT   CAC  ACCG
                                     C__   __
GAM2288  ITSN1    3'  AAACAAATGCATGCCTG     16649         GACTG
                                AGACAAATGT    GCCTG
                                ||||||||||    |||||
                                TTTGTTTACG    CGGAC
                                      TA___
GAM2288  OVOL1    5'  AACAGACAGGTGAGAGGC    21267        AAT    CT
                                AACAGACA   GTGA  GGC
                                ||||||||   ||||  |||
                                TTGTCTGT   CACT  CCG
                                     C__    CT
GAM2288  RRM2B    3'  TAACAAATAAAGTTATGGCCTG 42723        C   T  GAC
                                TAACAGA AAA GT   TGGCCTG
                                ||||||| ||| ||   |||||||
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                                ATTGTTT TTT CA   ACCGGAC
                                    A   _ AT_
GAM2288  TNR      3'  ACAGAAAATATTGGTTGGC    17620       C     GAC_
                                ACAGA AAATGT    TGGC
                                ||||| ||||||    ||||
                                TGTCT TTTATA    ACCG
                                  _     ACCA
GAM2288  TSN      3'  TAACACACAAATGTTATCTG   21496       G       GA_
                                TAACA ACAAATGT   CTG
                                ||||| ||||||||   |||
                                ATTGT TGTTTACA   GAC
                                   G       ATA
GAM2288  VIPR1    5'  CAGAGTGGCGCTGGCCTG    21505      CAAAT   A
                                CAGA    GTG CTGGCCTG
                                ||||    ||| ||||||||
                                GTCT    CGC GACCGGAC
                                  CAC__   _
GAM2289  GLRA3    3'  CTCATCTTTCTCATGACTT    41066       A       A
                                TTTAT TTTTCTCAT ACTT
                                ||||| |||||||| ||||
                                GAGTA GAAAGAGTA TGAA
                                  _       C
GAM2289  RFPL2    3'  CTTTATTTAACTCATAACTT   27351        A  TT
                                CTTTAT TT  CTCATAACTT
                                |||||| ||  ||||||||||
                                GAAATA AA  GAGTATTGAA
                                   _ TT
GAM2289  TAL1     3'  TACCTTTATGTTCTTTCCC    17288         A__
                                TACCTTTAT   TTTTCTC
                                |||||||||   |||||||
                                ATGGAAATA   GAAAGGG
                                     CAA
GAM2289  WDR4     5'  CCCCTTTATTTTCTTGTGACTT 38019       A       CATA
                                CCTTT TATTTTCT    ACTT
                                ||||| ||||||||    ||||
                                GGGGA ATAAAAGA    TGAA
                                   A       ACAC
GAM2290  CRP      3'  TGATGATGAGCACTCTGGA    43446         _____  C
                                TGATGGTGA    TC GGA
                                |||||||||    || |||
                                ACTACTACT    AG CCT
                                     CGTG  A
GAM2290  DOCK1    3'  TACGATGGCACATCCCGGA    10718         A__
                                TATGATGGTG   TCCGGA
                                ||||||||||   ||||||
                                ATGCTACCGT   GGGCCT
                                     GTA
GAM2290  EGFL5    5'  TATGATGGCTTTTCTCTTGGA  44534         GA___  C_
                                TATGATGGT    TC  GGA
                                |||||||||    ||  |||
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                                ATACTACCG    AG  CCT
                                     AAAAG  AA
GAM2290  H4F2     3'  TGATGGTAAGCTCCTGGA    18641        __  _
                                TGATGGTGA  TCC GGA
                                |||||||||  ||| |||
                                ACTACCATT  AGG CCT
                                     CG   A
GAM2290  MYL1     3'  ATGATGGTAAACAGATCTGGAT 38605       _____   C   III
                                ATGATGGT    GATC GGA   T
                                ||||||||    |||| |||   |
                                TACTACCA    CTAG CCT   A
                                    TTTGT    A   III
GAM2290  TFRC     3'  TATGATGGTTCACTCACGGA   17434        GA__  _
                                TATGATGGT    TC CGGA
                                |||||||||    || ||||
                                ATACTACCA    AG GCCT
                                     AGTG  T
GAM2290  CRP      3'  TGATGATGAGCACTCTGGA    43446        ____  C
                                TGATGGTGA    TC GGA
                                |||||||||    || |||
                                ACTACTACT    AG CCT
                                     CGTG  A
GAM2290  DOCK1    3'  TACGATGGCACATCCCGGA    10718         A__
                                TATGATGGTG   TCCGGA
                                ||||||||||   ||||||
                                ATGCTACCGT   GGGCCT
                                     GTA
GAM2290  EGFL5    5'  TATGATGGCTTTTCTCTTGGA  44534        GA___  C_
                                TATGATGGT    TC  GGA
                                |||||||||    ||  |||
                                ATACTACCG    AG  CCT
                                     AAAAG  AA
GAM2290  H4F2     3'  TGATGGTAAGCTCCTGGA    18641        __  _
                                TGATGGTGA  TCC GGA
                                |||||||||  ||| |||
                                ACTACCATT  AGG CCT
                                     CG   A
GAM2290  MYL1     3'  ATGATGGTAAACAGATCTGGAT 38605       _____   C   III
                                ATGATGGT    GATC GGA   T
                                ||||||||    |||| |||   |
                                TACTACCA    CTAG CCT   A
                                    TTTGT    A   III
GAM2290  TFRC     3'  TATGATGGTTCACTCACGGA   17434        GA__  _
                                TATGATGGT    TC CGGA
                                |||||||||    || ||||
                                ATACTACCA    AG GCCT
                                     AGTG  T
GAM2291  CLN5     3'  ACCATGAAAATGTCACTGAA   27077         CC  A
                                ACCGTGAAAATG  CA TGAA
                                ||||||||||||  || ||||
```

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                                TGGTACTTTTAC  GT ACTT
                                      A_  G
GAM2291  PCDH9    5'  GTGAAAATTTCCCCAGTG    44407        G__    A
                                GTGAAAAT   CCCA TG
                                ||||||||   |||| ||
                                CACTTTTA   GGGT AC
                                     AAG    C
GAM2291  TMSB4Y   5'  GTGAAAATGTCACAGCGC    20089         CC  ATGAA
                                GTGAAAATG  CA    CGC
                                |||||||||  ||    |||
                                CACTTTTAC  GT    GCG
                                     A_  GTC__
GAM2291  TNFRSF8  3'  CCGGAAGGGCCCAATG      10316     T   AAT
                                CCG GAA   GCCCAATG
                                ||| |||   ||||||||
                                GGC CTT   CGGGTTAC
                                  _   CC_
GAM2291  UBL1     3'  CCTGAAAATGCAATG       17840     G       CC
                                CC TGAAAATGC  AATG
                                || |||||||||  ||||
                                GG ACTTTTACG  TTAC
                                 _        __
GAM2292  KRT4     3'  GAAGATTCACCTGCAGAT    14005         A___
                                GAAGATTCA    CAGGT
                                |||||||||    |||||
                                CTTCTAAGT    GTCTA
                                     GGAC
GAM2292  KRT4     3'  GAAGATTCACCTGCAGAT    14005         A___
                                GAAGATTCA    CAGGT
                                |||||||||    |||||
                                CTTCTAAGT    GTCTA
                                     GGAC
GAM2293  B3GALT5  3'  GAGTACCGAGCCGATAACAT  37683    ATC   A
                                GA   ACC GAGCCGATAACAT
                                ||   ||| ||||||||||||||
                                CT   TGG CTCGGCTATTGTA
                                 CA_  _
GAM2293  BMX      5'  TAGACTCGCTAGAGCCGA     11890      A  ACC
                                TAGA TC   AGAGCCGA
                                ||||  ||   ||||||||
                                ATCT AG   TCTCGGCT
                                  G  CGA
GAM2293  FXYD6    3'  TAGGGTCCCAGAGCCCAT    35122     AA  A      G
                                TAG  TC CCAGAGCC AT
                                |||  || |||||||| ||
                                ATC  AG GGTCTCGG TA
                                  CC  _       G
GAM2293  HS2ST1   3'  TAAAATCATTAGAAACCAAT  29335         CC   _
                                TAGAATCA  AGAG CCGAT
                                ||||||||  |||| |||||
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                                ATTTTAGT  TCTT GGTTA
                                    AA    T
GAM2293  IGF2R    3'  TAGAACACCAGAGTCTATA    9339       T      CCG
                                TAGAA CACCAGAG   ATA
                                ||||| ||||||||   |||
                                ATCTT GTGGTCTC   TAT
                                   _       AGA
GAM2293  MSL3L1   3'  TAGATCACCAAAAATAACA    38602      A      GCC
                                TAGA TCACCAGA   GATAACA
                                |||| ||||||||   |||||||
                                ATCT AGTGGTTT   TTATTGT
                                  _      ____
GAM2293  NRAS     3'  AGAATAGAGCCGATAACAT    14846      CACC
                                AGAAT    AGAGCCGATAACAT
                                |||||    ||||||||||||||
                                TCTTA    TCTCGGCTATTGTA
                                  _____
GAM2293  PART1    3'  GATCACCAGAAAACA       32459    A       CCGAT
                                GA TCACCAGAG     AACA
                                || |||||||||     ||||
                                CT AGTGGTCTT     TTGT
                                  _       ______
GAM2293  PPP1CB   3'  TAGAATCACATCCAATA     15507         CAGAG
                                TAGAATCAC     CCGATA
                                |||||||||     ||||||
                                ATCTTAGTG     GGTTAT
                                     TA___
GAM2293  SLIT3    3'  GAATCACCAGGGGGTCCCACA  16867          AG___  G
                                GAATCACCAG     CC ATA
                                ||||||||||     || |||
                                CTTAGTGGTC     GG TGT
                                      CCCCA  G
GAM2293  B3GALT5  3'  GAGTACCGAGCCGATAACAT   37687    ATC   A
                                GA   ACC GAGCCGATAACAT
                                ||   ||| ||||||||||||||
                                CT   TGG CTCGGCTATTGTA
                                 CA_  _
GAM2293  BMX      5'  TAGACTCGCTAGAGCCGA     11890      A  ACC
                                TAGA TC   AGAGCCGA
                                |||| ||   ||||||||
                                ATCT AG   TCTCGGCT
                                  G  CGA
GAM2293  FXYD6    3'  TAGGGTCCCAGAGCCCAT    35122     AA  A      G
                                TAG  TC CCAGAGCC AT
                                |||  || |||||||| ||
                                ATC  AG GGTCTCGG TA
                                  CC  _       G
GAM2293  HS2ST1   3'  TAAAATCATTAGAAACCAAT   29335         CC   _
                                TAGAATCA  AGAG CCGAT
                                ||||||||  |||| |||||
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                                ATTTTAGT  TCTT GGTTA
                                    AA    T
GAM2293  IGF2R    3'  TAGAACACCAGAGTCTATA    9339       T      CCG
                                TAGAA CACCAGAG   ATA
                                ||||| ||||||||   |||
                                ATCTT GTGGTCTC   TAT
                                   _       AGA
GAM2293  MSL3L1   3'  TAGATCACCAAAAATAACA    38594      A      GCC
                                TAGA TCACCAGA   GATAACA
                                |||| ||||||||   |||||||
                                ATCT AGTGGTTT   TTATTGT
                                  _      ___
GAM2293  NRAS     3'  AGAATAGAGCCGATAACAT    14846      CACC
                                AGAAT    AGAGCCGATAACAT
                                |||||    ||||||||||||||
                                TCTTA    TCTCGGCTATTGTA
                                  _____
GAM2293  PART1    3'  GATCACCAGAAAACA       32459    A       CCGAT
                                GA TCACCAGAG     AACA
                                || |||||||||     ||||
                                CT AGTGGTCTT     TTGT
                                  _       ______
GAM2293  PPP1CB   3'  TAGAATCACATCCAATA     15507         CAGAG
                                TAGAATCAC     CCGATA
                                |||||||||     ||||||
                                ATCTTAGTG     GGTTAT
                                      TA___
GAM2293  SLIT3    3'  GAATCACCAGGGGGTCCCACA  16867          AG___  G
                                GAATCACCAG     CC ATA
                                ||||||||||     || |||
                                CTTAGTGGTC     GG TGT
                                      CCCCA  G
GAM2294  8D6A     3'  TGAGGGCTGGTGTGCCCG    32449    A   ACACC  G  C
                                C AGG     GC GG GTGCCCG
                                | |||     || || |||||||
                                A TCC     CG CC CACGGGC
                                 C  ______  A  A
GAM2294  ADRA1A   5'  AGGGGCGCGCGGGGCTGCCGG  37804     ACAC     C  GC
                                AGG    CGCGGG GT  CCGG
                                |||    |||||| ||  ||||
                                TCC    GCGCCC CG  GGCC
                                  CCGC     _  AC
GAM2294  CDKN1A   5'  CAGGGACACACGCGGGCACGCT 38502    A     _         CC
            TGG                    CA GGACAC CGCGGGCGTGC  GG
                                || |||||| ||||||||||  ||
                                GT CCTGTG GCGCCCGTGCG  CC
                                 C     T          AA
GAM2294  CTSS     3'  AGGCATGCACCACCGTGCTCGG 19845     A___     GGG    C
                                AGG    CACCGC   CGTGC CGG
                                |||    ||||||   ||||| |||
```

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                                TCC   GTGGTG  GCACG GCC
                                  GTAC    ___    A
GAM2294  DDX20   5'  AGGGCGCCGCGGGCCTGC   28506    ACA      G
                                AGG  CCGCGGGC TGC
                                |||  |||||||| |||
                                TCC  GGCGCCCG ACG
                                  CGC      G
GAM2294  DDX26   5'  GGACACCGGGGCCCGA     29095       C   GTGC
                                GGACACCG GGGC   CCGG
                                |||||||| ||||   ||||
                                CCTGTGGC CCCG   GGCT

                                   _   ____
GAM2294  E2F2    5'  AGGGCACCGCGACCCG     19867    A     GGCGT
                                AGG CACCGCG    GCCCG
                                ||| |||||||    |||||
                                TCC GTGGCGC    TGGGC
                                  C     _____
GAM2294  EHD3    3'  CAAGGACACTGCAGAGTCCCTG 31105        C    C  G  C
            G                    CAAGGACAC GCGGG GT CC GG
                                |||||||| ||||| || || ||
                                GTTCCTGTG CGTCT CA GG CC
                                     A    _  G  A
GAM2294  FBN2    3'  TGAGGACGCAGCGCACCCTGG  12807   A    ACC   G  TG  _
                                C AGGAC  GCGG CG  CCC GG
                                | |||||  |||| ||  ||| ||
                                A TCCTG  CGTC GC  GGG CC
                                 C   ___   _ GT   A
GAM2294  FCGRT   5'  GGACACCGCGGGCACG     19954           TGCC
                                GGACACCGCGGGCG   CG
                                ||||||||||||||  ||
                                CCTGTGGCGCCCGT   GC

                                      ____
GAM2294  GUCY1A2  5'  GGCGCTGCGGTCGCGCCCGG  9222    ACACC   G
                                GG    GCGG CGTGCCCGG
                                ||    |||| |||||||||
                                CC    CGCC GCGCGGGCC
                                 GCGA_   A
GAM2294  HCN4    5'  AGGGGCGCGGCGCGCCGCCCGG 24218    ACAC    _   _
                                AGG   CGCGG GCGT GCCCGG
                                |||   ||||| |||| ||||||
                                TCC   GCGCC CGCG CGGGCC
                                  CC__    G   G
GAM2294  HIP1    3'  AGGCATGCGCCACTGTGCCCGG 23749    A  CC   G_ _
                                AGG CA  GCG  GC GTGCCCGG
                                ||| ||  |||  || ||||||||
                                TCC GT  CGC  TG CACGGGCC
                                  _ A_  GG  A
GAM2294  ICMT    3'  GGATTACAGGCGTGCCCGG   29654    CACC
                                GGA   GCGGGCGTGCCCGG
                                |||   ||||||||||||||
```

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                                CCT   TGTCCGCACGGGCC
                                  AA__
GAM2294 ILVBL   5' GGAGCGTGGCCGTGCCCGG   27769    CAC  C  G
                                GGA   CG GG CGTGCCCGG
                                |||   || || |||||||||
                                CCT   GC CC GCACGGGCC
                                  C__  A  G
GAM2294 MAP3K5  5' AGGGCACGCCGCTGCCCGG   25435    A   C  GG  G
                                AGG CAC GC  GC TGCCCGG
                                ||| ||| ||  || |||||||
                                TCC GTG CG  CG ACGGGCC
                                  C   _  G_  _
GAM2294 MGEA5   5' CAGGGACCCGAATGCCCG    29211    A   A  CGGGC
                                CA GGAC CCG    GTGCCCG
                                || |||| |||    |||||||
                                GT CCTG GGC    TACGGGC
                                 C    _  T_____
GAM2294 NCAM2   3' CAAAGACACTGCGACGATTTGG 21223        C   G  TGCCC
                                CAAGGACAC GCGG CG    GG
                                ||||||||| |||| ||    ||
                                GTTTCTGTG CGCT GC    CC
                                     A   _  TAAA_
GAM2294 NFATC2  5' GGACGCACGCCGGGTCCGG   29588     AC_  G  C  GC
                                GGAC   CGC GG GT  CCGG
                                ||||   ||| || ||  ||||
                                CCTG   GCG CC CA  GGCC
                                  CGT   G  _  __
GAM2294 NLGN2   3' GGGGGCCGGCGTGTGCCCGG   44759    ACACC  G   __
                                GG    GC GGC  GTGCCCGG
                                ||    || |||  ||||||||
                                CC    CG CCG  CACGGGCC
                                 CC___  G   CA
GAM2294 NTSR1   5' AGGACAGCGCCCAGCCCGG   14875      C   GGG  T
                                AGGACA CGC   CG GCCCGG
                                |||||| |||   || ||||||
                                TCCTGT GCG   GT CGGGCC
                                   C   G__  _
GAM2294 OTOF    3' GGAAGACAGGGTGTGCCCGG   22059   A    CCGC   C
                                C AGGACA    GGG GTGCCCGG
                                | ||||||    ||| ||||||||
                                C TTCTGT    CCC CACGGGCC
                                 C      _____   A
GAM2294 OTP     3' GGGGACCGCGGGCGATCG    36998    AC       TGCC
                                GG  ACCGCGGGCG    CG
                                ||  ||||||||||    ||
                                CC  TGGCGCCCGC    GC
                                 CC         TA__
GAM2294 PTPN7   3' AGGGGCGGCGTGCCG      38709     ACACC   G     C
                                AGG    GCGG CGTGCC G
                                |||    |||| |||||| |
```

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                                TCC    CGCC GCACGG C
                                  C____   _     A
GAM2294  RAB26    3'  CAAGGTGGAGCGTGCTCG    30743      ACACCGC      C
                                CAAGG      GGGCGTGC CG
                                |||||      |||||||| ||
                                GTTCC      CTCGCACG GC
                                   AC_____       A
GAM2294  RB1CC1   5'  GGACACCGCCGCGGCTTGG   31316        GG   T  CC
                                GGACACCGC  GCG GC  GG
                                |||||||||  ||| ||  ||
                                CCTGTGGCG  CGC CG  CC
                                      G_   _ AA
GAM2294  RNF4     3'  GGACAAAAGGTGGTGTGCCCGG 16356      CCGCG_  C
                                GGACA     GG GTGCCCGG
                                |||||     || ||||||||
                                CCTGT     CC CACGGGCC
                                   TTTCCA  A
GAM2294  SEZ6L    5'  GGGGGGCAAGGCGTGCTTGG   34424    ACACC  _     CC
                                GG    GCG GGCGTGC  GG
                                ||    ||| |||||||  ||
                                CC    CGT CCGCACG  CC
                                 CCC__   T      AA
GAM2294  SKI      3'  AGGCGGCACGTGTGCCCG    16730     ACAC   GGC
                                AGG   CGCG   GTGCCCG
                                |||   ||||   |||||||
                                TCC   GTGC   CACGGGC
                                  GCC_   A__
GAM2294  SLC22A2  5'  AGGCTGCCCGACGTGCCCGG   40517     ACA  G   G
                                AGG   CC CGG CGTGCCCGG
                                |||   || ||| |||||||||
                                TCC   GG GCT GCACGGGCC
                                  GAC  _   _
GAM2294  SOX11    3'  GGGGCGCGCGTGCCCG      17028     ACACC   G
                                GG    GCG GCGTGCCCG
                                ||    ||| |||||||||
                                CC    CGC CGCACGGGC
                                 C____   G
GAM2294  SYBL1    5'  TGAGGGCGCGCGGGCTCG    24849   A  ACACC   G   T  C
                                C AGG    GCG GCG GC CG
                                | |||    ||| ||| || ||
                                A TCC    CGC CGC CG GC
                                 C  _____   G   C  A
GAM2294  TBL1X    5'  GGCGGCGCCGCGCGCCCG    24890    ACAC   GG
                                GG   CGC  GCGTGCCCG
                                ||   |||  |||||||||
                                CC   GCG  CGCGCGGGC
                                 GCC_   G_
GAM2294  TXNRD2   3'  GGCGCACCGTGTGCCCTGG   26977    A_    CGGGC     _
                                GG  CACCG    GTGCCC GG
                                ||  |||||    |||||| ||
```

```
                                CC  GTGGC    CACGGG CC
                                 GC    A____     A
GAM2294  USP6    5'  TGAGGACGTGCACAGGGCCTGG 45033   A    AC_    CGT   C
                                C AGGAC   CGCGGG   GCC GG
                                | |||||   ||||||   ||| ||
                                A TCCTG   GTGTCC   CGG CC
                                 C    CAC     ___   A
GAM2294  COLQ    5'  TGCTGTTTGCGTGCGC     38696     C     CACGGCC
                                TGC TGTTTGC      GCGC
                                ||| |||||||      ||||
                                ACG ACAAACG      CGCG
                                  _      CA_____
GAM2294  FZD3    5'  GCCTGCCGCGGGCGGCCGCGCG 32630       T  CA_
                                GCCTGTT GC   CGGCCGCGCG
                                ||||||| ||   ||||||||||
                                CGGACGG CG   GCCGGCGCGC
                                    _ CCC
GAM2294  HDAC4   5'  GCCTCCCACGGCCGCGCG    25770     G
                                GTTT CCACGGCCGCGCG
                                |||| ||||||||||||
                                CGGA GGTGCCGGCGCGC
                                  G
GAM2295  LNK     5'  CCAGCGCTTGACAGTTGCGGGA 24196        CC  __   A  A
            GGAT                  CTAGCGCT  GCG  TGCG GA GAT
                                |||||||  |||  |||| || |||
                                GGTCGCGA  TGT  ACGC CT CTA
                                     AC   CA   C  C
GAM2295  MLLT2   3'  CAGCGCTCTAGGCAATGGGGAG 25495       C__  _  C_
            A                   TAGCGCTC   GCG TG  GAGA
                                ||||||||   ||| ||  ||||
                                GTCGCGAG   CGT AC  CTCT
                                     ATC   T  CC
GAM2295  SGCB    3'  TAGGCTCTCTGAGAAGA    6928     C   CGCGTGC
                                TAG GCTC      GAGAAGA
                                ||| ||||      |||||||
                                ATC CGAG      CTCTTCT
                                  _   AGA____
GAM2295  AK3     3'  CTTTCATCCCAGGATGTC    30183        ___
                                CTTTCGTCC   GGTGTC
                                |||||||||   ||||||
                                GAAAGTAGG   CTACAG
                                     GTC
GAM2295  ATP11B  3'  CTTTGTCTGGTGTCAGTAC   44308     C  C      _
                                CTTT GTC GGTGTCGG AC
                                |||| ||| |||||||| ||
                                GAAA CAG CCACAGTC TG
                                  _  A       A
GAM2295  SMARCD2 3'  CCTTTGGTTCGGAAATGTC   16915      C  C  ___
                                CCTTT GT CGG   TGTC
                                ||||| || |||   ||||
```

```
                                GGAAA CA GCC   ACAG
                                  C  A   TTT
GAM2296 ASTN     3'  TCTGTTTGCTGACCTTTC    42953      CTCGG  CC
                                TCTG    GC  GACCTTTC
                                ||||    ||  ||||||||
                                AGAC    CG  CTGGAAAG
                                  AAA__  A_
GAM2296 B4GALT1  3'  CCTCTGCCTCTCTGATCTTTCC 11281       _  GGGCCC  C
                                CTTCTG CTC     GA CTTTCC
                                |||||| |||     || ||||||
                                GGAGAC GAG     CT GAAAGG
                                   G   AGA___  A
GAM2296 DPYSL3   5'  CTTCTGCTCCGGCTCGCC    10767         G   C  A
                                CTTCTGCTC GGC CG CC
                                ||||||||| ||| || ||
                                GAAGACGAG CCG GC GG
                                     G   A  _
GAM2296 GDI1     3'  CTTCTGCTTGGCTCACTTTTC  41013        CG   C G  C
                                CTTCTGCT  GGC C AC TTTC
                                ||||||||  ||| | || ||||
                                GAAGACGA  CCG G TG AAAG
                                     A_   A _  A
GAM2296 HSPA4    5'  CTACTGCTCGGGCTCGGGCC   44851    T        C  A_
                                CT CTGCTCGGGC CG  CC
                                || ||||||||| ||  ||
                                GA GACGAGCCCG GC  GG
                                 T         A  CC
GAM2296 MLLT7    3'  TTCTGCATAGACCTTTC     25536       TCGGGCCC
                                TTCTGC       GACCTTTC
                                ||||||       ||||||||
                                AAGACG       CTGGAAAG
                                   TAT_____
GAM2296 MTNR1B   3'  CTTCTGCCCCAGGCCTTTC   25552         _    CGACC
                                CTTCTGCTC GGGCC    TTTC
                                ||||||||| |||||    ||||
                                GAAGACGGG TCCGG    AAAG
                                     G    _____
GAM2296 ODF2     3'  CTGCTGCTTTTGGGACTTTTC  14928    T    CG_  CCC   C
                                CT CTGCT   GG   GAC TTTC
                                || |||||   ||   ||| ||||
                                GA GACGA   CC   CTG AAAG
                                 C    AAA  ___   A
GAM2296 OSBP     5'  TTCTCTCGGGCCTGTCATTC   14992      G       CGACCT
                                TTCT CTCGGGCC     TTC
                                |||| ||||||||     |||
                                AAGA GAGCCCGG     AAG
                                  _       ACAGT_
GAM2296 SERPINB6 5'  CTTCTGCTGGGAACGACCTTTC 21301         C   CC
                                CTTCTGCT GGG  CGACCTTTC
                                |||||||| |||  |||||||||
```

```
                                GAAGACGA CCC  GCTGGAAAG
                                     _  TT
GAM2296  SLC1A4   3'  TTCTGCTCAGGCTCATGTCC   16765          C  A__
                                TTCTGCTCGGGC CG   CC
                                |||||||||||| ||   ||
                                AAGACGAGTCCG GT   GG
                                      A  ACA
GAM2296  TRIM9    5'  CTTCCGCTCGGGTTTGAC    31562          CCC
                                CTTCTGCTCGGG   GAC
                                ||||||||||||   |||
                                GAAGGCGAGCCC   CTG
                                      AAA
GAM2296  AVP      5'  GGGCAGGGGACAGCCAGG    7939         ATCCTT  C  G
                                GGGCAGGG     CA GC CGGG
                                ||||||||     || || ||||
                                CCCGTCCC     GT CG GTCC
                                     CT_____  _  _
GAM2296  CLCN4    5'  AGGCAGGGAGGTGTGCGCGGG  12276         TCCTTCAC
                                GGGCAGGGA       GCGCGGG
                                |||||||||       |||||||
                                TCCGTCCCT       CGCGCCC
                                     CCACA___
GAM2296  EPHB1    5'  GGGCAGGAGTGTGTGCGCGTGG 20775         ATCCTTCA   C
           G                     GGGCAGGG       CGCG GGG
                                ||||||||       |||| |||
                                CCCGTCCT       GCGC CCC
                                     CACACAC_   A
GAM2296  GSTM3    5'  GGGCGGGGCCCACGCGCGGG   42763     A  AT  TTC
                                GGGC GGG  CC   ACGCGCGGG
                                |||| |||  ||   |||||||||
                                CCCG CCC  GG   TGCGCGCCC
                                  _   CG  ___
GAM2296  ILF1     5'  GGGCGGGAGCACGCGCGG    21116     A   TCCTT
                                GGGC GGGA    CACGCGCGG
                                |||| ||||    |||||||||
                                CCCG CCCT    GTGCGCGCC
                                  _    C____
GAM2296  MAPRE3   3'  GGGCAGGGGGCCTTGGG     29535        AT   CACGCGC
                                GGGCAGGG  CCTT      GGG
                                ||||||||  ||||      |||
                                CCCGTCCC  GGAA      CCC
                                     CC   ________
GAM2296  MKPX     5'  GGGCGGGGAGGAGGCGCGCGGG 33641     A   TCCTTCA
                                GGGC GGGA      CGCGCGGG
                                |||| ||||      ||||||||
                                CCCG CCCT      GCGCGCCC
                                  C   CCTCC__
GAM2296  PCSK1N   3'  GGGTAGGGATCCTCG      29977     C       TCACGCG
                                GGG AGGGATCCT      CG
                                ||| |||||||||      ||
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                                CCC TCCCTAGGA      GC
                                  A       ________
GAM2296  PTGDS    3'  GGGCAGGGGTGCTTTGGCGGG  9633         ATC   CACGC
                                GGGCAGGG   CTT    GCGGG
                                ||||||||   |||    |||||
                                CCCGTCCC   GAA    CGCCC
                                    CAC   AC___
GAM2296  SORD     3'  GGGAGGGGGTCCTTCACTTGG  16966     C   A_      GCGC
                                GGG AGGG  TCCTTCAC   GG
                                ||| ||||  ||||||||   ||
                                CCC TCCC  AGGAAGTG   CC
                                  _   CC       AA__
GAM2296  SPOCK    5'  AGGCAGGGGTCCTTGGATGGG  41731        A    CACGCGC
                                GGGCAGGG TCCTT      GGG
                                |||||||| |||||      |||
                                TCCGTCCC AGGAA      CCC
                                    C    CCTA___
GAM2297  ECGF1    5'  TCGCGCACAGCGGTCCACTGC  12641        C  C  ACA
                                TCGCGCACA GC GT   CACTGC
                                ||||||||| || ||   ||||||
                                AGCGCGTGT CG CA   GTGACG
                                     _ C  G__
GAM2297  ITGA5    3'  ACACAGCCTCACACTGC     41494      C   GTA
                                GCACA GCC   CACACTGC
                                ||||| |||   ||||||||
                                TGTGT CGG   GTGTGACG
                                  _   A__
GAM2297  ITGAM    3'  CGCACACATGCACACACTGC   43511        CC
                                CGCACACG  GTACACACTGC
                                ||||||||  ||||||||||
                                GCGTGTGT  CGTGTGTGACG
                                    A_
GAM2297  PTGS1    5'  GCGTGCGCCTCGCACACTGC   38737     CACA    GTA
                                GCG    CGCC   CACACTGC
                                |||    ||||   ||||||||
                                CGC    GCGG   GTGTGACG
                                  AC__    AGC
GAM2297  STX1A    3'  GCTCCTCGCTGTGCACACTGC  21412    GCACA   C  A
                                GC     CGC GT CACACTGC
                                ||     ||| || ||||||||
                                CG     GCG CA GTGTGACG
                                 AGGA_   A  C
GAM2297  TCF12    3'  GCAGAAGCGACACACTGC     17341     CAC  C T
                                GCA   GC G ACACACTGC
                                |||   || | |||||||||
                                CGT   CG C TGTGTGACG
                                  CTT  _ _
GAM2297  ADAR     3'  TGCCCTCTGAGGGGGAAAAGG  31912         AC  A  TGC
                                TGCCCTCT  GG GG   GGG
                                ||||||||  || ||   |||
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                                ACGGGAGA  CC CC   TCC
                                    CT  C  TTT
GAM2297 IL16     5'  CGCCCTCTGTGGAGGACTTGG  21097        AC    T  GG
                                TGCCCTCT  GGAGG GC  GG
                                ||||||||  ||||| ||  ||
                                GCGGGAGA  CCTCC TG  CC
                                    CA    _  AA
GAM2298 KAL1     3'  TAATCTTAGTTGATTTTTC   6872       AC
                                TAAT  TAGTTGATTTTTC
                                ||||  ||||||||||||
                                ATTA  ATCAACTAAAAAG
                                  GA
GAM2298 NAT2     3'  CAATATTAAATGTTTTCTAGCA 6143       C   T  AT
                                TAATA TAG TG  TTTTCTAGCA
                                ||||| ||| ||  ||||||||||
                                GTTAT ATT AC  AAAAGATCGT
                                   A   T  __
GAM2298 ASTN     3'  GTGTGTGCACACGTGTGTGTG  42951     _  ATCTA  A
                                GTGT TG    GT TGTGTG
                                |||| ||    || ||||||
                                CACA AC    CA ACACAC
                                  C  GTGTG  C
GAM2298 CRTL1    5'  GTGTGTGTGAGTGTGTGTGCA  12451     _  ATCT   A
                                GTGT TG    AGT TGTGTGCA
                                |||| ||    ||| ||||||||
                                CACA AC    TCA ACACACGT
                                  C  AC__   C
GAM2298 ELAVL4   3'  TCGTGTATGTGTGTGTGTG   34983      TGATCTA  A
                                TCGTGT      GT TGTGTG
                                ||||||      || ||||||
                                AGCACA      CA ACACAC
                                   TACA___  C
GAM2298 F7       3'  GTGTGCGCACTTGGTGTGTGTG 6559      _  AT  A_  A
                                GTGT TG  CT  GT TGTGTG
                                |||| ||  ||  || ||||||
                                CACA GC  GA  CA ACACAC
                                  C  GT  AC  C
GAM2298 GABRB3   3'  GTGTGTCTGTGTGTGTA    34875     T A   A  A
                                GTGT G TCT GT TGTGTG
                                |||| | ||| || ||||||
                                CACA C AGA CA ACACAT
                                  _ _   _  C
GAM2298 ITGAM    3'  GTGTGTGTGTATGTGTG    43516     _  ATCTA
                                GTGT TG    GTATGTGTG
                                |||| ||    |||||||||
                                CACA AC    CATACACAC
                                  C  A____
GAM2298 MUC4     3'  TCGTGTGTGTGTGTG      39677       TGATCTA  A
                                TCGTGT      GT TGTGTG
                                ||||||      || ||||||
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                                AGCACA      CA ACACAC
                                  _______ C
GAM2298 PAX6     5' GTGTTAATGTGTGTGTGC    11485        CTA  A
                                GTGTTGAT   GT TGTGTGC
                                ||||||||   || |||||||
                                CACAATTA   CA ACACACG
                                   ___ C
GAM2298 RARA     3' GTGTTTGTGTGTGTGC      9714       GATCTA  A
                                GTGTT     GT TGTGTGC
                                |||||     || |||||||
                                CACAA     CA ACACACG
                                  A_____ C
GAM2298 SORCS3   3' GTGTTGTATGTGTG       31425      GATCTA
                                GTGTT     GTATGTGTG
                                |||||     |||||||||
                                CACAA     CATACACAC

                                  _______
GAM2299 IHPK3    3' TCTGCCATATATAGAGAT    38375        _ C
                                TTTGTCGT TA AGAGAT
                                |||||||| || ||||||
                                AGACGGTA AT TCTCTA
                                     T  A
GAM2299 AK3      3' CAGACCAGCAGTTTAATAA   30179     AC  TG     C
                                TAG  GC  GTAGTT AATAA
                                |||  ||  |||||| |||||
                                GTC  TG  CGTCAA TTATT
                                  __ GT     A
GAM2299 PAICS    3' TCTGGACCTAATAATTCAATA  26983     A   G
                                TCT GAC CTGGTAGTTCAATA
                                ||| ||| ||||||||||||||
                                AGA CTG GATTATTAAGTTAT
                                  C  _
GAM2300 EGLN2    5' TCACCACTGCCACTGCTGCAGC 32762        C_   AGCA
           T                     TTACCAC  CCG    CTGCAGCT
                                |||||||  |||   ||||||||
                                AGTGGTG  GGT   GACGTCGA
                                    AC   GAC_
GAM2300 PSCD4    3' TCACCACCTCGCAAGGCAGCTA 30130        CCGA   CT
                                TTACCACC    GCA  GCAGCTA
                                ||||||||    |||  |||||||
                                AGTGGTGG    CGT  CGTCGAT
                                     AG__   TC
GAM2300 PTGFRN   3' TTACCACCATCGAGTGTCTG   42607        C_   CA_
                                TTACCACC  CGAG   CTG
                                ||||||||  ||||   |||
                                AATGGTGG  GCTC   GAC
                                     TA    ACA
GAM2300 SHC1     3' CCACCCCGGGCCTAGGCT    16697        A  A   CA
                                CCACCCCG GC CTG  GCT
                                |||||||| || |||  |||
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                                GGTGGGGC CG GAT  CGA
                                     C  _  C_
GAM2300  SLC21A9  3'  TTACTGCTCCCAGCACTA    28572      CAC_  G
                                TTAC   CCC AGCACTG
                                ||||   ||| |||||||
                                AATG   GGG TCGTGAT
                                  ACGA  _
GAM2300  ABR      3'  TGGCTGCAGCCTACCTGCCTGG 35021      A        __ _
            ACAC                   TGGC TGCAGCCTGCT  CC GGACAC
                                |||| ||||||||||  || ||||||
                                ACCG ACGTCGGATGG  GG CCTGTG
                                  _        AC  A
GAM2300  FCAR     3'  TGTGTGCAGCCTGGCCAG    39339    GCA       CT
                                TG   TGCAGCCTG  CCGG
                                ||   |||||||||  ||||
                                AC   ACGTCGGAC  GGTC
                                 AC_       C_
GAM2300  GLI4     3'  TGGCATGCGGTGCTGGGCA   39692        AGCC   CC  A
                                TGGCATGC   TGCT  GG CA
                                ||||||||   ||||  || ||
                                ACCGTACG   ACGA  CC GT
                                     CC__   __ C
GAM2300  NCALD    3'  GGCATGCAGTCCTCTGG     36766         _  G  CC
                                GGCATGCAG CCT CT  GG
                                ||||||||| ||| ||  ||
                                CCGTACGTC GGA GA  CC
                                     A  _ __
GAM2301  COL15A1  3'  TTCTAAACACTGACTTTATAAG 12361         G  T    C
            A                    TTCTGAACA TGG CTTTA AAGA
                                ||||||||| ||| ||||| ||||
                                AAGATTTGT ACT GAAAT TTCT
                                     G  _    A
GAM2301  HRH1     3'  TTCTGAACAATGGTTTCT    9258             C
                                TTCTGAACAGTGGT TTT
                                |||||||||||||| |||
                                AAGACTTGTTACCA AGA
                                       A
GAM2301  KLK10    3'  TGAACAGTGCAGACAAG     15775         GTCTTT
                                TGAACAGTG     ACAAG
                                |||||||||     |||||
                                ACTTGTCAC     TGTTC
                                     GTC___
GAM2301  TRPM8    3'  TTCTGAGTAGCTGGGATTACAG 35865       AC  _  TCT    A
            GA                     TTCTGA  AG TGG   TTACA GA
                                ||||||  || |||   ||||| ||
                                AAGACT  TC ACC   AATGT CT
                                   CA  G   CT_    C
GAM2301  COL15A1  3'  TTCTAAACACTGACTTTATAAG 12361         G  T    C
            A                    TTCTGAACA TGG CTTTA AAGA
                                ||||||||| ||| ||||| ||||
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                                AAGATTTGT ACT GAAAT TTCT
                                     G  _    A
GAM2301  HRH1    3'  TTCTGAACAATGGTTTCT   9258            C
                                TTCTGAACAGTGGT TTT
                                |||||||||||||| |||
                                AAGACTTGTTACCA AGA
                                       A
GAM2301  KLK10   3'  TGAACAGTGCAGACAAG    15775         GTCTTT
                                TGAACAGTG     ACAAG
                                |||||||||     |||||
                                ACTTGTCAC     TGTTC
                                     GTC___
GAM2301  TRPM8   3'  TTCTGAGTAGCTGGGATTACAG 35865       AC  _   TCT    A
           GA                     TTCTGA  AG TGG   TTACA GA
                                |||||| || |||   ||||| ||
                                AAGACT  TC ACC   AATGT CT
                                   CA  G   CT_    C
GAM2302  COL4A1  3'  TAAATTACTAATATATATA   12307          _
                                TAAATTACTA TATATATA
                                |||||||||| ||||||||
                                ATTTAATGAT ATATATAT
                                      T
GAM2302  HK3     3'  TAAATTATATATATATATT   13378        C
                                TAAATTA TATATATATATT
                                ||||||| ||||||||||||
                                ATTTAAT ATATATATATAA
                                     _
GAM2302  IFNGR2  3'  TAAATTACTAGGAGTATATTTA 24388          TATA
           CA                     TAAATTACTA    TATATTTACA
                                |||||||||    ||||||||||
                                ATTTAATGAT    ATATAAATGT
                                      CCTC
GAM2302  IGFBP1  3'  TTACTATATATATATACA    8251            TT
                                TTACTATATATATA  TACA
                                ||||||||||||||  ||||
                                AATGATATATATAT  ATGT
                                       __
GAM2302  NCSTN   3'  TCATTATATATATATTTACA  43942     C
                                TTA TATATATATATTTACA
                                ||| ||||||||||||||||
                                AGT ATATATATATAAATGT
                                  A
GAM2302  COL4A1  3'  TAAATTACTAATATATATA   12307          _
                                TAAATTACTA TATATATA
                                |||||||||| ||||||||
                                ATTTAATGAT ATATATAT
                                      T
GAM2302  HK3     3'  TAAATTATATATATATATT   13378        C
                                TAAATTA TATATATATATT
                                ||||||| ||||||||||||
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                                ATTTAAT ATATATATATAA
                                      _
GAM2302  IFNGR2   3'  TAAATTACTAGGAGTATATTTA 24388          TATA
           CA                   TAAATTACTA    TATATTTACA
                                ||||||||||    ||||||||||
                                ATTTAATGAT    ATATAAATGT
                                    CCTC
GAM2302  IGFBP1   3'  TTACTATATATATATACA    8251             TT
                                TTACTATATATATA  TACA
                                ||||||||||||||  ||||
                                AATGATATATATAT  ATGT
                                        __
GAM2302  NCSTN    3'  TCATTATATATATATTTACA  43942     C
                                TTA TATATATATATTTACA
                                ||| ||||||||||||||||
                                AGT ATATATATATAAATGT
                                  A
GAM2303  BBOX1    5'  TCAGGAGTAGATGCTGTCA   19602         C  C  _
                                TCAGGAGTA AT TTG CA
                                |||||||||  || ||| ||
                                AGTCCTCAT TA GAC GT
                                    C  C   A
GAM2303  FCRH3    5'  TCAGGAGTAATGTCTCCAAGAC 38114          CA_   G  CA
           T                     TCAGGAGTA   TCTT CA  ACT
                                 |||||||||   ||||  ||  |||
                                 AGTCCTCAT   AGAG GT  TGA
                                     TAC   _  TC
GAM2303  FGFR2    3'  GCATTCATCTTGCACGGCTA   35663     __         AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA         CC
GAM2303  KCNQ1    3'  AGGAAAAGCTTGCACAA     6881        TACAT
                                AGGAG     CTTGCACAA
                                |||||     |||||||||
                                TCCTT     GAACGTGTT
                                   TTC__
GAM2303  PRKCM    3'  AAGAGCACTAGGTCTTGCACAG 15636          A___        A
           CTA                    AGGAGTAC    TCTTGCACA CTA
                                  ||||||||    ||||||||| |||
                                  TTCTCGTG    AGAACGTGT GAT
                                      ATCC        C
GAM2303  BBOX1    5'  TCAGGAGTAGATGCTGTCA   19602         C  C  _
                                TCAGGAGTA AT TTG CA
                                |||||||||  || ||| ||
                                AGTCCTCAT TA GAC GT
                                    C  C   A
GAM2303  FCRH3    5'  TCAGGAGTAATGTCTCCAAGAC 38114          CA_   G  CA
           T                     TCAGGAGTA   TCTT CA  ACT
                                 |||||||||   ||||  ||  |||
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                                AGTCCTCAT   AGAG GT  TGA
                                     TAC    _ TC
GAM2303  FGFR2    3'  GCATTCATCTTGCACGGCTA   35663     __        AA
                                GTA  CATCTTGCAC  CTA
                                |||  ||||||||||  |||
                                CGT  GTAGAACGTG  GAT
                                  AA         CC
GAM2303  KCNQ1    3'  AGGAAAAGCTTGCACAA     6881       TACAT
                                AGGAG    CTTGCACAA
                                ||||||    |||||||||
                                TCCTT    GAACGTGTT
                                   TTC__
GAM2303  PRKCM    3'  AAGAGCACTAGGTCTTGCACAG 15636        A___       A
              CTA                   AGGAGTAC    TCTTGCACA CTA
                                ||||||||   ||||||||| |||
                                TTCTCGTG    AGAACGTGT GAT
                                     ATCC       C
GAM2304  DNASE1L1 3'  GCATATCTGCTGCACAAGTG   27497     CAAG    T
                                GCA    TGCT GCACAAGTG
                                |||    |||| |||||||||
                                CGT    ACGA CGTGTTCAC
                                  ATAG   _
GAM2304  IL1A     3'  TGCACAAGTGAGACAAGT     41677          CTTGC
                                TGCACAAGTG    ACAAGT
                                ||||||||||    ||||||
                                ACGTGTTCAC    TGTTCA
                                      TC___
GAM2304  IFNA17   3'  AGTACTAGTGCCTGCACA    34622      ATG
                                AGTA   AGTGCCTGCACA
                                ||||   ||||||||||||
                                TCAT   TCACGGACGTGT
                                  GA_
GAM2304  ZFY      3'  TATAGTAATGGATGTGAACAAG 18220          AG  CC  C
                                TATAGTAATG  TG  TG ACAAG
                                ||||||||||  ||  || |||||
                                ATATCATTAC  AC  AC TGTTC
                                      CT  __  T
GAM2305  C6       5'  TAGTACTTATCTACTACTATTT 45404        C    TCA
                                TAGTATT ATCT   TGCTATTT
                                |||||||  ||||   ||||||||
                                ATCATGA TAGA   ATGATAAA
                                    A    TG_
GAM2305  FGF5     3'  TAGCATTTCATTTTATGCTATT 37591        _   C  C
              TA                    TAGTATT CAT TT ATGCTATTTA
                                |||||||  |||  ||  ||||||||||
                                ATCGTAA GTA AA TACGATAAAT
                                    A   A  _
GAM2305  PRKAB1   3'  TAGCATTCATTTTTGGCT    26504          C  CAT
                                TAGTATTCAT TT   GCT
                                |||||||||  ||   |||
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                                ATCGTAAGTA AA   CGA
                                     A  AC_
GAM2305  PTTG1IP   3'  TAGCTATTCCCCAATGCTATTT 20290     _   A   TC
              A                   TAGT ATTC TCT  ATGCTATTTA
                                  |||| |||| |||  ||||||||||
                                  ATCG TAAG GGG  TACGATAAAT
                                    A   _  T_
GAM2305  SCGB3A2   3'  TAGTATTCATTGCT       38290          CTTCA
                                  TAGTATTCAT    TGCT
                                  ||||||||||    ||||
                                  ATCATAAGTA    ACGA
                                        _____
GAM2305  ROBO1     3'  TTGGTCATTAAAAACATC    39493            A
                                  TTGGTCATTAAAAA TATT
                                  |||||||||||||| ||||
                                  AACCAGTAATTTTT GTAG
                                        _
GAM2306  COL6A1    3'  AGGCAGCAGCGTTGTGTCCTGG 12327         TACATTTCAA
                                  AGGCAGCA        TCCTGG
                                  ||||||||        ||||||
                                  TCCGTCGT        AGGACC
                                      CGCAACAC__
GAM2306  OVOL1     3'  AGGCAGCTGGGAGGCAATCCTG 21270        ATACATTT
              G                    AGGCAGC       CAATCCTGG
                                  |||||||       |||||||||
                                  TCCGTCG       GTTAGGACC
                                     ACCCTCC_
GAM2306  PTPRM     3'  AGGCAGCAGCATTACT      15970        TA   TCAATC
                                  AGGCAGCA  CATT     CT
                                  ||||||||  ||||     ||
                                  TCCGTCGT  GTAA     GA
                                      C_   T_____
GAM2306  TEAD3     3'  AGGTAGATGAATCCTCAATCCT 17369     C  CATACA
              GG                    AGG AG     TTTCAATCCTGG
                                  ||| ||     ||||||||||||
                                  TCC TC     GGAGTTAGGACC
                                    A  TACTTA
GAM2306  BBOX1     5'  TCAGGAGTAGATGCTGTCA   19602         C  C  _
                                  TCAGGAGTA AT TTG CA
                                  |||||||| || ||| ||
                                  AGTCCTCAT TA GAC GT
                                       C  C   A
GAM2306  FCRH3     5'  TCAGGAGTAATGTCTCCAAGAC 38114         CA_   G  CA
              T                    TCAGGAGTA   TCTT CA  ACT
                                  |||||||||   |||| ||  |||
                                  AGTCCTCAT   AGAG GT  TGA
                                       TAC    _  TC
GAM2306  FGFR2     3'  GCATTCATCTTGCACGGCTA  35663     __        AA
                                  GTA  CATCTTGCAC  CTA
                                  |||  ||||||||||  |||
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                                CGT  GTAGAACGTG  GAT
                                  AA         CC
GAM2306  KCNQ1    3'  AGGAAAAGCTTGCACAA     6881        TACAT
                                AGGAG    CTTGCACAA
                                |||||    |||||||||
                                TCCTT    GAACGTGTT
                                   TTC__
GAM2306  PRKCM    3'  AAGAGCACTAGGTCTTGCACAG 15636         A___       A
             CTA                   AGGAGTAC    TCTTGCACA CTA
                                |||||||||    ||||||||| |||
                                TTCTCGTG    AGAACGTGT GAT
                                     ATCC        C
GAM2307  BHLHB3   3'  TGCGGGATGAGCAAAACAGGAA 36262     TA       __   AA
             CTC                   TGC  GATGAGCG  GCA  GAACTC
                                |||  ||||||||  |||  ||||||
                                ACG  CTACTCGT  TGT  CTTGAG
                                  CC       TT   C_
GAM2307  PRKAR1A  3'  TGCTAGATAGGAAAGCAG    15614         _____
                                TGCTAGAT    GAGCGG
                                ||||||||    ||||||
                                ACGATCTA    TTCGTC
                                     TCCT
GAM2307  SMARCD2  3'  TGTAGGAATGGCAAAGAACT   16922    C   AT   C
                                TG TAG  GAG GGCAAAGAACT
                                || |||  ||| ||||||||||
                                AC ATC  CTT CCGTTTCTTGA
                                 _  __   A
GAM2307  CRP      3'  TTTCTGGGGGTCATGGGT    43449         A_    TCT
                                TTTCTGGG  TTAT   GGT
                                ||||||||  ||||   |||
                                AAAGACCC  AGTA   CCA
                                     CC    C__
GAM2307  MAP3K13  3'  TTTCTAGGGGGTGGTAAA    21798         ATTATTC
                                TTTCTGGG      TGGTAAA
                                ||||||||      |||||||
                                AAAGATCC      ACCATTT
                                     CCC_____
GAM2307  NBS1     3'  TCTTTCCATTCTGGTGAAA   42989     GGGA        A
                                TCT    TTATTCTGGT AAA
                                |||    |||||||||| |||
                                AGA    GGTAAGACCA TTT
                                  AA__         C
GAM2307  NR2C2    3'  TCTGGGATTAACAGATAA    17675          TTCT
                                TCTGGGATTA    GGTAA
                                ||||||||||    |||||
                                AGACCCTAAT    CTATT
                                      TGT_
GAM2307  PTGES    3'  TTTCTGGGGTCAGTCTGA    22186         A   T
                                TTTCTGGG TTA TCTGG
                                |||||||| ||| |||||
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                                AAAGACCC AGT AGACT
                                     C   C
GAM2307  SLC2A5   3'  TTTCTGGAAAAGGATCTGGTAA 16770         TTAT_
                                TTTCTGGGA    TCTGGTAA
                                |||||||||    ||||||||
                                AAAGACCTT    AGACCATT
                                     TTCCT
GAM2307  TMEM2    3'  TTTCTGGGATTTTCCTGGCA  30158          A
                                TTTCTGGGATT TTCTGGTA
                                |||||||||||| ||||||||
                                AAAGACCCTAA AGGACCGT
                                      A
GAM2307  TPM1     3'  TTTCTGTGACAGTGGTAAAA  7489        G   TATTC
                                TTTCTG GAT    TGGTAAAA
                                |||||| |||    ||||||||
                                AAAGAC CTG    ACCATTTT
                                   A   TC___
GAM2308  ACATN    5'  TAGGTGCCCCCTGGAACGGC  21842           TAGA_
                                TAGGTGCCCCCT    GGT
                                ||||||||||||    |||
                                ATCCACGGGGGA    CCG
                                      CCTTG
GAM2308  CYP24    5'  GGTGCCTCCTTGCAC       8950        C    AGAG
                                GGTGCC CCTT   GTAC
                                |||||| ||||   ||||
                                CCACGG GGAA   CGTG
                                   A   _____
GAM2308  FCGR2A   3'  TAGGTATCTTCTTAGAAAGT  44280       CCCC     _
                                TAGGTG   CTTAGAG GT
                                ||||||   ||||||| ||
                                ATCCAT   GAATCTT CA
                                   AGAA      T
GAM2308  IL8RA    3'  AGGTGCCTTCTTAGGAGGT   8440        CC    _
                                AGGTGCC  CTTAG AGGT
                                |||||||  ||||| ||||
                                TCCACGG  GAATC TCCA
                                     AA    C
GAM2308  ITGA6    3'  TAGGTGCCTCCTCAGCTACAC  6833         C     AGG
                                TAGGTGCC CCTTAG   TACAC
                                |||||||| ||||||   |||||
                                ATCCACGG GGAGTC   ATGTG
                                     A     G__
GAM2308  LDHB     5'  TAGATGCCTTCTTGGT      14121         CC   AGA
                                TAGGTGCC  CTT   GGT
                                ||||||||  |||   |||
                                ATCTACGG  GAA   CCA
                                     AA   ___
GAM2308  MGAT5    5'  GATGCCCCCTTGGGGGTA    14473          AGA
                                GGTGCCCCCTT   GGTA
                                ||||||||||   ||||
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                                CTACGGGGGAA  CCAT
                                     CCC
GAM2308 MRC1    3' GGAGCTCCTTAAAATATGCC  14628   T CC     GTACA
                                GG GC  CCTTAGAG    CC
                                || ||  ||||||||    ||
                                CC CG  GGAATTTT    GG
                                 T A_      ATAC_
GAM2308 PTGS1   3' GGTGCCCCCTCTGTTGTA    38741         AGAG
                                GGTGCCCCCTT   GTA
                                ||||||||||   |||
                                CCACGGGGGAG   CAT
                                      ACAA
GAM2308 TIF1    3' TAAGTGCCTTCTTAATAGCA  41274       CC    A
                                TAGGTGCC  CTTAG GGTA
                                ||||||||  ||||| ||||
                                ATTCACGG  GAATT TCGT
                                     AA    A
GAM2308 XPC     3' GGTGCCCCTCTAGTGGGC    21551       C   A_
                                GGTGCCCC TTAG  GGT
                                |||||||| ||||  |||
                                CCACGGGG GATC  CCG
                                     A   AC
GAM2308 ATM     3' CCTCTTAGAAGCATATAAA   39632   _       CAT
                                CC CTTAGAGGCA   TATAGA
                                || ||||||||||   ||||||
                                GG GAATCTTCGT   ATATTT
                                 A       ____
GAM2308 CDH12   5' CCCCCTAGCGTTCATTGTAGAA 19773       AGGCA   A
                                CCCCTTAG    CATT TAGAA
                                ||||||||    |||| |||||
                                GGGGGATC    GTAA ATCTT
                                     GCAA_   C
GAM2308 CELL    3' CCCCTGTGGAGGGCATGGAAC  12222     TA_   CA   TATA
                                CCCCT   GAGG  CAT   GAAC
                                |||||   ||||  |||   ||||
                                GGGGA   CTCC  GTA   CTTG
                                   CAC   C_  C____
GAM2308 CRYZL1  3' CCCTTAAGATGTTAATTATAGA 23045     _ GGCAC
            A                    CCCTTA GA    ATTATAGAA
                                ||||||  ||    |||||||||
                                GGGAAT CT    TAATATCTT
                                   T  ACAAT
GAM2308 CTH     3' CCTTCAGAGGCAAACATAGA  12511   C       CAT
                                CC TTAGAGGCA   TATAGA
                                || |||||||||   ||||||
                                GG AGTCTCCGT   GTATCT
                                 A       TT_
GAM2308 IFNGR2  3' CCTTTTAGAGGCAGCAAAAGGG 24384   CC       _ TTATA
            AA                    CC  TTAGAGGCA CA    GAA
                                ||  |||||||||  ||    |||
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                                GG  AATCTCCGT GT    CTT
                                 AA       C  TTTCC
GAM2308  PMP22    3'  CCTTGGAGGCACAGAA      7160      A      TTATA
                                CCTT GAGGCACA    GAA
                                |||| ||||||||    |||
                                GGAA CTCCGTGT    CTT
                                  C      _____
GAM2308  PYGL     3'  CTAGAGACATTGTAGA      16054        CA  A
                                TTAGAGGCA  TT TAGA
                                |||||||||  || ||||
                                GATCTCTGT  AA ATCT
                                     __ C
GAM2309  AMFR     3'  TAGAAAGTATTACAAAGA    10080        _  TG
                                TAGAAAGT TTA  AAGA
                                |||||||| |||  ||||
                                ATCTTTCA AAT  TTCT
                                     T   GT
GAM2309  CHST1    3'  CAGGAAGGACACGAAGAT    18902    A   TT
                                TAG AAG  TATGAAGAT
                                ||| |||  |||||||||
                                GTC TTC  GTGCTTCTA
                                  C   CT
GAM2309  ESRRBL1  3'  TAGAAAGTTGCTCAGGAAGAT  32843        ___  T
                                TAGAAAGT   TTA GAAGAT
                                ||||||||   ||| ||||||
                                ATCTTTCA   AGT CTTCTA
                                     ACG   C
GAM2309  FSTL1    3'  GAAAGTTTTTTATGAAGAT   28215       ___
                                GAAAGTT   TATGAAGAT
                                |||||||   |||||||||
                                CTTTCAA   ATACTTCTA
                                    AAA
GAM2309  KIF5C    3'  TAGAAGTCCTATAAAGAT    21162      AG
                                TAGAA  TTTATGAAGAT
                                |||||  ||||||||||
                                ATCTT  GGATATTTCTA
                                   CA
GAM2309  SACM2L   3'  CAGAAGTCCATGGAGAT     38706      A     A
                                TAGAA GTTTATG AGAT
                                ||||| ||||||| ||||
                                GTCTT CAGGTAC TCTA
                                   _      C
GAM2309  SLC2A3   3'  TAAAAAGCCATTGAAGAT    27980        TA
                                TAGAAAGTT  TGAAGAT
                                |||||||||  |||||||
                                ATTTTTCGG  ACTTCTA
                                     TA
GAM2309  AXIN1    3'  GGGTCTTGGATGAAGAGGTG  41388    AA  AA      T
                                GG  CTT  ATGAAGAG TG
                                ||  |||  |||||||| ||
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                                CC  GAA  TACTTCTC AC
                                 CA   CC       C
GAM2309  CDR2     3'  GGAGCTTAAATGGAAGT     44022      A       AA
                                GGA CTTAAATG  GAGT
                                ||| ||||||||  ||||
                                CCT GAATTTAC  TTCA
                                  C       C_
GAM2309  DPYSL3   3'  GGAACTTACAATGAATGCTG   10772         _     GA
                                GGAACTTA AATGAA  GTTG
                                |||||||| ||||||  ||||
                                CCTTGAAT TTACTT  CGAC
                                     G     A_
GAM2309  MAN1A2   5'  GGCGACATCCGAGGAGTTGTAG 27456    AACTTAAA   A
                                GG       TGA GAGTTGTAG
                                ||       ||| |||||||||
                                CC       GCT CTCAACATC
                                 GCTGTAG_  C
GAM2309  MMP19    5'  GGAACTTAAGGGAGAAAAA   35594         AT__
                                GGAACTTAA    GAAGAG
                                |||||||||    ||||||
                                CCTTGAATT    CTTTTT
                                     CCCT
GAM2309  MMP3     3'  AGAGACTTAGGTGAAGAATTAT 14544    GA     AA
                                AG  ACTTA  TGAAGAGTTGT
                                ||  |||||  ||||||||||
                                TC  TGAAT  ACTTCTTAATA
                                 TC    CC
GAM2309  PLAG1    3'  AGCACCATGAAGAGTTGTA    15344    A   TAA
                                GG ACT   ATGAAGAGTTGTA
                                || |||   ||||||||||||
                                TC TGG   TACTTCTCAACAT
                                 G  ___
GAM2309  SMAC     5'  AGGAACCTAAATGAGGATGCAG 39892             A  GT
                                AGGAACTTAAATGA GA  TGTAG
                                |||||||||||||| ||  |||||
                                TCCTTGGATTTACT CT  ACGTC
                                         C  __
GAM2309  VSNL1    3'  GGAGCCTGGATGAAAAGTTG   18037     A   AA
                                GGA CTT  ATGAAGAGTTG
                                ||| |||  ||||||||||
                                CCT GGA  TACTTTTCAAC
                                  C   CC
GAM2309  ZNF146   3'  AGGAGTCTTAATATTAGTTGTA 28348      A_    ATGAAG
            G                    AGGA  CTTAA     AGTTGTAG
                                ||||  |||||     ||||||||
                                TCCT  GAATT     TCAACATC
                                  CA    ATAA__
GAM2310  ADCY7    3'  AATGTGTTTCTATGTTAT    9978        A  G
                                AATGTG TT TATGTTGT
                                |||||| || ||||||||
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                                TTACAC AA ATACAATA
                                   A  G
GAM2310  EIF4E    3'  AATGTAATTATGATGTTACATT 12690        TG    T
                                AATGTGAT  TATG TGTTACATT
                                ||||||||  |||| |||||||||
                                TTACATTA  ATAC ACAATGTAA
                                    __    T
GAM2310  HAO1     3'  ATGTGATTGGAAATCTACATT  32758         TATGTTG
                                ATGTGATTG      TTACATT
                                |||||||||      |||||||
                                TACACTAAC      GATGTAA
                                     CTTTA__
GAM2310  NPR2L    3'  TGTGATTGTGCCAC       27255         ATGTT
                                TGTGATTGT    GTTAC
                                |||||||||    |||||
                                ACACTAACA    CGGTG

                                _____
GAM2310  ADCY7    3'  AATGTGTTTCTATGTTAT    9978        A  G
                                AATGTG TT TATGTTGT
                                |||||| || ||||||||
                                TTACAC AA ATACAATA
                                   A  G
GAM2310  EIF4E    3'  AATGTAATTATGATGTTACATT 12690        TG    T
                                AATGTGAT  TATG TGTTACATT
                                ||||||||  |||| |||||||||
                                TTACATTA  ATAC ACAATGTAA
                                    __    T
GAM2310  HAO1     3'  ATGTGATTGGAAATCTACATT  32758         TATGTTG
                                ATGTGATTG      TTACATT
                                |||||||||      |||||||
                                TACACTAAC      GATGTAA
                                     CTTTA__
GAM2310  NPR2L    3'  TGTGATTGTGCCAC       27255         ATGTT
                                TGTGATTGT    GTTAC
                                |||||||||    |||||
                                ACACTAACA    CGGTG

                                _____
GAM2311  UTY      3'  CCAGTTGCTTGACATA      28310       _   ATTT
                                CTAGT GCT    TGACATA
                                ||||| |||    |||||||
                                GGTCA CGA    ACTGTAT
                                   A  ____
GAM2311  UTY      3'  CCAGTTGCTTGACATA      28310       _   ATTT
                                CTAGT GCT    TGACATA
                                ||||| |||    |||||||
                                GGTCA CGA    ACTGTAT
                                   A  ____
GAM2312  LAMC1    3'  TAAGGTATCATCTTGTAAA   14092      A       C
                                TAA GTATTATC TGTAAA
                                ||| |||||||| ||||||
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                                ATT CATAGTAG ACATTT
                                  C       A
GAM2312  LAMC1    3'  TAAGGTATCATCTTGTAAA   14092     A       C
                                TAA GTATTATC TGTAAA
                                ||| |||||||| ||||||
                                ATT CATAGTAG ACATTT
                                  C       A
GAM2313  BPHL     3'  TTTCAATATGTCATTATT    20260      TA
                                TTTCA  ATGTCATTATT
                                |||||  ||||||||||
                                AAAGT  TACAGTAATAA
                                   TA
GAM2313  HTR7     3'  TGTTTATTTCATCTCCATT   33389           AATG
                                TGTTTATTTCAT   TCATT
                                ||||||||||||   |||||
                                ACAAATAAAGTA   GGTAA
                                       GA__
GAM2313  PDGFRA   3'  TGTTTGTTTCTAATCCCATTAT 26289      A   A   G
              T                  TGTTT TTTC TAAT TCATTATT
                                |||||| |||| |||| ||||||||
                                ACAAA AAAG ATTA GGTAATAA
                                   C   _   G
GAM2313  PUM2     3'  GTTTATTTCATACAATGT    31663           __
                                GTTTATTTCATA  ATGT
                                ||||||||||||  ||||
                                CAAATAAAGTAT  TACA
                                       GT
GAM2313  CTBP2    5'  CAACTCTCAGATCAAAA     35599      AATA
                                CAACT   AGATCAAAA
                                |||||   |||||||||
                                GTTGA   TCTAGTTTT
                                   GAG_
GAM2313  FCMD     3'  TATTACAACTAATAATTACC  27523            G_
                                TATTACAACTAATAA  ATC
                                |||||||||||||||  |||
                                ATAATGTTGATTATT  TGG
                                       AA
GAM2313  NAGA     3'  TATTACAACTACTTGATTAAA 7043           ATAA  C
                                TATTACAACTA   GAT AAA
                                ||||||||||    ||| |||
                                ATAATGTTGAT   CTA TTT
                                      GAA_  A
GAM2313  PRKY     3'  TACAACTGGAGAAATCAAA   15705       AATA
                                TACAACT   AGATCAAA
                                |||||||   ||||||||
                                ATGTTGA   TTTAGTTT
                                    CCTC
GAM2314  ABL2     5'  TCCGCACCCGGCCTCCTCAC  28727     A  A    GC
                                TCCG AC CTGGC  CTCCTCAC
                                |||| || |||||  ||||||||
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                                AGGC TG GGCCG  GAGGAGTG
                                  G _    __
GAM2314 ASPH    3' CGAAATTCTATCCTCAC    37134     CA_  GCGCC
                                CGAA  CTG    TCCTCAC
                                ||||  |||    |||||||
                                GCTT  GAT    AGGAGTG
                                  TAA  _____
GAM2314 CNN1    5' TCTGCACACTCTTCCCTCCTCA 10541    CGA    GGCG
            CA                    TC  ACACT   CCTCCTCACA
                                ||  |||||   ||||||||||
                                AG  TGTGA   GGAGGAGTGT
                                 ACG    GAAG
GAM2314 GABRE   3' GAACACTGAGCATCAC     35075        _  CCTCC
                                GAACACTG GCG    TCAC
                                |||||||| |||    ||||
                                CTTGTGAC CGT    AGTG
                                     T  _____
GAM2314 HR      3' TCCTGATGCCACCCTCTCCTCA 32934    GAACAC  G   ___
            CA                    TCC     TG CGCC  TCCTCACA
                                |||     || ||||  ||||||||
                                AGG     AC GTGG  AGGAGTGT
                                  ACT___  G   GAG
GAM2314 HYAL2   5' CCCGGCTCAGCGCCTCCTC   37636     AACA  _
                                TCCG   CT GGCGCCTCCTC
                                ||||   || ||||||||||
                                GGGC   GA TCGCGGAGGAG
                                  C___  G
GAM2314 IL1F5   3' TCTGACATCACCACCTCCTCA  29359    C  A  CT G
                                TC GA CA  G CGCCTCCTCA
                                || || ||  | ||||||||||
                                AG CT GT  T GTGGAGGAGT
                                 A  _  AG G
GAM2314 MAGEA12  5' TCAGAACCTTGCCTCCTCAC  23852    C    A  GGC
                                TC GAAC CT   GCCTCCTCAC
                                || |||| ||   ||||||||||
                                AG CTTG GA   CGGAGGAGTG
                                 T    _  A__
GAM2314 MAGEA8   5' CGAACCTTGCCTCCTCACA   23846      A  GGC
                                CGAAC CT   GCCTCCTCACA
                                ||||| ||   ||||||||||
                                GCTTG GA   CGGAGGAGTGT
                                   _  A__
GAM2314 MBNL    5' GAAAGGGAATCTCCTCACA   34312     CACT  CGC
                                GAA   GG   CTCCTCACA
                                |||   ||   |||||||||
                                CTT   CC   GAGGAGTGT
                                  TC__  TTA
GAM2314 PMCHL1  3' GACACTGACGCTATTTCTTACA 36667    A       CTC__  C
                                GA CACTGGCGC    CT ACA
                                || |||||||||    || |||
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                                CT GTGACTGCG    GA TGT
                                 _       ATAAA  A
GAM2314  PRKAB1   5'  TCCCAACCGCTTCCTC     26506     G   ACTGG   C
                                TCC AAC     CGC TCCTC
                                ||| |||     ||| |||||
                                AGG TTG     GCG AGGAG
                                  G  _____   A
GAM2314  A1BG     3'  ACCAGATCACTAGCAAATTCGT 39084        A  GCAA
                                ACCGGG CG    CAAATTCGT
                                |||||| ||    |||||||||
                                TGGTCT GT    GTTTAAGCA
                                   A  GATC
GAM2314  B3GALT5  3'  AGGATGGTAACACCCATCA   37675     C  C    AA
                                GGGA GG AACA  TTCGTCA
                                |||| || ||||  |||||||
                                TCCT CC TTGT  GGGTAGT
                                  A  A   __
GAM2314  ITCH     5'  ACTCGGGGCGGCGGCGACTCCT 36452    _   A    AACAA    G
              CA                  AC CGGG CGGC     ATTC TCA
                                || |||| ||||     |||| |||
                                TG GCCC GCCG     TGAG AGT
                                 A    C    CCGC_    G
GAM2314  MUC4     3'  ACCGAGACGGTGGCCCAGCCGT 39655          CAACAAAT
              C                   ACCGGGACGG       TCGTC
                                ||||||||||       |||||
                                TGGCTCTGCC       GGCAG
                                      ACCGGGTC
GAM2315  AXIN1    5'  GGGCGCCGCAGGGGCCCA    41387    T      A   G
                                GG GCGCCGCA GGGT CG
                                || |||||||| |||| ||
                                CC CGCGGCGT CCCG GT
                                 _       C    G
GAM2315  DFNA5    3'  AGGGTCCCAAGCAGGGGTGTGT 20583     TGCG ___   A    C
              TA                  AGG    CC   GCA GGGTG GTTA
                                |||    ||   ||| ||||| ||||
                                TCC    GG   CGT CCCAC CAAT
                                  CA__  GTT   C    A
GAM2315  APG5L    3'  TCTGTATAAAACTACTCTG   22135     C   C_
                                TCTG ATA  GCTGCTCTG
                                |||| |||  |||||||||
                                AGAC TAT  TGATGAGAC
                                  A   TT
GAM2315  ATP7B    3'  CCGTTCTGCTGCTCT      6275      CA    ATACGC
                                CCG  TCTGC     TGCTCT
                                |||  |||||     ||||||
                                GGC  AGACG     ACGAGA
                                  A_    _______
GAM2315  C18orf1  3'  CCGCATCTGTGGGCACACCTG  41219         ____     G
                                CCGCATCT    GCATAC CTG
                                ||||||||    |||||| |||
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                              GGCGTAGA   CGTGTG GAC
                                  CACC    _
GAM2315 CENTD2   3' CCGCTTTCTGCTGTTCTG   31591     A_   ATACGC  C
                              CCGC  TCTGC     TG TCTG
                              ||||  |||||     || ||||
                              GGCG  AGACG     AC AGAC
                                AA    _______ A
GAM2315 F2RL3    5' CTGCACTCAGGCTGCTCTG   19517      AC__
                              CTGCAT   GCTGCTCTG
                              ||||||   |||||||||
                              GACGTG   CGACGAGAC
                                 AGTC
GAM2315 FACL2    3' CCTTATCTGCATGGTTCTG   34434    GC      ACGCTGC
                              CC  ATCTGCAT     TCTG
                              ||  ||||||||     ||||
                              GG  TAGACGTA     AGAC
                               AA      CCA____
GAM2315 GFRA1    5' CCGGACAGCTGTGCTGCTCTG 23565    C  CT  ATAC
                              CCG AT  GC   GCTGCTCTG
                              ||| ||  ||   |||||||||
                              GGC TG  CG   CGACGAGAC
                                C  T_  ACA_
GAM2315 GUCY1B2  3' CTGCATCTGCTGCGTTTCTG  19964      AC    ___
                              CTGCAT  GCTGC   TCTG
                              ||||||  |||||   ||||
                              GACGTA  CGACG   AGAC
                                 GA    CAA
GAM2315 HMGCS2   3' ATCTGCATGCACATTTCTG   24326       A   TGC
                              ATCTGCAT CGC   TCTG
                              |||||||| |||   ||||
                              TAGACGTA GTG   AGAC
                                   C   TAA
GAM2315 NHP2L1   3' GCTTCTGTCTGCTCTG     22681    A   CATACG
                              GC TCTG     CTGCTCTG
                              || ||||     ||||||||
                              CG AGAC     GACGAGAC
                               A   A_____
GAM2315 SLC6A6   3' CCCATCTGCATGCCT      16784    G      TACGC   T
                              CC CATCTGCA    TGC CT
                              || ||||||||    ||| ||
                              GG GTAGACGT    ACG GA
                                _      _____  _
GAM2315 TCF2     3' CATCTGCAGCTGGTTCTG    7844        TAC    C_
                              CATCTGCA   GCTG  TCTG
                              ||||||||   ||||  ||||
                              GTAGACGT   CGAC  AGAC
                                   ___    CA
GAM2315 TNFRSF8  3' CATTTGCATACACGTCTGA   10314     C       T C
                              CAT TGCATACGC G TCTGA
                              ||| ||||||||| | |||||
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                                GTA ACGTATGTG C AGACT
                                  A       _ _
GAM2315 ZNF79    5' CCGTTCTGCAGGGCTGCTCTGA 44353     CA     TAC
                                CCG  TCTGCA   GCTGCTCTGA
                                |||  ||||||   ||||||||||
                                GGC  AGACGT   CGACGAGACT
                                  A_     CC_
GAM2316 BACH2    3' TCACGTGATTCACATT      34805         GT
                                TCACGTGAT  TTATGTT
                                |||||||||  |||||||
                                AGTGCACTA  AGTGTAA
                                     __
GAM2316 DMD      3' CCATGTGATGTTTATGCT    19681     C
                                TCA GTGATGTTTATGTT
                                ||| ||||||||||||||
                                GGT CACTACAAATACGA
                                  A
GAM2316 DYRK1A   3' TCCATGCTGTTTATGTT     38999    A   A
                                TC CGTG TGTTTATGTT
                                || |||| ||||||||||
                                AG GTAC ACAAATACAA
                                  _   G
GAM2316 GNAZ     3' TCCGTAAATATTTATGTT    13185    A   _
                                TC CGTGA TGTTTATGTT
                                || ||||| ||||||||||
                                AG GCATT ATAAATACAA
                                  _    T
GAM2316 GRB14    3' TCACATGATAATGTT       21052         TTT
                                TCACGTGATG   ATGTT
                                ||||||||||   |||||
                                AGTGTACTAT   TACAA
                                     ___
GAM2316 IPP      3' TCACATAAAGTTTTATGTT   25322         TG_
                                TCACGTGA   TTTATGTT
                                ||||||||   ||||||||
                                AGTGTATT   AAATACAA
                                     TCA
GAM2316 SLC18A1  5' TCACTTGGAGCCCATGTT    16824     G  AT
                                TCAC TG  GTTTATGTT
                                |||| ||  |||||||||
                                AGTG AC  CGGGTACAA
                                  A  CT
GAM2316 ST7      3' TCACATGATTGTATGTT     30273         GTT
                                TCACGTGAT   TATGTT
                                |||||||||   ||||||
                                AGTGTACTA   ATACAA
                                     AC_
GAM2317 APCS     5' TTCCTGGCCTAGGGCTGT    11605     _       G C
                                TTCC GGCCTGGGG C GT
                                |||| ||||||||| | ||
```

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                                AAGG CCGGATCCC G CA
                                  A       _ A
GAM2317  ARNT2    3'  CTGCCGGCCCGGGTTGTC    31358    T       GGCC
                                CT CCGGCCTGGG   GTC
                                || ||||||||||   |||
                                GA GGCCGGGCCC   CAG
                                 C       AA__
GAM2317  CASP3    3'  CCTCCGGCTGGATGCCGTC   20295       C  GG
                                CTTCCGGC TGG  GCCGTC
                                |||||||| |||  ||||||
                                GGAGGCCG ACC  CGGCAG
                                     _  TA
GAM2317  CAV3     3'  CTTCTGTGGCTGGGCCGTC   37845     C__  CTGG
                                CTTC  GGC   GGGCCGTC
                                ||||  |||   ||||||||
                                GAAG  CCG   CCCGGCAG
                                  ACA  A___
GAM2317  DPH2L1   5'  CCTCTGCCAGGGCCGTC    10725     CG  TG
                                CTTC  GCC  GGGGCCGTC
                                ||||  |||  |||||||||
                                GGAG  CGG  TCCCGGCAG
                                  A_  __
GAM2317  DUSP7    5'  CTCCCGGCCTCCGT       42270        GGGGG
                                CTTCCGGCCT    CCGT
                                ||||||||||    ||||
                                GAGGGCCGGA    GGCA
                                      _____
GAM2317  DVL1     3'  CTTCCGGTCCCGTCGACGGCC  40410       _  _____ GGCCG
                                CTTCCGG CCTG    GG    T
                                ||||||| ||||    ||    |
                                GAAGGCC GGGC    CT    G
                                   A   AGIII  GCCGG
GAM2317  EGFL4    3'  CTTCCGGCCCGCACCAGTC   41568        GGG  _
                                CTTCCGGCCTG   GCC GTC
                                ||||||||||   ||| |||
                                GAAGGCCGGGC   TGG CAG
                                      G__   T
GAM2317  EN1      5'  TCTGGCCTGGATCGCTCGT   10924    C      G_ _
                                TC GGCCTGGG  GC CGT
                                || ||||||||  || |||
                                AG CCGGACCT  CG GCA
                                 A       AG  A
GAM2317  FBXL7    5'  CCTCCGGCCTGGAGAGGTC   29398           CC
                                CTTCCGGCCTGGGGG  GTC
                                ||||||||||||||  |||
                                GGAGGCCGGACCTCT  CAG
                                       C_
GAM2317  FZD2     3'  TTCCGGCCTGGGGGCGTC    11156           C
                                TTCCGGCCTGGGGGC GTC
                                ||||||||||||||| |||
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                                AAGGCCGGACCCCCG CAG
                                                _
GAM2317 GEM     5' CTCCGTCTCGGGCCGTC    23545      GC  G   G
                                TTCCG  CT GGG CCGTC
                                |||||  || ||| |||||
                                GAGGC  GA CCC GGCAG
                                  A_  G  _
GAM2317 GIPR    3' CTTCCGCCTAGAATCCTGT   6723       G      G _
                                CTTCCG CCTGGGG CC GT
                                |||||| ||||||| || ||
                                GAAGGC GGATCTT GG CA
                                   _     A  A
GAM2317 HDAC8   5' CTTCCGCTTAAAACCGT    32971      GC  GG
                                CTTCCG  CT  GGGCCGT
                                ||||||  ||  |||||||
                                GAAGGC  GA  TTTGGCA
                                   __  AT
GAM2317 KIF3B   3' CTTCCAGCCTGGATTAGTC   22035          GGCC
                                CTTCCGGCCTGGG   GTC
                                ||||||||||||   |||
                                GAAGGTCGGACCT   CAG
                                      AAT_
GAM2317 LIF     3' CTCCCGGCCTGGCAGAGCTGT 14144          __   C
                                CTTCCGGCCTGG  GGGC GT
                                ||||||||||||  |||| ||
                                GAGGGCCGGACC  CTCG CA
                                      GT   A
GAM2317 MADH2   5' CTCCCGGCCGCCGT       25343        TGGGG
                                CTTCCGGCC    GCCGT
                                |||||||||    |||||
                                GAGGGCCGG    CGGCA
                                          _____
GAM2317 PPT1    3' CTTTGGGCCTGGGCACAGT   41550    CC      G  C
                                CTT  GGCCTGGG GC GT
                                |||  |||||||| || ||
                                GAA  CCGGACCC TG CA
                                  AC       G  T
GAM2317 RAB31   5' TCCTCCGGGGCCGTC      27804    GG  TG
                                TCC  CC  GGGGCCGTC
                                |||  ||  |||||||||
                                AGG  GG  CCCCGGCAG
                                  A_  __
GAM2317 RBM10   5' TTCTCGGCCCGGGCTGTC   24986   _    GG   C
                                TTC CGGCCT  GGGC GTC
                                ||| ||||||  |||| |||
                                AAG GCCGGG  CCCG CAG
                                  A     __   A
GAM2317 ROR1    5' CTCCCGGCCGCCTCGTC    22699        TGGGG  __
                                CTTCCGGCC    GCC  GTC
                                |||||||||    |||  |||
```

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                                GAGGGCCGG    CGG  CAG
                                     _____  AG
GAM2317  SACM2L   5'  CTTCCGGCAACTGTCGACGGCC 38707        __  _____  GGCCG
                                CTTCCGGC  CTG    GG    T
                                ||||||||  |||    ||    |
                                GAAGGCCG  GAC    CT    G
                                    TT   AGIII  GCCGG
GAM2317  SORBS1   3'  CTTCCAGCACCCTAGTTGT   31706       _ GG  GCC
                                CTTCCGGC CT  GG   GT
                                |||||||| ||  ||   ||
                                GAAGGTCG GG  TC   CA
                                    T  GA  AA_
GAM2317  STIM1    3'  CTTCCGGCCTGGGCTGGAGTC  41127          __ CC
                                CTTCCGGCCTGGG  GG  GTC
                                ||||||||||||  ||  |||
                                GAAGGCCGGACCC  CC  CAG
                                      GA  T_
GAM2317  VAMP1    3'  CTTCGAGGGGGGCCGT     32575     C  CCT
                                CTTC GG   GGGGGCCGT
                                ||||  ||   |||||||||
                                GAAG TC   CCCCCGGCA
                                  C  ___
GAM2317  VIPR2    3'  CTCCCGGCACAGCTGTC     18012       CTGGG   C
                                CTTCCGGC    GGC GTC
                                ||||||||    ||| |||
                                GAGGGCCG    TCG CAG
                                    TG___   A
GAM2318  ATP2A3   3'  CGGGACCCGGTGGGCAAG    23192       AATGAC   A
                                CGGGACCC     TGG TAAG
                                ||||||||     ||| ||||
                                GCCCTGGG     ACC GTTC
                                    CC_____   C
GAM2318  MX2      3'  TACGGGACCCAAGGACTGGA   14697          T
                                TACGGGACCCAA GACTGGA
                                |||||||||||| |||||||
                                ATGCCCTGGGTT CTGACCT
                                      C
GAM2318  PACSIN1  3'  GGAACCCAGTGATTTTATGG   45152       A  C_____
                                GGGACCCA TGA    TGG
                                |||||||| |||    |||
                                CCTTGGGT ACT    ACC
                                    C   AAAAT
GAM2318  SPTBN1   5'  GGGACCCAATGAATCAGG    17103          CT__
                                GGGACCCAATGA   GG
                                ||||||||||||   ||
                                CCCTGGGTTACT   CC
                                      TAGT
GAM2319  RNF28    3'  TCAGTTACCACCCCGTATG   37201       A     TGAA
                                TCAGTTA CCACTCT   TATG
                                ||||||| |||||||   ||||
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                                AGTCAAT GGTGGGG   ATAC
                                   _     C___
GAM2319  RRM1    3'  TTAACCACTCCCTGTATGC   9756          GAA
                                TTAACCACTCTT  TATGC
                                ||||||||||||  |||||
                                AATTGGTGAGGG  ATACG
                                      AC_
GAM2319  TEM7    3'  AGTTAACCTGTGTCATATGC  33800       ACTCTTGA
                                AGTTAACC      ATATGC
                                ||||||||      ||||||
                                TCAATTGG      TATACG
                                    ACACAG__
GAM2319  ABCE1   3'  CAACACTGGTCAGCA      40498         GTCTCT
                                CAACACTGGT    TAGTA
                                ||||||||||    |||||
                                GTTGTGACCA    GTCGT
                                      _______
GAM2319  AKAP2   3'  TCAACACTGTTTTAGT     28501         GTGTCTC
                                TCAACACTG     TTAGT
                                |||||||||     |||||
                                AGTTGTGAC     AATCA
                                     AA_____
GAM2319  COL4A4  3'  TCAAACTGTTGCCTTGGTAC  6407     C   G    CTTA
                                TCAA ACTG TGTCT   GTAC
                                |||| |||| |||||   ||||
                                AGTT TGAC ACGGA   CATG
                                  _   A    AC__
GAM2319  CREBL2  3'  TCAACGTTCTCTTAGT     10585     ACTG  G
                                TCAAC   GT TCTCTTAGT
                                |||||   || |||||||||
                                AGTTG   CA AGAGAATCA
                                     _____ _
GAM2319  GABRP   3'  TCAACCCAGTACTTTTAGTAC  30559     A TG   T  C
                                TCAAC C  GTG CT TTAGTAC
                                ||||| |  ||| || |||||||
                                AGTTG G  CAT GA AATCATG
                                   _ GT   _  A
GAM2319  MAP3K9  3'  CCAACACTGGTGTTTGGGAAGC 41352          CTCTT_
                                TCAACACTGGTGT     AGT
                                ||||||||||||      |||
                                GGTTGTGACCACA     TCG
                                      AACCCT
GAM2319  PLP2    3'  TCAGAACTGGTGTCTCCTA   15409    AC
                                TCA  ACTGGTGTCTCTTA
                                |||  ||||||||||||||
                                AGT  TGACCACAGAGGAT
                                  CT
GAM2319  SEL1L   3'  AACACTGATCAGTTTTTAGT  22842       GTCTC_
                                AACACTGGT     TTAGT
                                |||||||||     |||||
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                                TTGTGACTA     AATCA
                                     GTCAAA
GAM2319  STAT4    3'  AACACTGGTTTCTTAAAGT   17142        G   CTT
                                AACACTGGT TCT   AGT
                                ||||||||| |||   |||
                                TTGTGACCA AGA   TCA
                                     A   ATT
GAM2319  TSN      3'  CTGGCACATACTCTTAGTAC  21492      TG ___
                                CTGG  T   CTCTTAGTAC
                                ||||  |   ||||||||||
                                GACC  G   GAGAATCATG
                                  GT TAT
GAM2319  USH2A    3'  AACACTGAGTTTTTTAGT    28298        T  CTC
                                AACACTGG GT   TTAGT
                                |||||||| ||   |||||
                                TTGTGACT CA   AATCA
                                     _  AAA
GAM2320  COLQ     3'  AGGTCTCAGGTTGGGCATGT  38692        CGA    A  C
                                AGGTCTCAG   GTTGG CA GT
                                |||||||||   ||||| || ||
                                TCCAGAGTC   CAACC GT CA
                                     ___    C  A
GAM2321  GPR34    3'  TGCTTGATTTTAATAACTACTT 23628         AC    TGA
                                TGCTTGATTT  AATA   TATTT
                                ||||||||||  ||||   |||||
                                ACGAACTAAA  TTAT   ATGAA
                                     A_    TG_
GAM2321  RNGTT    3'  TGTCTTGATTTCCTTGATATTT 19168    _      ACAATA
                                TG CTTGATTT     TGATATTT
                                || ||||||||     ||||||||
                                AC GAACTAAA     ACTATAAA
                                 A       GGA___
GAM2322  BMP2     5'  GGCACCGGCGCAAAGTGG    10185      GTATA       C
                                GGCAT    GGCGCAAAG GG
                                |||||    ||||||||| ||
                                CCGTG    CCGCGTTTC CC
                                   G____        A
GAM2322  CELSR2   3'  TGGCCTGCCCGGGGCGCGGGGC 10860     A   ATA_    AAA
            GGG                   TGGC TGT    GGCGC   GCGGG
                                |||| |||   |||||  |||||
                                ACCG ACG    CCGCG   CGCCC
                                  G   GGCC    CCC
GAM2322  DRD3     3'  TGGCATGTCTGGCAGTGG    38015        ATA   GCAA  C
                                TGGCATGT   GGC    AG GG
                                ||||||||   |||    || ||
                                ACCGTACA   CCG    TC CC
                                     GA_   ____  A
GAM2322  WISP2    3'  TGTGTGTGTAGGCAGGGAGTGG 19312    GCA   A     CAA  C
            G                    TG   TGT TAGGCG   AG GGG
                                ||   ||| ||||||   || |||
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                                AC   ACA ATCCGT   TC CCC
                                 AC_  C     CCC  A
GAM2322  BAT4     5'  GGTTAGGAAAGGCCCTCAGG  37691        TC_
                                GGTTAGGAG  CCCTCAGG
                                |||||||||  ||||||||
                                CCAATCCTT  GGGAGTCC
                                     TCC
GAM2322  GCKR     3'  GCTGGCACAAGTCCCCTTGGG  11241   _  T G       CA
                                GC GGT A GAGTCCCCT  GG
                                || ||| | |||||||||  ||
                                CG CCG T TTCAGGGGA  CC
                                 A  _ G       AC
GAM2322  SP3      5'  GCGGTTAGGGTCGGGCC     44377        A  _______
                                GCGGTTAGG GTC     CC
                                ||||||||| |||     ||
                                CGCCAATCC CAG     GG
                                     _  CCCIII
GAM2323  ALEX2    5'  TATAGACTGTCGACGTTAG   31327       _      C
                                TATAGA TGTCGACG TAG
                                |||||| |||||||| |||
                                ATATCT ACAGCTGC ATC
                                   G       A
GAM2324  AMD1     3'  GACAAGAAATATAAAATTTAG  11590          TAG__
                                GACAAGAAATATA    TAG
                                ||||||||||||    |||
                                CTGTTCTTTATAT    ATC
                                      TTTAA
GAM2324  CHRNA10  3'  GACAGGAAATGCAGCAG    33792     A    ATATA
                                GACA GAAAT    GTAGCAG
                                |||| |||||    |||||||
                                CTGT CTTTA    CGTCGTC
                                  C   _____
GAM2324  RRAS     3'  AGAAGGCACACAGTGGCAGT  26555     A_      A
                                AGAA  TATATAGT GCAGT
                                ||||  |||||||| |||||
                                TCTT  GTGTGTCA CGTCA
                                  CC       C
GAM2324  TRDN     3'  ACAAGAAATTTATAGCAG    25876         A
                                ACAAGAAAT TATAGTAG
                                ||||||||| ||||||||
                                TGTTCTTTA ATATCGTC
                                     A
GAM2324  XT3      3'  CAAGGAGTAACAGAGCAGT   33660     AAATAT   T
                                CAAG     ATAG AGCAGT
                                ||||     |||| ||||||
                                GTTC     TGTC TCGTCA
                                  CTCAT_   _
GAM2324  PIGN     3'  TCAAGATATTTTGCCCATTAGA 29550    T      TA   AT_
            A                    TC AGATATTT  TGT   TTAGAA
                                || ||||||||  |||   ||||||
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                                AG TCTATAAA  ACG   AATCTT
                                 T       __  GGT
GAM2324  STK31    3'  TCTAGATATTTCTGTGTATT   37277          A_
                                TCTAGATATTTT  TGTATT
                                ||||||||||||  ||||||
                                AGATCTATAAAG  ACATAA
                                      AC
GAM2324  TP63     3'  GATGTGGCATGTATTTAGAA   18998     ATTT
                                GAT   TATGTATTTAGAA
                                |||   ||||||||||||
                                CTA   GTACATAAATCTT
                                  CACC
GAM2325  ELMO2    3'  CCTATAGTAATGAAAATATATA 39313    _       CTT_
                                CC ATAGTAATG   TATATA
                                || |||||||||   ||||||
                                GG TATCATTAC   ATATAT
                                 A        TTTT
GAM2325  TGFBI    3'  TTAAAGTGTGATACTTGGT   7416        TCTATG  C
                                TTGAAGT     GA ACTTGGT
                                |||||||     || |||||||
                                AATTTCA     CT TGAACCA
                                    CA____  A
GAM2326  ADCY6    3'  GGTACGGGGATCCAGGGT    34174         CA   C
                                GGTACGGGGA  CGG GT
                                ||||||||||  ||| ||
                                CCATGCCCCT  GTC CA
                                      AG   C
GAM2326  AP2B1    3'  GGGTGAGGGGACAGCAT     10489     AC      CG
                                GGGT  GGGGACA  GCGT
                                ||||  |||||||  ||||
                                CCCA  CCCCTGT  CGTA
                                  CT      __
GAM2326  APOE     3'  GGGCGGGGACAGGGT       6218      TA       C  C
                                GGG  CGGGGACA GG GT
                                |||  |||||||| || ||
                                CCC  GCCCCTGT CC CA
                                   __       _ _
GAM2326  ATP11A   3'  GGGTACGGCGGTGCAT      44177         _ ACACG
                                GGGTACGG GG    GCGT
                                |||||||| ||    ||||
                                CCCATGCC CC    CGTA
                                    G  A____
GAM2326  BMP1     3'  GGGCACGGGGAAGGGT      25985          CAC  C
                                GGGTACGGGGA   GG GT
                                ||||||||||   || ||
                                CCCGTGCCCCT   CC CA
                                      T__  _
GAM2326  BTAF1    5'  GGGAGCGGCCGGTGCGGCGT  43667     TA  __  ACA
                                GGG  CGG  GG   CGGCGT
                                |||  |||  ||   ||||||
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                                CCC  GCC  CC   GCCGCA
                                  TC   GG  AC_
GAM2326  C1QG     5'  AGGCAAGAGGACACGGTGT   41686      C        C
                                GGGTA GGGGACACGG GT
                                ||||| |||||||||| ||
                                TCCGT CTCCTGTGCC CA
                                   T         A
GAM2326  CALM1    5'  GAGTAACGGCACGGCGT     27858      _  GGA
                                GGGTA CGG   CACGGCGT
                                ||||| |||   ||||||||
                                CTCAT GCC   GTGCCGCA
                                   T  ___
GAM2326  COX10    3'  GGGTGGGGGCCAGAGGT     10553      AC   A  C  C
                                GGGT  GGGG CA GG GT
                                ||||  |||| || || ||
                                CCCA  CCCC GT TC CA
                                  C_   G  C  _
GAM2326  FXYD6    3'  GGGTGGGGGACACACA      35120      AC        G
                                GGGT  GGGGACACG CG
                                ||||  ||||||||| ||
                                CCCA  CCCCTGTGT GT
                                  C_        _
GAM2326  GRIK3    3'  GGGTACAGGGGACG        9098          ACAC
                                GGGTACGGGG   GGCG
                                ||||||||||   ||||
                                CCCATGTCCC   CTGC
                                          _____
GAM2326  IGF2     3'  GGGCACGGGGACTGGGT     8311           AC  C
                                GGGTACGGGGAC  GG GT
                                ||||||||||||  || ||
                                CCCGTGCCCCTG  CC CA
                                       A_  _
GAM2326  ITGA4    5'  GGGTGGGGTCCCGGGCGT    9426       AC   ACA  _
                                GGGT  GGGG   CGG CGT
                                ||||  ||||   ||| |||
                                CCCA  CCCC   GCC GCA
                                  __   AGG   C
GAM2326  KIF5C    5'  GGGCACGGGGATGGGT      21156          CAC  C
                                GGGTACGGGGA   GG GT
                                ||||||||||   || ||
                                CCCGTGCCCCT   CC CA
                                       A__  _
GAM2326  LASS1    3'  GGGCACGGGGGGCGCGGGT   34611          ACA  C
                                GGGTACGGGGG   CGG GT
                                |||||||||   ||| ||
                                CCCGTGCCCC   GCC CA
                                      CGC   _
GAM2326  MYLK     5'  GGGTTGGACTCAGGCGT     38165      ACGG   A _
                                GGGT   GGAC C GGCGT
                                ||||   |||| | |||||
```

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                                CCCA   CCTG G CCGCA
                                  A___   A T
GAM2326 NCSTN   3' GGGTACAGGGGTGGGGGT   43940        ACAC  C
                                GGGTACGGGG   GG GT
                                ||||||||||   || ||
                                CCCATGTCCC   CC CA
                                     CACC  _
GAM2326 NONO    5' GGGTACAAAATGGCGT     44357         ACAC
                                GGGTACGGGG   GGCGT
                                ||||||||||   |||||
                                CCCATGTTTT   CCGCA
                                     A___
GAM2326 PFN1    3' GGGTAGGGGGAGGTGT     22720      C   CAC  C
                                GGGTA GGGGA   GG GT
                                ||||| |||||   || ||
                                CCCAT CCCCT   CC CA
                                   C    ___  A
GAM2326 POLG    5' AGGCCCACGGCACGGCGT   15442    TA  G  A
                                GGG  CG GG CACGGCGT
                                |||  || || ||||||||
                                TCC  GT CC GTGCCGCA
                                  GG  G  _
GAM2326 PPP2R5A 5' GGGCACGGGGGGTGCGGGT   26441        ACA   C
                                GGGTACGGGG   CGG GT
                                ||||||||||   ||| ||
                                CCCGTGCCCC   GCC CA
                                     CAC   _
GAM2326 PPP2R5D 3' GGGCACGGGGGTAGGGTGT   26461        ACAC  C
                                GGGTACGGGG   GG GT
                                ||||||||||   || ||
                                CCCGTGCCCC   CC CA
                                     ATC_  A
GAM2326 SH3GL1  3' GGGCGGGGACACGGGT     16673    TA        C
                                GGG  CGGGGACACGG GT
                                |||  |||||||||||| ||
                                CCC  GCCCCTGTGCC CA
                                   __        _
GAM2326 GCNT2   5' TCTCTTGTTGTTCGTG     11253    G    ACACGTC
                                TC CTTGT      GTTCGTG
                                || |||||      |||||||
                                AG GAACA      CAAGCAC
                                 A    A_______
GAM2327 ATRN    3' GAGGCTGTCCCTTTCCTG   40274    AAT  TTATA
                                GAG   CT    CCTTTCCTG
                                |||   ||    |||||||||
                                CTC   GA    GGAAAGGAC
                                  C__  CAG__
GAM2327 AVPR1A  5' GAAAGGACCTGCCTTTCCTG  8727      __   TTATA
                                GAGA  ATCT    CCTTTCCTG
                                ||||  ||||    |||||||||
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                                CTTT  TGGA    GGAAAGGAC
                                  CC   C____
GAM2327  BMX     3'  GAATCTTTTGTTTCCTG     11889        ATACC
                                GAATCTTT    TTTCCTG
                                ||||||||    |||||||
                                CTTAGAAA    AAAGGAC
                                    AC___
GAM2327  CAPON   3'  AGAATCTCAATACTTTCCTG  41917        T   C
                                AGAATCTT ATAC TTTCCTG
                                |||||||| |||| |||||||
                                TCTTAGAG TATG AAAGGAC
                                    T   _
GAM2327  NP      3'  ACAGGAATCTTTTCCTTTC   7074      A      ATA
                                ACG GAATCTTT   CCTTTC
                                ||| ||||||||   ||||||
                                TGT CTTAGAAA   GGAAAG
                                  C       A__
GAM2327  AK2     3'  AGAAATAATATTGTGTC     30186        TTC
                                GGAAATA   TGTTGTGTC
                                |||||||   |||||||||
                                TCTTTAT   ATAACACAG
                                    T__
GAM2327  ATP5G1  3'  TTAGAGAAACGTTGTGT     23202      _    ATTCT
                                TTAG GAAAT    GTTGTGT
                                |||| |||||    |||||||
                                AATC CTTTG    CAACACA
                                  T    _____
GAM2327  BMP6    3'  TTAGAAAATATTCTAAAAT   11871            TT
                                TTAGGAAATATTCTG  GT
                                ||||||||||||||  ||
                                AATCTTTTATAAGAT  TA
                                        TT
GAM2327  CCND3   3'  TTAGGAAAGACCTGTGT     12067        T  TCTG
                                TTAGGAAA AT    TTGTGT
                                |||||||| ||    ||||||
                                AATCCTTT TG    GACACA
                                    C  ____
GAM2327  DDX3    3'  TTAGGAAATTTTTGCCGT    35827        A  C
                                TTAGGAAAT TT TGTTGT
                                ||||||||| || ||||||
                                AATCCTTTA AA ACGGCA
                                    _  A
GAM2327  DISC1   3'  TCAGGAAATATTTTCGT     33050          CTG
                                TTAGGAAATATT   TTGT
                                ||||||||||||   ||||
                                AGTCCTTTATAA   AGCA
                                      A__
GAM2327  EPHB2   3'  TAGGAAATGTCAAAGTGTC   32676        AT  TGTT
                                TAGGAAAT  TC   GTGTC
                                ||||||||  ||   |||||
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                                ATCCTTTA  AG    CACAG
                                    C_  TTT_
GAM2327  LDHB     5'  TTAGGAAATTGTATATATGTGT 14127         ATTC  _
              C                  TTAGGAAAT    TGT TGTGTC
                                 |||||||||    ||| ||||||
                                 AATCCTTTA    ATA ACACAG
                                      ACAT   T
GAM2327  MAP3K5   3'  TTAGGAAATTTCAGTGTGT   25447         A   T  T
                                 TTAGGAAAT TTC GT GTGT
                                 ||||||||| ||| || ||||
                                 AATCCTTTA AAG CA CACA
                                      _  T  _
GAM2327  SEL1L    3'  TTAGGAAAAGTATGTCTGTGTC 22852        TATTCTG
                                 TTAGGAAA      TTGTGTC
                                 ||||||||      |||||||
                                 AATCCTTT      GACACAG
                                      TCATACA
GAM2327  SPON1    3'  GGAAATATTCTGATGTGT    41669          T
                                 GGAAATATTCTG TGTGT
                                 |||||||||||| |||||
                                 CCTTTATAAGAC ACACA
                                       T
GAM2327  TOP1     3'  TCAGGAAATATTTTCCCATC   17629         ___
                                 TTAGGAAATA   TTCTGTT
                                 ||||||||||   |||||||
                                 AGTCCTTTAT   AGGGTAG
                                      AAA
GAM2327  TSLP     3'  TTAAGAAATATATAGTGTC    39701          TCTGTT
                                 TTAGGAAATAT     GTGTC
                                 ||||||||||      |||||
                                 AATTCTTTATA     CACAG
                                       TAT___
GAM2328  BMP4     3'  TGTAGTGTGTGGGTGA      10197        TACA  TA
                                 TGTGGTGT   GT  GGTGA
                                 ||||||||   ||  |||||
                                 ACATCACA   CA  CCACT
                                     _____  C_
GAM2329  PCDH9    5'  TTTGTATTGACAGGATCTTTCT 44416     _     TTGT
                                 TTTG ATTGACA   GGTCTTTCT
                                 |||| |||||||   |||||||||
                                 AAAC TAACTGT   CTAGAAAGA
                                   A      C___
GAM2330  GABRP    3'  TAAAAACTCATCTTGGTATTG  30557        A   CAA
                                 TAAAAACT ATCT   GTATTG
                                 |||||||| ||||   ||||||
                                 ATTTTTGA TAGA   CATAAC
                                      G   AC_
GAM2330  STXBP1   3'  TCTGACGACTAATCTCAGT   17210     AAAA        A
                                 TCT   ACTAATCTCA GT
                                 |||   |||||||||| ||
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```
                                AGA   TGATTAGAGT CA
                                  CTGC       _
GAM2330  APP     3'  TGAAGCAATGGTTTTGC    7923         A    A
                                TGAAGTAAT GTTTT GC
                                ||||||||| ||||| ||
                                ACTTCGTTA CAAAA CG
                                    C   _
GAM2330  EDAR    3'  TGAAATAATACCTGGAGCA   35311        G  TT
                                TGAAGTAATA TT  AGCA
                                |||||||||| ||  ||||
                                ACTTTATTAT GA  TCGT
                                     G  CC
GAM2331  APPL    3'  GAGATTGGTTAAAAAGTA    29007       A  TTTA
                                GAGATT GTT   GAAAAGTA
                                |||||| |||   ||||||||
                                CTCTAA CAA   TTTTTCAT
                                   C  ____
GAM2331  DIAPH2  3'  GAGATTCACTGTTAGAAAAGT 28672       AG  T
                                GAGATT  TT TTAGAAAAGT
                                ||||||  || ||||||||||
                                CTCTAA  GA AATCTTTTCA
                                   GT  C
GAM2331  KIF5C   3'  TGAGCTTAGTTGTTCAGAA   21164      A    _
                                TGAG TTAGTT TTTAGAA
                                |||| |||||| |||||||
                                ACTC AATCAA AAGTCTT
                                  G     C
GAM2331  OGT     5'  TGAGATTAGTTGGACTCGAGGT 18788          TTTAGAAAA
            AT                   TGAGATTAGTT       GTAT
                                ||||||||||        ||||
                                ACTCTAATCAA       CATA
                                     CCTGAGCTC
GAM2332  BRCA1   5'  AGTGTCCCCCTCAAGGCA   28620     _       T
                                AGTG CCCCCTTAG GGCA
                                |||| ||||||||| ||||
                                TCAC GGGGGAGTT CCGT
                                  A       _
GAM2332  CDK7    3'  TAAGTTTTCCCTAATGCA    12209      GCCC      G
                                TAAGT   CCTTAGTG CA
                                |||||   |||||||| ||
                                ATTCA   GGGATTAC GT
                                   AAA_      _
GAM2332  CTPS    3'  TAAGTCCATGTGGCACAC    44800      G  CCCTTA
                                TAAGT CC     GTGGCACAC
                                ||||| ||     |||||||||
                                ATTCA GG     CACCGTGTG
                                   _ TA____
GAM2332  PLOD2   3'  GTGTTCCCTTAGTAACAC    9596      CC
                                GTG  CCCTTAGTGGCAC
                                |||  ||||||||||||
```

```
                                CAC  GGGAATCATTGTG
                                  AA
GAM2332  PTGS1    3'  GTGCCCCCTCTGTTGTATGC   38742          A___  _
                                GTGCCCCCTT   GTG GC
                                ||||||||||   ||| ||
                                CACGGGGGAG   CAT CG
                                     ACAA  A
GAM2332  PTPRG    3'  TAAGTGCCCTTTCAGGA    15942         CC   T
                                TAAGTGCCC  TTAG GG
                                |||||||||  |||| ||
                                ATTCACGGG  AGTC CT
                                     AA   _
GAM2332  TIF1     3'  TAAGTGCCTTCTTAATAGCA  41274         CC
                                TAAGTGCC  CTTAGTGGCA
                                ||||||||  ||||||||||
                                ATTCACGG  GAATTATCGT
                                     AA
GAM2332  FNTB     3'  TAGAGGCAGCAAATGGCCAGGT 13008         _  TTATATAA
                                TAGAGGCA CA       CCAGGT
                                ||||||||  ||       ||||||
                                ATCTCCGT GT       GGTCCA
                                     C  TTACC___
GAM2332  HTR2C    3'  AGAGGCACATTCTCAGG     9276           ATATAAC
                                AGAGGCACATT      CAGG
                                ||||||||||       ||||
                                TCTCCGTGTAA      GTCC
                                     GA_____
GAM2333  CEACAM1  3'  TGGATGAGGGAAAGTATGCACA 11836       _   AATTC  T
              GT                  TGGAT AGG     GT TGCACAGT
                                  ||||| |||     ||  ||||||||
                                  ACCTA TCC     CA ACGTGTCA
                                    C   CTTT_  T
GAM2333  ITPA     3'  TGGAAGGCGATTTGCA      37908      T   AATTC
                                TGGA AGG     GTTTGCA
                                ||||  |||    |||||||
                                ACCT TCC     TAAACGT
                                  _   GC___
GAM2333  REV3L    3'  GGTACTACTGTTTGCACAGT   16267    A   C__
                                GG ATT   GTTTGCACAGT
                                ||  |||   ||||||||||
                                CC TGA   CAAACGTGTCA
                                 A   TGA
GAM2334  FAAH     3'  AGCGCCCGAGTAGGGGCCTGAG 11043          AC    A
                                GGCGCCCGA  AGGG CCTGAG
                                |||||||||  |||| ||||||
                                TCGCGGGCT  TCCC GGACTC
                                     CA    C
GAM2334  FOXD2    5'  TTGGCGCCCGCAGCCTTGGGCC 20977          AACA___   A
              TG                  TTGGCGCCCG      GGG CCTG
                                  ||||||||||      ||| ||||
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                                AACCGCGGGC      CCC GGAC
                                     GTCGGAA  _
GAM2334  IL1RN    3'  TTGGCCCTGCAGGGACCTGAG  8218       G  CGAA
                                TTGGC CC    CAGGGACCTGAG
                                ||||| ||    ||||||||||||
                                AACCG GG    GTCCCTGGACTC
                                  _  AC__
GAM2334  RFX2     3'  TGGCTGCGCAGGGACCTG    8464       GCC  AA
                                TGGC   CG  CAGGGACCTG
                                ||||   ||  ||||||||||
                                ACCG   GC  GTCCCTGGAC
                                  AC_  __
GAM2334  TIA1     3'  TTGTGTTTGAAACAAGGATCTG 35288     GCGCCC       C
              AG                  TTG     GAACAGGGA CTGAG
                                ||||     ||||||||| |||||
                                AAC     TTTGTTCCT GACTC
                                  ACAAAC        A
GAM2334  TIA1     3'  TTGTGTTTGAAACAAGGATCTG 35288     GCGCCC       C
              AG                  TTG     GAACAGGGA CTGAG
                                ||||     ||||||||| |||||
                                AAC     TTTGTTCCT GACTC
                                  ACAAAC        A
GAM2334  ABH      3'  TCTCTGTTTTTGGCTTGTCTG  40742    C    CTCTA
                                TC CTGT     GTTTGTCTG
                                || ||||     |||||||||
                                AG GACA     CGAACAGAC
                                 A    AAAAC
GAM2334  CBFA2T2  3'  CCTTGTTTCTAGTTCAGTTC   22972    C   C       TCT
                                CC TGT TCTAGTTTG   GTTC
                                || ||| |||||||||   ||||
                                GG ACA AGATCAAGT   CAAG
                                 A  A       ____
GAM2334  COL4A3   3'  CTGTCTCTGGGTCATGTT    36379        AGTTT  _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC____   T
GAM2334  COL4A3   3'  CTGTCTCTGGGTCATGTT    36379        AGTTT  _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC____   T
GAM2334  COL4A3   3'  CTGTCTCTGGGTCATGTT    36379        AGTTT  _
                                CTGTCTCT    GTC TGTT
                                ||||||||    ||| ||||
                                GACAGAGA    CAG ACAA
                                     CC____   T
GAM2334  F7       3'  TCTCTGTCTCTGTCTCTCTCTG 33343    C       AG_  G
              TT                   TC CTGTCTCT   TTT TCTGTT
                                || ||||||||   ||| ||||||
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                                AG GACAGAGA   AGA AGACAA
                                 A       CAG   G
GAM2334  F7       3'  TCTCTGTCTCTGTCTCTCTCTG 33343     C       AG_   G
                TT                  TC CTGTCTCT   TTT TCTGTT
                                || ||||||||   ||| ||||||
                                AG GACAGAGA   AGA AGACAA
                                 A       CAG   G
GAM2334  HDAC4    3'  CCTGTTTCTGTCCAGTTTTGTT 25753       C____       GTC
                                CCTGT    TCTAGTTT   TGTT
                                |||||    ||||||||   ||||
                                GGACA    AGGTCAAA   ACAA
                                  AAGAC      ___
GAM2334  MEN1     5'  TGTTTGTTAGTTTGTCTGTT   39241     CTC_
                                TGT    TAGTTTGTCTGTT
                                |||    ||||||||||||
                                ACA    ATCAAACAGACAA
                                  AACA
GAM2334  NDRG1    3'  CCTGTTTTGCCTGT       40576       CTCTAG
                                CCTGT     TTTGTCTGT
                                |||||     |||||||||
                                GGACA     AAACGGACA
                                  _______
GAM2334  NKX3A    3'  TCACTGTCTCTGTTGT      26115     C       A   T
                                TC CTGTCTCT GTT GT
                                || |||||||| ||| ||
                                AG GACAGAGA CAA CA
                                 T       _   _
GAM2334  PACSIN1  3'  CTGTCTCTGCATACTTTGTT   45148         A  TTGTC_
                                CTGTCTCT GT     TGTT
                                |||||||| ||     ||||
                                GACAGAGA CG     ACAA
                                     _  TATGAA
GAM2334  PDCD2    3'  TCCCTGTCACTGGACACTTTTG 15143         T  AG_____
                T                   TCCCTGTC CT      TTTGT
                                |||||||| ||      |||||
                                AGGGACAG GA      AAACA
                                     T  CCTGTGA
GAM2334  PDE4D    3'  TCCTTGTCTGTAATTTGT    43900     C    C
                                TCC TGTCT TAGTTTGT
                                ||| ||||| ||||||||
                                AGG ACAGA ATTAAACA
                                  A    C
GAM2334  SLC2A4   3'  TCTCTGCTCTGGTTTGTC    9800     C   T   A
                                TC CTG CTCT GTTTGTC
                                || ||| |||| |||||||
                                AG GAC GAGA CAAACAG
                                 A   _    C
GAM2335  CLCN6    3'  CTGATACCATGTAGAAGG    34715          TGC   CAA
                                TTGATACCAT   GTG   AAGG
                                ||||||||||   |||   ||||
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                                GACTATGGTA  CAT  TTCC
                                    ____  C__
GAM2335 PPP1R12B 3' ATACCATTGAGTGAGGGGGT  36966       C  CAAAA
                                ATACCATTG GTG   GGT
                                ||||||||| |||   |||
                                TATGGTAAC CAC   CCA
                                     T  TCCC_
GAM2335 ILVBL   5' CCGTGCCCGGGTGGCCCA   27767       C   AA_
                                CCGTGCCC GGGT  TCA
                                |||||||| ||||  |||
                                GGCACGGG CCCA  GGT
                                    _  CCG
GAM2335 RPH3AL  3' CCGTGCCCTAGGTTTCA    28099       CG  AA
                                CCGTGCCC  GGT  TCA
                                ||||||||  |||  |||
                                GGCACGGG  CCA  AGT
                                    AT  A_
GAM2336 LLT1    3' TAATATTTTACTATGATTTT  29974      A   CG
                                TAATAT TTTAC  TGATTTT
                                |||||| |||||  |||||||
                                ATTATA AAATG  ACTAAAA
                                   _   AT
GAM2336 LLT1    3' TAATATTTTACTATGATTTT  29974      A   CG
                                TAATAT TTTAC  TGATTTT
                                |||||| |||||  |||||||
                                ATTATA AAATG  ACTAAAA
                                   _   AT
GAM2337 CLN2    3' TATAGCCCTAAACTAAGGTAG  7559      T   _
                                TATA GCTC AAACTAAGGTAG
                                |||| |||| ||||||||||||
                                ATAT CGGG TTTGATTCCATC
                                  _   A
GAM2337 ICMT    3' TATATGCTCAAATCCCTTTGG  29660         _  AA__
                                TATATGCTCAAA CT   GG
                                |||||||||||| ||   ||
                                ATATACGAGTTT GG   CC
                                       A  GAAA
GAM2337 CLN2    3' TATAGCCCTAAACTAAGGTAG  7559      T   _
                                TATA GCTC AAACTAAGGTAG
                                |||| |||| ||||||||||||
                                ATAT CGGG TTTGATTCCATC
                                  _   A
GAM2337 ICMT    3' TATATGCTCAAATCCCTTTGG  29660         _  AA__
                                TATATGCTCAAA CT   GG
                                |||||||||||| ||   ||
                                ATATACGAGTTT GG   CC
                                       A  GAAA
GAM2338 ADSS    3' TTGAACATTTCACTAAAT    43480          A
                                TTGAACATTTCAC AAAT
                                |||||||||||| ||||
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                                AACTTGTAAAGTG TTTA
                                      A
GAM2338 LARS2    3' TTGAACATTTCCTAAATG    31684          ACA
                                TTGAACATTTC   AAATG
                                ||||||||||   |||||
                                AACTTGTAAAG   TTTAC
                                      GA_
GAM2338 SVIL     3' CTTGAACATTTACAAAATA   34728          C
                                CTTGAACATTT ACAAAATG
                                |||||||||| ||||||||
                                GAACTTGTAAA TGTTTTAT
                                         _
GAM2338 CIT      3' TGTGAATGCTTTGAAAGAGT  43063          A  TCT
                                TGTGAATGCTTT GA   GAGT
                                |||||||||||| ||   ||||
                                ACACTTACGAAA CT   CTCA
                                      _  TT_
GAM2338 DLD      3' TGAATGCCCACGTATTTGAGT  6469          TAG_  C
                                TGAATGCTT    AT TGAGT
                                |||||||||    || |||||
                                ACTTACGGG    TA ACTCA
                                     TGCA  A
GAM2338 MASP1    3' CTGTGAATTGCTGTCCCTGAGT 12432         _   TTAGA
                                CTGTGAAT GCT     TCTGAGT
                                |||||||| |||    |||||||
                                GACACTTA CGA     GGACTCA
                                    A   CAG__
GAM2338 PCOLN3   3' ACTTGAATGTGGATCTGAG   15744     G     CTTTA
                                ACT TGAATG     GATCTGAG
                                ||| ||||||     ||||||||
                                TGA ACTTAC     CTAGACTC
                                  _     AC___
GAM2338 TAT      3' TGTGAATGAGGAGGATCTGAGT 7402          CTTTA
                                TGTGAATG     GATCTGAGT
                                ||||||||     |||||||||
                                ACACTTAC     CTAGACTCA
                                     TCCTC
GAM2339 GRINL1A  5' TCTGCGCGGGCTGAGGCTGG  43003     TA         _  C
                                TCT  CGCGGGCTGAG CT GG
                                |||  |||||||||| || ||
                                AGA  GCGCCCGACTC GA CC
                                  C_         C  _
GAM2340 B4GALT4  5' CCTGCCTCTTCCTTCATGAA  19099         GAAA_  C
                                CTTGCCTCT     CA GAA
                                |||||||||     || |||
                                GGACGGAGA     GT CTT
                                     AGGAA  A
GAM2340 CTLA1    3' CTTGCCTCTGTCCCAGA     37901          AAA  C
                                CTTGCCTCTG   CA GA
                                ||||||||||   || ||
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                                GAACGGAGAC   GT CT
                                      AGG  _
GAM2340  EFNA4    3'  CTTGCCTCTGCTTCAGA     23391          AAA  C
                                CTTGCCTCTG   CA GA
                                ||||||||||   || ||
                                GAACGGAGAC   GT CT
                                      GAA  _
GAM2340  GAB2     3'  CCTGCCTCTGACACCAA     38677          A  A
                                CTTGCCTCTGA AC CGA
                                |||||||||||| || |||
                                GGACGGAGACT TG GTT
                                       G  _
GAM2340  GAS7     3'  CTGGCCTCTGAGACGA      18884    T       AAC
                                CT GCCTCTGA   ACGA
                                || ||||||||   ||||
                                GA CGGAGACT   TGCT
                                 C       C__
GAM2340  HEPH     3'  TTGCTGTCTAAAACATGAA    39860      C_       C
                                TTGC  TCTGAAACA GAA
                                ||||  ||||||||| |||
                                AACG  AGATTTTGT CTT
                                   AC        A
GAM2340  HFE      3'  CTCTCCTGAAACATGAA      40004     GC T       C
                                CTT  C CTGAAACA GAA
                                |||  | |||||||| |||
                                GAG  G GACTTTGT CTT
                                  A_ _       A
GAM2340  LIMD1    3'  CTCCCTCTGAAGCATGAA     30629     G       A  C
                                CTT CCTCTGAA CA GAA
                                ||| |||||||| || |||
                                GAG GGAGACTT GT CTT
                                  _       C  A
GAM2340  MAGEA3   5'  CTTGCCTCCTCACCGA      23842          GAA  A
                                CTTGCCTCT   AC CGA
                                |||||||||   || |||
                                GAACGGAGG   TG GCT
                                      AG_  _
GAM2340  MAP3K7IP1 3'  CTTCCTCTGAAACAGGA     25926     G         C
                                CTT CCTCTGAAACA GA
                                ||| ||||||||||| ||
                                GAA GGAGACTTTGT CT
                                  _          C
GAM2340  NMI      5'  CTTCCCGGAAAACACGA      21720     G   CT
                                CTT CCT  GAAACACGA
                                ||| |||  |||||||||
                                GAA GGG  TTTTGTGCT
                                  _  CC
GAM2340  P2RY1    3'  CTTGTCCTGGAACACAA      15007      C T   A
                                CTTG C CTG AACACGA
                                |||| | ||| |||||||
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                                GAAC G GAC TTGTGTT
                                  A _  C
GAM2340  PAFAH1B1  3'  CTTACTGTAAAACACGA     7706       CTC
                                CTTGC  TGAAACACGA
                                |||||  ||||||||||
                                GAATG  ATTTTGTGCT
                                  AC_
GAM2340  PDE4D     3'  TTGCTTCAGACAACACGAA   43905      C  T  _
                                TTGC TC GA AACACGAA
                                |||| || || ||||||||
                                AACG AG CT TTGTGCTT
                                  A  T  G
GAM2340  PIGA      3'  CTGCTCAGAAAACACGAA    33830      C  T_
                                TTGC TC  GAAACACGAA
                                |||| ||  ||||||||||
                                GACG AG  TTTTGTGCTT
                                  _  TC
GAM2340  SIAT1     3'  CTGCCTCTCTCACTGAA     16721        GAAA  _
                                TTGCCTCT   CAC GAA
                                ||||||||   ||| |||
                                GACGGAGA   GTG CTT
                                    GA__   A
GAM2340  SIT       3'  TTGCCTCCTCCATCACGAA   30902        GAAA_
                                TTGCCTCT    CACGAA
                                ||||||||    ||||||
                                AACGGAGG    GTGCTT
                                    AGGTA
GAM2340  TEM7      3'  TTGCCTCTCAACAGAA      33820        GA   C
                                TTGCCTCT  AACA GAA
                                ||||||||  |||| |||
                                AACGGAGA  TTGT CTT
                                    G_   _
GAM2341  PTER      3'  TTCATTAAACTATATTAT    36219       _
                                TTCAT AAACTATATTAT
                                ||||| ||||||||||||
                                AAGTA TTTGATATAATA
                                  A
GAM2341  RHO       3'  CTGTCTCTCCATAGGCCACAT  8061     A        AA
                                CT TCTCTTCATA  CTATAT
                                || ||||||||||  ||||||
                                GA AGAGAGGTAT  GGTGTA
                                 C         CC
GAM2341  RNF12     5'  TATCTCTCATAAGCCTAT    32040        T    A_
                                TATCTCT CATAA  CTAT
                                ||||||| |||||  ||||
                                ATAGAGA GTATT  GATA
                                    _    CG
GAM2342  ADRA2A    5'  TATATATACATATCAATA    8641           _
                                TATATATGCATA CGATA
                                |||||||||||| |||||
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                                ATATATATGTAT GTTAT
                                       A
GAM2342  CDH13    3'  TATATATACATACAGATA    10371          _
                                TATATATGCATAC GATA
                                |||||||||||| ||||
                                ATATATATGTATG CTAT
                                       T
GAM2342  DAPK1    3'  TATATATACATATGATATAT  22367          C    III
                                TATATATGCATA GATATA  T
                                |||||||||||| ||||||  |
                                ATATATATGTAT CTATAT  A
                                       A     III
GAM2342  DXF68S1E 3'  TATACATGCATGCATAT    41037          A G
                                TATATATGCAT C ATAT
                                |||||||||| | ||||
                                ATATGTACGTA G TATA
                                       C _
GAM2342  FACL4    3'  TATATATGCATATATATA   35687          CG
                                TATATATGCATA  ATATA
                                |||||||||||  |||||
                                ATATATACGTAT  TATAT
                                       A_
GAM2342  ICOS     3'  TATGTATGCATAGATATA   29001    A     C
                                TAT TATGCATA GATATA
                                ||| |||||||| ||||||
                                ATA ATACGTAT CTATAT
                                  C       _
GAM2342  OTP      5'  TATAAGCTATACGATATA   37001    T  _
                                TATA GC ATACGATATA
                                |||| || ||||||||||
                                ATAT CG TATGCTATAT
                                   T  A
GAM2342  PLXNA1   3'  TATATATGCATATATATA   43627          CG
                                TATATATGCATA  ATATA
                                |||||||||||  |||||
                                ATATATACGTAT  TATAT
                                       A_
GAM2342  RBP3     3'  TATATATACATACACATATA 16191           _
                                TATATATGCATACG ATATA
                                |||||||||||||| |||||
                                ATATATATGTATGT TATAT
                                       G
GAM2342  RCN2     3'  TACATATGCAAAAATATA   16216         TAC
                                TATATATGCA   GATATA
                                ||||||||||   ||||||
                                ATGTATACGT   TTATAT
                                      TT_
GAM2342  SAR1     3'  CATATATGCACTCTGATA   33550          AC_
                                TATATATGCAT   GATA
                                ||||||||||   ||||
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                                GTATATACGTG  CTAT
                                      AGA
GAM2342  STAM    3'  TATATATACACACACATATA  18462          _
                                TATATATGCATACG ATATA
                                |||||||||||||| |||||
                                ATATATATGTGTGT TATAT
                                       G
GAM2342  TDO2    3'  ATATATGCATACATATA    24903          G
                                ATATATGCATAC ATATA
                                |||||||||||| |||||
                                TATATACGTATG TATAT
                                      _
GAM2343  BMP1    3'  TTTCTGCACTCGGAATTTGA  25997        _ C  CCCG
                                TTTCTGCAC CG AAT   TGA
                                ||||||||| || |||   |||
                                AAAGACGTG GC TTA   ACT
                                      A  C  A___
GAM2343  MLANA   3'  CTTCTGCACATTCTTGTGA  24298        CGCAA  CC
                                TTTCTGCAC    TC  GTGA
                                |||||||||    ||  ||||
                                GAAGACGTG    AG  CACT
                                      TA___  AA
GAM2343  PMX1    5'  CTCTCTGCACTCCTGTG    35508        CGCAA  C
                                CTTTCTGCAC    TCC GTG
                                ||||||||||    ||| |||
                                GAGAGACGTG    AGG CAC
                                      _____  A
GAM2344  APPBP2  3'  ATACCTAGGATTGCAAT    26873       CAT
                                ATACCTG  GTTGCAAT
                                |||||||  ||||||||
                                TATGGAT  TAACGTTA
                                   CC_
GAM2344  COCH    3'  AAAATACCTGGCAA       19859        CATGTT
                                AAAATACCTG    GCAA
                                ||||||||||    ||||
                                TTTTATGGAC    CGTT
                                      _______
GAM2344  CUL4B   3'  TAAAATACCTGGCCACA    18726         CAT  TG
                                TAAAATACCTG  GT  CA
                                ||||||||||  ||  ||
                                ATTTTATGGAC  CG  GT
                                      ___  GT
GAM2344  DCN     3'  TAAAACATCCACATTGCA    39446       C TG  GT
                                TAAAATA C  CAT  TGCA
                                ||||||| |  |||  ||||
                                ATTTTGT G  GTA  ACGT
                                   A GT  __
GAM2344  GAS41   3'  TAAAATACCTATATAGCA    27201         GC   T
                                TAAAATACCT  ATGT GCA
                                ||||||||||  |||| |||
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                                ATTTTATGGA  TATA CGT
                                      __    T
GAM2344  PPARGC1   3'  TAAAATACCTGCATTTAAC   29956          GTT
                                TAAAATACCTGCAT   GC
                                ||||||||||||||  ||
                                ATTTTATGGACGTA   TG
                                      AAT
GAM2344  TEM7      3'  CAAAATACCTGTGTGTGCA   33802         CA   T
                                TAAAATACCTG  TGT GCA
                                ||||||||||  ||| |||
                                GTTTTATGGAC  ACA CGT
                                      AC   _
GAM2345  EIF4E     3'  ATCAGAATCACTAATATTA   12692       TTT
                                ATCAGA   ATCATTAATATTA
                                ||||||   ||||||||||||
                                TAGTCT   TAGTGATTATAAT

                                   ___
GAM2345  IGF1      3'  ATCAGATTTATCTTTTGAAAAT 8334           ATT____
              ATT                  ATCAGATTTATC      AATATT
                                ||||||||||||      ||||||
                                TAGTCTAAATAG      TTATAA
                                      AAAACTT
GAM2345  SPS2      3'  AGATTTATCAACAATATT    29300         T
                                AGATTTATCA TAATATT
                                |||||||||| |||||||
                                TCTAAATAGT GTTATAA
                                      T
GAM2346  BIN2      3'  TCTATAGATACTTTTGC     32226        ACACT
                                TCTATAGA    TTTTTGC
                                ||||||||    |||||||
                                AGATATCT    GAAAACG
                                     AT___
GAM2346  CDH1      3'  AGAATACTTTTCTCAGCT    20358      C      G
                                AGAA ACTTTTTT CAGCT
                                |||| |||||||| |||||
                                TCTT TGAAAAGA GTCGA
                                  A      _
GAM2346  INMT      3'  TATAGAACATTCCCCCTGGCT  27682         C     GCA
                                TATAGAACA TTTTTT   GCT
                                |||||||||| ||||||   |||
                                ATATCTTGT AGGGGG   CGA
                                     A     AC_
GAM2347  ANGPT1    5'  GCTGCGTGTACATATTC     40242       ATA  T
                                GCTGCGT   GT ATGTATTC
                                |||||||   || ||||||||
                                CGACGCA   CA TGTATAAG
                                     ___  _
GAM2347  CYB561    3'  TGCGTTGTTTATGTATTC    12546      ATAG
                                TGCGT    TTATGTATTC
                                |||||    ||||||||||
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                              ACGCA   AATACATAAG
                                ACA_
GAM2347 F3      3' TGCGTTTCCATGTATTCT   42552      ATAG
                              TGCGT   TTATGTATTCT
                              |||||   ||||||||||
                              ACGCA   GGTACATAAGA
                                AA__
GAM2347 SCD     3' TGCGTTGTTTATGTATTC   22837      ATAG
                              TGCGT   TTATGTATTC
                              |||||   |||||||||
                              ACGCA   AATACATAAG
                                ACA_
GAM2347 UBE2B   3' CACTGAAGTTATGTATT    17789      CGTAT
                              CGCTG    AGTTATGTATT
                              |||||    ||||||||||
                              GTGAC    TCAATACATAA
                                T____
GAM2348 ASTN    3' TGAGGCAGGTGCATTAGAGAGT 42954       C      G
                              TGAGGC GGTGTAT TAGAGAGT
                              |||||| ||||||| ||||||||
                              ACTCCG CCACGTA ATCTCTCA
                                 T      _
GAM2348 PDE4A   5' GAGGCTGGGCTTGGGGAGTC  26256      C  T  A  TAGA
                              GAGGC GG GT TG   GAGTC
                              ||||| || || ||   |||||
                              CTCCG CC CG AC   CTCAG
                                A  _  A  CC__
GAM2349 AGTR1   3' TACAAAATGTGCAGTACCAGG  28918         TA   C
                              TACAAAGTGT  CAG ACCAGG
                              ||||||||||  ||| ||||||
                              ATGTTTTACA  GTC TGGTCC
                                    C_   A
GAM2349 CD28    3' TACAGGTGCCTGCCACCAGGC  26023     AA    ACAG
                              TACA  GTGTT   CACCAGGC
                              ||||  |||||   ||||||||
                              ATGT  CACGG   GTGGTCCG
                                C_    ACG_
GAM2349 CDC7L1  3' AAGAGCACCAGCACCAGG    18599     T  TA
                              AAG GT  CAGCACCAGG
                              ||| ||  ||||||||||
                              TTC CG  GTCGTGGTCC
                                T  TG
GAM2349 CX3CR1  3' CACAGCACAGCAGTGCCAGG  43292    A   GTT    ___
                              CA AGT   ACAGCA   CCAGG
                              || |||   ||||||   |||||
                              GT TCG   TGTCGT   GGTCC
                               G  ___     CAC
GAM2349 DBT     3' TACAGGCGTGAGCCACCAGGC  12552     AA   TAC  _
                              TACA  GTGT   AGC ACCAGGC
                              ||||  ||||   ||| |||||||
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                                ATGT  CGCA   TCG TGGTCCG
                                  C_   C__   G
GAM2349  EGFL5    5'  TACAGGGGTGGTCGGCGCCGGG 44533     AA_   TTACA  A  A
                C                  TACA   GTG    GC CC GGC
                                   ||||   |||    || || |||
                                ATGT   CAC    CG GG CCG
                                  CCC   CAGC_  C  C
GAM2349  F2RL3    3'  TACAGGCGTGAGCCACCAGGC  19530     AA    TAC   _
                                TACA  GTGT   AGC ACCAGGC
                                ||||  ||||   ||| |||||||
                                ATGT  CGCA   TCG TGGTCCG
                                  C_   C__   G
GAM2349  F2RL3    3'  ACAAAGTGCCACATGCCAGGC  19508           GCA
                                ACAAAGTGTTACA   CCAGGC
                                ||||||||||||   ||||||
                                TGTTTCACGGTGT   GGTCCG
                                       AC_
GAM2349  FOS      3'  TGAAAATATCCAGCACCAGG   23520   C      A
                                A AAAGTGTT CAGCACCAGG
                                | ||||||||  ||||||||||
                                A TTTTATAG GTCGTGGTCC
                                 C      _
GAM2349  GLI2     3'  GTGCACTCAGCACCAGGC    36119     TA_
                                GTGT   CAGCACCAGGC
                                ||||   ||||||||||
                                CACG   GTCGTGGTCCG
                                  TGA
GAM2349  GPM6B    3'  CAAAGTATTTTCCAGG      42541         ACAGCA
                                CAAAGTGTT     CCAGG
                                |||||||||     |||||
                                GTTTCATAA     GGTCC
                                     AA____
GAM2349  KLF8     5'  TACAGGTGTGAGCCACCAGGC  28539     AA    TAC   _
                                TACA  GTGT   AGC ACCAGGC
                                ||||  ||||   ||| |||||||
                                ATGT  CACA   TCG TGGTCCG
                                  C_   C__   G
GAM2349  NEBL     3'  CACAATTAGCAGCACCAGGC   26899     AAGT    _
                                TACA    GTTA CAGCACCAGGC
                                ||||    |||| ||||||||||
                                GTGT    TAAT GTCGTGGTCCG
                                  ____    C
GAM2349  PITX2    3'  TACGAAATGTTATACACAGG   7252      A       CA    C
                                TAC AAGTGTTA  GCAC AGG
                                ||| ||||||||  |||| |||
                                ATG TTTACAAT  TGTG TCC
                                  C       A_   _
GAM2349  POV1     5'  AGGGCTCGGGGCACCAGGC   18842    T   ACA_
                                AG GTT    GCACCAGGC
                                || |||    |||||||||
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                                TC CGA   CGTGGTCCG
                                 C  GCCC
GAM2349 PTTG1IP  3' AATGACAGCCACAGCGC    20276     TT   AC  _
                                AGTG  ACAGC  CAG GC
                                ||||  |||||  ||| ||
                                TTAC  TGTCG  GTC CG
                                  __    GT   G
GAM2349 RARG     3' GCATCACACAGCATTAGGC   9724       __    CC
                                GTGTT  ACAGCA  AGGC
                                |||||  ||||||  ||||
                                CGTAG  TGTCGT  TCCG
                                   TG     AA
GAM2349 SLC7A6   3' TGAAATGACCTAGCACCAGG  19599   A    TTAC
                                C AAGTG   AGCACCAGG
                                | |||||   |||||||||
                                A TTTAC   TCGTGGTCC
                                 C    TGGA
GAM2349 SYNGR1   3' AAAACACCCAGCACTGGGC   21747     TG  A     CA
                                AAAG  TT CAGCAC  GGC
                                ||||  || ||||||  |||
                                TTTT  GG GTCGTG  CCG
                                  GT  _     AC
GAM2349 TCEB1L   3' TACAGTGTTACAGTGTCAGGC 17312      AA       CAC
                                TACA  GTGTTACAG   CAGGC
                                ||||  |||||||||   |||||
                                ATGT  CACAATGTC   GTCCG
                                  __        ACA
GAM2349 TNFRSF5  3' CACAGCAGCAGCAGCACCAGGC 10354    A  _  TA
                                CA AGT GT  CAGCACCAGGC
                                || ||| ||  ||||||||||
                                GT TCG CG  GTCGTGGTCCG
                                 G   T  TC
GAM2349 XKRY     5' TACAAGGTGTGACAGCAC    21706      A    T
                                TACAA GTGT ACAGCAC
                                ||||| |||| |||||||
                                ATGTT CACA TGTCGTG
                                   C    C
GAM2349 ADRA2A   5' GCGCACTGTGCGGAGCTCGGG  8638         CAATACAA   C
                                GTGCATTG       AGC CGGG
                                ||||||||       ||| ||||
                                CGCGTGAC       TCG GCCC
                                     ACGCC___   A
GAM2349 SH3BP2   3' GCATTGCACTCCAGCCTGGG   16633        ATACAA    C
                                GCATTGCA     AGCC GGG
                                ||||||||     |||| |||
                                CGTAACGT     TCGG CCC
                                     GAGG__    A
GAM2349 SPN      3' GTGCATTGCACTCCAGCCTGGG 17088          ATACAA    C
                                GTGCATTGCA     AGCC GGG
                                ||||||||||     |||| |||
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                                CACGTAACGT     TCGG CCC
                                     GAGG__    A
GAM2349  WBSCR5   3'  GTGCCTGCCCCACAAAGCCTGG 37128      A   AA       C
             G                    GTGC TTGC  TACAAAGCC GGG
                                  |||| ||||  |||||||||| |||
                                  CACG GACG  GTGTTTCGG CCC
                                    _   GG       A
GAM2350  ENO2     5'  GAGCTGCCGGCGGAGGCGCACG 12710       __  ACTTCTT
                                  GAGCTGC  GC      GGCGCACG
                                  |||||||  ||      ||||||||
                                  CTCGACG  CG      CCGCGTGC
                                      GC  CCT____
GAM2350  INPP5B   5'  GAGCTGTCACCACAGGGCGCAC 45471       CG    TCTT
             G                    GAGCTG  CACT    GGCGCACG
                                  ||||||  ||||    ||||||||
                                  CTCGAC  GTGG    CCGCGTGC
                                     A_    TGTC
GAM2350  CBFA2T3  3'  TCTTTGTCCATTTCT      23268       C   GCGTCA
                                  TCTTTG TCC     ATTTCT
                                  |||||| |||     ||||||
                                  AGAAAC AGG     TAAAGA
                                     _   _______
GAM2350  DLEU2    5'  CCTTTGCTCCAAGTAATTTTTG 25691          C  C    C
                                  TCTTTGCTCCG GT AATTT TG
                                  |||||||||||| || ||||| ||
                                  GGAAACGAGGT CA TTAAA AC
                                        T  _    A
GAM2350  NELL2    3'  TCTTTGCTTTACTTCT      26051         CC  GTCAAT
                                  TCTTTGCT  GC     TTCT
                                  ||||||||  ||     ||||
                                  AGAAACGA  TG     AAGA
                                      AA  _______
GAM2350  ZFP36L1  3'  TTTGCTCTCCAATTTCTGA   22295        CGCG
                                  TTTGCTC    TCAATTTCTGA
                                  |||||||    ||||||||||||
                                  AAACGAG    GGTTAAAGACT
                                      A___
GAM2351  ADRBK1   3'  TGCCAGGCCTAACACTG     11542         TC   T
                                  TGCCAGGC  AAT ACTG
                                  ||||||||  ||| ||||
                                  ACGGTCCG  TTG TGAC
                                      GA  _
GAM2351  AKAP13   3'  TGCCAGGCACGTTACTAGCTGC 28489         TCA__   _
             TAC                    TGCCAGGC    ATTA CTGCTAC
                                    ||||||||    |||| |||||||
                                    ACGGTCCG    TGAT GACGATG
                                        TGCAA   C
GAM2351  BCL2L2   3'  CCAGGCTCAACAGCCCTGC   19735          TA__
                                  CCAGGCTCAAT    CTGC
                                  ||||||||||    ||||
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                                GGTCCGAGTTG   GACG
                                      TCGG
GAM2351  BMP1    3'  CCAACCCAATTGCTGCT    25976     G     A
                                CCAG CTCAATT CTGCT
                                |||| ||||||| |||||
                                GGTT GGGTTAA GACGA
                                  _     C
GAM2351  CASQ2   3'  TGCCATGTTCAGGCACTGC   10284     GGC   AT
                                TGCCA   TCA  TACTGC
                                |||||   |||  ||||||
                                ACGGT   AGT  GTGACG
                                   ACA   CC
GAM2351  CBS     3'  TGCCAGGCCAGGCAGTTAC   6311        ___  A
                                TGCCAGGCT   CA TTAC
                                |||||||||   || ||||
                                ACGGTCCGG   GT AATG
                                      TCC  C
GAM2351  DDX5    3'  ACCATAATTACTGCT      20534     GGCTC
                                GCCA    AATTACTGCT
                                ||||    ||||||||||
                                TGGT    TTAATGACGA
                                  A____
GAM2351  DFFB    3'  CCAGGATTACTGCT       44597     CTCA
                                CCAGG   ATTACTGCT
                                |||||   |||||||||
                                GGTCC   TAATGACGA
                                  _____
GAM2351  DRG2    3'  TGCAGGCTCAGCACTAC    10789     C     AT
                                TGC AGGCTCA  TACTGC
                                ||| |||||||  ||||||
                                ACG TCCGAGT  GTGATG
                                  _     C_
GAM2351  ELAVL2  5'  TGCCAGGCTCACAGTAACTA  20747         ATTACT
                                TGCCAGGCTCA    GCTA
                                ||||||||||     ||||
                                ACGGTCCGAGT    TGAT
                                      GTCAT_
GAM2351  FNTA    3'  TGCAGTTATTACTGCTA    12996     C  GCTCA
                                TGC AG    ATTACTGCTA
                                ||| ||    ||||||||||
                                ACG TC    TAATGACGAT
                                  _ AA___
GAM2351  HPCAL1  3'  GCCAGGCTCAGGGGGCTGC  39547        ATTA_
                                GCCAGGCTCA    CTGC
                                ||||||||||    ||||
                                CGGTCCGAGT    GACG
                                      CCCCC
GAM2351  LZTS1   3'  GCCAGGCTATTCACACTGCT  34267       CAAT_
                                GCCAGGCT    TACTGCT
                                ||||||||    |||||||
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                                CGGTCCGA    GTGACGA
                                    TAAGT
GAM2351  MAGEB4   3'  TGCCAGGCCCAGTTGC      14328          ATTAC
                                TGCCAGGCTCA    TGC
                                ||||||||||    |||
                                ACGGTCCGGGT    ACG
                                     CA___
GAM2351  NKTR     3'  TGCCAGACTCATGAGCTAC   23928          ATTACT
                                TGCCAGGCTCA    GCTAC
                                ||||||||||     |||||
                                ACGGTCTGAGT    CGATG
                                     ACT___
GAM2351  OPCML    3'  TGTGAGGCTCAATTTTTGC   14956    CC        AC
                                TG  AGGCTCAATT  TGC
                                ||  ||||||||||  |||
                                AC  TCCGAGTTAA  ACG
                                 AC         AA
GAM2351  PCDHAC1  5'  TGCCGGCCGTCACTGCT     36623     A    CAA
                                TGCC GGCT   TTACTGCT
                                |||| ||||   ||||||||
                                ACGG CCGG   AGTGACGA
                                  _    C__
GAM2351  PTGS2    3'  GCCAGGCTTGATTCCAATGC  9688         CA   AC__
                                GCCAGGCT  ATT    TGC
                                ||||||||  |||    |||
                                CGGTCCGA  TAA    ACG
                                     AC   GGTT
GAM2351  PTPN7    3'  TGCCAGGCCTGGTCACCTCT  38719         CAA    G
                                TGCCAGGCT   TTACT CT
                                |||||||||   ||||| ||
                                ACGGTCCGG   AGTGG GA
                                     ACC    A
GAM2351  S100A1   3'  TGCAGGCTTGGACCGCTAC   26564     C    CAATT
                                TGC AGGCT    ACTGCTAC
                                ||| |||||    ||||||||
                                ACG TCCGA    TGGCGATG
                                  _    ACC__
GAM2351  TNFRSF11A 3'  TGCCACAAATTACTGCT     19281      GGCTC
                                TGCCA    AATTACTGCT
                                |||||    ||||||||||
                                ACGGT    TTAATGACGA
                                   GT___
GAM2351  TRPV3    3'  CCAGGCTCCAGACTGCT     45439        AATT
                                CCAGGCTC    ACTGCT
                                ||||||||    ||||||
                                GGTCCGAG    TGACGA
                                     GTC_
GAM2351  WFS1     3'  TGACAGGCTCAAGCTGC     25643    C       TTA
                                TG CAGGCTCAA   CTGC
                                || |||||||||   ||||
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                                AC GTCCGAGTT   GACG
                                 T       C__
GAM2352  CYP4F3   3'  TGTATGGATGGACCATATT   9460        AGAAGTA
                                TGTATGGA      ACCATATT
                                ||||||||      ||||||||
                                ACATACCT      TGGTATAA
                                    ACC____
GAM2352  SORBS1   3'  TGTGGGAAGAGGTAACTCA   31718     AT     A    _
                                TGT  GGAAGA GTAAC CA
                                |||  |||||| ||||| ||
                                ACA  CCTTCT CATTG GT
                                  C_     C    A
GAM2353  PRM2     5'  GGAGATCTGGTGGCTCCTGG   15718        __    AATA
                                GGAGATCT  TGGC    TTCTGG
                                ||||||||  ||||    ||||||
                                CCTCTAGA  ACCG    AGGACC
                                    CC    ____
GAM2353  PVR      3'  GGAGTCTTGGGCCACTCTGG   27111      A     CAA
                                GGAG TCTTGG   TATTCTGG
                                |||| ||||||   ||||||||
                                CCTC AGAACC   GTGAGACC
                                  _     CG_
GAM2354  ADRA2B   3'  TGAGAACCAGGAAGCAGG    8653      A       C
                                TGA AACCGGGAA GCAGG
                                ||| ||||||||| |||||
                                ACT TTGGTCCTT CGTCC
                                  C       _
GAM2354  AGTR1    3'  TGAAAACCGGCACGAAAA    28923         GGAAC   G
                                TGAAAACCG     GCA GAAAA
                                |||||||||     ||| |||||
                                ACTTTTGGC     CGT CTTTT
                                    _____  G
GAM2354  ATF4     5'  GAGAATCGGGAACAGG      11724     A  C     AC
                                GA AA CGGGA  GCAGG
                                || || |||||  |||||
                                CT TT GCCCT  TGTCC
                                 C  A    __
GAM2354  AXUD1    3'  TGAAAACCAGGAGTGTGC    37494           AC__
                                TGAAAACCGGGA    GC
                                ||||||||||||    ||
                                ACTTTTGGTCCT    CG
                                      CACA
GAM2354  CAV1     3'  TGAAATTGGCACCAGGAAAA   11996       ACCG  A  G
                                TGAAA    GG AC CAGGAAAA
                                |||||    || || ||||||||
                                ACTTT    CC TG GTCCTTTT
                                  AA__  G  _
GAM2354  CIT      3'  GAAAGCGGGAACAGCAGG    43048       AC      _
                                GAAA  CGGGAAC GCAGG
                                ||||  ||||||| |||||
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                                CTTT  GCCCTTG CGTCC
                                  C_      T
GAM2354  CTNS     5'  TGAAAACCCGGAGGGGAGGA   22351        G   ACGC
                                TGAAAACC GGA    AGGA
                                |||||||| |||    ||||
                                ACTTTTGG CCT    TCCT
                                     G   CCCC
GAM2354  DLG5     5'  GAAAACTGGGAGCAGA      44456       C    AC
                                GAAAAC GGGA  GCAGG
                                |||||| ||||  |||||
                                CTTTTG CCCT  CGTCT
                                   A   __
GAM2354  FGFR1    3'  TGAAGGCAGGCCACACAGGAA  31956      AAC    A_
                                TGAA   CGGG  ACGCAGGAA
                                ||||   ||||  |||||||||
                                ACTT   GTCC  TGTGTCCTT
                                  CC_    GG
GAM2354  GRM6     3'  GAAAACAGCAAATGCAGGAAAA 9171        C  G  C_
              C                  GAAAAC GG AA  GCAGGAAAAC
                                 |||||| || ||  ||||||||||
                                 CTTTTG TC TT  CGTCCTTTTG
                                    _  G  TA
GAM2354  KCNE1L   3'  TGAAAACTGGGGAGGCAAGAAA 29376        C   AAC
              A                   TGAAAAC GGG   GCAGGAAAA
                                  ||||||| |||   |||||||||
                                  ACTTTTG CCC   CGTTCTTTT
                                      A   CTC
GAM2354  MYCN     3'  TGGAAACTTGGAACACACAA   23918    A    CG       G
                                TG AAAC  GGAACGCA GA
                                || ||||  |||||||| ||
                                AC TTTG  CCTTGTGT TT
                                 C    AA       G
GAM2354  MYLK2    3'  AACCGGGAGCGGCTTCAAC    37516         AC  A  AA__
                                AACCGGGA  GC GG    AAC
                                ||||||||  || ||    |||
                                TTGGCCCT  CG CC    TTG
                                     __  _  GAAG
GAM2354  NUP98    3'  TGAAAACCAGGGACCAAA     32235           A  G
                                TGAAAACCGGG AC CAGG
                                |||||||||| || ||||
                                ACTTTTGGTCC TG GTTT
                                       C  _
GAM2354  SLC9A1   5'  TGAAACCGGGAAGCGGCCGGGA 43241       A      _  _ A_
                                TGAAA CCGGGAA CG C  GGA
                                ||||| ||||||| || |  |||
                                ACTTT GGCCCTT GC G  CCT
                                   _      C  C GC
GAM2354  TCEA1    3'  TAAAAATTTGATTTGCAGGAAA 44328        CCG  AAC
              AC                   TGAAAA   GG   GCAGGAAAAC
                                   ||||||   ||   ||||||||||
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                                ATTTTT  CT  CGTCCTTTTG
                                   AAA  AAA
GAM2354 TMEPAI   3' TGAAAACCTGGAGAACAAGA  33626       G  AC
                                TGAAAACC GGA  GCAGGA
                                |||||||| |||  ||||||
                                ACTTTTGG CCT  TGTTCT
                                    A  CT
GAM2355 ATP8B2   3' TCCATAAAATGATATAATT   42214       TTC
                                TCCATAGA  GATATAATT
                                ||||||||  |||||||||
                                AGGTATTT  CTATATTAA
                                    TA_
GAM2355 MSR1     3' TTACTTCATGATTCAAT     14665      C  A
                                TTACT CAT GATTCGAT
                                ||||| ||| ||||||||
                                AATGA GTA CTAAGTTA
                                  A  _
GAM2356 HSD11B1  3' ACCTATGTTTACTAACAAT   24359      C      _
                                ACCTA GTTTATTA TAAT
                                ||||| |||||||| ||||
                                TGGAT CAAATGAT GTTA
                                  A       T
GAM2356 TERF1    3' TATGACCTTGTTTATTAT    32745       AC
                                TATGACCT  GTTTATTAT
                                ||||||||  |||||||||
                                ATACTGGA  CAAATAATA
                                    A_
GAM2356 AQP6     3' GGTTCCTACCACCCTTAGGGC  11644     A         A
                                GGTT CCTATTATCCTTA GGC
                                |||| |||||||||||| |||
                                CCAA GGATGGTGGGAAT CCG
                                  _         C
GAM2356 DGKI     3' GGTTACCTCTCTGAGG      21786       ATTATC  A_
                                GGTTACCT    CTT  AGG
                                ||||||||    |||  |||
                                CCAATGGA    GAG  TCC
                                    _______  AC
GAM2356 IRF1     5' AGGTTGCCGGGTTCTTAAGGC  42040     A  TATTATC
                                AGGTT CC     CTTAAGGC
                                ||||| ||     ||||||||
                                TCCAA GG     GAATTCCG
                                  C  CCCAA__
GAM2356 MSN      3' TAAGTTACTGACTTTAAGG   41248       CT  ATCC
                                TAGGTTAC  ATT   TTAAGG
                                ||||||||  |||   ||||||
                                ATTCAATG  TGA   AATTCC
                                    AC  ____
GAM2356 OPHN1    3' TAGGTTCTTTGTTATCCCT   14970      ACCTA
                                TAGGTT    TTATCCTT
                                ||||||    ||||||||
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                                ATCCAA    AATAGGGA
                                   GAAAC
GAM2356 RPL15   3' TAGCTTACCAATCTTAAGG  16392    G   TATTATC
                                TAG TTACC      CTTAAGG
                                ||| |||||      |||||||
                                ATC AATGG      GAATTCC
                                  G    TTA____
GAM2357 ATRN    3' GAATTAAGGGGCCAGTCCAC  40273       AAAA   A
                                GAATTAAG   CAGT TCGC
                                ||||||||   |||| ||||
                                CTTAATTC   GTCA GGTG
                                     CCCG   _
GAM2357 OPA1    3' AGAGTGAGAAAACAGCA    39267    ATTA
                                AGA   AGAAAACAGTA
                                |||   ||||||||||
                                TCT   TCTTTTGTCGT
                                  CAC_
GAM2357 TPP2    3' AGGCATTAAGAAAACACCAT  17651   A_        G
                                AG  ATTAAGAAAACA TAT
                                ||  |||||||||||| |||
                                TC  TAATTCTTTTGT GTA
                                 CG          G
GAM2358 FMN2    3' TAGAAATAACATTTTACCCA  44286     T        AA
                                TAGAA ATAACATTTTA  TA
                                ||||| ||||||||||  ||
                                ATCTT TATTGTAAAAT  GT
                                   _         GG
GAM2358 TLR3    3' TAGAATATAATCATTTACAAAT 17560         _    _
            A                    TAGAATATAA CATTT TAAATA
                                ||||||||||| ||||| ||||||
                                ATCTTATATT GTAAA GTTTAT
                                      A    T
GAM2359 APOBEC1 3' TACCTTGTGAACATTTCT   25258      A  A
                                TACCT GT AACATTTTT
                                ||||| || |||||||||
                                ATGGA CA TTGTAAAGA
                                   A  C
GAM2359 CHGB    3' CTGAGACAAACATTTTTCC   12241   _  _
                                CT AG TAAACATTTTTCC
                                || || ||||||||||||
                                GA TC GTTTGTAAAAAGG
                                 C  T
GAM2359 CTSF    3' TACCCAGTGCCTTTC      45366        AAACA
                                TACCTAGT    TTTTTC
                                ||||||||    ||||||
                                ATGGGTCA    GGAAAG
                                     C____
GAM2359 DUSP5   3' TACCTAGCAAGTACCCTTC   20661         AC
                                TACCTAGTAA  ATTTTTC
                                ||||||||||  |||||||
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                                ATGGATCGTT  TGGGAAG
                                     CA
GAM2359  GATM     3'  TACCTAGCAGAAGTTATTTTC  11232        AACAT__
                                TACCTAGTA     TTTTC
                                |||||||||     |||||
                                ATGGATCGT     AAAAG
                                     CTTCAAT
GAM2359  GRIN2A   3'  TACCCAGTAGGCATGTCC    9114         AA  TTT
                                TACCTAGTA  CAT   TCC
                                |||||||||  |||  |||
                                ATGGGTCAT  GTA   AGG
                                     CC   C__
GAM2359  HFE      5'  CCCAGTAAAACTTCC      40002        CATT
                                CCTAGTAAA   TTTCC
                                |||||||||   |||||
                                GGGTCATTT   GAAGG
                                     T___
GAM2359  MEOX1    3'  CCTTAGTCATTTTTCC     30396    _  AAA
                                CCT AGT   CATTTTTCC
                                ||| |||   |||||||||
                                GGA TCA   GTAAAAAGG
                                  A  ___
GAM2359  OPA1     3'  TACCCAGTAAGGTCATCT    39269        A__
                                TACCTAGTAA  CATTT
                                ||||||||||  |||||
                                ATGGGTCATT  GTAGA
                                     CCA
GAM2359  PCDH11X  3'  ACCTAGTAAAATTATTTTC   37290        CAT_
                                ACCTAGTAAA   TTTTC
                                ||||||||||   |||||
                                TGGATCATTT   AAAAG
                                     TAAT
GAM2359  PCDH11Y  3'  ACCTAGTAAAATTATTTTC   37330        CAT_
                                ACCTAGTAAA   TTTTC
                                ||||||||||   |||||
                                TGGATCATTT   AAAAG
                                     TAAT
GAM2359  PPP2R1B  3'  CTAGTAAAGGCCTTTTCC    15518        CA_
                                CTAGTAAA  TTTTTCC
                                ||||||||  |||||||
                                GATCATTT  GAAAAGG
                                    CCG
GAM2359  RAB5B    3'  TACCTAGGAACACCCTCC    16093       TA
                                TACCTAG  AACATTTTTC
                                |||||||  ||||||||||
                                ATGGATC  TTGTGGGAGG
                                   C_
GAM2359  RPA2     3'  CCTGGTAGCATCCTTCC     16377     A  AA
                                CCT GTA  CATTTTTCC
                                ||| |||  |||||||||
```

```
                                GGA CAT  GTAGGAAGG
                                  C  C_
GAM2359  SERPINA5  3'  CCCATTCCAACATTTTTCC   8413      GTA_
                                CCTA   AACATTTTTCC
                                ||||   ||||||||||
                                GGGT   TTGTAAAAAGG
                                  AAGG
GAM2359  T       3'  TACCTAGTAGGTCAATCC    17249        AACA  TT
                                TACCTAGTA   TT  TCC
                                |||||||||   ||  |||
                                ATGGATCAT   AG  AGG
                                     CC__  TT
GAM2359  TAF5     3'  TACCTAGTTACATACATTCC   40060       AA   TT_
                                TACCTAGT  ACAT   TTCC
                                ||||||||  ||||   ||||
                                ATGGATCA  TGTA   AAGG
                                    A_   TGT
GAM2360  CRACC    3'  GCCTTGGCCTCTCGAG     34521     C_  ACTTAG
                                GCT  GGC     CTCTCGAG
                                |||  |||     ||||||||
                                CGG  CCG     GAGAGCTC
                                  AA  _______
GAM2360  RANBP3   3'  GCGTCGGCACTATTGGTTGAGT 28760    _      TAGCTCTC
                                GC TCGGCACT       GAGT
                                || ||||||||       ||||
                                CG AGCCGTGA       CTCA
                                 C       TAACCAA_
GAM2361  BCL2L2   3'  CCCTATTTGTCCCTTTGGGC   19737          AGACG
                                CCCTGTTTGTCT    GGGC
                                ||||||||||||    ||||
                                GGGATAAACAGG    CCCG
                                      GAAA_
GAM2361  CENPB    3'  GCCCCTCTGCCCAGGATGGGGC 43013       GT       AC_
                                GCCCCT  TTGTCTAG   GGGGC
                                ||||||  ||||||||   |||||
                                CGGGGA  GACGGGTC   CCCCG
                                   __       CTA
GAM2361  CHRNA4   3'  ACCCCTGGCTGGATGGGG    8844        T   TCTA  C
                                GCCCCTG TTG    GA GGGG
                                ||||||| |||    || ||||
                                TGGGGAC GAC    CT CCCC
                                   C  _____  A
GAM2361  CYLN2    3'  GCCCCCGTTAGGAGATGGGGC  18051         TGTCT   C
                                GCCCCTGTT     AGA GGGGC
                                |||||||||     ||| |||||
                                CGGGGGCAA     TCT CCCCG
                                     TCC__   A
GAM2361  G6PT1    3'  CCTGTTTGTCTGAAGGC     11161          A  CG
                                CCTGTTTGTCT GA  GGGC
                                |||||||||| ||  ||||
```

```
                                GGACAAACAGA CT  TCCG
                                      _ __
GAM2361  GAS7    3'  GCCTCTGTTTGTTTCAGAGC  25272    C      CTAGA
                                GCC CTGTTTGT    CGGGGC
                                ||| ||||||||    ||||||
                                CGG GACAAACA    GTCTCG
                                  A       AA___
GAM2361  PBP     3'  GCCTCTGGTTGTCTAGGTGAG  15018    C  T      AC
                                GCC CTG TTGTCTAG  GGG
                                ||| ||| ||||||||  |||
                                CGG GAC AACAGATC  CTC
                                  A  C       CA
GAM2361  POLL    3'  GCTCCTGCTTAAAATGGGGC  29981    C      TCT  C
                                GC CCTGTTTG   AGA GGGGC
                                || ||||||||   ||| |||||
                                CG GGACGAAT   TTT CCCCG
                                 A       ___  A
GAM2361  RAB36   5'  CCTGGAGTCTGGGCGGGGC   22239    TTT   AGA
                                CCTG   GTCT   CGGGGC
                                ||||   ||||   ||||||
                                GGAC   CAGA   GCCCCG
                                  CT_   CCC
GAM2361  TFAP2C  3'  GCCCCCGTTTGAACACGGGG  17404        TCTAG
                                GCCCCTGTTTG    ACGGGG
                                ||||||||||    ||||||
                                CGGGGGCAAAC    TGCCCC
                                      TTG__
GAM2361  UBE2L3  3'  GCCTCTGCTGACGGG      17827    C    TGTCTA
                                GCC CTGTT     GACGGG
                                ||| |||||     ||||||
                                CGG GACGA     CTGCCC
                                 A   _______
GAM2362  CKAP1   5'  GCTTCGTGGGTATTCGCTTCTG 43883       TTT_  CCACCC
           C                     GCTTTGTG   TTC    CTGC
                                ||||||||   |||    ||||
                                CGAAGCAC   AAG    GACG
                                    CCAT   CGAA__
GAM2362  LAMA4   3'  GCTTTGTGTTTCTTTCAGTGC  14061         CC  CCCC
                                GCTTTGTGTTTTT  CA   TGC
                                ||||||||||||  ||   |||
                                CGAAACACAAAGA  GT   ACG
                                      AA  C___
GAM2362  PBX2    3'  GCCTTGTGAGAGCCCCCACCCC 15105       TTT_
           TG                    GCTTTGTG   TTCCCACCCCTG
                                ||||||||   ||||||||||||
                                CGGAACAC   GGGGGTGGGGAC
                                    TCTC
GAM2362  SH3GL1  3'  GCTGTGTGCTCATCTCTG    16671    T    T  CCACCC
                                GCT TGTGTTT TC    CTG
                                ||| ||||||| ||    |||
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                                CGA ACACGAG AG     GAC
                                  C      T  A_____
GAM2362  SLC4A1   3'  GCCTTTGCTTCTACCCCTG   7356       G      CCC
                                GCTTT TGTTTTT   ACCCCTG
                                ||||| |||||||   |||||||
                                CGGAA ACGAAGA   TGGGGAC
                                  _      ___
GAM2362  TEM7R    3'  TTTGTGTTTGTTCTCACTCTTG 37273         _  C   CCC
              C                  TTTGTGTTT TTC CAC   TGC
                                |||||||||| ||| |||   |||
                                AAACACAAA AAG GTG   ACG
                                     C   A   AGA
GAM2362  TRO      3'  GCTCTTGTACCCATCCCTG   32072      G   TTTT    C
                                GCTTT TGT    CCCA CCCTG
                                ||||| |||    |||| |||||
                                CGAGA ACA    GGGT GGGAC
                                  _  T___    A
GAM2363  APAF1    3'  TAAAACCTGATGTGTGTTGTTA 29825       A   A       A
                                TAAGAT TGA TGTGTGTT TTA
                                |||||| ||| |||||||| |||
                                ATTTTG ACT ACACACAA AAT
                                   G   _       C
GAM2363  DISC1    3'  GATATGAATAGGAGTTAC    33039          TGT
                                GATATGAATG   GTTAT
                                ||||||||||   |||||
                                CTATACTTAT   CAATG
                                     CCT
GAM2363  PLAUR    5'  AAATATGAATGTGGCTGATTA  15368            T   _
                                AGATATGAATGTG GTT ATTA
                                |||||||||||| ||| ||||
                                TTTATACTTACAC CGA TAAT
                                      _  C
GAM2364  GATA3    3'  TACAATATAAGTTATATGCAAT 13098           _   _
                                TACAATATAAGT ATAT TAAT
                                |||||||||||| |||| ||||
                                ATGTTATATTCA TATA GTTA
                                     A   C
GAM2364  RANBP9   3'  CACAATATAAGTGTGAGCTCTT 24248           ATATTAA
              G                  TACAATATAAGT      TTTTG
                                ||||||||||||      |||||
                                GTGTTATATTCA      AGAAC
                                     CACTCG_
GAM2365  NDRG3    3'  ACTTAGCTGGGTATGGTGG   36745        AAA   _
                                ACTTAGTT   TATG TGG
                                ||||||||   |||| |||
                                TGAATCGA   ATAC ACC
                                   CCC   C
GAM2366  GOT2     3'  TAAGTCTACATGGTTA      45235          TAATAA
                                TAAGTTTAC     ATGGTTA
                                |||||||||     |||||||
```

```
                                ATTCAGATG     TACCAAT
                                          _______
GAM2366 LMAN1    3'  TAAGTTTACTAACAAGTG    24528             A
                                TAAGTTTACTAATAA TG
                                |||||||||||||| ||
                                ATTCAAATGATTGTT AC
                                        C
GAM2366 OSR1     3'  TAAGTTTACTAACGGAACTCTG 23039           AAA____
              G                  TAAGTTTACTAAT      TGG
                                |||||||||||||      |||
                                ATTCAAATGATTG      ACC
                                        CCTTGAG
GAM2367 ADAMTS13 3'  CGCGGCACTGCTCGTTGGC   40031     AA   G  CA   C
                                CGC  GCAC GT  CGT GGC
                                |||  |||| ||  ||| |||
                                GCG  CGTG CG  GCA CCG
                                  C_   A  A_   A
GAM2367 ADM      3'  GCGAGCACGGCTGTGGC     10027    A      CAC  C
                                GC AGCACGGT   GT GGC
                                || ||||||||   || |||
                                CG TCGTGCCG   CA CCG
                                 C       A__  _
GAM2367 GASC1    5'  CGAGAGCACGACTCGG      42030    CA     GTC  G
                                CG  AGCACG   AC TCGG
                                ||  ||||||   || ||||
                                GC  TCGTGC   TG AGCC
                                 TC     ___  _
GAM2367 ITPKB    3'  GCAGGCACGGTCTTCCAGGC   13646     A      ACG  _
                                GCA GCACGGTC   TC GGC
                                ||| ||||||||   || |||
                                CGT CGTGCCAG   GG CCG
                                  C       AA_  T
GAM2367 KCNQ4    5'  CGGGCACGGTCCGGGGC     21729    CAA      A  TC
                                CG   GCACGGTC CG  GGC
                                ||   |||||||| ||  |||
                                GC   CGTGCCAG GC  CCG
                                 C__       _  C_
GAM2367 LAMB1    5'  GCAGCCACGGGGACGCGGC    14065     AG    TC   T
                                GCA  CACGG  ACG CGGC
                                |||  |||||  ||| ||||
                                CGT  GTGCC  TGC GCCG
                                  CG    CC   _
GAM2367 PTPN2    5'  CGTCAGCGCGCAGACTCGGC   15912    CA   A  GTC  G
                                CG  AGC CG   AC TCGGC
                                ||  ||| ||   || |||||
                                GC  TCG GC   TG AGCCG
                                 AG   C  GTC  _
GAM2367 TJP1     5'  CGCAGCCCGGCCACGTCGGC   17539     A  A
                                CGCA GC CGGTCACGTCGGC
                                |||| || ||||||||||||
```

```
                                GCGT CG GCCGGTGCAGCCG
                                  _ G
GAM2367 TMEM1    3' CGCAAGCACAGTGCTGGGC   17591          CAC  C_
                                CGCAAGCACGGT  GT  GGC
                                ||||||||||||  ||  |||
                                GCGTTCGTGTCA  CG  CCG
                                      ___ AC
GAM2367 HIS1     3' GTGGATAGCTTTTTTTTT    26993       TCAC
                                GTGGGT   AGCTTTTTTTTT
                                ||||||   ||||||||||||
                                CACCTA   TCGAAAAAAAAA
                                  ____
GAM2367 RPL23    3' ATGGGTTTAGTTTTTTTTTA  9735        CAC  C
                                GTGGGTT  AG TTTTTTTTTA
                                |||||||  || ||||||||||
                                TACCCAA  TC AAAAAAAAAT
                                   A__ _
GAM2367 TAX1BP1  3' GTGGTTTTTTTTTTTTTTTTT 25697     GTTCACAGC
             AC                   GTGG       TTTTTTTTTAC
                                ||||       ||||||||||||
                                CACC       AAAAAAAAATG
                                  AAAAAAAAA
GAM2368 CCND2    3' TAGAAAAAGACCAGGATA    12050     TTC  TA
                                TGGA  GG  ACCAGGATA
                                ||||  ||  |||||||||
                                ATCT  TC  TGGTCCTAT
                                  TTT __
GAM2368 GUCY1A3  3' TGGCATTCCACCAGGATA    41840     _   GGTA
                                TGG ATTC   ACCAGGATA
                                ||| ||||   |||||||||
                                ACC TAAG   TGGTCCTAT
                                  G   G___
GAM2368 HSPA4    3' TGAATAAACAGGCCAGGATA  44855      T__  TAA
                                TGGAT  CGG  CCAGGATA
                                |||||  |||  ||||||||
                                ACTTA  GTC  GGTCCTAT
                                   TTT  C__
GAM2368 RNF26    3' TGGATGTATGGCAGGAT     36759      TCG  AC_
                                TGGAT  GTA  CAGGAT
                                |||||  |||  ||||||
                                ACCTA  CAT  GTCCTA
                                   ___  ACC
GAM2368 SCRT1    3' CGGATTTGGCAGAGGAT     36362       C   ACC
                                TGGATT GGTA  AGGAT
                                |||||| ||||  |||||
                                GCCTAA CCGT  TCCTA
                                   A   C__
GAM2368 SIGLEC9  3' TGGATTCAGGTTTGAGATA   41646        TAACCA
                                TGGATTCGG    GGATA
                                |||||||||    |||||
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                                ACCTAAGTC     TCTAT
                                     CAAAC_
GAM2368 SLC17A5  3' TAGATTTAAACCAGGAT    29689       CGGT
                                TGGATT    AACCAGGAT
                                ||||||    |||||||||
                                ATCTAA    TTGGTCCTA
                                   AT__
GAM2368 TEC      3' TAGACTGACCAGGAT       17387       C GTA
                                TGGATT G   ACCAGGAT
                                |||||| |   ||||||||
                                ATCTGA C   TGGTCCTA
                                  _ ___
GAM2368 UBE2A    3' GGACCAGCCAGGAT        17785     T   TAA
                                GGAT CGG   CCAGGAT
                                |||| |||   |||||||
                                CCTG GTC   GGTCCTA
                                  _   ___
GAM2368 XRCC3    5' TGGGCTGGCCACCAGGAT    24111     AT C   A
                                TGG  T GGT ACCAGGAT
                                |||  | ||| ||||||||
                                ACC  A CCG TGGTCCTA
                                  CG _   G
GAM2368 APPBP2   3' TGGCACTGCCATCTGT      26885    A  T   GTTTG
                                TG CA CTGC    TATCTGT
                                || || ||||    |||||||
                                AC GT GACG    GTAGACA
                                 C  _   _____
GAM2368 EBP      3' CTTCTCTTGTATCTGTGT    27308    GCG
                                CT   TTTGTATCTGTGT
                                ||   ||||||||||||
                                GA   GAACATAGACACA
                                 AGA
GAM2368 F7       3' ATCTGTGTGTGCATCTGTGT  33334      C  T
                                ATCTG GT TGTATCTGTGT
                                ||||| || ||||||||||
                                TAGAC CA ACGTAGACACA
                                   A  C
GAM2368 F7       3' TGCATCTGTGTGTGCATCTGTG 33346    A     C  T
             T                   TG CATCTG GT TGTATCTGTGT
                                 || |||||| || ||||||||||
                                 AC GTAGAC CA ACGTAGACACA
                                  _     A  C
GAM2368 JAM3     3' TGGCATCTGTGTATGTAC    37269    A     C  T
                                TG CATCTG GT TGTAT
                                || |||||| || |||||
                                AC GTAGAC CA ACATG
                                 C     A  T
GAM2368 PARK2    3' TGAATCTGTGCTCTGGTATTTG 21278    C    C   __    C
             TGT                   TGA ATCTG GTTT  GTAT TGTGT
                                ||| ||||| ||||  |||| |||||
```

```
                                ACT TAGAC CGAG  CATA ACACA
                                  _    A   AC   A
GAM2368  TIMM44   3'  TGGCACTGTGTGACCTGTG   43428    A  T   C  TT T
                                TG CA CTG GT  G ATCTGTG
                                || || ||| ||  | |||||||
                                AC GT GAC CA  C TGGACAC
                                 C  _   A  __ _
GAM2368  TNFSF13B  5'  ATCTGTGTTTGTTGATGT    27298      C     ATCT
                                ATCTG GTTTGT    GTGT
                                ||||| ||||||    ||||
                                TAGAC CAAACA    TACA
                                   A     AC__
GAM2369  GABRP    3'  GCCACTGGGAGAGTGTT     30556      C      C
                                GTCAC GGGAGGGT GTT
                                ||||| |||||||| |||
                                CGGTG CCCTCTCA CAA
                                   A       _
GAM2369  ENDOGL1   3'  GCTGAGGGTGATGGTGTGT   23016     A      C
                                GTT GGGGGTGA GGTGTGT
                                ||| |||||||| |||||||
                                CGA CTCCCACT CCACACA
                                  _       A
GAM2369  EPB49    3'  TGTGAGGGGGTGCGTGGGTGT  12738     T      AC_  T
                                TGT AGGGGGTG   GG GTGT
                                ||| ||||||||   || ||||
                                ACA TCCCCCAC   CC CACA
                                  C       GCA  _
GAM2369  PSCD4    3'  TGTGAGGGGGTGAGAAGTGT   30136     T      C_
                                TGT AGGGGGTGA  GGTGT
                                ||| |||||||||  |||||
                                ACA TCCCCCACT  TCACA
                                  C        CT
GAM2370  IFNB1    3'  TAAAATTTAAATAAATAAAAAT 13482         T_
                AA                  TGAAATTT  ATAAATAAAAATAA
                                ||||||||  ||||||||||||||
                                ATTTTAAA  TATTTATTTTTATT
                                     TT
GAM2371  FACL2    3'  TCTTTTGATATGAAAACCAC   34439       A      TTACT
                                TCTTTT ATATGAA     TCAC
                                ||||||| |||||||     ||||
                                AGAAAA TATACTT     GGTG
                                   C      TT___
GAM2371  P23      5'  TCTTTTAAATGATCACATTCA  27347         T   A   _
                                TCTTTTAA ATGA TTAC TTCA
                                |||||||| |||| |||| ||||
                                AGAAAATT TACT AGTG AAGT
                                     _   _   T
GAM2371  PIGC     3'  TTTTAATAGAAACCACATCACT 15284         T      T
                                TTTTAATA GAATTAC TCACT
                                |||||||| ||||||| |||||
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                                AAAATTAT TTTGGTG AGTGA
                                    C      T
GAM2371  ZNF195   3'  TCTTTTAGTATGAACTCT    28382       A      A
                                TCTTTTA TATGAATT CT
                                ||||||| |||||||| ||
                                AGAAAAT ATACTTGA GA
                                    C      _
GAM2372  AGTR1    3'  GGAAATAAAAAATAACA     28915          CCGCA
                                GGAAATAAAAGA    TAACA
                                ||||||||||||    |||||
                                CCTTTATTTTTT    ATTGT
                                                _____
GAM2372  CLECSF12 3'  GGAAATAAAAATAGCACCAG   44124          ACC   AA
                                GGAAATAAAAG   GCAT  CAG
                                ||||||||||   ||||  |||
                                CCTTTATTTTT   CGTG  GTC
                                      AT_   __
GAM2372  GYPA     3'  CGGAAATAAAGTATCACA    44622         AGAC
                                CGGAAATAAA    CGCA
                                ||||||||||    ||||
                                GCCTTTATTT    GTGT
                                      CATA
GAM2372  JDP1     5'  CGGAAACAAGAGGCACA     34760         A  ACC
                                CGGAAATAA AG   GCATA
                                |||||||| ||   |||||
                                GCCTTTGTT TC   CGTGT
                                      C  ___
GAM2372  NPM1     5'  CGGAGATAAAAGAACGCTGCTC 14823      A      C   ATAA_
            CAG                    CGGA ATAAAAGA CGC     CAG
                                |||| |||||||| |||     |||
                                GCCT TATTTTCT GCG     GTC
                                  C       T   ACGAG
GAM2372  PCLO     3'  GGAAACAAAGGAGAAACA    45303         A  CCGCAT
                                GGAAATAAA GA     AACA
                                |||||||| ||     ||||
                                CCTTTGTTT CT     TTGT
                                      C  CT____
GAM2372  PTGER3   3'  GGAAACAGGACATAACA     9649         AAAGACC
                                GGAAATA      GCATAACA
                                |||||||      ||||||||
                                CCTTTGT      TGTATTGT
                                    CC_____
GAM2372  RECQL5   3'  GGAAATAAAAACACACA     20168          AC
                                GGAAATAAAAG  CGCATA
                                ||||||||||  ||||||
                                CCTTTATTTTT  GTGTGT
                                                __
GAM2372  SLC1A5   5'  CGGAAACAGGGGACCCA     24746         AAA   G
                                CGGAAATA   GACC CA
                                ||||||||   |||| ||
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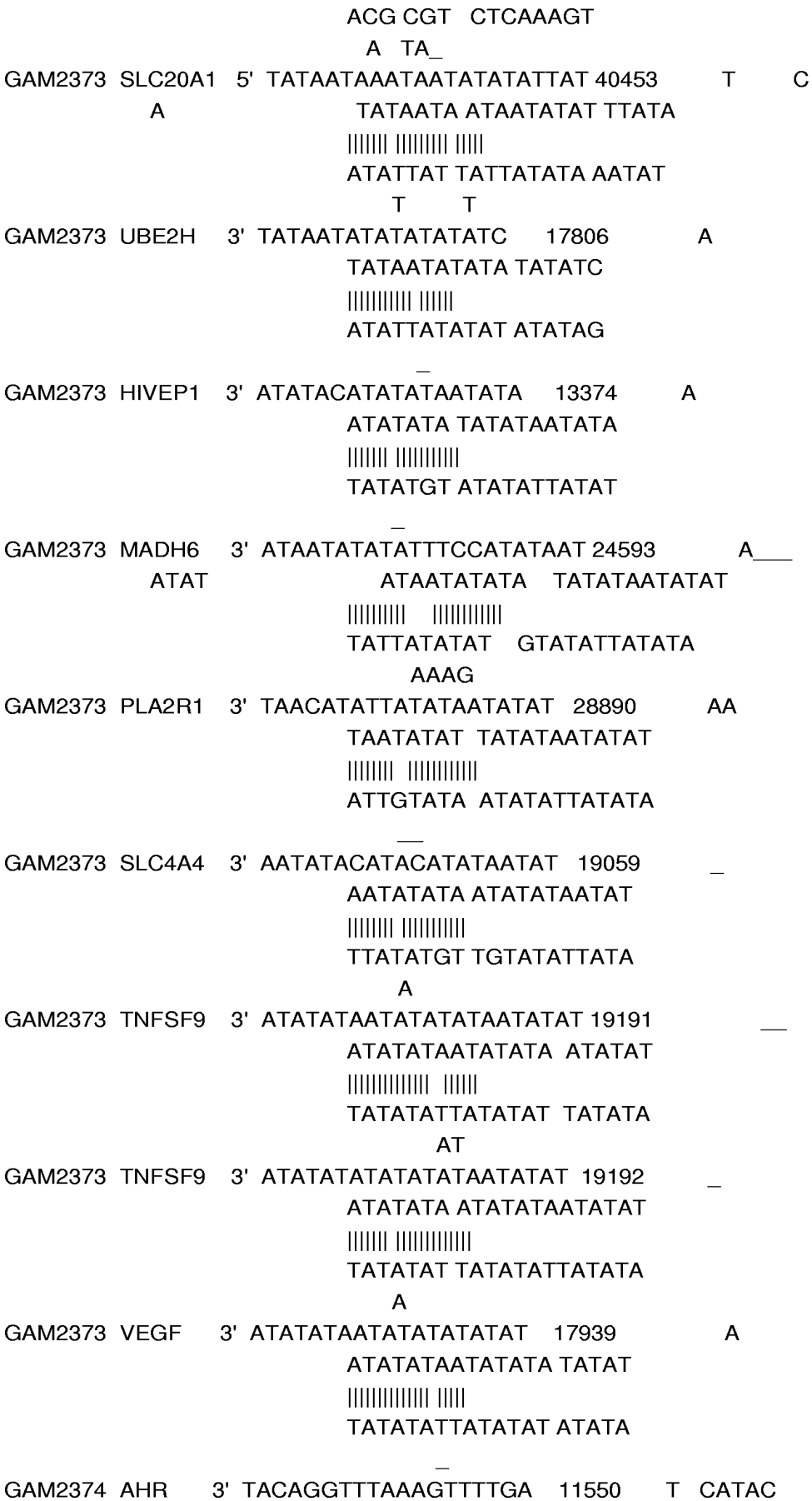
                                GCCTTTGT  CTGG GT
                                    CCC   _
GAM2372  STAU2    3'  CAGAAATAAAAGTAAC     30800          ACCGCA
                                CGGAAATAAAAG     TAAC
                                ||||||||||||    ||||
                                GTCTTTATTTTC     ATTG
                                        _______
GAM2372  THO2     3'  GGAAATAAAAACTGAACCCA  43285          ____   G
                                GGAAATAAAA   GACC CA
                                ||||||||||   |||| ||
                                CCTTTATTTT   TTGG GT
                                     TGAC   _
GAM2372  TPD52L2  3'  GAGATAAAAAATTGCGTAACAG 17635    A      CC  A
                                GA ATAAAAGA  GC TAACAG
                                || ||||||||  || ||||||
                                CT TATTTTTT  CG ATTGTC
                                 C       AA  C
GAM2372  BPAG1    3'  TGTGGCCAAGTTTCAAAA    31784       ATA
                                TGTGGT  CGAGTTTCAAAA
                                ||||||  ||||||||||||
                                ACACCG  GTTCAAAGTTTT
                                    ____
GAM2372  DVL3     3'  TAATGTGGGGTAAAGTC     20688        TA  C
                                TAATGTGG  TA GAGTT
                                ||||||||  || |||||
                                ATTACACC  AT TTCAG
                                     CC  _
GAM2372  GCGR     5'  TGTGTGTGTACGCTCCTC    6698      _  A   AG
                                TGTG GT TACG  TTTC
                                |||| || ||||  ||||
                                ACAC CA ATGC  GGAG
                                  A  C   GA
GAM2372  MBD3     3'  GTGGGTGATGTGAGTTTCAAAA 19423      TATAC__
                                GTGG      GAGTTTCAAAA
                                ||||      ||||||||||||
                                CACC      CTCAAAGTTTT
                                  CACTACA
GAM2372  RAD21    3'  TGAAGTCTGAGTTTCAAA    26532    T  ATAC
                                TG GGT    GAGTTTCAAA
                                || |||    ||||||||||
                                AC TCA    CTCAAAGTTT
                                 T  GA__
GAM2372  RAD51L1  3'  TAATGTGGTTAAACCGCTT   39451        AT_  GA
                                TAATGTGGT   AC  GTTT
                                |||||||||   ||  ||||
                                ATTACACCA   TG  CGAA
                                     ATT  G_
GAM2372  RAP1A    3'  TGCTGCAATGAGTTTCA     16155     G   TAC
                                TGT GTA   GAGTTTCA
                                ||| |||   ||||||||
```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A TA_
GAM2373 SLC20A1 5' TATAATAAATAATATATATTAT 40453 T C
A TATAATA ATAATATAT TTATA
ATATTAT TATTATATA AATAT
T T
GAM2373 UBE2H 3' TATAATATATATATATC 17806 A
TATAATATATA TATATC
ATATTATATAT ATATAG
_
GAM2373 HIVEP1 3' ATATACATATATAATATA 13374 A
ATATATA TATATAATATA
TATATGT ATATATTATAT
_
GAM2373 MADH6 3' ATAATATATATTTCCATATAAT 24593 A___
ATAT ATAATATATA TATATAATATAT
TATTATATAT GTATATTATATA
AAAG
GAM2373 PLA2R1 3' TAACATATTATATAATATAT 28890 AA
TAATATAT TATATAATATAT
ATTGTATA ATATATTATATA
__
GAM2373 SLC4A4 3' AATATACATACATATAATAT 19059 _
AATATATA ATATATAATAT
TTATATGT TGTATATTATA
A
GAM2373 TNFSF9 3' ATATATAATATATATAATATAT 19191 __
ATATATAATATATA ATATAT
TATATATTATATAT TATATA
AT
GAM2373 TNFSF9 3' ATATATATATATATAATATAT 19192 _
ATATATA ATATATAATATAT
TATATAT TATATATTATATA
A
GAM2373 VEGF 3' ATATATAATATATATATAT 17939 A
ATATATAATATATA TATAT
TATATATTATATAT ATATA
_
GAM2374 AHR 3' TACAGGTTTAAAGTTTTGA 11550 T CATAC
TACA GTT AAAGTTTTGA

```
                                ATGT CAA    TTTCAAAACT
                                  C  A____
GAM2374 FAT     3' ACATGTTCATGTATCTGA   23488        ACAAA _
                                ACATGTTCAT    GT TTTGA
                                ||||||||||    || |||||
                                TGTACAAGTA    CA AGACT
                                      _____ T
GAM2374 PUM2    3' ATGTTTATACAAAATACTGAC 31658     C       T
                                ATGTT ATACAAAGT TTGAC
                                ||||| ||||||||| |||||
                                TACAA TATGTTTTA GACTG
                                  A       T
GAM2374 ZNFN2A1 5' ACATCAGCTACAAAGTTTTG  41362     GTTCA
                                ACAT    TACAAAGTTTTG
                                ||||    ||||||||||||
                                TGTA    ATGTTTCAAAAC
                                  GTCG_
GAM2374 AKAP13  3' TAGAAAGCACTTCTGTGG    40353     C  TTCCG
                                TAGAAA CAT    TTCTGTGG
                                ||||||| |||    ||||||||
                                ATCTTT GTG    AAGACACC
                                   C  _____
GAM2374 GPR81   3' TAGAAACTGTATTCCGTGAAAG 37190      CAT_    TCTGT
           GA                     TAGAAAC   TTCCGT    GGA
                                ||||||||   ||||||    |||
                                ATCTTTG   AAGGCA    CCT
                                    ACAT    CTTT_
GAM2374 SALL2   3' GAAGCTGTTTCTGCTCTGTGG 41898    ACCA   C
                                GAA   TTTC GTTCTGTGG
                                |||   |||| |||||||||
                                CTT   AAAG CGAGACACC
                                  CGAC   A
GAM2375 ABCD4   3' AACTGATTAAAAGATTTCCA  33736        AA  GCG
                                AACTGGTTAAA  AGA  CCA
                                ||||||||||  |||  |||
                                TTGACTAATTT  TCT  GGT
                                      __  AAA
GAM2375 AICDA   3' AACTGATTGAAAGTGAGC    34034       A  AA
                                AACTGGTT AAA  GAGC
                                |||||||| |||  ||||
                                TTGACTAA TTT  CTCG
                                    C  CA
GAM2375 DXF68S1E 3' AACTGGTTAAGAGGAGCA   41034        AAAA
                                AACTGGTTAA   GAGCG
                                ||||||||||   |||||
                                TTGACCAATT   CTCGT
                                     CTC_
GAM2375 EGF     3' ACTGCTTAAAAGAGCA     12649     G    AA
                                ACTG TTAAA  AGAGCG
                                |||| |||||  ||||||
```

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                                TGAC AATTT  TCTCGT
                                  G    __
GAM2375  FOG2     3'  ACTGGTTAGAACAACA      28967        AAAAA     C
                                ACTGGTT     AGAGCG CA
                                |||||||     ||||||  ||
                                TGACCAA     TCTTGT GT
                                    _____      T
GAM2375  G22P1    3'  AACTGGCTGAGGACAAGGCCA  11172         AAAAAA   C
                                AACTGGTT     GAG GCCA
                                ||||||||     |||  ||||
                                TTGACCGA     TTC CGGT
                                    CTCCTG   _
GAM2375  HLCS     3'  AACTGGCTTAAAAGCTCCAAA  7630         AAAA     G
                                AACTGGTT    AAGAGC CCAAA
                                ||||||||    ||||||  |||||
                                TTGACCGA    TTTTCG GGTTT
                                    A___     A
GAM2375  HOXD4    3'  AACTGGTTGTAAGCAC      31164         AAAAAA
                                AACTGGTT     GAGCGC
                                ||||||||     ||||||
                                TTGACCAA     TTCGTG
                                    CA____
GAM2375  NEBL     5'  ACTGGTTAAGAAATCCAA    26897         AAAA    CG
                                ACTGGTTA    AGAG  CCAA
                                ||||||||    ||||  ||||
                                TGACCAAT    TCTT  GGTT
                                    _____   TA
GAM2375  PGM1     3'  AACTGGTTAGTGAAAAAGTCA  15255         AA_     _
                                AACTGGTTA   AAAGAG CG
                                |||||||||   ||||||  ||
                                TTGACCAAT   TTTTTC GT
                                    CAC     A
GAM2375  PIK3R3   3'  AACTGGTCAGAAAAGATACTGT 41429          A     _  GC_
              CAAA                  AACTGGTTA AAAAGA GC   CAAA
                                ||||||||| ||||||  ||   ||||
                                TTGACCAGT TTTTCT TG   GTTT
                                    C     A  ACA
GAM2375  PTGFRN   3'  GCAGAAAAGAGAGAGCGCCAA  42591    TA   ___
                                GT  AAAA   AGAGCGCCAA
                                ||  ||||   ||||||||||
                                CG  TTTT   TCTCGCGGTT
                                  TC    CTC
GAM2375  SIRT2    3'  CTGGTTAAGAGGGGGCCA    36146        AAAA    C__
                                CTGGTTA    AGAG   GCCA
                                |||||||    ||||   ||||
                                GACCAAT    TCTC   CGGT
                                    _____    CCC
GAM2375  SLC25A13 3'  CTGGTTAAGAAAACACC     30660         AAA
                                CTGGTTAA   AGAGCGCC
                                ||||||||   ||||||||
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                                GACCAATT   TTTTGTGG
                                     C__
GAM2375  UPF3A    3'  TGGTTAAAATCGCAGTGCCAAA 38787         AAG_  C
                                TGGTTAAAA    AG GCCAAA
                                |||||||||    || ||||||
                                ACCAATTTT    TC CGGTTT
                                     AGCG  A
GAM2375  VSX1     3'  AACTGGTTAAAGTGCCA     31095         AAAAA   C
                                AACTGGTTA     GAG GCCA
                                |||||||||     ||| ||||
                                TTGACCAAT     TTC CGGT
                                     _____  A
GAM2375  ZNF265   3'  CTGGATAAAAGAGACAC     24149      TTAA      _
                                CTGG    AAAAGAG CGC
                                ||||    ||||||| |||
                                GACC    TTTTCTC GTG
                                  TA__      T
GAM2375  CRACC    3'  CATTCTTGCCCAACAAGCATT  34519    C   CGGA
                                CA TCT    TTTAACAAGCATT
                                || |||    ||||||||||||
                                GT AGA    GGGTTGTTCGTAA
                                 A   AC__
GAM2375  CRIM1    3'  CTTTCACAACAAGCATT     32371    C   GATT
                                CT TCG    TAACAAGCATT
                                || |||    ||||||||||
                                GA AGT    GTTGTTCGTAA
                                 A  _____
GAM2375  P2RY6    3'  ACTCTTGGGCTCAAGCATT    19987      C  ATTTAA
                                ACTCT GG      CAAGCATT
                                ||||| ||      ||||||||
                                TGAGA CC      GTTCGTAA
                                   A  CGA___
GAM2376  COL4A3   3'  AACACTAGTTTAATGTTT     36374       ACTTT    A
                                AACACT     GGTT GATGTTT
                                ||||||     |||| |||||||
                                TTGTGA     TCAA TTACAAA
                                     _____   A
GAM2376  DPYSL2   3'  CTACTTTGTGATGTTT      10747        GTTA
                                CTACTTTG    GATGTTT
                                ||||||||    |||||||
                                GATGAAAC    CTACAAA
                                     A___
GAM2376  HK1      5'  AACACAGCAAGATAGATGTTTT 37914       TACTTT  T
                                AACAC      GG TAGATGTTTT
                                |||||      || ||||||||||
                                TTGTG      TC ATCTACAAAA
                                   TCGT__  T
GAM2376  HOXC13   3'  AACCCTGCTTTGGTTGGA    40661     A  A       A
                                AAC CT CTTTGGTT GA
                                ||| || |||||||| ||
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                                TTG GA GAAACCAA CT
                                  G C       C
GAM2376 TYR      3' ACATTACTTTGAGTTAGA    7498      C      _
                                ACA TACTTTG GTTAGA
                                ||| ||||||| ||||||
                                TGT ATGAAAC CAATCT
                                  A      T
GAM2376 IFNAR2   3' TATCAGCTGTACTGTTTGCTCT 9322      _ C    C   CT
              T                  TATC GC GTAC GTT  TGTTTTT
                                ||||  || |||| |||  |||||||
                                ATAG CG CATG CAA  ACGAGAA
                                  T A    A  __
GAM2377 BHLHB3   3' TGGGAATAGATGCACTTGA   36263        AAATAC    GT
                                TGGGAATA     TACT  TGA
                                ||||||||     ||||  |||
                                ACCCTTAT     GTGA  ACT
                                     CTAC__   __
GAM2377 ITK      3' TGGGAATAATAATATTACCTCA 24449        _   C    GT_
              TG                   TGGGAATAA AATA TACT   TG
                                ||||||||| |||| ||||   ||
                                ACCCTTATT TTAT ATGG   AC
                                     A    A    AGT
GAM2377 MPV17    3' TGGGAATAAGACTATTATCAAG 43264        AAT    C   TG
                                TGGGAATAA   ACTA TGT  AG
                                |||||||||   |||| |||  ||
                                ACCCTTATT   TGAT ATA  TC
                                     C__    A   GT
GAM2377 MSR1     3' TGGGAATAAAAATGCTGA    14664          TACTAC
                                TGGGAATAAAA     TGTTGA
                                ||||||||||      ||||||
                                ACCCTTATTTT     ACGACT
                                      T_____
GAM2377 RNMT     3' TGGGAATAATGGTGCTGA    19159         AATACTAC
                                TGGGAATAA       TGTTGA
                                |||||||||       ||||||
                                ACCCTTATT       ACGACT
                                     ACC_____
GAM2377 SCP2     3' TGGGAAGAAAATACTGTTTCTG 16486       T       ACTG
                                TGGGAA AAAATACT    TTG
                                ||||||  ||||||||    |||
                                ACCCTT TTTTATGA    GAC
                                   C       CAAA
GAM2377 SFRP4    3' TGGGTATAAAATACTTGA    16588      A        ACTGT
                                TGGG ATAAAATACT    TGA
                                ||||  ||||||||||    |||
                                ACCC TATTTTATGA     ACT
                                  A        _____
GAM2377 WASF1    3' TGGGAAGGGGATACTGCTA    19448       TAAAATAC
                                TGGGAA       TACTGTTG
                                ||||||       ||||||||
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                                ACCCTT       ATGACGAT
                                   CCCCT___
GAM2378 BHLHB3   3' TGGGAATAGATGCACTTGA   36263        AAATAC   GT
                                TGGGAATA     TACT  TGA
                                ||||||||     ||||  |||
                                ACCCTTAT     GTGA  ACT
                                    CTAC__   __
GAM2378 ITK      3' TGGGAATAATAATATTACCTCA 24449        _   C   GT_
             TG                   TGGGAATAA AATA TACT   TG
                                ||||||||| |||| ||||   ||
                                ACCCTTATT TTAT ATGG   AC
                                     A   A   AGT
GAM2378 MPV17    3' TGGGAATAAGACTATTATCAAG 43264        AAT   C   TG
                                TGGGAATAA   ACTA TGT  AG
                                |||||||||   |||| |||  ||
                                ACCCTTATT   TGAT ATA  TC
                                     C__    A   GT
GAM2378 MSR1     3' TGGGAATAAAAATGCTGA    14664         TACTAC
                                TGGGAATAAAA     TGTTGA
                                ||||||||||      ||||||
                                ACCCTTATTTT     ACGACT
                                      T_____
GAM2378 RNMT     3' TGGGAATAATGGTGCTGA    19159        AATACTAC
                                TGGGAATAA       TGTTGA
                                |||||||||       ||||||
                                ACCCTTATT       ACGACT
                                     ACC_____
GAM2378 SCP2     3' TGGGAAGAAAATACTGTTTCTG 16486       T       ACTG
                                TGGGAA AAAATACT    TTG
                                ||||||| ||||||||    |||
                                ACCCTT TTTTATGA    GAC
                                   C       CAAA
GAM2378 SFRP4    3' TGGGTATAAAATACTTGA    16588     A       ACTGT
                                TGGG ATAAAATACT     TGA
                                |||| ||||||||||     |||
                                ACCC TATTTTATGA     ACT
                                  A        _____
GAM2378 WASF1    3' TGGGAAGGGGATACTGCTA    19448       TAAAATAC
                                TGGGAA       TACTGTTG
                                ||||||       ||||||||
                                ACCCTT       ATGACGAT
                                   CCCCT___
GAM2379 CRIM1    3' TGATTGGCTTGGAAGAAAA    32385    T      ___
                                TG ATTGGCTT   AGAAAA
                                || ||||||||   ||||||
                                AC TAACCGAA   TCTTTT
                                 _       CCT
GAM2379 GHR      3' TGTTTTGGCTTAAACGTTATT  6722      A       AAAC
                                TGT TTGGCTTAGA    TATT
                                ||| ||||||||||    ||||
```

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                                ACA AACCGAATTT   ATAA
                                  A        GCA_
GAM2380 AGTR1   5' CTCCCGCCCGCCGCCTCGG   28910          GA  C
                                CTCCCGCCCGC  CC CGG
                                ||||||||||  || |||
                                GAGGGCGGGCG  GG GCC
                                      GC  A
GAM2380 AP2A1   5' CTCCGCCCGCGGTCCGG    39103     C      ACC
                                CTCC GCCCGCG   CCGG
                                |||| |||||||   ||||
                                GAGG CGGGCGC   GGCC
                                  _      CA_
GAM2380 BAALC   5' CTCCCGCCCGCGCTGCAGCCGC 36038           ACC___   G
            GCGG                   CTCCCGCCCGCG     CCG CGCGG
                                ||||||||||||     ||| |||||
                                GAGGGCGGGCGC     GGC GCGCC
                                      GACGTC  _
GAM2380 BMPR1A  5' CTCCAGCCCTCGGCGC     20254     C   GCGACCC
                                CTCC GCCC      CGGCGC
                                |||| ||||      ||||||
                                GAGG CGGG      GCCGCG
                                  T   A_______
GAM2380 BTEB1   5' CCCGCCCGGCACGGCGCGG   10213        _ ACCC
                                CCCGCCCG CG   CGGCGCGG
                                |||||||| ||   ||||||||
                                GGGCGGGC GT   GCCGCGCC
                                    C  _____
GAM2380 CD63    5' CTCCCGCCGCGGCTCCGG    12132        C   ACC
                                CTCCCGCC GCG   CCGG
                                |||||||| |||   ||||
                                GAGGGCGG CGC   GGCC
                                    _  CGA
GAM2380 COL1A1  5' CTCCTGCTCCGACCCCGA    6372      C  CCG
                                CTCC GC   CGACCCCGG
                                |||| ||   |||||||||
                                GAGG CG   GCTGGGGCT
                                  A  AG_
GAM2380 DVL1    3' CTCCCGTCCTGGCCCCCACG   40409       C  GCGA   G
                                CTCCCG CC    CCCC GCG
                                |||||| ||    |||| |||
                                GAGGGC GG    GGGG TGC
                                   A  ACC_    G
GAM2380 EDNRA   5' TCCCGGGCTCCGGCGCG     41999      CCC  GACC
                                TCCCG   GC    CCGGCGCG
                                |||||   ||    ||||||||
                                AGGGC   CG    GGCCGCGC
                                  C__  A___
GAM2380 EGLN1   5' CTTCCTCCAGGCCGGCGCGG  35165    C  GC   CGACC
                                CT CC  CCG    CCGGCGCGG
                                || ||  |||    |||||||||
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                                GA GG  GGT    GGCCGCGCC
                                 A  A_  CC___
GAM2380  HDAC1    5'  CTCCCGCCCGCGGCTCCG    22442          ACC
                                CTCCCGCCCGCG  CCG
                                ||||||||||||  |||
                                GAGGGCGGGCGC  GGC
                                      CGA
GAM2380  KCNA7    5'  CCCCGACGCCCGGCCCCGGTGC 36644     __     CGA     C
              GG                  CTCC  CGCCCG  CCCCGG GCGG
                                ||||  ||||||  |||||| ||||
                                GGGG  GCGGGC  GGGGCC CGCC
                                  CT    C__     A
GAM2380  KIF5C    5'  CCTGCCCGCGACCACGCGG   21150    C       CCG
                                CC GCCCGCGACC  GCGCGG
                                || ||||||||||  ||||||
                                GG CGGGCGCTGG  TGCGCC
                                 A       ___
GAM2380  LRP3     5'  CTCCTGCCCCGCGGCTCCG   42165     C   G  ACCC   G_
                                CTCC GCCC CG   CGGC  CG
                                |||| |||| ||   ||||  ||
                                GAGG CGGG GC   GCCG  GC
                                  A   _ _____   AG
GAM2380  MYO1D    5'  CTCCCGCCGCGGCTGCCGG   43495       C   ACC_
                                CTCCCGCC GCG   CCGG
                                |||||||| |||   ||||
                                GAGGGCGG CGC   GGCC
                                     _  CGAC
GAM2380  NCKAP1   5'  CTCCCGCCCGCGACCTCCG   30256           _
                                CTCCCGCCCGCGACC CCG
                                |||||||||||||| |||
                                GAGGGCGGGCGCTGG GGC
                                         A
GAM2380  PIK3R2   3'  TCCTGCCCTGACCCCAG    22751    C   GC
                                TCC GCCC  GACCCCGG
                                ||| ||||  ||||||||
                                AGG CGGG  CTGGGGTC
                                  A   A_
GAM2380  PITPN    5'  CTCCCGCCCGCTGCCCGCCG  26336         GAC   G
                                CTCCCGCCCGC   CCCG CG
                                ||||||||||   |||| ||
                                GAGGGCGGGCG   GGGC GC
                                      AC_   G
GAM2380  POU2AF1  3'  CTCACGCCTGTGATCCCAG   26367    C   CGC  C
                                CTC CGCC   GA CCCGG
                                ||| ||||   || |||||
                                GAG GCGG   CT GGGTC
                                  T   ACA  A
GAM2380  PRDM16   3'  TCCCTTCCGCGACCCCACGCGG 35248     GC        G
                                TCCC  CCGCGACCCCG CGCGG
                                ||||  |||||||||| |||||
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                                AGGG  GGCGCTGGGGT GCGCC
                                  AA        _
GAM2380  PSMD9    3'  CTCACGCCTGTGATCCCAG   15844    C   CGC  C
                                CTC CGCC   GA CCCGG
                                ||| ||||   || |||||
                                GAG GCGG   CT GGGTC
                                  T   ACA  A
GAM2380  SERPINE1 3'  CTCCCGCCTTGGCCTCCCAA  8287       C__  GAC
                                CTCCCGCC   GC   CCCGG
                                ||||||||   ||   |||||
                                GAGGGCGG   CG   GGGTT
                                    AAC  GA_
GAM2380  SLC20A2  5'  CCCGCCCGGTCCCGGCGCGG  27570       CGAC
                                CCCGCCCG   CCCGGCGCGG
                                ||||||||   ||||||||||
                                GGGCGGGC   GGGCCGCGCC
                                    CA__
GAM2380  SNX9     5'  CTCCGGCTGGGCCCCGGCGCGG 32153     C  CCGCGA
                                CTCC GC     CCCCGGCGCGG
                                |||| ||     ||||||||||
                                GAGG CG     GGGGCCGCGCC
                                  C  ACCC__
GAM2380  STK6     5'  CTCCCACCTGCGACCCAAG   18776       C      C
                                CTCCCGCC GCGACCC GG
                                |||||||| ||||||| ||
                                GAGGGTGG CGCTGGG TC
                                    A      T
GAM2380  XPR1     5'  CCCACATGGGCCCCGGCGCGG  21846      A___
                                CCCGCG   CCCCGGCGCGG
                                ||||||   ||||||||||
                                GGGTGT   GGGGCCGCGCC
                                   ACCC
GAM2380  ARIX     5'  CGGGGTCCGGGTGGAGGTCGG  23180       GC____     CC
                                CGGGGTC     GAGGTC  GG
                                |||||||     ||||||  ||
                                GCCCCAG     CTCCAG  CC
                                    GCCCAC     __
GAM2380  BRF1     5'  CGGGGACGCGAGGACTGG    11333      T     TCCC
                                CGGGG CGCGAGG   GG
                                ||||| |||||||   ||
                                GCCCC GCGCTCC   CC
                                   T      TGA_
GAM2380  BSN      5'  CGGGGTCGCGCTGCGCCCGGGC 18399         AG  _    A
            CG                    CGGGGTCGCG  GT CCCGG CCG
                                ||||||||||  || ||||| |||
                                GCCCCAGCGC  CG GGGCC GGC
                                      GA  C    C
GAM2380  EEF1A2   3'  CGGGGGTGCGGGGCGCCGGACC 41516      TC   A   C
            G                    CGGGG  GCG GGT CCGGACCG
                                |||||  ||| ||| ||||||||
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                                GCCCC  CGC CCG GGCCTGGC
                                   CA   C   C
GAM2380  KIF1B    5'  CGGGGGCGCGGGGGGCCGG   31462      T   A  TC
                                CGGGG CGCG GG  CCGG
                                ||||| |||| ||  ||||
                                GCCCC GCGC CC  GGCC
                                   C   C  CC
GAM2380  MMP25    5'  CAGGGTCGCGCCGCTGGGTCG  35378         AG  CCC  AC
                                CGGGGTCGCG  GT   GG  CG
                                ||||||||||  ||   ||  ||
                                GTCCCAGCGC  CG   CC  GC
                                      GG  A__  CA
GAM2380  PABPC1   5'  CGGGGCCGCGGGCGGGCGGGTC 15022          A  CC_  AC
            G                    CGGGGTCGCG GGT   CGG  CG
                                ||||||||||  |||   |||  ||
                                GCCCCGGCGC CCG   GCC  GC
                                      _  CCC   CA
GAM2380  RERE     5'  CGGGGCCGCGGGGCGCAGGGCC 29026         A   CCC  A
            GA                    CGGGGTCGCG GGT   GG CCGA
                                ||||||||||  |||   ||  ||||
                                GCCCCGGCGC CCG   CC GGCT
                                      C   CGT  C
GAM2380  SDC1     5'  GGGTCGCGGCTGCGGGCCG   16510       GA   CC   A
                                GGGTCGC  GGT  CGG CCG
                                |||||||  |||  ||| |||
                                CCCAGCG  CCG  GCC GGC
                                   __  AC   C
GAM2380  SFRP4    5'  CGGGGCCGCGGGGTCCGG    16584         A    C
                                CGGGGTCGCG GGTCC GG
                                ||||||||||  |||||  ||
                                GCCCCGGCGC CCAGG CC
                                      C    _
GAM2380  SLC21A2  5'  CGGGGTCGGGGCGCCTCGG   24797        CGA  _  _
                                CGGGGTCG   GGT CC CGG
                                ||||||||   ||| || |||
                                GCCCCAGC   CCG GG GCC
                                     C__   C  A
GAM2380  ZNF144   5'  CGGGGTCGGGAGTGGGGGGAC  28339        C   GTCCC
                                CGGGGTCG GAG    GGAC
                                ||||||||  |||    ||||
                                GCCCCAGC CTC    CCTG
                                     C   ACCCC
GAM2381  ANK1     3'  ACACTCCCGCAGAGCG     33845          CAC
                                GCACTTTTGC   AGAGCG
                                ||||||||||   ||||||
                                TGTGAGGGCG   TCTCGC
                                      ____
GAM2381  ATP7A    3'  AAAAGATATTTTTGCCAACAG  6256        CAC_      _
                                AAAAG   TTTTGCCA CAG
                                |||||   |||||||| |||
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                                TTTTC    AAAACGGT GTC
                                  TATA       T
GAM2381  CTNND2    3'  AAAAAGCACTTTGTTGACAAGG 10630           __  C  CA
              AG                   AAAAAGCACTTT  TG CA  GAG
                                   ||||||||||||  || ||  |||
                                   TTTTTCGTGAAA  AC GT  CTC
                                         CA  T  TC
GAM2381  HD        3'  AAAGAGCACTTCTGCCACA    13339     A
                                   AAA AGCACTTTTGCCACA
                                   ||| ||||||||||||||||
                                   TTT TCGTGAAGACGGTGT
                                     C
GAM2381  MTAP      5'  AAGCGAGCCACAGAGCG     14673      ACTTTT
                                   AAGC     GCCACAGAGCG
                                   ||||     ||||||||||
                                   TTCG     CGGTGTCTCGC
                                     CT____
GAM2381  ODC1      3'  GCACTCTTGAGTAGCG      14916         CCAC  _
                                   GCACTTTTG    AG AGCG
                                   |||||||||    || ||||
                                   CGTGAGAAC    TC TCGC
                                        ____  A
GAM2381  PCDH7     5'  GGAGACTACTCGCGTCACAGAG 37118    A  C  _    __
              CG                     A AG ACT TTTGC  CACAGAGCG
                                     | || ||| |||||  |||||||||
                                     C TC TGA GAGCG  GTGTCTCGC
                                      C  _   T    CA
GAM2381  WNT7A     5'  AGCACGGGAGCCACGGAGCG   21519       TTTT    A
                                   AGCAC    GCCAC GAGCG
                                   |||||    ||||| |||||
                                   TCGTG    CGGTG CTCGC
                                      CCCT    C
GAM2381  YWHAG     5'  AGGACCGACCCACAGAGCG    29785    C   TTTG
                                   AG ACT    CCACAGAGCG
                                   || |||    ||||||||||
                                   TC TGG    GGTGTCTCGC
                                    C   CTG_
GAM2381  BRCA1     3'  CCTGGGTGTTTGTATTTGCAGT 28627      C  ACGC       A
                                   TCTG GT    TTGTATTT CAGT
                                   |||| ||    |||||||| ||||
                                   GGAC CA    AACATAAA GTCA
                                     C  CA__       C
GAM2381  TCEA1     3'  CTGTGTATGTTTCACAG     44325     C   CGCT   A
                                   CTG GTA    TGT TTTACAG
                                   ||| |||    ||| |||||||
                                   GAC CAT    ACA AAGTGTC
                                     A  _____  _
GAM2382  AP2B1     3'  TGTAGGAAAAGAGGGTT     10498           A A
                                   TGTAGGAAAAGA G GTT
                                   |||||||||||| | |||
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                                ACATCCTTTTCT C CAA
                                      _ C
GAM2382  CKM      3'  GGAAAAGAAGAGGACCC     12261          TTC TT
                                GGAAAAGAAGAG   G  C
                                ||||||||||||  | |
                                CCTTTTCTTCTC   T  G
                                      C__ GG
GAM2382  CSN10    3'  TGTAAGGAGAGAAGAGCT    23317     _   AA
                                TGTA GGA  AGAAGAGTT
                                |||| |||  |||||||||
                                ACAT CCT  TCTTCTCGA
                                  T   C_
GAM2382  IL2RG    3'  TGAGGGAGAAGAAAAACATGTT 6817     TA   A       TTC
              CG                  TG  GGA AAGAAGAG   GTTCG
                                ||  ||| ||||||||   |||||
                                AC  CCT TTCTTTTT   CAAGC
                                 TC   C       GTA
GAM2382  MAGEA10  5'  TGTAGAAAAGAGGGGTTCCCT  34333      G     AGA    G
                                TGTAG AAAAGA   GTTC TT
                                |||||| ||||||   |||| ||
                                ACATC TTTTCT   CAAG GA
                                   _     CCC    G
GAM2382  RGS5     3'  GTGGGGAAAGAAGGCCTTCG   18833    A  A      A   CG
                                GT GG AAAGAAG GTT  TTCG
                                || || ||||||| |||  ||||
                                CA CC TTTCTTC CGG  AAGC
                                 C  C      _  __
GAM2382  TRPC5    3'  TGTGGAAAAGAATTTGTT    29772     A       GA_
                                TGT GGAAAAGAA   GTT
                                ||| |||||||||   |||
                                ACA CCTTTTCTT   CAA
                                  _       AAA
GAM2382  VEGFB    3'  TGAGGGGAGGAAGAGCCAGTT  17982    T   AAAA      TC
                                TG AGG    GAAGAGT  GTT
                                || |||    |||||||  |||
                                AC TCC    CTTCTCG  CAA
                                 _   CCTC      GT
GAM2383  HLA-DQA1 3'  TCTGTGTTACTGGACATGAC   45569        T  CACT
                                TCTGTGTT AC    CGTGAC
                                |||||||| ||    ||||||
                                AGACACAA TG    GTACTG
                                     _  ACCT
GAM2383  KCNJ5    3'  TCTGTGTTCACTGAAGCCAGTG 9442          CA___  C
              AC                   TCTGTGTTTAC     CT GTGAC
                                ||||||||||||     || |||||
                                AGACACAAGTG     GG CACTG
                                       ACTTC  T
GAM2383  MUC12    3'  TCTGTGTTTGCAGCTCTCCTGA 45334         ACCA__   G
                                TCTGTGTTT      CTC TGA
                                |||||||||      ||| |||
```

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                                AGACACAAA     GAG ACT
                                     CGTCGA   G
GAM2383  PDPK1    3'  TCTGCGTTCCCCTTGTGA    15211         A  A  C
                                TCTGTGTTT CC CT GTGA
                                ||||||||| || || ||||
                                AGACGCAAG GG GA CACT
                                     _ _ A
GAM2383  SIGLEC6  3'  TCTGTGTTTATGTCACTCG   40934          C__
                                TCTGTGTTTA   CACTCG
                                ||||||||||   ||||||
                                AGACACAAAT   GTGAGC
                                     ACA
GAM2384  AMPH     3'  TAGAGGAGCTGTTTTTATAGTG 11602     CA     CTC
              TT                   TGG  GAGCTG   TTATAGTGTT
                                ||| ||||||   ||||||||||
                                ATC  CTCGAC   AATATCACAA
                                  TC     AAA
GAM2385  PPIF     3'  TTAGTGTTGCAGTTTCAC    25061       C  A
                                TTAGTG TG AGTTTCAC
                                |||||| || ||||||||
                                AATCAC AC TCAAAGTG
                                   A  G
GAM2385  RNPEPL1  5'  GTGCACTTCACGGCAG      32889      TGAAG      A
                                GTGC     TTTCACG CAG
                                ||||     ||||||| |||
                                CACG     GAAGTGC GTC
                                  T_____       C
GAM2385  TTC3     5'  GTGCTAAAGTTTCAGACTAAGG 17715             C   __
                                GTGCTGAAGTTTCA GAC  AGG
                                |||||||||||||| |||  |||
                                CACGATTTCAAAGT CTG  TCC
                                      _   AT
GAM2386  GNAZ     3'  TGTTGTATTGGTTTTTGCTGCA 13193    C       CTCAA__
              TA                   TG TGTATTGGT      GCATA
                                || |||||||||      |||||
                                AC ACATAACCA      CGTAT
                                 A        AAAACGA
GAM2386  KLHL3    3'  TGCTGTAACTGATCAAGCAT   44652        _   TC
                                TGCTGTA TTGG  TCAAGCAT
                                ||||||| ||||  ||||||||
                                ACGACAT GACT  AGTTCGTA
                                    T   __
GAM2387  C11orf8  3'  ACAGTTGTGCAAATCTGTGTTG 11478    CA     TG___     A
              GTTTT                AC  TTGTGT    TGTGTT GTTTT
                                ||  ||||||    |||||| |||||
                                TG  AACACG    ACACAA CAAAA
                                 TC     TTTAG     C
GAM2387  CALB1    3'  CATTTGTTGAATTTTAGTTTT  22310      G    TGTG
                                CATT TGTTG    TTAGTTTT
                                |||| |||||    ||||||||
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                                GTAA ACAAC    AATCAAAA
                                  _     TTAA
GAM2387  CEACAM1   3'  ACTATTGGTTATATATTTGGTT 11828    C    T        A_
              TT                   AC ATTG GTTGTGTGTT  GTTTT
                                   || |||| ||||||||||  |||||
                                   TG TAAC CAATATATAA  CAAAA
                                    A    _         AC
GAM2387  NRXN1     3'  TTATGTTTTGTGTTGGTTTT   39855        G      A
                                   TTGTGTT TGTGTT GTTTT
                                   ||||||| |||||| |||||
                                   AATACAA ACACAA CAAAA
                                       A     C
GAM2387  TFDP2     3'  ATTGTGTTTCTCTAGTTTT    26617         GTGTG
                                   ATTGTGTT    TTAGTTTT
                                   ||||||||    ||||||||
                                   TAACACAA    GATCAAAA
                                       AGA__
GAM2387  TLL2      5'  ACCGTCGTGAGACAGGTTAGTT 29743     A    TTGTGT
              TT                   ACC TTGTG     GTTAGTTTT
                                   ||| |||||     |||||||||
                                   TGG AGCAC     CAATCAAAA
                                     C    TCTGTC
GAM2388  NEDD4     3'  TTATATGCTTGTAATTTCTAG  43105        AC       C
                                   TTGTGT  CTTGTAAT TCTAG
                                   ||||||  |||||||| |||||
                                   AATATA  GAACATTA AGATC
                                      C_       A
GAM2389  AQP6      5'  GGGAAAGTAAGGGGGGCGAAGG 38252         TTGTAA  ACA
                                   GGGAAGGT     GG   AAGG
                                   ||||||||     ||   ||||
                                   CCCTTTCA     CC   TTCC
                                        TTCCCC  GC_
GAM2389  ARPC2     5'  GGTAAGGGAGGCAAGGACGGAG 25064    G    TTT       AA
              G                    GG AAGG   GTAAGGAC  AGG
                                   || ||||   ||||||||  |||
                                   CC TTCC   CGTTCCTG  TCC
                                    A    CTC       CC
GAM2389  CEBPA     3'  GGGAAAGCTGAGGGCAAAGGA  20398         TGTA   A
                                   GGGAAGGTT    AGG CAAAGGA
                                   |||||||||    ||| |||||||
                                   CCCTTTCGA    TCC GTTTCCT
                                         C___    C
GAM2389  CYLN2     3'  GGGAAGATGGCAGGGCGAGG   18059         TT   A  ACAA
                                   GGGAAGGT  GTA GG    AGG
                                   ||||||||  ||| ||    |||
                                   CCCTTCTA  CGT CC    TCC
                                        C_   C  GC__
GAM2389  DNLC2A    3'  GGGAAGGTTGGTGCACACAGG  30507         T  AAGG   A
                                   GGGAAGGTT GT    ACA AGG
                                   ||||||||| ||    ||| |||
```

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                                CCCTTCCAA CA    TGT TCC
                                     C  CG__   G
GAM2389  EFNB1    3'  GGGAAGGTGGCAAGGGGGGCGA 20724         TT     ACAA__
              GG                   GGGAAGGT  GTAAGG     AGG
                                ||||||||  ||||||     |||
                                CCCTTCCA  CGTTCC     TCC
                                     C_     CCCCGC
GAM2389  EGFL4    5'  GGTGAGGGTGAGTGGGGGACAG 41579    _ A   TT  AA_    A
              AGG                   GG GA GGT  GT   GGACA AGG
                                || || |||  ||   ||||| |||
                                CC CT CCA  CA   CCTGT TCC
                                 A  C   CT  CCC    C
GAM2389  ELK1     3'  GGGAGGTTGGCAGACAAAGGA  23413      A    T  AA
                                GGGA GGTT GT  GGACAAAGGA
                                |||| |||| ||  ||||||||||
                                CCCT CCAA CG  TCTGTTTCCT
                                  _    C  __
GAM2389  EZH1     3'  GGGGGACAGCAGGGACAAAGGA 12785     AA  TTT   A
                                GGG  GG   GTA GGACAAAGGA
                                |||  ||   ||| ||||||||||
                                CCC  CC   CGT CCTGTTTCCT
                                  __  TGT   C
GAM2389  HNF3A    3'  GGGTAGAGAGGACAAAGG    40728     A   TTTGTA
                                GGG AGG     AGGACAAAGG
                                ||| |||     ||||||||||
                                CCC TCT     TCCTGTTTCC
                                  A   C_____
GAM2389  IL2RB    3'  GGGAAGTTTGTCACCTAGATGA 9391        G    AA___   CAA
              GG                   GGGAAG TTTGT    GGA   AGG
                                |||||| |||||    |||   |||
                                CCCTTC AAACA    TCT   TCC
                                   _    GTGGA   AC_
GAM2389  ITGAL    3'  GGAAGGTTCAGGCAGAGG    13619         GTA   A  A
                                GGAAGGTTT   AGG CA AGG
                                |||||||||   ||| || |||
                                CCTTCCAAG   TCC GT TCC
                                     ___   _  C
GAM2389  JUNB     3'  GGGGTGTCCGTAAAGGGGCAGG 13763     AAG        ACAA
                                GGG   GTTTGTAAGG    AGG
                                |||   ||||||||||    |||
                                CCC   CAGGCATTTC    TCC
                                  CA_         CCCG
GAM2389  MYO1D    3'  GGACAGTAAGGACAGAGGA    43499    TTT        A
                                GG   GTAAGGACA AGGA
                                ||   ||||||||| ||||
                                CC   CATTCCTGT TCCT
                                 TGT        C
GAM2389  PLA2G2D  3'  GGGGGTGAGGAAGGACAAGGG  29637     AA   TTGT       A
                                GGG  GGT    AAGGACAA GG
                                |||  |||    |||||||| ||
```

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                                CCC  CCA    TTCCTGTT CC
                                  __   CTCC       C
GAM2389  PMX1     5'  GGAGGCCAGCAGGGCGGGGGA  27911     A   TT   A  ACAAA
                                GGA GGT  GTA GG     GGA
                                ||| |||  ||| ||     |||
                                CCT CCG  CGT CC     CCT
                                  _   GT   C  GCCC_
GAM2389  PRKACA   3'  GGGAGAGGGGGCAGGAGGGTGA 15582      _   TTT   A   CA___
              AGG                   GGGA AGG   GTA GGA     AAGG
                                |||| |||   ||| |||    ||||
                                CCCT TCC   CGT CCT     TTCC
                                  C   CC_   _   CCCAC
GAM2389  PRKACG   3'  AGGAAGGCATGGGGCGGGGG   15599        T  TAA  ACAAA
                                GGGAAGGT TG   GG     GG
                                |||||||| ||   ||     ||
                                TCCTTCCG AC   CC     CC
                                     T  C__  GCCC_
GAM2389  PRKCH    3'  GGGAAGGTCCGATAGAGGA    26510          TA__
                                GGGAAGGTTTG    AGGA
                                ||||||||||    ||||
                                CCCTTCCAGGC    TCCT
                                       TATC
GAM2389  SOX12    3'  GGGGTGTCAGAGGGACAAAGGA 28052     AAG   TGTAA
                                GGG   GTT     GGACAAAGGA
                                |||   |||     ||||||||||
                                CCC   CAG     CCTGTTTCCT
                                  CA_   TCTC_
GAM2389  SYN2     3'  GGGAAAGTTGGAGGTGGGGGA  39463         TGTA   ACAAA
                                GGGAAGGTT    AGG    GGA
                                |||||||||    |||    |||
                                CCCTTTCAA    TCC    CCT
                                     CC__    ACCC_
GAM2389  SYNGR2   3'  GGGAAAGTCCAGGGCAGAGG   21743          GTA   A  A
                                GGGAAGGTTT   AGG CA AGG
                                ||||||||||   ||| || |||
                                CCCTTTCAGG   TCC GT TCC
                                       ___   C  C
GAM2389  TBX6     3'  GGGAGGTTTGTGATGGAGGCAG 38858      A      A____   A  A
              AGG                   GGGA GGTTTGT     AGG CA AGG
                                |||| |||||||     ||| || |||
                                CCCT CCAAACA     TCC GT TCC
                                  _      CTACC   _  C
GAM2389  UBTF     3'  GGGGAGGCCAGGGGGGCAAGGG 30616     A    TGTAA  A   A
              A                    GGG AGGTT     GG CAA GGA
                                ||| |||||     || ||| |||
                                CCC TCCGG     CC GTT CCT
                                  C    TCCCC  _   C
GAM2389  UCP2     3'  GGGAAGGTGGTAGGTAAAGGA  17846         TT   A  AC
                                GGGAAGGT  GTA GG  AAAGGA
                                ||||||||  ||| ||  ||||||
```

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                                CCCTTCCA  CAT CC  TTTCCT
                                    C_  _ A_
GAM2389  UGCG    5'  GGGAGAGGAAAGGGCGGAGG  17876     _  TTTGT   ACAA
                                GGGA AGG    AAGG   AGG
                                |||| |||    ||||   |||
                                CCCT TCC    TTCC   TCC
                                  C  T_____   CGCC
GAM2390  ATP2A3   3'  GCAGACAGCGCGGCGG     23195      CACCT
                                GCAGAC    CGCGGCGG
                                ||||||    ||||||||
                                CGTCTG    GCGCCGCC
                                   TC___
GAM2390  CACNA1A  5'  TGCCGGGGCTGGGAGCGCGGCG 35744      CAGACCACCT
            GC                    TGCCG        CGCGGCGGC
                                |||||        |||||||||
                                ACGGC        GCGCCGCCG
                                   CCCGACCCTC
GAM2390  COG2    5'  TGCGCAGACCGACTCGGCGGC  28881    C     AC   GC
                                TGC GCAGACC  CTC  GGCGGC
                                ||| |||||||  |||  ||||||
                                ACG CGTCTGG  GAG  CCGCCG
                                  _      CT   __
GAM2390  DVL3    3'  GCCGCAGGCTGCCACACGTGG  20682       ACCA  T   GC
                                GCCGCAG   CC CGCG  GG
                                |||||||   || ||||  ||
                                CGGCGTC   GG GTGC  CC
                                    CGAC  T   A_
GAM2390  GRAF    5'  TGCTGCAACCACCTGCCCGGGC 31457    C   A    C ___
                                TGC GCAG CCACCT GC   GGC
                                ||| |||| |||||| ||   |||
                                ACG CGTT GGTGGA CG   CCG
                                  A   _    _ GGC
GAM2390  HMOX2   5'  TGCCGCAGGTCGCTGTCG   42174       ACCACC   GG_
                                TGCCGCAG    TCGC   CG
                                ||||||||    ||||   ||
                                ACGGCGTC    AGCG   GC
                                    C_____   ACA
GAM2390  ISLR    3'  TGCTTCAGACCACCTCCCAGC  24438    CG        G
                                TGC  CAGACCACCTC CGGC
                                |||  |||||||||| ||||
                                ACG  GTCTGGTGGAG GTCG
                                  AA         G
GAM2390  LASS1   3'  TGCGCAGGGTCCGCGGCGG   34619    C   ACCACC
                                TGC GCAG    TCGCGGCGG
                                ||| ||||    |||||||||
                                ACG CGTC    GGCGCCGCC
                                  _   CCA___
GAM2390  MATK    5'  TGCCACAGGCCAGGCG     40319       A   CCTCGC
                                TGCCGCAG CCA    GGCG
                                |||||||| |||    ||||
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                                ACGGTGTC GGT     CCGC
                                    C  _______
GAM2390  POLR2E   3'  TGCCCTGGGCCACCTCAGC   40927     GCAGA     GC
                                TGCC    CCACCTC  GGC
                                ||||    |||||||  |||
                                ACGG    GGTGGAG  TCG
                                  GACCC      __
GAM2390  POU4F1   5'  GCCGCGGCGGTCGCGGCGGC   26388      AGACCACC
                                GCCGC      TCGCGGCGGC
                                |||||      ||||||||||
                                CGGCG      AGCGCCGCCG
                                   CCGCC___
GAM2390  PPP2R5E  5'  TGCCCCGGACCCGGCGGCGGC  26479     GCA   ACCTC
                                TGCC   GACC    GCGGCGGC
                                ||||   ||||    ||||||||
                                ACGG   CTGG    CGCCGCCG
                                  GGC   GC___
GAM2390  PTGER3   5'  TGCTGGGACCGCGGCCGCGGCG 9651     CGCA   ACC_
           GC                     TGC   GACC   TCGCGGCGGC
                                |||   ||||   ||||||||||
                                ACG   CTGG   GGCGCCGCCG
                                 ACC_   CGCC
GAM2390  SGT     3'  GCTGCAGGGCCGCGGCGG    16618    C   ACCACC
                                GC GCAG     TCGCGGCGG
                                || ||||     |||||||||
                                CG CGTC     GGCGCCGCC
                                 A   CC_____
GAM2390  SNRP70   5'  TGTCCGGAGGCTCGCGGCGGC  44217    _   C  ACCAC
                                TG CCG AG    CTCGCGGCGGC
                                || ||| ||    ||||||||||
                                AC GGC TC    GAGCGCCGCCG
                                 A  C  C_____
GAM2391  APBA1    5'  TCCGCGGGCCCGCGGGAG    43090     A        CCC
                                TTC CGGGCCCGCG   GAG
                                ||| ||||||||||   |||
                                AGG GCCCGGGCGC   CTC
                                  C        C__
GAM2391  EML1     3'  GGTACGCTCGAGAGAG      40723    CCC    C
                                GG   GCGC CGAGAGAG
                                ||   |||| ||||||||
                                CC   TGCG GCTCTCTC
                                 A__    A
GAM2391  HTR1D    3'  TTCACGGACAACTGGGAGAG   9268          CC  GCCC
                                TTCACGGGC  GC   GAGAG
                                |||||||||  ||   |||||
                                AAGTGCCTG  TG   CTCTC
                                     T_  ACC_
GAM2391  MYO1D    5'  GGGCCCGCGATGAGCTCGGGAG 43501         _____  C  A
                                GGGCCCGC    GC CG GAG
                                ||||||||    || || |||
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                                CCCGGGCG    CG GC CTC
                                     CTACT  A  C
GAM2392  ABCA1    3'  CTAGTGATTGAAGAGATGAAA  24270       CGAATC
                                TTAGTGA     AAGAGATGAAA
                                |||||||     ||||||||||
                                GATCACT     TTCTCTACTTT
                                    AAC___
GAM2392  ATP8A2   3'  ATGGATCCCAGGAGATGAA   45252     ACGAA   A
                                GTG    TCA GAGATGAA
                                |||    ||| ||||||||
                                TAC    GGT CTCTACTT
                                  CTAG_   C
GAM2392  OGG1     3'  CTAGTGACAGTGTTGGGAGGTG 32562         AATCAA_   A
                                TTAGTGACG      GAG TG
                                |||||||||      ||| ||
                                GATCACTGT      CTC AC
                                     CACAACC   C
GAM2392  FMR1     3'  TAACAGAACACTTTCTATAGAT 12943        _   GGAGA
                                TAACAGA TAC    CTATAGAT
                                ||||||| |||    ||||||||
                                ATTGTCT GTG    GATATCTA
                                    T   AAA__
GAM2392  FOXE1    3'  TAACAGATGGGGGAGACTGAAG 20947        AC_      AT
                                TAACAGAT   GGAGACT  AG
                                ||||||||   |||||||  ||
                                ATTGTCTA   CCTCTGA  TC
                                     CCC      CT
GAM2392  RFX5     3'  GATACAGAATAGAT       7794         GACT
                                GATACGGA    ATAGAT
                                ||||||||    ||||||
                                CTATGTCT    TATCTA
                                     ____
GAM2393  EN1      3'  TCAACGTCATTGTCCATT    10922          _  G
                                TCAACGTCATT TC ATT
                                |||||||||| || |||
                                AGTTGCAGTAA AG TAA
                                      C  G
GAM2393  MS4A1    3'  TCCACGTCACTTTATTT     6602     A       CGAT
                                TC ACGTCATTT    TATTT
                                || |||||||||    |||||
                                AG TGCAGTGAA    ATAAA
                                  G       ____
GAM2393  ACLY     3'  GAGGTGGTAATCTTCT      42154     A  C  TG
                                GGG TG GT  AATCTTCT
                                ||| || ||  ||||||||
                                CTC AC CA  TTAGAAGA
                                  C  _  __
GAM2393  BPAG1    3'  AAGGGACGTGTTTTATTTC   31779        C   GAATC
                                AAGGGATG GTT     TTC
                                |||||||| |||    |||
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```
                                TTCCCTGC CAA     AAG
                                    A   AATA_
GAM2393  COL9A1    3'  TCAAGGGAGGTGTTTGGTTTTC 38537         TGC   GAATC
             T                   TCAAGGGA   GTT     TTCT
                                 ||||||||   |||     ||||
                                 AGTTCCCT   CAA     AAGA
                                     CCA   ACCAA
GAM2393  PNN       3'  CAAGGGATGTTAATCTT     43401          CGTTG
                                 CAAGGGATG     AATCTT
                                 |||||||||     ||||||
                                 GTTCCCTAC     TTAGAA
                                      AA___
GAM2393  TTC3      3'  TCAACGGATGTTCCTCTTCTC  17716      G    CGTTGAA
                                 TCAA GGATG      TCTTCTC
                                 |||| |||||      |||||||
                                 AGTT CCTAC      AGAAGAG
                                   G    AAGG___
GAM2393  ZNF144    3'  TCAGGGCCTGAATCTTCT    28344     A   ATGCGT
                                 TCA GGG     TGAATCTTCT
                                 ||| |||     ||||||||||
                                 AGT CCC     ACTTAGAAGA
                                   _   GG____
GAM2394  ITGA4     5'  TTAACGGTGGTTGGGGCCTAGA 9428           TGTACGA
             A                   TTAACGGTGGTT      TAGAA
                                 ||||||||||||      |||||
                                 AATTGCCACCAA      ATCTT
                                       CCCCGG_
GAM2394  MRPL49    3'  GGGGTTTGTGTCACAGAA    43025    T     ACG
                                 GG GGTTTGT   ATAGAA
                                 || |||||||   ||||||
                                 CC CCAAACA   TGTCTT
                                  _      CAG
GAM2394  MRPS12    3'  TTAATAGTGGTCCTGATGGAA  37893     CG     GTAC   A
                                 TTAA  GTGGTTT    GAT GAA
                                 ||||  |||||||    ||| |||
                                 AATT  CACCAGG    CTA CTT
                                   AT      A___   C
GAM2394  PCDHA11   5'  AACGGTGGCATCCGGTATGATG 36571         TT___   C   A
             GA                    AACGGTGGT     GTA GAT GA
                                   |||||||||     ||| ||| ||
                                   TTGCCACCG     CAT CTA CT
                                       TAGGC   A   C
GAM2394  DAPP1     3'  GCAGCGCCGCGATCTG      30816    C  T  CAAC      C
                                 GC GC CC    GCGATCT G
                                 || || ||    ||||||| |
                                 CG CG GG    CGCTAGA C
                                  T  C  _____      A
GAM2394  F2R       3'  GCACAGTGGCGCGATCTCGG   12796    C  TCCCAA
                                 GC GC      CGCGATCTCGG
                                 || ||      ||||||||||
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                                CG TG     GCGCTAGAGCC
                                 _ TCACC_
GAM2394 FLII    5' CGCCGCTCTCGCTGCCG     12897        CCAA   GATC
                                CGCCGCTC   CGC   TCG
                                ||||||||   |||   |||
                                GCGGCGAG   GCG   GGC
                                    A___   AC__
GAM2394 MAN2A2  5' CGCCGCTCCGGGCCCAGTCGG 25944        CAAC  GATC
                                CGCCGCTCC   GC   TCGG
                                |||||||||   ||   ||||
                                GCGGCGAGG   CG   AGCC
                                     CC__  GGTC
GAM2394 MAP3K5  5' ACGCCGCTGCCCGGCGGCG   25433        _   AAC   ATCT
                                ACGCCGCT CCC   GCG   CG
                                |||||||| |||   |||   ||
                                TGCGGCGA GGG   CGC   GC
                                    C   C__   C___
GAM2394 MS4A1   3' GCACTGGTGCGATCTCGG    6599     C   CCCAAC
                                GC GCT     GCGATCTCGG
                                || |||     ||||||||||
                                CG TGA     CGCTAGAGCC
                                 _  CCA___
GAM2394 NFIB    3' ACGCCGCCTCCTAGCCTTCG  24637       TC  AAC  GATC
                                ACGCCGC  CC   GC   TCG
                                |||||||  ||   ||   |||
                                TGCGGCG  GG   CG   AGC
                                    GA  AT_  GA__
GAM2394 NKX2H   5' ACGCCGCTCCTACGGAT     30753         CA   C
                                ACGCCGCTCC  ACG GAT
                                ||||||||||  ||| |||
                                TGCGGCGAGG  TGC CTA
                                     A_  _
GAM2394 NPTX1   5' CGCCGCTCTGGGCGCGCTCTTC 14835       CCAA   A  _
           GG                    CGCCGCTC   CGCG TCT CGG
                                ||||||||   |||| ||| |||
                                GCGGCGAG   GCGC AGA GCC
                                    ACCC   G   A
GAM2394 SFN     3' GCTTTCCCTCAATCTCG    43969    CGC   AACG
                                GC   TCCC   CGATCTCG
                                ||   ||||   ||||||||
                                CG   AGGG   GTTAGAGC
                                 AA_   A___
GAM2394 SORL1   5' CGCCGCTCCCGGGGCTCCAGG  16970        AAC  GA   C
                                CGCCGCTCCC   GC  TCT GG
                                ||||||||||   ||  ||| ||
                                GCGGCGAGGG   CG  AGG CC
                                      CCC  __   T
GAM2395 C18orf1 3' TCTGCAACAACAAAAATGTGC  41232        T   TCCAG_
                                TCTGCAACA CAA     GC
                                ||||||||| |||     ||
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                                AGACGTTGT GTT     CG
                                     T  TTTACA
GAM2395 CTBP1    3' TCTCTGCAGTGCCAGGGCCAC 42751        ACATCAAT   __
                                TCTCTGCA      CCAGG  CAC
                                ||||||||      |||||  |||
                                AGAGACGT      GGTCC  GTG
                                     CAC_____    CG
GAM2395 JPH3     3' TCCCTGCAGCGCCTCCCCGGGC 34024        ACA  AA   A
             AC                   TCTCTGCA   TC  TCC GGCAC
                                ||||||||   ||  ||| |||||
                                AGGGACGT   GG  GGG CCGTG
                                     CGC  AG   C
GAM2395 KCNK10   5' TCTCTGCAGCTCAAAACCTGC  39682        ACA   T_  AG
                                TCTCTGCA   TCAA  CC  GC
                                ||||||||   ||||  ||  ||
                                AGAGACGT   AGTT  GG  CG
                                     CG_   TT  A_
GAM2395 KLHL1    3' TCTTTCAACATCAGTAGG    34085     CTG      ATCC
                                TCT   CAACATCA    AGG
                                |||   ||||||||    |||
                                AGA   GTTGTAGT    TCC
                                  AA_       CA__
GAM2395 MBP      3' TCTGCAACGCCCATGTCCAGGC 44894        A_   A_
             AC                   TCTGCAAC  TCA  TCCAGGCAC
                                ||||||||  |||  |||||||||
                                AGACGTTG  GGT  AGGTCCGTG
                                     CG   AC
GAM2395 MEN1     3' TCTCTGTGTACTCCCAGGCA  39233      CAACA  AAT
                                TCTCTG    TC   CCAGGCA
                                ||||||    ||   |||||||
                                AGAGAC    AG   GGTCCGT
                                   ACATG  ___
GAM2395 PAG      3' CTCTGCAATGTCAGACA     32953        CATCAATC
                                CTCTGCAA       CAGGCA
                                ||||||||       ||||||
                                GAGACGTT       GTCTGT
                                     ACA_____
GAM2395 PDHB     3' TCTTGCAGTACAAATCCAGG  44608     C    AC  C
                                TCT TGCA  AT AATCCAGG
                                ||| ||||  || ||||||||
                                AGA ACGT  TG TTAGGTCC
                                  _   CA  T
GAM2395 PIGA     3' TCTGCAACATTCCTCCAGG   33833         CAA
                                TCTGCAACAT   TCCAGG
                                ||||||||||   ||||||
                                AGACGTTGTA   AGGTCC
                                      AGG
GAM2395 PPIA     3' CTCTGCAATCCAGCTAGGCA  34444       AC   AATCC
                                CTCTGCA ATC    AGGCA
                                |||||||  |||    |||||
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                                GAGACGT  TAG    TCCGT
                                   __  GTCGA
GAM2395  RB1CC1   3'  TGAAACATCAAAGGGCA    31319    C      TCCA
                                TG AACATCAA   GGCA
                                || ||||||||   ||||
                                AC TTGTAGTT   CCGT
                                 T      TC__
GAM2395  RXRG     5'  TCTCGGCTCCCAGGCA     27944     T  AACATCAA
                                TCTC GC      TCCAGGCA
                                |||| ||      ||||||||
                                AGAG CG      GGGTCCGT
                                  C A_______
GAM2395  SHANK2   3'  TCTGCAACACACAGTAC     29471        T  ATC  _
                                TCTGCAACA CA   CAG GC
                                ||||||||| ||   ||| ||
                                AGACGTTGT GT   GTC TG
                                    _ ___   A
GAM2395  SLC21A2  3'  TCTCTCAACCCAGGC      24804     TGCAACA
                                TCTC      TCAATCCAGGC
                                ||||      ||||||||||
                                AGAG      AGTTGGGTCCG
                                   _______
GAM2395  STAC     3'  TCCCTGCAACGTAGGC      17139         ATCAATCC
                                TCTCTGCAAC       AGGC
                                ||||||||||       ||||
                                AGGGACGTTG       TCCG
                                     CA_______
GAM2395  TAF6     5'  TCTCTCCAATGCAGGC      24860      GCAACA    C
                                TCTCT     TCAAT CAGGC
                                |||||     ||||| |||||
                                AGAGA     GGTTA GTCCG
                                   _______   C
GAM2395  GARP     3'  GAAGATTTGTTGATCTGACA  24310    TT   G       CA
                                GA  GGT TTGTTGATC  ACA
                                ||  ||| |||||||||  |||
                                CT  CTA AACAACTAG  TGT
                                 T_  _       AC
GAM2395  KCNJ1    5'  TGGATTGGGTTCCA        6891         T  TGTTGA
                                TGGATTGG GT     TCCA
                                |||||||| ||     ||||
                                ACCTAACC CA     AGGT
                                    _ _______
GAM2395  PDE4D    3'  TGTATTGGTGTTTGTTAAT   43902    G       _
                                TG ATTGGTGTT GTTGAT
                                || ||||||||| ||||||
                                AC TAACCACAA CAATTA
                                 A       A
GAM2395  SLC13A3  3'  TGGGCTGGTGTCTTTTCCAA  41302     AT      GTTGA
                                TGG  TGGTGTT    TCCAA
                                |||  |||||||    |||||
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                                ACC  ACCACAG    AGGTT
                                  CG      AAA__
GAM2396  CACNB1   3'  TGCACCTTTTCTCTA      8786        ACAC
                                TGCACCTT    TCTCTA
                                ||||||||    ||||||
                                ACGTGGAA    AGAGAT
                                    A___
GAM2396  CCND2    3'  TTGCACCTCGGTTTCTCT    12056        ACAC
                                TTGCACCTT    TCTCT
                                |||||||||    |||||
                                AACGTGGAG    AGAGA
                                     CCAA
GAM2396  CRTAP    3'  CTGCACTCTACACTCTCTA   26840       C
                                TTGCAC TTACACTCTCTA
                                ||||||| ||||||||||||
                                GACGTG GATGTGAGAGAT
                                   A
GAM2396  DLEC1    3'  CTGCACCTCACTCTCTCTA   28825         A
                                TTGCACCTTAC CTCTCTA
                                |||||||||||| |||||||
                                GACGTGGAGTG GAGAGAT
                                      A
GAM2396  DMXL1    3'  TGCATATAAACTCTCTA     24292      CCT  C
                                TGCA   TA ACTCTCTA
                                ||||   || ||||||||
                                ACGT   AT TGAGAGAT
                                  AT_  T
GAM2396  EFG2     3'  TTGAACCTTTGACCCTCTA   37037     C    AC
                                TTG ACCTT  ACTCTCTA
                                ||| |||||  ||||||||
                                AAC TGGAA  TGGGAGAT
                                  T    AC
GAM2396  FCN2     3'  TCGCACCTTCATCTCT      31896         A  C
                                TTGCACCTT CA TCTCT
                                ||||||||| || |||||
                                AGCGTGGAA GT AGAGA
                                      _  _
GAM2396  HOXD4    5'  TTGTACCTCACTCCCTA     31186     C   TA
                                TTG ACCT  CACTCTCTA
                                ||| ||||  |||||||||
                                AAC TGGA  GTGAGGGAT
                                  A   __
GAM2396  ITCH     3'  TTACACTCAGATAACTCTCTA  36458       C  C___
                                TTGCAC TTA    ACTCTCTA
                                |||||| |||    ||||||||
                                AATGTG AGT    TGAGAGAT
                                   _   CTAT
GAM2396  LECT2    5'  TTGCCCCCACACTCTCT     14131      A
                                TTGC CCTTACACTCTCT
                                |||| ||||||||||||
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                                AACG GGGGTGTGAGAGA
                                   _
GAM2396 LMO2     3'  TACACAACAACTCTCTA     24548      CT  C
                                TGCAC  TA ACTCTCTA
                                |||||  || ||||||||
                                ATGTG  GT TGAGAGAT
                                   TT  _
GAM2396 PTGFRN   3'  TTGCACCTGGCACCACTCT   42610        TA   _
                                TTGCACCT  CACT CTCT
                                ||||||||  |||| ||||
                                AACGTGGA  GTGG GAGA
                                     CC    T
GAM2396 RAF1     3'  CTGCACCACTCTCT       44332        TTAC
                                TTGCACC    ACTCTCT
                                |||||||    |||||||
                                GACGTGG    TGAGAGA
                                   ____
GAM2396 SCML2    3'  TGCACCTTTAAATTCTCTA   25888        ACAC_
                                TGCACCTT    TCTCTA
                                ||||||||    ||||||
                                ACGTGGAA    AGAGAT
                                     ATTTA
GAM2396 SLC19A1  5'  TTGCACCTACAAAGCTTCT   16853        T  ___  C
                                TTGCACCT ACA   CT TCT
                                |||||||| |||   || |||
                                AACGTGGA TGT   GA AGA
                                     _  TTC  _
GAM2397 ANKRA2   5'  TAAGAGCAGTATCCAGTG    35754        TAGG
                                TAAGAGCA    TCGGTG
                                ||||||||    ||||||
                                ATTCTCGT    GGTCAC
                                     CATA
GAM2397 ATP2A3   3'  GAGAGCGGGTGCCCT       23194     CATA   C
                                GAG    GGT GGTGCCCT
                                |||    ||| ||||||||
                                CTC    TCG CCACGGGA
                                  ____   C
GAM2397 DLC1     5'  GAGCGAAGCGCCCTC       25905     ATA  TC
                                GAGC   GG  GGTGCCCTC
                                ||||   ||  |||||||||
                                CTCG   CT  TCGCGGGAG
                                   ___  __
GAM2397 SUFU     3'  TGTGTGATGTGCTGAACCTCAC 32098        AA   CG
                                TGTGTGAT  TGC  GGGCTTCAC
                                ||||||||  |||  |||||||||
                                ACACACTA  ACG  CTTGGAGTG
                                     C_   A_
GAM2397 TARBP2   3'  TGAGTCCAGCTGGGGCTTCAC  39539     TAAT_  C
                                TGA    GC GGGGCTTCAC
                                |||    || ||||||||||
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                                ACT    CG CCCCGAAGTG
                                  CAGGT  A
GAM2397  UCP3    3'  TGTGTGATGGTGCAGCT    17859       AA  CGG
                                TGTGTGAT  TGC  GGCT
                                ||||||||  |||  ||||
                                ACACACTA  ACG  TCGA
                                    CC  ___
GAM2398  E2F1    3'  TGCAGATTGGAGGGTGG    44492     CT     A
                                TGTAG  ATTGGAGG TGG
                                |||||  |||||||| |||
                                ACGTC  TAACCTCC ACC
                                   __      C
GAM2398  FMR2    3'  TGTACTTGCTCAGATGGAG   12986    G  ATTGGA
                                TGTA CT    GGATGGAG
                                ||||  ||    ||||||||
                                ACAT GA    TCTACCTC
                                  _  ACGAG_
GAM2398  FPGS    3'  GTGGCTGGAAGATGG      22431    A  ATT
                                GT GCT   GGAGGATGG
                                ||  |||  |||||||||
                                CA CGA   CCTTCTACC
                                 C  ___
GAM2398  ITGA11  3'  GTTTCTCTGGAGGATGG    29203    AG  A
                                GT  CT TTGGAGGATGG
                                ||  ||  ||||||||||
                                CA  GA GACCTCCTACC
                                 AA  _
GAM2398  CDC2L2  5'  ACTTTTTCTTTCCGAGAC   37934          TTTT
                                ACTTTTTTTTTCCGA   GAC
                                ||||||||||||||   |||
                                TGAAAAAGAAAGGCT   CTG
                                          ____
GAM2398  CRIM1   3'  TTTTTTTTTTTGATTTCAACTC 32389       CC    TG
                                TTTTTTTTT  GATTT  ACTC
                                |||||||||  |||||  ||||
                                AAAAAAAAA  CTAAA  TGAG
                                     AA    GT
GAM2398  FALZ    3'  CTTTTTTTTTTTTTTTTTTGAC 20890       CCGA_
            T                   CTTTTTTTTT    TTTTGACT
                                ||||||||||    ||||||||
                                GAAAAAAAAA    AAAACTGA
                                     AAAAA
GAM2398  FAP     5'  TTTTTCTTTCCACGGACT    20894         ATTTT
                                TTTTTTTTTCCG    GACT
                                ||||||||||||    ||||
                                AAAAAGAAAGGT    CTGA
                                      GC___
GAM2398  MBNL    5'  TTTTTTTTTCCTCCTTGA    34329         GA
                                TTTTTTTTTCC  TTTTGA
                                ||||||||||  ||||||
```

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                              AAAAAAAAAGG  GGAACT
                                    A_
GAM2398  NSD1    3'  TTTTTTTTTTTTTTTTTGACTC 35363        CCGA
                              TTTTTTTTT   TTTTGACTC
                              |||||||||   |||||||||
                              AAAAAAAAA   AAAACTGAG
                                   AAAA
GAM2398  OTOF    3'  TTTTTTTTTCAGTGCTTGACT  22066        CGAT
                              TTTTTTTTTC   TTTGACT
                              ||||||||||   |||||||
                              AAAAAAAAAG   GAACTGA
                                   TCAC
GAM2398  PHKG1   3'  TTTTTTTTTACCCCTTTGACT  26313        _ GA
                              TTTTTTTTT CC  TTTTGACT
                              ||||||||| ||  ||||||||
                              AAAAAAAAA GG  GAAACTGA
                                   T  G_
GAM2398  PLAG1   3'  TTTTCTTTTCTATTTTGACTC  15365        CG
                              TTTTTTTTTC  ATTTTGACTC
                              ||||||||||  ||||||||||
                              AAAAGAAAAG  TAAAACTGAG
                                   A_
GAM2398  PPP5C   3'  TTTTTTTTTCCGATAATGACT  26497          TT
                              TTTTTTTTTCCGAT  TGACT
                              |||||||||||||  |||||
                              AAAAAAAAAGGCTA  ACTGA
                                    TT
GAM2398  RAI14   3'  TTTTTTTTCCGAGACC     31810          TTTT
                              TTTTTTTTCCGA   GACT
                              ||||||||||||   ||||
                              AAAAAAAAGGCT   CTGG
                                   ____
GAM2398  RGS16   3'  TTTTTTTTTCATATTTGACT  16331        CGAT
                              TTTTTTTTTC   TTTGACT
                              |||||||||   |||||||
                              AAAAAAAAAG   AAACTGA
                                   TAT_
GAM2398  SOX4    3'  TTTTTTTTTCCGAAACCACTC  16996          TT  G
                              TTTTTTTTTCCGA  TT ACTC
                              ||||||||||||  ||  ||||
                              AAAAAAAAAGGCT  GG TGAG
                                    TT  _
GAM2398  UBE2L6  3'  TTTTTTTTTCATCTCTGACT  20125        CGA
                              TTTTTTTTTC   TTTTGACT
                              |||||||||   ||||||||
                              AAAAAAAAAG   GAGACTGA
                                   TA_
GAM2398  USP6    3'  TTTTTTCCTCTGACTC     45036        GAT
                              TTTTTTCC   TTTGACTC
                              ||||||||   ||||||||
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                                AAAAAAGG  AGACTGAG
                                   ___
GAM2399 JDP1    3' CAGCATAGGGGACAGTCT   34759       ATTTTA
                                CAGTATAGG    AGTCT
                                |||||||||    |||||
                                GTCGTATCC    TCAGA
                                     CCTG__
GAM2399 NKX3A   3' CAACAGTAGAGACTGGGTCT  26109       TA   TTAA
                                CAACAGTA GGATT   GTCT
                                ||||||||  |||||  ||||
                                GTTGTCAT TCTGA   CAGA
                                     C_   CC__
GAM2399 ORC4L   3' CAGTAGATGGGCAAGTCT   41606    ATA   TT_
                                CAGT  GGAT  TAAGTCT
                                ||||  ||||  |||||||
                                GTCA  TCTA  GTTCAGA
                                  ___   CCC
GAM2400 NLGN2   5' AGACGGTAGTTGAGCGTGG   44745    _   ATC   GT
                                AGA GGTA  GAGCG  TGG
                                ||| ||||  |||||  |||
                                TCT CCAT  CTCGC  ACC
                                  G   CAA   __
GAM2400 VARS2   5' GAGGAGTCGAGCGGGCAG   26660    TAA     TT
                                GAGG  TCGAGCGG  GG
                                ||||  ||||||||  ||
                                CTCC  AGCTCGCC  TC
                                  TC_      CG
GAM2400 ZIC3    5' AGGGGTGGCGGCGGTTGG   18243   A  AAT  A
                                AG GGT  CG GCGGTTGG
                                || |||  || ||||||||
                                TC CCA  GC CGCCAACC
                                 C  CC_ _
GAM2400 LGALS3BP 3' TACCACCTGGAAACTGGTGAGG 42937       TCTT  CGATA
                                TACCGCCTG   CT   AGG
                                |||||||||   ||   |||
                                ATGGTGGAC   GA   TCC
                                     CTTT  CCAC_
GAM2400 MAZ     5' GCTCTTTGTCTTCTTCTCCAAG 43852   _ __    _ GA
            GC                   GC CT  GTCTTCT C  TAAGGC
                                || ||  ||||||| |  ||||||
                                CG GA  CAGAAGA G  GTTCCG
                                 A  AA      A AG
GAM2400 NEK6    3' GCTGGCTTTGATAAGGC    30826   C  T  CTC
                                GC TG CTT   GATAAGGC
                                || || |||   ||||||||
                                CG AC GAA   CTATTCCG
                                 _  C   A__
GAM2400 OXTR    3' CACCTTCTTGATAGGG     9521      G   CTC   A
                                CGCCT TCTT   GATA GG
                                ||||| ||||   |||| ||
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                                GTGGA AGAA   CTAT CC
                                  _   ___    C
GAM2400  WAS      5'  GCCCTTGTCTTCTCTGG     7535       __       GATAA
                                GCCT  GTCTTCTC    GG
                                ||||  ||||||||    ||
                                CGGG  CAGAAGAG    CC
                                  AA       A____
GAM2401  AXUD1    3'  TAGGACTACAAGGCAAAAGGGG 37492         ____     AATC
                                TAGGACTA   GCAAAA   GGGG
                                ||||||||   ||||||   ||||
                                ATCCTGAT   CGTTTT   CCCC
                                     GTTC    ____
GAM2401  BPGM     3'  CTAGCTCTGGAAAATCGGGG   11893      AA___
                                CTAGC    AAAATCGGGG
                                |||||    ||||||||||
                                GATCG    TTTTAGCCCC
                                   AGACC
GAM2401  BTG2     3'  TAGGACAGTAGGAATCAGG    27621       T  CAAAA
                                TAGGAC AG    AATCGGG
                                |||||| ||    |||||||
                                ATCCTG TC    TTAGTCC
                                   _ ATCC_
GAM2401  DHCR7    3'  AGGACTAGTAAAGGTGACTGGG 10681         C   AA__  C
                                AGGACTAG AAA    AT GGG
                                |||||||| |||    || |||
                                TCCTGATC TTT    TG CCC
                                     A   CCAC  A
GAM2401  EIF2AK3  3'  TAGGACTATAAAACTACGG   22108        GC    AAT
                                TAGGACTA  AAAA   CGG
                                ||||||||  ||||   |||
                                ATCCTGAT  TTTT   GCC
                                     A_    GAT
GAM2401  SOST     3'  GGACCAGCAAAGGTAGG     36106          AAATC
                                GGACTAGCAAA     GGG
                                ||||||||||     |||
                                CCTGGTCGTTT     TCC
                                      CCA__
GAM2401  TM4SF2   3'  TAGGACTAGCTGCAGG      21450          AAAAAAT
                                TAGGACTAGC      CGGG
                                ||||||||||      ||||
                                ATCCTGATCG      GTCC
                                      AC_____
GAM2401  TTC1     3'  TAGGACAGCCAGAATCGGGG   17708       T   AAAA
                                TAGGAC AGC    AATCGGGG
                                |||||| |||    ||||||||
                                ATCCTG TCG    TTAGCCCC
                                   _  GTC_
GAM2401  VAV1     3'  GGACCCAAGAGGAAATCGGGG  24073       AGCAAA_
                                GGACT      AAATCGGGG
                                |||||      |||||||||
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                                CCTGG      TTTAGCCCC
                                   GTTCTCC
GAM2401  B4GALT5  3'  GAAGGCCAAGAGGCTCCA    21939         AAA    AA
                                GAAGGCCGA   GGGCT  CCA
                                |||||||||   |||||  |||
                                CTTCCGGTT   TCCGA  GGT
                                     C__    __
GAM2401  CTSD     3'  AGGCCGGAGGCCAAC       12525       AAAA
                                AGGCCG    GGGCTAAC
                                ||||||    ||||||||
                                TCCGGC    TCCGGTTG
                                   C___
GAM2401  EMS1     3'  CCAAGGCCGAGAGGCCA     23425   G      AAA
                                C AAGGCCGA   GGGCTA
                                | ||||||||   ||||||
                                G TTCCGGCT   TCCGGT
                                 G       C__
GAM2401  GOCAP1   3'  AGGCAGCAAGGGGCTAACCAT  35546     CGA  A
                                AGGC   AA GGGCTAACCAT
                                ||||   || ||||||||||
                                TCCG   TT CCCGATTGGTA
                                  TCG  C
GAM2401  GRLF1    3'  CGGGAGCCGAAGGGCCACTCC  44226    AA     AA      A_
                                CG  GGCCGA  AGGGCTA  CC
                                ||  ||||||  |||||||  ||
                                GC  TCGGCT  TCCCGGT  GG
                                 CC      __      GA
GAM2401  LENG4    3'  CGAAGGCCAAGGCAAAC     35882         AAAA   T
                                CGAAGGCCG    GGGC AAC
                                |||||||||    |||| |||
                                GCTTCCGGT    TCCG TTG
                                     _____   T
GAM2401  NGFR     3'  GGCCAAAAGGGTTCCAT     14781      G      CTAA
                                GGCC AAAAGGG    CCAT
                                |||| |||||||    ||||
                                CCGG TTTTCCC    GGTA
                                  _      AA__
GAM2401  RFX5     3'  AGGTAGAAAAAAAGGGACTA   7792      CC___       _
                                AGG     GAAAAGGG CTA
                                |||     |||||||| |||
                                TCC     TTTTTCCC GAT
                                  ATCTT       T
GAM2401  SP100    3'  GAAGGTGAAAAAACTACCAT   17055      CC      G   A
                                GAAGG  GAAAAGG CTA CCAT
                                |||||  ||||||| ||| ||||
                                CTTCC  CTTTTTT GAT GGTA
                                   A_      _  _
GAM2401  ZFP93    3'  AAGGCTGAAGGATGGGAGCCAT 20145       C   AA__   CTAA
                                AAGGC GAA    GGG    CCAT
                                ||||| |||    |||    ||||
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                                TTCCG CTT   CCC   GGTA
                                  A  CCTA  TC__
GAM2402  APOL1   3'  GGGCAGATCAAGAGGTCAGG  18937   A       C  AC
                                GG CAGATCGAGA GG  CAGG
                                || |||||||||| ||  ||||
                                CC GTCTAGTTCT CC  GTCC
                                 C        _ A_
GAM2402  CALM3   3'  CGGGAGGTGCTGGCGGACCAGG 23232    AC  ATCGAGA
                                CGG  AG     CGGACCAGG
                                |||  ||     |||||||||
                                GCC  TC     GCCTGGTCC
                                  C_  CACGACC
GAM2402  DFFB    3'  CGGGCAGATCACCTGAGGTCAG 44598    A     AGAC  AC
           G                     CGG CAGATCG   GG  CAGG
                                ||| |||||||   ||  ||||
                                GCC GTCTAGT   TC  GTCC
                                  C     GGAC  CA
GAM2402  DVL3    3'  ACGGACGGATGGAGAGAG   20668      A  C   C
                                ACGGAC GAT GAGA GG
                                |||||| ||| |||| ||
                                TGCCTG CTA CTCT TC
                                   C  C   C
GAM2402  FUS1    3'  CAGGTAGGTCGGAAGAATCAGG 28583    AC  A  A  C  C
                                CGG  AG TCG GA GGA CAGG
                                |||  || ||| || ||| ||||
                                GTC  TC AGC CT CTT GTCC
                                  CA  C  _ T  A
GAM2402  HDAC5   5'  ACGGACGGGACGGGAGCCCGG  40157      A_  C_  A_
                                ACGGAC  GAT  GAG  CGG
                                ||||||  |||  |||  |||
                                TGCCTG  CTG  CTC  GCC
                                   CC   CC   GG
GAM2402  HDLBP   3'  ACTGACATGCCGGGTGGACCAG 42743   G   GA  AGAC
           G                     AC GACA  TCG   GGACCAGG
                                || ||||  |||   ||||||||
                                TG CTGT  GGC   CCTGGTCC
                                 A   AC   CCA_
GAM2402  HLCS    5'  ACAGGTGGATCACGAGGTCAGG 7631     ACA   A  C  AC
                                ACGG   GATCG GA GG  CAGG
                                ||||   ||||| || ||  ||||
                                TGTC   CTAGT CT CC  GTCC
                                  CAC    G  _  A_
GAM2402  KIF1B   5'  CAGACCGACGGGCGGACCGGG  31460       GA__    A
                                CAGATCGA   CGGACC GG
                                ||||||||   |||||| ||
                                GTCTGGCT   GCCTGG CC
                                     GCCC    C
GAM2402  LIF     3'  GGACAGATGGACAACTCCGGG  14149       CGA   A_  A
                                GGACAGAT   GACGG  CC GG
                                ||||||||   |||||  || ||
```

```
                                CCTGTCTA  CTGTT  GG CC
                                    C__    GA  C
GAM2402  LMO1     3'  GGACAGACGGGCCTGGAGGCCA 14182        ____ GA  C  A
              GG                  GGACAGAT   C  GA GG CCAGG
                                  ||||||||   |  || || |||||
                                  CCTGTCTG   G  CT CC GGTCC
                                      CCCG AC  _  _
GAM2402  MDFI     3'  GGGTAGGAGAGGACCAGG   24620    AC  ATC   C
                                  GG  AG   GAGA GGACCAGG
                                  ||  ||   |||| ||||||||
                                  CC  TC   CTCT CCTGGTCC
                                   CA  ___   _
GAM2402  MRPL49   3'  ACAGGCCAAGGTGGACCAG   43020     AT   AC
                                  ACAG  CGAG  GGACCAG
                                  ||||  ||||  |||||||
                                  TGTC  GTTC  CCTGGTC
                                    CG   CA
GAM2402  NCOA6    5'  ACGGGTGGATCACTTGAGGTCA 30432     ACA    AGAC  AC
              GG                  ACGG   GATCG   GG  CAGG
                                  ||||   |||||   ||  ||||
                                  TGCC   CTAGT   TC  GTCC
                                    CAC    GAAC  CA
GAM2402  NR3C2    3'  CAGACAGACAATTTGGACTGGG 9468        T   GAC   CA
                                  CGGACAGA CGA   GGAC  GG
                                  |||||||| |||   ||||  ||
                                  GTCTGTCT GTT   CCTG  CC
                                      _  AAA   AC
GAM2402  PRX      3'  GGACAGATCGAGGGCAG     34128          AC  AC
                                  GGACAGATCGAG  GG  CAG
                                  ||||||||||||  ||  |||
                                  CCTGTCTAGCTC  CC  GTC
                                                __  __
GAM2402  RPH3AL   3'  CGGGCGGATCACTTGAGACCAG 28100     ACA    AGAC
              G                    CGG   GATCG   GGACCAGG
                                   |||   |||||   ||||||||
                                   GCC   CTAGT   TCTGGTCC
                                     CGC    GAAC
GAM2402  SNX15    3'  ACAGACAGACATGGGCCG    43930         CGAGAC  A  A
                                  ACGGACAGAT     GG CC G
                                  ||||||||||     || || |
                                  TGTCTGTCTG     CC GG C
                                       TAC___  _  C
GAM2402  ERBB2    5'  GGTGGGGGCCGGGCGCGCG   20822    _    ATC   A_
                                  GG GGGGG   TCG  CGCGCG
                                  || |||||   |||  ||||||
                                  CC CCCCC   GGC  GCGCGC
                                   A    ___   CC
GAM2402  JUND     3'  GCGGGGGGGGTCATGCGC     23805         A  TCGAC
                                  GCGGGGGGG TC     GCGC
                                  |||||||| ||     ||||
```

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                                CGCCCCCCC AG    CGCG
                                     _ TA___
GAM2402 LMO2    5' GCGGGGAGGGGACCGTGCG  24544       ATCTCGA  C
                                GCGGGGGGG     CG GCG
                                |||||||||     || |||
                                CGCCCCTCC     GC CGC
                                     CCTG___  A
GAM2402 PPP3R1  5' GCGGGGAGGGGGCGCGCG   44077       ATCTCGA
                                GCGGGGGGG     CGCGCG
                                |||||||||     ||||||
                                CGCCCCTCC     GCGCGC
                                     CCC____
GAM2402 SLC6A5  5' AGCGGGAGGGGGCTGCG    20107       AT  CGAC
                                AGCGGGGGGG  CT   GCG
                                ||||||||||  ||   |||
                                TCGCCCTCCC  GA   CGC
                                     CC  ____
GAM2402 VGF     3' AGGGGGGCGCCGGCGCGCGC  17984      ATC   A
                                GGGGGGG   TCG CGCGCGC
                                |||||||   ||| |||||||
                                TCCCCCC   GGC GCGCGCG
                                    GC_   C
GAM2403 ABCD4   3' GTTTTGTCTAATTTGCTG   33748   C     AGACC
                                GT TTGTCTGG    GCTG
                                || ||||||||    ||||
                                CA AACAGATT    CGAC
                                 A       AAA__
GAM2403 ABH     3' TGGCTTGTCTGGGTGCTG   40744   T     AGACC
                                TG CTTGTCTGG    GCTG
                                || |||||||||    ||||
                                AC GAACAGACC    CGAC
                                 C       CA___
GAM2403 DNASE1  5' TCTTGTCTGGGGGCCCCA   23358       AGACC  G
                                TCTTGTCTGG    GCT CCG
                                ||||||||||    ||| |||
                                AGAACAGACC    CGG GGT
                                     CC___  _
GAM2403 GJB3    5' TGCCTTGTTTCTGTGCTGC   35839      __   GAGACC
                                TGTCTTG  TCTG    GCTGC
                                |||||||  ||||    |||||
                                ACGGAAC  AGAC    CGACG
                                    AA   A_____
GAM2403 NAT1    5' TGTCTGGTTTGGGGGAACC   8555     T  C  A__
                                TGTCT GT TGG   GACC
                                ||||| || |||   ||||
                                ACAGA CA ACC   TTGG
                                   C  A  CCC
GAM2403 SCN4A   3' TGTCTTGTTTTGAAGGTTTTGC 7331       C_    ACC__
            TG                   TGTCTTGT  TGGAG    GCTG
                                |||||||  |||||    ||||
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                                ACAGAACA  ACTTC    CGAC
                                    AA    CAAAA
GAM2404  APP     3'  TATCAAAGACCCAAAGAT    7919         A   TAT
                                TATCAAAGA CCT   GAT
                                ||||||||| |||   |||
                                ATAGTTTCT GGG   CTA
                                    _  TTT
GAM2404  CCND2   3'  TACCAAAGAACGCCAGAT    12049          C   T
                                TATCAAAGAAC TTA GAT
                                |||||||||| ||| |||
                                ATGGTTTCTTG GGT CTA
                                    C  _
GAM2404  EIF1AY  3'  TATCAGAAACCTTATGA     21717       AA
                                TATCA  GAACCTTATGA
                                |||||  ||||||||||
                                ATAGT  TTTGGAATACT
                                   C_
GAM2404  RAD51L1  3'  TATCAAATCAGCTTATGAT   39453        GAAC
                                TATCAAA   CTTATGAT
                                |||||||   ||||||||
                                ATAGTTT   GAATACTA
                                    AGTC
GAM2404  RASGRP1  3'  TATCAAAAAACTTTACAAT   25080          C   TG
                                TATCAAAGAAC TTA  AT
                                |||||||||| |||  ||
                                ATAGTTTTTTG AAT  TA
                                    A   GT
GAM2404  RDS     3'  TCAAAGAATCTCCTTTGAT   7246         ___   A
                                TCAAAGAA   CCTT TGAT
                                ||||||||   |||| ||||
                                AGTTTCTT   GGAA ACTA
                                    AGA   _
GAM2405  CDH11    5'  GCTGCGAGCGGCCCCCGC    38033    CA_  A
                                GC   GA GCGGCCCTCGC
                                ||   || ||||||||||
                                CG   CT CGCCGGGGGCG
                                 ACG  _
GAM2405  CELSR2   3'  AGCCAGAGGCTGGCCTCACAAA 10844       A  _   C
                                AGCCAGA GC GGCC TCGCAGA
                                ||||||| || |||| |||||||
                                TCGGTCT CG CCGG AGTGTTT
                                    C  A   _
GAM2405  CHRNA2   5'  AGCCAGAACGGCTTCATGCAG  8828         G   CC  __
                                AGCCAGAA CGGC  TC  GCAG
                                |||||||| ||||  ||  ||||
                                TCGGTCTT GCCG  AG  CGTC
                                    _   A_  TA
GAM2405  EXTL3    3'  GCCAGGGGCGGCCCACAG    11035      AA      TC
                                GCCAG  GCGGCCC  GCAG
                                |||||  |||||||  ||||
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                                CGGTC  CGCCGGG  TGTC
                                  CC      __
GAM2405  FBXO7    5'  CCGGAAGCGGCGACGGGGACG  29136    A       CCT  CA
                                CC GAAGCGGC   CG  GACG
                                || ||||||||   ||  ||||
                                GG CTTCGCCG   GC  CTGC
                                 C       CT_  CC
GAM2405  KCNK4    3'  GCCAGAGGTGCCCCCAC     37834       A CG
                                GCCAGA G  GCCCTCGC
                                |||||| |  ||||||||
                                CGGTCT C  CGGGGGTG
                                   _ CA
GAM2405  MAPK8IP1  3'  CCAGAAGCCCCGCAGA      24153       AGC    T
                                CCAGA   GGCCC CGCAGA
                                |||||   ||||| ||||||
                                GGTCT   TCGGG GCGTCT
                                  ____    _
GAM2405  NPAS2    5'  GCCGGAGCGGCCCCGC      14820     A  A      T
                                GCC GA GCGGCCC CGC
                                ||| || ||||||| |||
                                CGG CT CGCCGGG GCG
                                 C  _      _
GAM2405  PIM2     5'  GCCCGGAAGCGCCCGCAGACG  41026     A_     G   TC
                                GCC  GAAGCG CCC  GCAGACG
                                |||  |||||| |||  |||||||
                                CGG  CTTCGC GGG  CGTCTGC
                                 GC     _  __
GAM2405  RAB6A    5'  AGCCGGAACCGCAGA       16096      A   GCGGCCC
                                AGCC GAA      TCGCAGA
                                |||| |||      |||||||
                                TCGG CTT      GGCGTCT
                                  C  ________
GAM2405  SLC6A8   5'  AGTCAGAAGCAGTCCACG    24753    C       C  T
                                AG CAGAAGCGG CC CG
                                || |||||||| || ||
                                TC GTCTTCGTC GG GC
                                 A        A  T
GAM2405  SLC7A5   3'  GCCAGAAGGGGCTGCCGGGC   18547        C   __  TC
                                GCCAGAAG GGC  CC  GC
                                |||||||| |||  ||  ||
                                CGGTCTTC CCG  GG  CG
                                     C   AC  CC
GAM2405  STAT4    5'  AGTCAGAAGCGCCCCTCACAG  17143    C       G
                                AG CAGAAGCG CCCTCGCAG
                                || |||||||| |||||||||
                                TC GTCTTCGC GGGAGTGTC
                                 A       G
GAM2405  TLX1     5'  GCCAGAAGCCGAGGACAGA   24338         ___  CCCTC
                                GCCAGAAGC   GG    GCAGA
                                |||||||||   ||    |||||
```

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                                CGGTCTTCG  CC    TGTCT
                                     GCT _____
GAM2405 ZNF278   5' AGCGAGAAGCGGGGCGCAGCAG 36784    C      CCCTC_
            ACG                   AGC AGAAGCGG     GCAGACG
                                ||| ||||||||     |||||||
                                TCG TCTTCGCC     CGTCTGC
                                  C       CCGCGT
GAM2405 AANAT    3' CTTTATTTAGCCCTGCTC    9899     GTT      C
                                CT   TTTGGCCC GCTC
                                ||   |||||||| ||||
                                GA   AAATCGGG CGAG
                                 AAT       A
GAM2405 ADAMTS13 3' CCCCTGGCACACAGGTCTCGTT 40029       TTTTT__ CCC __
            CTCC                  CCCCTG      GG   CG  CTCC
                                ||||||      ||   ||  ||||
                                GGGGAC      CC   GC  GAGG
                                   CGTGTGT  AGA  AA
GAM2405 ANK1     3' CCTCTCTCTCCCCGCT     33857     G    GG
                                CCT TTTTT  CCCCGCT
                                ||| |||||  |||||||
                                GGA AGAGA  GGGGCGA
                                  G    __
GAM2405 AR       5' CCGGACCGTCCCGCTCTCC   6230     TTT   GC     _
                                CTG   TTG  CCCGCTC CC
                                |||   |||  ||||||| ||
                                GGC   GGC  GGGCGAG GG
                                  CT_   A_      A
GAM2405 BACE     3' CCCTGTCTTTGTACTCCC    39956          GCCCC
                                CCCTGTTTTTG    GCTCCC
                                ||||||||||    ||||||
                                GGGACAGAAAC    TGAGGG
                                      A____
GAM2405 BAZ1B    3' CCTGCTTTTCTTCTGCTCCCC  37085         GGCCCC
                                CCTGTTTTT     GCTCCCC
                                |||||||||     |||||||
                                GGACGAAAA     CGAGGGG
                                     GAAGA_
GAM2405 BMPR1B   3' CTGTCTTTGCCCAGGTCGCTCC 10203         G  ____
            C                    CTGTTTTTG CCC    CGCTCCC
                                ||||||||| |||    |||||||
                                GACAGAAAC GGG    GCGAGGG
                                     _   TCCA
GAM2405 BRCA1    3' CTGTTTTTGCCTTCCC      28631         G  CCGC
                                CTGTTTTTG CC    TCCC
                                ||||||||| ||    ||||
                                GACAAAAAC GG    AGGG
                                     _ A___
GAM2405 BRF2     3' CCCCAGTTCCCGCTCC      32897      T   TTTGGC
                                CCCC GTT     CCCGCTCC
                                |||| |||     ||||||||
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                                GGGG CAA     GGGCGAGG
                                  T  _______
GAM2405  C1orf6   3'  CCTGTTTCACCTGCTCC     33525        TG   CC
                                CCTGTTTT  GCC  GCTCC
                                ||||||||  |||  |||||
                                GGACAAAG  TGG  CGAGG
                                    __   A_
GAM2405  CDH18    5'  CCCTGTTTCTGTTCTTGCTCC  22339          GCCCC
                                CCCTGTTTTTG    GCTCC
                                ||||||||||     |||||
                                GGGACAAAGAC    CGAGG
                                     AAGAA
GAM2405  CDH4     3'  CCTCTGCTCAGTCCTGCTCC   12173    _     TT  C  C
                                CC CTGTTT  GG CC GCTCC
                                || ||||||  || || |||||
                                GG GACGAG  TC GG CGAGG
                                 A     __  A  A
GAM2405  CDKN2B   3'  GTCGCGGTGGCCCCGCTCC   38550     TT__
                                GTT    TGGCCCCGCTCC
                                |||    ||||||||||||
                                CAG    ACCGGGGCGAGG
                                  CGCC
GAM2405  CELSR3   3'  CCCTTGTTTCTGCTCC      10833     C      GGCCCC
                                CCC TGTTTTT     GCTCC
                                ||| |||||||     |||||
                                GGG ACAAAGA     CGAGG
                                  A     _______
GAM2405  COL7A1   5'  GCCTCTGTCCCTTGCTCCC   6425        G   C_
                                GTTTTTG CCC  GCTCCC
                                ||||||| |||  ||||||
                                CGGAGAC GGG  CGAGGG
                                    A   AA
GAM2405  COPA     5'  CCCGTGAGCTCCGTTCTC    20410      TTTT   C   __
                                CCTGT    GGC CCG  CTC
                                |||||    ||| |||  |||
                                GGGCA    TCG GGC  GAG
                                   C___   A   AA
GAM2405  CRY2     3'  CCCCTGTGCCCTGCTCCC    43579       TTTTG    C
                                CCCCTGT     GCCC GCTCCC
                                |||||||     |||| ||||||
                                GGGGACA     CGGG CGAGGG
                                    _____    A
GAM2405  DBCCR1   5'  CTGTTGCTCGCTCGCTC     31145      T  G  CC
                                CTGTT TT GC  CGCTC
                                ||||| || ||  |||||
                                GACAA GA CG  GCGAG
                                   C  G  A_
GAM2405  DBN1     5'  CCCCAGCCCGCTCCGCTCC   38925     T    TTG  C
                                CCCC GTTT   GC CCGCTCC
                                |||| ||||   || |||||||
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                                GGGG CGGG   CG GGCGAGG
                                  T   ___  A
GAM2405  DDX26    5'  CCCGTCCCCGCTCC       29087       TTTTGG
                                CCTGT     CCCCGCTCC
                                |||||     |||||||||
                                GGGCA     GGGGCGAGG
                                  _______
GAM2405  DLG2     3'  CCCTTTGGCCCCTCT       10696      GTTT       G
                                CCCT    TTGGCCCC CT
                                ||||    |||||||| ||
                                GGGA    AACCGGGG GA
                                  ____       A
GAM2405  DXYS155E 3'  CCTCCGCTCCCGGCTCCGCTCC 22948    _         C
              C                  CC CTGTTTTTGGC CCGCTCCC
                                || ||||||||||| ||||||||
                                GG GGCGAGGGCCG GGCGAGGG
                                 A          A
GAM2405  EDG6     3'  CCCGTTCCCTGCTCC       19093       TTTGG   C
                                CCTGTT    CCC GCTCC
                                ||||||    ||| |||||
                                GGGCAA    GGG CGAGG
                                  ______  A
GAM2405  EMX2     3'  CCCCCGTCGTCCTGCTCCC    44679        TTT GC  C
                                CCCCTGTT   G  CC GCTCCC
                                ||||||||   |  || ||||||
                                GGGGGCAG   C  GG CGAGGG
                                    ___ A_  A
GAM2405  EPB41    5'  CCTCTGCTTTCTGATGTCCGCT 20764    _       GGCC__
              CC                   CC CTGTTTTT     CCGCTCC
                                || ||||||||     |||||||
                                GG GACGAAAG     GGCGAGG
                                 A       ACTACA
GAM2405  EPHA1    3'  CCCCGTCCTTGCTCC       23433          GGCCCC
                                CCCTGTTTTT     GCTCC
                                ||||||||||     |||||
                                GGGGCAGGAA     CGAGG
                                  _______
GAM2405  EXTL1    3'  TGTTCCCATCCCGCTTTCC    20875       TT GC     CC
                                TGTTT  G  CCCGCT  CC
                                |||||  |  ||||||  ||
                                ACAAG  T  GGGCGA  GG
                                   GG A_     AA
GAM2405  FANCC    3'  CTGTATTTTTGGCTCTC     43274      __      CCCG
                                CTGT  TTTTGGC   CTC
                                ||||  |||||||   |||
                                GACA  AAAACCG   GAG
                                  TA      A___
GAM2405  FGFR4    3'  CCTGTTTTCGGCAGGCT     35653           CCC
                                CCTGTTTTTGGC   GCT
                                ||||||||||||   |||
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                                GGACAAAAGCCG  CGA
                                      TC_
GAM2405  FMR2    3'  CTGTTCCTGATGGTTCTGCTCC 12964         CCCC___
                                CTGTTTTTGG      GCTCC
                                ||||||||||      |||||
                                GACAAGGACT      CGAGG
                                      ACCAAGA
GAM2405  FOXF1   3'  GCTCTTGTCACTTCCCGCTCCC 11119       GC____
                                GTTTTTG     CCCGCTCCC
                                |||||||     |||||||||
                                CGAGAAC     GGGCGAGGG
                                    AGTGAA
GAM2405  FZD5    5'  CCGCTGGCAGCGCTCCGCTCC  41043    _  TTTTTG  C
                                CC CTG     GC CCGCTCC
                                || |||     || |||||||
                                GG GAC     CG GGCGAGG
                                 C  CGTCG_  A
GAM2405  GAB2    3'  CCTCTTTTAGTGGCCTTGCT  29379    G   __    CC
                                CCT TTTT  TGGCC  GCT
                                ||| ||||  |||||  |||
                                GGA AAAA  ACCGG  CGA
                                  G   TC    AA
GAM2405  GALNT7  3'  TGTTTTTGTCACCCTCGCT   38363        __   _
                                TGTTTTTG  GCCC CGCT
                                ||||||||  |||| ||||
                                ACAAAAAC  TGGG GCGA
                                     AG   A
GAM2405  GNB1    5'  CCACTCCCGGCCCCGCTCCCC  13198   TG
                                C  TTTTTGGCCCCGCTCCCC
                                |  ||||||||||||||||||
                                G  GAGGGCCGGGGCGAGGGG
                                 GT
GAM2405  GPR48   3'  CCCTTTTTTGGCCCTGC    32983     G       C
                                CCCT TTTTTGGCCC GC
                                |||| |||||||||| ||
                                GGGA AAAAACCGGG CG
                                  _        A
GAM2405  GPR62   5'  CCTGTCCTCTGCTCC      44874        GGCCCC
                                CCTGTTTTT    GCTCC
                                |||||||||    |||||
                                GGACAGGAG    CGAGG
                                     A_____
GAM2405  GPR62   5'  CTCCTCTTGTCCCTTGCTCC  44875   G    G   C_
                                CT TTTTTG CCC  GCTCC
                                || ||||||  |||  |||||
                                GA GAGAAC GGG  CGAGG
                                 G     A   AA
GAM2405  GRIA2   5'  CCTTCTTTGGCTGTTTTCC   9082     G      CCCGC
                                CCT TTTTTGGC    TCC
                                ||| ||||||||    |||
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                                GGA AGAAACCG    AGG
                                  _      ACAAA
GAM2405 HCS     3' CCCTTGTTTTTGATTCTACC  33227    C       CCCCG  C
                                CCC TGTTTTTGG    CT CC
                                ||| |||||||||    || ||
                                GGG ACAAAAACT    GA GG
                                  A       AA___  T
GAM2405 IGFBP4  3' CCTTTGACCCCCTTCGCTCTCC 11398          ____   _
                                TTTTTGGCCCC   GCTC CC
                                ||||||||||   |||| ||
                                GGAAACTGGGG   CGAG GG
                                      GAAG   A
GAM2405 JRK     5' CCCTCTCCTCCTGCTCCC    44497     G   TGGC  C
                                CCCT TTTT   CC GCTCCC
                                |||| ||||   || ||||||
                                GGGA AGGA   GG CGAGGG
                                  G   ____ A
GAM2405 KCNK3   3' CCTTCTTTCTGTCCTGCT    13902     G_    GC  C
                                CCT  TTTTTG  CC GCT
                                |||  ||||||  || |||
                                GGA  AAAGAC  GG CGA
                                  AG     A_ A
GAM2405 KITLG   5' CCACTGTCCCTGCTTCC     19643   _   TTTTGG   C  _
                                CC CTGT     CCC GCT CC
                                || ||||     ||| ||| ||
                                GG GACA     GGG CGA GG
                                 T   _______  A   A
GAM2405 LDB1    3' CTGTCTTCTGCTCCC       19336        GGCCCC
                                CTGTTTTT     GCTCCC
                                ||||||||     ||||||
                                GACAGAAG     CGAGGG
                                    A_____
GAM2405 LHX4    5' CCCTTTGATCTCGCTCTCC   37851     GTTT   CCC   _
                                CCCT   TTGG   CGCTC CC
                                ||||   ||||   ||||| ||
                                GGGA   AACT   GCGAG GG
                                  ____   AGA    A
GAM2405 MAP1B   3' CCTTACCCCACCCTGCTC    25393    GTT   G   C
                                CCT   TTT GCCC GCTC
                                |||   ||| |||| ||||
                                GGA   GGG TGGG CGAG
                                  AT_   G    A
GAM2405 MASP1   3' CCTCCTGTCCCTGCTTCTC   40097   _       G CCCG
                                CC CCTGTTTTTG C    CTC
                                || ||||||||| |    |||
                                GG GGACAGGGAC G    GAG
                                 A        _ AA__
GAM2405 MDS1    5' CCTGTTTCTCTCCTGTTTCTC 22560        GG  CCG__
                                CCTGTTTTT  CC    CTC
                                |||||||||  ||    |||
```

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                                GGACAAAGA  GG    GAG
                                    GA  ACAAA
GAM2405  MMP14    3'  CCCTCTCCTCTTGCTCCC    22635     G    GGCCCC
                                CCCT TTTTT     GCTCCC
                                |||| |||||     ||||||
                                GGGA AGGAG     CGAGGG
                                  G    AA____
GAM2405  OPCML    3'  CCCCTTTTTTGGTCACT     14950      G     CCC
                                CCCCT TTTTTGG   CGCT
                                ||||| |||||||   ||||
                                GGGGA AAAAACC   GTGA
                                  _      A__
GAM2405  PCSK5    5'  CCGACTCGGTCTCGCTCC    26233     TT    CCC
                                CTG  TTTGG   CGCTCC
                                |||  |||||   ||||||
                                GGC  GAGCC   GCGAGG
                                  T_    AGA
GAM2405  PDE4C    3'  CCCTTCTTTTCTGCTCC     9557      G    GGCCCC
                                CCCT TTTTT     GCTCC
                                |||| |||||     |||||
                                GGGA AGAAA     CGAGG
                                  _    AGA___
GAM2405  PIK3R1   3'  CCTCTCTCTCCTCCGCTCTCC  42860     G    GG _    _
                                CCT TTTTT  CC CCGCTC CC
                                ||| |||||  || |||||| ||
                                GGA AGAGA  GG GGCGAG GG
                                  G    __ A     A
GAM2405  POLG     5'  CCTGTCTCTGCTCTCC      15444          GCCCCG
                                CCTGTTTTTG     CTCC
                                ||||||||||     ||||
                                GGACAGAGAC     GAGG
                                     GA____
GAM2405  POLK     5'  CTCCTTTCTCCGCTCC      32137    G    GGCC
                                CT TTTTT    CCGCTCC
                                || |||||    |||||||
                                GA GAAAG    GGCGAGG
                                 G    A___
GAM2405  POU4F1   3'  CCCCTGCTCGGGTCTCCGCTTT 26383         TT  CC_    CC
            CC                   CCCCTGTTT  GG   CCGCT  CC
                                |||||||||  ||   |||||  ||
                                GGGGACGAG  CC   GGCGA  GG
                                     C_  AGA     AA
GAM2405  PPP1R3D  5'  CCCTTGGTTCGCCACCTTGCTC 26425      GTTT  G  _ __
            C                    CCCT    TT GCC CC  GCTCC
                                ||||    || ||| ||  |||||
                                GGGA    AA CGG GG  CGAGG
                                  ACC_  G   T  AA
GAM2405  PRG2     5'  CCCTGTCTTTCTTGCTTCC    15561          GGCCCC   C
                                CCCTGTTTTT     GCT CC
                                ||||||||||     ||| ||
```

```
                                GGGACAGAAA     CGA GG
                                     GAA___   A
GAM2405  PUM1    5'  TCTCTGGCGCTCTCGCTCCCC  31240        CC___
                                TTTTTGGC    CGCTCCCC
                                ||||||||    ||||||||
                                AGAGACCG    GCGAGGGG
                                    CGAGA
GAM2405  RIMS1   5'  CCTTTGTTTTGGTCGCCC    43732    GT_    CCC
                                CCT   TTTTGG   CGCTC
                                |||   ||||||   |||||
                                GGA   AAAACC   GCGGG
                                  AAC     A__
GAM2405  SALL2   5'  CTGTTCTTGACTCTC      41897          CCCG
                                CTGTTTTTGGC    CTC
                                ||||||||||    |||
                                GACAAGAACTG    GAG
                                      A___
GAM2405  SLC39A4  5'  CCCCAGGCCCCTGTCCTGCTTC 39294     T_     GC  C  _
            CC                    CCCC  GTTTTTG  CC GCT CCC
                                ||||  |||||||  || ||| |||
                                GGGG  CGGGGAC  GG CGA GGG
                                  TC      A_  A   A
GAM2405  SLC4A4   3'  TTTCTGTTCCCTTGCTCC    19067       GC   __
                                TTTTTG  CCC  GCTCC
                                ||||||  |||  |||||
                                AAAGAC  GGG  CGAGG
                                   AA   AA
GAM2405  SMCX    5'  CCTCTTCGTCCCGCTCC     20069     GT    GC
                                CCT  TTTTG  CCCGCTCC
                                |||  |||||  ||||||||
                                GGA  GAAGC  GGGCGAGG
                                  __     A_
GAM2405  SPTBN2   5'  CCTGCTCCTGTGCTCCGCTCTC 28068          _  C     _
            C                     CCTGTTTTTG GC CCGCTC CC
                                ||||||||||  ||  ||||||  ||
                                GGACGAGGAC CG GGCGAG GG
                                      A  A     A
GAM2405  SUPT5H   5'  CCCCAGTTTCCGAATCTGTTCT 17217      T       CCCCG__
            C                     CCCC GTTTTTGG      CTC
                                ||||  ||||||||      |||
                                GGGG CAAAGGCT      GAG
                                  T       TAGACAA
GAM2405  TCFL4   3'  CCTTGTTTTTGGTTGGCT    41826    C       CCCC
                                CC TGTTTTTGG    GCT
                                ||  |||||||||   |||
                                GG ACAAAAACC    CGA
                                 A        AAC_
GAM2405  TEL2    5'  CTGTCTTGAGCGCTCCCC    32044        T   CCC
                                CTGTTTT GGC   GCTCCCC
                                |||||||  |||   |||||||
```

```
                                GACAGAA TCG   CGAGGGG
                                   C  ___
GAM2405  TLX1     5'  CCTCTCTGGCTTCTGCTTCCC  24332     GT      CCC_  _
                                CCT  TTTTGGC    GCT CCC
                                |||  |||||||    ||| |||
                                GGA  GAGACCG    CGA GGG
                                  __      AAGA   A
GAM2405  TNFSF4   3'  TCCTTCACTCCTTGCTCC    17754      G  _  C_
                                TTTTT GC CC  GCTCC
                                ||||| || ||  |||||
                                AGGAA TG GG  CGAGG
                                   G  A  AA
GAM2405  TRIM39   3'  TGTTTCTGGAAAAGCCTCTCC  34577         CC___  G
                                TGTTTTTGG     CC CTCC
                                |||||||||     || ||||
                                ACAAAGACC     GG GAGG
                                      TTTTC  A
GAM2405  WASF3    3'  CCCTGTTTGTTGAACCTTTCC  27380         _  GC  CGC
                                CCCTGTTT TTG  CC   TCC
                                |||||||| |||  ||   |||
                                GGGACAAA AAC  GG   AGG
                                     C   TT  AA_
GAM2405  YY1      5'  CCGGGCCGGCGCTCCGCTTCCC 18168     TTT    C__    _
                                CTG   TTGGC   CCGCT CCC
                                |||   |||||   ||||| |||
                                GGC   GGCCG   GGCGA GGG
                                  CC_    CGA    A
GAM2405  ZIC1     5'  CCGTTTTTCCCTCTC       18231         GGC   G
                                CTGTTTTT   CCC CTC
                                ||||||||   ||| |||
                                GGCAAAAA   GGG GAG
                                     ___   A
GAM2405  ZNF205   5'  CCCTCTTTTTGGCCAAGCCCC  18376      G        CC
                                CCCT TTTTTGGCC  GCTCC
                                |||| |||||||||  |||||
                                GGGA AAAAACCGG  CGGGG
                                  G        TT
GAM2405  ZNF205   3'  CCCTGGGCGCCCCGCTCCCC   18377      TTTTTG
                                CCCTG     GCCCCGCTCCCC
                                |||||     ||||||||||||
                                GGGAC     CGGGGCGAGGGG
                                   CCG___
GAM2406  CMRF35   3'  GGAGTGTGGGCCATT       27434       GCGAACC  C
                                GGAGTG      GG GTCATT
                                ||||||      || ||||||
                                CCTCAC      CC CGGTAA
                                   A_______  _
GAM2406  MAP1B    3'  GGGTGGGAGGTATCATTA    25397    A   C  ACC  CG
                                GG GTGG GA   GG  TCATTA
                                || |||| ||   ||  ||||||
```

```
                                CC CACC CT   CC  AGTAAT
                                 _   _ ___  AT
GAM2406 ABL1    5' GCCCTCACCGCCGCCCGCC   28714    GGA
                                GCC  GTCGCCGCCCGCC
                                |||  ||||||||||||
                                CGG  TGGCGGCGGGCGG
                                  GAG
GAM2406 ACCN2   5' GCCGGAGCCCGCGGCCGCC   33446       CG  __
                                GCCGGAGT  CCGC  CCGCC
                                ||||||||  ||||  |||||
                                CGGCCTCG  GGCG  GGCGG
                                    __   CC
GAM2406 ADCY6   5' CCTGGCCGTCCCGCCCGCC   34170   _ A_  G
                                CC GG  GTC CCGCCCGCC
                                || ||  ||| |||||||||
                                GG CC  CAG GGCGGGCGG
                                 A  GG  _
GAM2406 ANK1    3' GCCGGAGCGTGCAGCCA    33865       T  CC  CC
                                GCCGGAG CG  GC  GCCA
                                |||||||  ||  ||  ||||
                                CGGCCTC GC  CG  CGGT
                                   _  A_  T_
GAM2406 AOC2    3' ACCACGCCGCCCGCCAC    41816     GAGT
                                GCCG   CGCCGCCCGCCAC
                                ||||   ||||||||||||
                                TGGT   GCGGCGGGCGGTG
                                  ____
GAM2406 BMP6    5' GCCGGAGCGCGGCCGC     11866       T   C   C
                                GCCGGAG CGC GCC GC
                                ||||||| ||| ||| ||
                                CGGCCTC GCG CGG CG
                                   _  C  _
GAM2406 CACNA1A 3' GCCTGGCCACCGCCTGC    35735    GGA       C
                                GCC  GTCGCCGCC GC
                                |||  |||||||| ||
                                CGG  CGGTGGCGG CG
                                  AC_       A
GAM2406 CACNA1G 3' GCCAGAGTTGCCGGGGC    33130       C   CCC
                                GCCGGAGT GCCG  GC
                                |||||||| ||||  ||
                                CGGTCTCA CGGC  CG
                                    A   CC_
GAM2406 CCND1   5' GCGGACTCTGCTGCTCGC   38210   C  G  _  C  C
                                GC GGA TC GC GC CGC
                                || ||| || || || |||
                                CG CCT AG CG CG GCG
                                 _  G  A  A  A
GAM2406 CCNDBP1 5' GCCGGAGCCGCACTGC     29101        C  CC
                                GCCGGAGTCGC GC  GC
                                |||||||||| ||  ||
```

```
                                CGGCCTCGGCG TG  CG
                                      _  A_
GAM2406  CDC2L2   5'  GCCGCTCCTCCGCCCGCC    37939      GAG  G
                                GCCG   TC CCGCCCGCC
                                ||||   || |||||||||
                                CGGC   GG GGCGGGCGG
                                  GA_  A
GAM2406  CDH15    5'  GCCGGAGTGCACCCGC      22335        C  C
                                GCCGGAGT GC GCCCGC
                                |||||||| || ||||||
                                CGGCCTCA CG TGGGCG
                                    _ _
GAM2406  CDH6     5'  GCCGCGGTCGCCGGCTCTGCC  22328      GA      _ CC_
                                GCCG  GTCGCCG C   GCC
                                ||||  ||||||| |   |||
                                CGGC  CAGCGGC G   CGG
                                  GC      C AGA
GAM2406  CDK6     5'  GCCTGGACGCCGCCCGCC    10385     _  GT
                                GCC GGA  CGCCGCCCGCC
                                ||| |||  ||||||||||||
                                CGG CCT  GCGGCGGGCGG
                                 A  __
GAM2406  CDS1     5'  GCGGGGCGCCCCGCCAC     10400    C  A T   GC
                                GC GG G CGCC  CCGCCAC
                                || || | ||||  |||||||
                                CG CC C GCGG  GGCGGTG
                                 C  _ _   __
GAM2406  CLK2     5'  GCCGGAGTCCCGGCAC      41278         G   CC
                                GCCGGAGTC CCG  CGC
                                ||||||||| |||  |||
                                CGGCCTCAG GGC  GTG
                                     _  C_
GAM2406  CLTB     5'  GCCGGAGCCTCCGCTGC     28225         G   CC
                                GCCGGAGTC CCGC  GC
                                ||||||||| ||||  ||
                                CGGCCTCGG GGCG  CG
                                     A   A_
GAM2406  COL9A1   5'  GCCCGCCGCCCGCC       38534     GGAGT
                                GCC    CGCCGCCCGCC
                                |||    ||||||||||
                                CGG    GCGGCGGGCGG
                                  _____
GAM2406  COL9A3   3'  CCTGGACGTCACCCGCCTGCCA 12345   _  _    _  C
           C                     CC GGA GTCGCC GCC GCCAC
                                || ||| |||||| ||| |||||
                                GG CCT CAGTGG CGG CGGTG
                                 A  G    G  A
GAM2406  CORO1C   5'  GCCGAAGTCCCCGCTGC     30724         G   CC
                                GCCGGAGTC CCGC  GC
                                |||||||| ||||  ||
```

```
                                CGGCTTCAG GGCG  CG
                                     G    A_
GAM2406  COX4I1   5'  GCCGCCACTGCCCGCC      12403     GGA    C
                                GCC   GTCGC GCCCGCC
                                |||   ||||| |||||||
                                CGG   CGGTG CGGGCGG
                                  ___     A
GAM2406  CRACC    3'  GCCGGAGTGCAGTGGTGCCA   34520         C  CGCCC_
                                GCCGGAGT GC     GCCA
                                |||||||| ||     ||||
                                CGGCCTCA CG     CGGT
                                     _  TCACCA
GAM2406  CRMP1    5'  GCTCGGCCCGCCCGCC      10598    _   AGTCG
                                GC CGG    CCGCCCGCC
                                || |||    |||||||||
                                CG GCC    GGCGGGCGG
                                 A  G____
GAM2406  CYP51    5'  GCCGAGGTCGCCACCGC     8958       GA       C
                                GCCG  GTCGCCGCC GC
                                ||||  ||||||||| ||
                                CGGC  CAGCGGTGG CG
                                  TC       _
GAM2406  DDX6     5'  GCCGAAGTCGCCGCCTGGC   20552             C_
                                GCCGGAGTCGCCGCC  GC
                                |||||||||||||||  ||
                                CGGCTTCAGCGGCGG  CG
                                       AC
GAM2406  DSCAM    5'  GCCCGCCCGCCGCCCGCC    10801     GGAG
                                GCC   TCGCCGCCCGCC
                                |||   ||||||||||||
                                CGG   GGCGGCGGGCGG
                                 GCG_
GAM2406  DUSP7    5'  GCCGAGCTGCGCGCCCGCC   42273      G   C  _
                                GCCG AGT GC CGCCCGCC
                                |||| ||| || ||||||||
                                CGGC TCG CG GCGGGCGG
                                  _   A  C
GAM2406  DVL3     5'  CCAGCGCCGCCCGCC       20674      AGT
                                CCGG   CGCCGCCCGCC
                                ||||   ||||||||||||
                                GGTC   GCGGCGGGCGG
                                  ___
GAM2406  EMX2     5'  GCCTCCGCCGCCCGC       44689     GGAG
                                GCC   TCGCCGCCCGC
                                |||   ||||||||||||
                                CGG   GGCGGCGGGCG
                                 A___
GAM2406  EPHB6    5'  CCGGGTCCCGCCGCCCGC    20797      A   __
                                CCGG GTC  GCCGCCCGC
                                |||| |||  |||||||||
```

```
                                GGCC CAG  CGGCGGGCG
                                  _  GG
GAM2406  EVC     5'  CCGCATCCCGCCGCC      30976    GA  G   C
                                CCG  GTC CCGCC GCC
                                |||  ||| ||||| |||
                                GGC  TAG GGCGG CGG
                                 G_  _   _
GAM2406  F2R     5'  GCTGGAGCCGCTCGGCGC    12798    C      _ CC
                                GC GGAGTCGC CG  CGC
                                || |||||||| ||  |||
                                CG CCTCGGCG GC  GCG
                                 A       A  C_
GAM2406  FGFR1   5'  CCGCTAGCTGCCGCCCGCC   31932    G_  C
                                CCG  AGT GCCGCCCGCC
                                |||  ||| ||||||||||
                                GGC  TCG CGGCGGGCGG
                                 GA  A
GAM2406  FOXD1   5'  GCCGGAGCTGCGCCGGGGC   20927       __   CCC
                                GCCGGAGT  CGCCG  GC
                                ||||||||  |||||  ||
                                CGGCCTCG  GCGGC  CG
                                    AC    CC_
GAM2406  FOXD2   5'  GCCGGCGGCCCCCGCCAC    20968     AGTC  G
                                GCCGG   GCC CCCGCCAC
                                |||||   ||| ||||||||
                                CGGCC   CGG GGGCGGTG
                                  GC__  _
GAM2406  GALR1   5'  CCGGGCGCCTCCGCCCGC    11199     A_  G
                                CCGG  GTC CCGCCCGC
                                ||||  ||| ||||||||
                                GGCC  CGG GGCGGGCG
                                  CG  A
GAM2406  GARP    3'  GCTGGAGCCGCCGTGGCCCAC  24314    C      ___
                                GC GGAGTCGCC  GCCCGC
                                || |||||||||  ||||||
                                CG CCTCGGCGG  CGGGTG
                                 A       CAC
GAM2406  GARS    5'  GCCGGGTCGCCGCCGC     13058     A      C
                                GCCGG GTCGCCGCC GC
                                ||||| ||||||||| ||
                                CGGCC CAGCGGCGG CG
                                  _       _
GAM2406  GNA11   5'  GCCGGAGCCGCCTCGGCCGCC  44045         GC__
                                GCCGGAGTCGCC   CCGCC
                                ||||||||||||   |||||
                                CGGCCTCGGCGG   GGCGG
                                       AGCC
GAM2406  GNB3    5'  GCCCGCGCCCGCCCGTCAC   13221    GGA T   _   C
                                GCC  G CGCC GCCCG CAC
                                |||  | |||| ||||| |||
```

```
                                CGG   C GCGG CGGGC GTG
                                  G__ _   G    A
GAM2406  HNRPD    5'  GCCGAGACTACACCCGCC    36392     GA TC  C
                                GCCG  G  GC GCCCGCC
                                ||||  |  || |||||||
                                CGGC  T  TG TGGGCGG
                                  TC GA  _
GAM2406  HPN      3'  GCTGAGTGGGCCCGCCAC    13460    CG   CGCC
                                GC  GAGT   GCCCGCCAC
                                ||  ||||   |||||||||
                                CG  CTCA   CGGGCGGTG
                                 A_   CC__
GAM2406  KCNK1    5'  GCCGGAGCGCGGCCCGCC    13890       T   C
                                GCCGGAG CGC GCCCGCC
                                ||||||| ||| |||||||
                                CGGCCTC GCG CGGGCGG
                                    _  C
GAM2406  KCNK1    5'  GCCTGGCTCCCGCCCGCC    13891    _ AG  G
                                GCC GG  TC CCGCCCGCC
                                ||| ||  || |||||||||
                                CGG CC  AG GGCGGGCGG
                                 A  G_  _
GAM2406  LASS1    5'  ACCGCCCGCTCGCCCGCC    34589     GAG   _
                                GCCG   TCGC CGCCCGCC
                                ||||   |||| ||||||||
                                TGGC   GGCG GCGGGCGG
                                  G__   A
GAM2406  LYN      5'  GCCGCCCCGCCCGC       14286    GGA   G
                                GCC   GTC CCGCCCGC
                                |||   ||| ||||||||
                                CGG   CGG GGCGGGCG
                                  ___   _
GAM2406  MAFK     5'  GCCCCCGCGCCGCCCGCC    14318    GGA T
                                GCC   G CGCCGCCCGCC
                                |||   | ||||||||||
                                CGG   C GCGGCGGGCGG
                                  GGG _
GAM2406  MN1      5'  GCCACGTCCGCCGCCTGCC    14583    GA   _    C
                                GCCG  GTC GCCGCC GCC
                                ||||  ||| |||||| |||
                                CGGT  CAG CGGCGG CGG
                                  G_   G    A
GAM2406  MUCDHL   3'  GCCGGAGTCACTGGCGCCA   34937          CGCC
                                GCCGGAGTCGC   CGCCA
                                ||||||||||   |||||
                                CGGCCTCAGTG   GCGGT
                                      ACC_
GAM2406  MXI1     5'  GCCAGCCGCGCCCGCC     39021    GG    C
                                GCC  AGTCGC GCCCGCC
                                |||  |||||| |||||||
```

```
                                CGG  TCGGCG CGGGCGG
                                  __     _
GAM2406  MYCL1    5'  CGCTCCAGCCGCCCGCCAC   23887    GAG  _
                                CG   TC GCCGCCCGCCAC
                                ||   || ||||||||||||
                                GC   GG CGGCGGGCGGTG
                                 GA_  T
GAM2406  NEK2     5'  GCCAGAGTCGCGCTGC      14747          C  CC
                                GCCGGAGTCGC GC  GC
                                |||||||||| ||  ||
                                CGGTCTCAGCG CG  CG
                                      _  A_
GAM2406  NLGN2    5'  GCCGGGGCCGCCCGGGGCGCCG 44756       A     _____  _
              C                  GCCGG GTCGCC    GC CCGC
                                ||||| ||||||    || ||||
                                CGGCC CGGCGG    CG GGCG
                                   C     GCCC  C
GAM2406  NMB      5'  GCCGTGCCCCGCGCCCGCC   43954      GAG_   C
                                GCCG    TCGC GCCCGCC
                                ||||    |||| |||||||
                                CGGC    GGCG CGGGCGG
                                  ACGG    _
GAM2406  NRAS     5'  CCGGCCCCGCCCGCTAC     14849      AG  G       C
                                CCGG  TC CCGCCCGC AC
                                ||||  || |||||||| ||
                                GGCC  GG GGCGGGCG TG
                                  __  _       A
GAM2406  ODC1     5'  GCCTGAGTCGCAGCCGC     14918     G      C   C
                                GCC GAGTCGC GCC GC
                                ||| ||||||| ||| ||
                                CGG CTCAGCG CGG CG
                                 A      T  _
GAM2406  ODC1     5'  GCCGGAGACGCCGGC       14917        T    CCC
                                GCCGGAG CGCCG   GC
                                ||||||| |||||   ||
                                CGGCCTC GCGGC   CG
                                    T    ____
GAM2406  OGG1     5'  GCCACAGCTGCTGCCTGCC   32565      G   C  C   C
                                GCCG AGT GC GCC GCC
                                |||| ||| || ||| |||
                                CGGT TCG CG CGG CGG
                                  G   A  A   A
GAM2406  ORC2L    5'  GCTGAGTCGCCGCCGC      26193    CG         C
                                GC  GAGTCGCCGCC GC
                                ||  ||||||||||| ||
                                CG  CTCAGCGGCGG CG
                                 A_          _
GAM2406  PAX2     5'  GCCGGAGCTTGCAACTGC    19628         C_  C  CC
                                GCCGGAGT  GC GC  GC
                                ||||||||  || ||  ||
```

```
                                CGGCCTCG  CG TG  CG
                                    AA  T  A_
GAM2406  PAX7     5'  GCCGGAATCGAGGCCGC     30332          CC   C
                                GCCGGAGTCG  GCC GC
                                ||||||||||  ||| ||
                                CGGCCTTAGC  CGG CG
                                     TC  _
GAM2406  PDE5A    5'  GCCGGAGCGCGGCCGC      37905        T   C   C
                                GCCGGAG CGC GCC GC
                                ||||||| ||| ||| ||
                                CGGCCTC GCG CGG CG
                                   _  C  _
GAM2406  PITPN    5'  GCCGCGGTCGCCGCGC      26338      GA       CC
                                GCCG  GTCGCCGC  GC
                                ||||  ||||||||  ||
                                CGGC  CAGCGGCG  CG
                                  GC       __
GAM2406  PITX1    5'  GCTGGGCGCGCCCGCC      15326    C  A T   C
                                GC GG G CGC GCCCGCC
                                || || | ||| |||||||
                                CG CC C GCG CGGGCGG
                                 A  _ _  _
GAM2406  PKIA     5'  GCCGCAGTCCCGCCGC      27742      G   G    C
                                GCCG AGTC CCGCC GC
                                |||| |||| ||||| ||
                                CGGC TCAG GGCGG CG
                                  G   _   _
GAM2406  PPM1D    5'  GCCGGAGCGCCGGAGC      18838        T    CCC
                                GCCGGAG CGCCG   GC
                                |||||||  |||||   ||
                                CGGCCTC GCGGC   CG
                                   _    CT_
GAM2406  PPP1R8   5'  GCCGGAGTTCGCGGCTGCCGC  39729          _  C __
                                GCCGGAGT CGC GC  CCGC
                                |||||||| ||| ||  ||||
                                CGGCCTCA GCG CG  GGCG
                                    A   C  AC
GAM2406  PPP4C    5'  CAGAGTCGGGGCCGCCGC     15531         ___     C
                                CGGAGTC   GCCGCC GC
                                |||||||   |||||| ||
                                GTCTCAG   CGGCGG CG
                                   CCC     _
GAM2406  PTPRF    5'  GCTGGAGCCGCCGCCTCTGCC  39035    C          C__
                                GC GGAGTCGCCGCC   GCC
                                || ||||||||||||   |||
                                CG CCTCGGCGGCGG   CGG
                                 A          AGA
GAM2406  PURA     5'  GCCGCGCCGCCGCCGCC     25207      GA       C
                                GCCG  GTCGCCGCC GCC
                                ||||  ||||||||| |||
```

```
                                CGGC  CGGCGGCGG CGG
                                  G_       _
GAM2406 PURA    5' GCCTGCCGCTCCGCCCGCC   25208    GGA   __
                                GCC   GTCGC  CGCCCGCC
                                |||   |||||  ||||||||
                                CGG   CGGCG  GCGGGCGG
                                  A__    AG
GAM2406 RAD51L3  5' GCCGGGTCGCGCCGC      39471      A    C  C
                                GCCGG GTCGC GCC GC
                                ||||| ||||| ||| ||
                                CGGCC CAGCG CGG CG
                                  _    _  _
GAM2406 RANBP9   5' CGGCGCTGCTGCCCGCCAC   24251     A  C  C
                                CGG GT GC GCCCGCCAC
                                ||| || || |||||||||
                                GCC CG CG CGGGCGGTG
                                  G  A  A
GAM2406 RB1CC1   5' CCGGGCGCCCGCCCGCC    31311     A T   _
                                CCGG G CGCC GCCCGCC
                                |||| | |||| |||||||
                                GGCC C GCGG CGGGCGG
                                  _ _   G
GAM2406 SIAH2    5' GCCGGGGCGCTGGCTCCGC   22864      A T   C_  _
                                GCCGG G CGC  GC CCGC
                                ||||| | |||  || ||||
                                CGGCC C GCG  CG GGCG
                                   C _  AC  A
GAM2406 SLC12A4  5' GCCGTCCCAGCCGCCCGCC   22897     GAGTC
                                GCCG    GCCGCCCGCC
                                ||||    ||||||||||
                                CGGC    CGGCGGGCGG
                                  AGGGT
GAM2406 SLC22A5  5' GCGCGGGGCACCCGCC      16860    _  AGTC  C
                                GC CGG   GC GCCCGCC
                                || |||   || |||||||
                                CG GCC   CG TGGGCGG
                                 C   C___  _
GAM2406 SLC30A4  5' GCCCGCCGCGCCCGC       30016    GGA    C
                                GCC   GTCGC GCCCGC
                                |||   ||||| ||||||
                                CGG   CGGCG CGGGCG
                                  G__    _
GAM2406 SMARCB1  5' GCCGGAGCCGGGCTGC      42312         CC  CC
                                GCCGGAGTCG  GC  GC
                                ||||||||||  ||  ||
                                CGGCCTCGGC  CG  CG
                                      C_  A_
GAM2406 SMURF1   5' GCCGGACGCCCGCC        45196       GTCGC
                                GCCGGA    CGCCCGCC
                                ||||||    ||||||||
```

```
                              CGGCCT    GCGGGCGG
                                    _____
GAM2406 SOX11    3' CCGGGTGCCCTCTGCCAC    17012     A  C   GCCC
                              CCGG GT GCC    GCCAC
                              |||| || |||    |||||
                              GGCC CA CGG    CGGTG
                                _ _  GAGA
GAM2406 SPI1     3' CGGAGCCCGGCCCGCCAC    17075       GCC
                              CGGAGTC   GCCCGCCAC
                              |||||||   |||||||||
                              GCCTCGG   CGGGCGGTG
                                  GC_
GAM2406 SRRM2    5' GCCGCCTCCGCCCGCC     32275    GGA   G
                              GCC   GTC CCGCCCGCC
                              |||   ||| |||||||||
                              CGG   CGG GGCGGGCGG
                                ___  A
GAM2406 ST7      5' CCGGAGCCCGCCCGCC     32937       CG
                              CCGGAGT  CCGCCCGCC
                              |||||||  |||||||||
                              GGCCTCG  GGCGGGCGG
                                    __
GAM2406 SYK      5' GCCGGGGTGGCCTCAGCCGC  17237      A  C   GC__
                              GCCGG GT GCC    CCGC
                              ||||| || |||    ||||
                              CGGCC CA CGG    GGCG
                                 C  C   AGTC
GAM2406 TARBP2   5' GCCGGTAGGGCCCGCC     39532      _  TCGCC
                              GCCGG AG     GCCCGCC
                              ||||| ||     |||||||
                              CGGCC TC     CGGGCGG
                                 A  C_____
GAM2406 TIF1     5' GCGCGGTCTCCGCCCGCC    41273    _  AG  G
                              GC CGG  TC CCGCCCGCC
                              || |||  || |||||||||
                              CG GCC  AG GGCGGGCGG
                               C   __  A
GAM2406 TIMP3    5' GCCGGGGCTGCTGCTCGCC    7456       A  C  C  C
                              GCCGG GT GC GC CGCC
                              ||||| || || || ||||
                              CGGCC CG CG CG GCGG
                                 C  A  A  A
GAM2406 TMEM1    5' GCCGCAGCTGCCGCCCGC    17595      G   C
                              GCCG AGT GCCGCCCGC
                              |||| ||| |||||||||
                              CGGC TCG CGGCGGGCG
                                G   A
GAM2406 TMEM4    5' GCGCTTCGCCGCCTGCCAC   30674    CGGAG       C
                              GC     TCGCCGCC GCCAC
                              ||     |||||||| |||||
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                                CG    AGCGGCGG CGGTG
                                 CGA__       A
GAM2406 UBE3A    5' GCCGCCTCCGCCCGCCAC    39279    GGA  G
                                GCC  GTC CCGCCCGCCAC
                                |||  ||| ||||||||||
                                CGG  CGG GGCGGGCGGTG
                                 ___  A
GAM2406 VEGF     5' GCCGAGTCGCCACTGC      17957     G       CC
                                GCCG AGTCGCCGC  GC
                                |||| |||||||||  ||
                                CGGC TCAGCGGTG  CG
                                  _       A_
GAM2406 VEGF     5' GCCGCGTCCACTGTCCGCC   17958     GAGT  _   ___
                                GCCG   CG CCGC   CCGCC
                                ||||   || ||||   |||||
                                CGGC   GC GGTG   GGCGG
                                  _____ A   ACA
GAM2406 VEGFB    5' GCCGGGGCCGCCCGC       17979      AGTC
                                GCCGG   GCCGCCCGC
                                |||||   |||||||||
                                CGGCC   CGGCGGGCG
                                  C___
GAM2406 VIPR2    5' GCCGCCCAGCGCCCGCC     18016     GAG  C
                                GCCG  TCG CGCCCGCC
                                ||||  ||| ||||||||
                                CGGC  GGT GCGGGCGG
                                  G__  C
GAM2406 WHSC1    3' ACCAGCTGCCCGCCA       39347     GAGTC  C
                                GCCG    GC GCCCGCCA
                                ||||    || ||||||||
                                TGGT    CG CGGGCGGT
                                  _____ A
GAM2406 ZNF148   5' GCCGAAGTCGTCAGCGGTCAC 35025         C _  C__
                                GCCGGAGTCG C GC  CGC
                                |||||||||| | ||  |||
                                CGGCTTCAGC G CG  GTG
                                      A T  CCA
GAM2406 ZYX      5' GCCGGAGCGTGCGCGCCGC   18435       CGC  _
                                GCCGGAGT  CGC CCGC
                                ||||||||  ||| ||||
                                CGGCCTCG  GCG GGCG
                                    CAC  C
GAM2407 SLC25A13 3' CTTTGGGACTACAATCCTA   30661    GAC_      ACA
                                CT   GACTACGA  CCTA
                                ||   ||||||||  ||||
                                GA   CTGATGTT  GGAT
                                 AACC      A__
GAM2407 SPTBN2   3' TCCCTGTCGACTGTCCCT    28073       A    ACGAACA
                                TCCCTG CGACT      CCT
                                |||||| |||||      |||
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                                AGGGAC GCTGA      GGA
                                   A    CAG____
GAM2407  CDC42    3'  TTCATTTGGTGCATTTCAA   12164          ACCC_
                                TTCATTTGGTG    CGA
                                ||||||||||    |||
                                AAGTAAACCAC    GTT
                                      GTAAA
GAM2408  ACP1     5'  GTGGGGTCACCTGGAGGGAG   28245     C  ____
                                GTGG GTC   GGAGGGAG
                                |||| |||   ||||||||
                                CACC CAG   CCTCCCTC
                                  C  TGGA
GAM2408  AGPAT2   3'  GCTGAGTGAGAGCTGGGGGAGC 26928        _ C  C  A
                                GCTGAGTG G GT GG GGGAGC
                                |||||||| | || || ||||||
                                CGACTCAC C CG CC CCCTCG
                                     T T  A  _
GAM2408  ASIC4    5'  AGCGAGTGAGCGAGGGAG    33063     T    _ GTCG
                                AGC GAGTG GC   GAGGGAG
                                ||| ||||| ||   |||||||
                                TCG CTCAC CG   CTCCCTC
                                  _    T  ____
GAM2408  CD74     3'  GCTGGGGGCTGAAGGGAGC   20338     AGT  GTC
                                GCTG  GGC  GGAGGGAGC
                                ||||  |||  |||||||||
                                CGAC  CCG  CTTCCCTCG
                                  CC_  A__
GAM2408  CDO1     5'  AGCTGGGGGCGAGGGAG     12214      AGT  GTCG
                                AGCTG  GGC   GAGGGAG
                                |||||  |||   |||||||
                                TCGAC  CCG   CTCCCTC
                                  CC_  ____
GAM2408  COL1A1   3'  AAGTTGGTTGGGTGGGAGGGAG 6360     C  AG  C  C
            C                    AAG TG  TGG GT GGAGGGAGC
                                ||| ||  ||| || |||||||||
                                TTC AC  ACC CA CCTCCCTCG
                                  A  CA  _  C
GAM2408  CORO2A   3'  AGCCGAGTGGTGTCCCTGAGGG 38058         C  G__
                                AGCTGAGTGG GTC  GAGGG
                                |||||||||| |||  |||||
                                TCGGCTCACC CAG  CTCCC
                                     A  GGA
GAM2408  CTRB1    3'  GAGCAGGGTCGGAGGGAG    12521     TG C
                                GAG  G GTCGGAGGGAG
                                |||  | ||||||||||
                                CTC  C CAGCCTCCCTC
                                  GT C
GAM2408  DDAH2    5'  AGTTGGTGGAGAAGGGAG    30354    C  A   CGTC
                                AG TG GTGG   GGAGGGAG
                                || || ||||   ||||||||
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                                TC AC CACC   CTTCCCTC
                                 A  _   T___
GAM2408  DMPK    5'  GCTGGGTGGGAGAAAGGG   20615     A   CGTC
                                GCTG GTGG   GGAGGG
                                |||| ||||   ||||||
                                CGAC CACC   TTTCCC
                                  C   CTC_
GAM2408  FAT2    3'  GACTGGGTGGGAGGGAG    11075    G  C  C
                                GA TGG GT GGAGGGAG
                                || ||| || ||||||||
                                CT ACC CA CCTCCCTC
                                 G  _  C
GAM2408  GALNT2  3'  GCGGGGTGTGGGAGGGAGC  21007     C__  C
                                GTGG  GT GGAGGGAGC
                                ||||  || |||||||||
                                CGCC  CA CCTCCCTCG
                                  CCA  C
GAM2408  GPR56   3'  GCTGAGGGAGGGAGGGGGC  25000      T  CGTC    A
                                GCTGAG GG   GGAGGG GC
                                |||||| ||   |||||| ||
                                CGACTC CC   CCTCCC CG
                                   _ TC__     C
GAM2408  HCFC1   3'  AGCAGGGTGGGCCGGGGGAGC 43383    TGA   C    A
                                AGC  GTGG GTCGG GGGAGC
                                |||  |||| ||||| ||||||
                                TCG  CACC CGGCC CCCTCG
                                 TCC   _   _
GAM2408  HDAC5   3'  GCTGGTGGTCAGCAAAGGGAGC 40171     A   _  T
                                GCTG GTGG CG CGGAGGGAGC
                                |||| |||| || ||||||||||
                                CGAC CACC GT GTTTCCCTCG
                                  _   A  C
GAM2408  IGF2    5'  AGCTGGGGGGGGACGGGAGGGAG 8307      AGT__   TC
            C                    AGCTG    GGCG  GGAGGGAGC
                                |||||    ||||  |||||||||
                                TCGAC    CTGC  CCTCCCTCG
                                  CCCCC   __
GAM2408  IMPDH1  3'  GCTGGTCTCGGAGGGG     9411      A  GGCG      A
                                GCTG GT   TCGGAGGG G
                                |||| ||   |||||||| |
                                CGAC CA   AGCCTCCC C
                                  _ G___      C
GAM2408  ITPR3   3'  CTGAGGCACGGAGGGAGC    13688     GT   T
                                CTGA  GGCG CGGAGGGAGC
                                ||||  |||| ||||||||||
                                GACT  CCGT GCCTCCCTCG
                                  __   _
GAM2408  KCNQ4   5'  GCTGGGGGCGCCGGGG     21732     AGT      A
                                GCTG   GGCGTCGG GG
                                ||||   |||||||| ||
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                                CGAC   CCGCGGCC CC
                                  CC_      _
GAM2408  NOTCH3   3'  GCTGGGGCAGAGGGAG     7736      AGT  C T
                                GCTG   GG G CGGAGGGAG
                                ||||   || | |||||||||
                                CGAC   CC C GTCTCCCTC
                                   ___  _ _
GAM2408  PACSIN1  3'  AGTGGAGTGGGACGGAGGGAG  45141    CT     CGT
                                AG  GAGTGG   CGGAGGGAG
                                ||  ||||||   |||||||||
                                TC  CTCACC   GCCTCCCTC
                                 AC     CT_
GAM2408  PEA15    3'  AACTGAGTGGAAGAGGGG    19073         CGTC     A
                                AGCTGAGTGG    GGAGGG G
                                ||||||||||    |||||| |
                                TTGACTCACC    TCTCCC C
                                      T___     C
GAM2408  PIM2     3'  CTGCAAAAGTTGGAGGGAGC   41023     AGT  C  C
                                CTG   GG GT GGAGGGAGC
                                |||   || || |||||||||
                                GAC   TT CA CCTCCCTCG
                                  GT_  T  A
GAM2408  POLL     3'  AGCTGAGGCTGGAGGGAG    29978       GT   GTC
                                AGCTGA  GGC   GGAGGGAG
                                ||||||  |||   ||||||||
                                TCGACT  CCG   CCTCCCTC
                                   __   A__
GAM2408  PPFIA3   3'  AGCTGAGTGGCACAGGGGGC   41412           T   A   A
                                AGCTGAGTGGCG CGG GGG GC
                                |||||||||||| ||| ||| ||
                                TCGACTCACCGT GTC CCC CG
                                      _   _   _
GAM2408  RAB6A    5'  AAGCTGAGGGTGGCGGAG    16094         T  CGTC  AG
                                AAGCTGAG GG    GG  GGAG
                                |||||||| ||    ||  ||||
                                TTCGACTC CC    CC  CCTC
                                   _  A___  G_
GAM2408  TFAP4    3'  TGAGTGGCTTCGTTCAAAGG   17416         G  ___
                                TGAGTGGC TCG   GAGGG
                                |||||||| |||   |||||
                                ACTCACCG AGC   TTTCC
                                    A   AAG
GAM2408  WNT3A    5'  AGCGTGAGCGCCGGGGGGGGC  37535     TGA  _     A  A
                                AGC   GTG GCGTCGG GGG GC
                                |||   ||| ||||||| ||| ||
                                TCG   CAC CGCGGCC CCC CG
                                  ___   T      C   C
GAM2408  XRCC3    3'  CTGAGTGGTGGGGGAG      24104         CGTC  A
                                CTGAGTGG    GG GGGAG
                                ||||||||    || |||||
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                                GACTCACC    CC CCCTC
                                    A___  _
GAM2409  OTP      3'  TCCCTAACATTGTGCTGTCCCT 37002          AT_  GAACA
                                TCCCTAACG   TGC    CCT
                                |||||||||   |||    |||
                                AGGGATTGT   ACG    GGA
                                    AAC   ACAG_
GAM2409  PEX13    3'  CTAGCAGCAAAACACCTGA   15225     A  ATT    _
                                CTA CG   GCGAA CACCTGA
                                ||| ||   ||||| |||||||
                                GAT GT   CGTTT GTGGACT
                                  C ___    T
GAM2409  CDC42    3'  TTCATTTGGTGCATTTCAA   12164          ACCC_
                                TTCATTTGGTG    CGA
                                ||||||||||     |||
                                AAGTAAACCAC    GTT
                                    GTAAA
GAM2410  EDNRA    5'  TTCACTTTTTTTTCACC     42008        GCTC
                                TTCACTT    TTTCACT
                                |||||||    |||||||
                                AAGTGAA    AAAGTGG
                                   AAA_
GAM2410  IRTA2    3'  TTCTCTTGCTCCACGTCTAT   36351     A       TTCA
                                TTC CTTGCTCT    CTAT
                                ||| ||||||||    ||||
                                AAG GAACGAGG    GATA
                                  A       TGCA
GAM2410  SPG4     3'  TCCACTTGCTTATAATTATCC  31402          CTTTCAC
                                TTCACTTGCT      TATCC
                                ||||||||||      |||||
                                AGGTGAACGA      ATAGG
                                    ATATTA_
GAM2410  SYT4     5'  TTCACTTGCCTGGATCTCA    41664          C___
                                TTCACTTGCT    TTTCA
                                ||||||||||    |||||
                                AAGTGAACGG    AGAGT
                                    ACCT
GAM2410  XDH      3'  TTCACTTGTCTTCCAAATCCCA 40462         C      CT
                                TTCACTTG TCTTTCA  ATCCCA
                                ||||||||| |||||||  ||||||
                                AAGTGAAC AGAAGGT  TAGGGT
                                   _      T_
GAM2410  ZNF9     3'  TTCAGTTGCTCTTTCCATC    18280      C        AC
                                TTCA TTGCTCTTTC  TATC
                                |||| ||||||||||  ||||
                                AAGT AACGAGAAAG  GTAG
                                  C        __
GAM2410  EGLN2    5'  TCCAAGGATAATTTGCTGGGTA 38835            ACAT
                                TTCAAGGATAATT    CTGGGTA
                                ||||||||||||    |||||||
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                                AGGTTCCTATTAA   GACCCAT
                                      AC__
GAM2410 HTR2C   3' AGGATAATTACCAGGTTGGGTA 9278          ATC__
                                AGGATAATTAC    TGGGTA
                                ||||||||||    ||||||
                                TCCTATTAATG    ACCCAT
                                      GTCCA
GAM2410 LZTR1   3' TTCAAGGAGGCTTCTGGGT   27645       TAATTACA
                                TTCAAGGA      TCTGGGT
                                ||||||||      |||||||
                                AAGTTCCT      AGACCCA
                                    CCGA____
GAM2410 RCN1    3' TTCAAGGATATTTAGG     16209         A  ACATC
                                TTCAAGGATA TT    TGGG
                                ||||||||||| ||    ||||
                                AAGTTCCTAT AA    ATCC
                                      _ _____
GAM2411 CELSR1  3' GCGAACACTGGGGACCCAG   30653       C  AAT  AG
                                GCGAACAC TG   GA  CGG
                                |||||||| ||   ||  |||
                                CGCTTGTG AC   CT  GTC
                                    _ CC_  GG
GAM2411 GNB3    3' GAACACCTGAATGAGATGG   13218          AGC
                                GAACACCTGAATGA   GG
                                ||||||||||||||   ||
                                CTTGTGGACTTACT   CC
                                      CTA
GAM2411 HS2ST1  3' GAATCAACTGAATGGAGTGG  29329    _ C     A  C
                                GAA CA CTGAATG AG GG
                                ||| || ||||||| || ||
                                CTT GT GACTTAC TC CC
                                  A  T     C  A
GAM2411 ID1     5' GCGAAAAAAATGAGGTGGAAG 43116     CACCT    AGC
                                GCGAA    GAATGA   GGAAG
                                |||||    ||||||   |||||
                                CGCTT    TTTACT   CCTTC
                                   TT___     CCA
GAM2411 NRXN2   5' GCGGGGTAGGGATGAAGCGGA 31483    AACACCT  A
                                GCG      GA TGAAGCGGA
                                |||      || |||||||||
                                CGC      CT ACTTCGCCT
                                  CCCATCC  _
GAM2411 POLR2E  5' GCGAATGCCTGAATGCAG    40921     CA     GAA
                                GCGAA  CCTGAAT   GCGG
                                |||||  |||||||   ||||
                                CGCTT  GGACTTA   CGTC
                                   AC      ___
GAM2411 USH3A   5' GCTGACACCTGAATGTTGAGAA 38157   GA        AAGC
            G                    GC  ACACCTGAATG   GGAAG
                                ||  ||||||||||    |||||
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                                CG  TGTGGACTTAC    TCTTC
                                 AC          AAC_
GAM2411  CDC42    3'  TTCATTTGGTGCATTTCAA   12164          ACCC_
                                TTCATTTGGTG     CGA
                                ||||||||||     |||
                                AAGTAAACCAC     GTT
                                      GTAAA
GAM2412  DIAPH2   3'  TGTCACTATATACTTTTTTT   28684       A   AT
                                TGTCAC ATA  TATTTTTTTT
                                ||||||  |||  ||||||||||
                                ACAGTG TAT  ATGAAAAAAA
                                   A  __
GAM2412  FGF5     3'  TGTCTGCAATACTACTTTTTTT 37596      A_    A
               AA                  TGTC  CAATA TTATTTTTTTTAA
                                ||||  |||||  ||||||||||||
                                ACAG  GTTAT GATGAAAAAAATT
                                  AC    _
GAM2412  PPAT     3'  TGTCACAGTATTATTTTC     15488        ATA
                                TGTCACA   ATTATTTTT
                                |||||||   |||||||||
                                ACAGTGT   TAATAAAAG
                                    CA_
GAM2412  RGS16    3'  TGTCACAATAAATAAATATTTA 16330          T  TTTTT
               A                   TGTCACAATAA TA     TTTAA
                                ||||||||||| ||     |||||
                                ACAGTGTTATT AT     AAATT
                                      T  TTAT_
GAM2413  BCL7A    3'  GAGAGGAACCGCATCA      34208          ACAGAA
                                GAGAGGAACC      CATCA
                                ||||||||||      |||||
                                CTCTCCTTGG      GTAGT
                                      C_____
GAM2413  CHRNA2   3'  GAGAGGAATGACGTCAA     8830         CCACA  ACA
                                GAGAGGAA    GA   TCAA
                                ||||||||    ||  ||||
                                CTCTCCTT    CT   AGTT
                                    A____  GC_
GAM2413  CTF1     3'  TGAAGGAAAGGAGGACATCAAA 10629     G    CCAC  A
                                TGA AGGAA    AG ACATCAAA
                                ||| |||||    || ||||||||
                                ACT TCCTT    TC TGTAGTTT
                                  _     TCC_  C
GAM2413  CYP19    3'  TGAGAGGAGTACCCCTTAGA   36308         __  AC__
                                TGAGAGGA  ACC    AGA
                                ||||||||  |||   |||
                                ACTCTCCT  TGG    TCT
                                     CA   GGAA
GAM2413  DBY      3'  GAGCCAACAGGACATCAA    21658     GAA  _  A
                                GAG   CCA CAG ACATCAA
                                |||   ||| ||| |||||||
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                                CTC   GGT GTC TGTAGTT
                                  ___   T   C
GAM2413  DDX3     3'  GAGCCAACAGGACATCAA    35818     GAA   _   A
                                GAG   CCA CAG ACATCAA
                                |||   ||| ||| |||||||
                                CTC   GGT GTC TGTAGTT
                                  ___   T   C
GAM2413  DMD      3'  TGAGAGGAGTTCAAATATACAT 19695         ACCA   ___
              CAAA                  TGAGAGGA   CAGA   ACATCAAA
                                |||||||||   ||||   |||||||||
                                ACTCTCCT    GTTT   TGTAGTTT
                                     CAA_   ATA
GAM2413  FCMD     3'  TGAGAGAATTACATCAGA    27526         AC_  _
                                TGAGAGGA   CA CAGA
                                ||||||||   || ||||
                                ACTCTCTT   GT GTCT
                                     AAT  A
GAM2413  MEF2D    3'  TGAGAGGAAGAAGACAT     25424         CCAC   A
                                TGAGAGGAA    AGA CAT
                                |||||||||    ||| |||
                                ACTCTCCTT    TCT GTA
                                     CT__   _
GAM2413  MGAT1    3'  TGAGAGGAGCCTGTGTGTCAAA 14439         A  ACAGAACA
                                TGAGAGGA CC       TCAAA
                                |||||||| ||       |||||
                                ACTCTCCT GG       AGTTT
                                     C  ACACAC__
GAM2413  MTMR2    3'  TGAGGGGAACCACTGGAA    32068      A       A_
                                TGAG GGAACCAC  GAA
                                |||| ||||||||  |||
                                ACTC CCTTGGTG  CTT
                                  C       AC
GAM2413  OXCT     3'  TGAGAGGAGGTACAGTACA   7747         ACC    A
                                TGAGAGGA   ACAG ACA
                                ||||||||   |||| |||
                                ACTCTCCT   TGTC TGT
                                     CCA    A
GAM2413  SET      3'  TGAGAGAAAAGCATCA      16563         CCAC  AA
                                TGAGAGGAA    AG  CATCA
                                |||||||||    ||  |||||
                                ACTCTCTTT    TC  GTAGT
                                             ____  __
GAM2413  TLL2     5'  GAGAGGAACCGCAGGTTCA   29751          A   AACA
                                GAGAGGAACC CAG    TCA
                                |||||||||| |||    |||
                                CTCTCCTTGG GTC    AGT
                                      C   CA__
GAM2413  Z39IG    3'  GAGAGAGTCAGAACAT      28577        AACCA
                                GAGAGG     CAGAACAT
                                ||||||     ||||||||
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                                CTCTCT    GTCTTGTA
                                   CA___
GAM2413 ZYX     3' TGGGAGGGGCTAGACATCAAA 18440    A   AACCAC  A
                                TG GAGG     AGA CATCAAA
                                || ||||     ||| |||||||
                                AC CTCC     TCT GTAGTTT
                                 C   CCGA__  _
GAM2413 AVPR1A  5' GTGGGGACATCTTTTTGGGT  8732     AC_      CA
                                GTG  GCATCTTTT  GGT
                                |||  |||||||||  |||
                                CAC  TGTAGAAAA  CCA
                                  CCC       AC
GAM2413 BCL11A  3' TAATGGGTCATCTTTTTAGGTA 39718   T  ACG      C
             G                   A GTG  CATCTTTT AGGTAG
                                | |||  |||||||| ||||||
                                A TAC  GTAGAAAA TCCATC
                                 T  CCA      A
GAM2413 CD28    3' TGTGATTCATCTTTAGTAG   26027      CG     TCA
                                TGTGA  CATCTTT   GGTAG
                                |||||  |||||||  |||||
                                ACACT  GTAGAAA   TCATC
                                   AA     ___
GAM2413 KIR2DS2 3' TGTGATTGCAGCCTCAGGTAG  29482      C_  T  TT
                                TGTGA  GCA CT  TCAGGTAG
                                |||||  ||| ||  ||||||||
                                ACACT  CGT GG  AGTCCATC
                                   AA  C  __
GAM2413 RET     3' TGTTGTGCATCTTTCACAAA  33943    GAC      _
                                TGT   GCATCTTTT CAGG
                                |||   ||||||||| ||||
                                ACA   CGTAGAAAG GTTT
                                  ACA       T
GAM2414 CAV1    5' CGCTGGAGGGGGGCGGTGGCTG 11989    C    A_  TCCAC  C
             G                   CGT GGAGGG  GC    GGC GG
                                ||| ||||||  ||    ||| ||
                                GCG CCTCCC  CG    CCG CC
                                  A     CC  CCA__  A
GAM2414 FGFR1   5' GTCGCAAGAGCTCCGCGGCCGG 35790     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                   G_       C
GAM2414 FGFR1   5' GTCGCAAGAGCTCCGCGGCCGG 31949     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                   G_       C
GAM2414 FGFR1   5' GTCGCAAGAGCTCCGCGGCCGG 31949     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
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                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2414  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 31949     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2414  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 31949     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2414  FGFR1    5'  GTCGCAAGAGCTCCGCGGCCGG 31949     GA       A
                                GTCG  GGGAGCTCC CGGCCGG
                                ||||  ||||||||| |||||||
                                CAGC  TTCTCGAGG GCCGGCC
                                  G_       C
GAM2414  FLOT2    3'  GCTGGAGGGAGGGCC      20983    C      CTCCAC
                                GT GGAGGGAG     GGCC
                                || ||||||||     ||||
                                CG CCTCCCTC     CCGG
                                 A      _______
GAM2414  MAPRE3   3'  GCTGGAGGGAGTGGCG      29533    C      CTCCAC   C
                                GT GGAGGGAG     GGC G
                                || ||||||||     ||| |
                                CG CCTCCCTC     CCG C
                                 A       A_____   A
GAM2414  MYO3A    3'  CGTCGGGGGGAGGTTTCCCGA   41114      A    C__   A
                                CGTCGG GGGAG   TCC CGG
                                |||||| |||||   ||| |||
                                GCAGCC CCCTC   AGG GCT
                                   _    CAA   _
GAM2414  PPP4C    3'  GTTGGAGGGGGGCAGGGGCCGG  15537    C     A  TCCAC
                                GT GGAGGG GC    GGCCGG
                                || |||||| ||    ||||||
                                CA CCTCCC CG    CCGGCC
                                 A     C  TCC__
GAM2414  SLC23A1  5'  CGTTGGGGAGAGCAGCG     44054     C  A     TCCAC   C
                                CGT GG GGGAGC    GGC G
                                ||| || ||||||    ||| |
                                GCA CC CTCTCG    TCG C
                                  A  C     _____   A
GAM2414  SOX12    3'  ATCGGAGGGGGCTGGCTGCTGG 28029         A   CCACG  C
                                GTCGGAGGG GCT    GC GG
                                ||||||||| |||    || ||
                                TAGCCTCCC CGA    CG CC
                                     C   CCGA_  A
GAM2414  APOL1    5'  CCAAGATATACCGAGGAATTC  18933        ACC      _  C
                                CCAAGATA   TACCGAG AA TC
                                ||||||||   ||||||| || ||
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                                GGTTCTAT   ATGGCTC TT AG
                                   ___       C  A
GAM2414  ARF3     3'  CCAAGATCACTTACTGCCCCC  11669        A  C   CGAGAA
                                CCAAGAT AC TAC     CTC
                                ||||||| || |||     |||
                                GGTTCTA TG ATG     GGG
                                    G  A   ACGG__
GAM2414  CHD2     3'  CCAAATAACCTGCAACTC    10443     A       ACCGAG
                                CCA GATAACCT     AACTC
                                ||| ||||||||     |||||
                                GGT TTATTGGA     TTGAG
                                  _      CG____
GAM2414  DDX3     5'  GAAGAGTACCGAGAACTC    35816    TAACC
                                GA     TACCGAGAACTC
                                ||     ||||||||||||
                                CT     ATGGCTCTTGAG
                                 TCTC_
GAM2414  DDX3     5'  GAAGAGTACCGAGAACTC    35816    TAACC
                                GA     TACCGAGAACTC
                                ||     ||||||||||||
                                CT     ATGGCTCTTGAG
                                 TCTC_
GAM2414  ENTPD6   3'  CCGAGACACCGAGAGCT     10336    A   AACCT      A
                                CC AGAT     ACCGAGA CT
                                || ||||     ||||||| ||
                                GG TCTG     TGGCTCT GA
                                 C   ______      C
GAM2414  GNL1     5'  CCGGGAGAACCTACCACTC    45562    AA  T       GAGA
                                CC  GA AACCTACC    ACTC
                                ||  || ||||||||    ||||
                                GG  CT TTGGATGG    TGAG
                                 CC  C       _____
GAM2414  GNL1     5'  CCGGGAGAACCTACCACTC    45562    AA  T       GAGA
                                CC  GA AACCTACC    ACTC
                                ||  || ||||||||    ||||
                                GG  CT TTGGATGG    TGAG
                                 CC  C       _____
GAM2414  KCNMB1   3'  AGACAACAGGGAGAACTCA    19980        CTACC
                                AGATAAC     GAGAACTCA
                                |||||||     |||||||||
                                TCTGTTG     CTCTTGAGT
                                    TCC__
GAM2414  RGS16    3'  CCAAGAGACAGCACAGAACTCA 16319       TAACC   CG
                                CCAAGA     TAC  AGAACTCA
                                ||||||     |||  ||||||||
                                GGTTCT     GTG  TCTTGAGT
                                   CTGTC   __
GAM2414  SYN3     3'  GAGTAACCTACCAATACC     18564    _        GA
                                GA TAACCTACCGA  ACT
                                || ||||||||||  |||
```

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                                CT ATTGGATGGTT  TGG
                                 C         A_
GAM2414  SYN3     3'  GAGTAACCTACCAATACC    39494    _        GA
                                GA TAACCTACCGA  ACT
                                || ||||||||||  |||
                                CT ATTGGATGGTT  TGG
                                 C         A_
GAM2414  SYN3     3'  GAGTAACCTACCAATACC    18564    _        GA
                                GA TAACCTACCGA  ACT
                                || ||||||||||  |||
                                CT ATTGGATGGTT  TGG
                                 C         A_
GAM2415  COL2A1   3'  CCTGCGCCCGGCACCTG     12305      A  A  A  A
                                CCTG CG CT CG GCACCTG
                                |||| || || || |||||||
                                GGAC GC GG GC CGTGGAC
                                  _  _  _  _
GAM2415  EXTL3    3'  TCCCGTGGTGAGAAGCACCTGA 11038      _  AC  CTAC
                                TCCC TG  GA   GAGCACCTGA
                                |||| ||  ||   ||||||||||
                                AGGG AC  CT   TTCGTGGACT
                                  C  CA  C___
GAM2415  PUNC     5'  CCTGTGCCCAGCACCTG     44879      ACGA  ACG
                                CCTG   CT   AGCACCTG
                                ||||   ||   ||||||||
                                GGAC   GG   TCGTGGAC
                                  ACG_  ___
GAM2415  SPTBN2   3'  TCCCTGTCGACTGTCCCTG   28074       A    ACGAGCA
                                TCCCTG CGACT      CCTG
                                |||||| |||||      ||||
                                AGGGAC GCTGA      GGAC
                                   A    CAG____
GAM2415  CDC42    3'  TTCATTTGGTGCATTTCAA    12164          ACCC_
                                TTCATTTGGTG    CGA
                                ||||||||||    |||
                                AAGTAAACCAC    GTT
                                      GTAAA
GAM2416  CUL4B    3'  GAATCTTGTGTAATAGTCT    18724         CAC  T_  A
                                GAATCTTGT   GT  TAG TCT
                                |||||||||   ||  ||| |||
                                CTTAGAACA   CA  ATC AGA
                                     ___  TT  _
GAM2416  PML      5'  TCGATTCTCGGTTTAGATC    37736      A    TCAC
                                TCGA TCTTG   GTTTAGATC
                                |||| |||||   |||||||||
                                AGCT AGAGC   CAAATCTAG
                                  A    ____
GAM2416  SIP      3'  TCTATTATTGTCATGTTTAGAT 30847    GAATC     C
                                TC    TTGTCA GTTTAGAT
                                ||    |||||| ||||||||
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                                AG    AACAGT CAAATCTA
                                 ATAAT     A
GAM2417  MAK     3'  TTCGAAGTGTCTATTTAAA   25383    A       CG
                                TTC AAGTGTCTA  TTAGA
                                ||| |||||||||  |||||
                                AAG TTCACAGAT  AATTT
                                  C        A_
GAM2417  AXL     3'  ACTTGAGAAGATAACATT    34878          CT
                                ACTTGAGAAGATA  ACGTT
                                ||||||||||||  |||||
                                TGAACTCTTCTAT  TGTAA
                                              __
GAM2417  IFNA4   5'  TACTTGAGATGGATAACC    34336        A_   _
                                TACTTGAGA  GATA CT
                                |||||||||  |||| ||
                                ATGAACTCT  CTAT GG
                                      AC    T
GAM2417  TPM4    3'  CTTGAGAAGATGTTTGTCC    17646         ACTAC
                                CTTGAGAAGAT    GTTC
                                ||||||||||    ||||
                                GAACTCTTCTA    CAGG
                                       CAAA_
GAM2418  CTNNB1  3'  GTAGCAGTATTCACTATAAC   12517      AC   GG
                                GTAGCA  ATT  TTGTAAC
                                ||||||  |||  |||||||
                                CATCGT  TAA  GATATTG
                                   CA   GT
GAM2418  HMG20A  3'  GTAGCAACATGACAGGTAGT   32870        T___   T
                                GTAGCAACAT    GGT GT
                                ||||||||||    ||| ||
                                CATCGTTGTA    CCA CA
                                       CTGT   T
GAM2418  SALL2   3'  TCTAGCAACATTCCTTA     41902    G       GG
                                TC TAGCAACATT  TTG
                                || ||||||||||  |||
                                AG ATCGTTGTAA  AAT
                                 _        GG
GAM2418  HHEX    3'  TCAAGTTACTTATTAAAAA   15567        CAA
                                TCAAGTTAC   TATTAAAAA
                                |||||||||   |||||||||
                                AGTTCAATG   ATAATTTTT
                                      A__
GAM2418  SFRS2IP 5'  TCAAGTTATCCATGAATTAA  21794       _   AT_
                                TCAAGTTA CCA   ATTAA
                                |||||||| |||   |||||
                                AGTTCAAT GGT   TAATT
                                     A   ACT
GAM2419  ELK4    3'  TAACTTTGTTCTTAATTGC   34748      ATAT   GAG
                                TAACT    TTGT   TAATTGC
                                |||||    ||||   |||||||
```

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                                ATTGA   AACA  ATTAACG
                                  _____   AGA
GAM2420 CDC25C   3' CTCATTCTGTAGTGTTTATTTT 35614      AA__   A
           TC                    CTCGT   TAGT TTTATTTTTC
                                 |||||   |||| ||||||||||
                                 GAGTA   ATCA AAATAAAAAG
                                   AGAC   C
GAM2420 ZNF165   3' CACTTGCCCAATATTTATTTTT 18356     C  AA
                                 CACT GT  TAGTATTTATTTTT
                                 |||| ||  |||||||||||||
                                 GTGA CG  GTTATAAATAAAAA
                                   A  G_
GAM2421 B4GALT1  3' TCAGTGGTAGGAGTGTCTT   11289    ATA       G
                                 TCA  GTAGGAGTG TTTT
                                 |||  ||||||||| ||||
                                 AGT  CATCCTCAC AGAA
                                   CAC       _
GAM2421 CLASP1   3' CAGTATGGCTCTTTTCTG    42235     GGA  GG
                                 TAGTA  GT  TTTTCTG
                                 |||||  ||  |||||||
                                 GTCAT  CG  AAAAGAC
                                   AC_  AG
GAM2421 RPS6KA5  3' TCACATAGTACTTGTTTTCTGT 21915    _     GGAGTG
                                 TCA ATAGTA     GTTTTCTGT
                                 ||| ||||||     |||||||||
                                 AGT TATCAT     CAAAAGACA
                                   G     GAA___
GAM2421 TRPM8    3' CAGTATTGGGCAAGTTTTCTGT 35855      ___  AGT
                                 TAGTA  GG  GGTTTTCTGT
                                 |||||  ||  ||||||||||
                                 GTCAT  CC  TCAAAAGACA
                                   AAC  GT_
GAM2421 AP1B1    3' TCAGAAAACCATCCCCAAC   10041    AT        T
                                 TCA  AAACCATCCC CAAT
                                 |||  |||||||||| ||||
                                 AGT  TTTGGTAGGG GTTG
                                   CT        _
GAM2421 GAS7     3' TCAATCATACCTCAATAAA   25281     AAAC  C
                                 TCAAT   CAT CCTCAATAAA
                                 |||||   ||| ||||||||||
                                 AGTTA   GTA GGAGTTATTT
                                   _____  T
GAM2421 HSD11B1  3' AAAGAACCATCCTGAATAA   24357    TA      CTC
                                 AA  AACCATCC   AATAA
                                 ||  ||||||||   |||||
                                 TT  TTGGTAGG   TTATT
                                  TC       AC_
GAM2421 NEU3     3' TCAGGAACCACCCTAATAAA  27407    ATA    T   C
                                 TCA  AACCA CCCT AATAAA
                                 |||  ||||| |||| ||||||
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                                AGT   TTGGT GGGA TTATTT
                                  CC_    _   _
GAM2421  OPHN1    3'  AAACCATCATTCTCAGTAAAC  14960        C__    A
                                AAACCATC   CTCA TAAAC
                                ||||||||   |||| |||||
                                TTTGGTAG   GAGT ATTTG
                                     TAA    C
GAM2422  ABCA2    3'  AGGGTGTACGCAGCCCGG    11490    C    AGCC  A
                                GG GGTG    AC CAGCCCGG
                                || ||||    || ||||||||
                                TC CCAC    TG GTCGGGCC
                                 _   A___  C
GAM2422  ABCA2    3'  GGCGGTGAGCAGTGCCAGG   45525         CACACA   C
                                GGCGGTGAGC     GCC GG
                                ||||||||||     ||| ||
                                CCGCCACTCG     CGG CC
                                      TCA___   T
GAM2422  ALPI     3'  AGACGGTGGGGCACGCGG    11573        A_  CACACA  C
                                AGGCGGTG  GC     GC CGG
                                ||||||||  ||     || |||
                                TCTGCCAC  CG     TG GCC
                                     CC  _______  C
GAM2422  APOBEC3B 5'  ACGTTCGCCACACAGTCCGGG  22223     GTGA       C
                                GCG    GCCACACAG CCGGG
                                |||    ||||||||| |||||
                                TGC    CGGTGTGTC GGCCC
                                  AAG_        A
GAM2422  CAPNS1   3'  AGGCGGTGAGGGGGCGGG    11974          CCACACAGCC
                                AGGCGGTGAG         CGGG
                                ||||||||||         ||||
                                TCCGCCACTC         GCCC
                                      CCCC_______
GAM2422  CLPS     3'  AGGAGGTGGCCAGCCCGG    12295     C    A    CACA
                                AGG GGTG GCCA    GCCCGG
                                ||| |||| ||||    ||||||
                                TCC CCAC CGGT    CGGGCC
                                  T   _   _____
GAM2422  CRACC    3'  AGGTGTGAGCCACCATGCCGGG 34516     CG        A  GC
                                AGG  GTGAGCCAC CA  CCGGG
                                |||  ||||||||| ||  |||||
                                TCC  CACTCGGTG GT  GGCCC
                                  A_         _  AC
GAM2422  EGR1     5'  GGCGGGGGGGGTGCAGCCCGGG  12663       TGAGCCACA
                                GGCGG        CAGCCCGGG
                                |||||        |||||||||
                                CCGCC        GTCGGGCCC
                                   CCCCCAC__
GAM2422  ELL      3'  AGGCAGTGGGCTTCCTGG    27206         A  CACACAG  C
                                AGGCGGTG GC      CC GG
                                |||||||| ||      || ||
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                                TCCGTCAC CG      GG CC
                                    C  AA_____  A
GAM2422  GNA11    5'  AGGCGGGGCGGGCCGGCCCGGG 13160     __    A   ACACA
                                AGGC  GGTG GCC    GCCCGGG
                                ||||  |||| |||    |||||||
                                TCCG  CCGC CGG    CGGGCCC
                                  CC    C   C____
GAM2422  GRM3     5'  GGCGGTGAGCCTGCACCCGGG  9152          ACACA
                                GGCGGTGAGCC    GCCCGGG
                                ||||||||||    |||||||
                                CCGCCACTCGG    TGGGCCC
                                      ACG__
GAM2422  IFNAR1   3'  AGGTGTGAGCCACCGTGCCCGG 8429     CG       ACA
             G                   AGG  GTGAGCCAC   GCCCGGG
                                |||  |||||||||   |||||||
                                TCC  CACTCGGTG   CGGGCCC
                                  A_       GCA
GAM2422  IL1R1    3'  AGGCGTGAGCCACCACACCGGG 9355      G      A  GC
                                AGGCG TGAGCCAC CA  CCGGG
                                ||||| |||||||| ||  |||||
                                TCCGC ACTCGGTG GT  GGCCC
                                  _       _ GT
GAM2422  KCNC3    3'  AGGCGGTGACAAGAGCCCGGG  22492        GC  CAC
                                AGGCGGTGA  CA   AGCCCGGG
                                |||||||||  ||   |||||||
                                TCCGCCACT  GT   TCGGGCCC
                                     __  TC_
GAM2422  MSL3L1   5'  AGGCGGTGCGCCGTGGCCGGG  38576        A   ACACA   C
                                AGGCGGTG GCC    GCC GGG
                                ||||||||| |||    ||| |||
                                TCCGCCAC CGG    CGG CCC
                                    G   CAC__   _
GAM2422  MUC4     3'  AGGCGATGAAGTTGGTGGCCTG 39660          CCACACA   C
             GG                   AGGCGGTGAG      GCC GGG
                                ||||||||||      ||| |||
                                TCCGCTACTT      CGG CCC
                                     CAACCAC   A
GAM2422  OVOL1    5'  AGCTGGGCCACCACACAGCCCG 21269     __   GA
             GG                   GGC  GGT  GCCACACAGCCCGGG
                                |||  |||  ||||||||||||||||
                                TCG  CCG  TGGTGTGTCGGGCCC
                                  AC   G_
GAM2422  PKD2L1   5'  AGCTGTTTCCACACAGCCTGGG 32016     G  GAG        C
                                GGC GT   CCACACAGCC GGG
                                ||| ||   |||||||||| |||
                                TCG CA   GGTGTGTCGG CCC
                                  A  AA_        A
GAM2422  PPFIA3   3'  GGCGGTGAGGCCCCG       41424          _  ACACAGC
                                GGCGGTGAG CC      CCG
                                |||||||| ||      |||
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                                CCGCCACTC GG      GGC
                                     C ________
GAM2422 PRG4     3' AGGTGTGAGCCATGCAATGGG 25149     CG      CA  CCC
                                AGG GTGAGCCA CAG  GGG
                                ||| |||||||| |||  |||
                                TCC CACTCGGT GTT  CCC
                                  A_      AC  A__
GAM2422 PSA      5' GGCGGTGAGTCAGCCAAG    38454        CCACA    C
                                GGCGGTGAG    CAGCC GG
                                |||||||||    ||||| ||
                                CCGCCACTC    GTCGG TC
                                     A____    T
GAM2422 REGL     3' AGGCAGTATTGGCACAGCTTGG 27117        AGCCA    CC
             G                   AGGCGGTG    CACAGC  GGG
                                ||||||||    ||||||  |||
                                TCCGTCAT    GTGTCG  CCC
                                     AACC_    AA
GAM2422 RNH      5' GGCGGGACAGCAGCAGCCCGGG 40606      T  G CA  _
                                GGCGG GA C  CA CAGCCCGGG
                                ||||| || |  || |||||||||
                                CCGCC CT G  GT GTCGGGCCC
                                  _ _ TC  C
GAM2422 SERPINE2 5' AGACGCCGCGCAGCCCGG    44001      G  A  CACAC
                                AGGCG TG GC    AGCCCGG
                                ||||| || ||    |||||||
                                TCTGC GC CG    TCGGGCC
                                  G  G  _____
GAM2422 SIM2     3' AGGTGTGAGCCACTGAGCCCGG 22872     CG       AC
                                AGG  GTGAGCCAC  AGCCCGG
                                |||  |||||||||  |||||||
                                TCC  CACTCGGTG  TCGGGCC
                                  A_       AC
GAM2422 SLC21A2  3' GGCCCACACAGCCCG      24800     GGTGAG
                                GGC     CCACACAGCCCG
                                |||     ||||||||||||
                                CCG     GGTGTGTCGGGC
                                 _______
GAM2422 TEAD2    3' GGGGTGAGCCAGTTTTGGG    18767    C       CACAGCCC
                                GG GGTGAGCCA       GGG
                                || |||||||||       |||
                                CC CCACTCGGT       CCC
                                 _       CAAAA___
GAM2422 VMD2     5' AGGCAGTGGGCTGCAGCAGGTG 20053        A  CACA   CC__
             GG                   AGGCGGTG GC    CAGC    GGG
                                ||||||||  ||    ||||    |||
                                TCCGTCAC CG    GTCG    CCC
                                     C  AC__    TCCA
GAM2422 WSX1     3' AGGCGTGAGCCACTGTGCTGGG 22112      G       ACA  CC
                                AGGCG TGAGCCAC   GC  GGG
                                ||||| ||||||||   ||  |||
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                                TCCGC ACTCGGTG  CG  CCC
                                  _      ACA  A_
GAM2422  ZNF137   3'  AGGTGTGAGCCACCGCTCCGGG 18334    CG      ACA  _
                                AGG  GTGAGCCAC   GC CCGGG
                                |||  |||||||||   || |||||
                                TCC  CACTCGGTG   CG GGCCC
                                  A_       G__  A
GAM2422  BSN      3'  GGGGTGAGCAGGGAGCATAG   18406    A     G    CG
                                GG GGTGAGC AGGGA  GCGTAG
                                || ||||||| |||||  ||||||
                                CC CCACTCG TCCCT  CGTATC
                                 _     _    __
GAM2422  EGFL4    5'  GAGGGTGAGTGGGGGACAG   41571   GA     CGA
                                G  GGTGAG   GGGACGG
                                |  ||||||   |||||||
                                C  CCACTC   CCCTGTC
                                 TC     ACC
GAM2422  HTR6     5'  GGAGGTGAGTGGGGGGACA   9311         CGA_
                                GGAGGTGAG   GGGACG
                                |||||||||   ||||||
                                CCTCCACTC   CCCTGT
                                     ACCC
GAM2422  IL1RL1   3'  GGAGGGAGTGGGGGAGG    32171      T  CGA   C
                                GGAGG GAG   GGGA GG
                                ||||| |||   |||| ||
                                CCTCC CTC   CCCT CC
                                  _  ACC   _
GAM2422  KRT14    5'  GGAGGTGAGCGAGCGAGCAG   8019          G  _
                                GGAGGTGAGCGAG GA CGG
                                |||||||||||| || |||
                                CCTCCACTCGCTC CT GTC
                                       G  C
GAM2422  KRT16    5'  GGAGGTGAGCGAGCGAGCAG   45451          G  _
                                GGAGGTGAGCGAG GA CGG
                                |||||||||||| || |||
                                CCTCCACTCGCTC CT GTC
                                       G  C
GAM2422  TGM2     3'  GGGGTGAGTGGGGACCCACA   21441    A     CGA    G_
                                GG GGTGAG   GGGAC  GCG
                                || ||||||   |||||  |||
                                CC CCACTC   CCCTG  TGT
                                 _     AC_    GG
GAM2423  ADAM29   3'  GAGGGTGTCACCCGAGGTT    44620     ACACA  GGAG
                                GAGG    AC    TCGAGGTT
                                ||||    ||    ||||||||
                                CTCC    TG    GGCTCCAA
                                  CACAG  ____
GAM2423  CYP24    5'  GAGGATGGGGTGGGGCGAGGTT 8946       CACAAC  A T
            G                    GAGGA     GG G CGAGGTTG
                                |||||     || | ||||||||
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                                CTCCT     CC C GCTCCAAC
                                   ACCCCA  C _
GAM2423  MAD2L2   3'  GAGGCTGAGAAGTCGAGGTTG  26805     ACACAAC
                                GAGG      GGAGTCGAGGTTG
                                ||||      ||||||||||||
                                CTCC      CTTCAGCTCCAAC
                                  GACT___
GAM2423  PITX1    3'  GGGGGCGCGGGATACGAGGTTG 15328    ACACAA   AG _
                                GG     CGG  T CGAGGTTG
                                ||     |||  | ||||||||
                                CC     GCC  A GCTCCAAC
                                 CCCGC_   CT T
GAM2423  PUNC     5'  AGGACACAATGGGGCGCGGGTT 44878         C  A  _  A
            G                    AGGACACAA GG GT CG GGTTG
                                |||||||||  || || || |||||
                                TCCTGTGTT CC CG GC CCAAC
                                     A  C  C  _
GAM2423  TCF2     3'  GAGGACACAGAGGGGAAATTG  27025         ACG   TC
                                GAGGACACA   GAG  GAGGTTG
                                |||||||||   |||  |||||||
                                CTCCTGTGT   CTC  CTTTAAC
                                     ___  CC
GAM2423  SLC22A2  3'  GGGTGTTTTATTTCTTT     40526     C       G
                                GGG GTTTTATT TCTTT
                                ||| |||||||| |||||
                                CCC CAAAATAA AGAAA
                                  A       _
GAM2424  SOS2     3'  TGACAAAATAATAAACACT    42853          ACTG     _
                                TGACGAAATA    ATAGAC CT
                                ||||||||||    |||||| ||
                                ACTGTTTTAT    TATTTG GA
                                     _____     T
GAM2425  ADAT1    3'  CCTGAGCCACCAAGCC      28993       AAGA
                                TCTGA    TATCAAGCC
                                |||||    |||||||||
                                GGACT    GTGGTTCGG
                                   CG__
GAM2425  ADM      5'  TCCGAAGTCCAAGCCC      10028       A ATA
                                TCTGAA G   TCAAGCCC
                                |||||| |   ||||||||
                                AGGCTT C   GGTTCGGG
                                   _ A__
GAM2425  ATP6V0B  3'  CCTGAACACCAAGCC       19725       AAG
                                TCTGA   ATATCAAGCC
                                |||||   ||||||||||
                                GGACT   TGTGGTTCGG
                                  ____
GAM2425  CACNG3   5'  TCTGCCCAGTCAAGCCC     27242      AA_  ATA
                                TCTG   AG   TCAAGCCC
                                ||||   ||   ||||||||
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                                AGAC   TC   AGTTCGGG
                                  GGG  ___
GAM2425  CENPA    3'  TCTGAAAATTATTTTCAGGCC  12233        A  ___   A
                                TCTGAAAG TA   TCA GCC
                                |||||||| ||   ||| |||
                                AGACTTTT AT   AGT CGG
                                     A  AAA   C
GAM2425  DPH2L1   3'  TCTGAAAACCACCAGCC     10730        A    A
                                TCTGAAAG TATCA GCC
                                |||||||| ||||| |||
                                AGACTTTT GTGGT CGG
                                     G    _
GAM2425  ENC1     3'  AAGACAGGTGTCAAGCCC    18857        _____
                                AAGATA    TCAAGCCC
                                ||||||    ||||||||
                                TTCTGT    AGTTCGGG
                                    CCAC
GAM2425  EPB41L2  3'  TCTGAAAGAGATAGGCC     11008         T  CAA
                                TCTGAAAGA AT   GCC
                                ||||||||| ||   |||
                                AGACTTTCT TA   CGG
                                     C  TC_
GAM2425  EZH1     3'  CCTGGGAGACCAAGCCC     12781      AA    AT
                                TCTG  AGAT  CAAGCCC
                                ||||  ||||  |||||||
                                GGAC  TCTG  GTTCGGG
                                  CC   __
GAM2425  FOXE1    3'  TCTGAAAGCTGTGAATGGAGCC 20950         AT_____  CA
                                TCTGAAAG     AT  AGCC
                                ||||||||     ||  ||||
                                AGACTTTC     TA  TCGG
                                     GACACT  CC
GAM2425  HBE1     3'  TCTCAAGGCCAAGCCC      23727     GA   ATA
                                TCT  AAG   TCAAGCCC
                                |||  |||   ||||||||
                                AGA  TTC   GGTTCGGG
                                  G_   C__
GAM2425  IL1R1    3'  TAAAAGATCTTCCCAAGCCC  9365         A___
                                TGAAAGAT    TCAAGCCC
                                ||||||||    ||||||||
                                ATTTTCTA    GGTTCGGG
                                     GAAG
GAM2425  INPP5D   3'  CCTGAAAACACAAAGCC     44419        A    C
                                TCTGAA GATAT AAGCC
                                |||||| ||||| |||||
                                GGACTT TTGTG TTCGG
                                    _    T
GAM2425  LDB1     3'  TCTGTAGAGGCCAGGCCC    19346      AA   TA   A
                                TCTG  AGA  TCA GCCC
                                ||||  |||  ||| ||||
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                                AGAC  TCT  GGT CGGG
                                  A_   CC   C
GAM2425  LHX4     3'  CTGAGCAGCCAAGCCC      37852      A_  ATA
                                CTGA  AG   TCAAGCCC
                                ||||  ||   ||||||||
                                GACT  TC   GGTTCGGG
                                  CG  ___
GAM2425  PARK2    3'  TCTAAAAAGAGAAGCCC      21277        _  TATC
                                TCTGAAA GA    AAGCCC
                                |||||||  ||    ||||||
                                AGATTTT CT    TTCGGG
                                    T  C___
GAM2425  PIP5K1A  3'  CCTGAGATACCAGGCCC      18652       AA      A
                                TCTGA  GATATCA GCCC
                                |||||  |||||||  ||||
                                GGACT  CTATGGT CGGG
                                  __       C
GAM2425  POLS     3'  TCTGGAGCCAAGCCC       28127      AA  ATA
                                TCTG  AG   TCAAGCCC
                                ||||  ||   ||||||||
                                AGAC  TC   GGTTCGGG
                                  C_  ___
GAM2425  PVT1     3'  TCTAGAGACACCAGGCC      42309      AA       A
                                TCTG  AGATATCA GCC
                                ||||  ||||||||  |||
                                AGAT  TCTGTGGT CGG
                                  C_       C
GAM2425  RNMT     3'  TCTGAAAAGAAAGCCC       19156        _  TATC
                                TCTGAAA GA    AAGCCC
                                |||||||  ||    ||||||
                                AGACTTT CT    TTCGGG
                                    T  _____
GAM2425  SF3A2    5'  CTGGGAGACACCAGAGCCC    28403      AA       _
                                CTG  AGATATCA AGCCC
                                |||  ||||||||  |||||
                                GAC  TCTGTGGT TCGGG
                                  CC       C
GAM2425  SH3BP5   3'  TCTGAAAAACCAGCCC       22125          ATCA
                                TCTGAAAGAT    AGCCC
                                ||||||||||    |||||
                                AGACTTTTTG    TCGGG
                                     G___
GAM2425  SLC2A2   3'  CTGAAAGATTTTGATAAGCC   7347          ATC___
                                CTGAAAGAT     AAGCC
                                |||||||||     |||||
                                GACTTTCTA     TTCGG
                                     AAACTA
GAM2425  SLC2A3   5'  CCTGAAAGGGCGACAAGCCC   27975         ATAT_
                                TCTGAAAG    CAAGCCC
                                ||||||||    |||||||
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                                GGACTTTC    GTTCGGG
                                    CCGCT
GAM2425  SLC7A7   3'  TCTAAAACAACCAAGCCC    19579       GAT
                                TCTGAAA   ATCAAGCCC
                                |||||||   |||||||||
                                AGATTTT   TGGTTCGGG
                                    GT_
GAM2425  SYCP1    5'  CCTGAAAAGAAAGCCC      17230       _ TATC
                                TCTGAAA GA    AAGCCC
                                ||||||| ||    ||||||
                                GGACTTT CT    TTCGGG
                                    T ____
GAM2425  TMEM1    3'  CCTGAAAGACAAATGGCC    17590         TCAA
                                TCTGAAAGATA    GCC
                                ||||||||||    |||
                                GGACTTTCTGT    CGG
                                      TTAC
GAM2425  TMEPAI   3'  TCTGAAAAGCAGGAGCCC    33625       A  TCA
                                TCTGAAAG TA   AGCCC
                                ||||||| ||   |||||
                                AGACTTTT GT   TCGGG
                                    C  CC_
GAM2425  TRIM9    3'  CCTGAAAGATCTTGCCC     31559        ATCAA
                                TCTGAAAGAT    GCCC
                                |||||||||    ||||
                                GGACTTTCTA    CGGG
                                     GAA__
GAM2425  TTC3     5'  TCCGAAAGATTCTCGTCC    17718        A_  AAG
                                TCTGAAAGAT  TC   CC
                                |||||||||  ||   ||
                                AGGCTTTCTA  AG   GG
                                     AG  CA_
GAM2425  VANGL2   3'  CCTGAGAACCAAGCCC     43456      AA  T
                                TCTGA  GA ATCAAGCCC
                                |||||  || |||||||||
                                GGACT  CT TGGTTCGGG
                                   __  _
GAM2425  WW45     3'  CCTGAAAGATTAAAAGGCCC  34819        ATCAA_
                                TCTGAAAGAT     GCCC
                                |||||||||     ||||
                                GGACTTTCTA     CGGG
                                     ATTTTC
GAM2425  ZNF198   3'  TCCGAAAGACACTGCAAG    18370          __
                                TCTGAAAGATAT  CAAG
                                ||||||||||||  ||||
                                AGGCTTTCTGTG  GTTC
                                      AC
GAM2426  ASPH     3'  TGTAACAAACTGCAATCT    37144        C   TC
                                TGTAACAAAC GCG  CT
                                |||||||||| |||  ||
```

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                                ACATTGTTTG CGT  GA
                                     A   TA
GAM2426  GPM6B    3'  TGTAACAAAATTGCAGAAACCT 42544          CC_   TCCTC
              A                   TGTAACAAA   GCG     ACCTA
                                  |||||||||   |||     |||||
                                  ACATTGTTT   CGT     TGGAT
                                       TAA   CTT__
GAM2426  PRDM2    3'  TGTGACAAACCGTGCTCA    31976     A       C TC
                                  TGT ACAAACCG G  CTCA
                                  ||| |||||||| |  ||||
                                  ACA TGTTTGGC C  GAGT
                                    C       A __
GAM2426  STAU2    3'  TGTAACAAGCTGGTCCT     30807         ACC  __
                                  TGTAACAA   GC  GTCCT
                                  ||||||||   ||  |||||
                                  ACATTGTT   CG  CAGGA
                                       ___  AC
GAM2427  ADAM17   3'  GCTGTTATCAATATAAAAGATT 34831    GCAG___
              A                   GC       AGTATAAAAGATTA
                                  ||       ||||||||||||||
                                  CG       TTATATTTTCTAAT
                                   ACAATAG
GAM2427  PDCD2    3'  GCAAGGTATAAAAGATTA     15141      A
                                  GCAG GTATAAAAGATTA
                                  |||| ||||||||||||
                                  CGTT CATATTTTCTAAT
                                    C
GAM2428  CD2AP    3'  TGACAAGATAATGAGAAATATT 29075     _     _    TA
              T                    TGA AAGATA TGAG  AAATATTT
                                  ||| |||||| ||||  ||||||||
                                  ACT TTCTAT ACTC  TTTATAAA
                                    G     T   __
GAM2428  DMXL1    3'  AAAATTTAAGTAAAATATTT   24287       A
                                  AAGAT TGAGTAAAATATTT
                                  ||||| ||||||||||||||
                                  TTTTA ATTCATTTTATAAA
                                     A
GAM2428  EIF4G2   3'  AAAGATACTCCTAAAATATTT  10871         GAG
                                  AAAGATAT   TAAAATATTT
                                  ||||||||   ||||||||||
                                  TTTCTATG   ATTTTATAAA
                                       AGG
GAM2428  FLRT2    5'  AAAGATGAAAGCAAAATGTTTA 29831        AT        A
                                  AAAGAT  GAGTAAAAT TTTA
                                  ||||||  ||||||||| ||||
                                  TTTCTA  TTCGTTTTA AAAT
                                     CT        C
GAM2428  NEDD4L   3'  GAAAGGATGTAAAATATTTA   31618       ATAT  _
                                  GAAAG    GA GTAAAATATTTA
                                  |||||    || ||||||||||||
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                                CTTTC   CT CATTTTATAAAT
                                  ____  A
GAM2429  CSPG2    5'  TCGGCGTTGCCCAGGCGGGTCA 20480     ____       A
                                TTGG   GCCCAGGCGG TCA
                                ||||   |||||||||| |||
                                AGCC   CGGGTCCGCC AGT
                                  GCAA        C
GAM2429  NCALD    3'  TTAAAGTTGGGCCCTAGTCA  36777     _     A  _
                                TTAAA TTGGGCCC GG CG
                                ||||| |||||||| || ||
                                AATTT AACCCGGG TC GT
                                  C       A  A
GAM2429  STARD4   3'  TTTAAATTGGGGCCAGGCA   40129         C
                                TTTAAATTGGG CCAGGCG
                                |||||||||| |||||||
                                AAATTTAACCC GGTCCGT
                                       C
GAM2430  ABCC3    3'  CACCAGCACTCGCGT      19121        GT   A
                                CACCGGCAC  TCG CGT
                                |||||||||  ||| |||
                                GTGGTCGTG  AGC GCA
                                      __  _
GAM2430  B3GALT5  3'  CACCGACATTCTGGCGT    37677       CG   GA_
                                CACCGGCA  TTC   CGT
                                ||||||||  |||   |||
                                GTGGCTGT  AAG   GCA
                                     __  ACC
GAM2430  COL7A1   3'  CACTCGCACGCTCACGT    6423     CG      G
                                CAC  GCACGTTC ACGT
                                |||  |||||||| ||||
                                GTG  CGTGCGAG TGCA
                                  AG      _
GAM2430  KCNA6    5'  ACCGGCACACAGGCGCGT   13804        TT__  A
                                ACCGGCACG   CG CGT
                                |||||||||   || |||
                                TGGCCGTGT   GC GCA
                                     GTCC  _
GAM2430  LYL1     5'  CACATGGACCCCGACGT    24575    C_  C  G
                                CAC  GG AC TTCGACGT
                                |||  || || ||||||||
                                GTG  CC TG GGGCTGCA
                                  TA  _  _
GAM2430  NOC4     3'  CACCAGCACTCCACGT     25864        GT  G
                                CACCGGCAC  TC ACGT
                                |||||||||  || ||||
                                GTGGTCGTG  AG TGCA
                                     __  G
GAM2430  PFKL     3'  CACCGACAGCGCCACGT    15229        _   CG
                                CACCGGCA CGTT  ACGT
                                |||||||| ||||  ||||
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                                GTGGCTGT GCGG  TGCA
                                    C   __
GAM2430  SOX11    3'  CACCAGCACGGAGCACGT    17005         TTCG
                                CACCGGCACG   ACGT
                                ||||||||||   ||||
                                GTGGTCGTGC   TGCA
                                     CTCG
GAM2430  SSPN     3'  CACCGACAGTGCAGCGT     22934        C  T  A
                                CACCGGCA GT CG CGT
                                |||||||| || || |||
                                GTGGCTGT CA GT GCA
                                    _ C  C
GAM2431  GABRP    3'  TTCATTATTTAAAAACTCAT  30563     CTC
                                TTCA  ATTTAAAAACTTAT
                                ||||  ||||||||||||||
                                AAGT  TAAATTTTTGAGTA
                                  AA_
GAM2431  TIMELESS 3'  TTCACTCACTCCTCTTAT    19399         AAAAA
                                TTCACTCATTT    CTTAT
                                ||||||||||    |||||
                                AAGTGAGTGAG    GAATA
                                     GA___
GAM2432  AP1B1    3'  GGCACAGCTTCTGTGGCT    10039           A
                                GGCATGGTTTCTGTG CT
                                |||||||||||||| ||
                                CCGTGTCGAAGACAC GA
                                       C
GAM2432  ARF1     3'  CGGCATAGTGGGGTGGCT    43306        TTCT  A
                                CGGCATGGT   GTG CT
                                |||||||||   ||| ||
                                GCCGTATCA   CAC GA
                                     CCC_  C
GAM2432  ARHGDIB  3'  GGCAGGGGATGTGACTA     10126     T  TTTC
                                GGCA GG   TGTGACTA
                                ||||  ||  ||||||||
                                CCGT CC   ACACTGAT
                                  C  CT__
GAM2432  BBS2     5'  CGGCGCCTTCTGTGGCT     36638     AT G      A
                                CGGC  G TTTCTGTG CT
                                ||||  | ||||||||  ||
                                GCCG  C GAAGACAC GA
                                  __ G      C
GAM2432  CARPX    5'  GGCATGGTCGGAGGGTGGCT  33576        TCT__  A
                                GGCATGGTT    GTG CT
                                |||||||||    ||| ||
                                CCGTACCAG    CAC GA
                                     CCTCC  C
GAM2432  CCND1    3'  GGATGGTTTGTCACT      38212    C    TC  G
                                GG ATGGTT  TGT ACT
                                || ||||||  ||| |||
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                                CC TACCAA  ACA TGA
                                 _    __  G
GAM2432 DCN     5' GGTGCTGCTCTGTGACTA   39445   CATG  T
                                GG   GTT CTGTGACTA
                                ||   ||| |||||||||
                                CC   CGA GACACTGAT
                                 ACGA  _
GAM2432 FAT2    3' GGCAGGCCCTGACT       11077     T   CTG
                                GGCA GGTTT  TGACT
                                |||| |||||  |||||
                                CCGT CCGGG  ACTGA
                                  _   ___
GAM2432 FGFRL1  3' GCGTGTGTGTGTGACTA    34912   A _ TTC
                                GC TG GT  TGTGACTA
                                || || ||  ||||||||
                                CG AC CA  ACACTGAT
                                 C  A  C__
GAM2432 FRK     5' CGGCTTGCTTTCTGTGGCT  13012    A  G      A
                                CGGC TG TTTCTGTG CT
                                |||| || |||||||| ||
                                GCCG AC AAAGACAC GA
                                  A  G      C
GAM2432 GOCAP1  3' GGGGTTTGTGACTA       35548   CAT   TC
                                GG  GGTT  TGTGACTA
                                ||  ||||  ||||||||
                                CC  CCAA  ACACTGAT
                                 ___  __
GAM2432 HSPD1   3' GGAATTTCTGTGACTA     41153   CAT
                                GG  GGTTTCTGTGACTA
                                ||  ||||||||||||||
                                CC  TTAAAGACACTGAT
                                 ___
GAM2432 IFI27   3' GGCATGGTTCTCTTCTCTG  24377       ____  G
                                GGCATGGTT   TCT TG
                                |||||||||   ||| ||
                                CCGTACCAA   AGA AC
                                     GAGA  G
GAM2432 IL20RA  3' GGCATAGTTTAGTTCCTA   30878       CT  GA
                                GGCATGGTTT  GT  CTA
                                ||||||||||  ||  |||
                                CCGTATCAAA  CA  GAT
                                     T_  AG
GAM2432 ITK     3' CGGCAGGAAGCTGTGGCT   24442     T  TTT   A
                                CGGCA GG  CTGTG CT
                                |||||  ||  |||||  ||
                                GCCGT CC  GACAC GA
                                  _  TTC    C
GAM2432 KRT5    3' GGCTTGGTCTAGACTA     7690    A  TT   T
                                GGC TGG  TCTG GACTA
                                |||  |||  ||||  |||||
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                                CCG ACC  AGAT CTGAT
                                  A  __   _
GAM2432  LAMC3    3'  CGGCAGGGAGTGTGACTA    25863      T  TTTC
                                CGGCA GG    TGTGACTA
                                ||||| ||    ||||||||
                                GCCGT CC    ACACTGAT
                                   C  TC__
GAM2432  MAPK7    3'  CGGTGGTGGCTCAGGTGGCT   40044     CA_     CT   A
                                CGG   TGGTTT  GTG CT
                                |||   ||||||  ||| ||
                                GCC   ACCGAG  CAC GA
                                  ACC     TC   C
GAM2432  MEST     3'  CAGCATGGTGACTTGACTA    43079         TT  G
                                CGGCATGGT  CT TGACTA
                                |||||||||  || ||||||
                                GTCGTACCA  GA ACTGAT
                                     CT  _
GAM2432  MKI67    3'  GACATCTCCTGTGGCT      14522       GG       A
                                GGCAT  TTTCTGTG CT
                                |||||  |||||||| ||
                                CTGTA  GAGGACAC GA
                                   __       C
GAM2432  MMP19    3'  AACGTGGTTTCTGTGGCT    35575     A         A
                                GGC TGGTTTCTGTG CT
                                ||| ||||||||||| ||
                                TTG ACCAAAGACAC GA
                                  C         C
GAM2432  MS4A8B   3'  CAGCATGGTTTCCTAGACT   36435           GT
                                CGGCATGGTTTCT  GACT
                                ||||||||||||  ||||
                                GTCGTACCAAAGG  CTGA
                                       AT
GAM2432  PFKFB4   3'  GCATGGCATGGTGACTA     21291        TTCT
                                GCATGGT    GTGACTA
                                |||||||    |||||||
                                CGTACCG    CACTGAT
                                    TAC_
GAM2432  PSMD9    3'  CAGCATGTCTGTGGCTA     15843        GTT     A
                                CGGCATG   TCTGTG CTA
                                |||||||   |||||| |||
                                GTCGTAC   AGACAC GAT
                                   ___      C
GAM2432  SH3GL2   3'  CAGCAGTTCTGTGACTA     16680       TGGT
                                CGGCA    TTCTGTGACTA
                                |||||    ||||||||||
                                GTCGT    AAGACACTGAT
                                  C___
GAM2432  SPTAN1   3'  GACATGATGATTGTGACT    17102         TTC
                                GGCATGGT   TGTGACT
                                ||||||||   |||||||
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                                CTGTACTA  ACACTGA
                                    CTA
GAM2432 SYNGR1   3' GGCAGGACAGTCTGTGACT   21762     T  TT__
                                GGCA GG   TCTGTGACT
                                |||| ||   |||||||||
                                CCGT CC   AGACACTGA
                                  _ TGTC
GAM2432 TRIM9    3' GACCCCCAGTTCTGTGACT   31568    AT__   T
                                GGC   GGTT CTGTGACT
                                |||   |||| ||||||||
                                CTG   TCAA GACACTGA
                                 GGGG   _
GAM2432 TRPM2    5' CGACATGGTTTCGCAACT    17691          T TG
                                CGGCATGGTTTC G  ACT
                                |||||||||||| |  |||
                                GCTGTACCAAAG C  TGA
                                       _ GT
GAM2432 WISP1    3' GGCATGGTCTGCAGCT     38902       TT    GA
                                GGCATGG  TCTGT  CT
                                |||||||  |||||  ||
                                CCGTACC  AGACG  GA
                                   __    TC
GAM2432 ZIC3     3' GGCACGGTTTAAGACT     18252         CTGT
                                GGCATGGTTT   GACT
                                |||||||||   ||||
                                CCGTGCCAAA   CTGA
                                     TT__
GAM2432 ZNFN2A1  3' GGGTGGTCTCTGACTA     41364    CA      GT
                                GG  TGGTTTCT  GACTA
                                ||  ||||||||  |||||
                                CC  ACCAGAGA  CTGAT
                                 C_      __
GAM2432 ATP7A    3' CTGAAATTATCTCTTTGATTAT 6260        AACCGCG_
             TT                  CTGAAAT      TGATTATTT
                                |||||||      |||||||||
                                GACTTTA      ACTAATAAA
                                   ATAGAGAA
GAM2432 GAN      3' ACTGAAATAACTGTAATT    35137         CGC
                                ACTGAAATAAC   GTGATT
                                ||||||||||   ||||||
                                TGACTTTATTG   CATTAA
                                      A__
GAM2432 KCND2    3' TGAAATAACCTAACTGCAT   29369         _____
                                TGAAATAACC    GCGT
                                ||||||||||    ||||
                                ACTTTATTGG    CGTA
                                      ATTGA
GAM2432 MBL2     3' TGAAATAAGAATGATTATTT  6965        CCGC
                                TGAAATAA   GTGATTATTT
                                ||||||||   ||||||||||
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                                ACTTTATT   TACTAATAAA
                                    CT__
GAM2432 ULBP2   3' CTGAAGTCTAACGTGATTATTT 36097      ATAACC
                                CTGAA    GCGTGATTATTT
                                |||||    ||||||||||||
                                GACTT    TGCACTAATAAA
                                  CAGAT_
GAM2433 ALDH1A1 3' CGAATTTGTCTTTTTTTATT  8664    TT  A
                                CG  TTT TCTTTTTTTATT
                                ||  ||| ||||||||||||
                                GC  AAA AGAAAAAAATAA
                                 TT  C
GAM2433 APBA2   3' AAGAGACGACGGGAGAG    24274      GCGA   AA
                                GAGAGAC   GACG  AGAG
                                |||||||   ||||  ||||
                                TTCTCTG   CTGC  TCTC
                                   ____   CC
GAM2433 C18orf1 3' AGATGAAATAAAGGTGAAAGAG 41204    _   CGC   AC
            A                    AGA GAGA   GAG  GAAAGAGA
                                 ||| ||||   |||  ||||||||
                                 TCT CTTT   TTC  CTTTCTCT
                                   A   AT_   CA
GAM2433 CCNF    3' GAGACACGGAAGGGA      12074       A  CGAA  A
                                GAGACGCG GA   AG GA
                                |||||||| ||   || ||
                                CTCTGTGC CT   TC CT
                                  _  ____  C
GAM2433 CSK     3' AGAGAGACGGGGCCGGAG   20457       CGAGA  AAA
                                AGAGAGACG    CG   GAG
                                |||||||||    ||   |||
                                TCTCTCTGC    GC   CTC
                                    CCCG_  ___
GAM2433 DUX4    5' GAGAGACGTGAGCAACAG   43759       C   A   A
                                GAGAGACG GAG CGA AG
                                |||||||| ||| ||| ||
                                CTCTCTGC CTC GTT TC
                                    A   _   G
GAM2433 EHD2    5' GAGAGACGTGCAGATGGAGAG  31131       CG_   CGAA
                                GAGAGACG   AGA   AGAG
                                ||||||||   |||   ||||
                                CTCTCTGC   TCT   TCTC
                                    ACG   ACC_
GAM2433 F8A     3' GAGGAAGGAGACGAAAGGGA  29108    A  CGC       A
                                GAG GA   GAGACGAAAG GA
                                ||| ||   ||||||||||| ||
                                CTC CT   CTCTGCTTTC CT
                                  _  TC_        C
GAM2433 FVT1    3' AGAGAGAGAGAGAGAG     13025       CGC   C  AA
                                AGAGAGA   GAGA GA  GAG
                                |||||||   |||| ||  |||
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                                TCTCTCT   CTCT CT  CTC
                                   ___   _ __
GAM2433  GPC4     5'  AGGAGACGCGGGGCGAAAA   11082    A      AGA
                                AG GAGACGCG   CGAAAG
                                || ||||||||   ||||||
                                TC CTCTGCGC   GCTTTT
                                 _       CCC
GAM2433  HDGF     3'  AGAGAGGCATAGAGAG      21058       AC  _  CGAAA
                                AGAGAG  GCG AGA    GAG
                                ||||||  ||| |||    |||
                                TCTCTC  CGT TCT    CTC
                                   __   A   _____
GAM2433  HK2      5'  GAGACGCGAGAGGGGAG     6788           CGAAA
                                GAGACGCGAGA    GAG
                                ||||||||||    |||
                                CTCTGCGCTCT    CTC
                                      CCC__
GAM2433  MEN1     3'  AGAGGGATGCAAAAGAGA    39144     ACGC  GA
                                AGAG   GA  CGAAAGAGA
                                ||||   ||  |||||||||
                                TCTC   CT  GTTTTCTCT
                                  C___  AC
GAM2433  NCSTN    5'  AGAAAGACAGAAGGCGAAGGAG 43939         C   A   A
            AC                    AGAGAGACG GAG CGAA GAGAC
                                ||||||||| ||| |||| |||||
                                TCTTTCTGT TTC GCTT CTCTG
                                     C   C   C
GAM2433  RCN2     5'  GAGGGACGCGAGGAGGGAG   16213     A      AC  AA
                                GAG GACGCGAG  GA  GAG
                                ||| ||||||||  ||  |||
                                CTC CTGCGCTC  CT  CTC
                                  C       __  CC
GAM2433  SCN4A    3'  GAAAGGTGAGAAAGAGA     7320       ACGC   CGA
                                GAGAG   GAGA   AAGAGA
                                |||||   ||||   ||||||
                                CTTTC   CTCT   TTCTCT
                                   CA__   ___
GAM2433  SH3GL2   3'  GAGAAATGCAAAGAG       16681       C   GACGAA
                                GAGAGA GCGA     AGAG
                                |||||| ||||     ||||
                                CTCTTT CGTT     TCTC
                                   A   _______
GAM2433  SIX2     3'  GAGAGAGAAAGGGAGAGA    32606       CGC   CGAA
                                GAGAGA   GAGA   AGAGA
                                ||||||   ||||   |||||
                                CTCTCT   CTTT   TCTCT
                                   ___   CCC_
GAM2433  SIX2     3'  AGAGAGGGTAAAAGGAAGAGAC 32600       ACGC   C   A
                                AGAGAG   GAGA GAA GAGAC
                                ||||||   |||| ||| |||||
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                                TCTCTC    TTTT CTT CTCTG
                                   CCA_    C  _
GAM2433  SNX6     5'  GAGACACAAAGGGAGA      34561          ACGAAA
                                GAGACGCGAG     GAGA
                                ||||||||||     ||||
                                CTCTGTGTTT     CTCT
                                     CC_____
GAM2433  SOX13    3'  AGAGAGACGAGGACAGAGAGAG 25005         CGA  _  A
              AC                   AGAGAGACG   GAC GA AGAGAC
                                ||||||||||   ||| || ||||||
                                TCTCTCTGC   CTG CT TCTCTG
                                     TC_   T  C
GAM2433  SPS2     3'  GAGAGACGTCATTAACAGAGAC 29304         _  AGACGAA
                                GAGAGACG CG      AGAGAC
                                ||||||||| ||      ||||||
                                CTCTCTGC GT      TCTCTG
                                     A  AATTG__
GAM2433  TG737    5'  GAGAGACGCGGCGCCAAG    27202          AGA  AAA
                                GAGAGACGCG   CG   GAG
                                ||||||||||   ||   |||
                                CTCTCTGCGC   GC   TTC
                                     C__  GG_
GAM2433  TLL1     3'  AAGAGAAAAATGAAAGAGAC   29730       CGC    C
                                GAGAGA   GAGA GAAAGAGAC
                                ||||||   |||| |||||||||
                                TTCTCT   TTTT CTTTCTCTG
                                   ___    A
GAM2433  TNFSF5   3'  AGAGAGATGGAGAGAGAGAGA  6319        CGC    C  A
                                AGAGAGA   GAGA GA AGAGA
                                |||||||   |||| || |||||
                                TCTCTCT   CTCT CT TCTCT
                                     AC_    _  C
GAM2433  TNFSF5   3'  AGAGAGATTGAGAAAGAGA    6320        CGC    CGA
                                AGAGAGA   GAGA   AAGAGA
                                |||||||   ||||   ||||||
                                TCTCTCT   CTCT   TTCTCT
                                     AA_    ____
GAM2433  TNFSF5   3'  AGAGAGATTGGAAGAAAGAG   6321        CGCGA  C
                                AGAGAGA     GA GAAAGAG
                                |||||||     || |||||||
                                TCTCTCT     CT CTTTCTC
                                     AAC__  T
GAM2433  TNFSF5   3'  AGAGAGACTGAAAGAGAGAGA  6317         GC    C  A
                                AGAGAGAC  GAGA GA AGAGA
                                ||||||||  |||| || |||||
                                TCTCTCTG  CTTT CT TCTCT
                                     A_    _  C
GAM2433  TNFSF5   3'  AGAGAGACTGGGGGAGGGAAGA 6318         GC___   AC   A
              GAC                   AGAGAGAC    GAG  GAA GAGAC
                                ||||||||     |||  ||| |||||
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                                TCTCTCTG    CTC  CTT CTCTG
                                    ACCCC   C_  _
GAM2434  AMELX    5'  TGATGGTTCTTTGAATGTATTC 10078     T   CAATG
                                TGAT GGT    TGAATGTATTC
                                |||| |||    ||||||||||
                                ACTA CCA    ACTTACATAAG
                                  _  AGAA_
GAM2434  APOBEC2  3'  TGATTGGTTGGTGTCAAATGT  27708       CAA  _
                                TGATTGGT   TGT GAATGT
                                ||||||||   ||| ||||||
                                ACTAACCA   ACA TTTACA
                                    ACC   G
GAM2434  ATP6V1A1 3'  TGATTGGTCAACTGGCTGT   11782         G  AA
                                TGATTGGTCAAT TG  TGT
                                ||||||||||| ||  |||
                                ACTAACCAGTTG AC  ACA
                                      _ CG
GAM2434  RUNX1    3'  TGGTTGGCAATGTCTCTGT   12032    A   T    GAA
                                TG TTGG CAATGT   TGT
                                || |||| ||||||   |||
                                AC AACC GTTACA   ACA
                                 C   _     GAG
GAM2435  PCSK2    3'  TATCACCCATTTGAATGACAG  15134         A____
                                TATCGCCCATTT    ACAG
                                ||||||||||||    ||||
                                ATAGTGGGTAAA    TGTC
                                      CTTAC
GAM2435  RRM2     3'  TATCGCCGCCGTGAGTACAAAA 9762       CATTTAAC
                                TATCGCC       AGTACAAAA
                                |||||||       |||||||||
                                ATAGCGG       TCATGTTTT
                                   CGGCAC__
GAM2436  AMELX    5'  TGATGGTTCTTTGAATGTATTC 10078     T   CAATG
                                TGAT GGT    TGAATGTATTC
                                |||| |||    ||||||||||
                                ACTA CCA    ACTTACATAAG
                                  _  AGAA_
GAM2436  APOBEC2  3'  TGATTGGTTGGTGTCAAATGT  27708       CAA  _
                                TGATTGGT   TGT GAATGT
                                ||||||||   ||| ||||||
                                ACTAACCA   ACA TTTACA
                                    ACC   G
GAM2436  ATP6V1A1 3'  TGATTGGTCAACTGGCTGT   11782         G  AA
                                TGATTGGTCAAT TG  TGT
                                ||||||||||| ||  |||
                                ACTAACCAGTTG AC  ACA
                                      _ CG
GAM2436  RUNX1    3'  TGGTTGGCAATGTCTCTGT   12032    A   T    GAA
                                TG TTGG CAATGT   TGT
                                || |||| ||||||   |||
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                                AC AACC GTTACA   ACA
                                 C   _     GAG
GAM2437  DDEF2    3'  TATGAATCTTACCCTCGC    19326       TC    C
                                TATGAAT  TACCC CGT
                                |||||||  ||||| |||
                                ATACTTA  ATGGG GCG
                                    GA    A
GAM2438  BCL2L2   3'  CGTTCCCTAAATCCCACTC   19740         A G  GT
                                CGTTCCCTAAA T CT  GCTC
                                |||||||||||| | ||  ||||
                                GCAAGGGATTT A GG  TGAG
                                      _ G  __
GAM2438  ESR2     5'  TTCTCTAAAATGCGGAC     11015     C       T TG
                                TTC CTAAAATGC G  C
                                ||| |||||||| |  |
                                AAG GATTTTACG C  G
                                  A       _ CT
GAM2438  MECP2    3'  ACGCTTGAAATGCTGTGTTC   22567      CCCTA       C
                                ACGTT    AAATGCTGTG TC
                                |||||    |||||||||| ||
                                TGCGA    TTTACGACAC AG
                                  AC___        A
GAM2438  NCAM2    3'  TACGTTCCCTGAAATTCC    21225         A   G
                                TACGTTCCCT AAAT CT
                                |||||||||| |||| ||
                                ATGCAAGGGA TTTA GG
                                      C   A
GAM2438  SYT1     3'  GCTTGACAAAATGCTGTGTTC  24854     CCC         C
                                GTT   TAAAATGCTGTG TC
                                |||   |||||||||||| ||
                                CGA   GTTTTACGACAC AG
                                  ACT         A
GAM2439  BCL2     3'  AAGGTTGTCATTAAATATC    8516          CGAAC
                                AAGGTTGTCGTTA    ATATC
                                ||||||||||||    |||||
                                TTCCAACAGTAAT    TATAG
                                       T____
GAM2440  ADRB3    3'  CCACAGCCAGCCCATCC     6177           TTA
                                CTACAGCCAGTTCA   TCC
                                ||||||||||||||   |||
                                GGTGTCGGTCGGGT   AGG
                                         ___
GAM2440  MTMR8    3'  TACAGTGAGCCTCATTATC    31755      CC  _
                                TACAG  AGT TCATTATC
                                |||||  ||| ||||||||
                                ATGTC  TCG AGTAATAG
                                  AC   G
GAM2440  NR1I2    3'  GACCTACAGGTCAGTGCACTCT 35103        C_   T   A
              C                  GACCTACAG  CAGT CATT TC
                                |||||||||  |||| |||| ||
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                                CTGGATGTC  GTCA GTGA AG
                                     CA   C   G
GAM2440  RUNX1    3'  GACCTACAGCGAGATC      12021         C  TTCATT
                                GACCTACAGC AG     ATC
                                |||||||||| ||     |||
                                CTGGATGTCG TC     TAG
                                     C  _______
GAM2440  SLC21A2  3'  TACAGCCAGTCTCC       24803          CATTA
                                TACAGCCAGTT    TCC
                                ||||||||||    |||
                                ATGTCGGTCAG    AGG
                                      _____
GAM2441  DAB2     3'  TATGAAGGGATGTGGTGG    10643      T
                                TATGA GGGATGTGGTGG
                                ||||| ||||||||||||
                                ATACT CCCTACACCACC
                                   T
GAM2441  LNK      3'  TGGTGGGATGTGCTGTGCC   24210    A       G  GGT
                                TG TGGGATGTG TG   TGCC
                                || |||||||| ||   ||||
                                AC ACCCTACAC AC   ACGG
                                 C       G  ___
GAM2441  PEA15    3'  TGGGTAGATGGTGGGTTGC   19084     AT_
                                TGGG   GTGGTGGGTTGC
                                ||||   ||||||||||||
                                ACCC   TACCACCCAACG
                                  ATC
GAM2442  NEU1     3'  TGAAGGCAGAATACCCCTGT  7731     T  A      AATG
                                TGA AG CAGAATGC    CTGT
                                ||| || ||||||||    ||||
                                ACT TC GTCTTATG    GACA
                                  _ C       GG__
GAM2443  ABCD4    3'  GGAGATTCAGTGTCCC      33747        C  CAT
                                GGAGATTC AG   TGTTCC
                                |||||||| ||   ||||||
                                CCTCTAAG TC   ACAGGG
                                      _ ___
GAM2443  APBA2    5'  CAGGAGATTCAGCAACGC    24277         C    T
                                CAGGAGATTC AGCA TGT
                                |||||||||| |||| |||
                                GTCCTCTAAG TCGT GCG
                                     _   T
GAM2443  ATBF1    5'  GGAAATTCCAGTGGCACCC   27849          CATTGT
                                GGAGATTCCAG     TCC
                                ||||||||||     |||
                                CCTTTAAGGTC     GGG
                                      ACCGT_
GAM2443  CKTSF1B1 3'  AGGAGATTCTGGTCCC      30079        CAGCATT
                                AGGAGATTC      GTTCC
                                |||||||||      |||||
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                                TCCTCTAAG      CAGGG
                                     AC_____
GAM2443  DIAPH2   3'  CAGGAGACTCCATTCC      28669          GCATTG
                                CAGGAGATTCCA      TTCC
                                ||||||||||||     ||||
                                GTCCTCTGAGGT     AAGG
                                      _______
GAM2443  ETV5     5'  TGAGAGGTTTCAGCATTG    20856   A    A  C
                                C GGAG TT CAGCATTG
                                | |||| || ||||||||
                                A TCTC AA GTCGTAAC
                                 C    C  A
GAM2443  FAAH     5'  CAGGAGACTCGCGTGTTCC   11047          CA  AT
                                CAGGAGATTC  GC  TGTTCC
                                ||||||||||  ||  ||||||
                                GTCCTCTGAG  CG  ACAAGG
                                     __  C_
GAM2443  FOSB     3'  GAGATTCCAGCCCC       27538          ATTGT
                                GAGATTCCAGC    TCC
                                ||||||||||||    |||
                                CTCTAAGGTCG    GGG
                                      _____
GAM2443  GAD1     3'  CAGGAGATCTAGTTATTATCCA 9051          CCAGC    T
              A                  CAGGAGATT    ATTGT CCAA
                                ||||||||||    ||||| ||||
                                GTCCTCTAG    TAATA GGTT
                                     ATCAA    _
GAM2443  HUNK     3'  CAGGGGTTCCAGCAAGTTCC  31056     AGA      TT
                                CAGG   TTCCAGCA  GTTCC
                                ||||   ||||||||  |||||
                                GTCC   AAGGTCGT  CAAGG
                                  CC_      T_
GAM2443  IMPA2    3'  CAGGAGATTTGAGTTTTG    45455         CC  CA
                                CAGGAGATT  AG  TTG
                                |||||||||  ||  |||
                                GTCCTCTAA  TC  AAC
                                     AC  AA
GAM2443  IRF2     3'  GGAGATCCAGCAGGCTC     13586       T     TT
                                GGAGAT CCAGCA  GTTC
                                ||||||  ||||||  ||||
                                CCTCTA GGTCGT  CGAG
                                   _     C_
GAM2443  NEU3     3'  GGAAATTCTGTCCA       27404         CAGCAT   T
                                GGAGATTC     TGT CCA
                                ||||||||     ||| |||
                                CCTTTAAG     ACA GGT
                                      _______  _
GAM2443  NUCB1    3'  GGGGATTCCAGTAGCTGT    26159    A       CA_
                                GG GATTCCAG   TTGT
                                || ||||||||   ||||
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                                CC CTAAGGTC  GACA
                                 C      ATC
GAM2443 PPP2R2B  3' CAGGAGATACTGACTAGTTC  21329       TCCA ATT
                                CAGGAGAT   GC  GTTC
                                ||||||||   ||  ||||
                                GTCCTCTA   TG  CAAG
                                    TGAC AT_
GAM2443 RABIF    3' AGAGATTCCAGTTGAACCAA  16121        CA  TT
                                GGAGATTCCAG TTG CCAA
                                |||||||||||  |||  ||||
                                TCTCTAAGGTC AAC GGTT
                                      __  TT
GAM2443 RBP5     5' TGAGAGATTCCAGCCAGCTCC 36463  A       ATT
                                C GGAGATTCCAGC  GTTCC
                                | ||||||||||||  |||||
                                A TCTCTAAGGTCG  CGAGG
                                 C         GT_
GAM2443 RDS      3' GGAGATTCAGACTTTC     7245       C C  G
                                GGAGATTC AG ATT TTC
                                |||||||| || ||| |||
                                CCTCTAAG TC TGA AAG
                                      _ _  _
GAM2443 TACC1    3' AGGAGGCTCCAGCACTGTC  26588     AT
                                AGGAG TCCAGCATTGTT
                                |||||  ||||||||||||
                                TCCTC AGGTCGTGACAG
                                  CG
GAM2443 TTN      3' CAGGAGATGTTACTTTTCCAA 39420      TCCA ATTG
                                CAGGAGAT   GC   TTCCAA
                                ||||||||   ||   ||||||
                                GTCCTCTA   TG   AAGGTT
                                    CAA_ AA__
GAM2444 AMD1     3' TCACTGCATCAATCCAGAA   11591        CGTGC
                                TTACTGCATCAA    TCAGAA
                                ||||||||||||    ||||||
                                AGTGACGTAGTT    GGTCTT
                                      A____
GAM2444 BRCA1    3' TACATCCGTCTCAGAAA    28642      AA  G
                                TGCATC CGT CTCAGAAA
                                ||||||  ||| ||||||||
                                ATGTAG GCA GAGTCTTT
                                     __  _
GAM2444 BRCA1    5' TACATCCGTCTCAGAAA    28642      AA  G
                                TGCATC CGT CTCAGAAA
                                ||||||  ||| ||||||||
                                ATGTAG GCA GAGTCTTT
                                     __  _
GAM2444 CLC      3' CTACTGCATTGTAAACTTTCAG 29897       C___  GTGC
                                TTACTGCAT   AAC   TCAG
                                |||||||||   |||   ||||
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                                GATGACGTA   TTG   AGTC
                                     ACAT  AA__
GAM2444  CREBL2   3'  TACTCTGTTTACTCAGAA    10583     A  AACG
                                TGC TC   TGCTCAGAA
                                ||| ||   |||||||||
                                ATG AG   ATGAGTCTT
                                  _ ACAA
GAM2444  CSE1L    3'  TTAATGCAGCTGTGCTCAGAA  41589     C    TCAAC
                                TTA TGCA    GTGCTCAGAA
                                ||| ||||    ||||||||||
                                AAT ACGT    CACGAGTCTT
                                  T   CGA__
GAM2444  ENPP2    3'  TACTGCAGATGCTCAGAAA   26303       TCAAC
                                TACTGCA    GTGCTCAGAAA
                                |||||||    ||||||||||
                                ATGACGT    TACGAGTCTTT
                                    C____
GAM2444  ITGA1    3'  TTACTACATTATCAGA      41862         CAACG  C
                                TTACTGCAT    TG TCAGA
                                |||||||||    || |||||
                                AATGATGTA    AT AGTCT
                                     _____ _
GAM2444  NLGN1    3'  TTACTGCAGTTAGTTTGTCAGA 31392        TCAACG_  C
                                TTACTGCA     TG TCAGA
                                ||||||||     || |||||
                                AATGACGT     AC AGTCT
                                    CAATCAA  _
GAM2444  PAX5     3'  TACTGCATCGGTCCCAGA    32520         AAC  G
                                TACTGCATC   GT CTCAGA
                                |||||||||   || ||||||
                                ATGACGTAG   CA GGGTCT
                                    C__  _
GAM2444  RB1CC1   5'  TTACTGGTTAAACTCAGAA   31320      CATCAACGT
                                TTACTG       GCTCAGAA
                                ||||||       ||||||||
                                AATGAC       TGAGTCTT
                                   CAATT____
GAM2444  TSG      3'  TTACTGCATTTTTTCAGAA   34012        CAACGTGC
                                TTACTGCAT      TCAGAA
                                |||||||||      ||||||
                                AATGACGTA      AGTCTT
                                    AAAA____
GAM2445  AIM2     5'  ACCGGGTCTGCCACC      22105     AAT  CTAG
                                ACCG  GG   CTGCCACC
                                ||||  ||   ||||||||
                                TGGC  CC   GACGGTGG
                                  ___ A___
GAM2445  DAD1     3'  CCAATAAGCTGCCATCTC    10644     ATGGCT      C
                                CCGA     AGCTGCCA CTC
                                ||||     |||||||| |||
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                                GGTT     TCGACGGT GAG
                                  AT____      A
GAM2445  DLG5    5'  GAAAGGAGCTGCTGCCTC    44457     T  CT     CA
                                GAA GG  AGCTGC  CCTC
                                ||| ||  ||||||  ||||
                                CTT CC  TCGACG  GGAG
                                  T __     AC
GAM2445  GCNT2   5'  CCGAGAGTCCAGCTGCTGTCTC 11249      ATGG       CAC
                                CCGA   CTAGCTGC   CTC
                                ||||   ||||||||   |||
                                GGCT   GGTCGACG   GAG
                                  CTCA       ACA
GAM2445  HD      3'  CCGGCCCCAGCTGCCGCCTC   13346     AATGG       A
                                CCG    CTAGCTGCC CCTC
                                |||    ||||||||| ||||
                                GGC    GGTCGACGG GGAG
                                  CGG__       C
GAM2445  LAD1    3'  GAGTGGCAAGCCACCACCT    24490    A   T   TG
                                GA TGGC AGC  CCACCT
                                || |||| |||  ||||||
                                CT ACCG TCG  GGTGGA
                                 C   T   GT
GAM2445  MAPK1   3'  CGAGTGAAGCTGCCAC      15649     A   CT
                                CGA TGG  AGCTGCCAC
                                ||| |||  |||||||||
                                GCT ACT  TCGACGGTG
                                  C  __
GAM2445  MASP1   3'  TGGGTCCCATTGCCACCT    40118     ___   GC
                                TGG   CTA  TGCCACCT
                                |||   |||  ||||||||
                                ACC   GGT  ACGGTGGA
                                  CAG   A_
GAM2445  PIGF    5'  ATGGCTAGCTAACTCTC     15285          CC  _
                                ATGGCTAGCTG  AC CTC
                                ||||||||||  || |||
                                TACCGATCGAT  TG GAG
                                       __ A
GAM2445  UBE3A   5'  CACCAGTCTAGCTGCTACCT   39276      AATGG       C
                                TACCG    CTAGCTGC ACCT
                                |||||    |||||||| ||||
                                GTGGT    GATCGACG TGGA
                                   CA___       A
GAM2446  NCYM    5'  GCGAGTGCGGTTGTCTGCGTGC 26745           _   CACA
                                GCGAGTGCGGTT TCT    TGC
                                |||||||||||| |||    |||
                                CGCTCACGCCAA AGA    ACG
                                       C   CGC_
GAM2446  TRH     3'  GCTGATTTTCTCACATGC    28290    GG__
                                GC    TTTCTCACATGC
                                ||    ||||||||||||
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                                CG   AAAGAGTGTACG
                                 ACTA
GAM2447  DDEF2    3'  TAAAAAGTGGGATGTTTGGGAG 19323        TA  AG  A
              TA                  TAAAAAGTG  GTG  TG GAGTA
                                  |||||||||  |||  || |||||
                                  ATTTTTCAC  TAC  AC CTCAT
                                       CC   AA  C
GAM2447  DMXL1    3'  AGTGTGGTGAATTAAGT     24288      A     GA
                                  AGTGT GTGAGT  GAGT
                                  ||||| ||||||  ||||
                                  TCACA CACTTA  TTCA
                                    C     A_
GAM2447  EGFL5    3'  TAAAAAGTGTAGGACCAAGGT  44532          T  G    A
                                  TAAAAAGTGTAG GA TGAG GT
                                  |||||||||||| || |||| ||
                                  ATTTTTCACATC CT GTTC CA
                                         _  G   _
GAM2447  ITGBL1   3'  GTGAGTTTAAAGTGAGAGTA   21987     T  ___
                                  GTG AGT   GAGTGAGAGTA
                                  ||| |||   ||||||||||
                                  CAC TCA   TTCACTCTCAT
                                    _   AAT
GAM2447  MGAT2    3'  AAGTGTGTCAAGAGAGT     14442       A  G  T
                                  AAGTGT GT AG GAGAGT
                                  |||||| || || ||||||
                                  TTCACA CA TT CTCTCA
                                     _  G  _
GAM2447  OAS2     3'  AAAAGTTTAAGTGAGGGT    32545       GTAG       A
                                  AAAAGT    TGAGTGAG GT
                                  ||||||    |||||||| ||
                                  TTTTCA    ATTCACTC CA
                                     A___       C
GAM2447  PTPN7    3'  AAGAGTAGTTGGTGGGAGT   38708     T    GA   A
                                  AAG GTAGT  GTG GAGT
                                  ||| |||||  ||| ||||
                                  TTC CATCA  CAC CTCA
                                    T    AC   C
GAM2447  CALU     3'  AGGGATCATTCAAGAT      10255     CA      CTCAT
                                  AGG  ATCATTC    AAGAT
                                  |||  |||||||    |||||
                                  TCC  TAGTAAG    TTCTA
                                    C_      _____
GAM2448  SERPINB5 3'  GCAGCATATTAAGGTGTTGAT  15281        AG   TA   C
                                  GCAGCATA  TAG  TGT GAT
                                  ||||||||  |||  ||| |||
                                  CGTCGTAT  ATT  ACA CTA
                                       A_   CC   A
GAM2448  HDAC7A   3'  TTGAAGACTTTGCCAGAG    32479         CTT
                                  TTGAAGACT   CCAGAG
                                  |||||||||   ||||||
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                                AACTTCTGA   GGTCTC
                                     AAC
GAM2448  LTBP1    3'  TCGAAGACTTTTTCATTTGAGA 8426          C  C  ___
                                TTGAAGACT TT CA   GAGA
                                ||||||||| || ||   ||||
                                AGCTTCTGA AA GT   CTCT
                                     A  A  AAA
GAM2448  PDCL     3'  TTCAAGACTCTTTTACAG    23935    G       C__
                                TT AAGACTCTT   CAG
                                || |||||||||   |||
                                AA TTCTGAGAA   GTC
                                 G        AAT
GAM2448  PDGFB    3'  TTGGAGACCTTCTCCCAG    15200     A    __
                                TTG AGAC  TCTTCCAG
                                ||| ||||  ||||||||
                                AAC TCTG  AGAGGGTC
                                  C    GA
GAM2448  PRDM4    3'  TTAGAGACTCTTCTGTAAG   29666     A       CA_
                                TTG AGACTCTTC   GAG
                                ||| |||||||||   |||
                                AAT TCTGAGAAG   TTC
                                  C        ACA
GAM2448  SIRT6    3'  TTGAGGACTTTTCCAGAA    32419      A    C
                                TTGA GACT TTCCAGAG
                                |||| |||| ||||||||
                                AACT CTGA AAGGTCTT
                                   C    A
GAM2448  XYLB     3'  TTGGAAATTCTTCCAGAGA   23032     A   C
                                TTG AGA TCTTCCAGAGA
                                ||| ||| ||||||||||
                                AAC TTT AGAAGGTCTCT
                                  C   A
GAM2449  CAPN2    3'  TCCCTGCATTTTTTTTTCCTGA 11970    A     C____
                                TC CTGCAT     TTTCTTGA
                                || ||||||     ||||||||
                                AG GACGTA     AAAGGACT
                                 G      AAAAA
GAM2449  EIF3S6   3'  CATCTTTCTTTGATAGTT    11468          _  GGC
                                CATCTTTCTT GA   GTT
                                |||||||||| ||   |||
                                GTAGAAAGAA CT   CAA
                                     A  AT_
GAM2449  MAP3K7   3'  TCACTGCATCTGTTTTGAAG  17273          TTC
                                TCACTGCATCT   TTGAGG
                                ||||||||||   ||||||
                                AGTGACGTAGA   AACTTC
                                      CAA
GAM2449  NDP      3'  TGCATCCTTTTTTGCCTT    7054          C  GAG  G
                                TGCATCTTT TT   GC TT
                                |||||||| ||   || ||
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                                ACGTAGGAA AA   CG AA
                                      _ AA_  G
GAM2450  DUOX1    3'  GAAGCAGAGGTTTCACTTTGC  32653     A  T  T  A
                                GAA CA GA GT TCACTTTGC
                                ||| || || || |||||||||
                                CTT GT CT CA AGTGAAACG
                                  C  _  C  A
GAM2450  EIF4EBP2 3'  TAGGAGCAGACAAAATCACTTT 19895     AAA  T    T_
            GC                    TAG   CA GATG  ATCACTTTGC
                                |||   || ||||  ||||||||||
                                ATC   GT CTGT  TAGTGAAACG
                                  CTC  _    TT
GAM2450  GP2      5'  GAGGCATGCAGGTCACTTTGC  11303    AA    ATGTA
                                GA  CATG    TCACTTTGC
                                ||  ||||    |||||||||
                                CT  GTAC    AGTGAAACG
                                 CC    GTCC_
GAM2450  GPR30    3'  TAGAGACATGACGTGGCCGTGC 11316      A       ATCA  T
                                TAGA ACATGATGT    CT TGC
                                |||| |||||||||    || |||
                                ATCT TGTACTGCA    GG ACG
                                  C       CC__  C
GAM2450  HOXD4    3'  TAGAAACAATGATGTGAATAAT 31180        _     ATCACTT
            GC                    TAGAAACA TGATGT      TGC
                                |||||||| ||||||      |||
                                ATCTTTGT ACTACA      ACG
                                     T     CTTATT_
GAM2450  HUNK     3'  GAGACAGGGTCTCACTTTGC   31068    A   TGAT  A
                                GA ACA    GT TCACTTTGC
                                || |||    || |||||||||
                                CT TGT    CA AGTGAAACG
                                 C   CC__  G
GAM2450  PCDH9    5'  AAAACAGATCACTTT       44394       T  TGTA
                                GAAACA GA    TCACTTT
                                |||||| ||    |||||||
                                TTTTGT CT    AGTGAAA
                                   _ _____
GAM2450  PDE4D    3'  TAGAACAAATAGTCACTTTGC  43897      ACAT    TA
                                TAGAA    GATG  TCACTTTGC
                                |||||    ||||  |||||||||
                                ATCTT    TTAT  AGTGAAACG
                                   GT__    C_
GAM2450  POLS     3'  GAAACATGATATCTTTTTG   28119          ATCAC
                                GAAACATGATGT    TTTG
                                ||||||||||||    ||||
                                CTTTGTACTATA    AAAC
                                       GAA__
GAM2450  TSN      3'  TAGAGATGGAGTCTCACTTTG  21497      AAC   AT  A
                                TAGA   ATG  GT TCACTTTG
                                ||||   |||  || ||||||||
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                                ATCT   TAC  CA AGTGAAAC
                                  C__   CT  G
GAM2451  IL2RB    3'  TGCAGAGAGGATTAGTAGGTT  9395      TA    CGTAG
                                TGC  AGAGA    AGTAGGTT
                                |||  |||||    ||||||||
                                ACG  TCTCT    TCATCCAA
                                  __    CCTAA
GAM2451  P23      3'  TGCTAAGAGATGTAAAAGCT   27348         C    GTA
                                TGCTAAGAGA GTAGA   GGTT
                                |||||||||| |||||   ||||
                                ACGATTCTCT CATTT   TCGA
                                      A    ___
GAM2452  ACPT     3'  CCTCCCGCAGCAGCTCGTG   38887        C___
                                CCTCCCGC    GCTTGTG
                                ||||||||    |||||||
                                GGAGGGCG    CGAGCAC
                                     TCGT
GAM2452  AKAP13   3'  CCTCCCTTTTATGGCAGCA   40350       GCCGCT  T
                                CCTCCC     TG GCAGCA
                                ||||||     || ||||||
                                GGAGGG     AC CGTCGT
                                   AAAAT_ _
GAM2452  AMD1     5'  CTCCCGCCGCTGCCGC      11589          TGT  A
                                CTCCCGCCGCT   GC GC
                                ||||||||||   || ||
                                GAGGGCGGCGA   CG CG
                                      ___  G
GAM2452  B3GAT1   3'  CCTCCCGCCCTGCATCA     38297         G  TGT   G
                                CCTCCCGCC CT   GCA CA
                                |||||||| ||   ||| ||
                                GGAGGGCGG GA   CGT GT
                                     _ ___   A
GAM2452  BCL7B    5'  CCGCCCGCCGCCGCCGCAGC   11802    T       TG
                                CC CCCGCCGCT  TGCAGC
                                || |||||||||  ||||||
                                GG GGGCGGCGG  GCGTCG
                                 C        CG
GAM2452  BTG3     5'  TCCCGCCGCTGCCGC       27716          TGT  A
                                TCCCGCCGCT   GC GC
                                ||||||||||   || ||
                                AGGGCGGCGA   CG CG
                                      ___  G
GAM2452  C20orf1  3'  TCCCTGTTGTTATCAGCACCA  29056      GCCGC    G
                                TCCC     TTGT CAGCACCA
                                ||||     |||| ||||||||
                                AGGG     AATA GTCGTGGT
                                  ACAAC    _
GAM2452  C4orf1   5'  CCTCCGCGCCGCCACCGGTACC 40489       _      TGT  AGC_
            A                    CCTCC CGCCGCT   GC    ACCA
                                |||||| |||||||   ||    ||||
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                                GGAGG GCGGCGG   TG    TGGT
                                  C      ___  GCCA
GAM2452  CELSR3   5'  CCCCCGCCGCCCTCTGGGCACC 10829          GTGCA
                A                  CTCCCGCCGCTT    GCACCA
                                   ||||||||||||    ||||||
                                   GGGGGCGGCGGG    CGTGGT
                                         AGACC
GAM2452  EFNB1    5'  CCTCCCGCCGGCTTCGGTG   20712         _  __
                                   CCTCCCGCCG CTT  GTG
                                   |||||||||| |||  |||
                                   GGAGGGCGGC GAA  CAC
                                         C   GC
GAM2452  EIF2AK3  5'  CTCCCGCCGCTTGGAGCTCCCA 22106          TGC   A_
                                   CTCCCGCCGCTTG   AGC  CCA
                                   ||||||||||||   |||  |||
                                   GAGGGCGGCGAAC   TCG  GGT
                                           C__   AG
GAM2452  GUCY1A2  5'  CCTCTGCTGCTGCTCGCGCGGC 9214      CC__  C       A  A
                GCC                   CCTC    GC GCTTGTGC GC CC
                                   ||||    || |||||||| || ||
                                   GGAG    CG CGAGCGCG CG GG
                                     ACGA  A       C  C
GAM2452  HOXC5    3'  CCACTTGCTGGGGTCCAGTGCC 33244     C_   T__  G   CA
                A                  CCGC  GCT   GT CAG  CCA
                                   ||||  |||   || |||  |||
                                   GGTG  CGA   CA GTC  GGT
                                     AA   CCC  G   AC
GAM2452  KCNN2    5'  CCCCCGCCGCCGGGGCACC   34665          TGTGCA
                                   CTCCCGCCGCT     GCACC
                                   ||||||||||     |||||
                                   GGGGGCGGCGG     CGTGG
                                         CCC___
GAM2452  MLLT4    3'  CCTTGCTGTGCAGGCACC    25524    GCC   T     _
                                   CC   GCT GTGCAG CACC
                                   ||   ||| |||||| ||||
                                   GG   CGA CACGTC GTGG
                                    AA_  _     C
GAM2452  NDRG2    3'  CCTTCCTGTTGCCCCAGCACCA 32195     C  GCC_   GTG
                                   CCT CC    GCTT   CAGCACCA
                                   ||| ||    ||||   ||||||||
                                   GGA GG    CGGG   GTCGTGGT
                                     A  ACAA   ___
GAM2452  NRXN2    3'  CCTCCCGCCCTTCTCCCACC   31480         G   GTGCAG
                                   CCTCCCGCC CTT     CACC
                                   |||||||| |||     ||||
                                   GGAGGGCGG GAA     GTGG
                                         _  GAGG__
GAM2452  RAP1     5'  CCTCTGCCGCGAAGCGCAGCAC 33267      CC    TT_
                                   CCTC  GCCGC   GTGCAGCAC
                                   ||||  |||||   |||||||||
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                                GGAG  CGGCG   CGCGTCGTG
                                  A_    CTT
GAM2452 REPS2    5' CCCCCGCCCGCGGCC      21807     G       CA  A
                                CCC CCGCTTGTG  GC C
                                ||| |||||||||  || |
                                GGG GGCGGGCGC  CG G
                                  _       __ C
GAM2452 RRP22    5' CCTCCGCCCCGCAGCGCC    27005      C   G  TGT    A
                                CCTCC GCC CT   GCAGC CC
                                ||||| ||| ||   ||||| ||
                                GGAGG CGG GG   CGTCG GG
                                  _  _ ___    C
GAM2452 STXBP1   3' TCCCTCGGGATCACAGCAC   17209     GC  CTTG
                                TCCC  CG   TGCAGCAC
                                ||||  ||   ||||||||
                                AGGG  GC   GTGTCGTG
                                  A_ CCTA
GAM2452 TCFL4    3' CCTCTGCCATGCAGCAC     41825     CC   GCTT      C
                                CCTC  GCC   GTGCAGCA C
                                ||||  |||   |||||||| |
                                GGAG  CGG   TACGTCGT G
                                  A_  ____      A
GAM2452 TNFRSF1A 3' CCTCTCTCCGCGCGCACAGC  9868      CCG   T  TG
                                CCTC   CCGC TG  CAGC
                                ||||   |||| ||  ||||
                                GGAG   GGCG GC  GTCG
                                  AGA   C  GT
GAM2452 WWOX     3' CCTCGCCGCGCCGCGCAG    39111     _   C   T
                                CCTC CCGC GCT GTGCAG
                                |||| |||| ||| ||||||
                                GGAG GGCG CGG CGCGTC
                                  C   _  _
GAM2452 ZNF278   5' CCTCCCGCCCGCCAGGCGGCGC 36787        _  TGT  A  A
            C                    CCTCCCGCC GCT   GC GC CC
                                |||||||| |||   || || ||
                                GGAGGGCGG CGG   CG CG GG
                                     G   TC_  C  C
GAM2453 CARKL    3' AGTTCAAGTGATTTTCCT    29987      TA
                                AGTTCA  TGATTTTTCT
                                ||||||  ||||||||||
                                TCAAGT  ACTAAAAGGA
                                   TC
GAM2453 HCS      3' CAAGTTCAAGTGATTCTT    33221       TA
                                CAAGTTCA  TGATTTTT
                                ||||||||  ||||||||
                                GTTCAAGT  ACTAAGAA
                                     TC
GAM2453 PFN2     3' AGTTCATATGCTTTCTT     15242         AT
                                AGTTCATATG  TTTTCTT
                                ||||||||||  |||||||
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                                TCAAGTATAC  GAAAGAA
                                          __
GAM2453  SH2D1A   3'  CAAGTTCATGTGATGCTTTTA  14289         A    TTTT
                                CAAGTTCAT TGAT    CTTTTA
                                ||||||||| ||||    ||||||
                                GTTCAAGTA ACTA    GAAAAT
                                     C    C___
GAM2453  SLC1A3   3'  AAGTTGATATGATTAAGTCTTT 20038      C       TT_
                                AAGTT ATATGATT   TCTTT
                                ||||| ||||||||   |||||
                                TTCAA TATACTAA   AGAAA
                                   C       TTC
GAM2454  GNB1     3'  ACAGAGCAGCAACGAGAA    13195      AA  ATA
                                ATAGA  CA   CAACGAGAA
                                |||||  ||   |||||||||
                                TGTCT  GT   GTTGCTCTT
                                   C_  C__
GAM2454  HF1      3'  AAAACAATACATAAAAAAT    6778           AC
                                GAAACAATACA  GAGAAAT
                                ||||||||||  |||||||
                                TTTTGTTATGT  TTTTTTA
                                      A_
GAM2454  MCL1     3'  ATAGAAACAAAACAGTAAG    34995          T   AC
                                ATAGAAACAA ACA  GAG
                                |||||||||| |||  |||
                                TATCTTTGTT TGT  TTC
                                      T   CA
GAM2454  MOX2     3'  TAAGAAACAATACAGAATTAAA 42520    T          ACGAG
              TA                    A AGAAACAATACA     AAATA
                                | ||||||||||||     |||||
                                A TCTTTGTTATGT     TTTAT
                                 T          CTTAA
GAM2454  ORC2L    3'  TAGAAACAATAAGAGA      26194          CAAC
                                TAGAAACAATA    GAGA
                                ||||||||||    ||||
                                ATCTTTGTTAT    CTCT
                                      T___
GAM2454  PCDH15   3'  GAAAGCACAATGAGAAATA    37505      CAA    C
                                GAAA   TACAA GAGAAATA
                                ||||   ||||| ||||||||
                                CTTT   GTGTT CTCTTTAT
                                  C__     A
GAM2454  RNGTT    3'  TAGAAACAATGCAATTCACAAA 19166          A  ____
              AA                    TAGAAACAAT CA    ACGAGAA
                                |||||||||| ||    |||||||
                                ATCTTTGTTA GT    TGTTTTT
                                      C  TAAG
GAM2454  STMN1    3'  TAGAAAAGATGCAACAAGAAA  24516       CA  A
                                TAGAAA  AT CAACGAGAAA
                                ||||||  || ||||||||||
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                                ATCTTT  TA GTTGTTCTTT
                                   TC  C
GAM2454  ZNF74    5'  ACAGAAACAGCATCGAGGAATA 18297         ATA  A    A
                                ATAGAAACA   CA CGAG AATA
                                |||||||||   || |||| ||||
                                TGTCTTTGT   GT GCTC TTAT
                                     C__  A   C
GAM2454  FGF2     3'  ATCTTTCCATAGCTATTA    12828       AG   G
                                ATCTTT  TAT AGCTATTA
                                ||||||  ||| ||||||||
                                TAGAAA  GTA TCGATAAT
                                   G_  _
GAM2454  SERPIND1 3'  GAGCTTACAGCATGGGCTATT  6773     AT  _      A
                                GA  CTT TAGTATG GCTATT
                                ||  ||| ||||||| ||||||
                                CT  GAA GTCGTAC CGATAA
                                 C_  T      C
GAM2454  UCN      3'  ACGGGTCTTCAGTACTTTTATT 17841     AA        GAGC
            A                    ACG  TCTTTAGTAT    TATTA
                                |||  ||||||||||    |||||
                                TGC  AGAAGTCATG    ATAAT
                                  CC         AAA_
GAM2455  KCNA7    3'  TAAATGCAAAACAGCCCGATGT 36661    C       __    TT   C
            G                    A AATGCAAA  AGCC  CGA GTG
                                | ||||||||  ||||  ||| |||
                                A TTACGTTT  TCGG  GCT CAC
                                 T       TG   __   A
GAM2455  KIF3C    3'  ACAATGCAAAGGCGATGT    13945          A  CTTC  C
                                ACAATGCAAA GC    GA GT
                                |||||||||| ||    || ||
                                TGTTACGTTT CG    CT CA
                                     C  ____  A
GAM2455  PAFAH1B2 3'  TACAATGCAAAGTGCCTT    15074          A_
                                TACAATGCAAA  GCCTT
                                ||||||||||  |||||
                                ATGTTACGTTT  CGGAA
                                      CA
GAM2455  A1BG     3'  TTGGGAGGCTGAGGCGG     39098         GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
                                AACCCTCCG     TCCGCC
                                     AC_____
GAM2455  ACADSB   3'  TTGGGAGGCCAAGGTGG     11502         G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GT   TCC CC
                                     _ ___   A
GAM2455  ALDH1B1  3'  TTGGGAGGCTGAGGCGG     8674          GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
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                                AACCCTCCG     TCCGCC
                                     AC____
GAM2455  APAF1    3'  TTGGGAGGCCAAGGCGG     29830        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                     _  ___
GAM2455  APM1     3'  TTGGGAGGTCGAGGCGG     22024        _  CGGGT
                                TTGGGAGG CG    AGGCGG
                                |||||||| ||    ||||||
                                AACCCTCC GC    TCCGCC
                                     A  _____
GAM2455  APM1     3'  TTGGGAGGCCGAGGCGG     22023        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                     _  ___
GAM2455  APOL1    3'  TTGGGAGGCCAAGGTGG     18941        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GT   TCC CC
                                     _  ___   A
GAM2455  APPL     3'  TTGGGAGGCCGAGGCGG     29017        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                     _  ___
GAM2455  AQP6     3'  TTGGGAGGCCGAGGTGG     38260        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                     _  ___   A
GAM2455  ARCN1    3'  TTGGGAGGCTGAGGTGG     11660        GCGGGT   C
                                TTGGGAGGC      AGG GG
                                |||||||||      ||| ||
                                AACCCTCCG      TCC CC
                                     AC____   A
GAM2455  ATP6V1A1 3'  TTGGGAGGCCGAGGTGG     11783        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                     _  ___   A
GAM2455  ATP7A    3'  TTGGGAGGCCAAGGCGG     6271         G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                     _  ___
GAM2455  ATP8B2   3'  TTGGGAGGTTGAGGTGGG    42224        CGC    A
                                TTGGGAGG   GGGT GG
                                ||||||||   |||| ||
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                                AACCCTCC  TCCA CC
                                   AAC   C
GAM2455 AXL     3' TTGGGAGGCTGAGGTGG    34893       GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
                                AACCCTCCG    TCC CC
                                   AC____  A
GAM2455 CAMLG   3' TTGGGAGGCCGAGGTGG    11957       G GGT  C
                                TTGGGAGGC CG  AGG GG
                                |||||||||  ||  ||| ||
                                AACCCTCCG GC  TCC CC
                                   _ ___  A
GAM2455 CASP2   3' TTGGGAGGCTGAGGTGG    37406       GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
                                AACCCTCCG    TCC CC
                                   AC____  A
GAM2455 CASP8   3' TTGGGAGGCCGAGGTGG    37882       G GGT  C
                                TTGGGAGGC CG  AGG GG
                                |||||||||  ||  ||| ||
                                AACCCTCCG GC  TCC CC
                                   _ ___  A
GAM2455 CBFA2T2 3' TTGGGAGGCCAAGGTGG    22985       G GGT  C
                                TTGGGAGGC CG  AGG GG
                                |||||||||  ||  ||| ||
                                AACCCTCCG GT  TCC CC
                                   _ ___  A
GAM2455 CLECSF11 5' TTGGGAGGCTGAGGTGG    39046       GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
                                AACCCTCCG    TCC CC
                                   AC____  A
GAM2455 CLECSF12 3' TTGGGAGGCCAAGGCGG    44129       G GGT
                                TTGGGAGGC CG  AGGCGG
                                |||||||||  ||  ||||||
                                AACCCTCCG GT  TCCGCC
                                   _ ___
GAM2455 CNGA1   5' TTGGGAGGCTGAGGTGG    40496       GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
                                AACCCTCCG    TCC CC
                                   AC____  A
GAM2455 CR1     3' TTGGGAGGCCGAGGCGG    8204        G GGT
                                TTGGGAGGC CG  AGGCGG
                                |||||||||  ||  ||||||
                                AACCCTCCG GC  TCCGCC
                                   _ ___
GAM2455 CXCL16  3' TTGGGAGGCCTGGGTGGG   35203       GC  A
                                TTGGGAGGC  GGGT GG
                                |||||||||  ||||  ||
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                                AACCCTCCG  CCCA CC
                                     GA    C
GAM2455  CYP1A2   3'  TTGGGAGGCTGAGGCGG     8918         GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
                                AACCCTCCG     TCCGCC
                                     AC_____
GAM2455  CYP2B6   3'  TTGGGAGGCTAAGGTGG     8926         GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                     AT_____   A
GAM2455  CYP51    3'  TTGGGAGGCCAAGGCGG     8963         G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                     _  ____
GAM2455  DDX3     3'  TTGGGATGGGGGTAGGCGGG   35830       _  CGC
                                TTGGGA GG   GGGTAGGCGGG
                                ||||||  ||   ||||||||||
                                AACCCT CC   CCCATCCGCCC
                                   A  ____
GAM2455  DFFB     3'  TTGGGAGGCTGAGGTGG     44606        GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                     AC_____   A
GAM2455  DHFR     3'  TTGGGAGGCTGAGGTGG     8999         GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                     AC_____   A
GAM2455  DNASE1L1 5'  TTGGGAGGCTGAGGCGG     27505          GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
                                AACCCTCCG     TCCGCC
                                     AC_____
GAM2455  DSCR3    3'  TTGGGAGGCCAAGGCGG     25831         G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                     _  ____
GAM2455  F3       3'  TTGGGAGGCCAAGGTGG     42553         G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                |||||||||  ||   ||| ||
                                AACCCTCCG GT   TCC CC
                                     _  ____  A
GAM2455  FCAR     3'  TTGGGAGGCCAAGGTGG     39340         G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                |||||||||  ||   ||| ||
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                                AACCCTCCG GT   TCC CC
                                    _ ___  A
GAM2455  FCGR2A   3' TTGGGAGGCCGAGGCGG    44282        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                    _ ___
GAM2455  FEZ1     3' TTGGGAGGCCAAGGCGG    23009        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                    _ ___
GAM2455  FUT1     3' TGGGAGGCCGAGGTGG     6636        G  GGT   C
                                TGGGAGGC CG   AGG GG
                                |||||||| ||   ||| ||
                                ACCCTCCG GC   TCC CC
                                    _ ___  A
GAM2455  HCS      3' TTGGGAGGCCAAGGTGG    33238        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GT   TCC CC
                                    _ ___  A
GAM2455  HTR1E    5' TTGGGAGGCCGAGGCGG     9273        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                    _ ___
GAM2455  HUNK     3' TTGGGAGGCCAAGGTGG    31092        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GT   TCC CC
                                    _ ___  A
GAM2455  IGF1     3' TTGGGAGGCTGAGGCGG    8363         GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
                                AACCCTCCG     TCCGCC
                                    AC____
GAM2455  INMT     3' TTGGGAGGCCGAGGTGG    27686        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                    _ ___  A
GAM2455  KMO      3' TTGGGAGGCTGAGGTGG    18964        GCGGGT  C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                    AC____  A
GAM2455  KRTHB6   3' TATTGGGAGGCCGGCGCGG  14036          G  GTAG
                                TATTGGGAGGC CGG   GCGG
                                |||||||||| |||   ||||
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                                ATAACCCTCCG GCC   CGCC
                                      _  G___
GAM2455 LNK     3' TTGGGAGGCCAAGGCGG    24212       G  GGT
                                TTGGGAGGC CG  AGGCGG
                                ||||||||| ||  ||||||
                                AACCCTCCG GT  TCCGCC
                                      _ ___
GAM2455 LYZ     3' TTGGGAGGCCGAGGTGG    6956        G  GGT  C
                                TTGGGAGGC CG  AGG GG
                                ||||||||| ||  ||| ||
                                AACCCTCCG GC  TCC CC
                                      _ ___  A
GAM2455 MDM2    3' TTGGGAGGCCGAGGTGG    27810       G  GGT  C
                                TTGGGAGGC CG  AGG GG
                                ||||||||| ||  ||| ||
                                AACCCTCCG GC  TCC CC
                                      _ ___  A
GAM2455 MEFV    3' TTGGGAGGCTGAGGTGG    6976        GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
                                AACCCTCCG    TCC CC
                                     AC____  A
GAM2455 MEFV    3' TTGGGAGGCTGAGGCGG    6975        GCGGGT
                                TTGGGAGGC    AGGCGG
                                |||||||||    ||||||
                                AACCCTCCG    TCCGCC
                                     AC____
GAM2455 MHC2TA  3' TTGGGAGGCTGAGGTGG    6995        GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
                                AACCCTCCG    TCC CC
                                     AC____  A
GAM2455 MLANA   3' TTGGGAGGCTGAGGCGG    24301       GCGGGT
                                TTGGGAGGC    AGGCGG
                                |||||||||    ||||||
                                AACCCTCCG    TCCGCC
                                     AC____
GAM2455 MPL     3' TTGGGAGGCCAAGGTGG    23884       G  GGT  C
                                TTGGGAGGC CG  AGG GG
                                ||||||||| ||  ||| ||
                                AACCCTCCG GT  TCC CC
                                      _ ___  A
GAM2455 MRPL49  3' TTGGGAGGCCAAGGTGG    43031       G  GGT  C
                                TTGGGAGGC CG  AGG GG
                                ||||||||| ||  ||| ||
                                AACCCTCCG GT  TCC CC
                                      _ ___  A
GAM2455 MTR     3' TTGGGAGGCTGAGGTGG    7021        GCGGGT  C
                                TTGGGAGGC    AGG GG
                                |||||||||    ||| ||
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```
                                AACCCTCCG     TCC CC
                                     AC____   A
GAM2455  NFRKB    5'  TTGGGAGGTCCAGGCGG     26107        CGCGGG
                                TTGGGAGG     TAGGCGG
                                ||||||||     |||||||
                                AACCCTCC     GTCCGCC
                                     AG____
GAM2455  NONO     3'  TTGGGAGGCCGAGGTGG     44363        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                     _ ___   A
GAM2455  PCDHA9   3'  TTGGGAGGCCGAGGTGG     36557        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                     _ ___   A
GAM2455  PCDHA9   3'  TTGGGAGGCTGAGGCGG     36558        GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
                                AACCCTCCG     TCCGCC
                                     AC____
GAM2455  PER2     3'  TTGGGAGGCCGAGGTGG     19349        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                     _ ___   A
GAM2455  PIK3CD   3'  TTGGGAGGCTCAGGCGG     22739        GCGGG
                                TTGGGAGGC     TAGGCGG
                                |||||||||     |||||||
                                AACCCTCCG     GTCCGCC
                                     A____
GAM2455  PPID     3'  TTGGGAGGCCAAGGCGG     44618        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                     _ ___
GAM2455  PTGIS    3'  TTGGGAGGCCGAGGCGG     9683         G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                     _ ___
GAM2455  RAB36    3'  TTGGGAGGCCGAGGTGG     22250        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                     _ ___   A
GAM2455  RAB36    3'  TTGGGAGGCCGAGGCGG     22249        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
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                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  RABL2A   3'  TTGGGAGGCCGAGGCGG     30199        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  RABL2B   3'  TTGGGAGGCCGAGGCGG     28208        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  RCE1     3'  TTGGGGGGTGGGGGGTGGG   23072      A  CGC   TA  C
                              TTGGG GG   GGG  GG GGG
                              ||||| ||   |||  || |||
                              AACCC CC   CCC  CC CCC
                                 _  CA_   C_  A
GAM2455  RHD      3'  TTGGGAGGCCGAGGCGG     32170        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  RPH3AL   3'  TTGGGAGGCCGAGGCGG     28107        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  RPP30    3'  TTGGGAGGCCGAGGCGG     26941        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  SEDL     3'  TTGGGAGGCTGAGGCGG     31016        GCGGGT
                              TTGGGAGGC      AGGCGG
                              |||||||||      ||||||
                              AACCCTCCG      TCCGCC
                                    AC____
GAM2455  SEDL     3'  TTGGGAGGCCAAGGCGG     31015        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GT   TCCGCC
                                    _  ___
GAM2455  SERPINB9 3'  TTGGGAGGCCGAGGCGG     20000        G  GGT
                              TTGGGAGGC CG   AGGCGG
                              ||||||||| ||   ||||||
                              AACCCTCCG GC   TCCGCC
                                    _  ___
GAM2455  SH3BP2   3'  TTGGGAGGCCAAGGTGG     16647        G  GGT   C
                              TTGGGAGGC CG   AGG GG
                              ||||||||| ||   ||| ||
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                                AACCCTCCG GT   TCC CC
                                    _ ___  A
GAM2455  SHOX     3'  TTGGGAGGCTAAGGCGG     27837        GCGGGT
                                TTGGGAGGC     AGGCGG
                                |||||||||     ||||||
                                AACCCTCCG     TCCGCC
                                    AT____
GAM2455  SHOX     3'  TTGGGAGGCCGAGGCGG     27836        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GC   TCCGCC

                                    _ ___
GAM2455  SIL      5'  TTGGGAGGCCGAGGCGG     16729        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GC   TCCGCC

                                    _ ___
GAM2455  SLA2     3'  TTGGGAGGCCAAGGTGG     37018        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                |||||||||  ||   ||| ||
                                AACCCTCCG GT   TCC CC
                                    _ ___  A
GAM2455  SLC24A1  3'  TTGGGAGGCCGAGGCGG     21826        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GC   TCCGCC

                                    _ ___
GAM2455  SNAP23   3'  TTGGGAGGCCAAGGCGG     19253        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GT   TCCGCC

                                    _ ___
GAM2455  STARD4   3'  TTGGGAGGCTAAGGTGG     40128        GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                    AT____   A
GAM2455  TAPBP    3'  TTGGGAGGCCGAGGCGG     17310        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
                                AACCCTCCG GC   TCCGCC

                                    _ ___
GAM2455  TAPBP    3'  TTGGGAGGCTGAGGTGG     17311        GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                    AC____   A
GAM2455  TAPBP    3'  TTGGGAGGCCGAGGCGG     17310        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                |||||||||  ||   ||||||
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                                AACCCTCCG GC   TCCGCC
                                      _  ___
GAM2455  TERF1    3'  TTGGGAGGCCGAGGTGG     32747        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                      _  ___   A
GAM2455  TPMT     3'  TTGGGAGGCCGAGGTGG     7495         G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                      _  ___   A
GAM2455  TRAF5    3'  TTGGGAGGCCGAGGCGG     21478        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                      _  ___
GAM2455  TRPV1    3'  TTGGGAGGCCAAGGCGG     38805        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GT   TCCGCC
                                      _  ___
GAM2455  TRPV1    3'  TTGGGAGGCCGAGGTGG     38806        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
                                AACCCTCCG GC   TCC CC
                                      _  ___   A
GAM2455  VENTX2   3'  TTGGGAGGCCGAGGCGG     30928        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                      _  ___
GAM2455  VHL      3'  TTGGGAGGCTGAGGTGG     8124         GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                     AC____   A
GAM2455  VHL      3'  TTGGGAGGCTGAGGTGG     8124         GCGGGT   C
                                TTGGGAGGC     AGG GG
                                |||||||||     ||| ||
                                AACCCTCCG     TCC CC
                                     AC____   A
GAM2455  VIPR2    3'  TTGGGAGGCCGAGGCGG     18032        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                      _  ___
GAM2455  XRCC2    3'  TTGGGAGGCCGAGGTGG     24097        G  GGT   C
                                TTGGGAGGC CG   AGG GG
                                ||||||||| ||   ||| ||
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                                AACCCTCCG GC   TCC CC
                                   _ ___  A
GAM2455  YES1     3'  TTGGGAGGCCGAGGCGG     24124        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                   _ ___
GAM2455  ZNF74    5'  TTGGGAGGCCGAGGCGG     18302        G  GGT
                                TTGGGAGGC CG   AGGCGG
                                ||||||||| ||   ||||||
                                AACCCTCCG GC   TCCGCC
                                   _ ___
GAM2456  ABCB6    5'  AGAGGGGCGCGGACATCC    25030      AAACA  C     _
                                AGAGG    GGC GCGGACA CC
                                |||||    ||| ||||||| ||
                                TCTCC    CCG CGCCTGT GG
                                  _____  _     A
GAM2456  ADAR     3'  AGAGGAAATGGACCGCAG    9973         CA
                                AGAGGAAA  GGCCGCGG
                                ||||||||  ||||||||
                                TCTCCTTT  CTGGCGTC
                                    AC
GAM2456  AKAP2    5'  AAGGAAACTGATGGGCACC   28491         A  CCGC  A
                                GAGGAAAC GG    GG CACC
                                |||||||| ||    || ||||
                                TTCCTTTG CT    CC GTGG
                                    A  AC__  _
GAM2456  ANGPT4   3'  AGAGGGATGGGCCCCGAACACC 31986       AAACA   G
           C                     AGAGG    GGCC CGGACACCC
                                |||||    |||| |||||||||
                                TCTCC    CCGG GCTTGTGGG
                                   CTAC_   G
GAM2456  APBA2    3'  AGAGGGGGCAGACACC      24275      AAACA  CC
                                AGAGG    GG  GCGGACACC
                                |||||    ||  |||||||||
                                TCTCC    CC  CGTCTGTGG
                                  _____  __
GAM2456  APM1     3'  GAGGTGGGAAACAGACACC   22014      AAACA  CC
                                GAGG    GG  GCGGACACC
                                ||||    ||  |||||||||
                                CTCC    CC  TGTCTGTGG
                                  AC___  TT
GAM2456  ARHGAP6  5'  GGAGCAGGCTCTGCGCGGACA 30220     AA   ____
                                GGA  CAGGC   CGCGGACA
                                |||  |||||   ||||||||
                                CCT  GTCCG   GCGCCTGT
                                  C_   AGAC
GAM2456  BAK1     3'  GAGGAGACGGCCACAGCC    45107      A  A      ACA
                                GAGGA AC GGCCGCGG  CC
                                ||||| || ||||||||  ||
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                                CTCCT TG CCGGTGTC   GG
                                  C _      ___
GAM2456 BARHL1   3' GAGGGCACAGGCCACAGAC   33464     AA
                                GAGG  ACAGGCCGCGGAC
                                ||||  ||||||||||||
                                CTCC  TGTCCGGTGTCTG
                                  CG
GAM2456 CA7      3' GAGGGAGAAGGCCACGTCACC 41197     AAAC      GA
                                GAGG   AGGCCGCG  CACC
                                ||||   ||||||||  ||||
                                CTCC   TCCGGTGC  GTGG
                                  CTCT      A_
GAM2456 CDH19    5' AGAGGAAACAGGACGTCAC   34500         CC   GA
                                AGAGGAAACAGG  GCG  CAC
                                ||||||||||||  |||  |||
                                TCTCCTTTGTCC  TGC  GTG
                                      __  A_
GAM2456 CDKN1B   5' GAGGGGGAGAAAAACACCC   19798     AAACA  CCGC
                                GAGG    GG   GGACACCC
                                ||||    ||   ||||||||
                                CTCC    CC   TTTGTGGG
                                  C____  TCTT
GAM2456 CGTHBA   3' GAGGGGGCCACAGGGCAC    28961     AAACA      A_
                                GAGG    GGCCGCGG  CAC
                                ||||    ||||||||  |||
                                CTCC    CCGGTGTC  GTG
                                  C____       CC
GAM2456 COG3     3' AGAGGAAAGGATGACACC    36413       AC   CCGCG
                                AGAGGAA  AGG    GACACC
                                |||||||  |||    ||||||
                                TCTCCTT  TCC    CTGTGG
                                   __  TA___
GAM2456 COL4A6   5' AGGGAAACAGGCTCAGCGGTGC 37973    A       _ _   ACA
             CC                   AG GGAAACAGGC C GCGG   CCC
                                || ||||||||| | ||||  |||
                                TC CCTTTGTCCG G CGCC   GGG
                                 _        A T    AC_
GAM2456 COX7A1   5' GAGGAGGCGGTCCAGACCC   12410     AACA  CG__    A
                                GAGGA   GGC   CGGAC CC
                                |||||   |||   ||||| ||
                                CTCCT   CCG   GTCTG GG
                                  _____  CCAG    _
GAM2456 ELK1     3' GAGGAAACAGGCAGGACCC   23410         CGC   A
                                GAGGAAACAGGC   GGAC CC
                                ||||||||||||  |||| ||
                                CTCCTTTGTCCG   CCTG GG
                                      T__   _
GAM2456 FANCG    5' GAGGAAACGAGTCAGCAACCC  21556       AG CCG   AC
                                GAGGAAAC  G   CGG  ACCC
                                ||||||||  |   |||  ||||
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                                CTCCTTTG C  GTC TGGG
                                    CT A__  GT
GAM2456 FANCG   3' AGGAGAAACAGGAAAAAAGGTG 21553   AG     CCGC__ ACA
            CC                   AG GAAACAGG    GG  CC
                                || ||||||||    ||  ||
                                TC CTTTGTCC    CC  GG
                                 CT      TTTTTT AC_
GAM2456 GGT1    3' GGAGACAGGCCAGGGAGGCACC 23572    A     C  __
                                GGA ACAGGCCG GGA CACC
                                ||| |||||||| |||  ||||
                                CCT TGTCCGGT CCT  GTGG
                                  C      C  CC
GAM2456 GLS     5' AGAGGAAAGGGCAGCTAC   31374       CA  C  GG
                                AGAGGAAA  GGC GC  AC
                                ||||||||  ||| ||  ||
                                TCTCCTTT  CCG CG  TG
                                    C_  T  A_
GAM2456 GNAQ    3' AGAGGAAATGTGCTGGGAC   13173       CAG  CGC
                                AGAGGAAA  GC  GGAC
                                ||||||||  ||  ||||
                                TCTCCTTT  CG  CCTG
                                    ACA  AC_
GAM2456 GNPI    3' GAGGAGGCAGCATCCAC    24184     AACA  C  GA
                                GAGGA   GGC GCG  CAC
                                |||||   ||| |||  |||
                                CTCCT   CCG CGT  GTG
                                  _____  T  AG
GAM2456 HAP1    3' GGATGGGAGCCTGGACACC   19502    AACA   GC
                                GGA   GGCC  GGACACC
                                |||   ||||  |||||||
                                CCT   TCGG  CCTGTGG
                                  ACCC   A_
GAM2456 INMT    3' AGATGAAATACAGGACACC   27672    G   CAG  CGC
                                AGA GAAA  GC  GGACACC
                                ||| ||||  ||  |||||||
                                TCT CTTT  TG  CCTGTGG
                                  A   A__  T__
GAM2456 JRK     3' AGAGGAAATGGGCCCAGGGACA 44494       CA   GC_   __
            TGCC                AGAGGAAA  GGCC  GGACA  CC
                                ||||||||  ||||  |||||  ||
                                TCTCCTTT  CCGG  CCTGT  GG
                                    AC   GTC   AC
GAM2456 KCNS3   3' AGAGAAACAGGCACAAACACCC 13930     G      C
                                AGAG AAACAGGC GCGGACACCC
                                |||| |||||||| ||||||||||
                                TCTC TTTGTCCG TGTTTGTGGG
                                  _      _
GAM2456 LTBP3   3' GAGGAAGGCAGGCAGCGCCC  34339      A_    C  GACA
                                GAGGAA  CAGGC GCG   CCC
                                ||||||  ||||| |||   |||
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                                CTCCTT  GTCCG CGC    GGG
                                   CC    T  ____
GAM2456  MAB21L1   5'  AGAAACGGGCCGCAACAC    24583       A      G
                                GGAAAC GGCCGCG ACAC
                                |||||| ||||||| ||||
                                TCTTTG CCGGCGT TGTG
                                   C      _
GAM2456  MECP2     3'  GAGGGGGCAGACACCC      22589      AAACA  CC
                                GAGG    GG  GCGGACACCC
                                ||||    ||  ||||||||||
                                CTCC    CC  CGTCTGTGGG
                                  _____  __
GAM2456  NDST2     3'  GAGGGGCCAGGCCACTCGGGTG 18877      AAA      _______  ACA
            C                    GAGG   CAGGCCGC     GG   C
                                ||||   ||||||||     ||  |
                                CTCC   GTCCGGTG     CC   G
                                  CCG       AGIIIC  ACA
GAM2456  NIPSNAP1  3'  GGAAACAGCCAAGCCAC     18872       G    C  A
                                GGAAACA GCCG GG CAC
                                ||||||| |||| || |||
                                CCTTTGT CGGT TC GTG
                                   _   _ G
GAM2456  NRD1      5'  GGGAACAGGCCTGAACCC    14857    A      GC    A
                                GG AACAGGCC  GGAC CC
                                || ||||||||  |||| ||
                                CC TTGTCCGG  CTTG GG
                                 C       A_   _
GAM2456  PACSIN1   3'  AGGGGAAACAGGGCTGG     45138    A       CC  _
                                AG GGAAACAGG  GC GG
                                || |||||||||  || ||
                                TC CCTTTGTCC  CG CC
                                 C        __  A
GAM2456  PGAM1     3'  GAGGAAACAGTTGTCACA    44057         GC__
                                GAGGAAACAG    CGCG
                                ||||||||||    ||||
                                CTCCTTTGTC    GTGT
                                      AACA
GAM2456  POU4F1    3'  GAGAAAACAGGAGAGA      26385          CCGC
                                GAGGAAACAGG    GGA
                                ||||||||||    |||
                                CTCTTTTGTCC    TCT
                                      TC__
GAM2456  PPFIA3    3'  AAAGGAAAGCGGAC        41411         CAGGCC
                                AGAGGAAA     GCGGAC
                                ||||||||     ||||||
                                TTTCCTTT     CGCCTG
                                   _______
GAM2456  PPP1R11   5'  GAGGAAGGGGGATGAGACACCC 34992        ACA  CCGC
                                GAGGAA   GG    GGACACCC
                                ||||||   ||    ||||||||
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                                CTCCTT  CC   TCTGTGGG
                                   CC_  CTAC
GAM2456 PPT2    5' GAGGAAACAGGCGGAGCGATCC 39919          C__   ACA
                                GAGGAAACAGGC  GCGG  CC
                                ||||||||||||  ||||  ||
                                CTCCTTTGTCCG  CGCT  GG
                                      CCT   A__
GAM2456 SFN     3' AGAGGAAACATGGTCACACCC  43964         _ C GCGG
                                AGAGGAAACA GG C   ACACCC
                                |||||||||| || |   ||||||
                                TCTCCTTTGT CC G   TGTGGG
                                      A  A ____
GAM2456 SH3BP2  3' AGAGGTGGCCTTGGACACC   16623     AAACA   GC
                                AGAGG   GGCC  GGACACC
                                |||||   ||||  |||||||
                                TCTCC   CCGG  CCTGTGG
                                   A____   AA
GAM2456 SIX3    5' GAGGAAGGGCGTAAGGGACACC 24019     ACA  CGC__
             C                   GAGGAA  GGC   GGACACCC
                                ||||||  |||   ||||||||
                                CTCCTT  CCG   CCTGTGGG
                                   C__  CATTC
GAM2456 SLC1A3  3' AGGGGAAACAGAGGGCAG   20040   A      CC
                                AG GGAAACAGG  GCGG
                                || |||||||||  ||||
                                TC CCTTTGTCT  CGTC
                                 C       CC
GAM2456 SLC7A5  3' AGGGAGCAGGCATGGCACC   18537   A  AA   CGC  A
                                AG GGA  CAGGC  GG CACC
                                || |||  |||||  || ||||
                                TC CCT  GTCCG  CC GTGG
                                 _  C_   TA_ _
GAM2456 SLC7A7  3' AGAGGAGTAGGTAGGCACACCC 19576     AAC  CCGC  _
                                AGAGGA  AGG   GG ACACCC
                                ||||||  |||   || ||||||
                                TCTCCT  TCC   CC TGTGGG
                                   CA_  AT__  G
GAM2456 SMARCD2 3' AGAGGGTGACAGCAGACAC   16909     AAACA  C
                                AGAGG   GGC GCGGACAC
                                |||||   ||| ||||||||
                                TCTCC   CTG CGTCTGTG
                                  CA___  T
GAM2456 SORCS2  3' AGAGGAGACACCCTGGGCAC  34042     A  GG  GC  A
                                AGAGGA ACA  CC  GG CAC
                                |||||| |||  ||  || |||
                                TCTCCT TGT  GG  CC GTG
                                   C  G_  A_  C
GAM2456 STUB1   3' AGGGGAAACAGTCCAGAGTCC  44060   A      G  C  ACA
                                AG GGAAACAG CCG GG  CC
                                || |||||||| ||| ||  ||
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                                TC CCTTTGTC GGT TC   GG
                                 C       A   C  A__
GAM2456  SURF4    3'  AGGAGAAACAGGAACACC    37649    AG      CCGCG
                                AG  GAAACAGG    GACACC
                                ||  ||||||||    ||||||
                                TC  CTTTGTCC    TTGTGG
                                 CT      _____
GAM2456  TMEPAI   3'  AGAGGAAAGGGTGCAC     33588       AC   CC  GGAC
                                AGAGGAA  AGG  GC   AC
                                |||||||  |||  ||   ||
                                TCTCCTT  TCC  CG   TG
                                    __   CA  ____
GAM2456  TOMM22   3'  AGAGGAAATGAGCTCCTGC   33672        C_  G_  _
                                AGAGGAAA  AG  CC GC
                                ||||||||  ||  || ||
                                TCTCCTTT  TC  GG CG
                                     AC  GA  A
GAM2456  TTID     3'  AGAGAAAACGGGTAAAACAG  27711         A  CC__
                                AGAGGAAAC GG    GCGG
                                |||||||||  ||    ||||
                                TCTCTTTTG CC    TGTC
                                     C  ATTT
GAM2456  UCP1     5'  AGAGGAAAAGGCTCCAGCC   34834        C    CG   ACA
                                AGAGGAAA AGGC  CGG   CC
                                |||||||| ||||  |||   ||
                                TCTCCTTT TCCG  GTC   GG
                                    _    AG   ___
GAM2456  ZNF26    3'  AGAGAAAACAGGGG       43793           CCGC
                                AGAGGAAACAGG    GG
                                ||||||||||||    ||
                                TCTCTTTTGTCC    CC
                                          ____
GAM2456  ANK1     3'  TTTTCTTTCCAGGAAGCCCACA 33880          T_____
                                TTTTCTTTCT     CCCACA
                                ||||||||||     ||||||
                                AAAAGAAAGG     GGGTGT
                                      TCCTTC
GAM2456  ATP1B3   3'  CTTTTTTTCCTTCCTCACA    11742       C      _
                                CTTTT TTTCTTCC CACA
                                ||||| |||||||| ||||
                                GAAAA AAGGAAGG GTGT
                                   A       A
GAM2456  BACE     3'  TTCTCTTTTCTGTTTCCTACA  29048     C      TTC    C
                                TTC CTTTTCT   TTCC ACA
                                ||| |||||||   |||| |||
                                AAG GAAAAGA   AAGG TGT
                                  A      CA_   A
GAM2456  BCAS1    3'  TTCCTTTTTCTATACCCCACAC 18927      C      TTCT
              A                  TTCC TTTTCT    TCCCACACA
                                 |||| ||||||    |||||||||
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                                AAGG AAAAGA    GGGGTGTGT
                                  A     TAT_
GAM2456  BRCA2    3'  TCCCCTTTTTTTTTTTCTTC   6293          C___
                                TTCCCTTTT    TTTCTTC
                                |||||||||    |||||||
                                AGGGGAAAA    AAAGAAG
                                     AAAA
GAM2456  CALCRL   3'  CCAGGATTTCTTTTTTCCCACA 25127    CT__      C
                                CC    TTTCTTT TTCCCACA
                                ||    ||||||| ||||||||
                                GG    AAAGAAA AAGGGTGT
                                 TCCT      A
GAM2456  CARP     3'  CCTTTCCTGTCCCTACA     30794         TTCT   _
                                CCTTTTCT    TCCC ACA
                                ||||||||    |||| |||
                                GGAAAGGA    AGGG TGT
                                     C___    A
GAM2456  CEACAM1  3'  CTTCTCTTTGCTAGTTCACACA 11831          _  TCC_
                                CTTTTCTTT CT    CACACA
                                ||||||||| ||    ||||||
                                GAAGAGAAA GA    GTGTGT
                                     C  TCAA
GAM2456  COL1A2   3'  TTCTTTTTCTCTTTTGCCCACA 6389      CC       C  _
                                TTC  TTTTCTTT TT CCCACA
                                |||  |||||||| || ||||||
                                AAG  AAAAGAGA AA GGGTGT
                                  A_       A  C
GAM2456  DGKG     3'  TTTTTTTCCTTCCCTTTTTACA 10663      C        _____
              CA                  TTTT TTTCTTCCC     ACACA
                                ||||| |||||||||     |||||
                                AAAA AAGGAAGGG     TGTGT
                                  A        AAAAA
GAM2456  DHCR24   3'  TTCCTCTGACTTTCCACACA   31303     CTTT   TT   C
                                TTCC    TCT  CTT CCACACA
                                ||||    |||  ||| |||||||
                                AAGG    AGA  GAA GGTGTGT
                                  _____  CT   A
GAM2456  FLT1     3'  CCTTTTCCTCCTCACA      12908           TCC
                                CCTTTTCTTTCT   CACA
                                ||||||||||||   ||||
                                GGAAAAGGAGGA   GTGT
                                       ___
GAM2456  GNAZ     3'  TTCTCTTTCCCCCGTACA    13194            C_
                                TTTTCTTTCTTCC  ACA
                                ||||||||||||||  |||
                                AAGAGAAAGGGGGG  TGT
                                       CA
GAM2456  GPR23    3'  TTCTTTTTCTTCCCACCCAC   41319     CC        T
                                TTC  TTTTCTTTCT CCCAC
                                |||  |||||||||| |||||
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                                AAG  AAAAGAAGGG GGGTG
                                  A_         T
GAM2456  HD       3'  TTCCTTCTTCTCACTCCTACAC 13370      C      TC    C
                                TTCC TTTTCTT  TTCC ACAC
                                |||| |||||||  |||| ||||
                                AAGG AGAAGAG  GAGG TGTG
                                  A      T_   A
GAM2456  HDC      5'  TTCCCTCTTGCCAGTCC     13372          _ TTCT
                                TTCCCTTTT CT    TCC
                                |||||||| ||    |||
                                AAGGGAGAA GG    AGG
                                     C  TC__
GAM2456  HIP2     3'  TTCCCCTTTTTAAATTTACACA 23772         CTTTCTTCCC
                                TTCCCTTTT        ACACA
                                |||||||||        |||||
                                AAGGGGAAA        TGTGT
                                     AATTTAAA__
GAM2456  HOXC10   3'  TTTCCTTTTTTTCCCCTACA   41493        C_    AC
                                TTTTCTTT  TTCCC  ACA
                                |||||||  |||||  |||
                                AAAGGAAA  AAGGG  TGT
                                   AA    GA
GAM2456  IL2RA    3'  TTCCTTCTTTCTTTCCTTCC   7675       __   TC
                                TTCC  CTTT  TTTCTTCC
                                ||||  ||||  ||||||||
                                AAGG  GAAA  AAGGAAGG
                                  AA   GA
GAM2456  JMJ      3'  TTCCCTTTTTTATTCCACACA  22486         CTTTCTTC
                                TTCCCTTTT       CCACACA
                                |||||||||       |||||||
                                AAGGGAAAA       GGTGTGT
                                     AATAA___
GAM2456  LIMD1    3'  TTCCCTTTTTGTTCTTTCTCAA 30639         ____       CC
              CA                  TTCCCTTT    TCTTTCTT  CA
                                |||||||    ||||||||  ||
                                AAGGGAAA    AGAAAGAG  GT
                                     AACA       TT
GAM2456  LPHH1    5'  TTTTCTCTTTTCTCCACAC    29393         C  _
                                TTTTCTTT TTC CCACAC
                                |||||||| ||| ||||||
                                AAAAGAGA AAG GGTGTG
                                     A   A
GAM2456  LRRC2    3'  TTCTCCTTTGGAATCTTTCTGC 36031     _    ____      TCC
              ACA                   TTC CCTTT    TCTTTCT   CACA
                                ||| |||||    |||||||   ||||
                                AAG GGAAA    AGAAAGA   GTGT
                                  A    CCTT      C__
GAM2456  LTBP1    3'  CTCCCTTTTCCTTTACAC    8425            CTTCCC
                                TTCCCTTTTCTTT     ACAC
                                ||||||||||||     ||||
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                                GAGGGAAAAGGAA     TGTG
                                      A_____
GAM2456  MAML1    3'  TTCTCTTTTCTCTCCACCA   31297     C        TC
                                TTC CTTTTCTTTCT  CCA
                                ||| ||||||||||  |||
                                AAG GAAAAGAGAGG  GGT
                                  A         T_
GAM2456  NOTCH2   3'  TTCCCTTTTATTAGATACCACA 35917         C  TCTTC
              CA                  TTCCCTTTT TT    CCACACA
                                ||||||||| ||    |||||||
                                AAGGGAAAA AA    GGTGTGT
                                     T  TCTAT
GAM2456  NRCAM    5'  CCTTTTCTTCTTTCACA     22689         T   CC
                                CCTTTTCTT CTT  CACA
                                ||||||||| |||  ||||
                                GGAAAAGAA GAA  GTGT
                                     _   A_
GAM2456  NRXN2    3'  TTTTCTTTTTCCCACACA    31497         C
                                TTTTCTTT TTCCCACACA
                                |||||||| ||||||||||
                                AAAAGAAA AAGGGTGTGT
                                     _
GAM2456  OTC      3'  TTCTCTTCTCTTTTCCCCA   8046      C       C
                                TTC CTTTTCTTT TTCCCA
                                ||| ||||||||| ||||||
                                AAG GAAGAGAAA AGGGGT
                                  A       _
GAM2456  OTP      3'  TTCCCTTCTACACTCTCACACA 37009         CT_   TCC
                                TTCCCTTTT   TTCT   CACACA
                                |||||||||   ||||   ||||||
                                AAGGGAAGA   GAGA   GTGTGT
                                     TGT   ___
GAM2456  PCDH11X  3'  CCTTTTCTTTTTAAATACACA  37300         CTTCCC
                                CCTTTTCTTT     ACACA
                                ||||||||||     |||||
                                GGAAAAGAAA     TGTGT
                                     AATTTA
GAM2456  PCDH11Y  3'  CCTTTTCTTTTTAAATACACA  37339         CTTCCC
                                CCTTTTCTTT     ACACA
                                ||||||||||     |||||
                                GGAAAAGAAA     TGTGT
                                     AATTTA
GAM2456  PCDH8    3'  TTTTTTTTCTTCAAACACA   15116      C      CC
                                TTTT TTTCTTC  ACACA
                                |||| |||||||  |||||
                                AAAA AAAGAAG  TGTGT
                                  A      TT
GAM2456  PLA2R1   3'  CTTTCCTTTTCCCCTCA     28888         C    A
                                CTTTTCTTT TTCCC CA
                                ||||||||| ||||| ||
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                                GAAAGGAAA AGGGG GT
                                    _    A
GAM2456  PLAUR    3'  CTCTTCTGCTTCACACA     15370        TT   C
                                CTTTTCT  CTTC CACA
                                |||||||  |||| ||||
                                GAGAAGA  GAAG GTGT
                                   C_   T
GAM2456  PLD2     3'  CCCTTTTCAGCTATTTCTCAC  15377        TTTC__  C
                                CCCTTTTC     TTC CAC
                                ||||||||     ||| |||
                                GGGAAAAG     AAG GTG
                                     TCGATA   A
GAM2456  PRKCM    3'  CCTCATTCATTTTTTTCCCACA 15638      _  __  C
                                CCTT TTC  TTT TTCCCACA
                                |||| |||  ||| ||||||||
                                GGAG AAG  AAA AAGGGTGT
                                  T   TA   A
GAM2456  RORB     5'  TTCTTTTTCTTTCTCTCCA   27926     CC        TC
                                TTC  TTTTCTTTCT  CCA
                                |||  ||||||||||  |||
                                AAG  AAAAGAAAGA  GGT
                                  A_         GA
GAM2456  RPA3     5'  TTCCCTCTTGCCAGTTCT    16387         _ __
                                TTCCCTTTT CT  TTCT
                                |||||||| ||  ||||
                                AAGGGAGAA GG  AAGA
                                     C  TC
GAM2456  SHOX2    3'  TTCTCTTTTCTTGCTCTTCCAT 27843     C       __     C_
              ACA                   TTC CTTTTCTT  TCTTCC  ACA
                                |||  ||||||||  ||||||  |||
                                AAG GAAAAGAA  AGAAGG  TGT
                                  A       CG     TA
GAM2456  SLC11A3  5'  TTCTTTTTTCCTTCTTTCCA  31053     CC         C
                                TTC  TTTTCTTTCTT CCA
                                |||  |||||||||| |||
                                AAG  AAAAGGAAGAA GGT
                                  AA          A
GAM2456  SMT3H1   3'  TTCCCTTCAACTTTTCC     41005        T_   CT
                                TTCCCTTT  CTTT  TCC
                                ||||||||  ||||  |||
                                AAGGGAAG  GAAA  AGG
                                     TT   __
GAM2456  SNX6     3'  TTCTGCTTTTCTTTCCCCACA  34568     C_        TT
                                TTC  CTTTTCTTTC  CCCACA
                                |||  ||||||||||  ||||||
                                AAG  GAAAAGAAAG  GGGTGT
                                  AC         __
GAM2456  SOX4     3'  TTTTCTTTCTTTTTTCCC    16995          ____
                                TTTTCTTTCT    TCCC
                                ||||||||||    ||||
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                                AAAAGAAAGA   AGGG
                                     AAAA
GAM2456 TCFL4    3' CTCTTTTTCTCCCATACA    41827      C    T   C
                                CTTTT TTTCT CCCA ACA
                                ||||| ||||| |||| |||
                                GAGAA AAAGA GGGT TGT
                                  _    _   A
GAM2456 THBD     5' TCCTCCTTTCTTTCTTTTCATA 7430     _         CC  C
           CA                     TCC CTTTTCTTTCTT  CA ACA
                                ||| ||||||||||||  || |||
                                AGG GGAAAGAAAGAA  GT TGT
                                  A          AA  A
GAM2456 TOMM22   3' CTTCTCTTTTTTTAAACACACA 33674         CTTCC__
                                CTTTTCTTT      CACACA
                                |||||||||      ||||||
                                GAAGAGAAA      GTGTGT
                                     AAAATTT
GAM2456 TRIM37   3' TTCCCATACTGTTTTTCCCA   31628      TTTT  _  C
                                TTCCC    CT TT TTCCCA
                                |||||    || || ||||||
                                AAGGG    GA AA AAGGGT
                                   TAT_  C  A
GAM2456 TRIP12   3' TCCCTTTTTTAAATTTCACACA 20161        CTTTCTTCC
                                TCCCTTTT       CACACA
                                ||||||||       ||||||
                                AGGGAAAA       GTGTGT
                                     AATTTAAA_
GAM2456 TXNRD1   3' TTCCCATTTCTTTACA      17775      T      CTTCCC
                                TTCCC TTTCTTT      ACA
                                ||||| |||||||      |||
                                AAGGG AAAGAAA      TGT
                                   T     _______
GAM2456 WFS1     3' TTCCCTTTGTCGGGGTCCACGC 25645        _  TTTCTTC   A
           A                     TTCCCTTT TC      CCAC CA
                                ||||||||  ||      ||||  ||
                                AAGGGAAA AG      GGTG GT
                                     C  CCCCA__   C
GAM2456 XK       3' CCTGGCTTCTTCCCATACA   34359     TTTC        C
                                CCT    TTTCTTCCCA ACA
                                |||    |||||||||| |||
                                GGA    GAAGAAGGGT TGT
                                  CC__         A
GAM2457 PCDHB9   3' AAGGATGGCAAACCA       33316        T   TGAATA
                                AAGGATG GCA     AACCA
                                ||||||| |||     |||||
                                TTCCTAC CGT     TTGGT
                                   _  _______
GAM2457 SRR      3' AGGATGTGCTGTGGTTTAAACC 34963         A_  AA_
           A                     AGGATGTGC  TG   TAAACCA
                                |||||||||  ||   |||||||
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                                TCCTACACG  AC   ATTTGGT
                                     AC  CAA
GAM2457  DIAPH2   3'  TATCTTAACTTTATTGAA    28679           A
                                TATCTTAACTTTAT GAG
                                ||||||||||||| |||
                                ATAGAATTGAAATA CTT
                                      A
GAM2457  ITK      3'  TCTTGGCTTTTTAAAGCCTC   24447      AA   A
                                TCTT  CTTT TAGAGCTTT
                                ||||  |||| |||||||||
                                AGAA  GAAA ATTTCGGAG
                                  CC   A
GAM2457  PCDHB6   3'  TATCTTACTTTATATAAAATTT 33200       A     _  C
              CA                  TATCTTA CTTTATA GAG TTTCA
                                ||||||| ||||||| ||| |||||
                                ATAGAAT GAAATAT TTT AAAGT
                                   _     A  T
GAM2457  SSPN     3'  TATCTTAATTTCTGCTTTC   22938        C  ATAGA
                                TATCTTAA TTT    GCTTTC
                                |||||||| |||    ||||||
                                ATAGAATT AAA    CGAAAG
                                     _  GA___
GAM2458  ATP11A   3'  TAAGGCTGAAGGATGGCAA   44181       CA  A
                                TAAGGT  AA GATGGTAA
                                ||||||  || ||||||||
                                ATTCCG  TT CTACCGTT
                                    AC  C
GAM2458  BAZ2A    3'  CAAGGTCAAAAATCAGGGT   30302          AT__
                                TAAGGTCAAAAG   GGT
                                ||||||||||||   |||
                                GTTCCAGTTTTT   CCA
                                       AGTC
GAM2458  CLCN6    3'  CAAGGTCAGGAGCAAATC    10509        AAAGAT  TA_
                                TAAGGTCA    GG   AAATC
                                ||||||||    ||   |||||
                                GTTCCAGT    CC   TTTAG
                                     _______ TCG
GAM2458  PPP1R8   5'  GGTCAATGGTAAAGTCA    39732      AAAG      A
                                GGTCA   ATGGTAAA TCA
                                |||||   |||||||| |||
                                CCAGT   TACCATTT AGT
                                   ____       C
GAM2458  TRAF5    3'  TAAGGCCAGGTCTAGAATC   21474        AAAGAT   AA__
                                TAAGGTCA    GGT   AATC
                                ||||||||    |||   ||||
                                ATTCCGGT    CCA   TTAG
                                     _______ GATC
GAM2458  ZNF133   5'  AGGTCAGCAGTTCAAAATCA  18320       AA  ATGG
                                AGGTCA  AG   TAAAATCA
                                ||||||  ||   ||||||||
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                                TCCAGT  TC    GTTTTAGT
                                   CG  AA__
GAM2459  CHST1    3'  TCAAAAGCTTGAGAAGTCGCCT 18914         C  ACAA_
              C                    TCAAAAGCT GA    CGCCTC
                                   ||||||||| ||    ||||||
                                   AGTTTTCGA CT    GCGGAG
                                       A  CTTCA
GAM2459  GRLF1    3'  CCAAGGGCTCGAACCCT    44224     AA      AACG
                                   TCAA  GCTCGAAC   CCT
                                   ||||  ||||||||   |||
                                   GGTT  CGAGCTTG   GGA
                                     CC      _____
GAM2459  HLCS     3'  CTTAAAAGCTCCAAATCCTC  7640    C      G  CAACG
                                   CT AAAAGCTC AA    CCTC
                                   || |||||||| ||    ||||
                                   GA TTTTCGAG TT    GGAG
                                    A       G  TA___
GAM2459  MGAT2    3'  ACTCAAAACTTGTAGAATGCCT 14443         G  CGAACAAC
                                   ACTCAAAA CT       GCCT
                                   |||||||| ||       ||||
                                   TGAGTTTT GA       CGGA
                                       _  ACATCTTA
GAM2459  RB1CC1   5'  ACTCAGAAAACCGGCAACGCCT 31306       _    T  AA
              C                    ACTCA AAAGC CG  CAACGCCTC
                                   ||||| ||||| ||  |||||||||
                                   TGAGT TTTTG GC  GTTGCGGAG
                                     C    _  C_
GAM2459  SCD      3'  CTCAAAAGACAAGGATGCCT   22824        CT   ACAAC
                                   CTCAAAAG  CGA    GCCT
                                   ||||||||  |||    ||||
                                   GAGTTTTC  GTT    CGGA
                                       T_   CCTA_
GAM2459  TAF7     5'  CTCAGCGAGCTCTCTTCGCCTC 24863      AA_    GAACAA
                                   CTCA   AGCTC     CGCCTC
                                   ||||   |||||     ||||||
                                   GAGT   TCGAG     GCGGAG
                                     CGC    AGAA__
GAM2459  TM4SF4   5'  TCAAAAGCTCCTCACTGCCTC  21457         GAA  AC
                                   TCAAAAGCTC   CA  GCCTC
                                   ||||||||||   ||  |||||
                                   AGTTTTCGAG   GT  CGGAG
                                        GA_  GA
GAM2459  WNT2     5'  CCCGAAAGCTCTGCGCGCCTC  18101     A      GAACAA
                                   CTC AAAGCTC      CGCCTC
                                   ||| |||||||      ||||||
                                   GGG TTTCGAG      GCGGAG
                                     C      ACGC__
GAM2459  COG3     3'  ACGTATCTATGATGAGAA    36412         CGCTT
                                   ACGTATTTA    TGAGAA
                                   |||||||||    ||||||
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                                TGCATAGAT    ACTCTT
                                     ACT__
GAM2459  CYBB     3'  GTATTTACGGAAAA       44097         CTTTGA
                                GTATTTACG    GAAAA
                                |||||||||    |||||
                                CATAAATGC    CTTTT
                                     _______
GAM2459  NR4A2    3'  ACCTATTTTACAATTGAGAAAA 26161    G    _  CT
              T                  AC TATTT ACG  TTGAGAAAAT
                                 || ||||| |||  ||||||||||
                                 TG ATAAA TGT  AACTCTTTTA
                                  G    A   T_
GAM2460  C18orf1  3'  AGGGATTTGGATGGATTCTTC  41207        A  GACCT
                                AGGGATTT GA    TTCTTC
                                |||||||| ||    ||||||
                                TCCCTAAA CT    AAGAAG
                                     C  ACCT_
GAM2460  CYP4F3   3'  AAAGGGATTTTCTTTTCTT   9447          AGAGACC
                                AGAGGGATTT     TTTCTT
                                ||||||||||     ||||||
                                TTTCCCTAAA     AAAGAA
                                     AGA____
GAM2460  DLG3     3'  AGAGGGACTTGATTTCTT    34429         A  GACC
                                AGAGGGATTT GA   TTTCTT
                                |||||||||| ||   ||||||
                                TCTCCCTGAA CT   AAAGAA
                                     _ _____
GAM2460  IL1R1    3'  AGAGGGCATTTATTGCCCTTT  9354        _    GAGA
                                AGAGGG ATTTA   CCTTT
                                |||||| |||||   |||||
                                TCTCCC TAAAT   GGAAA
                                   G    AACG
GAM2460  MLANA    3'  AGAGGGATTTGGGAACCC    24297         AGA
                                AGAGGGATTT   GACCT
                                ||||||||||   |||||
                                TCTCCCTAAA   TTGGG
                                     CCC
GAM2460  MUC4     3'  AGACGGTAGTTGGGCCTTTCTT 39658    G  ATT   AGA__
              C                  AGA GG   TAG    CCTTTCTTC
                                 ||| ||   |||    |||||||||
                                 TCT CC   ATC    GGAAAGAAG
                                   G  ___   AACCC
GAM2460  RRM2B    3'  AAGGGATTAAATCCTTTCTTC  42707        T   GA
                                GAGGGATT AGA  CCTTTCTTC
                                |||||||| |||  |||||||||
                                TTCCCTAA TTT  GGAAAGAAG
                                     _  A_
GAM2461  PCDH11X  3'  TACATCTGTAGAATATGATTG  37308         T_
                                TATATCTGT  GATATGATTG
                                |||||||||  ||||||||||
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                                ATGTAGACA  TTATACTAAC
                                      TC
GAM2461  RHEB2    3'  ATATAAATTGAAAATATGATTG 24714      TC_  TT
                                ATATA   TG  GATATGATTG
                                |||||   ||  ||||||||||
                                TATAT   AC  TTATACTAAC
                                   TTA  TT
GAM2462  MAPK4    3'  GGTCCAGTTCAAACCCGC    15663    C   A_  C
                                GG CCA  TC AATCCGT
                                || |||  || |||||||
                                CC GGT  AG TTGGGCG
                                 A   CA  T
GAM2462  RECQL5   3'  CAGGGCCCAATTCAATCCA   20164    A       C
                                CA GGCCCAAT CAATCCG
                                || |||||||| |||||||
                                GT CCGGGTTA GTTAGGT
                                 C       A
GAM2462  SMARCD1  3'  TGAGGCCCAATCCATTCCA   40089    A          A
                                C AGGCCCAATCCA TCCG
                                | ||||||||||| ||||
                                A TCCGGGTTAGGT AGGT
                                 C          A
GAM2463  ADAM12   3'  TCTCTATCCTGGTGTGGC    18478    _   A       A
                                TC CTG TTCTGGTGT GC
                                || ||| |||||||| ||
                                AG GAT AGGACCACA CG
                                 A  _       C
GAM2463  AMPD1    5'  TCCTTGATTCTAGGATAGC   6212       _       TG
                                TCCT GATTCTGG  TAGC
                                |||| ||||||||  ||||
                                AGGA CTAAGATC  ATCG
                                  A       CT
GAM2463  AMT      3'  TTCCTGACTTGCAG        7909           CTGG
                                TTCCTGATT    TGTAG
                                |||||||||    |||||
                                AAGGACTGA    ACGTC
                                      ____
GAM2463  CHD2     3'  TCCCTGATACCTAGTGTGGC  10451          _       A
                                TTCCTGAT TCTGGTGT GC
                                |||||||| |||||||| ||
                                AGGGACTA GGATCACA CG
                                     T       C
GAM2463  CLASPIN  5'  TCTCTGATTCCCTCAGC     35225    _      GGTG
                                TC CTGATTCT    TAGC
                                || ||||||||    ||||
                                AG GACTAAGG    GTCG
                                 A       GA__
GAM2463  DLEC1    3'  TTCCTGATGCTGACAAAGC   28842         T   GT T
                                TTCCTGAT CTG  G AGC
                                |||||||| |||  | |||
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                                AAGGACTA GAC  T TCG
                                    C   TG T
GAM2463  DNAI2    3'  TTCCTGATTTGTAG       35749        CTGG
                                TTCCTGATT    TGTAG
                                |||||||||    |||||
                                AAGGACTAA    ACATC
                                     ____
GAM2463  DRIL1    3'  TCCTGGCCCCTGTGTGGC    23387      AT   G    A
                                TCCTG  TCT GTGT GC
                                |||||  ||| |||| ||
                                AGGAC  GGG CACA CG
                                   CG   A    C
GAM2463  ETS2     3'  TTCCTGGGTCCTCGGAGC    23475      A_   _ T
                                TTCCTG  TTCT GG GT
                                ||||||  |||| || ||
                                AAGGAC  AGGA CC CG
                                    CC    G  T
GAM2463  FAP      3'  TTCAGATTCTGATACAG     20893     CT
                                TTC  GATTCTGGTGTAG
                                |||  ||||||||||||
                                AAG  CTAAGACTATGTC
                                  T_
GAM2463  FCN2     3'  TCTCTGACACCTTGTAGC    31897    _    T  GG
                                TC CTGAT CT  TGTAGC
                                || ||||| ||  ||||||
                                AG GACTG GG  ACATCG
                                 A    T  A_
GAM2463  FREB     3'  TTCCTGATCTAGACAGC     37227       T    TGT
                                TTCCTGAT CTGG   AGC
                                |||||||| ||||   |||
                                AAGGACTA GATC   TCG
                                    _   TG_
GAM2463  GUCY1A3  5'  CTCCTGATGAGCTGTAG     41836       TCT  _
                                TTCCTGAT   GG TGTAG
                                ||||||||   || |||||
                                GAGGACTA   TC ACATC
                                    C__  G
GAM2463  LRP8     3'  TTCCTGACTTCCTGGGGT    37801        __    T
                                TTCCTGAT  TCTGG GT
                                ||||||||  ||||| ||
                                AAGGACTG  GGACC CA
                                    AA    C
GAM2463  MAP3K11  3'  TTCCTGTGCAGTGTAG      14537       ATTC
                                TTCCTG    TGGTGTAG
                                ||||||    ||||||||
                                AAGGAC    GTCACATC
                                   AC__
GAM2463  MYLK2    3'  TTCCTAATTCTCCTGGGC    37531          ____
                                TTCCTGATTCT    GGT
                                ||||||||||    |||
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                                AAGGATTAAGA   CCG
                                      GGAC
GAM2463 NFRKB   5' TTCCTGGTGCCGCAGC     26106      ATTC  G
                                TTCCTG   TG TGTAGC
                                ||||||   || ||||||
                                AAGGAC   AC GCGTCG
                                   C___  G
GAM2463 PLA2G2D 3' TTCTTGGTTCTGGTGTTGC   29642    C A      A
                                TTC TG TTCTGGTGT GC
                                ||| || ||||||||| ||
                                AAG AC AAGACCACA CG
                                  A C       A
GAM2463 PML     3' CTCCTGGCCCTGGTGTAG    37752      AT
                                TTCCTG  TCTGGTGTAG
                                ||||||  ||||||||||
                                GAGGAC  GGACCACATC
                                   CG
GAM2463 RELN    3' TTCCTGATATCAGATGTAG   45360       _  T
                                TTCCTGAT TC GGTGTAG
                                |||||||| || |||||||
                                AAGGACTA AG CTACATC
                                     T  T
GAM2463 SH3BP2  3' TTCCTGGTGTGACCCTGGT   16646     _____
                                TTCCT    GATTCTGGT
                                |||||    |||||||||
                                AAGGA    CTGGGACCA
                                  CCACA
GAM2463 YES1    3' TTCCTGATTAGATTTAG     24123       CT   G
                                TTCCTGATT  GGT TAG
                                |||||||||  ||| |||
                                AAGGACTAA  CTA ATC
                                     T_   A
GAM2463 APOB48R 3' GGGTAGGTGGTCCACCAGCC  33091          G  _
                                GGGTAGGTGGTC AT AGCC
                                |||||||||||| || ||||
                                CCCATCCACCAG TG TCGG
                                       G  G
GAM2463 DIRC1   5' AGGGTGGGTGGTCGGGC     38125      A      ATA
                                AGGGT GGTGGTCG   GC
                                ||||| ||||||||   ||
                                TCCCA CCACCAGC   CG
                                  C       C__
GAM2463 KCNA7   3' GAGGGTAGGTGACAGGCC    36655          T  ATA
                                GAGGGTAGGTGG CG   GCC
                                |||||||||||| ||   |||
                                CTCCCATCCACT GT   CGG
                                       _  C__
GAM2463 KLHL1   5' CGAGGATGCCCCGATAGCC   34078       AG  GG
                                CGAGGGT  GT  TCGATAGCC
                                |||||||  ||  |||||||||
```

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                                GCTCCTA  CG  GGCTATCGG
                                   __  G_
GAM2463  OBP2A    3'  GAGGGTAGGTCCAGGTGGTC  31040      _______
                                GAGGGT     AGGTGGTC
                                ||||||     ||||||||
                                CTCCCA     TCCACCAG
                                   TCCAGG
GAM2463  OBP2B    3'  GAGGGTAGGTCCAGGTGGTC  31035      _______
                                GAGGGT     AGGTGGTC
                                ||||||     ||||||||
                                CTCCCA     TCCACCAG
                                   TCCAGG
GAM2463  RAD23A   3'  AGGGTGGGGGCTTCGGTGGCC  22792      A  T  __  ATA
                                AGGGT GG GGT  CG   GCC
                                ||||| || |||  ||   |||
                                TCCCA CC CCG  GC   CGG
                                   C  _   AA  CAC
GAM2464  CRP      3'  ACAACATATTTATACCTA    43441       ATGC
                                ACAACA    TATACCTA
                                ||||||    ||||||||
                                TGTTGT    ATATGGAT
                                   ATAA
GAM2464  SCML2    3'  TACAACAAATGGCTAATAC    25886        TGCTATAC
                                TACAACAA       CTAATAC
                                ||||||||       |||||||
                                ATGTTGTT       GATTATG
                                     TACC____
GAM2464  TACC1    3'  CAACAGGATCACCTAATA    26589      ATGCTA
                                CAACA     TACCTAATA
                                |||||     |||||||||
                                GTTGT     GTGGATTAT
                                   CCTA__
GAM2464  DMRT2    3'  TATTATTATCCATGTCATCTT  27266      G    TTCT
                                TATTA TATTC    TGTCATCTT
                                ||||| |||||    |||||||||
                                ATAAT ATAGG    ACAGTAGAA
                                   A    T___
GAM2464  E2F3     3'  TATTAGTATTCCTTTCAT    12631          TCTTG
                                TATTAGTATTCT    TCAT
                                ||||||||||||    ||||
                                ATAATCATAAGG    AGTA
                                      AA___
GAM2464  MEN1     5'  TTAGTATTCATTTTGCTATCTT 39243        TTC   TC
                                TTAGTATTC   TTG  ATCTT
                                |||||||||   |||  |||||
                                AATCATAAG   AAC  TAGAA
                                     TAA   GA
GAM2464  PUM2     3'  TAGTATTCTCTACTTGTCAT   31664         __
                                TAGTATTCTT  CTTGTCAT
                                ||||||||||  ||||||||
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```
                                ATCATAAGAG  GAACAGTA
                                      AT
GAM2465 A1BG    3'  TAGCTGGGTGTGGTGGT    39093     A  CCGTCA
                                TAGT GG     TGTGGTGGT
                                |||| ||     |||||||||
                                ATCG CC     ACACCACCA
                                  A  C_____
GAM2465 CNP     3'  TAGGGGCATAAGTGGTGGT   37562     TA   CGTCAT
                                TAG  GGC     GTGGTGGT
                                |||  |||     ||||||||
                                ATC  CCG     CACCACCA
                                  C_   TATT__
GAM2465 DMD     3'  TAGTAGTCATTTGGTGTGGTGG 19706       GC   CA__
              TA                  TAGTAG  CGT    TGTGGTGGTA
                                ||||||  |||    ||||||||||
                                ATCATC  GTA    ACACCACCAT
                                   A_   AACC
GAM2465 DYRK1A  3'  GGTGGTGATGGTGGTGGT    38996    CC  C   _
                                GG  GT ATG TGGTGGT
                                ||  || ||| |||||||
                                CC  CA TAC ACCACCA
                                 AC  C   C
GAM2465 FCGR2A  3'  TAGTAGGCTGCTTGTGATTGG  44281        C  CA     _
                                TAGTAGGC GT  TGTGGT GG
                                |||||||| ||  |||||| ||
                                ATCATCCG CG  ACACTA CC
                                     A  A_     A
GAM2465 LLGL1   3'  TAGCTGGGCGTGGTGGTGG   42509     A  C   CAT
                                TAGT GG CGT   GTGGTGG
                                |||| || |||   |||||||
                                ATCG CC GCA   CACCACC
                                  A  C   C__
GAM2465 MRPL49  3'  TAGCAGGCTGTGGTGGT     43028        CGTCA
                                TAGTAGGC    TGTGGTGGT
                                ||||||||    |||||||||
                                ATCGTCCG    ACACCACCA
                                            _____
GAM2465 MXI1    3'  TAGAGGCTGTCATGCATGG   39023     T   C       G
                                TAG AGGC GTCATGTG TGG
                                ||| |||| |||||||| |||
                                ATC TCCG CAGTACGT ACC
                                  _   A       _
GAM2465 MYH11   3'  TAGGGGTGGTGGTGGT      35628     CC  CAT
                                TAGG  GT   GTGGTGGT
                                ||||  ||   ||||||||
                                ATCC  CA   CACCACCA
                                  C_  C__
GAM2465 PLN     3'  TAGTAGGCTATTAGGTAG    15406        CG CATGT
                                TAGTAGGC  T    GGTGG
                                ||||||||  |    |||||
```

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                                ATCATCCG A    CCATC
                                   AT AT___
GAM2465 PPP1R12B 3' TAGGGGGCGGTGGTGGTGG  36979    TA  C  CAT
                                TAG  GGC GT   GTGGTGG
                                |||  ||| ||   |||||||
                                ATC  CCG CA   CACCACC
                                  CC   C  C__
GAM2465 RANBP3   3' TAGTGTGCCGTCATCGGTGG  28765     AG      G
                                TAGT  GCCGTCAT TGGTGG
                                ||||  |||||||| ||||||
                                ATCA  CGGCAGTA GCCACC
                                  CA       _
GAM2465 SHOX     3' TAGCTGGGTGTGGTGGT     27828     A  CCGTCA
                                TAGT GG     TGTGGTGGT
                                ||||| ||     |||||||||
                                ATCG CC     ACACCACCA
                                  A  C_____
GAM2465 STC1     3' TAGTAGGCCTTATCACACTGTA 17182         __   TG G
             A                   TAGTAGGCC  GTCA  T GTGG
                                |||||||||  ||||  | ||||
                                ATCATCCGG  TAGT  G CATT
                                     AA    GT A
GAM2466 LIPA     3' TGTGATCAATAACGACAGTA   6939           AC  T
                                TGTGATCAATAA  AC GTG
                                ||||||||||||  || |||
                                ACACTAGTTATT  TG CAT
                                      GC  T
GAM2466 MADH3    3' TGTGATAATAGACACTATA    25353       C    A
                                TGTGAT AATA ACACTGTG
                                |||||| |||| ||||||||
                                ACACTA TTAT TGTGATAT
                                   _   C
GAM2466 NLGN1    3' TCTATATTGAAACTACTGTGAA 31390      C   ATTAA
             T                   TTTA ATT     TACTGTGAAT
                                |||| |||    ||||||||||
                                AGAT TAA     ATGACACTTA
                                  A   CTTTG
GAM2466 PDE4D    3' TCTACATTATTGTGAA      43901          TAATAC
                                TTTACATTAT     TGTGAA
                                ||||||||||     ||||||
                                AGATGTAATA     ACACTT
                                               _______
GAM2466 SNAP25   3' TTTACAAGAACAATACTGTG   39265       TTAT
                                TTTACA    TAATACTGTG
                                ||||||    ||||||||||
                                AAATGT    GTTATGACAC
                                   TCTT
GAM2467 ADAM12   3' TACAGAAACACCACC       18477     G   CT
                                TAC AGAA  GCACCACC
                                ||| ||||  ||||||||
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                                ATG TCTT  TGTGGTGG
                                  _   __
GAM2467 ATRN    3' CATGAAAACACCACCATCT   40268    A  CT       C
                                CG GAA  GCACCACCA CT
                                || |||  |||||||||  ||
                                GT CTT  TGTGGTGGT GA
                                 A  T_       A
GAM2467 CBFB    3' GAGGTCATCACCACCACCT   35632    AACTG
                                GAG    CACCACCACCT
                                |||    ||||||||||
                                CTC    GTGGTGGTGGA
                                  CAGTA
GAM2467 ERCC5   5' ACGACGGACTGCACCGCCGCCT 6523      GA_      A A
                                ACGA   ACTGCACC CC CCT
                                ||||   ||||||||  || |||
                                TGCT   TGACGTGG GG GGA
                                   GCC       C  C
GAM2467 F7      3' GAGAGCTAAACAACCGCCT   33340     A  C C  A
                                GAGA CTG AC ACC CCT
                                |||| ||| || ||| |||
                                CTCT GAT TG TGG GGA
                                  C  T T  C
GAM2467 IRS2    3' CGAGAACTGCCACACAC     40699         AC  _
                                CGAGAACTGC  CAC CAC
                                ||||||||||  ||| |||
                                GCTCTTGACG  GTG GTG
                                      __  T
GAM2467 MICB    3' TACGAGAAGTGCTTGAACC   25476       C  ACC_
                                TACGAGAA TGC    ACC
                                ||||||||  |||    |||
                                ATGCTCTT ACG    TGG
                                    C   AACT
GAM2467 PLD1    3' TACGAGAATGCGTCAGGCCT  15376       C  AC  CCA
                                TACGAGAA TGC  CA   CCT
                                ||||||||  |||  ||   |||
                                ATGCTCTT ACG  GT   GGA
                                    _  CA  CC_
GAM2467 SLC7A1  5' ACGGGAAGCCTCACCACCT   16805    A  CT  AC
                                ACG GAA  GC  CACCACCT
                                |||  |||  ||  ||||||||
                                TGC CTT  CG  GTGGTGGA
                                  C  __  GA
GAM2467 STK4    3' TACAGAGATGCCACCACCT   26584    _  AC  AC
                                TAC GAGA  TGC  CACCACCT
                                |||  ||||  |||  ||||||||
                                ATG CTCT  ACG  GTGGTGGA
                                  T   __  __
GAM2468 CDH5    3' CATTTCCCTGAATGTGGTTCAG 12184      A  A  CGC
                                CATTTC CT GAA   TGGTTCAG
                                ||||||  ||  |||   ||||||||
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                                GTAAAG GG CTT   ACCAAGTC
                                   _ A   AC_
GAM2468  DKC1     3'  CATTTCACTGAGCAGACT    10695         _ AAC
                                CATTTCACT AG   GCT
                                |||||||||  ||   |||
                                GTAAAGTGA TC   TGA
                                    C  GTC
GAM2468  GLS      3'  CATTTCACTAAACACAGCTTCA 31375           A   T   _
              G                  CATTTCACTAGA CGC GGTT CAG
                                |||||||||||| ||| |||| |||
                                GTAAAGTGATTT GTG TCGA GTC
                                      _  _   A
GAM2468  MNAT1    3'  TTTTGCTAGCTCCCTGGTTCAG 14604     CA   AACG
                                TTT  CTAG   CTGGTTCAG
                                |||  ||||   |||||||||
                                AAA  GATC   GACCAAGTC
                                  AC   GAGG
GAM2468  OSCAR    3'  CATTTTACAGAGCGCTGATT   39307      C  T   A
                                CATTT AC AGA CGCTGGTT
                                ||||| || ||| ||||||||
                                GTAAA TG TCT GCGACTAA
                                   A  _  C
GAM2468  PMX1     3'  CATTTCACCAGAGCTC      35505          ACGCTG
                                CATTTCACTAGA     GTTC
                                ||||||||||||     ||||
                                GTAAAGTGGTCT     CGAG
                                      _______
GAM2468  RPP30    3'  ATTTCCAAAGTTGGTTCA    26933      ACT  AACGC
                                ATTTC   AG    TGGTTCA
                                |||||   ||    |||||||
                                TAAAG   TC    ACCAAGT
                                   GTT  A____
GAM2468  CDH5     3'  CATTTCCCTGAATGTGGTTCAG 12184       A  A   CGC
                                CATTTC CT GAA   TGGTTCAG
                                |||||| || |||   ||||||||
                                GTAAAG GG CTT   ACCAAGTC
                                   _ A   AC_
GAM2468  DKC1     3'  CATTTCACTGAGCAGACT    10695         _ AAC
                                CATTTCACT AG   GCT
                                |||||||||  ||   |||
                                GTAAAGTGA TC   TGA
                                    C  GTC
GAM2468  GLS      3'  CATTTCACTAAACACAGCTTCA 31375           A   T   _
              G                  CATTTCACTAGA CGC GGTT CAG
                                |||||||||||| ||| |||| |||
                                GTAAAGTGATTT GTG TCGA GTC
                                      _  _   A
GAM2468  MNAT1    3'  TTTTGCTAGCTCCCTGGTTCAG 14604     CA   AACG
                                TTT  CTAG   CTGGTTCAG
                                |||  ||||   |||||||||
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                                AAA  GATC   GACCAAGTC
                                  AC   GAGG
GAM2468  OSCAR    3'  CATTTTACAGAGCGCTGATT  39076      C  T   A
                                CATTT AC AGA CGCTGGTT
                                ||||| || ||| ||||||||
                                GTAAA TG TCT GCGACTAA
                                   A  _   C
GAM2468  PMX1     3'  CATTTCACCAGAGCTC     27910          ACGCTG
                                CATTTCACTAGA     GTTC
                                ||||||||||||     ||||
                                GTAAAGTGGTCT     CGAG
                                                 _____
GAM2468  RPP30    3'  ATTTCCAAAGTTGGTTCA    26933      ACT  AACGC
                                ATTTC   AG    TGGTTCA
                                |||||   ||    |||||||
                                TAAAG   TC    ACCAAGT
                                   GTT  A____
GAM2469  GPC3     3'  TTCGAAAACATAACACA     21025         ATCC
                                TTCGAAAATA   TAACACA
                                ||||||||||   |||||||
                                AAGCTTTTGT   ATTGTGT
                                             _____
GAM2469  NYX      3'  AAACGCCTCCTAACACAT    35441      AA_
                                AAAT   TCCTAACACAT
                                ||||   ||||||||||
                                TTTG   AGGATTGTGTA
                                  CGG
GAM2469  RAG1     3'  CATTCAAAATAGTTCCTACA  7784         ATAA    A
                                CATTCGAAA    TCCTA CA
                                |||||||||    ||||| ||
                                GTAAGTTTT    AGGAT GT
                                     ATCA    _
GAM2470  ADORA2A  3'  CTCTGTGGAGACAAGGTGGTGC 8600      ACATA      CACAA
           T                     CTC    GAGACAAG    GCT
                                 |||    ||||||||    |||
                                 GAG    CTCTGTTC    CGA
                                   ACAC_       CACCA
GAM2470  BTEB1    3'  CATAAAGACAGCTGTGCT    10211         A  ACAA
                                CATAGAGACA GC    GCT
                                |||||||||| ||    |||
                                GTATTTCTGT CG    CGA
                                     _  ACA_
GAM2470  C18orf1  3'  CACACAGGTTGTAAGCATGAGC 41211       AGAC_    CA
           T                     CACATAG    AAGCA  AGCT
                                 |||||||    |||||  ||||
                                 GTGTGTC    TTCGT  TCGA
                                    CAACA    AC
GAM2470  FADD     3'  CTCACACAGGGGCCAAGAGCT  19246         AGA_   CACA
                                CTCACATAG   CAAG   AGCT
                                |||||||||   ||||   ||||
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                                GAGTGTGTC   GTTC   TCGA
                                     CCCG   ____
GAM2470  GAB2    3'  CACAGCCCATGGGCACAAGCT  38674      AGA  A__
                                CATAG  CA  GCACAAGCT
                                |||||  ||  |||||||||
                                GTGTC  GT  CGTGTTCGA
                                  GG_  ACC
GAM2470  GARP    3'  TCACATAGGGGCAGACACAAGG 24317        AGA  AG    _
           CT                    TCACATAG  CA  CACAAG CT
                                ||||||||  ||  |||||| ||
                                AGTGTATC  GT  GTGTTC GA
                                     CCC  CT    C
GAM2470  IL6     3'  CTCCATAGAGAACAACATAAG  8278     A      CA   C
                                CTC CATAGAGA  AGCA AAG
                                ||| ||||||||  |||| |||
                                GAG GTATCTCT  TTGT TTC
                                  _      TG   A
GAM2470  MCC     3'  TAGAGACAGGTCCAGAGCT   14383       AGCA  _
                                TAGAGACA   CA AGCT
                                ||||||||   || ||||
                                ATCTCTGT   GT TCGA
                                     CCAG  C
GAM2470  RNF4    3'  TCACATAGAGGAGGGACAC   16357        ACAA_
                                TCACATAGAG    GCAC
                                ||||||||||    ||||
                                AGTGTATCTC    TGTG
                                      CTCCC
GAM2470  SFRP1   3'  CTGACACAAAGGCAGGCACAGG 16572   C      A  A    A
           CT                    CT ACATAGAG CA GCACA GCT
                                || |||||||| || ||||| |||
                                GA TGTGTTTC GT CGTGT CGA
                                 C       C  C    C
GAM2470  SH3BP2  3'  CTCGTCTAGAGACAAGCACGGC 16630    ACA         AA
           C                     CTC   TAGAGACAAGCAC  GCT
                                |||   ||||||||||||  |||
                                GAG   ATCTCTGTTCGTG  CGG
                                  CAG          C_
GAM2470  VAT1    3'  CACACACACACAAGCACA    26846      GAG
                                CACATA   ACAAGCACA
                                ||||||   |||||||||
                                GTGTGT   TGTTCGTGT
                                   GTG
GAM2471  OGG1    3'  CTGGTGGCTCCTGAG      32569        GCT
                                CTGGTGGCT   TCTGGG
                                |||||||||   ||||||
                                GACCACCGA   GGACTC
                                            ___
GAM2471  ORM1    5'  CTGGTGGCTGCAGGG      8297          TTCT
                                CTGGTGGCTGC   GGG
                                ||||||||||    |||
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                                GACCACCGACG   CCC
                                      T___
GAM2471  SLC6A8   3'  CTGCCACTGCTGCTTCTGGG  24766    GTG__
                                CTG    GCTGCTTCTGGG
                                |||    ||||||||||||
                                GAC    CGACGAAGACCC
                                  GGTGA
GAM2471  TZFP     3'  CTGGGGCGCTTCTGGGGCG   30788     T  T      A
                                CTGG GGC GCTTCTGGG CG
                                |||| ||| ||||||||| ||
                                GACC CCG CGAAGACCC GC
                                  _  _       C
GAM2472  CASP4    5'  TTAGTGCATTCCAACAGGTGAG 37822        C   TAAAAAC
            A                    TTAGTGCA TCTA      GAGA
                                |||||||| ||||      ||||
                                AATCACGT AGGT      CTCT
                                     A   TGTCCA_
GAM2472  HADHA    3'  TTAGTGCACTGACTGAGCGAG  6766          CTATAAAAA
                                TTAGTGCACT       CGAG
                                ||||||||||       ||||
                                AATCACGTGA       GCTC
                                      CTGACTC__
GAM2472  HNRPF    3'  GCATTTTATAAAAACGAGA   22456    CTC
                                GCA   TATAAAAACGAGA
                                |||   ||||||||||||
                                CGT   ATATTTTTGCTCT
                                  AAA
GAM2472  PRKG2    3'  TTAGTAGTACTCAAACGAG   26523      C_   TATAA
                                TTAGTG  ACTC    AAACGAG
                                ||||||  ||||    |||||||
                                AATCAT  TGAG    TTTGCTC
                                   CA   ______
GAM2473  JAM2     5'  GGGGGTGTGGGGGTAGGGGCT  34548       TCCTTAA    A
                                GGGGGTGT      TAGGG CT
                                ||||||||      ||||| ||
                                CCCCCACA      ATCCC GA
                                     CCCCC__    C
GAM2473  ANGPT1   3'  CCCATAGGAATATTTCCA    40239         GGAAC
                                CCCATGGGAG    ATTTCCA
                                ||||||||||    |||||||
                                GGGTATCCTT    TAAAGGT
                                      A_____
GAM2473  BCL3     3'  GCTCTGGGAGGGGACAT     23206    CCA      A
                                GC   TGGGAGGG ACAT
                                ||   |||||||| ||||
                                CG   ACCCTCCC TGTA
                                 AG_       C
GAM2473  EMR1     3'  TGGTGGGATCCTCATTTCCA  12705    GA   A___
                                TGG  GGGA   CATTTCCA
                                |||  ||||   ||||||||
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                              ACC  CCCT   GTAAAGGT
                                A_   AGGA
GAM2473  HOXD3    3'  GCCCATGGAGGGGAGGCCC   27897       GA   ACATT
                              GCCCATGG  GGGA    TCC
                              ||||||||  ||||    |||
                              CGGGTACC  CCCT    GGG
                                   TC   CC___
GAM2473  LY95     5'  GCTCGTGGGAGGGGACAC    22099    CCA      A
                              GC   TGGGAGGG ACAT
                              ||   |||||||| ||||
                              CG   ACCCTCCC TGTG
                               AGC       C
GAM2473  MBP      3'  GCCTCTGGGAGGGTCTCTTC   44889     CA      AACA
                              GCC  TGGGAGGG    TTTC
                              |||  ||||||||    ||||
                              CGG  ACCCTCCC    GAAG
                                AG       AGA_
GAM2473  MYL3     3'  GCCCATGGGGTGGGGACA    41905        A_   A
                              GCCCATGGG  GGG ACA
                              |||||||||  ||| |||
                              CGGGTACCC  CCC TGT
                                   CA   C
GAM2473  NCF4     3'  GCTTCTGGGAGGGGAGGCCAC  8437     CCA      AACATTT
                              GC   TGGGAGGG      CCAC
                              ||   ||||||||      ||||
                              CG   ACCCTCCC      GGTG
                               AAG       CTCC___
GAM2473  RPH3AL   3'  GCCCATGGGAGGGGGGCACT   28101           AA_
                              GCCCATGGGAGGG   CATT
                              ||||||||||||   ||||
                              CGGGTACCCTCCC   GTGA
                                     CCC
GAM2473  SIRT6    3'  GCCCAGGGAGGGACC       32418       T      ACATTT
                              GCCCA GGGAGGGA     CC
                              ||||| ||||||||     ||
                              CGGGT CCCTCCCT     GG
                                   _      _______
GAM2473  SLC6A6   3'  GCCCTTGGGAGGGGGACAC    16792      A      A_
                              GCCC TGGGAGGG  ACAT
                              |||| ||||||||  ||||
                              CGGG ACCCTCCC  TGTG
                                A       CC
GAM2473  SLC9A6   3'  CATGGGAGGGATTCC       26828          ACAT
                              CATGGGAGGGA    TTCC
                              ||||||||||    ||||
                              GTACCCTCCCT    AAGG
                                        ____
GAM2473  SURF5    3'  GCCTGCGGGAGGGGACAC    39505     CA      A
                              GCC  TGGGAGGG ACAT
                              |||  |||||||| ||||
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                                CGG  GCCCTCCC TGTG
                                  AC       C
GAM2473  WBSCR5   3'  TAGCAAGTGACATTTCCAC   37129     G   GA
                                TGG AGG  ACATTTCCAC
                                ||| |||  ||||||||||
                                ATC TTC  TGTAAAGGTG
                                  G   AC
GAM2474  PSMC6    3'  CTTTAACTTTATTTTTACAATA 15833           C    TT
            A                    CTTTAATTTTATT TTAT  TAA
                                ||||||||||||| ||||  |||
                                GAAATTGAAATAA AATG  ATT
                                        A    TT
GAM2474  TYRO3    3'  CTTCAATTTTATTTCTATTTTA 26651           CT
            AA                   CTTTAATTTTATT  TATTTTAAA
                                ||||||||||||  |||||||||
                                GAAGTTAAAATAA  ATAAAATTT
                                        AG
GAM2475  HHLA1    5'  GCGATGGCTTGGCTTGGG    25051    A  A  ATTG
                                GC AT GG    GGCTTGGG
                                || || ||    ||||||||
                                CG TA CC    CCGAACCC
                                 C  _  GAA_
GAM2475  AF3P21   3'  CCCAGACCATGGTCCCCAATCC 32399       A  CAAG__
            TA                   CCCAGA CC     CCCAATCCTA
                                ||||||  ||     ||||||||||
                                GGGTCT GG     GGGTTAGGAT
                                   _  TACCAG
GAM2475  ASTN     3'  CAAAACCCAAGTGGCCCA    42939          ___
                                CAGAACCCAA   GCCCA
                                ||||||||||   |||||
                                GTTTTGGGTT   CGGGT
                                      CAC
GAM2475  ATP5B    5'  CCACCAAAAAGCCCAAT     40648    _     CCCA
                                CC CCAGAA    AGCCCAAT
                                || ||||||    ||||||||
                                GG GGTTTT    TCGGGTTA
                                 T     _____
GAM2475  DUSP4    5'  CCCCGGAAGCCCAAGGGCCGAG 38412      A  _    __  CAA_
            GTCCT                  CCCC GAA CCCAA  GCC    TCCT
                                |||| ||| |||||  |||    ||||
                                GGGG CTT GGGTT  CGG    AGGA
                                  C  C    CC   CTCC
GAM2475  ERBB4    3'  CCATGGAATTCAAGCCAATCCT 23454     __  CC     C
                                CCA  GAA  CAAGCC AATCCT
                                |||  |||  |||||| ||||||
                                GGT  CTT  GTTCGG TTAGGA
                                  AC   AA     _
GAM2475  GNAT1    5'  CCCCAGAACCTGGCCTCCC    6738          CAA   CAA
                                CCCCAGAACC   GCC   TCCT
                                ||||||||||   |||   ||||
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                                GGGGTCTTGG  CGG  AGGG
                                     AC_  ___
GAM2475 HUNK    3' CCCTGGAGCCAACCCTCCT  31062    CA A CA   AA
                                CCC  GA CC  AGCCC  TCCT
                                |||  || ||  |||||  ||||
                                GGG  CT GG  TTGGG  AGGA
                                  AC  C  __   __
GAM2475 LIF     3' CCCCAGGCCTCAGGACCT   14141      AACCCAA  _ AT_
                                CCCCAG     GCC CA  CCT
                                ||||||     ||| ||  |||
                                GGGGTC     CGG GT  GGA
                                   ________  A  CCT
GAM2475 PEX6    3' CCCCAGAACCCAAGGCCC   7107           _
                                CCCCAGAACCCAAG CCC
                                |||||||||||||| |||
                                GGGGTCTTGGGTTC GGG
                                        C
GAM2475 PIK3R3  3' CCCCAGAACTAGAGCTTTCCTA 41440       CCA  CCAA
                                CCCCAGAAC  AGC   TCCTA
                                |||||||||  |||   |||||
                                GGGGTCTTG  TCG   AGGAT
                                     ATC  AA__
GAM2475 S100A10 5' CCCCAGAAGCCGGGCTTCCC  40387       C  AA  CCAA
                                CCCCAGAA CC  GC   TCCT
                                |||||||| ||  ||   ||||
                                GGGGTCTT GG  CG   AGGG
                                    C  CC  A___
GAM2475 SH3BP2  3' CCCCAGAACTGAGCCCACCT  16627       CCA    AT
                                CCCCAGAAC  AGCCCA  CCT
                                |||||||||  ||||||  |||
                                GGGGTCTTG  TCGGGT  GGA
                                     AC_    __
GAM2475 SLC4A7  3' CACAACCCCATTCATCCAGTCC 18821   G    AAGC___  A
           TA                    CA AACCC     CCA TCCTA
                                || |||||     ||| |||||
                                GT TTGGG     GGT AGGAT
                                 G   GTAAGTA  C
GAM2475 STS     5' GAAGCAGGCCAATCCTA    7394     CCCA  C
                                GAA   AG CCAATCCTA
                                |||   || |||||||||
                                CTT   TC GGTTAGGAT
                                  CG__  C
GAM2475 TDG     5' CCCCAGAGACCTGGGCCC   17353       _  CAA
                                CCCCAGA ACC  GCCC
                                ||||||| |||  ||||
                                GGGGTCT TGG  CGGG
                                    C  ACC
GAM2475 TFAP4   3' CCCCAGAATGCCCCAGCC   17410       __  A
                                CCCCAGAA  CCC AGCC
                                ||||||||  ||| ||||
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                              GGGGTCTT  GGG TCGG
                                  AC   G
GAM2476 DNASE1L1 5' GTTGGGACAAATGAGGT    27499    GA_    TGTA
                              GT   GATAA   ATGAGGT
                              ||   |||||   |||||||
                              CA   CTGTT   TACTCCA
                                ACC    ____
GAM2476 ERBB3    3' GTGAGATAATGTAGGT     12758          AATG
                              GTGAGATAATGT   AGGT
                              ||||||||||||   ||||
                              CACTCTATTACA   TCCA
                                           ____
GAM2476 CLDN14   5' AACGGCCTGCGTGGGCACAC  29080        A   ACTT
                              AATGGCCT CGTG   GGTATAC
                              |||||||| ||||   |||||||
                              TTGCCGGA GCAC   CCGTGTG
                                  C   ____
GAM2476 DSG1     3' ATGGCTTGTGGACTTGACTAT  12600      CTAC  _    _
                              ATGGC   GTG ACTTGG TAT
                              |||||   ||| |||||| |||
                              TACCG   CAC TGAACT ATA
                                AA__  C    G
GAM2476 GAD1     3' AATGGCCTGTGTGTTTCAGC   30285        AC   AC TG
                              AATGGCCT  GTG  T  GT
                              ||||||||  |||  |  ||
                              TTACCGGA  CAC  A  CG
                                  CA   AA GT
GAM2476 HSPA1A   3' AATGGCCTGAGTTAAGTGTAT  23780        AC  GACTTG
                              AATGGCCT  GT    GTAT
                              ||||||||  ||    ||||
                              TTACCGGA  CA    CATA
                                  CT  ATTCA_
GAM2476 IL13RA1  3' AATGTTCTACGTGAAGATAC   11437     GC      CTT
                              AATG  CTACGTGA   GGTAT
                              ||||  ||||||||   |||||
                              TTAC  GATGCACT   CTATG
                                AA       T__
GAM2476 PPARG    5' AATGGCCTTGTTGTAT      39814        ACG  ACTTG
                              AATGGCCT   TG    GTAT
                              ||||||||   ||    ||||
                              TTACCGGA   AC    CATA
                                  ___  AA___
GAM2477 CMAR     3' TGATGAGTGAGCTGGATG    23297   C      ___
                              A ATGGGTGG   GGATG
                              | ||||||||   |||||
                              A TACTCACT   CCTAC
                               C       CGA
GAM2477 CPA3     3' TAACATGGGACTTAAATG    12417         TGG_
                              TGACATGGG    GGATG
                              |||||||||    |||||
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                                ATTGTACCC   TTTAC
                                     TGAA
GAM2477 LDOC1    3' GGATGTGGTGAGTGGATG    29491   C  _   _ _
                                A ATG GGTG G GGATG
                                | ||| |||| | |||||
                                C TAC CCAC C CCTAC
                                 C   A   T A
GAM2477 PCDH11Y  5' TAACATGGGTTTAAAATG    37347         GG_
                                TGACATGGGT   GGATG
                                ||||||||||   |||||
                                ATTGTACCCA   TTTAC
                                     AAT
GAM2477 PIM2     3' TGACATGGCCATGGGATG    41028        G  _
                                TGACATGG TG GGGATG
                                |||||||| || ||||||
                                ACTGTACC GT CCCTAC
                                     G  A
GAM2477 PTMS     3' GACATGACGCTGGGGGATG   15883       _ __
                                GACATGG GT  GGGGATG
                                ||||||| ||  |||||||
                                CTGTACT CG  CCCCTAC
                                    G  AC
GAM2477 SPG7     3' TGATGAGTGAGCTGGATG    17072   C      ___
                                A ATGGGTGG   GGATG
                                | ||||||||   |||||
                                A TACTCACT   CCTAC
                                 C       CGA
GAM2477 AKT2     3' ACCCAGCGGTGATGGCAGC   11563        C  GA   G
                                ACCCAGTGG GA  GGC AGC
                                ||||||||| ||  ||| |||
                                TGGGTCGCC CT  CCG TCG
                                     A  A_  _
GAM2477 ALPPL2   3' CCCAGTGGAGGGACA      42875        CGAG   C  G
                                CCCAGTGG    AGG GA CA
                                ||||||||    ||| || ||
                                GGGTCACC    TCC CT GT
                                     _____  _ _
GAM2477 APOBEC3B 5' CCCAGTAGTAGTAGAGGCGGGC 22224         CG__      A  A
           GGC                    CCCAGTGG    AGAGGCG GC GC
                                ||||||||    ||||||| || ||
                                GGGTCATC    TCTCCGC CG CG
                                     ATCA      C  C
GAM2477 BAIAP3   3' ACCCAGTGGTGCCAGTGGC   19451         __  G  A
                                ACCCAGTG  GC AG GGC
                                ||||||||  || || |||
                                TGGGTCAC  CG TC CCG
                                     CA  G  A
GAM2477 EXT1     5' ACCCAGGGCGGGCGAGCAG   6547        T    AGA
                                ACCCAG GGCG   GGCGAGCAG
                                ||||||| ||||   |||||||||
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                                TGGGTC CCGC   CCGCTCGTC
                                   _   ___
GAM2477  FLRT1    3'  CCAGTGGCGGGAGAGC      40598         AGA  C
                                CCAGTGGCG   GG GAGC
                                |||||||||   || ||||
                                GGTCACCGC   CC CTCG
                                    ___  T
GAM2477  GAB2     3'  CCCAGTGGCCGGAGGGAAGATA 38676         GA   C   C_
              GC                  CCCAGTGGC  GAGG GAG  AGC
                                |||||||||  |||| |||  |||
                                GGGTCACCG  CTCC TTC  TCG
                                     GC   C   TA
GAM2477  GTF2H1   5'  ACCCAGTGGCCGCAGCAG    23685         GAGAG  G
                                ACCCAGTGGC    GC AGCAG
                                ||||||||||    || |||||
                                TGGGTCACCG    CG TCGTC
                                     G____  _
GAM2477  GYG2     5'  CAGTGGCGCCGCGGGCAG    19388         AGAG   A
                                CAGTGGCG    GCG GCAG
                                ||||||||    ||| ||||
                                GTCACCGC    CGC CGTC
                                    GG__   C
GAM2477  HSPB3    5'  CAGTGGCGAGCCCCTGCAG    26711          AGGCGA
                                CAGTGGCGAG     GCAG
                                ||||||||||     ||||
                                GTCACCGCTC     CGTC
                                     GGGGA_
GAM2477  MMP25    3'  CCAGCGGCGGGGGACTCGGC   35379         A__  GG  A
                                CCAGTGGCG   GA  CG GC
                                |||||||||   ||  || ||
                                GGTCGCCGC   CT  GC CG
                                     CCC  GA  _
GAM2477  PCSK1    3'  ACTCAGTGGGAGAAAGCCAGC  7749     C     C    _  G
                                AC CAGTGG GAGAG GC AGC
                                || |||||| ||||| || |||
                                TG GTCACC CTCTT CG TCG
                                 A     _    T  G
GAM2477  PSD      5'  CCCAGGGTGAGGGAGC      15779       T  CGA    C
                                CCCAG GG   GAGG GAGC
                                |||||  ||   |||| ||||
                                GGGTC CC   CTCC CTCG
                                   _  A__   _
GAM2477  RANBP3   3'  ACCTGGGGTGGGAAACAAGTAG 28746     CA__   CGA      C
                                ACC    GTGG   GAGGCGAG AG
                                |||    ||||   |||||||| ||
                                TGG    CACC   CTTTGTTC TC
                                  ACCC    ___       A
GAM2477  RUNX1    3'  CCCGGAGGCGAAGGCGGC    12016     AGT    G    A
                                CCC   GGCGA AGGCG GC
                                |||   ||||| ||||| ||
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                                GGG   CCGCT TCCGC CG
                                  CCT    _   _
GAM2477 SLC22A2  5' CCCAGTGGCAGGCGGC     40520        GAG    A
                                CCCAGTGGC   AGGCG GC
                                |||||||||   ||||| ||
                                GGGTCACCG   TCCGC CG
                                        ___    _
GAM2477 SMARCC2  3' CCCAGTGGTGGGGGAAGGGC  40071        C____  A
                                CCCAGTGG    GAG GGC
                                ||||||||    ||| |||
                                GGGTCACC    CTT CCG
                                     ACCCC   C
GAM2477 SRP46    5' CCGGGCGGAGAGGCGGGCGGC 36953    AGT   _     A  A
                                CC   GGCG AGAGGCG GC GC
                                ||   |||| ||||||| || ||
                                GG   CCGC TCTCCGC CG CG
                                 C__   C      C  C
GAM2477 TNS      5' CCAGTGGCGGAGGCAGC     35468        A    G
                                CCAGTGGCG GAGGC AGC
                                ||||||||| ||||| |||
                                GGTCACCGC CTCCG TCG
                                        _    _
GAM2477 TNXB     3' GCGAGAGAGGTGGGCAGC    37157     C     CGA
                                GTGG GAGAGG   GCAGC
                                |||| ||||||   |||||
                                CGCT CTCTCC   CGTCG
                                  _     ACC
GAM2477 TPST2    5' CCCGTGGCGAGACGCGGC    18758    A       G   A
                                CCC GTGGCGAGA GCG GC
                                ||| ||||||||| ||| ||
                                GGG CACCGCTCT CGC CG
                                  _       G  _
GAM2477 UBE2G2   3' CAGTGGCGGGACTTCAGC    42118        AGA   GAG
                                CAGTGGCG   GGC   CAGC
                                ||||||||   |||   ||||
                                GTCACCGC   CTG   GTCG
                                     C__   AA_
GAM2477 UBE4A    5' ACCTAGTGGGAGAGGCAGAGC 21968    C    C     _
                                ACC AGTGG GAGAGGC GAGC
                                ||| ||||| ||||||| ||||
                                TGG TCACC CTCTCCG CTCG
                                  A    _      T
GAM2478 APPL     3' AGAATGCATTGTAGAAGTAG  29004        CC      GG
                                AGAATGCA  GTAGGAG  G
                                ||||||||  |||||||  |
                                TCTTACGT  CATCTTC  C
                                     AA      AT
GAM2478 CARPX    3' GCATCACAGGGGGGCATG    33571    C     A
                                GCA CGTAGG GGGGCATG
                                ||| |||||| ||||||||
```

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                                CGT GTGTCC CCCCGTAC
                                  A     _
GAM2478 CD7     3' AGAAGCACCGTGGGGC     26001     T     AGGA
                                AGAA GCACCGT    GGGGC
                                |||| |||||||    |||||
                                TCTT CGTGGCA    CCCCG
                                  _     _____
GAM2478 EPB41L2  3' GAATGCTGCCGAAGGGCATG  11005      ACC  AG
                                GAATGC   GT  GAGGGGCATG
                                ||||||   ||  ||||||||||
                                CTTACG   CG  CTTCCCGTAC
                                   A__   G_
GAM2478 FGFR1    3' GAGTACTGGTCCAGGGGCATG 31941    A   ACC  AGG
                                GA TGC   GT   AGGGGCATG
                                || |||   ||   |||||||||
                                CT ATG   CA   TCCCCGTAC
                                 C   AC_  GG_
GAM2478 AP1B1    5' CACCTCTCGCTCTCCCGG    10034       _ _
                                CGCCTC CG TTTCCCGG
                                |||||| || ||||||||
                                GTGGAG GC AGAGGGCC
                                   A  G
GAM2478 ATF4     5' CCTGCCGCCGCCATCTTGGT   11722         T     CCC
                                CCTGCCGCC CCGTTT   GGT
                                ||||||||| ||||||   |||
                                GGACGGCGG GGTAGA   CCA
                                     C     A__
GAM2478 BLTR2    5' TGCCTGTTTCCAGTCTCCTGGT 33374     GCC_  _     C
                                TGCC    TCC GTTTCC GGT
                                ||||    ||| |||||| |||
                                ACGG    AGG CAGAGG CCA
                                  ACAA   T     A
GAM2478 CXorf6   3' CCTTGCCGCTTCCCCAG     24237     _    CTCCG
                                CCT GCCGC    TTTCCCGG
                                ||| |||||    ||||||||
                                GGA CGGCG    AAGGGGTC
                                  A    ______
GAM2478 DBH      3' TGCCGCCTCGTCTTTTGGT    8973          C    CCC
                                TGCCGCCTC GTTT   GGT
                                ||||||||| ||||   |||
                                ACGGCGGAG CAGA   CCA
                                     _    AAA
GAM2478 DMD      5' CACCTGTTTCTTCCACTCCGGT 19678       CCGCC    TTTC
                                CACCTG    TCCG    CCGGT
                                ||||||    ||||    |||||
                                GTGGAC    AGGT    GGCCA
                                   AAAGA    GA__
GAM2478 FCER2    3' GCTGCCTCCGTTTGGGT     12814    C        CCC
                                GC GCCTCCGTTT   GGT
                                || ||||||||||   |||
```

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                                CG CGGAGGCAAA   CCA
                                 A        C__
GAM2478  M6PR     3'  CACTTCTGCTTCCGTTCCC    14305     __    CGCC
                                CAC  CTGC    TCCGTTTCC
                                |||  ||||    |||||||||
                                GTG  GACG    AGGCAAGGG
                                  AA    A___
GAM2478  MN1      5'  CGCCTGCCGCTTCTGTTC    14575    A       C  C
                                C CCTGCCGC TC GTTT
                                | |||||||| || ||||
                                G GGACGGCG AG CAAG
                                 C       A  A
GAM2478  MPP6     5'  CTGCCGCCGCTCCCGG      32393         TCC   T
                                CTGCCGCC   GTT CCCGG
                                ||||||||   ||| |||||
                                GACGGCGG   CGA GGGCC
                                     ___   _
GAM2478  PPAT     3'  CACCTGCCTTCTCTGACCAGGT 15482         GC   CGTTT  C
                                CACCTGCC  CTC    CC GGT
                                ||||||||  |||    || |||
                                GTGGACGG  GAG    GG CCA
                                     AA   ACT__  T
GAM2478  PRKY     5'  CCCGCCGCTTCCTCCAGCTCGG 15691         C   GTT  ____
                T                CCTGCCGC TCC   TCC    CGGT
                                ||||||||  |||   |||    ||||
                                GGGCGGCG AGG   AGG    GCCA
                                     A   ___   TCGA
GAM2478  PTPRF    5'  CCGCCGCCTCCACCTGG     39031          TTT  C
                                CTGCCGCCTCCG   CC GG
                                ||||||||||||   || ||
                                GGCGGCGGAGGT   GG CC
                                       ___  A
GAM2478  RAD51L3  5'  CGCGCTGCCGCTTCCGGG    39468     _  _      C
                                CGC CT CCGTTTCC GG
                                ||| || ||||||||  ||
                                GCG GA GGCGAAGG CC
                                  C  C       C
GAM2478  SMAC     3'  CTGCCGCCTCTTCTCGGT    39896         CGT   C
                                CTGCCGCCTC   TTC CGGT
                                |||||||||   ||| ||||
                                GACGGCGGAG   AAG GCCA
                                       ___   A
GAM2478  SMCX     5'  CCGCCGCCGCCATCTTGGT   20068         T     CCC
                                CTGCCGCC CCGTTT   GGT
                                |||||||| ||||||   |||
                                GGCGGCGG GGTAGA   CCA
                                     C     A__
GAM2478  VIPR2    5'  CCCGCCGCCTCCGTCCTAGGT  18007              CCC
                                CCTGCCGCCTCCGTTT   GGT
                                ||||||||||||||||   |||
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                                GGGCGGCGGAGGCAGG   CCA
                                      AT_
GAM2478  ZNF278   3'  TGCCGGCTGTCCCACCTTCCTG 36812      _ C_   G__    C
           GT                   TGCCG C  TCC   TTTCC GGT
                                ||||| |  |||   ||||| |||
                                ACGGC G  AGG   GAAGG CCA
                                  C AC   GTG    A
GAM2479  CKMT2    5'  TCACTTGGCTTGTGACT     12266         CC   A
                                TCGCTTGGT  TGT ACT
                                |||||||||  ||| |||
                                AGTGAACCG  ACA TGA
                                     A_   C
GAM2479  DLG5     3'  CCACTCTGCCTGTAACT     44452       G T
                                TCGCTT G CCTGTAACT
                                |||||| | |||||||||
                                GGTGAG C GGACATTGA
                                   A _
GAM2479  E2F3     3'  TCCCTTGGTCCAACT       12634    G      TGT
                                TC CTTGGTCC   AACT
                                || ||||||||   ||||
                                AG GAACCAGG   TTGA
                                 G      ___
GAM2479  EGLN1    5'  TCACTTGAGTATACTGTAACT  35176        _  C__
                                TCGCTTG GT   CTGTAACT
                                ||||||| ||   ||||||||
                                AGTGAAC CA   GACATTGA
                                     T  TAT
GAM2479  HTR2C    5'  TCGTTGGCCCCTAACT      9292      C      G
                                TCG TTGGTCCT TAACT
                                ||| |||||||| |||||
                                AGC AACCGGGG ATTGA
                                  _      _
GAM2479  HUNK     3'  CCAGGCCATTCTGTAACT    31058    T   ___
                                CT GGTC   CTGTAACT
                                || ||||   ||||||||
                                GG CCGG   GACATTGA
                                 T   TAA
GAM2479  MTMR6    3'  TCACTTAAGATGTAACT     45280        TCC
                                TCGCTTGG   TGTAACT
                                ||||||||   |||||||
                                AGTGAATT   ACATTGA
                                     CT_
GAM2479  NCAM1    3'  TCACTAAGCTGTAACT      8319       T  TC
                                TCGCT GG  CTGTAACT
                                ||||| ||  ||||||||
                                AGTGA TC  GACATTGA
                                   T  __
GAM2479  SNX5     3'  TCACCTGCTGTAACT       30866        GTC
                                TCGCTTG   CTGTAACT
                                |||||||   ||||||||
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                                AGTGGAC  GACATTGA
                                   ___
GAM2479 TDGF1    3' TCACTTGGTTTACAACT    17364       CC
                                TCGCTTGGT TGTAACT
                                ||||||||| |||||||
                                AGTGAACCA ATGTTGA
                                    A_
GAM2479 TNFRSF10B 3' TCTTTGGTCCCGACT     19289   GC      TA
                                TC TTGGTCCTG ACT
                                || ||||||||| |||
                                AG AACCAGGGC TGA
                                 A_      __
GAM2479 TPO      5' TCACGGCTGTAACT      8098     TT TC
                                TCGC GG CTGTAACT
                                |||| || ||||||||
                                AGTG CC GACATTGA
                                  __ __
GAM2479 YY1      3' CCACTTTCTGTAACT      18166      GGTC
                                TCGCTT  CTGTAACT
                                ||||||  ||||||||
                                GGTGAA  GACATTGA
                                   A___
GAM2479 CA3      3' TGTGGAAAAATGAAATA    23223        CA
                                TGTGGAAAAAT AAATA
                                |||||||||| |||||
                                ACACCTTTTTA TTTAT
                                     C_
GAM2479 CSN10    3' TGTGCAAGAATCAAAATA    23318    G A
                                TGTG AA AATCAAAATA
                                |||| || ||||||||||
                                ACAC TT TTAGTTTTAT
                                  G C
GAM2479 PKHD1    3' TGTGGAAAAAAAACTTAAAAAG 39812        TC AA
             T                   TGTGGAAAAA AA TAAAAAGT
                                ||||||||| || ||||||||
                                ACACCTTTTT TT ATTTTTCA
                                     T_ GA
GAM2479 RBMX     3' TGGGAAAAATCAGATAGGAAGT 42812   T       AA  AA
                                TG GGAAAAATCA ATA AAGT
                                || |||||||||| ||| ||||
                                AC CCTTTTTAGT TAT TTCA
                                 _       C_  CC
GAM2479 SIRT5    3' TGTGCAAAAATCAGAATA    29267    G      A
                                TGTG AAAAATCA AATA
                                |||| |||||||| ||||
                                ACAC TTTTTAGT TTAT
                                  G      C
GAM2480 TRIM9    3' AAAGATCTTGCCCATGAGTCT 31549       CG  G   A
                                AAGGATCT TGC CTAT AGTCT
                                |||||||| ||| |||| |||||
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                                TTTCTAGA  ACG GGTA TCAGA
                                   __  _   C
GAM2480  CDC42    3'  TGAGCTGCAAATCTAT     12162       T   CATGG
                                TGAGCT GCAA    GTCTAT
                                |||||| ||||    ||||||
                                ACTCGA CGTT    TAGATA
                                  _   _____
GAM2480  CDKN2B   3'  TGAGTTTGCAACAGTGCCATTG 38554     C      TGG   TA
           C                     TGAG TTGCAACA   GTC  TGC
                                |||| ||||||||   |||  |||
                                ACTC AACGTTGT   CGG  ACG
                                  A      CA_   TA
GAM2480  CXCR6    3'  GAGCTTGGGCACCCAGTGTGC  27295       CA_  ATG   CTA
                                GAGCTTG   AC   GGT   TGC
                                |||||||   ||   |||   |||
                                CTCGAAC   TG   TCA   ACG
                                    CCG  GG_   C__
GAM2480  HPCA     3'  GAGCTCCGTGGGTCTGTG    13425      GCAACA      A
                                GAGCTT     TGGGTCT TG
                                ||||||     ||||||| ||
                                CTCGAG     ACCCAGA AC
                                   GC____      C
GAM2480  SERPIND1 3'  TGAGCTTACAGCATGGGCTAT  6777          A     T
                                TGAGCTTGCA CATGGG CTAT
                                |||||||||| |||||| ||||
                                ACTCGAATGT GTACCC GATA
                                     C     _
GAM2481  AQP6     5'  CTGGTGCCTTGGCCGTTCCTT  38242        AC    TCACCC
                                CTGGTGCC  GGTT     CCTT
                                ||||||||  ||||     ||||
                                GACCACGG  CCGG     GGAA
                                    AA    CAA___
GAM2481  WNT5A    5'  CTGGTGCCAGGCGCTGCCTCCT 18117        C   TTCA  C
           T                     CTGGTGCCA GGT    CC CCTT
                                ||||||||| |||    || ||||
                                GACCACGGT CCG    GG GGAA
                                     _   CGAC  A
GAM2481  AES      3'  GGCTGCTGCGCTTCGCGAGGT  10057        ACCCA   T_
                                GGCTGCTGC    CGT  GGT
                                |||||||||    |||  |||
                                CCGACGACG    GCG  CCA
                                    CGAA_   CT
GAM2481  APP      3'  GAGGCTGCTGTGGC       7916          CACCCACGT
                                GAGGCTGCTG       TGGT
                                ||||||||||       ||||
                                CTCCGACGAC       ACCG
                                  _________
GAM2481  C6       3'  GAGACTGCTGTGGAAGTTGGT  45402         CACCCAC
                                GAGGCTGCTG     GTTGGT
                                ||||||||||     ||||||
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                                CTCTGACGAC      CAACCA
                                     ACCTT__
GAM2481  CALM3    3'  GAGGCTGCTGTAGCTGCCG   23235         CACCCAC
                                GAGGCTGCTG      GTTG
                                ||||||||||      ||||
                                CTCCGACGAC      CGGC
                                     ATCGA__
GAM2481  CAV1     3'  GAGGCTGCTGACCTAAAGCGAG 11992         C   CAC_  T
           T                     GAGGCTGCTG ACC    GT GGT
                                ||||||||||  |||    ||  |||
                                CTCCGACGAC TGG    CG TCA
                                     _   ATTT  C
GAM2481  CMAR     3'  GAGGCTGCTGGGTCTCTTCGGT 23294         CACCCACG
                                GAGGCTGCTG       TTGGT
                                ||||||||||       |||||
                                CTCCGACGAC       AGCCA
                                     CCAGAGA_
GAM2481  EGFL4    3'  AGGCGGATGTCCACGTTGGT   41558     TGC  CAC
                                AGGC   TG   CCACGTTGGT
                                ||||   ||   ||||||||||
                                TCCG   AC   GGTGCAACCA
                                  CCT  A__
GAM2481  GNA11    3'  GGCTGCTGCCGCCCGGGC    44050        AC  A  TT
                                GGCTGCTGC  CC CG  GGT
                                |||||||||  || ||  |||
                                CCGACGACG  GG GC  CCG
                                     GC  _  __
GAM2481  HD       3'  GAGGCTGCTGTCCCTGACTGGT 13351         CA   ACG
                                GAGGCTGCTG  CCC   TTGGT
                                ||||||||||  |||   |||||
                                CTCCGACGAC  GGG   GACCA
                                     A_   ACT
GAM2481  HOXA3    3'  GGCTGCTGCGTCCGGC      36196         AC  ACGTT
                                GGCTGCTGC  CC     GGT
                                |||||||||  ||     |||
                                CCGACGACG  GG     CCG
                                     CA  _____
GAM2481  IRS2     5'  GGCTGCTGCTGCTGCTGGT   40710         ACCCAC
                                GGCTGCTGC     GTTGGT
                                |||||||||     ||||||
                                CCGACGACG     CGACCA
                                     ACGA__
GAM2481  LMO4     5'  GGCTGTTGCTGCCCGGC     27658       C   A_   ACGTT
                                GGCTG TGC  CCC     GGT
                                |||||  |||  |||     |||
                                CCGAC ACG  GGG     CCG
                                   A   AC   _____
GAM2481  NFATC3   3'  GAGCCTGCTGCATTCACACT   21249     G       CC
                                GAG CTGCTGCA  CACGTT
                                |||  ||||||||  ||||||
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                                CTC GACGACGT  GTGTGA
                                  G       AA
GAM2481  NFATC4   5'  GAGGCTGCTGTATCTTCACCC  21244          _______
                                GAGGCTGCTG     CACCC
                                ||||||||||     |||||
                                CTCCGACGAC     GTGGG
                                     ATAGAA
GAM2481  PDE4A    5'  GGCTGCTGCACACAGAGGC   26263          CC   TT
                                GGCTGCTGCAC  ACG  GGT
                                ||||||||||| |||  |||
                                CCGACGACGTG  TGT  CCG
                                     __  CT
GAM2481  PLOD     3'  GAGGCTGCTGGGCAGTGG    7158          CACC  C  T
                                GAGGCTGCTG   CA GT GG
                                ||||||||||   || || ||
                                CTCCGACGAC   GT CA CC
                                     CC__  _  _
GAM2481  RFX2     5'  GGCTGCTGCGTGTTGG      8456          ACCCAC
                                GGCTGCTGC     GTTGG
                                |||||||||     |||||
                                CCGACGACG     CAACC
                                     CA_____
GAM2481  SCGB2A2  5'  GAGGCTGCTGCTGTCGG     14484          ACCCAC
                                GAGGCTGCTGC     GTTGG
                                ||||||||||     |||||
                                CTCCGACGACG     CAGCC
                                     A______
GAM2481  SHOX     5'  GGGCTGCTGCGTCCTGG     7809    A      AC  ACGT
                                G GGCTGCTGC  CC   TGG
                                | |||||||||  ||   |||
                                C CCGACGACG  GG   ACC
                                _       CA  _____
GAM2481  SIAT7D   5'  GGCTGCTGTCTCCAGGGC    30832          CAC   CGTT
                                GGCTGCTG   CCA   GGT
                                ||||||||   |||   |||
                                CCGACGAC   GGT   CCG
                                     AGA   C___
GAM2481  TCF2     3'  GAGGCTGCTACACTTTGTGGT  7845           CCACGT
                                GAGGCTGCTGCAC     TGGT
                                ||||||||||||      ||||
                                CTCCGACGATGTG     ACCA
                                     AAAC__
GAM2481  TIMP3    5'  GGCTGCTGCAGCCCGAGCT   7461           _  AC
                                GGCTGCTGCA CCC  GTT
                                |||||||||| |||  |||
                                CCGACGACGT GGG  CGA
                                     C   CT
GAM2481  TNA      5'  GGCTGCTGCTGCCTGCAGCGGG 17613         A_  __  C  T
           T                     GGCTGCTGC  CC  CA GT GGT
                                |||||||||  ||  || || |||
```

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                                CCGACGACG  GG  GT CG CCA
                                     AC  AC  _  C
GAM2482  ALDH3B2  3'  GGGCATGTGTGTGTGAGG    8684     T    AC  ACAT
                                GG GCAT  TG    TGTGAGG
                                || ||||  ||    |||||||
                                CC CGTA  AC    ACACTCC
                                 _    C_  AC__
GAM2482  COL4A6   3'  GGTGACTGTTGTGAG      12325      CAT    ACA
                                GGTG   ACTG   TTGTGAG
                                ||||   ||||   |||||||
                                CCAC   TGAC   AACACTC
                                  ___    ___
GAM2482  ITSN2    3'  GTGCATGGCTTTGTGAGGG   33327       A_  GACA
                                GTGCAT  CT    TTGTGAGGG
                                ||||||  ||    |||||||||
                                CACGTA  GA    AACACTCCC
                                   CC  ____
GAM2482  NHLH1    5'  GGTACACATTGTGGG       24654       ATACTG       A
                                GGTGC     ACATTGTG GG
                                |||||     |||||||| ||
                                CCATG     TGTAACAC CC
                                  _______      _
GAM2482  PSMB9    3'  AGTGTATGCTGACATCTAGGAG 15826      C  A       GT_
            GG                    GGTG AT CTGACATT   GAGGG
                                |||| || ||||||||   |||||
                                TCAC TA GACTGTAG   CTCCC
                                  A  C       ATC
GAM2482  GIF      3'  GAGATGTTTGATAGAAGCTGA  23106    A    CA  C
                                GA ATGTT  GT GGAAGCTGA
                                || |||||  || |||||||||
                                CT TACAA  TA TCTTCGACT
                                 C    AC  _
GAM2482  HPGD     3'  GAAATGTTCAGTTGAAAG    9242            C
                                GAAATGTTCAGT GGAAG
                                |||||||||||| |||||
                                CTTTACAAGTCA CTTTC
                                       A
GAM2482  LTB4R    5'  GAACTGGTTGGAAGCTGA    8883      A  TTCA  C
                                GAA TG    GT GGAAGCTGA
                                ||| ||    || |||||||||
                                CTT AC    CA CCTTCGACT
                                  G  ____  A
GAM2482  OCLN     3'  TGTTCAGCCCAGTTGA      14910         GGA  C
                                TGTTCAGTC   AG TGA
                                |||||||||   || |||
                                ACAAGTCGG   TC ACT
                                     G__  A
GAM2482  ZNF146   3'  ATGTTTATATAAAAAGCTGA  28349       CA_  CG
                                ATGTT   GT  GAAGCTGA
                                |||||   ||  ||||||||
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                                TACAA   TA  TTTCGACT
                                   ATA  TT
GAM2483  AGL      3'  ATTACTGTCACAACTGTCC   8487          _    A
                                GTTACTGTC TAACT TCC
                                ||||||||| ||||| |||
                                TAATGACAG GTTGA AGG
                                     T    C
GAM2483  ALDH1B1  3'  ATTACTCCTCTATCCCC    8668        G   AA
                                GTTACT TCT  CTATCCCC
                                |||||| |||  ||||||||
                                TAATGA GGA  GATAGGGG
                                  _  __
GAM2483  CD79B    5'  GTCACTGCTCTGTCCCC    8422         CTAA  A
                                GTTACTGT    CT TCCCC
                                ||||||||    || |||||
                                CAGTGACG    GA AGGGG
                                     A___  C
GAM2483  CDKN2A   3'  GTTACTGCCTCTGGTGCCCC  38476          AACTAT
                                GTTACTGTCT     CCCC
                                ||||||||||     ||||
                                CAATGACGGA     GGGG
                                     GACCAC
GAM2483  DIAPH2   3'  GTTACTGCTATGTCCC      28676        T   ACTA
                                GTTACTG CTA    TCCC
                                ||||||| |||    ||||
                                CAATGAC GAT    AGGG
                                   _   AC__
GAM2483  GLB1     3'  GTTACTGTGCTGTCAGCCCC  7616          _ AAC  T
                                GTTACTGT CT   TA CCCC
                                |||||||| ||   || ||||
                                CAATGACA GA   GT GGGG
                                     C  CA_  C
GAM2483  HOXB5    3'  CTGACCCAGACTATCCCC    13446     _   _
                                CTG TCTA ACTATCCCC
                                ||| |||| |||||||||
                                GAC GGGT TGATAGGGG
                                  T    C
GAM2483  MTMR8    3'  ATTACTCATAAACTATCC    31749       GTCT
                                GTTACT    AACTATCC
                                ||||||    ||||||||
                                TAATGA    TTGATAGG
                                   GTAT
GAM2483  PTPRJ    3'  GCTACTGTTTAAATATTCC   15958         C   C   C
                                GTTACTGT TAA TAT CC
                                |||||||| ||| ||| ||
                                CGATGACA ATT ATA GG
                                     A   T   A
GAM2483  S100B    3'  GTTACTGTTAACAAGAGTCCC 26573         C    TA___
                                GTTACTGT TAAC     TCCC
                                |||||||| ||||     ||||
```

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                                CAATGACA ATTG    AGGG
                                    _   TTCTC
GAM2483 TMPRSS3  5' TTACAAATTTAACTATCC    37065     T_ C
                                TTAC  GT TAACTATCC
                                ||||  || |||||||||
                                AATG  TA ATTGATAGG
                                  TT  A
GAM2483 ZFP36    3' ATTACTGTCCCCCAAGTCCCC  18210         AA  __
                                GTTACTGTCT  CTA  TCCCC
                                ||||||||||  |||  |||||
                                TAATGACAGG  GGT  AGGGG
                                      G_  TC
GAM2483 ARHGDIA  3' AGGGGGCTGGCCAGGGAGCAGC 20198    AA      AA_  TTC
            GG                    AGG  GTTGGCCA   GGT   CGG
                                ||| ||||||||  |||  |||
                                TCC  CGACCGGT   TCG   GCC
                                  CC      CCC   TC_
GAM2483 BIN3     3' GGAAGCTGGCTGAGGGCCT   33082         CAAA
                                GGAAGTTGGC   GGTTT
                                ||||||||||   |||||
                                CCTTCGACCG   CCGGA
                                      ACTC
GAM2483 CIT      3' GGAGGTTGGCCAACTGACCGG  43053    A       AGGTTT
                                GGA GTTGGCCAA    CCGG
                                ||| |||||||||     ||||
                                CCT CAACCGGTT    GGCC
                                  C       GACT__
GAM2483 CUL3     5' GGGAGCTGGCCGGCCCCTGG   18742    A      AAA   TT C
                                GG AGTTGGCC   GGT  C GG
                                || ||||||||   |||  | ||
                                CC TCGACCGG   CCG  G CC
                                 C       ____   GG A
GAM2483 DISC1    3' AGAAAGTTGGCCGGGTGCG   33024          AAA   TTC
                                AGGAAGTTGGCC   GGT   CG
                                ||||||||||||   |||   ||
                                TCTTTCAACCGG   CCA   GC
                                      C__   C__
GAM2483 FOXO1A   3' AGGGAGTTGGTGAAAGACATC  12883    A    CC    TT
                                AGG AGTTGG  AAAGG  TC
                                ||| ||||||  |||||  ||
                                TCC TCAACC  TTTCT  AG
                                  C     AC    GT
GAM2483 HEBP1    3' GAAAGTTGGTTAAGTT      31990         CCAA
                                GGAAGTTGG    AGGTT
                                |||||||||    |||||
                                CTTTCAACC    TTCAA
                                      AA__
GAM2483 P4HB     3' AGAGAGGTTCCCTGGGTTTCCG 9542     GA  TTGG  AAA
            G                    AG  AG   CC   GGTTTCCGG
                                || ||   ||   |||||||||
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                                TC  TC   GG  CCAAAGGCC
                                 TC  CAA_  GAC
GAM2483  RNPEP    3'  AGGAAGTTGATCAGGGAACAG  42157        GC  AA  TTTC
                                AGGAAGTTG  CA  GG   CGG
                                |||||||||  ||  ||   |||
                                TCCTTCAAC  GT  CC   GTC
                                     TA  C_  TT__
GAM2483  RUNX1    3'  AGGAAGTTTGCTGGTTT     12004        G  CAAA
                                AGGAAGTT GC   GGTTT
                                ||||||||  ||   |||||
                                TCCTTCAA CG   CCAAA
                                    A  A___
GAM2483  TCF3     3'  GGAGGCTGGCCAGGCCCCTGG  43322     A       AA   TT C
                                GGA GTTGGCCA  GGT  C GG
                                |||  ||||||||  |||  | ||
                                CCT CGACCGGT  CCG  G CC
                                  C        __   GG A
GAM2483  TLL1     5'  AGAAGTTGGCTAGGGGCCCACG 29732         CAAA   TC
              G                   GGAAGTTGGC   GGTT  CGG
                                |||||||||||   ||||  |||
                                TCTTCAACCG   CCGG  GCC
                                     ATCC   GT
GAM2484  ANGPT1   5'  AGATATTTATTGCATAGTAGCT 40237      C    TTC
                                AGATA TTATT   TAGTAGCT
                                |||||  |||||   ||||||||
                                TCTAT AATAA   ATCATCGA
                                   A    CGT
GAM2484  BNC      3'  AGATATTTTTCCCCTAGC    11851      C  A  TT
                                AGATA TT TT  CTAGT
                                |||||  ||  ||  |||||
                                TCTAT AA AG  GATCG
                                   A  A  GG
GAM2484  DCN      3'  TAAGAATATCTCTAGTAGC   39447      TACTTAT
                                TAAGA      TTTCTAGTAGC
                                |||||      ||||||||||
                                ATTCT      AGAGATCATCG
                                   TAT_____
GAM2484  SACM2L   3'  AAATATTTATTTTCTGCAGACT 38705      C       A   _
                                AGATA TTATTTTCT GTAG CT
                                |||||  |||||||||  ||||  ||
                                TTTAT AATAAAAGA CGTC GA
                                   A        _    T
GAM2484  CASP1    3'  TCATTTTTCTACCAGATTT   37787         A   T
                                TCATTTTTCTA TAG GTTT
                                ||||||||||  |||  ||||
                                AGTAAAAAGAT GTC TAAA
                                      G   _
GAM2484  CDS1     3'  TTACTCATTTTATAGTGTT   10403          TCTA
                                TTGCTCATTTT    ATAGTGTT
                                ||||||||||    ||||||||
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                                AATGAGTAAAA    TATCACAA
                                       ____
GAM2484  EXTL2    3'  TTACTCATTTTTTTCAGGTTT  11023          CTAA   T
                                TTGCTCATTTTT    TAG GTTT
                                ||||||||||||    ||| ||||
                                AATGAGTAAAAA    GTC CAAA
                                       AA__   _
GAM2484  KRAS2    3'  TTGCTCATCTTTTCTTTATGTT 37889          _  AATA
                T                TTGCTCATTTTT CT    GTGTTT
                                ||||||||||||| ||    ||||||
                                AACGAGTAGAAA GA    TACAAA
                                       A  AA__
GAM2484  PDE4A    3'  TTGTTCTTTTTCTAAAAATGTT 26281     C  A       T
                                TTG TC TTTTTCTAA AGTGTT
                                ||| || ||||||||| ||||||
                                AAC AG AAAAAGATT TTACAA
                                  A  _       T
GAM2485  ABCG5    3'  TAAACATATTTTTAAGCT    35331          _
                                TAAACATATTTT AAGCT
                                |||||||||||| |||||
                                ATTTGTATAAAA TTCGA
                                       A
GAM2485  IL26     3'  TATAAACATATTTCTAGC    32902            A
                                TATAAACATATTTT AGC
                                |||||||||||||| |||
                                ATATTTGTATAAAG TCG
                                        A
GAM2486  PLN      3'  CAACAGTTGCATTTT       15404      TAT
                                CAGC   AGTTGCATTTT
                                ||||   ||||||||||
                                GTTG   TCAACGTAAAA
                                  ___
GAM2486  RDS      3'  TTAACAGCATAGTTACACTT   7249         T
                                TTAACAGC ATAGTTGCATTT
                                |||||||| ||||||||||||
                                AATTGTCG TATCAATGTGAA
                                       _
GAM2487  RU2      3'  TCTTGCGATCCATATACTCTCT 32294     C      GC   A C
                T                TCT GCGATCT  GTG C CTCTT
                                ||| |||||||  ||| | |||||
                                AGA CGCTAGG  TAT G GAGAA
                                  A      TA  _ A
GAM2488  NRGN     3'  CTTAGGGCGCCCTCCGCA    26126      C  A       T
                                CTTA GG CGCCCTCC CG
                                |||| || |||||||| ||
                                GAAT CC GCGGGAGG GT
                                  C  _       C
GAM2488  TES      3'  ACTTCTGGGTGCCCTCCT    43536      AC  AC
                                ACTT  GG  GCCCTCCT
                                ||||  ||  ||||||||
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                                TGAA  CC  CGGGAGGA
                                  GA  CA
GAM2489  HOXB9    5'  GCAGGGGGAAGGGAAGCGCTC  35843     AATATATT  A
                                GCA       AG GAAGCGCTC
                                |||       || |||||||||
                                CGT       TC CTTCGCGAG
                                  CCCCCT__  C
GAM2489  JAG2     3'  CAAATATACAGAGTGCT     13701          T    AAGC
                                CAAATATAT AGAG    GCT
                                |||||||||| ||||    |||
                                GTTTATATG TCTC    CGA
                                      _   A___
GAM2489  PMX1     5'  GCAGATGTATTAGAGAGC    35512     A  A       A
                                GCA AT TATTAGAGA GC
                                ||| || ||||||||| ||
                                CGT TA ATAATCTCT CG
                                  C  C       _
GAM2490  GRINL1A  3'  TGAAAGACATGTAATAAATGCT 43004      CA       TA
                                TGAA  ACATGTAAT  GAATGCT
                                ||||  |||||||||  |||||||
                                ACTT  TGTACATTA  TTTACGA
                                  TC       __
GAM2490  OTP      3'  TGACCAGTATGTAACAAGAATG 37005     A  AC      T
              CT                  TGA CA  ATGTAAT AGAATGCT
                                ||| ||  ||||||| ||||||||
                                ACT GT  TACATTG TCTTACGA
                                  G  CA      T
GAM2490  PIN4     3'  TGACTAACATGTAAAACAAATG 26329     AC       TTA
                                TGA  AACATGTAA   GAATG
                                |||  |||||||||   |||||
                                ACT  TTGTACATT   TTTAC
                                  GA       TTG
GAM2490  STC1     3'  CAACATGTGAGAACTGCT    17171         AATT   _
                                CAACATGT    AGAA TGCT
                                ||||||||    |||| ||||
                                GTTGTACA    TCTT ACGA
                                     C___    G
GAM2490  ATP6IP1  3'  AATATGTACACCTTGTTGG   10142          AAGT
                                AATATGTACAC    TTGG
                                ||||||||||    ||||
                                TTATACATGTG    AACC
                                      GAAC
GAM2490  CRY1     3'  ATACTTCCACAAGTTTGG    19831      GTA
                                ATAT   CACAAGTTTGG
                                ||||   ||||||||||
                                TATG   GTGTTCAAACC
                                  AAG
GAM2490  FCMD     3'  AATATGTAGCCATAAGTTTGG  27508         __  C
                                AATATGTA  CA AAGTTTGG
                                ||||||||  || ||||||||
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                                TTATACAT  GT TTCAAACC
                                    CG  A
GAM2490  FGF5     3'  TAATATATACACAAACTTGG   20917           GT
                                TAATATGTACACAA  TTGG
                                ||||||||||||||  ||||
                                ATTATATATGTGTT  AACC
                                      TG
GAM2490  PACE4    3'  TAAAATGCCTACACAGGTTTGG 15058    T   __    A
                                TAA ATGT  ACACA GTTTGG
                                ||| ||||  ||||| ||||||
                                ATT TACG  TGTGT CAAACC
                                  T   GA    C
GAM2490  PTGFRN   3'  TATATACTCCAAGTTTGG    42597       A_
                                TATGTAC  CAAGTTTGG
                                |||||||  |||||||||
                                ATATATG  GTTCAAACC
                                    AG
GAM2491  CNP      3'  TTCTAGGGGCATAAGTGGTGGT 37564    CG     TGT
                                TTC  GGGGGT   GGTGGTGGT
                                |||  ||||||   |||||||||
                                AAG  TCCCCG   TCACCACCA
                                  A_     TAT
GAM2491  PIK3C2B  5'  TTCTGGAGGGTTGTGACATGGT 15298     C         GT G
                                TTC GGGGGGTTGTG  G TGGT
                                ||| ||||||||||  | ||||
                                AAG CCTCCCAACAC  T ACCA
                                  A         TG _
GAM2491  PX19     3'  TCTGGGGTGCTGTGGTGGTGGT 29876    C   G
                                TC GGGG GTTGTGGTGGTGGT
                                || |||| ||||||||||||||
                                AG CCCC CGACACCACCACCA
                                 A   A
GAM2491  SLC1A4   3'  CTCTGGGGTGGTGGTGG     16746     C   GGTTG
                                TTC GGGG    TGGTGGTGG
                                ||| ||||    |||||||||
                                GAG CCCC    ACCACCACC
                                  A   _____
GAM2491  TOX      3'  CGGGGGGCGGGGGGGTGGTGGT  31270        TGT_
                                CGGGGGGT   GGTGGTGGT
                                ||||||||   |||||||||
                                GCCCCCCG   CCACCACCA
                                    CCCC
GAM2491  EGFR     3'  CCCAAAATGTGCCCGAGGTG   23396        TTTC  A  A
                                CCCAAAAT   GCT CGA GTG
                                ||||||||   ||| ||| |||
                                GGGTTTTA   CGG GCT CAC
                                    CA__   _  C
GAM2491  ETV5     3'  CCAAGGGTTTTCACCAGGTGA  20848     AA_       CGAA
                                CCAA  TTTTCGCTA   GTGA
                                ||||  |||||||||   ||||
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                                GGTT   AAAAGTGGT    CACT
                                  CCC        C___
GAM2492  KCNQ1    3'  TCCAAATCACCACAAATTAT   6887        T    G   T
                                TCCAAAT CACCA CGA TTAT
                                ||||||| ||||| ||| ||||
                                AGGTTTA GTGGT GTT AATA
                                   _    _  T
GAM2493  ARL2     3'  TTGGTGAAGGTTGAGGGACCT  11694        ATCCAA_
                                TTGGTGAA      GGATTT
                                ||||||||      ||||||
                                AACCACTT      CCTGGA
                                     CCAACTC
GAM2493  COG6     3'  TTGGTTGGATTTAGGACCCAT  43768      GAAATCCA
                                TTGGT       AGGATTTAT
                                |||||       |||||||||
                                AACCA       TCCTGGGTA
                                   ACCTAAA_
GAM2493  GAGED2   3'  TTGGTGAAAGCTGCAAAACTTT 39419         TC__    A
            ATT                   TTGGTGAAA    CAAGG TTTATT
                                |||||||||    ||||| ||||||
                                AACCACTTT    GTTTT AAATAA
                                     CGAC    G
GAM2493  SCN1A    3'  TGGTGAAATTTAAGAATTT    44821         CC
                                TGGTGAAAT  AAGGATTT
                                |||||||||  ||||||||
                                ACCACTTTA  TTCTTAAA
                                     AA
GAM2493  WHSC1L1  3'  TTGGTGAAGTGGCATTTATT   35722        ATCCAA _
                                TTGGTGAA     GG ATTTATT
                                ||||||||     || |||||||
                                AACCACTT     CC TAAATAA
                                     CA_____  G
GAM2493  MADD     5'  TCCAATTCATCAGTTTATCT   39069      A   C   CGA
                                TCCAA TTCA CAG   TTTATCT
                                ||||| |||| |||   |||||||
                                AGGTT AAGT GTC   AAATAGA
                                   _    A   ___
GAM2494  PIN1L    3'  GCTGCAAAGTTGCTCAGAGGG  26324         TC  ATT
                                GCTGCAAAGTT  CT   AGGG
                                ||||||||||  ||   ||||
                                CGACGTTTCAA  GA   TCCC
                                      C_  GTC
GAM2494  SFRP4    3'  GCACTGCAGTGAGTTGTTAGGG 16586        A__   TCCTA
                                GCGCTGCA   AGTT    TTAGGG
                                ||||||||   ||||    ||||||
                                CGTGACGT   TCAA    AATCCC
                                     CAC    C_____
GAM2495  BNC      3'  TGTATCAGTGAAAGACCTCTTG 11857     T    ATT   A
                                TGT ATCGG   AAA ACCTCTTG
                                ||| |||||   ||| ||||||||
```

```
                                ACA TAGTC   TTT TGGAGAAC
                                  _    AC_   C
GAM2495  GPC4     3'  TAGAGTGATAAAATCACAAA   11086        T   C
                                TAGAGTGAT AAAA CATAAG
                                ||||||||| |||| ||||||
                                ATCTCACTA TTTT GTGTTT
                                      _   A
GAM2495  GSTT1    3'  AGTGATTAAAGGACACAAGGCC 43863         AC_    _
              T                  AGTGATTAAA   CATAAG CCT
                                ||||||||||   |||||| |||
                                TCACTAATTT   GTGTTC GGA
                                      CCT     C
GAM2495  IL1F5    3'  AGAGTGATTGTCCGCC      29347         AAAA  ATAA
                                AGAGTGATT    CC    GCC
                                |||||||||    ||    |||
                                TCTCACTAA    GG    CGG
                                     CA__  ____
GAM2495  PIAS3    3'  TAACTACAGGGCCATGAGCCT  25911       AAA__    A
                                TGATTA     CCAT AGCCT
                                ||||||     |||| |||||
                                ATTGAT     GGTA TCGGA
                                   GTCCC    C
GAM2495  RAD52    3'  TAGAGTGATGGACAAGC     39561         TAAAACC
                                TAGAGTGAT      ATAAGC
                                |||||||||      ||||||
                                ATCTCACTA      TGTTCG
                                     CC_____
GAM2496  ARHGEF6  3'  TCTGTGACTGTCTTCTAAAC   42806           G   CG
                                TCTGTGACTGTCT CTG  GAC
                                |||||||||||| |||  |||
                                AGACACTGACAGA GAT  TTG
                                       A   __
GAM2496  CACNG3   5'  TGCCTTTTGCTGCGGGCAC    27245      ___      A
                                TGTCT   GCTGCGG CAC
                                |||||   ||||||| |||
                                ACGGA   CGACGCC GTG
                                   AAA      C
GAM2496  GAB2     3'  TGTGGCTGCTGCGG        38688      ACT T
                                TGTG   G CTGCTGCGG
                                ||||   | |||||||||
                                ACAC   C GACGACGCC
                                     ___ _
GAM2496  GGCX     3'  TCTGTGACTGGCTGCTTCTAC  9062          T    GCGG
                                TCTGTGACTG CTGCT    AC
                                |||||||||| |||||    ||
                                AGACACTGAC GACGA    TG
                                     C     AGA_
GAM2496  HPS4     5'  CTGTGGCTGTCTGCAGAAC    35216       A       TGC
                                CTGTG CTGTCTGC   GGAC
                                ||||| ||||||||   ||||
```

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                                GACAC GACAGACG   CTTG
                                  C       T__
GAM2496  MS4A1    3'  TGTGACTGTGACTGTGTGG   6604          __  C  C
                                TGTGACTGT  CTG TG GG
                                |||||||||  ||| || ||
                                ACACTGACA  GAC AC CC
                                     CT   _  A
GAM2496  NONO     3'  CCTGTGACCTTTGTGGAC    44355         GTCTGC  C
                                TCTGTGACT     TG GGAC
                                |||||||||     || ||||
                                GGACACTGG     AC CCTG
                                     AA____  A
GAM2496  CHRNE    3'  CTTGCTTTCTGGAAGACTGG  6344        G  ___
                                TTTGCT TC   AAGACTGG
                                ||||||  ||   ||||||||
                                GAACGA AG   TTCTGACC
                                   A  ACC
GAM2496  ENTPD1   3'  TCACACTCGTCAAGACTGG   12128         GCT
                                TTACATTT   GTCAAGACTGG
                                ||||||||   ||||||||||
                                AGTGTGAG   CAGTTCTGACC
                                           ___
GAM2496  ETS2     3'  CATTTGCTGTTCCTGG      23467          CAAGA
                                CATTTGCTGT    CTGG
                                ||||||||||    ||||
                                GTAAACGACA    GACC
                                     AG___
GAM2496  PCDH11X  3'  CTTTCCATTTGCTACATACTGG 37325     A_       T  AG
                                CTT  CATTTGCTG CA  ACTGG
                                |||  |||||||||  ||  |||||
                                GAA  GTAAACGAT GT  TGACC
                                  AG        _  A_
GAM2496  PCDH11Y  3'  CTTTCCATTTGCTACATACTGG 37342     A_       T  AG
                                CTT  CATTTGCTG CA  ACTGG
                                |||  |||||||||  ||  |||||
                                GAA  GTAAACGAT GT  TGACC
                                  AG        _  A_
GAM2496  PLAC1    5'  ATTTGCCCCCAGGATTGG    34750         G  A  C
                                ATTTGCT TCA GA TGG
                                ||||||| ||| || |||
                                TAAACGG GGT CT ACC
                                   G  C  A
GAM2496  RUNX1    3'  TTACATTTGCTGACATTTTATG 12034           T  AGAC_
            G                   TTACATTTGCTG CA    TGG
                                ||||||||||||  ||    |||
                                AATGTAAACGAC GT    ACC
                                      T  AAAAT
GAM2496  SLC28A2  3'  TTACATTTACTGTTACTTACTG 20111           CAAG_
                                TTACATTTGCTGT    ACTG
                                ||||||||||||     ||||
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                                AATGTAAATGACA    TGAC
                                      ATGAA
GAM2497 TBX2    3' CCGTTGACCACGGCTGGGA  25629    C      AC  GC_
                                TCG TGACCACG  GC   GA
                                ||| ||||||||  ||   ||
                                GGC ACTGGTGC  CG   CT
                                  A       __  ACC
GAM2497 ZNF268  5' CCGTTGACCACGACGGGCG  41760    C        C
                                TCG TGACCACGACG GCG
                                ||| |||||||||||| |||
                                GGC ACTGGTGCTGC CGC
                                  A         C
GAM2497 CNP     3' TTCTAGGGGCATAAGTGGTGGT 37564    CG     TGT
                                TTC  GGGGGT   GGTGGTGGT
                                |||  ||||||   |||||||||
                                AAG  TCCCCG   TCACCACCA
                                  A_     TAT
GAM2497 PIK3C2B 5' TTCTGGAGGGTTGTGACATGGT 15298    C        GT G
                                TTC GGGGGGTTGTG  G TGGT
                                ||| ||||||||||  | ||||
                                AAG CCTCCCAACAC  T ACCA
                                  A         TG _
GAM2497 PX19    3' TCTGGGGTGCTGTGGTGGTGGT 29876    C    G
                                TC GGGG GTTGTGGTGGTGGT
                                || |||| ||||||||||||||
                                AG CCCC CGACACCACCACCA
                                 A   A
GAM2497 SLC1A4  3' CTCTGGGGTGGTGGTGG    16746    C    GGTTG
                                TTC GGGG    TGGTGGTGG
                                ||| ||||    |||||||||
                                GAG CCCC    ACCACCACC
                                  A   _____
GAM2497 TOX     3' CGGGGGGCGGGGGGGTGGTGGT  31270        TGT_
                                CGGGGGGT   GGTGGTGGT
                                ||||||||   |||||||||
                                GCCCCCCG   CCACCACCA
                                     CCCC
GAM2498 BRCA1   3' CCTGGAAAGGCCACTTTG    28626          __
                                CTTGGAAAGG  ATTTTG
                                ||||||||||  ||||||
                                GGACCTTTCC  TGAAAC
                                      GG
GAM2498 CPNE3   3' TTGGAAAGATTGCCTAA     19386         ATT    A
                                TTGGAAAGG   TTGCT TAA
                                |||||||||   ||||| |||
                                AACCTTTCT   AACGG ATT
                                     ___    _
GAM2498 EDNRA   3' TTGGAAAGCATTTCTTCT    42009         G    G_
                                TTGGAAAG ATTTT  CT
                                |||||||| |||||  ||
```

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                                AACCTTTC TAAAG  GA
                                    G    AA
GAM2498  GRB10    3'  CTTGAAAAGGGTTTACC    23655         AT
                                CTTGGAAAGG  TTTGCT
                                ||||||||||  ||||||
                                GAACTTTTCC  AAATGG
                                     C_
GAM2498  OGT      5'  TGGGAAGTCAGTTGCTATAAG  18790    A   GATT
                                TGG AAG   TTGCTATAAG
                                ||| |||   ||||||||||
                                ACC TTC   AACGATATTC
                                  C   AGTC
GAM2498  TH1L     3'  CTTGGAAAGGAGTTCCCC    32307         T   G
                                CTTGGAAAGGA TTT CT
                                |||||||||| ||| ||
                                GAACCTTTCCT AAG GG
                                     C   G
GAM2498  WHSC1    3'  TTGGAGAGACACCCTGCTGTAA 39399      A   _      A
             G                   TTGGA AGG ATTTTGCT TAAG
                                |||||  ||| ||||||||  ||||
                                AACCT  TCT TGGGACGA ATTC
                                   C   G      C
GAM2498  CYP51    3'  TGTAGAACTAGATACATA    8962          TTCGCC
                                TGTAGAGCTA    ACATA
                                ||||||||||    |||||
                                ACATCTTGAT    TGTAT
                                     CTA___
GAM2498  MAFG     3'  TGCAGCCAAATTCGCCATGTGC 43133      AGCT      CATA
             CT                   TGTAG   ATTCGCCA   CCT
                                |||||   ||||||||   |||
                                ACGTC   TAAGCGGT   GGA
                                  GGTT      ACAC
GAM2499  A1BG     3'  CCATTTCCACAGCGTCCAG   39090         ACC  AA
                                CCATTTCCACA  GC  CCGG
                                ||||||||||  ||  ||||
                                GGTAAAGGTGT  CG  GGTC
                                     ___  CA
GAM2499  ADD2     5'  CCATTTCCCGCACGAGG    32725       ACAAC   ACC
                                CCATTTCC    CGCA  GG
                                ||||||||    ||||  ||
                                GGTAAAGG    GCGT  CC
                                     _____   GCT
GAM2499  CTNNB1   3'  AACCATTTTTTATAACCGCA  12515       CCAC_
                                AACCATTT    AACCGCA
                                ||||||||    |||||||
                                TTGGTAAA    TTGGCGT
                                     AAATA
GAM2499  IFNA4    3'  CATTTCCATGTTGAACCAG   34335       CAACCGC
                                CATTTCCA     AACCGG
                                ||||||||     ||||||
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                                GTAAAGGT     TTGGTC
                                    ACAAC__
GAM2499 IL1R1    3' AACCAGTTTTAACAACCG    9351       _  CC
                                AACCA TTT  ACAACCG
                                ||||| |||  |||||||
                                TTGGT AAA  TGTTGGC
                                   C   AT
GAM2499 MAP3K12  3' CATTTCCACAGCTGCCAG    26681         ACC  AA
                                CATTTCCACA   GC  CCGG
                                ||||||||||   ||  ||||
                                GTAAAGGTGT   CG  GGTC
                                      ___  AC
GAM2499 MNT      3' CACAGTGACTGCAACCGG    33704      ___  C
                                CACA   AC GCAACCGG
                                ||||   || ||||||||
                                GTGT   TG CGTTGGCC
                                  CAC  A
GAM2499 SLC7A6   3' CCATTCTCATACAGCAACCGG  19588      TC  CA  C
                                CCATT  CA  AC GCAACCGG
                                |||||  ||  || ||||||||
                                GGTAA  GT  TG CGTTGGCC
                                   GA  A_  T
GAM2499 FGF7     3' GTGTGGCTTGATTATCTGACA  12860     TAT A  A__
                                GTGT   G GC   ATTATCTGACA
                                ||||   | ||   ||||||||||
                                CACA   C CG   TAATAGACTGT
                                  ___ _  AAC
GAM2499 HTR2C    3' TGTGCTATGAGCTTGCCCTGA  9295          AATTA
                                TGTGTTATGAGC    TCTGA
                                ||||||||||||    |||||
                                ACACGATACTCG    GGACT
                                      AACG_
GAM2500 ZNF268   5' CCGTTGACCACGACGGGCG   41760     C         C
                                TCG TGACCACGACG GCG
                                ||| |||||||||| |||
                                GGC ACTGGTGCTGC CGC
                                  A         C
GAM2500 CNP      3' TTCTAGGGGCATAAGTGGTGGT 37564     CG     TGT
                                TTC  GGGGGT   GGTGGTGGT
                                |||  ||||||   |||||||||
                                AAG  TCCCCG   TCACCACCA
                                  A_     TAT
GAM2500 PIK3C2B  5' TTCTGGAGGGTTGTGACATGGT 15298     C         GT G
                                TTC GGGGGGTTGTG  G TGGT
                                ||| ||||||||||  | ||||
                                AAG CCTCCCAACAC  T ACCA
                                  A         TG _
GAM2500 PX19     3' TCTGGGGTGCTGTGGTGGTGGT 29876    C   G
                                TC GGGG GTTGTGGTGGTGGT
                                || |||| ||||||||||||||
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                                AG CCCC CGACACCACCACCA
                                 A   A
GAM2500 SLC1A4   3' CTCTGGGGTGGTGGTGG    16746    C   GGTTG
                                TTC GGGG    TGGTGGTGG
                                ||| ||||    |||||||||
                                GAG CCCC    ACCACCACC
                                  A  _____
GAM2500 TOX     3' CGGGGGGCGGGGGGGTGGTGGT 31270       TGT_
                                CGGGGGGT   GGTGGTGGT
                                ||||||||   |||||||||
                                GCCCCCCG   CCACCACCA
                                     CCCC
GAM2501 ABCA4    3' GATGGCCCGGGGTTTC     42555         TAGCTT
                                GATGGCCCGGG    GTTTC
                                ||||||||||     |||||
                                CTACCGGGCCC    CAAAG

                                       _______
GAM2501 ADCY6    3' TAGCCCCTTGTTTC      34176      GGGTAG     _
                                TGGCCC     CTTGTTT C
                                ||||||     ||||||| |
                                ATCGGG     GAACAAA G
                                   _______     A
GAM2501 COL4A6   5' GATGCTTGGAGGCTGTTTCC  37975     G CCG  TA   T
                                GATG C   GG  GCT GTTTCC
                                |||| |   ||  ||| ||||||
                                CTAC G   CC  CGA CAAAGG
                                  _ AA_  TC  _
GAM2501 COX6A1   3' GCCCGGGTAGTGGTCC     20414         CT  TT
                                GCCCGGGTAG  TG  TCC
                                ||||||||||  ||  |||
                                CGGGCCCATC  AC  AGG
                                      __  C_
GAM2501 FRAT2    3' GATGGCCCGGGAAATTCTC   28971          TAG__
                                GATGGCCCGGG    CTT
                                ||||||||||     |||
                                CTACCGGGCCC    GAG
                                       TTTAA
GAM2501 GPR81    3' TGGCCTGGAATGTTTCC     37193      C   TAGCT
                                TGGCC GGG    TGTTTCC
                                ||||| |||    |||||||
                                ACCGG CCT    ACAAAGG
                                   A  T____
GAM2501 LFG      5' GGCCCGGGTGGCCGCTT     44142         A   T
                                GGCCCGGGT GCT GTTT
                                ||||||||| ||| ||||
                                CCGGGCCCA CGG CGAA
                                      C  _
GAM2501 LILRB4   3' TGGTCCGGGCAAGGTTT     27783     C      CTT
                                TGG CCGGGTAG   GTTT
                                ||| ||||||||   ||||
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                                ACC GGCCCGTT   CAAA
                                  A       C__
GAM2501  MSF      3'  GAGGCCCCTTCCCTTGTTTCC  44729    T    GGGTAG
                                GA GGCCC     CTTGTTTCC
                                || |||||     |||||||||
                                CT CCGGG     GAACAAAGG
                                 _    GAAGG_
GAM2501  ADCY9    3'  GGTGGGCAATGGGGGGTGG   10024       GA      A
                                GGTGGG  GGTGGGG GGTGG
                                ||||||  ||||||| |||||
                                CCACCC  TTACCCC CCACC
                                   G_      _
GAM2501  AGRN     3'  GGGGTGGGGATGGGATGGGGGT 44255    A      _ TG_   A
              GG                  GG GGTGGGGA GG   GGG GGTGG
                                || |||||||| ||   ||| |||||
                                CC CCACCCCT CC   CCC CCACC
                                 _       A  CTA   _
GAM2501  AP2M1    3'  GGAGGAGGGTGGCTGGGGAGGT 19820       T   GA  _
              GG                  GGAGG GGG  GG TGGGGAGGTGG
                                ||||| |||  || ||||||||||
                                CCTCC CCC  CC ACCCCTCCACC
                                   T   A_  G
GAM2501  AR       5'  GGCGGGTGGGGAGAAGGGTGG  6237     A_        T    A
                                GG  GGTGGGGAGG GGGG GG
                                ||  |||||||||| |||| ||
                                CC  CCACCCCTCT TCCC CC
                                 GC          _    A
GAM2501  ARHC     5'  GGAGCTGGGGAGAGGGGTGG   23172      G       T    A
                                GGAG TGGGGAGG GGGG GG
                                |||| |||||||| |||| ||
                                CCTC ACCCCTCT CCCC CC
                                  G       _    A
GAM2501  ASH1     5'  GGAAGTGGGGAAGAGGGGGTGG 32977            T    A
                                GGAGGTGGGGAGG GGGG GGTGG
                                |||||||||||| |||| |||||
                                CCTTCACCCCTTC TCCC CCACC
                                                _   _
GAM2501  ASNA1    3'  GGGGTGGGGAGGGTGGAGG    41775    A        TGG
                                GG GGTGGGGAGG   GGAGG
                                || ||||||||||   |||||
                                CC CCACCCCTCC   CCTCC
                                 _         CA_
GAM2501  BAT1     3'  GGGGTGGGGGCTGTCAGGGGTG 21589    A      AG_  G   A
              G                   GG GGTGGGG   GT GGG GGTGG
                                || |||||||   || ||| |||||
                                CC CCACCCC   CA TCC CCACC
                                 _      CGA  G   _
GAM2501  BAZ2A    3'  GGGGTGGGAGGTGGGAAAA   30310    A     G
                                GG GGTGGG AGGTGGGGAGG
                                || |||||| ||||||||||
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                                CC CCACCC TCCACCCTTTT
                                  _    _
GAM2501  BMP1    3'  GGAGGTGGGGGGTTGGTG    25982         A   GGGGA
                                GGAGGTGGGG GGT    GGTG
                                |||||||||| |||    ||||
                                CCTCCACCCC CCA    CCAC
                                     _  A____
GAM2501  C5R1    3'  GGGGTGGGGGGTGGGAGG    11923    A     A     G
                                GG GGTGGGG GGTGGG AGG
                                || ||||||| |||||| |||
                                CC CCACCCC CCACCC TCC
                                  _    _    _
GAM2501  C5R1    3'  GGGGGGGGTGGGGGGTG     11922    T   A     A
                                GG GGGG GGTGGGG GGTG
                                || |||| ||||||| ||||
                                CC CCCC CCACCCC CCAC
                                  _  _     _
GAM2501  CACNB1  3'  GGAGGTGGGGGGGTGGGG     8784          A
                                GGAGGTGGGG GGTGGGG
                                |||||||||| |||||||
                                CCTCCACCCC CCACCCC
                                     _
GAM2501  CALM3   3'  GGGGTGGGGAGGTGGTGG    23238    A          _
                                GG GGTGGGGAGGTGG GG
                                || ||||||||||||| ||
                                CC CCACCCCTCCACC CC
                                  _          A
GAM2501  CD34    3'  GGAAGTGGGGGGCAGGGGTG    12119         AG TG   AG
                                GGAGGTGGGG  G  GGG  GTG
                                ||||||||||  |  |||  |||
                                CCTTCACCCC  C  CCC  CAC
                                     __ GT  __
GAM2501  CDH5    3'  GGGGGTGGGTGTGGAGGTG    12190    T   GA   G
                                GG GGG  GGTG GGAGGTG
                                || |||  |||| |||||||
                                CC CCC  CCAC CCTCCAC
                                  _  AC   A
GAM2501  COL11A2 3'  GAAGGTGGGAGGGAGGTG    38775         GAGGT
                                GGAGGTGGG    GGGGAGGTG
                                |||||||||    |||||||||
                                CTTCCACCC    TCCCTCCAC
                                     _____
GAM2501  COL5A3  3'  GGGGTGGGGAGGTGAGGCTTGG 31855    A          A___
           GTGG                    GG GGTGGGGAGGTGGGG   GGTGG
                                || ||||||||||||||   |||||
                                CC CCACCCCTCCACTCC    CCACC
                                  _           GAAC
GAM2501  DES     3'  GGAGGGCGTGGGGAGGTG    43568    T   AG
                                GG GGGG  GTGGGGAGGTG
                                || ||||  ||||||||||
```

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                                CC TCCC  CACCCCTCCAC
                                 _   G_
GAM2501  DMPK     5'  GGAGGTGGGGAAGGGGTGG   20617           T  GA
                                GGAGGTGGGGAGG GGG  GG
                                |||||||||||| |||  ||
                                CCTCCACCCCTTC CCC  CC
                                       _  A_
GAM2501  EGFL4    3'  GGAGGTGGTGGGGCTGGGGGTG 41575        _ A  G  A
           G                     GGAGGTGG GG GGT GGG GGTGG
                                |||||||| || ||| ||| |||||
                                CCTCCACC CC CCG CCC CCACC
                                    A  _  A  _
GAM2501  EGFL4    3'  GGGGTGGTGGAGGTGGTGG   41578    A   _      _
                                GG GGTGG GGAGGTGG GG
                                || ||||| |||||||| ||
                                CC CCACC CCTCCACC CC
                                 _    A       A
GAM2501  ELAVL3   3'  GGGGTGGGAGGGCAGGCGGGGT 10888    A    GA  _ _ A
           GG                    GG GGTGGG  GGT GG GG GGTGG
                                || ||||||  ||| || || |||||
                                CC CCACCC  CCG CC CC CCACC
                                 _     TC  T  G  _
GAM2501  EN1      3'  GGAGGTGGGGGGAGAAGAGGTGG 10916          A  T
                                GGAGGTGGGG GG GGGGAGGTGG
                                |||||||||| || ||||||||||
                                CCTCCACCCC CT CTTCTCCACC
                                       _ _
GAM2501  ESPN     3'  GGAGGTGGGGCCAGAGGTG   36446          AGGTGG
                                GGAGGTGGGG     GGAGGTG
                                ||||||||||     |||||||
                                CCTCCACCCC     TCTCCAC
                                     GG____
GAM2501  EYA2     3'  GGAGTTCTCGGTGGGGAGGTGG 23485      GTGGGGA
                                GGAG      GGTGGGGAGGTGG
                                ||||      ||||||||||||||
                                CCTC      CCACCCCTCCACC
                                  AAGAG__
GAM2501  FGF20    5'  GGGGTGGGATGGAGGTG     33386    A    GAGGTGG
                                GG GGTGGG      GGAGGTG
                                || ||||||      |||||||
                                CC CCACCC      CCTCCAC
                                 _     TA_____
GAM2501  HMGA2    5'  GGAGGTGGCGGTGGAGGTG   18524       GGGGA   _
                                GGAGGT    GGTGG GGAGGTG
                                ||||||    ||||| |||||||
                                CCTCCA    CCGCC CCTCCAC
                                   _____    A
GAM2501  HTR6     5'  GGAAGTGGGAACGCGGGGAGGT 9309           G
           GG                    GGAGGTGGGGA GTGGGGAGGTGG
                                |||||||||| ||||||||||||
```

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                                CCTTCACCCTT CGCCCCTCCACC
                                       G
GAM2501  HYOU1    3'  GGGGTGGGGTGAGGGGTG    40637    A     AGG    A
                                GG GGTGGGG   TGGGG GGTG
                                || |||||||   ||||| ||||
                                CC CCACCCC   ACTCC CCAC
                                 _     ___    _
GAM2501  ITGB4    5'  GGGGTTGGGGGGTGGGG     6847     A  _   A
                                GG GGT GGGG GGTGGGG
                                || ||| |||| |||||||
                                CC CCA CCCC CCACCCC
                                 _  A   _
GAM2501  KCNA6    3'  GGAGGTGGGCAGGTGGATAGAT 13816         G     GG
              GG                  GGAGGTGGG AGGTGG  AGGTGG
                                |||||||||| ||||||  ||||||
                                CCTCCACCC TCCACC  TCTACC
                                      G     TA
GAM2501  LASS1    3'  GGGGCGGGGTCCCAGGGGAGGT 34612    A     AGGT_
              GG                  GG GGTGGGG    GGGGAGGTGG
                                || |||||||    ||||||||||
                                CC CCGCCCC    CCCCTCCACC
                                 _      AGGGT
GAM2501  LLGL1    3'  GGAGGGGGGGAGGTGGCACAGG 42506      T       GG_
                                GGAGG GGGGAGGTGG   AGG
                                ||||| ||||||||||   |||
                                CCTCC CCCCTCCACC   TCC
                                   C         GTG
GAM2501  LRP1     5'  GGGGTGGGGGGCGTGGACCGG  14224    A     A   _  A_
                                GG GGTGGGG GGTG GGG  GG
                                || ||||||| |||| |||  ||
                                CC CCACCCC CCGC CCT  CC
                                 _      _   A  GG
GAM2501  LRP1     5'  GGAGGCGGGGAGGGGGGGTGG  14215          T   AG
                                GGAGGTGGGGAGG GGGG  GTGG
                                |||||||||||| ||||  ||||
                                CCTCCGCCCCTCC CCCC  CACC
                                       _  __
GAM2501  MAPRE3   3'  GGGGGTGGGGAGGGCAGGTGG  29537    A     GGT  G
                                GG GGTGGGGA   GGG AGGTGG
                                || ||||||||   ||| ||||||
                                CC CCACCCCT   CCC TCCACC
                                 C       ___   G
GAM2501  MEOX1    3'  GGGGTGGGGAGGTGGGG     30400    A
                                GG GGTGGGGAGGTGGGG
                                || ||||||||||||||
                                CC CCACCCCTCCACCCC
                                 _
GAM2501  MYLK2    3'  GGAGTGGGGAGGTGGCGG    37526     G       _
                                GGAG TGGGGAGGTGG GG
                                |||| ||||||||||| ||
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                                CCTC ACCCCTCCACC CC
                                  _        G
GAM2501  NTSR1    3'  GGAGATGGGGGAGGGGTG    14883         AGGT   A
                                GGAGGTGGGG   GGGG GGTG
                                ||||||||||   |||| ||||
                                CCTCTACCCC   CTCC CCAC
                                     _____   _
GAM2501  PCTK3    3'  GGAGGGTGGGGGGCCTGAGGTGG 43780      TG  A  GGG
                                GGAGG  GGG GGT  GAGGTGG
                                |||||  ||| |||  |||||||
                                CCTCC  CCC CCG  CTCCACC
                                   CA  _  GA_
GAM2501  PDE4A    3'  GGGGCGGGGGGGGTGAGTGG   26270    A     A    GA
                                GG GGTGGGG GGTGGG  GG
                                || ||||||| ||||||  ||
                                CC CCGCCCC CCACTC  CC
                                 _     C     A_
GAM2501  PDGFB    3'  AGGTGGGAAGGGAGGTG     15169        AGGT
                                AGGTGGGG   GGGGAGGTG
                                ||||||||   |||||||||
                                TCCACCCT   TCCCTCCAC
                                     _____
GAM2501  PDGFB    5'  GGGGCTGGGGAGGGGGGTGG  15191    A _      T   A
                                GG GG TGGGGAGG GGGG GG
                                || || |||||||| |||| ||
                                CC CC ACCCCTCC CCCC CC
                                 _ G       _   A
GAM2501  PRDM2    3'  GAAGGTGGGGAGAGAGGGGTGG 31971           T   A
                                GGAGGTGGGGAGG GGGG GGTGG
                                |||||||||||| |||| |||||
                                CTTCCACCCCTCT CTCC CCACC
                                      _   _
GAM2501  PTMS     5'  GGGGTGGGGCGGGGGTG     15896    A     AGGTG  A
                                GG GGTGGGG    GGG GGTG
                                || |||||||    ||| ||||
                                CC CCACCCC    CCC CCAC
                                 _     G_____  _
GAM2501  RCE1     3'  GGGGTGGGGGGGTGGGG      23070    A     A
                                GG GGTGGGG GGTGGGG
                                || ||||||| |||||||
                                CC CCACCCC CCACCCC
                                 _     _
GAM2501  RPA1     3'  GGGATGGGGGGGGGGTG     16369    A     AGGT   A
                                GG GGTGGGG   GGGG GGTG
                                || |||||||   |||| ||||
                                CC CTACCCC   CCCC CCAC
                                 _     _____   _
GAM2501  SDC1     3'  GGGGCTGGAATGCTGGGGAGGT 16509    A  G   GG_
           GG                     GG GGT GGGA  TGGGGAGGTGG
                                || ||| ||||  ||||||||||
```

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                                CC CCG CCTT   ACCCCTCCACC
                                 _  A   ACG
GAM2501  SLC22A5  3'  GGGAGTGGGGAAAGGGGTGG  16862    AG      T   A
                                GG  GTGGGGAGG GGGG GG
                                ||  ||||||||| |||| ||
                                CC  CACCCCTTT CCCC CC
                                 CT       _   A
GAM2501  SOD3     3'  GGTGGGTGGGGAGGGGTG    16958      GA  T   A
                                GGTGGG  GG GGGG GGTG
                                ||||||  || |||| ||||
                                CCACCC  CC CTCC CCAC
                                   AC  _   _
GAM2501  TCF2     5'  GGGGTGAGGGGGTGGGTGG   27030    A     A    GA
                                GG GGTGGGG GGTGGG  GG
                                || ||||||| ||||||  ||
                                CC CCACTCC CCACCC  CC
                                 _     C     A_
GAM2501  TCF8     3'  GGGGTGGGGAGGGGGG     36238    A       T
                                GG GGTGGGGAGG GGGG
                                || ||||||||| ||||
                                CC CCACCCCTCC CCCC
                                 _       _
GAM2501  TFAP4    3'  AGAGGTGGGGGCTGGGGGGTGG 17408         AGG    A
                                GGAGGTGGGG   TGGGG GGTGG
                                |||||||||   ||||| |||||
                                TCTCCACCCC   ACCCC CCACC
                                     CG_    _
GAM2501  ZNF278   3'  GGAGTGGGGAAAGGGGTGG   36801     G      T   A
                                GGAG TGGGGAGG GGGG GG
                                |||| |||||||| |||| ||
                                CCTC ACCCCTTT CCCC CC
                                  _      _   A
GAM2502  ADCY7    3'  ATCCTTCTAGTTTTGAAG    9980       TAGGG
                                ATCCT    TTTAGTTTTGAAG
                                |||||    ||||||||||||
                                TAGGA    AGATCAAAACTTC
                                  _____
GAM2502  ASH1     3'  CTCTGGGGTAGCTCTTGGAGC  32975    A  TT     GA_
                                CTT GGG  TAGTTTT   AGC
                                ||| |||  |||||||   |||
                                GAG CCC  ATCGAGA   TCG
                                  A  C_      ACC
GAM2502  CENTD1   3'  CTTATAGTTCAGTTTTGGAG   40138     G        A
                                CTTA GGTTTAGTTTTG AG
                                |||| |||||||||||| ||
                                GAAT TCAAGTCAAAAC TC
                                  A         C
GAM2502  DGCR6    3'  ATCCTAGGGTTTGACAGC    24982      T    ___
                                ATCCT AGGGTT   TAGT
                                ||||| ||||||   ||||
```

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                                TAGGA TCCCAA   GTCG
                                  _     ACT
GAM2502  GPR86    3'  CTAGGGCCTTTGAG       35793        TTAG     A
                                TTAGGGT    TTTTGA G
                                |||||||    |||||| |
                                GATCCCG    GAAACT C
                                   _____     C
GAM2502  IRS1     3'  TCCTTAAGGTTGAAGATGAAG  24428          TAGTTT
                                TCCTTAGGGTT     TGAAG
                                ||||||||||     |||||
                                AGGAATTCCAA     ACTTC
                                      CTTCT_
GAM2502  MKI67    3'  TCCTACTGAAAGTTTTGA    14528      TAG  TTT
                                TCCT   GG   AGTTTTGA
                                ||||   ||   ||||||||
                                AGGA   CT   TCAAAACT
                                  TGA  T__
GAM2502  PCYT1A   3'  TCCTTAGGTTTAGTGTTG    22706        G     T
                                TCCTTAGG TTTAGT TTG
                                |||||||| |||||| |||
                                AGGAATCC AAATCA AAC
                                   _     C
GAM2502  SDC2     3'  CTTTGGGTTTGCTGAG      42566     A     A  TT   A
                                CTT GGGTTT GT  TGA G
                                ||| |||||| ||  ||| |
                                GAA CCCAAA CG  ACT C
                                  A     _ __  C
GAM2502  SECTM1   3'  CCTTAGGGACGTTTTGGGGC   16540        TTTA     AA
                                CCTTAGGG    GTTTTG  GC
                                ||||||||    ||||||  ||
                                GGAATCCC    CAAAAC  CG
                                    TG__     CC
GAM2503  ERBB2IP  5'  TTGGTGGGGGTTGGGGT     33105      T   T
                                TTGGT GGG GGTTGGGGT
                                ||||| ||| |||||||||
                                AACCA CCC CCAACCCCA
                                  _   _
GAM2504  ADORA2A  3'  TGGTGTGTGGGTGGC       8609           GAGTGAT
                                TGGTGTGTGGGT      GGC
                                ||||||||||||      |||
                                ACCACACACCCA      CCG
                                          ________
GAM2504  BAZ1B    3'  TGGTATGTGGGTGGGCTGG   37097           A  GA
                                TGGTGTGTGGGTG GT  TGG
                                |||||||||||| ||  |||
                                ACCATACACCCAC CG  ACC
                                       C  __
GAM2504  C5R1     3'  TGGTGTGTGGGGGGGGGTG   11930          TGA__
                                TGGTGTGTGGG    GTG
                                ||||||||||     |||
```

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                                ACCACACACCC    CAC
                                     CCCCC
GAM2504  CSRP1    3'  GGTGTGGTGGGTGATGGTGG  19843       _     G  A
                                GGTGTG TGGGTGA TG TGG
                                |||||| ||||||| || |||
                                CCACAC ACCCACT AC ACC
                                   C      _ C
GAM2504  EFNB1    3'  GTGTGTGGAAGGGTGGCA    20728       GT   TGA
                                GTGTGTGG  GAG   TGGCA
                                ||||||||  |||   |||||
                                CACACACC  TTC   ACCGT
                                     __   CC_
GAM2504  HS3ST4   3'  GTGTGTGGGTGGGTGTG     43869         A   A
                                GTGTGTGGGTG GTG TG
                                |||||||||| ||| ||
                                CACACACCCAC CAC AC
                                     C  _
GAM2504  LGMN     5'  TGGTGGCAGTGGTGGC      24687      T  GGGTG    A
                                TGGTG GT    AGTG TGGC
                                ||||| ||    |||| ||||
                                ACCAC CG    TCAC ACCG
                                  _ _____   C
GAM2504  MAPK4    3'  TGGTGTGAGGGTGAACGCA   15673       T     TGATG
                                TGGTGTG GGGTGAG    GCA
                                ||||||| |||||||    |||
                                ACCACAC CCCACTT    CGT
                                    T     G____
GAM2504  MNT      3'  TGGTGTGTGTGTGTCCAGGTGG 33730        G   AGTGA_
                                TGGTGTGTG GTG     TGG
                                ||||||||| |||     |||
                                ACCACACAC CAC     ACC
                                     A  AGGTCC
GAM2504  POU2AF1  5'  GTGTGTGGGTGTGAAGG     26375         GA   T
                                GTGTGTGGGT  GTGA GG
                                ||||||||||  |||| ||
                                CACACACCCA  CACT CC
                                     __   T
GAM2504  RAD18    3'  TGATGTGTTTGGGCTGGGTGAT 33558        __   GA_
            GGCAG                  TGGTGTGT  GGGT   GTGATGGCAG
                                ||||||||  ||||  ||||||||||
                                ACTACACA  CCCG   CACTACCGTC
                                    AA    ACC
GAM2504  SH3GL1   3'  TGGGTGGCTGGTGGTGGCA   16678     TGT   G  A   A
                                TGG   GTGG TG GTG TGGCA
                                |||   |||| || ||| |||||
                                ACC   CACC AC CAC ACCGT
                                  ___   G  _   C
GAM2504  SH3GL1   3'  TGGGTGTGGGTGGCTGGTGG   16679     T       AG  A
                                TGG GTGTGGGTG  TG TGG
                                ||| |||||||||  || |||
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                                ACC CACACCCAC  AC ACC
                                  _       CG  C
GAM2504  SLC1A4   3'  TGGTTTTCTCTGGGGTGGTGGT 16760     GTGT____    A   A
              GG                  TGGT       GGGTG GTG TGG
                                  ||||       ||||| ||| |||
                                  ACCA       CCCAC CAC ACC
                                    AAAGAGAC    _   C
GAM2504  CDC7L1   3'  AACCTCTATCTTGGGTCCTT   18598         C____
                                  AATCTCTATC    TCCTT
                                  ||||||||||    |||||
                                  TTGGAGATAG    AGGAA
                                        AACCC
GAM2504  CSF1R    5'  CTGATCCTCTTCTTCCCCTTTT 23310    _     __
                                  CT ATCCTC  CTTCCCCTTTT
                                  || ||||||  ||||||||||
                                  GA TAGGAG  GAAGGGGAAAA
                                   C     AA
GAM2504  TAL1     5'  TCTTTGCTTTCCCCCTTTT    17291     ATC  CC
                                  TCT   CT  TTCCCCTTTT
                                  |||   ||  ||||||||||
                                  AGA   GA  AGGGGGAAAA
                                    AAC  A_
GAM2504  V1RL1    3'  AATCTCTAAAGAATTCCCTTTT 33945         TCCTCC    C
              T                    AATCTCTA     TTCCC TTTT
                                  ||||||||     ||||| ||||
                                  TTAGAGAT     AAGGG AAAA
                                       TTCTT_    A
GAM2505  FGF5     3'  CTGTGATTTATGTCCAGCA   37588      T       GCATC
                                  CTGT GATTTATG     GCA
                                  |||| ||||||||     |||
                                  GACA CTAAATAC     CGT
                                    _       AGGT_
GAM2505  PIK3CG   3'  TCCCTGTTGATTCTTCTTTGCA 15308           ATG___
                                  TCCCTGTTGATTT      GCA
                                  |||||||||||||      |||
                                  AGGGACAACTAAG      CGT
                                         AAGAAA
GAM2505  PRKCM    3'  CTGTTGATTTGTCTTGGCA   15641          A___
                                  CTGTTGATTT    TGGCA
                                  ||||||||||    |||||
                                  GACAACTAAA    ACCGT
                                        CAGA
GAM2505  TBL1X    3'  TCCCTGTTTGGTTTATCACAGC 24898         GA_    G   TC
              A                    TCCCTGTT   TTTAT GCA  GCA
                                  ||||||||   ||||| |||  |||
                                  AGGGACAA   AAATA TGT  CGT
                                       ACC    G   __
GAM2506  ADAMTS13 3'  GGGACGTGAGCTGGGTGAT    40041    A        CTA
                                  GG ACGTGGGCTG   GAT
                                  || ||||||||||   |||
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                                CC TGCACTCGAC   CTA
                                 C         CCA
GAM2506  CHD2     3'  TAAGGACTGTGGGCTGGTA   10449       AC       C
                                TAAGGA  GTGGGCTG TA
                                ||||||  |||||||| ||
                                ATTCCT  CACCCGAC AT
                                   GA       C
GAM2506  FXYD7    5'  AGGGGGCTGCTGGAT      35127     AACGT      A
                                AGG    GGGCTGCT GAT
                                |||    |||||||| |||
                                TCC    CCCGACGA CTA
                                 _____       C
GAM2506  KCND2    5'  AGAAACGTGGTCCAGA      29363         GCTG
                                AGGAACGTGG    CTAGA
                                ||||||||||    |||||
                                TCTTTGCACC    GGTCT
                                      A___
GAM2506  LIFR     3'  GGAACTAACGCTGCTAGATA   14159      GTGG
                                GGAAC    GCTGCTAGATA
                                |||||    ||||||||||
                                CCTTG    CGACGATCTAT
                                   ATTG
GAM2506  MTAP     3'  TAAAGAGAAATTGCTAGAT    14679       ACGT  GC
                                TAAGGA    GG  TGCTAGAT
                                ||||||    ||  ||||||||
                                ATTTCT    TT  ACGATCTA
                                   CT__  A_
GAM2506  NGB      3'  GGAGCCTGGGCTACAACAGATA 34587     ACG       __
            C                    GGA   TGGGCTGC  TAGATAC
                                |||   ||||||||  |||||||
                                CCT   ACCCGATG  GTCTATG
                                  CGG       TT
GAM2506  VDR      3'  TAAGGAACGTGGCTTTCAGAT  7527           G  GC
                                TAAGGAACGTGG CT  TAGAT
                                ||||||||||| ||  |||||
                                ATTCCTTGCACC GA  GTCTA
                                      _  AA
GAM2506  C18orf1  3'  TTCATTCCCACCAAATGT    41237        T  ___
                                TTCGTTCC CAC   ATGT
                                |||||||| |||   ||||
                                AAGTAAGG GTG   TACA
                                    _  GTT
GAM2506  EYA4     5'  CTCGTTCCTTCCAGTGTC     19907         CA  _
                                TTCGTTCCT  CA TGTC
                                |||||||||  || ||||
                                GAGCAAGGA  GT ACAG
                                     AG  C
GAM2506  M17S2    5'  TTCGTTCCGCAATGCATGT    36592        T  ___
                                TTCGTTCC CA   CATGT
                                |||||||| ||   |||||
```

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                                AAGCAAGG GT   GTACA
                                    C  TAC
GAM2506  MAPK4    3'  CTCGGATCCTTCACGTGT    15659      T_   _  A
                                TTCG  TCCT CAC TGT
                                ||||  |||| ||| |||
                                GAGC  AGGA GTG ACA
                                  CT    A   C
GAM2507  ALDH1B1  3'  GGAATTGCTGGACTGTGACTGG 8672         CA   ___  C
                                GGAATTGC  GGAC   GAC GG
                                ||||||||  ||||   ||| ||
                                CCTTAACG  CCTG   CTG CC
                                    A_    ACA   A
GAM2507  ASC      3'  GGGATTGCCAGGGGCTGACCGG 29943    A       AC__
                                GG ATTGCCAGG    GACCGG
                                || |||||||||    ||||||
                                CC TAACGGTCC    CTGGCC
                                 C        CCGA
GAM2507  FZD1     5'  GGGGCTGCCAGGGGCACGGCCG 18618    AA      ___  A
           G                     GG  TTGCCAGG   ACG CCGG
                                ||  ||||||||   ||| ||||
                                CC  GACGGTCC   TGC GGCC
                                 CC       CCG   C
GAM2507  PFKFB2   3'  CACCGGAATGCTGAC       26305         T  CAG
                                CACCGGAAT GC   GAC
                                |||||||||  ||   |||
                                GTGGCCTTA CG   CTG
                                    _  A__
GAM2507  PIG3     5'  CACCGGAATGGACG        22190         TGCCA
                                CACCGGAAT    GGACG
                                |||||||||    |||||
                                GTGGCCTTA    CCTGC
                                     _____
GAM2507  AVPR2    5'  GCCTGGAGGTGATGTGC     6287         ATT   GC
                                GCCTGGAG   TGG  GTGC
                                ||||||||   |||  ||||
                                CGGACCTC   ACT  CACG
                                    C__   A_
GAM2507  BCL7A    3'  TGCCTGGTGCTTGGGGCGTGC  34223        AGA  T
                                TGCCTGG   TT GGGCGTGC
                                |||||||   || ||||||||
                                ACGGACC   AA CCCGCACG
                                   ACG  C
GAM2507  CACNA1S  3'  GCCTGGAGATTTTAATG     6303           GGGC
                                GCCTGGAGATTT    GTG
                                ||||||||||||    |||
                                CGGACCTCTAAA    TAC
                                      AT__
GAM2507  COL4A3   3'  TGCCTGGACATGCTTGGTGC   36387        G __   _
                                TGCCTGGA AT  TTGG GC
                                |||||||| ||  |||| ||
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                                ACGGACCT TA  AACC CG
                                    G  CG   A
GAM2507  FLG     3'  TGCCTGGAGCTGTCTCGTGC  43364       AT  GG_
                                TGCCTGGAG  TTG  CGTGC
                                |||||||||  |||  |||||
                                ACGGACCTC  GAC  GCACG
                                    __  AGA
GAM2507  FLG     5'  TGCCTGGAGCTGTCTCGTGC  43364       AT  GG_
                                TGCCTGGAG  TTG  CGTGC
                                |||||||||  |||  |||||
                                ACGGACCTC  GAC  GCACG
                                    __  AGA
GAM2507  JAG2    5'  GCCTGGGCGGCGGGCGTGC  13723      AGATT
                                GCCTGG    TGGGCGTGC
                                ||||||    |||||||||
                                CGGACC    GCCCGCACG
                                   CGCC_
GAM2507  NEBL    3'  TGCTTGGACATTTACACA   26914    C   G   G
                                TGC TGGA ATTTG GCG
                                ||| |||| ||||| |||
                                ACG ACCT TAAAT TGT
                                  A   G   G
GAM2507  NLGN3   3'  GCCTGGAGATTGGCTGTGC  33284        TG  _
                                GCCTGGAGATT  GGC GTGC
                                ||||||||||  ||| ||||
                                CGGACCTCTAA  CCG CACG
                                    __  A
GAM2507  NOLA2   3'  TGCCTGGGAAGAAGGCGTGC  45398      A  TTT
                                TGCCTGG GA  GGGCGTGC
                                |||||||  ||  ||||||||
                                ACGGACC CT  TCCGCACG
                                   _  TCT
GAM2507  NTRK2   5'  TGCTTGTTGCGGGCGTGC   26148    C  GAGATT
                                TGC TG    TGGGCGTGC
                                |||  ||    |||||||||
                                ACG AC    GCCCGCACG
                                  A  AAC___
GAM2507  PFKFB3  5'  TGCCAGGGGAAACGTG     44440    T  A  TTTG
                                TGCC GG GA   GGCGTG
                                ||||  ||  ||   ||||||
                                ACGG CC CT   TTGCAC
                                  T  C  ____
GAM2507  PIK3CD  3'  TGCTGGGAACAGGCGTG    22737    C  A  TT
                                TGC TGG GA  TGGGCGTG
                                |||  |||  ||  ||||||||
                                ACG ACC CT  GTCCGCAC
                                  _  _  T_
GAM2507  PLAT    3'  CCTGGAGAGGCTAGTGTGC  37447       TTTG  C
                                CCTGGAGA   GG GTGC
                                ||||||||   ||  ||||
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                                GGACCTCT   TC CACG
                                    CCGA  A
GAM2507 PPP2R5A  3' GCCTGGAGATTTAAGGT    26438          C
                                GCCTGGAGATTTGGG GT
                                |||||||||||||| ||
                                CGGACCTCTAAATTC CA
                                                _
GAM2507 RGL     5' TGCTGGGCGCCCGGGTGTGC  31547    C  AGA    C
                                TGC TGG  TTTGGG GTGC
                                ||| |||  |||||| ||||
                                ACG ACC  GGGCCC CACG
                                  _  CGC    A
GAM2507 SFRP2   3' TGCTGGGGATGCAAACGTGC  43546    C  A  T GG
                                TGC TGG GAT T  GCGTGC
                                ||| ||| ||| |  ||||||
                                ACG ACC CTA G  TGCACG
                                  _  C  C TT
GAM2507 SLC14A2  3' CCTGGGGATCTGGACGGCGTGC 28396     A    ___
                                CCTGG GATTTGG  GCGTGC
                                ||||| |||||||  ||||||
                                GGACC CTAGACC  CGCACG
                                   C      TGC
GAM2507 TAT     3' TGCCTGGAGAGAGCGTG    7401         TTT
                                TGCCTGGAGA  GGGCGTG
                                ||||||||||  |||||||
                                ACGGACCTCT  CTCGCAC
                                                ___
GAM2507 TIMP3   3' TGCCTGGGCACTTGTGTG   7470       AG   GGC
                                TGCCTGG  ATTTG  GTG
                                |||||||  |||||  |||
                                ACGGACC  TGAAC  CAC
                                    CG    A__
GAM2507 TNFRSF8  3' TGCCTGGCAGGCGTG     10324       AGATT
                                TGCCTGG    TGGGCGTG
                                |||||||    ||||||||
                                ACGGACC    GTCCGCAC
                                                _____
GAM2507 TRPS1   3' TGCCTGAAGATTGTTTGC   30474          TGG_
                                TGCCTGGAGATT   GC
                                ||||||||||||   ||
                                ACGGACTTCTAA   CG
                                      CAAA
GAM2508 MEF2A   3' ATCAATTCATAAGGGTGT   24623        TACC   C
                                ATCAATTTAT   GAGGG GT
                                ||||||||||   ||||| ||
                                TAGTTAAGTA   TTCCC CA
                                                ____   A
GAM2508 NDUFS2  5' TCATCTTTACTGAGGGCGT  21239    A  A   C
                                TCA TTT TTAC GAGGGCGT
                                ||| ||| |||| ||||||||
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                                AGT AGA AATG CTCCCGCA
                                  _  _   A
GAM2508 PCDHA9   3' AATTTATTACTAAGGTGTTC  36534        CG  GCG
                                AATTTATTAC  AGG  TC
                                ||||||||||  |||  ||
                                TTAAATAATG  TCC  AG
                                     AT  ACA
GAM2509 OAT      3' TAGATGCCATTACATTATTTAG 7086          ATGATA
                                TAGATGCTATTA     ATTTAG
                                ||||||||||||     ||||||
                                ATCTACGGTAAT     TAAATC
                                      GTAA__
GAM2509 B3GALT3  5' AGATGAAATTAAAGCTTAAGTT 37668    C      TAA
             TT                   AGA GAAATTAG   TTAAGTTTT
                                ||| ||||||||  |||||||||
                                TCT CTTTAATT   AATTCAAAA
                                  A       TCG
GAM2510 ATM      3' TAAAGTATGTTGGCAGGTTAA  39635         CAAT_
                                TAAAGTATGTT    GTTAA
                                ||||||||||    |||||
                                ATTTCATACAA    CAATT
                                      CCGTC
GAM2510 PUM1     3' TACCTTTCAATGTTAATA    31235    G_
                                TAT  TTCAATGTTAATA
                                |||  ||||||||||||
                                ATG  AAGTTACAATTAT
                                  GA
GAM2510 RAD54B   3' TGAATATGTTCAGATGTC    39585   A       _
                                A AGTATGTTCA ATGTT
                                | ||||||||| |||||
                                A TTATACAAGT TACAG
                                 C        C
GAM2510 WEE1     3' AATATGCCAATCAATGTTAATA 18077       ___
             AA                   AGTATGT   TCAATGTTAATAAA
                                |||||||   ||||||||||||||
                                TTATACG   AGTTACAATTATTT
                                    GTT
GAM2511 CLN5     5' AATGTGTATTTGGAGCTGA   27075       ___
                                GATGTGT   TGGAGCTGA
                                |||||||   |||||||||
                                TTACACA   ACCTCGACT
                                    TAA
GAM2511 GBF1     3' AGGCTGCAGATGACAGCTG   20076    AT      TGTTGG
                                AG  TGCAGATG     AGCTG
                                ||  ||||||||     |||||
                                TC  ACGTCTAC     TCGAC
                                 CG       TG____
GAM2511 GPR62    3' AGGGTGCAGATGGGAAAGCTGA 44869    AT      TGTT
                                AG  TGCAGATG   GGAGCTGA
                                ||  ||||||||   ||||||||
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                                TC  ACGTCTAC    TTTCGACT
                                 CC       CC__
GAM2511  MUC3B    5'  AGTTGTGGATGTGCTGA     45337    A   CA
                                AG TTG  GATGTGTTGG
                                || |||  ||||||||||
                                TC AAC  CTACACGACT
                                 _   AC
GAM2511  MYCL1    3'  AGATGGCAGAAAGCTGGAGCTG 23885      T     TGT
            A                    AGAT GCAGA   GTTGGAGCTGA
                                |||| |||||   ||||||||||
                                TCTA CGTCT   CGACCTCGACT
                                  C    TT_
GAM2511  PDK4     5'  GACTGCAGGTGCGCTGGCTG   15204        A      GA
                                GATTGCAG TGTGTTG  GCTG
                                |||||||| |||||||  ||||
                                CTGACGTC ACGCGAC  CGAC
                                     C      __
GAM2511  PPP1R12B 3'  AGATTGGGATGGGGCT      36962       CA    TGTT  A
                                AGATTG  GATG    GG GCT
                                ||||||  ||||    || |||
                                TCTAAC  CTAC    CC CGA
                                   C_   _____ _
GAM2511  PRKY     3'  GATTACAGGTGTGAGCC     15697        AT    TG
                                GATTGCAG  GTGT  GAGCT
                                ||||||||  ||||  |||||
                                CTAATGTC  CACA  CTCGG
                                          __   __
GAM2511  S100A1   5'  AGGTTGCAAATGTGGCTGCTG  26559    A         TTGGA
                                AG TTGCAGATGTG     GCTG
                                || ||||||||||     ||||
                                TC AACGTTTACAC     CGAC
                                 C          CGA__
GAM2511  SIM2     3'  GATTACAGGTGTGAGCCACTGA 22874         A    TTGGA
                                GATTGCAG TGTG     GCTGA
                                |||||||| ||||     |||||
                                CTAATGTC ACAC     TGACT
                                     C    TCGG_
GAM2511  DDX3     3'  TTGCACTTTAGGAAATTTT   35829     ATTT
                                TTG    TTTTAGGAAATTTT
                                |||    ||||||||||||||
                                AAC    GAAATCCTTTAAAA
                                  GT__
GAM2511  ICOS     3'  ATTTGATTTCACAGAAATTTT  28998          TTTA
                                ATTTGATTTT    GGAAATTTT
                                ||||||||||    |||||||||
                                TAAACTAAAG    TCTTTAAAA
                                      TG__
GAM2511  MLLT2    3'  TTTGATTTCTCGAAATTTT   25519          TAG
                                TTTGATTTTTT   GAAATTTT
                                ||||||||||   ||||||||
```

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                                AAACTAAAGAG  CTTTAAAA
                                    ___
GAM2511 NAT2    3' TATTTGATGTTTAGGA     6145        TTT
                                TATTTGAT  TTTAGGA
                                ||||||||  |||||||
                                ATAAACTA  AAATCCT
                                    C__
GAM2512 CAV1    3' TGAAGGTTTAAGAAAAGTC   11997     A_     AACC
                                TGAAG  TTAAGAAA   AGTC
                                |||||  ||||||||   ||||
                                ACTTC  AATTCTTT   TCAG
                                  CA      ____
GAM2512 IL13RA1  3' TGGAGATTAAAAAAAAAAGTGG 11447   A         CC  C
                                TG AGATTAAGAAAAA  AGT GG
                                || ||||||||||||  ||| ||
                                AC TCTAATTTTTTTT  TCA CC
                                 C          T_  _
GAM2512 NR5A2   5' TGAAAGTTAAGAAAAAGCAA  19237     A       C
                                TGAAG TTAAGAAAAA CAG
                                ||||| |||||||||| |||
                                ACTTT AATTCTTTTT GTT
                                  C        C
GAM2513 KNSL1   3' AGCCATTAGTCAGATGTCTGGG 21175       __  TA_  C
                                AGCCATTG  CGG   TC GGG
                                ||||||||  |||   || |||
                                TCGGTAAT  GTC   AG CCC
                                    CA   TAC  A
GAM2513 MAN2B1   5' GCTGTAGCCCTGGGCAAT   8034    G  _  _
                                GC GTA TCC GGGCAAT
                                || ||| ||| |||||||
                                CG CAT GGG CCCGTTA
                                 A  C  A
GAM2513 WARS    5' GCCACTGGTCACGCTGGGCA  42622      CGG  CC_
                                GCCATTG   TAT   GGGCA
                                |||||||   |||   |||||
                                CGGTGAC   GTG   CCCGT
                                    CA_   CGA
GAM2513 AF3P21   5' TGGCAAGGGCTGCGGCGC   32405       C  C_  GA
                                TGGCAAGG GC  CGG  GC
                                |||||||| ||  |||  ||
                                ACCGTTCC CG  GCC  CG
                                    _ AC   G_
GAM2513 AFP     5' TGGCAGTGGTGGAAGCAC   10068     A_ CGCCC
                                TGGCA  GG    GGGAGCAC
                                |||||  ||    ||||||||
                                ACCGT  CC    CCTTCGTG
                                  CA  A____
GAM2513 BCL2L2   5' TGGCAAGGAGCCCCCAGC   19752       C   GGG
                                TGGCAAGG GCCC   AGC
                                |||||||| ||||   |||
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                                ACCGTTCC CGGG   TCG
                                    T   GG_
GAM2513 CBFA2T3  3' TGGCTGGGCAGGAGCA     23273     AA  GCCC
                                TGGC  GGC   GGGAGCA
                                ||||  |||   |||||||
                                ACCG  CCG   TCCTCGT
                                  AC  ____
GAM2513 CCNF     3' TGGCAAGGCAGTCCTCGC    12080        C_  GGGA
                                TGGCAAGGCG  CC   GC
                                ||||||||||  ||   ||
                                ACCGTTCCGT  GG   CG
                                     CA  AG__
GAM2513 CCR9     3' TGGCAAAGCCAGGGTGC     36300       GC  C  A
                                TGGCAAG  GCC GGG GC
                                |||||||  ||| ||| ||
                                ACCGTTT  CGG CCC CG
                                   __  T  A
GAM2513 CUTL1    3' TGGCAAAGGCAGGCTGGGG   12536      _  __ CC
                                TGGCAA GGC  GC  GGG
                                ||||||| |||  ||  |||
                                ACCGTT CCG  CG  CCC
                                   T  TC  AC
GAM2513 CYP51    3' TGGCAAGAGCGATGAGTAC   8961       _  CCC  A
                                TGGCAAG GCG   GGG GC
                                ||||||| |||   ||| ||
                                ACCGTTC CGC   CTC TG
                                   T  TA_  A
GAM2513 DISC1    3' TGGCAAGGGCTTAGCA      33054       C  CCGGG
                                TGGCAAGG GC    AGCA
                                |||||||| ||    ||||
                                ACCGTTCC CG    TCGT
                                   _ AA___
GAM2513 DTR      3' TGGCAAAGGTGGGTGGCAC   12620       CGCCC  A_
                                TGGCAAGG    GGG  GCAC
                                ||||||||    |||  ||||
                                ACCGTTTC    CCC  CGTG
                                   CA___   AC
GAM2513 EGLN2    5' TGGCAAGATGAGGTAGCAC   38840       CGCCC  _
                                TGGCAAGG    GGG AGCAC
                                ||||||||    ||| |||||
                                ACCGTTCT    TCC TCGTG
                                   AC___   A
GAM2513 EGR4     5' TGGGGCGCCCGGGGC      12679    CAA       A
                                TGG   GGCGCCCGGG GC
                                |||   |||||||||| ||
                                ACC   CCGCGGGCCC CG
                                  ___       _
GAM2513 EP300    3' GCAAGGCAGGAGCA       10985       GCCC
                                GCAAGGC   GGGAGCA
                                |||||||   |||||||
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                                CGTTCCG   TCCTCGT
                                     ____
GAM2513  FUT3    3'  TGGCAAGGTCTCTGGGAGC   6643        CGCCC
                                TGGCAAGG    GGGAGC
                                ||||||||    ||||||
                                ACCGTTCC    CCCTCG
                                    AGAGA
GAM2513  FUT5    3'  TGGCAAGGTCTCTGGGAGC   13023       CGCCC
                                TGGCAAGG    GGGAGC
                                ||||||||    ||||||
                                ACCGTTCC    CCCTCG
                                    AGAGA
GAM2513  G22P1   5'  TAGCAAGGCTATGGGGGCGC  11174        GCCC_  A
                                TGGCAAGGC    GGG GC
                                |||||||||    ||| ||
                                ATCGTTCCG    CCC CG
                                     ATACC   G
GAM2513  GNA15   5'  TGGCAAGGCTTGAGTGC    40910        GCCC   A
                                TGGCAAGGC   GGG GC
                                |||||||||   ||| ||
                                ACCGTTCCG   CTC CG
                                    AA__    A
GAM2513  GNAZ    3'  TGGCAAGGGCTCCGGCAG    13187       C _    G
                                TGGCAAGG GC CCGG AG
                                |||||||| || |||| ||
                                ACCGTTCC CG GGCC TC
                                    _ A    G
GAM2513  GRLF1   3'  TGACAAGGCGCTGCATTGGGAG 44234         CC____
                                TGGCAAGGCGC     GGGAG
                                ||||||||||      |||||
                                ACTGTTCCGCG     CCCTC
                                     ACGTAA
GAM2513  HMGA2   5'  GCGGGCACCGGGAGCAC    18522    AA     C
                                GC  GGCGCC GGGAGCAC
                                ||  |||||| ||||||||
                                CG  CCGTGG CCCTCGTG
                                 C_     _
GAM2513  HUNK    3'  TGGCAAGGCTGCCTGC      31087        _  CGGGA
                                TGGCAAGGC GCC    GC
                                ||||||||| |||    ||
                                ACCGTTCCG CGG    CG
                                    A  A_____
GAM2513  IL8     3'  TGACAAGACTGGGAG       45392        GCCC
                                TGGCAAGGC   GGGAG
                                |||||||||   |||||
                                ACTGTTCTG   CCCTC
                                    A___
GAM2513  ILF1    5'  GGCGAGGGGCGGGAGCAC    21113    A  C  CC
                                GGC AGG GC  GGGAGCAC
                                ||| ||| ||  ||||||||
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                                CCG TCC CG  CCCTCGTG
                                  C   C __
GAM2513  ILVBL    5'  TGTCACGTGACCCGGGAGC   27771    G  AGGC
                                TG CA   GCCCGGGAGC
                                || ||   ||||||||||
                                AC GT   TGGGCCCTCG
                                 A  GCAC
GAM2513  ITPKB    3'  TGGCAAGCCCCAAGGAGCA   13660       G G  C
                                TGGCAAG C CC GGGAGCA
                                ||||||| | || |||||||
                                ACCGTTC G GG TCCTCGT
                                    _ G  T
GAM2513  KCNK10   5'  TGGCAAAGCGCTGCTACCGGGC 39683          _____    A
              AC                  TGGCAAGGCGC    CCGGG GC
                                ||||||||||     ||||| ||
                                ACCGTTTCGCG    GGCCC TG
                                      ACGAT    G
GAM2513  KCNS2    5'  GGCGCTACACCTGGGAGCAC  42836    AAG    C
                                GGC   GCGCC GGGAGCAC
                                |||   ||||| ||||||||
                                CCG   TGTGG CCCTCGTG
                                  CGA    A
GAM2513  KIT      3'  TGGAAAGGTGCGAGAGCA    6901     C    C  CC
                                TGG AAGG GC  GGGAGCA
                                ||| |||| ||  |||||||
                                ACC TTCC CG  CTCTCGT
                                  T   A __
GAM2513  LIF      3'  GCTGGGGCGCCCAAGAACA   14148    AA_
                                GC   GGCGCCCGGGAGCA
                                ||   ||||||||||||||
                                CG   CCGCGGGTTCTTGT
                                 ACC
GAM2513  MAFF     5'  AACCGGGCGCCCGGGAGC    29507     AA
                                GGC  GGCGCCCGGGAGC
                                |||  ||||||||||||
                                TTG  CCGCGGGCCCTCG
                                  GC
GAM2513  MBD3     3'  GGCAGGGCCCAGGAGCAC    19420     A  C
                                GGCA GG GCCCGGGAGCAC
                                |||| || ||||||||||||
                                CCGT CC CGGGTCCTCGTG
                                   _ _
GAM2513  MSX1     3'  GCCGAGCAGGGGAGCAC     14670    AA   CCC
                                GC  GGCG   GGGAGCAC
                                ||  ||||   ||||||||
                                CG  TCGT   CCCTCGTG
                                 GC   C__
GAM2513  MSX1     5'  GGCAGAGTTCCCGGGAGCAC  14671      AG CG
                                GGCA  G  CCCGGGAGCAC
                                ||||  |  ||||||||||
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                                CCGT  C  GGGCCCTCGTG
                                  CT AA
GAM2513  NONO     3'  TGGCACAGGAGCAGGGGGCA  44362      _  C  CC   A
                                TGGCA AGG GC  GGG GCA
                                ||||| ||| ||  ||| |||
                                ACCGT TCC CG  CCC CGT
                                   G   T  TC  _
GAM2513  PACE4    5'  TAGCAAGGTTGCAGGGTAC   15060       C_  CC   A
                                TGGCAAGG  GC  GGG GC
                                ||||||||  ||  ||| ||
                                ATCGTTCC  CG  CCC TG
                                    AA  T_  A
GAM2513  PTGFRN   3'  TGGTGAGCCAGGAGGAGCAC  42603    CA  G  CCC
                                TGG  AG CG   GGGAGCAC
                                |||  || ||   ||||||||
                                ACC  TC GT   TCCTCGTG
                                  AC  G  CC_
GAM2513  PTGIS    3'  TGGTGAAGCCGAGAGCAC    9681     CA   GCC
                                TGG  AGGC   CGGGAGCAC
                                |||  ||||   |||||||||
                                ACC  TTCG   GCTCTCGTG
                                  AC   ____
GAM2513  PXN      3'  TGGAAGGGTAGGAGGAGCAC  16034    C   CGCCC
                                TGG AAGG    GGGAGCAC
                                ||| ||||    ||||||||
                                ACC TTCC    TCCTCGTG
                                  _   CATCC
GAM2513  SBF1     5'  TGGCAAGGGTGGAATGTGC   42283       CGCCC   ____
                                TGGCAAGG    GGGA   GC
                                ||||||||    ||||   ||
                                ACCGTTCC    CCTT   CG
                                    CA____   ACA
GAM2513  SCAMP3   3'  TGGCCATAGGATTGGGAGCAC  25034     A__  CGCCC
                                TGGC   AGG    GGGAGCAC
                                ||||   |||    ||||||||
                                ACCG   TCC    CCCTCGTG
                                  GTA   TAA__
GAM2513  SFRP5    3'  TGGCAGGGCAAGGAGGAG    16599      A   CCC
                                TGGCA GGCG   GGGAG
                                ||||| ||||   |||||
                                ACCGT CCGT   TCCTC
                                   C    TCC
GAM2513  SFRS7    3'  GCAAGGCGCCTCAGCA      40469         CGGG
                                GCAAGGCGCC   AGCA
                                ||||||||||   ||||
                                CGTTCCGCGG   TCGT
                                     AG__
GAM2513  SLC1A4   3'  TGGCAAGGGCAGTGC       16758        C  CC  GA
                                TGGCAAGG GC  GG  GC
                                |||||||| ||  ||  ||
```

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                                ACCGTTCC CG  TC  CG
                                   _ __  A_
GAM2513  SNAI2   5'  TGGCGGGCGCCCGGCGC    16887     AA       GA
                                TGGC  GGCGCCCGG  GC
                                ||||  |||||||||  ||
                                ACCG  CCGCGGGCC  CG
                                  C_       G_
GAM2513  SOX13   3'  TGGCAGGAAGGGGAGCAC   25017      A  CGCCC
                                TGGCA GG    GGGAGCAC
                                ||||| ||    ||||||||
                                ACCGT CC    CCCTCGTG
                                   _ TTC__
GAM2513  SPON2   5'  GGCAGGAGCAGCGGGAGC   29714     A  C  C_
                                GGCA GG GC  CGGGAGC
                                |||| || ||  |||||||
                                CCGT CC CG  GCCCTCG
                                  _ T  TC
GAM2513  TEM6    3'  TGGCAAGGAGCAGCA      35564        C  CCGGG
                                TGGCAAGG GC    AGCA
                                |||||||| ||    ||||
                                ACCGTTCC CG    TCGT
                                     T _____
GAM2513  TFPI2   5'  GGCAAGGCGTCCGAGAAAGC  45284         C    __
                                GGCAAGGCG CCGGGA  GC
                                ||||||||| ||||||  ||
                                CCGTTCCGC GGCTCT  CG
                                     A     TT
GAM2513  TPD52L2 3'  TGGCAGAGCCGGGCAC     17642      A  C   C   A
                                TGGCA GG GCC GGG GC
                                ||||| || ||| ||| ||
                                ACCGT CT CGG CCC TG
                                   _ _  _  G
GAM2513  UBE3A   5'  TGGCGGGCGCCCGCGC     39286     AA       GGA
                                TGGC  GGCGCCCG   GC
                                ||||  ||||||||   ||
                                ACCG  CCGCGGGC   CG
                                  C_       G__
GAM2513  VAV1    3'  GGCACATCCCGGGAGCAC   24074     AGGCG
                                GGCA    CCCGGGAGCAC
                                ||||    ||||||||||
                                CCGT    GGGCCCTCGTG
                                  GTA__
GAM2514  CALCR   3'  TGATATGTTCGGTTCCTGGG  11947         CA  GAC   C
                                TGATATGTTT  GT   CCT GG
                                ||||||||||  ||   ||| ||
                                ACTATACAAG  CA   GGA CC
                                     C_  A__   C
GAM2514  EHD3    3'  CACGGTTTGCTTCTGTGAC   31106         CA  _
                                CACGGTTTGCT  TG GGC
                                ||||||||||  || |||
```

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                                GTGCCAAACGA  AC CTG
                                      AG  A
GAM2514  HS3ST2   5'  GGTTTCCGAGGGGGCACCG   25815      G  CAT_
                                GGTTT CT   GGGCACCG
                                ||||| ||   ||||||||
                                CCAAA GG   CCCGTGGC
                                  _ CTCC
GAM2514  PLOD     3'  ACGGTTTGCTCTCATGAC    7156          ATG_
                                ACGGTTTGCTC   GGC
                                ||||||||||   |||
                                TGCCAAACGAG   CTG
                                      AGTA
GAM2514  PTPN1    3'  CACGGTCTGCTCAAGAAGAGTG 15899          T___  CACC
            TTGAC                  CACGGTTTGCTCA   GGG   GAC
                                ||||||||||||   |||   |||
                                GTGCCAGACGAGT   CTC   CTG
                                       TCTT  ACAA
GAM2514  PTPRK    3'  ACAGTTTGCTCAAATTTGAC  15964          TG___
                                ACGGTTTGCTCA   GGC
                                ||||||||||   |||
                                TGTCAAACGAGT   CTG
                                      TTAAA
GAM2515  CACNB1   3'  ATGGGGGGCTCAGATGCAGA  8775      ACATA_
                                GTGG    TAGATGCAGA
                                ||||    ||||||||||
                                TACC    GTCTACGTCT
                                  CCCCGA
GAM2515  CHAC     3'  ATAAATGGACATATGGGCA   37812          AGAT
                                ATAAGTGGACATAT   GCA
                                ||||||||||||   |||
                                TATTTACCTGTATA   CGT
                                       CC__
GAM2515  GGCX     3'  ACAAGTGGCAGGGTGCAG    9059        A  TATAGA
                                ATAAGTGG CA    TGCAG
                                |||||||| ||    |||||
                                TGTTCACC GT    ACGTC
                                    _ CCC___
GAM2515  ITPKB    3'  GTGGACAGATGCAGA      13651       TATA
                                GTGGACA   GATGCAGA
                                |||||||   ||||||||
                                CACCTGT   CTACGTCT
                                    ____
GAM2515  KCNAB1   3'  TAAGTGGACATAACATTAGA  41404          ____
                                TAAGTGGACATA   TAGA
                                ||||||||||||   ||||
                                ATTCACCTGTAT   ATCT
                                       TGTA
GAM2515  KLRC4    5'  ATAAGTGGTGTATATTTTGACA 30236        ACA   GA_ _
            G                   ATAAGTGG   TATA   TG CAG
                                ||||||||   ||||   || |||
```

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                                TATTCACC  ATAT  AC GTC
                                    AC_   AAA  T
GAM2515  MDM1    3'  GTGGACATGAACCAGA     33517       ATA  TG
                                GTGGACAT  GA  CAGA
                                ||||||||  ||  ||||
                                CACCTGTA  CT  GTCT
                                    ___  TG
GAM2515  MLF2    3'  CAAGTCAGTAGATGCAGA    24142     _  ACATA
                                TAAGT GG    TAGATGCAGA
                                ||||| ||    ||||||||||
                                GTTCA TC    ATCTACGTCT
                                  G  _____
GAM2515  NR1I2   3'  GTGTTCAAATGGATGCAGA   35107    GA  T  A
                                GTG  CA AT GATGCAGA
                                |||  || || ||||||||
                                CAC  GT TA CTACGTCT
                                  AA  T  C
GAM2515  OGDH    3'  AATGGACACTGCAG       45008        ATAGA
                                AGTGGACAT    TGCAG
                                |||||||||    |||||
                                TTACCTGTG    ACGTC
                                    _____
GAM2515  SCA1    3'  AAGTGGACATAGTACAGA    7270         TA  A
                                AAGTGGACA  TAG TGCAGA
                                |||||||||  ||| ||||||
                                TTCACCTGT  ATC ATGTCT
                                    __  _
GAM2515  ACOX3   3'  AATTTCTTTTCCACGGTGCA  18596         _  A
                                AATTTCTTTTC ACG TGCA
                                |||||||||||| ||| ||||
                                TTAAAGAAAAG TGC ACGT
                                     G  C
GAM2515  DMRT2   3'  AATTTCTTTACACAAACATCTT 27256        T   T
          A                      AATTTCTTT CACGA GCATCTTA
                                |||||||||  ||||| ||||||||
                                TTAAAGAAA GTGTT TGTAGAAT
                                    T   _
GAM2515  DYRK2   3'  AATTTTTTTCACGTGC     27034      C      A
                                AATTT TTTTCACG TGC
                                |||||  ||||||||  |||
                                TTAAA AAAAGTGC ACG
                                  _      _
GAM2515  F8      5'  AATTTCTTTGCAGAGCAT    6561         T  C  T
                                AATTTCTTT CA GA GCAT
                                |||||||||  ||  ||  ||||
                                TTAAAGAAA GT CT CGTA
                                    C  _  _
GAM2515  NPAT    3'  ATTTCTCTTTTTACATCTTA  42611        CACGA
                                ATTTCTTTT    TGCATCTTA
                                |||||||||    |||||||||
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                              TAAAGAGAA    ATGTAGAAT
                                   AA___
GAM2515 SOX11    3' AATTTCTTTGCGTCACGACATC 17000        ___    AT
            TTA                  AATTTCTTT   TCACG  GCATCTTA
                                 |||||||||   |||||  ||||||||
                                 TTAAAGAAA   AGTGC  TGTAGAAT
                                     CGC    __
GAM2516 AKAP2    3' TCTTAAGCTTTTCTC      28503       T   TGTTAG
                                 TCTTAAG CTTT     TCTC
                                 ||||||| ||||     ||||
                                 AGAATTC GAAA     AGAG
                                     _   _______
GAM2516 CDC7L1   3' TCTTGGGTCCTTTTCTCT    18604     AA     GTTAG
                                 TCTT  GTCTTTT    TCTCT
                                 ||||  |||||||    |||||
                                 AGAA  CAGGAAA    AGAGA
                                   CC     ______
GAM2516 FZD10    3' TCTTAGTTCTTTTGTTAG    28461      AG
                                 TCTTA  TCTTTTGTTAG
                                 |||||  ||||||||||||
                                 AGAAT  AGAAAACAATC
                                    CA
GAM2516 LAD1     3' TCTAAGGTCTCATCAGTCTCTT 24493     TAA    TT
                                 TCT   GTCTT  GTTAGTCTCTT
                                 |||   |||||  ||||||||||||
                                 AGA   CAGAG  TAGTCAGAGAA
                                   TTC    __
GAM2516 LGS      3' CTTAAGTCTTTTTTTTCT    32443          GTTAG
                                 CTTAAGTCTTTT    TCT
                                 ||||||||||||    |||
                                 GAATTCAGAAAA    AGA
                                       AAA__
GAM2517 CGTHBA   3' AGCTAGCTCTTCCTCCAG    28958          ATAACG
                                 AGCTAGTTCTTC     TCCAG
                                 ||||||||||||     |||||
                                 TCGATCGAGAAG     AGGTC
                                       G_____
GAM2517 CIT      3' AGCTAGTTCTATATAGCAG   43037         TC   ACGTC
                                 AGCTAGTTCT  ATA    CAG
                                 |||||||||  |||    |||
                                 TCGATCAAGA  TAT    GTC
                                      TA   C____
GAM2517 LPIN1    3' GCCTGGACCCGGTGGCGTCCAG 42639     AGTT   CATAA
            A                     GCT    CTT    CGTCCAGA
                                  |||    |||    ||||||||
                                  CGG    GGG    GCAGGTCT
                                    ACCT   CCACC
GAM2517 PIP5K1B  3' AGCTAGTTTTCTATAAAGT   18663        C   _    C
                                 AGCTAGTT TTC ATAA GT
                                 ||||||||  ||| |||| ||
```

```
                                TCGATCAA AAG TATT CA
                                    _  A   T
GAM2517  CCNT2    3'  TGAGATTAAACTCTAATATTTA 38497   T   ____
                CA                  A AGGTT   TCTAATATTTACA
                                    | |||||   ||||||||||||||
                                    A TCTAA   AGATTATAAATGT
                                     C    TTTG
GAM2517  ESRRA    3'  TGAGATAGGTTTCTGCCTCCCA 20838   TA       AATA
                C                    TG  ATAGGTTTCT   TTTAC
                                    ||  ||||||||||   |||||
                                    AC  TATCCAAAGA   GGGTG
                                     TC        CGGA
GAM2518  ABCA3    3'  TGGGACGGTGCCCGGC     9904    AT      AGCCC
                                    TG  ACGGTGCC    TGGC
                                    ||  ||||||||    ||||
                                    AC  TGCCACGG    GCCG
                                     CC      _____
GAM2518  ACN      3'  GGTGACCCAGTCCTGGCCCC   31412     __   C
                                    GGTG  CCAG CCTGGCCCC
                                    ||||  |||| |||||||||
                                    CCAC  GGTC GGACCGGGG
                                      TG   A
GAM2518  CBS      5'  TGAAACGTGCGTCCTGGCCC   6310     T   G   CAGC
                                    TGA ACG TGC    CCTGGCCC
                                    ||| ||| |||    ||||||||
                                    ACT TGC ACG    GGACCGGG
                                      T   _   CA__
GAM2518  CD34     3'  TGAGCTATAGCCCTGGCC    12122   C   GCC
                                    A GGT   AGCCCTGGCC
                                    | |||   ||||||||||
                                    A TCG   TCGGGACCGG
                                     C   ATA
GAM2518  CHRNB4   5'  AGCGCCGGTCCTGGCCCC    8866       AGC
                                    GGTGCC   CCTGGCCCC
                                    ||||||   |||||||||
                                    TCGCGG   GGACCGGGG
                                       CCA
GAM2518  DBN1     5'  GGCGGGGCGCCCTGGCCCC    38938     CCA_
                                    GGTG    GCCCTGGCCCC
                                    ||||    ||||||||||
                                    CCGC    CGGGACCGGGG
                                      CCCG
GAM2518  ENG      5'  TGACAGCAGCAGTCCTGGCCCC 6507    T    GC   C
                                    A ACGGT  CAG CCTGGCCCC
                                    | |||||  ||| |||||||||
                                    A TGTCG  GTC GGACCGGGG
                                     C    TC   A
GAM2518  ESRRA    3'  GATGGCATTGCCCTGGCCC    20831     C __
                                    GGTG CA  GCCCTGGCCC
                                    |||| ||  ||||||||||
```

```
                                CTAC GT  CGGGACCGGG
                                  C  AA
GAM2518 GGA1     3'  GGGCCTGAGGTCCTGGCCC   30047    T  __ C_
                                GG GCC  AG  CCTGGCCC
                                || |||  ||  ||||||||
                                CC CGG  TC  GGACCGGG
                                 _   AC  CA
GAM2518 MAP3K11  5'  GGCATCCGGGCCCTGGCCC   14534     _ A_
                                GGTG CC  GCCCTGGCCC
                                |||| ||  ||||||||||
                                CCGT GG  CGGGACCGGG
                                  A  CC
GAM2518 MTM1     3'  TAATGCGGTGCCAGGGTCCC   7006      A       CCCT  _
                                TGAT CGGTGCCAG    GG CCC
                                |||| |||||||||    || |||
                                ATTA GCCACGGTC    CC GGG
                                  C        _____  A
GAM2518 MYO1A    5'  GGGGCATAAGAGTCCTGGCCCC 23922    T  C____  C
                                GG GC     AG CCTGGCCCC
                                || ||     || |||||||||
                                CC CG     TC GGACCGGGG
                                 C  TATTC  A
GAM2518 PACSIN1  3'  CGGTGGGGCAGCCCTGGTTCC  45147      C__       CC
                                CGGTG   CAGCCCTGG  CC
                                |||||   |||||||||  ||
                                GCCAC   GTCGGGACC  GG
                                   CCC        AA
GAM2518 RNPEPL1  3'  GGTGTGTGCGGGCTGGCCCC   32888     CCA  C__
                                GGTG   GC   CTGGCCCC
                                ||||   ||   ||||||||
                                CCAC   CG   GACCGGGG
                                  ACA  CCC
GAM2518 RP2      3'  AATACCAAGTCCTGGTC     27929        _ C     CC
                                GGTGCCA G CCTGG  C
                                ||||||| | |||||  |
                                TTATGGT C GGACC  G
                                    T A    AA
GAM2518 TNXB     5'  CACAGGCTCTGGCCCC      37148       TGCCA  C
                                TACGG     GC CTGGCCCC
                                |||||     || ||||||||
                                GTGTC     CG GACCGGGG
                                   _____  A
GAM2518 VHL      3'  TGATCTGCCTGCCCTGGCC   8120       ACGG    A
                                TGAT    TGCC GCCCTGGCC
                                ||||    |||| |||||||||
                                ACTA    ACGG CGGGACCGG
                                  G___    A
GAM2519 ADAM22   5'  CCGCCGAGTCCGTTTCCCTC   20083         _   __
                                CCGCCGAG CCGT  TCCTC
                                |||||||| ||||  |||||
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                              GGCGGCTC GGCA  GGGAG
                                   A   AA
GAM2519  ADRA1D   3'  GCCCAGTTCCTCAGGGA    8616     G GCC
                              GCC A  GTTCCTCAGGGA
                              ||| |  ||||||||||||
                              CGG T  CAAGGAGTCCCT
                                G ___
GAM2519  ANK1     5'  CCGCCGAAGGGCCTTGGGG   33856       CCGTT  CA
                              CCGCCGAG   CCT  GGG
                              ||||||||   |||  |||
                              GGCGGCTT   GGA  CCC
                                   CCC__  AC
GAM2519  ANK1     5'  CCCCTGAGTCCCCCAGGGAC  33854   G  GAGCC
                              CC CC   GTTCCTCAGGGAC
                              || ||   ||||||||||||
                              GG GG   CAGGGGGTCCCTG
                               _ ACT__
GAM2519  AP1G1    3'  GCTGCTTATTTCCTCAGGG   10049   CGA  CG__
                              GC  GC   TTCCTCAGGG
                              ||  ||   ||||||||||
                              CG  CG   AAGGAGTCCC
                               A__ AATA
GAM2519  ARHGAP6  3'  CCACCGAGGCCAATTTGGGGAC 30210       _  TTCCTCA
                              CCGCCGAG CCG     GGGAC
                              |||||||| |||     |||||
                              GGTGGCTC GGT     CCCTG
                                   C  TAAAC__
GAM2519  CDC25B   3'  GACCCATCCTCAGGGAC    34847   G   T
                              GA CCGT CCTCAGGGAC
                              || |||| ||||||||||
                              CT GGTA GGAGTCCCTG
                               G  _
GAM2519  CYP1B1   5'  CGCCGAGCCCCGCTGCCCTTGG 6447        __  _  CA_
           GGAC                   CGCCGAGCC  GTT CCT   GGGAC
                              |||||||||  ||| |||  |||||
                              GCGGCTCGG  CGA GGG   CCCTG
                                   GG  C   AAC
GAM2519  DDX26    5'  GAGAAGTTTCAGGGAC     29093    CC   CC
                              GAG  GTT  TCAGGGAC
                              |||  |||  ||||||||
                              CTC  CAA  AGTCCCTG
                                TT  __
GAM2519  DTX1     5'  CCGCCACTGCCTCAGGG     20649      AGCCGTT
                              CCGCCG     CCTCAGGG
                              ||||||     ||||||||
                              GGCGGT     GGAGTCCC
                                 GAC_____
GAM2519  EGLN3    5'  CCGCTGCAGCGTCGGGGA    35206     CGA  C  TCC  A
                              CCGC   GC GT   TC GGGA
                              ||||   || ||   || ||||
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                              GGCG  CG CG  AG CCCT
                                A__  T  C__  C
GAM2519  EN2     5'  CCGCCGAGTCTTCCGAGGG   10936       CCG   TC
                              CCGCCGAG  TTCC  AGGG
                              ||||||||  ||||  ||||
                              GGCGGCTC  AAGG  TCCC
                                  AG_   C_
GAM2519  FBXL7   3'  GCTGAGCTGTTTCCCCAG    29405    C   CG_
                              GC GAGC  TTCCTCAG
                              || ||||  ||||||||
                              CG CTCG  AAGGGGTC
                               A   ACA
GAM2519  GNAI2   3'  CCCCCATCTTCCTCAGGG    42646    G  AGCCG
                              CC CCG    TTCCTCAGGG
                              || |||    ||||||||||
                              GG GGT    AAGGAGTCCC
                               G  AG___
GAM2519  ID3     3'  CCGCCGAGCGTGCCGAGGCGGG 44270        C  T  TCA__
                              CCGCCGAGC GT CC    GGG
                              ||||||||| || ||    |||
                              GGCGGCTCG CA GG    CCC
                                   _ C  CTCCG
GAM2519  IHPK1   3'  GCCAAGCCCACCAGGG      45489       GTT C
                              GCCGAGCC  C TCAGGG
                              ||||||||  | ||||||
                              CGGTTCGG  G GGTCCC
                                  ___ T
GAM2519  IL27    3'  GCTGGCCCTTTCAGGGAC    42107    CGA  G  CC
                              GC  GCC TT  TCAGGGAC
                              ||  ||| ||  ||||||||
                              CG  CGG AA  AGTCCCTG
                               AC_  G  __
GAM2519  KRT1    3'  GCTGAACTGTTTCTCAGGGA  25938    C   C   C
                              GC GAGC GTT CTCAGGGA
                              || |||| ||| ||||||||
                              CG CTTG CAA GAGTCCCT
                               A   A  A
GAM2519  LAMA5   5'  CCCCGAGCTCCAGGGA     24497    G    CGT  TC
                              CC CCGAGC  TCC  AGGGA
                              || ||||||  |||  |||||
                              GG GGCTCG  AGG  TCCCT
                                _    ____  __
GAM2519  LSS     3'  CGCTGTGCCTCCTCAGGG    14248    CGA  GT
                              CGC  GCC  TCCTCAGGG
                              |||  |||  |||||||||
                              GCG  CGG  AGGAGTCCC
                                ACA  __
GAM2519  MALT1   5'  CCTCCGAGCCGCGGAGGCAGGG 27692    G       TCCT_
                              CC CCGAGCCGT    CAGGG
                              || |||||||||    |||||
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                                GG GGCTCGGCG    GTCCC
                                 A       CCTCC
GAM2519 NFKB1    5' CGCCGGGCCGCTCCGG     19650      A      TCA
                                CGCCG GCCGTTCC   GG
                                ||||| ||||||||   ||
                                GCGGC CGGCGAGG   CC
                                   C      ___
GAM2519 NFKBIB   5' CCGCCGCCTCAGGG       14766       AGCCGTT
                                CCGCCG     CCTCAGGG
                                ||||||     ||||||||
                                GGCGGC     GGAGTCCC
                                          ________
GAM2519 PPP2R2B  3' CCAGCCTTTCTCAGGGA    21330    G   G   C
                                CC AGCC TTC TCAGGGA
                                || |||| ||| |||||||
                                GG TCGG AAG AGTCCCT
                                 _   A   _
GAM2519 PRKCABP  3' CCGCCGAGGTGTGATGGGGAC 29669        CC  TCCTCA
                                CCGCCGAG  GT     GGGAC
                                ||||||||  ||     |||||
                                GGCGGCTC  CA     CCCTG
                                     CA  CTAC__
GAM2519 PSD      5' CGCGGTAGCACCTCAGGG    15783     CG_  CGTT
                                CGC   AGC   CCTCAGGG
                                |||   |||   ||||||||
                                GCG   TCG   GGAGTCCC
                                  CCA   T___
GAM2519 RANBP3   3' GCCGACTCAGCCAGGGAC    28759     _  C_
                                GCCG TTC  TCAGGGAC
                                |||| |||  ||||||||
                                CGGC GAG  GGTCCCTG
                                   T   TC
GAM2519 RFC4     5' CCGCCGGCTCGTTCCTCAGG   16286       A  _
                                CCGCCG GC CGTTCCTCAGG
                                |||||| || ||||||||||
                                GGCGGC CG GCAAGGAGTCC
                                   _ A
GAM2519 RXRA     3' CCAGCCGGGCCAAGGCGGGGAC 16416    _   A   TTCCTCA
                                CC GCCG GCCG      GGGAC
                                || |||| ||||      |||||
                                GG CGGC CGGT      CCCTG
                                 T   C   TCCGC__
GAM2519 SRRM2    5' CCTCCTCGCTTCCTCAGGG   32273    G  GA  CG
                                CC CC  GC  TTCCTCAGGG
                                || ||  ||  ||||||||||
                                GG GG  CG  AAGGAGTCCC
                                 A AG  __
GAM2519 TEM8     5' CGCCACGACCCTCAGGGAC   38178      AGC  TT
                                CGCCG   CG  CCTCAGGGAC
                                |||||   ||  ||||||||||
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                                GCGGT  GC  GGAGTCCCTG
                                   ___ TG
GAM2520 COL10A1  3'  TTCACATACGTTTTTACGTTGC 7966          CTGGCC  C
                                TTCACGTACGTT     CG TGC
                                ||||||||||||     || |||
                                AAGTGTATGCAA     GC ACG
                                       AAAT__  A
GAM2520 GRB14    5'  CGCGAGGCCGGGACCGCCGC  21030     C  TCGA  A
                                CGC GA   CC GGACCGCCGC
                                ||| ||   || ||||||||||
                                GCG CT   GG CCTGGCGGCG
                                  _ CC__  C
GAM2521 C9       3'  GCATGTTGCTATTTA      11931       TCCG
                                GCATGTT   GTTATTTA
                                |||||||   ||||||||
                                CGTACAA   CGATAAAT

                                   _____
GAM2521 NT5C2    3'  TAATGCATGTTCTGTAGT    29233          CC_
                                TAATGCATGTTT   GGT
                                ||||||||||||   |||
                                ATTACGTACAAG   TCA
                                       ACA
GAM2522 CEACAM6  3'  TTTGGATCTATCTTCTTCCTTA 14736       _    GTG  C_
           ACAT                    TTTGGATT ATCTT   CC  AACAT
                                ||||||||| |||||   ||  |||||
                                AAACCTAG TAGAA   GG  TTGTA
                                     A    GAA  AA
GAM2522 CELSR1   3'  TTTGGTCTGTGCCC       30657      ATTA   T
                                TTTGG    TCT GTGCCC
                                |||||    ||| ||||||
                                AAACC    AGA CACGGG

                                   _____  _
GAM2522 SRGAP2   3'  TTTGGATTTTCCCCAATCCAAC 43995        A   GTGC
           AT                     TTTGGATT TCTT    CCAACAT
                                ||||||||| ||||    |||||||
                                AAACCTAA AGGG    GGTTGTA
                                     A   GTTA
GAM2523 IGF2R    3'  TCTCAAACCTGAGTAATT    9343     _     TTGCAC
                                TCT AAACCT     GAGTAATT
                                ||| ||||||     ||||||||
                                AGA TTTGGA     CTCATTAA
                                  G    _______
GAM2523 ING1     3'  TAAACCTTTGTTACTGAAT   24397         C_ _
                                TAAACCTTTG  AC GAGT
                                ||||||||||  || ||||
                                ATTTGGAAAC  TG CTTA
                                       AA  A
GAM2523 KCNJ4    5'  TCTGGGCCTTTGCACTGGC   22541     AAA       GA
                                TCT   CCTTTGCAC  GT
                                |||   |||||||||  ||
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                                AGA  GGAAACGTG  CG
                                  CCC       AC
GAM2523  PRKY    3'  TCTACATTTTGCACAGTGATT  15710     AACC     G  A
                                TCTA   TTTGCAC AGT ATT
                                ||||   ||||||| ||| |||
                                AGAT   AAACGTG TCA TAA
                                  GTA_     _  C
GAM2523  ST14    3'  CAAACCTTTGCCCCCAGT   35058         ACG_
                                TAAACCTTTGC   AGT
                                ||||||||||   |||
                                GTTTGGAAACG   TCA
                                      GGGG
GAM2523  TGFBR2  3'  TCCAAACCTTTGCATGTA   17483           CGA
                                TCTAAACCTTTGCA  GTA
                                ||||||||||||||  |||
                                AGGTTTGGAAACGT  CAT
                                       A__
GAM2523  TMEM2   3'  AACCCTTACAAGTAATT    30146         CG
                                AACCTTTGCA  AGTAATT
                                ||||||||||  |||||||
                                TTGGGAATGT  TCATTAA
                                       __
GAM2523  CD1B    5'  TGGCAGAGCTGGTATTTG    12084    A    GTGCCA
                                TGG AGAGC     GGTATTTG
                                ||| |||||     ||||||||
                                ACC TCTCG     CCATAAAC
                                  G    A_____
GAM2523  RASA1   3'  TGGAAAAGTGTGCTATTTTTTG 35489        C   CAGGTA
                                TGGAAGAG GTGC     TTTG
                                |||||||| ||||     ||||
                                ACCTTTTC CACG     AAAC
                                     A   ATAAA_
GAM2523  SLC10A1 3'  TGGAATGGGATTTGGGTATTTG 16810      GAGCGTGCCA
           A                     TGGAA        GGTATTTGA
                                |||||         |||||||||
                                ACCTT         CCATAAACT
                                   ACCCTAAAC_
GAM2524  APTX    5'  TTGACATATCCCTTGTTACAC  32813         G    T
                                TTGACATATCC TTGTT CAC
                                |||||||||| ||||| |||
                                AACTGTATAGG AACAA GTG
                                       G    T
GAM2524  EGFL4   3'  GACATGGGGTTTCACCA    41570      ATCCGTT
                                GACAT      GTTTCACCA
                                |||||      |||||||||
                                CTGTA      CAAAGTGGT
                                   CCC____
GAM2524  NKX3A   3'  TTCACTGTCTCTGTTGTTTCA  26119   G  ATA_  C
                                TT AC   TC GTTGTTTCA
                                || ||   || |||||||||
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                                AA TG    AG CAACAAAGT
                                 G  ACAG  A
GAM2524  PAH      3'  TTGACTTATTTGTTGTTTCTCC 7097       A   CC       A
              AT                   TTGAC TAT  GTTGTTTC CCAT
                                   ||||| |||  |||||||| ||||
                                   AACTG ATA  CAACAAAG GGTA
                                     A   AA       A
GAM2524  PDE4D    3'  TTGACATATTTGTTGCTTC    43904         CC
                                   TTGACATAT  GTTGTTTC
                                   |||||||||  ||||||||
                                   AACTGTATA  CAACGAAG
                                        AA
GAM2525  ADAMTS13  3'  GAGCTGGGCTCTGACA      40034        T    GCTA
                                   GAGCTGG GCTT    GACA
                                   ||||||| ||||    ||||
                                   CTCGACC CGAG    CTGT
                                      _    A___
GAM2525  B4GALT5   3'  AGCTGGTAATGTAGGCAC    21935         CT  C   A
                                   AGCTGGTG  TG TAG CAC
                                   ||||||||  || ||| |||
                                   TCGACCAT  AC ATC GTG
                                        T_ _   C
GAM2525  EGR4      3'  CGAGCTGGTGCTGAATAG    12674           TGC
                                   CGAGCTGGTGCT   TAG
                                   ||||||||||||   |||
                                   GCTCGACCACGA   ATC
                                          CTT
GAM2525  FMR2      3'  CGAGCTGGTTGTTAAACA    12957         GCT  C
                                   CGAGCTGGT   TG TAGACA
                                   |||||||||   || ||||||
                                   GCTCGACCA   AC ATTTGT
                                        ___  A
GAM2525  GYPC      3'  GAGCTGATGTTGTCCTGC    13325         ____
                                   GAGCTGGTG    CTTGC
                                   |||||||||    |||||
                                   CTCGACTAC    GGACG
                                        AACA
GAM2525  KCNK3     3'  CGGCTGGTGCAAGCAGGCAC   13904    A       TT  T  A
                                   CG GCTGGTGC  GC AG CAC
                                   || ||||||||  || || |||
                                   GC CGACCACG  CG TC GTG
                                    _       TT  _  C
GAM2525  S100A10   5'  CGAGCTGGGCGAGCTGGAC   40390         T  TT   A
                                   CGAGCTGG GC  GCT GAC
                                   |||||||| ||  ||| |||
                                   GCTCGACC CG  CGA CTG
                                        _ CT   C
GAM2525  SHANK2    3'  ACAAGCTGGTGGGATTCCTAGA 29447           C__  G
              CAC                    ACGAGCTGGTG   TT CTAGACAC
                                   ||||||||||   || ||||||||
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                                TGTTCGACCAC   AA GATCTGTG
                                      CCT  G
GAM2525  SMTN     3'  CGGGCGGGCAGGCTAGACA   39521    A  T  T  TT
                                CG GC GG GC  GCTAGACA
                                || || || ||  ||||||||
                                GC CG CC CG  CGATCTGT
                                 C  _  _  TC
GAM2525  TPK1     3'  AGCCCTTGTTGTTAGACA    35353     GG  C   C
                                AGCT  TG TTG TAGACA
                                ||||  || ||| ||||||
                                TCGG  AC AAC ATCTGT
                                  GA  _   A
GAM2525  LUM      5'  TTTGGCAAATGGTTTGAATCC  14273        TAGTCCG  T
                                TTTGGCAA      TG AATCC
                                ||||||||      || |||||
                                AAACCGTT      AC TTAGG
                                     TACCAA_  _
GAM2525  TCFL4    3'  TTTGGCAATATTTATTATAAT  41833         GTCCG
                                TTTGGCAATA    TGTAAT
                                ||||||||||    ||||||
                                AAACCGTTAT    ATATTA
                                      AAATA
GAM2526  APPBP2   3'  CTAGATATCTATATATAGGA   26878        AGT  _
                                TTAGATAT   TA ATAGGA
                                ||||||||   || ||||||
                                GATCTATA   AT TATCCT
                                     GAT  A
GAM2526  GCLC     3'  TTAGATATGTTATTAAAATACA 11297        A   A    C
              T                  TTAGATAT GTTA TAGGA ACAT
                                ||||||||| |||| ||||| ||||
                                AATCTATA CAAT ATTTT TGTA
                                     _   A    A
GAM2526  NRG1     3'  TTAGATCTGGTAAGACACA   30352       ATAGTTAA
                                TTAGAT       TAGGACACA
                                ||||||       |||||||||
                                AATCTA       ATTCTGTGT
                                   GACC____
GAM2526  RB1      3'  GAAGATAGATAGGACACAT   44934    T_   TTA
                                GA  ATAG   ATAGGACACAT
                                ||  ||||   ||||||||||
                                CT  TATC   TATCCTGTGTA
                                 TC   ___
GAM2526  SMARCC2  3'  TTAGAAGTGGTTAATAGAAC  40075      TATA
                                TTAGA   GTTAATAGGAC
                                |||||   ||||||||||
                                AATCT   CAATTATCTTG
                                   TCAC
GAM2527  CARP     3'  TTTAAGAACTACCTATGGGT  30798        CAAG   A
                                TTTAAGAAC    TGTG GGT
                                |||||||||    |||| |||
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                                AAATTCTTG   ATAC CCA
                                     ATGG   _
GAM2527  CHST7    3'  TTTAAAAATCAGTTCTGGGTAG 33390        CCA  G_  A
             A                    TTTAAGAA  AGT  TG GGTAGA
                                  ||||||||  |||  || ||||||
                                  AAATTTTT  TCA  AC CCATCT
                                      AG_   AG  _
GAM2527  CYP1A2   3'  TTTAAGAATGTAAGTTAG    8919        ACCAA     G
                                  TTTAAGA    GTGTGAG TAG
                                  |||||||    ||||||| |||
                                  AAATTCT    TACATTC ATC
                                      _____      A
GAM2527  CYP1A2   3'  GAAGCCAAGGCAGGTGGA    8914     _    T  G   A
                                  GAA CCAAG GT AGGT GA
                                  ||| ||||| || |||| ||
                                  CTT GGTTC CG TCCA CT
                                    C    _ _   C
GAM2527  LMO7     3'  TTTAAAAATCAGAATAATAGGT 31917        C  _   TG
             AGA                    TTTAAGAA CA AGTG  AGGTAGA
                                  |||||||| || ||||  |||||||
                                  AAATTTTT GT TTAT  TCCATCT
                                      A  C   TA
GAM2527  LZTS1    3'  GAGGCCAAGGCAGGTGGA    34264    A_    T  G   A
                                  GA  CCAAG GT AGGT GA
                                  ||  ||||| || |||| ||
                                  CT  GGTTC CG TCCA CT
                                   CC    _ _   C
GAM2527  RNASE4   3'  TTTAAGGAGTAAGTGTAAGG   16348       AACC
                                  TTTAAG    AAGTGTGAGG
                                  ||||||    ||||||||||
                                  AAATTC    TTCACATTCC
                                     CTCA
GAM2527  TRPM6    3'  GAAGCCAAGGCAGGTGGA    32789    _    T  G   A
                                  GAA CCAAG GT AGGT GA
                                  ||| ||||| || |||| ||
                                  CTT GGTTC CG TCCA CT
                                    C    _ _   C
GAM2527  ZIC3     3'  TTTAAGAATGGGGTGTGCAGA  18257        CCAA    _
                                  TTTAAGAA   GTGTG AGG
                                  ||||||||   ||||| |||
                                  AAATTCTT   CACAC TCT
                                      ACCC    G
GAM2528  APM1     3'  TGAAAGCCTTTAATTGAC    22019     T       CAA
                                  TGA AGCCTTTAA   GC
                                  ||| |||||||||   ||
                                  ACT TCGGAAATT   TG
                                    T       AAC
GAM2528  F2RL2    3'  TGATATCTTTTCTCCTGCATTA 19911      GC   AACAA_
             AC                     TGATA  CTTT     GCATTAAC
                                  |||||  ||||     ||||||||
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                                ACTAT  GAAA     CGTAATTG
                                  A_    AGAGGA
GAM2529  ARCN1    3'  GAGAGCTTGCTTTCCTG     11654    AT   CATTA    T
                                GA  GCT     GCTTT CCTG
                                ||  |||     ||||| ||||
                                CT  CGA     CGAAA GGAC
                                 CT   A____    _
GAM2529  CD59     3'  AGGATGCTCATATACTCCTGC  8303     A       TAGCTT
                                AG ATGCTCAT     TTCCTGC
                                || |||||||      |||||||
                                TC TACGAGTA     GAGGACG
                                 C       TAT___
GAM2529  GRIN2B   3'  GATTGCTCACCGCCTTT     9122     A       A
                                GA TGCTCATT GCTTTT
                                || |||||||| ||||||
                                CT ACGAGTGG CGGAAA
                                 A       _
GAM2529  NRAP     3'  AGACTGCTCATTTCCT      40186     A       AGCTTT
                                AGA TGCTCATT     TCCT
                                ||| ||||||||      ||||
                                TCT ACGAGTAA     AGGA
                                  G       _______
GAM2529  PRKACB   3'  ATATCATTAGTTTTTCCTGC   15594     C       C
                                ATG TCATTAG TTTTCCTGC
                                ||| ||||||| |||||||||
                                TAT AGTAATC AAAAGGACG
                                  _       A
GAM2529  PTGS1    3'  AGAATGCTGCTTTCCT      38726         CATTA    T
                                AGAATGCT     GCTTT CCT
                                ||||||||     ||||| |||
                                TCTTACGA     CGAAA GGA
                                     ______    _
GAM2529  SOCS5    3'  AGACTGTTCATTAACTCTG   30420     A  C        TTTC
                                AGA TG TCATTAGCT    CTG
                                ||| || |||||||||    |||
                                TCT AC AGTAATTGA    GAC
                                  G  A        _____
GAM2530  ACP1     3'  AGTTGTATTTTTATAACTC   28232           G  G
                                AGTTGTATTTTTA AA TC
                                |||||||||||| || ||
                                TCAACATAAAAAT TT AG
                                        A  G
GAM2530  GPC1     3'  GTTGTATTTTTGGCAAAGTC  13257           A__
                                GTTGTATTTTT   GAAGTC
                                ||||||||||   ||||||
                                CAACATAAAAA   TTTCAG
                                       CCG
GAM2530  GPR85    3'  AGTTGTATATTTAGAACCCCAA 33258         T      G  G
                                AGTTGTAT TTTAGAA TC AA
                                |||||||| ||||||| || ||
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                                TCAACATA AAATCTT GG TT
                                     T      G  G
GAM2530  KAL1     3'  AGTTGATTTTTCATATCGAATC 6868       T     AGAA
                                AGTTG ATTTTT    GTCGAATC
                                ||||| ||||||    ||||||||
                                TCAAC TAAAAA    TAGCTTAG
                                  _     GTA_
GAM2530  VCAM1    3'  AGTTGCATTTTTAGGCCA    38780            AA
                                AGTTGTATTTTTAG  GTCG
                                ||||||||||||||  ||||
                                TCAACGTAAAAATC  CGGT
                                        __
GAM2530  GAGEC1   3'  AGAAAACTCAAACTTTAT    28129        A
                                AGAAAAT TAAACTTTAT
                                ||||||| ||||||||||
                                TCTTTTG GTTTGAAATA
                                    A
GAM2530  RAB26    3'  CAGAAAACACAACTTTAT    30744           A
                                TAGAAAATATAA CTTTAT
                                |||||||||||| ||||||
                                GTCTTTTGTGTT GAAATA
                                        _
GAM2530  UBE2G2   3'  GAAAACACAGAACTTTAT    42122         _
                                GAAAATATA AACTTTAT
                                ||||||||| ||||||||
                                CTTTTGTGT TTGAAATA
                                     C
GAM2531  AKAP13   3'  CACGCCCCATGGCCTGTGC   28473          _ AC
                                CACGCCCCATG C  GTGC
                                |||||||||||| |  ||||
                                GTGCGGGGTAC G  CACG
                                      C GA
GAM2531  APTX     5'  CCACGCCCAATCACAACTGC  32806        C  G   __
                                CCACGCCC AT CACG  TGC
                                |||||||| || ||||  |||
                                GGTGCGGG TA GTGT  ACG
                                     T  _    TG
GAM2531  ASK      5'  CACGCCACGCGCCGTGCCC   27471       CC   A_
                                CACGCC  ATGC  CGTGCCC
                                ||||||  ||||  |||||||
                                GTGCGG  TGCG  GCACGGG
                                   __    CG
GAM2531  ATP8B2   5'  CACCCCCATGCAAACC      42201     G       CGT
                                CAC CCCCATGCA   GCC
                                ||| |||||||||   |||
                                GTG GGGGTACGT   TGG
                                  _       T__
GAM2531  B29      5'  CCACGCCATGCTGAGGTG    36709        CC   AC__
                                CCACGCC  ATGC   GTG
                                |||||||  ||||   |||
```

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                                GGTGCGG  TACG   CAC
                                   __    ACTC
GAM2531  CAD     3'  CCACCCCCATGCCAGAGAGC   20293     G      ACGT__
                                CCAC CCCCATGC     GC
                                |||| ||||||||     ||
                                GGTG GGGGTACG     CG
                                  _       GTCTCT
GAM2531  CCNF    3'  ACCCAGGTCACACGTGCC    12068     CA__
                                GCCC   TGCACGTGCC
                                ||||   ||||||||||
                                TGGG   GTGTGCACGG
                                  TCCA
GAM2531  CD209   5'  CCACTCTCCCCCAGTGTCC   34505     G__   ATG  C  _
                                CCAC   CCCC   CA GTG CC
                                ||||   ||||   || ||| ||
                                GGTG   GGGG   GT CAC GG
                                  AGA   ___  _  A
GAM2531  CDKN1A  3'  CCAGCCCCATATGAGCCC    38504     C      CACGT
                                CCA GCCCCATG    GCCC
                                ||| ||||||||    ||||
                                GGT CGGGGTAT    CGGG
                                  _       ACT__
GAM2531  DDX3    5'  CACGTACAACGTGTGCCC    10675     CCC  T  AC
                                CACG   CA GC  GTGCCC
                                ||||   || ||  ||||||
                                GTGC   GT TG  CACGGG
                                  AT_ _  CA
GAM2531  DSCAM   5'  CCGCGCCCCACGCTGCGGCC   10793    A       A_  T
                                CC CGCCCCATGC  CG GCC
                                || ||||||||||  || |||
                                GG GCGGGGTGCG  GC CGG
                                 C        AC  _
GAM2531  EGFL4   3'  CCACGCCTATGACAGTGCC   41562       CC  _  C
                                CCACGCC  ATG CA GTGCC
                                |||||||  ||| || |||||
                                GGTGCGG  TAC GT CACGG
                                   A_   T  _
GAM2531  ESPN    5'  GGACGCCATGCACGTG     36445   C    CC
                                C ACGCC  ATGCACGTG
                                | |||||  |||||||||
                                C TGCGG  TACGTGCAC
                                 C    __
GAM2531  FUT5    3'  CCAGGCCCCATGCCGGCC    13020     C       A  T
                                CCA GCCCCATGC CG GCC
                                ||| |||||||| || |||
                                GGT CGGGGTACG GC CGG
                                  C       _ _
GAM2531  GLTSCR1 3'  CAAACACATGCGCGTGTCC   31832    C  CC    A   _
                                CA GC  CATGC CGTG CC
                                || ||  ||||| |||| ||
```

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                                GT TG  GTACG GCAC GG
                                 T T_    C    A
GAM2531  GPR44    3'  CCAGCCCCATGTGGCC      21953     C       CACGT
                                CCA GCCCCATG    GCC
                                ||| ||||||||    |||
                                GGT CGGGGTAC    CGG
                                  _       AC___
GAM2531  HOXA3    3'  CCAGGCCCCATGCTGGAGCC   36192     C        ACGT
                                CCA GCCCCATGC    GCC
                                ||| |||||||||   |||
                                GGT CGGGGTACG    CGG
                                  C        ACCT
GAM2531  HR       5'  CACGCCCCACTGGCCTGTG   32910          __ AC
                                CACGCCCCAT  GC  GTG
                                ||||||||||  ||  |||
                                GTGCGGGGTG  CG  CAC
                                      AC  GA
GAM2531  ID3      3'  CCGCGCCCCACGCTGCCC    44271    A        ACG
                                CC CGCCCCATGC   TGCCC
                                || ||||||||||   |||||
                                GG GCGGGGTGCG   ACGGG
                                 C         ___
GAM2531  IHPK1    3'  CACGTGCCAACAGGTGCC    45482     CC   T   C
                                CACG  CCA GCA GTGCC
                                ||||  ||| ||| |||||
                                GTGC  GGT TGT CACGG
                                  AC   _   C
GAM2531  KCNQ1    3'  CCACTCAACCACGTGCCC    6884      GCCC  TG
                                CCAC    CA  CACGTGCCC
                                ||||    ||  |||||||||
                                GGTG    GT  GTGCACGGG
                                  A___  TG
GAM2531  LRP4     3'  CCAGGCTGAGACACGTGCCC   42058     C  CCCAT
                                CCA GC     GCACGTGCCC
                                ||| ||     ||||||||||
                                GGT CG     TGTGCACGGG
                                  C  ACTC_
GAM2531  LY9      3'  CCAGGCCCCATGAGGTCC    43468     C       CAC  G
                                CCA GCCCCATG   GT CC
                                ||| ||||||||   || ||
                                GGT CGGGGTAC   CA GG
                                  C       TC_  _
GAM2531  MAP3K7IP1 3'  CCTGCCCCATGCCAGGCCC   25924    AC       A  T
                                CC  GCCCCATGC CG GCCC
                                ||  ||||||||| || ||||
                                GG  CGGGGTACG GT CGGG
                                 A_        _  C
GAM2531  MAPRE3   3'  CCATCCCTCACATGCC      29528     CG   CATG
                                CCA  CCC    CACGTGCC
                                |||  |||    ||||||||
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                                GGT  GGG   GTGTACGG
                                  A_  A___
GAM2531  MDK     3'  CCAGGCCCCATGTGACACC   14392    C      CAC TG
                                CCA GCCCCATG  G  CC
                                ||| ||||||||  |  ||
                                GGT CGGGGTAC  T  GG
                                  C       AC_ GT
GAM2531  MFGE8   3'  CACGCCCTACTTTGCCC    25460      CA  ACG
                                CACGCCC  TGC  TGCCC
                                |||||||  |||  |||||
                                GTGCGGG  ATG  ACGGG
                                    __  AA_
GAM2531  MKPX    5'  CCGCGCCCCACTCCGCCC   33636    A     GCACG
                                CC CGCCCCAT    TGCCC
                                || ||||||||    |||||
                                GG GCGGGGTG    GCGGG
                                 C       AG___
GAM2531  MN1     3'  CCATCCCCCATGCAGACC    14572    CG      CGT
                                CCA  CCCCATGCA  GCC
                                |||  |||||||||  |||
                                GGT  GGGGTACGT  TGG
                                  AG       C__
GAM2531  MSF     3'  CCACGGCCCACACGTGCCC   44719     C  AT
                                CCACG CCC  GCACGTGCCC
                                ||||| |||  ||||||||||
                                GGTGC GGG  TGTGCACGGG
                                   C  __
GAM2531  MYO1D   3'  CCACGCTGTGCTGCTGCCC   43488     CCCA_  ACG
                                CCACGC    TGC  TGCCC
                                ||||||    |||  |||||
                                GGTGCG    ACG  ACGGG
                                   ACACG  ___
GAM2531  MYOM2   3'  CCACACCCATGTGCC      19558       C  GCAC
                                CCACGCCC AT   GTGCC
                                |||||||| ||   |||||
                                GGTGTGGG TA   CACGG
                                  _ _____
GAM2531  NCAM1   5'  CACGCGCCATGGTACCC    8316      C    CAC
                                CACGC CCATG  GTGCCC
                                ||||| |||||  ||||||
                                GTGCG GGTAC  CATGGG
                                   C   ___
GAM2531  NCOR2   3'  CACGCCTGCCGTGCCC     26726      CCA  A
                                CACGCC  TGC CGTGCCC
                                ||||||  ||| |||||||
                                GTGCGG  ACG GCACGGG
                                  ___  _
GAM2531  P2RY6   3'  CACGCAAGGCCATGTGTCC  19988     C___   CAC  G
                                CACGC   CCATG  GT CC
                                |||||   |||||  || ||
```

```
                                GTGCG   GGTAC  CA GG
                                  TTCC    A__ _
GAM2531  PGLS    3'  CCAGCCCCATGGGCCGCGTGCC 28982    C     __ A_
                                CCA GCCCCAT  GC  CGTGCC
                                ||| |||||||  ||  ||||||
                                GGT CGGGGTA  CG  GCACGG
                                  _     CC  GC
GAM2531  PKD2    3'  CACCCCACTCCCCACGTGTCC  41069       G___    _
                                CGCCCCAT   CACGTG CC
                                ||||||||   |||||| ||
                                GTGGGGTG   GTGCAC GG
                                     AGGG    A
GAM2531  POLD1   3'  CCCGCCCCATGGGATGC    15437   A      CAC
                                CC CGCCCCATG  GTGC
                                || |||||||||  ||||
                                GG GCGGGGTAC  TACG
                                 _      CC_
GAM2531  POLR2A  3'  CCGCACCCCACGTGCCC    9599    A    ATGC
                                CC CGCCCC   ACGTGCCC
                                || ||||||   ||||||||
                                GG GTGGGG   TGCACGGG
                                 C    _____
GAM2531  PPFIA3  3'  CCACGCCACGTCGCC      41414       CCATGC   _
                                CCACGCC    ACGT GCC
                                |||||||    |||| |||
                                GGTGCGG    TGCA CGG
                                   _______   G
GAM2531  PTPRJ   5'  CGCGCCCTGGAACGTGCCC   15951    _  A  C_
                                CGC CCC TG  ACGTGCCC
                                ||| ||| ||  ||||||||
                                GCG GGG AC  TGCACGGG
                                  C  _ CT
GAM2531  RAD50   5'  CCCGCCCCATTGGGTCC    39434    A     GCAC  G
                                CC CGCCCCAT   GT CC
                                || ||||||||   || ||
                                GG GCGGGGTA   CA GG
                                 _      ACC_ _
GAM2531  RPL10   3'  CCATGCCACACACGTG     25669    C   CC
                                CCA GCC  ATGCACGTG
                                ||| |||  |||||||||
                                GGT CGG  TGTGTGCAC
                                  A  __
GAM2531  RPS6KA2 3'  CCCGCCCTGTGTGCACACCC  34456   A   CA__   GT
                                CC CGCCC   TGCAC  GCCC
                                || |||||   |||||  ||||
                                GG GCGGG   ACGTG  TGGG
                                 _    ACAC   __
GAM2531  S100A11 5'  CCACGCCCTTCCCGGCCC   24729       CATGCA  T
                                CCACGCCC    CG GCCC
                                ||||||||    || ||||
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                                GGTGCGGG    GC CGGG
                                    AAGG__ _
GAM2531 S100B   3' CCACGCCCTTGCAGGGCC   26566       CA   CGT
                                CCACGCCC TGCA  GCC
                                |||||||| ||||  |||
                                GGTGCGGG ACGT  CGG
                                    A_   CC_
GAM2531 SCTR    3' CCTGCCCCACAGTGCC     16488   AC   AT  C
                                CC GCCCC GCA GTGCC
                                || ||||| ||| |||||
                                GG CGGGG TGT CACGG
                                 A_    __  _
GAM2531 SLC21A2 3' CCAGTCCCACACTGCC     24796    CG  CAT   G
                                CCA CCC  GCAC TGCC
                                ||| |||  |||| ||||
                                GGT GGG  TGTG ACGG
                                  CA  ___  _
GAM2531 SLC6A6  3' CCACGTGCCACCTGCC     16781     CCCCA  _ G
                                CCACG   TGC AC TGCC
                                |||||    ||| || ||||
                                GGTGC   ACG TG ACGG
                                   _____  G  G
GAM2531 SRC     3' CAGCCCCACATCTGCC     24031   C   AT  CG
                                CA GCCCC GCA  TGCC
                                || ||||| |||  ||||
                                GT CGGGG TGT  ACGG
                                 _   __  AG
GAM2531 STX1A   3' CACGCCCCGCTGGCTGCC   21409       AT  ACG_
                                CACGCCCC GC   TGCC
                                |||||||| ||   ||||
                                GTGCGGGG CG   ACGG
                                    __ ACCG
GAM2531 TCF2    3' CGCTTCCCATGACACGCCC   27024    __    C
                                CGC CCCATG ACGTGCCC
                                ||| |||||| ||||||||
                                GCG GGGTAC TGTGCGGG
                                  AA    _
GAM2531 TNXB    5' CCACACCCCGGTGTCC     37150       ATGCAC  _
                                CCACGCCCC    GTG CC
                                |||||||||    ||| ||
                                GGTGTGGGG    CAC GG
                                    C_____  A
GAM2531 TYRO3   3' CCACTCCTGCCAGCTGCC   26650    G __  T  ACG
                                CCAC CC  CCA GC  TGCC
                                |||| ||  ||| ||  ||||
                                GGTG GG  GGT CG  ACGG
                                  A AC  _ ___
GAM2531 VASP    5' CCCGCCCCATAGAGTCC    17914   A      CAC  G
                                CC CGCCCCATG  GT CC
                                || |||||||||  || ||
```

```
                                GG GCGGGGTAT   CA GG
                                 _       CT_ _
GAM2531  WFDC1    5'  CGCGTCCAGCACATGCCC    34523     C_   T
                                CGC  CCA GCACGTGCCC
                                |||  ||| ||||||||||
                                GCG  GGT CGTGTACGGG
                                  CA   _
GAM2531  XRCC3    3'  CCAGCCCTGCGCTGCC      24103     C   CA   ACG
                                CCA GCCC  TGC   TGCC
                                ||| ||||  |||   ||||
                                GGT CGGG  GCG   ACGG
                                  _   AC  ____
GAM2531  ZNF26    5'  CCACGTTCGCGCGCTGCC    43797      CCCCA   A _
                                CCACG    TGC CG TGCC
                                |||||    ||| || ||||
                                GGTGC    GCG GC ACGG
                                   AA___   C  G
GAM2531  ZNF74    5'  CACGCCCCGGCACACCC     18299        AT    GT
                                CACGCCCC  GCAC  GCCC
                                ||||||||  ||||  ||||
                                GTGCGGGG  CGTG  TGGG
                                    C_    __
GAM2532  ESRRG    3'  TTAATAAATGGCTGAAAAGTG  42450           CAT    T
                                TTAATAAATGGCT   GGAA GTG
                                ||||||||||||   |||| |||
                                AATTATTTACCGA   CTTT CAC
                                      ___    T
GAM2533  APPL     3'  TAACTGGTTTCCTATCTACTGA 29011        CTGCATA
                                TAGCTGG      TATCTACTGA
                                |||||||      ||||||||||
                                ATTGACC      ATAGATGACT
                                   AAAGG__
GAM2533  FN1      3'  TGGCTGCATATGCTTTCCTATT 38340          A____    C
            GA                    TGGCTGCATAT    TCTA TGA
                                ||||||||||    |||| |||
                                ACCGACGTATA    GGAT ACT
                                      CGAAA    A
GAM2533  MNDA     3'  GCTAGAATATATCTACTGA    14605      CTGC
                                GCTGG    ATATATCTACTGA
                                |||||    ||||||||||||
                                CGATC    TATATAGATGACT
                                  T___
GAM2533  PRKCN    3'  TAGCTGGCTGCTGGAGCTG    25162          ATATATCTA
                                TAGCTGGCTGC       CTG
                                ||||||||||        |||
                                ATCGACCGACG       GAC
                                      ACCTC____
GAM2533  PTPN23   5'  TAGCTGCTGCAGCTGCTG    41893       G    TATAT  A
                                TAGCTG CTGCA    CT CTG
                                ||||||  |||||    || |||
```

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                                ATCGAC GACGT    GA GAC
                                   _    C____  C
GAM2533  TPD52L2  3'  GCTGGCTGCTCCGCTG     17638        ATATA  TA
                                GCTGGCTGC    TC  CTG
                                |||||||||    ||  |||
                                CGACCGACG    AG  GAC
                                     _____  GC
GAM2533  APPL     3'  TAACTGGTTTCCTATCTACTGA 29011       CTGCATA
                                TAGCTGG      TATCTACTGA
                                |||||||      ||||||||||
                                ATTGACC      ATAGATGACT
                                   AAAGG__
GAM2533  FN1      3'  TGGCTGCATATGCTTTCCTATT 38340         A____   C
            GA                   TGGCTGCATAT    TCTA TGA
                                ||||||||||     |||| |||
                                ACCGACGTATA    GGAT ACT
                                      CGAAA    A
GAM2533  MNDA     3'  GCTAGAATATATCTACTGA   14605      CTGC
                                GCTGG   ATATATCTACTGA
                                |||||   ||||||||||||
                                CGATC   TATATAGATGACT
                                  T___
GAM2533  PRKCN    3'  TAGCTGGCTGCTGGAGCTG   25162         ATATATCTA
                                TAGCTGGCTGC       CTG
                                ||||||||||        |||
                                ATCGACCGACG       GAC
                                      ACCTC____
GAM2533  PTPN23   5'  TAGCTGCTGCAGCTGCTG    41893      G    TATAT  A
                                TAGCTG CTGCA    CT CTG
                                ||||||  |||||    || |||
                                ATCGAC GACGT    GA GAC
                                   _    C____  C
GAM2533  TPD52L2  3'  GCTGGCTGCTCCGCTG     17638        ATATA  TA
                                GCTGGCTGC    TC  CTG
                                |||||||||    ||  |||
                                CGACCGACG    AG  GAC
                                     _____  GC
GAM2534  CACNA1G  3'  CCGGGGCTGCTGCTT      33129        T  TTACC
                                CCGGGGTT TT    GCTT
                                ||||||||  ||    ||||
                                GGCCCCGA GA    CGAA
                                   C  _____
GAM2534  DPP6     5'  GGGGCTTTTTAATATTTTGCTT 39132         TACC____
            T                    GGGGTTTTTT      GCTTT
                                ||||||||||      |||||
                                CCCCGAAAAA      CGAAA
                                     TTATAAAA
GAM2534  IL13     3'  TCCTGGGGTCCACTGCTT    13528     CC     TTTT   C
                                TCC  GGGGTT    TAC GCTT
                                |||  ||||||    ||| ||||
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                                AGG  CCCCAG    GTG CGAA
                                  A_      ____   A
GAM2534  JAM3     3'  GGGTTTTTTTGAAGCTTT    37265          ACC
                                GGGTTTTTTT   GCTTT
                                ||||||||||   |||||
                                CCCAAAAAAA   CGAAA
                                     CTT
GAM2534  RNPEPL1  3'  TCCCTGGGGTATTGCTT     32890      C    T  TTTACC
                                TCCC GGGGT TT     GCTT
                                |||| ||||| ||     ||||
                                AGGG CCCCA AA     CGAA
                                  A    T _______
GAM2534  CACNA1G  3'  CCGGGGCTGCTGCTT       33129         T  TTACC
                                CCGGGGTT TT    GCTT
                                |||||||| ||    ||||
                                GGCCCCGA GA    CGAA
                                     C ______
GAM2534  DPP6     5'  GGGGCTTTTTAATATTTTGCTT 39132          TACC____
                T                GGGGTTTTTT       GCTTT
                                ||||||||||       |||||
                                CCCCGAAAAA       CGAAA
                                     TTATAAAA
GAM2534  IL13     3'  TCCTGGGGTCCACTGCTT    13528     CC     TTTT   C
                                TCC  GGGGTT    TAC GCTT
                                |||  ||||||    ||| ||||
                                AGG  CCCCAG    GTG CGAA
                                  A_      ____   A
GAM2534  JAM3     3'  GGGTTTTTTTGAAGCTTT    37265          ACC
                                GGGTTTTTTT   GCTTT
                                ||||||||||   |||||
                                CCCAAAAAAA   CGAAA
                                     CTT
GAM2534  RNPEPL1  3'  TCCCTGGGGTATTGCTT     32890      C    T  TTTACC
                                TCCC GGGGT TT     GCTT
                                |||| ||||| ||     ||||
                                AGGG CCCCA AA     CGAA
                                  A    T _______
GAM2535  MYOZ1    5'  CACGAGCTGGGCAGGCG     34553        AC    A
                                CACGAGC  GGGCG GCG
                                |||||||  ||||| |||
                                GTGCTCG  CCCGT CGC
                                     A_    C
GAM2535  SORCS3   5'  CGCGCCGGCGAGCGAGCGAGC  31416    A  A__
                                CG GC   CGGGCGAGCGAGC
                                || ||   ||||||||||||||
                                GC CG   GCTCGCTCGCTCG
                                 G  GCC
GAM2535  UPF3A    3'  CACAGCACGCTTTGCGGGCAT  38786     G     GGCGA   A
                                CAC AGCACG     GCG GCAT
                                ||| ||||||     ||| ||||
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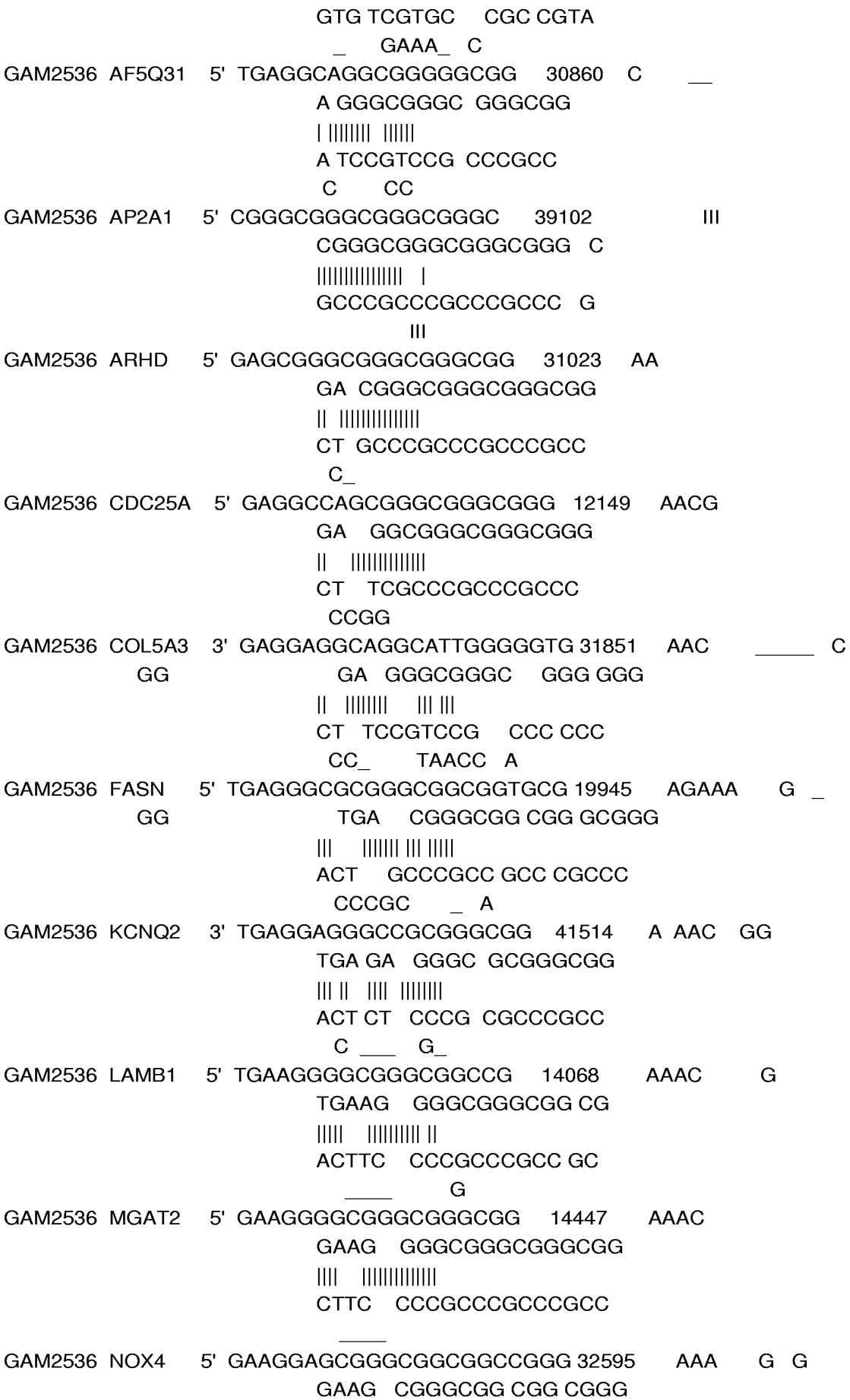
GTG TCGTGC CGC CGTA
_ GAAA_ C
GAM2536 AF5Q31 5' TGAGGCAGGCGGGGGCGG 30860 C __
A GGGCGGGC GGGCGG
| |||||||| ||||||
A TCCGTCCG CCCGCC
C CC
GAM2536 AP2A1 5' CGGGCGGGCGGGCGGGC 39102 III
CGGGCGGGCGGGCGGG C
|||||||||||||||| |
GCCCGCCCGCCCGCCC G
III
GAM2536 ARHD 5' GAGCGGGCGGGCGGGCGG 31023 AA
GA CGGGCGGGCGGGCGG
|| ||||||||||||||
CT GCCCGCCCGCCCGCC
C_
GAM2536 CDC25A 5' GAGGCCAGCGGGCGGGCGGG 12149 AACG
GA GGCGGGCGGGCGGG
|| ||||||||||||||
CT TCGCCCGCCCGCCC
CCGG
GAM2536 COL5A3 3' GAGGAGGCAGGCATTGGGGGTG 31851 AAC _____ C
GG GA GGGCGGGC GGG GGG
|| |||||||| ||| |||
CT TCCGTCCG CCC CCC
CC_ TAACC A
GAM2536 FASN 5' TGAGGGCGCGGGCGGCGGTGCG 19945 AGAAA G _
GG TGA CGGGCGG CGG GCGGG
||| ||||||| ||| |||||
ACT GCCCGCC GCC CGCCC
CCCGC _ A
GAM2536 KCNQ2 3' TGAGGAGGGCCGCGGGCGG 41514 A AAC GG
TGA GA GGGC GCGGGCGG
||| || |||| ||||||||
ACT CT CCCG CGCCCGCC
C ___ G_
GAM2536 LAMB1 5' TGAAGGGGCGGGCGGCCG 14068 AAAC G
TGAAG GGGCGGGCGG CG
||||| |||||||||| ||
ACTTC CCCGCCCGCC GC
____ G
GAM2536 MGAT2 5' GAAGGGGCGGGCGGGCGG 14447 AAAC
GAAG GGGCGGGCGGGCGG
|||| ||||||||||||||
CTTC CCCGCCCGCCCGCC
____
GAM2536 NOX4 5' GAAGGAGCGGGCGGCGGCCGGG 32595 AAA G G
GAAG CGGGCGG CGG CGGG
|||| ||||||| ||| ||||

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                                CTTC   GCCCGCC GCC GCCC
                                  CTC      _  G
GAM2536 SCA2     5' TGAGGAGCGGGCGGCGCGCTGG 16479     A  AA      G  G  _
             G                    TGA GA  CGGGCGG CG GC GGG
                                  ||| ||  ||||||| || || |||
                                  ACT CT  GCCCGCC GC CG CCC
                                   C  C_     _  G  A
GAM2536 TAZ      5' GAGGAAACGGGAAGGCGGG   31766    A      C
                                  GA GAAACGGG GGGCGGG
                                  || |||||||| |||||||
                                  CT CTTTGCCC TCCGCCC
                                   C       T
GAM2536 TBX6     3' GAGGGGGTGGGTGGGCAG    38856    AAC   C   C
                                  GA   GGG GGG GGGCGG
                                  ||   ||| ||| ||||||
                                  CT   CCC CCC CCCGTC
                                   CC_   A   A
GAM2536 YY1      5' AGAGGGGGCGGGCGGCGG    18162     AAC        G
                                  AGA   GGGCGGGCGG CGG
                                  |||   |||||||||| |||
                                  TCT   CCCGCCCGCC GCC
                                    CC_        _
GAM2537 ACADL    3' TTAGTGATCTTGCCAGTTTTGT 11499      ATTCT       TC_
                                  TTAGT    TCTTGTCA   TTGT
                                  |||||    ||||||||   ||||
                                  AATCA    AGAACGGT   AACA
                                     CT___       CAA
GAM2537 ATP1A2   3' TTAGTATTTTTCCTCTTGT   8717         ___
                                  TTAGTAT   TCTTCTTGT
                                  |||||||   |||||||||
                                  AATCATA   AGGAGAACA
                                      AAA
GAM2537 KLHL3    3' GTTGTTCTCCAAGCATCTTGT  44644    A_     TT T
                                  GT  TTCTTC  G CATCTTGT
                                  ||  ||||||  | ||||||||
                                  CA  AAGAGG  C GTAGAACA
                                   AC     TT _
GAM2537 PDE1A    3' TTCTTCTTAATTCCTTGT    22710         TCA
                                  TTCTTCTTG   TCTTGT
                                  |||||||||   ||||||
                                  AAGAAGAAT   GGAACA
                                       TAA
GAM2538 COL10A1  3' TTTATTGTGTCGTAAATAAGGA 7967         AT____
                                  TTTATTGT     GGTAAGGA
                                  ||||||||     ||||||||
                                  AAATAACA     TTATTCCT
                                       CAGCAT
GAM2538 ENIGMA   3' TTTATTGTGGCACTGGA     41638         AT   A_
                                  TTTATTGT  GGTA  GGA
                                  ||||||||  ||||  |||
```

```
                                AAATAACA  CCGT  CCT
                                   __   GA
GAM2538  ETV5    3'  TATTGTCCATGGTAAGGA    20855       __
                                TATTGT  ATGGTAAGGA
                                ||||||  ||||||||||
                                ATAACA  TACCATTCCT
                                   GG
GAM2538  LPHH1   3'  TTCATTGTACAGTTGAGGAA  29392          A_
                                TTTATTGTATGGT  AGGAA
                                ||||||||||||  |||||
                                AAGTAACATGTCA  TCCTT
                                      AC
GAM2538  PDYN    3'  ATTTATTGTACTGGAGGA    35920         _  TA
                                ATTTATTGTA TGG  AGGA
                                ||||||||||  |||  ||||
                                TAAATAACAT ACC  TCCT
                                      G  __
GAM2538  PTGIS   3'  TAATCACAATGGTAAGGAA   9676       TATTGT
                                TAATT     ATGGTAAGGAA
                                |||||     ||||||||||
                                ATTAG     TACCATTCCTT
                                   TGT___
GAM2539  DLG5    5'  GCTGTATCAAGTTCCGTTTGTT 44459     A   TT_      A
            AT                    GCT TATC   TTCCGTTT TTAT
                                |||  ||||   |||||||| ||||
                                CGA ATAG   AAGGCAAA AATA
                                  C   TTC       C
GAM2540  PMP2    3'  TGGCAGATAGGATTAGTA    15424          GG
                                TGGCAGATAGG  TGGTA
                                ||||||||||  |||||
                                ACCGTCTATCC  ATCAT
                                      TA
GAM2540  CCRL1   3'  TCTTGTATTAAAACTTAGATAA 32431     _     TTAAGT
                                TCT GTATTA     CTTAGATAA
                                |||  ||||||     |||||||||
                                AGA CATAAT     GAATCTATT
                                  A     TTT___
GAM2540  HDAC4   3'  TGTATTATTAGATCTTTGA   25790         AG   A
                                TGTATTATTA  TCTT GA
                                ||||||||||  ||||  ||
                                ACATAATAAT  AGAA CT
                                      CT   A
GAM2540  XPR1    3'  TCTGTATGGTTAAGTTTCA   21853       TA     C
                                TCTGTAT  TTAAGT TTA
                                |||||||  ||||||  |||
                                AGACATA  AATTCA AGT
                                   CC     A
GAM2541  PCDHB14 3'  TGTCTAGATTTAAGTTAC    33191          _
                                TGTCTGGATTTA GTTAC
                                ||||||||||||  |||||
```

```
                                ACAGATCTAAAT CAATG
                                      T
GAM2541  PPP3CB   3'  TGCCTGGAGCTCTGAGTT    34451        _  __
                                TGTCTGGA TTT  AGTT
                                |||||||| |||  ||||
                                ACGGACCT GAG  TCAA
                                    C   AC
GAM2542  C8orf1   3'  AGCATACATATCCCTTGGGGA  20269         CACGG  C
                                AGCATATATA    CT GGGGA
                                ||||||||||    || |||||
                                TCGTATGTAT    GA CCCCT
                                      AGG__  A
GAM2542  DIAPH2   3'  ATATATACAGAGGGG       28666         C  CTC
                                ATATATACA GG   GGGG
                                ||||||||| ||   ||||
                                TATATATGT CT   CCCC
                                      _ ___
GAM2542  ITPKB    3'  TATATACACATGGGG       13655         GCTC
                                TATATACACG    GGGG
                                ||||||||||    ||||
                                ATATATGTGT    CCCC
                                      A___
GAM2542  ITSN1    3'  AAGCATATTATGTGAGGTTGGG 16651        ATACAC_  CTC
              G                  AAGCATAT      GG   GGGG
                                ||||||||      ||   ||||
                                TTCGTATA      CC   CCCC
                                    ATACACT  AA_
GAM2543  ASCL1    5'  TCTAAGAAAAAAAAAAGCA    43747      _
                                TCTAA AAAAAAAAAGCA
                                ||||| ||||||||||||
                                AGATT TTTTTTTTTTCGT
                                   C
GAM2543  CPNE3    3'  TCTTAAAAAAAAAAAAGCACA   19384     A
                                TCT AAAAAAAAAAAGCACA
                                ||| ||||||||||||||||
                                AGA TTTTTTTTTTTCGTGT
                                  A
GAM2543  HNMT     5'  TCCAAAAAAAAAAAAAAATGCT 27887             CACAC
                                TCTAAAAAAAAAAAAG    GCT
                                ||||||||||||||||    |||
                                AGGTTTTTTTTTTTTT    CGA
                                      TTA__
GAM2543  HNRPH2   3'  AAAAAAAAAAAAGTGTACACT  33328           CAC
                                AAAAAAAAAAAAG   ACGCT
                                ||||||||||||   |||||
                                TTTTTTTTTTTTC   TGTGA
                                      ACA
GAM2543  LARS     3'  AAAAAAAAAAAAGCTGCT    33477           ACAC
                                AAAAAAAAAAAAGC    GCT
                                ||||||||||||||    |||
```

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                                TTTTTTTTTTTTCG    CGA
                                      A___
GAM2543  MAK      3'  TCTAAAAAAAAAAAAAAAAGC 25381              CACAC
                T                  TCTAAAAAAAAAAAG     GCT
                                   ||||||||||||||||    |||
                                   AGATTTTTTTTTTTTT    CGA
                                         TTTT_
GAM2543  PER2     3'  TCTAAAACAAAAAAAGCAACA  35620        A        C
                                   TCTAAAA AAAAAAAGCA ACG
                                   ||||||| |||||||||| |||
                                   AGATTTT TTTTTTTCGT TGT
                                       G        _
GAM2543  PIAS1    3'  CCTAAAAAAAGGAAAAAAAACA 32075          __     C
                CGCT                   TCTAAAAAAA  AAAAAG ACACGCT
                                   ||||||||||  |||||| |||||||
                                   GGATTTTTTT  TTTTTT TGTGCGA
                                         CC     T
GAM2543  PPP1R12A 3'  TAAAAAAAAAAAGGCCAC    14728           A  A
                                   TAAAAAAAAAAA GC CAC
                                   |||||||||||| || |||
                                   ATTTTTTTTTTT CG GTG
                                         C  _
GAM2543  RAB30    3'  TAAAAAAACAAAAGCAACATGC 30935        A      _  C
                T                  TAAAAAAA AAAAGCA CA GCT
                                   |||||||| ||||||| || |||
                                   ATTTTTTT TTTTCGT GT CGA
                                       G      T  A
GAM2543  SEDL     3'  TCAAAAAAAAAAAAAAGCGAGCT 31012    T          ACAC
                                   TC AAAAAAAAAAAAGC    GCT
                                   || ||||||||||||||    |||
                                   AG TTTTTTTTTTTTCG    CGA
                                    T           CT__
GAM2543  SHANK2   3'  TCTAAAAAGAATAAAAGCAC   29470        _  A
                                   TCTAAAAA AA AAAAGCAC
                                   |||||||| || ||||||||
                                   AGATTTTT TT TTTTCGTG
                                       C  A
GAM2543  TBXA2R   3'  TCTAAAAAAAAAAATAGCA    9860            _
                                   TCTAAAAAAAAAAA AGCA
                                   |||||||||||||| ||||
                                   AGATTTTTTTTTTT TCGT
                                         A
GAM2544  CDC25B   3'  TCTGACCCATCCTCAGGG    34859     A  A   C
                                   TCT ACC ATCC CAGGG
                                   ||| ||| |||| |||||
                                   AGA TGG TAGG GTCCC
                                     C  G   A
GAM2544  CYLN2    3'  TCTGGTCAACCCCCAGGG     18064     AAC   T
                                   TCT   CAA CCCCAGGG
                                   |||   ||| ||||||||
```

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                                AGA  GTT GGGGTCCC
                                  CCA  _
GAM2544  FPRL1    3'  TCTAACCAACTCCTGTGAG   11150        TC  CAG
                                TCTAACCAA  CC  GGG
                                |||||||||  ||  |||
                                AGATTGGTT  GG  CTC
                                     GA  ACA
GAM2544  FREB     3'  TCTAATCACTTCCCAAAG   37225      C  ATC
                                TCTAA CA  CCCAGGG
                                |||||  ||  |||||||
                                AGATT GT  GGGTTTC
                                   A  GAA
GAM2544  NLGN2    3'  CAGGGCCCCGGGGGCCAA   44747    AT_   A
                                CA  CCCC GGGGCCAA
                                ||  |||| ||||||||
                                GT  GGGG CCCCGGTT
                                 CCC   C
GAM2544  PRLR     3'  TAACCAATCATTCCATTAGTCA 9625         C__  GG  C
           AG                     TAACCAATC  CCA  GG CAAG
                                |||||||||  |||  || ||||
                                ATTGGTTAG  GGT  TC GTTC
                                     TAA  AA  A
GAM2544  SFTPD    3'  TCTGGCCAAACTCCTGGGCCAA 16601    AA   TCC  AG
           G                     TCT  CCAA  CC  GGGCCAAG
                                |||  ||||  ||  ||||||||
                                AGA  GGTT  GG  CCCGGTTC
                                  CC   TGA  A_
GAM2544  TACC3    5'  TCTGCTCCACGCCGGGGGCCAA 26811    AA_  ATCC  A
           G                     TCT  CCA   CC GGGGCCAAG
                                |||  |||   || |||||||||
                                AGA  GGT   GG CCCCGGTTC
                                  CGA  GC__  C
GAM2544  TCP10    3'  TCTAACCAAGTTTCCTAAATAG 21429        ___  CCAG_
           G                     TCTAACCAA  TCC   GGG
                                |||||||||  |||   |||
                                AGATTGGTT  AGG   TCC
                                     CAA  ATTTA
GAM2544  THBD     3'  TCTAACCAGCTCCCATGGG   7431        A_   CA
                                TCTAACCA  TCCC  GGG
                                ||||||||  ||||  |||
                                AGATTGGT  AGGG  CCC
                                     CG   TA
GAM2545  AKAP13   3'  AGGCAGGTTTTTCTTTTTCATT 28467      T   GA
                                AGGCAG GTT  TTTTTTTTCATT
                                ||||||  |||  ||||||||||||
                                TCCGTC CAA  AAGAAAAAGTAA
                                   _  A_
GAM2545  FCAR     3'  AGGTTGTGTTTTCTTTTCATT  39332    CA    GAT
                                AGG  GTGTT  TTTTTTTCATT
                                |||  |||||  ||||||||||
```

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                                TCC  CACAA   AAGAAAAGTAA
                                  AA    ___
GAM2545  GALNT1   3'  TGTTGATTTTTTTTCATT    33844
                                TGTTGATTTTTTTTCATT
                                ||||||||||||||||||
                                ACAACTAAAAAAAAGTAA

GAM2545  MYF5     3'  AGGCAGTATTATATTTTT    24630          _
                                AGGCAGTGTTG ATTTTT
                                |||||||||| ||||||
                                TCCGTCATAAT TAAAAA
                                      A
GAM2545  ONECUT2  5'  AGGCGGTGTAGGCAGCCTTCAT 22137     A   TGATTTT
            T                    AGGC GTGT      TTTTCATT
                                |||| ||||      ||||||||
                                TCCG CACA      GGAAGTAA
                                  C   TCCGTC_
GAM2546  RPL27A   3'  TTTTAAAAGTAGTTAGCATTTA 9742           CT  TAA_
            ATG                   TTTTAAAAGTAGT  GT   GATG
                                ||||||||||||  ||   ||||
                                AAAATTTTCATCA  CG   TTAC
                                       AT  TAAA
GAM2547  ALPL     5'  GCGGGCGCGGAGTGG      7888      A   GCAC  C  C
                                GCGG GCGC   GG AG GG
                                |||| ||||   || || ||
                                CGCC CGCG   CC TC CC
                                  _   _____ _ A
GAM2547  AMPH     5'  GCGCAGCGGGGCTGGCGGCGGC 11599    G   C_ AC   A
            G                    GCG AGCG  GC  GGC GCGGCG
                                ||| ||||  ||  ||| ||||||
                                CGC TCGC  CG  CCG CGCCGC
                                  G   CC  A_  C
GAM2547  AP1M1    5'  GCCGAGGGCGGTGGCGGC    37169    G   C  GCAC  CA
                                GC GAG GC    GG  GCGGC
                                || ||| ||    ||  |||||
                                CG CTC CG    CC  CGCCG
                                 G   C _____  AC
GAM2547  ASL      5'  GAGCGCGCGCCACGG       43532         ACG  A
                                GAGCGCGC   GC GCGG
                                ||||||||   || ||||
                                CTCGCGCG   CG TGCC
                                     ___  G
GAM2547  ASS      5'  CGGGCTCGGGCAGCGG      38263     A  G  CAC
                                CGG GC CG   GGCAGCGG
                                ||| || ||   ||||||||
                                GCC CG GC   CCGTCGCC
                                  _  A  ___
GAM2547  BCR      5'  GCGGGGCCCGTCTCAGCGGCG  34638      A  G  CACGG
                                GCGG GC CG    CAGCGGCG
                                |||| || ||    ||||||||
```

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                                CGCC CG GC    GTCGCCGC
                                  C  G  AGA__
GAM2547 BIN1     5'  GCGGAGCGTGCGCCGGACGGGC 40299       __   A  CA   _
                G                  GCGGAGC  GCGC CGG  GCGG CG
                                   |||||||  |||| |||  |||| ||
                                   CGCCTCG  CGCG GCC  TGCC GC
                                      CA   _  __   C
GAM2547 CALCA    5'  GCGGTGGCAGCGGCGGCGGCG  11939     AGCGC  _   A
                                   GCGG    GCA CGGC GCGGCG
                                   ||||    ||| |||| ||||||
                                   CGCC    CGT GCCG CGCCGC
                                     AC___  C   C
GAM2547 CCND3    5'  GCGGGGCGCGGGTCTGGC    12062     A    CAC  CAGC
                                   GCGG GCGCG  GG   GGC
                                   |||| |||||  ||   |||
                                   CGCC CGCGC  CC   CCG
                                     C    ___ AGA_
GAM2547 CELSR2   5'  CGGGTCAACGGCGGCGGCG   10847    AG  CGC    A
                                   CGG  CG  ACGGC GCGGCG
                                   |||  ||  ||||| ||||||
                                   GCC  GT  TGCCG CGCCGC
                                    CA  ___    C
GAM2547 CHAD     5'  GCGGGGCGCGGGCAGCGGCG  10415     A    CAC
                                   GCGG GCGCG  GGCAGCGGCG
                                   |||| |||||  ||||||||||
                                   CGCC CGCGC  CCGTCGCCGC
                                     C    ___
GAM2547 COL15A1  5'  GCGGCGCTCGGCAGCGGC    12356    GAGC   A
                                   GCG   GCGC CGGCAGCGGC
                                   |||   |||| ||||||||||
                                   CGC   CGCG GCCGTCGCCG
                                     _____   A
GAM2547 COL4A2   5'  GCGGAGCGCGGAGCCCTGG   12318        CAC  AGC
                                   GCGGAGCGCG  GGC  GG
                                   ||||||||||  |||  ||
                                   CGCCTCGCGC  TCG  CC
                                        C__  GGA
GAM2547 CPT1A    5'  GCGGCAGCGGCAGCGGCAGCGG 12424     _   C  _
                CG                   GCGG AGCG GCA CGGCAGCGGCG
                                     |||| |||| ||| ||||||||||
                                     CGCC TCGC CGT GCCGTCGCCGC
                                       G   _  C
GAM2547 CTGF     5'  GCGGAGCGGAGGGCGCGGTGGC 12502       C___  A  CA
                GGCG                   GCGGAGCG   GC CGG  GCGGCG
                                       ||||||||   || |||  ||||||
                                       CGCCTCGC   CG GCC  CGCCGC
                                          CTCC  C   AC
GAM2547 DDEF2    5'  GCGGGCGCGCACAGCCGGCG   19321     A        AG
                                     GCGG GCGCGCACGGC  CGGCG
                                     |||| ||||||||||  |||||
```

```
                                CGCC CGCGCGTGTCG  GCCGC
                                  _      __
GAM2547  DGCR2    3'  GGAGCCACAGTGGCAGCGG   23096      G   C_
                                GGAGC CGCA  GGCAGCGG
                                ||||| ||||  ||||||||
                                CCTCG GTGT  CCGTCGCC
                                  _   CA
GAM2547  EVX1     5'  GGAGCGCGACCGCGGCGG    12772        C  G  A
                                GGAGCGCG AC GC GCGG
                                |||||||| || || ||||
                                CCTCGCGC TG CG CGCC
                                    _ G  C
GAM2547  FACL4    5'  GCGGAGCGGGGGCGCGCGG   35680        CGCAC   A_
                                GCGGAGCG    GGC  GCGG
                                ||||||||    |||  ||||
                                CGCCTCGC    CCG  CGCC
                                    CC___   CG
GAM2547  FGD1     5'  GCAGCCGTGGCAGCGG     20905    G   G  CAC
                                G AGC CG   GGCAGCGG
                                | ||| ||   ||||||||
                                C TCG GC   CCGTCGCC
                                 G   _ A__
GAM2547  FMR2     5'  GCGGGCCGGCGGCGGCAGCGGC 12970      A  __   CA
           G                     GCGG GC  GCG  CGGCAGCGGCG
                                ||||  ||  |||  ||||||||||
                                CGCC CG  CGC  GCCGTCGCCGC
                                  _ GC   C_
GAM2547  FMR2     5'  CGGGGCAGAGGCAGCGGCG    12962     A   CGCAC
                                CGG GCG    GGCAGCGGCG
                                ||| |||    ||||||||||
                                GCC CGT    CCGTCGCCGC
                                  C   CT___
GAM2547  FMR2     5'  GGGCGGCAGCGGCGGCGGCG   12976    A   C   _   A
                                GG GCG GCA CGGC GCGGCG
                                || ||| ||| |||| ||||||
                                CC CGC CGT GCCG CGCCGC
                                 _  _  C    C
GAM2547  FOXG1B   5'  GCGGCGCGCGGGCGGCG     23506      A    CAC   A
                                GCGG GCGCG   GGC GCG
                                |||| |||||   ||| |||
                                CGCC CGCGC   CCG CGC
                                  G    ___   C
GAM2547  FOXG1B   5'  GGGGCGGCGGGCGGCAGCGGCG 23511    A   _  CA
                                GG GCG CG  CGGCAGCGGCG
                                || ||| ||  ||||||||||
                                CC CGC GC  GCCGTCGCCGC
                                 C   C  CC
GAM2547  GALGT    5'  GGAGCGCGGCGCGG        11187        GCAC   A
                                GGAGCGC    GGC GCGG
                                |||||||    ||| ||||
```

```
                              CCTCGCG   CCG CGCC
                                   ____  _
GAM2547 GDA     5' GCGGAGCGCAGCGCGG     20186        GCAC  A
                              GCGGAGCGC   GGC GCGG
                              |||||||||   ||| ||||
                              CGCCTCGCG   TCG CGCC
                                   ____  _
GAM2547 GPI     5' GCGAGGCGCGTGGGCGCGCGGC 6748     GA   CAC  A_
            G                  GCG  GCGCG  GGC  GCGGCG
                              |||  |||||  |||  ||||||
                              CGC  CGCGC  CCG  CGCCGC
                                TC    AC_  CG
GAM2547 GRM3    5' GCTGACCGCGGTGGCAGCGGCG 9150    G  G   CAC
                              GC GA CGCG  GGCAGCGGCG
                              || || ||||  ||||||||||
                              CG CT GCGC  CCGTCGCCGC
                               A  G   CA_
GAM2547 GTF2E2  5' GCGGCGGCGGCGGCAGCGGCG  13317     AGC  CA
                              GCGG  GCG  CGGCAGCGGCG
                              ||||  |||  ||||||||||||
                              CGCC  CGC  GCCGTCGCCGC
                                GC_  C_
GAM2547 GUCY1A2  5' GCGGCCGAGGCGGTGGCGGCG  9221      AG  CGCA  CA
                              GCGG  CG   CGG  GCGGCG
                              ||||  ||   |||  ||||||
                              CGCC  GC   GCC  CGCCGC
                                G_  TCC_  AC
GAM2547 GUCY1B3  5' GCAGAGGCGGCAGCGGC    9227       C  GCAC
                              GCGGAG GC   GGCAGCGGC
                              |||||| ||   |||||||||
                              CGTCTC CG   CCGTCGCCG
                                 _ _____
GAM2547 HDAC5   5' GCGGCGGCGGCAGCAGCGGCG  40169     A_  C  CG
                              GCGG  GCG GCA  GCAGCGGCG
                              ||||  ||| |||  |||||||||
                              CGCC  CGC CGT  CGTCGCCGC
                                GC  _  __
GAM2547 HMGA2   5' GCGGGAGCAGGCAGCGGC    18521     _   CGCAC
                              GCGG AGCG    GGCAGCGGC
                              |||| ||||    |||||||||
                              CGCC TCGT    CCGTCGCCG
                                C  ______
GAM2547 IGFBP4  5' GCGGCGCGCGGGCGAGCGGCG  11402     A    CAC  _
                              GCGG GCGCG   GGC AGCGGCG
                              |||| |||||   ||| |||||||
                              CGCC CGCGC   CCG TCGCCGC
                                G    ___  C
GAM2547 IGFBP7  5' GCGGGGTGCGGTGGCAGCGG  11412     AGC  CAC
                              GCGG  GCG  GGCAGCGG
                              ||||  |||  ||||||||
```

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                                CGCC  CGC  CCGTCGCC
                                  CCA  CA_
GAM2547 ISL1    5' GCGGAGGCGCTGCGGCGGCG  13596      C   ACG  A
                                GCGGAG GCGC  GC GCGGCG
                                |||||| ||||  || ||||||
                                CGCCTC CGCG  CG CGCCGC
                                   _   A__  C
GAM2547 KCNF1   5' CGGGGCGCGCAGGCAGCGGCG 13832    A     C
                                CGG GCGCGCA GGCAGCGGCG
                                ||| ||||||| ||||||||||
                                GCC CGCGCGT CCGTCGCCGC
                                  C     _
GAM2547 KCNMB4  5' GCGGGGAGCGCACGGACCG  30947    AGC      CAG
                                GCGG  GCGCACGG  CG
                                ||||  ||||||||  ||
                                CGCC  CGCGTGCC  GC
                                  CCT      TG_
GAM2547 KCNQ2   5' GCGGAGCGCGGGGGGCGGCG  41509        CAC  CA
                                GCGGAGCGCG  GG  GCGGCG
                                ||||||||||  ||  ||||||
                                CGCCTCGCGC  CC  CGCCGC
                                     ___  CC
GAM2547 LBX1    5' GCGGGCCAGGCAGCGGCG   27285     A  G  CAC
                                GCGG GC CG  GGCAGCGGCG
                                |||| || ||  ||||||||||
                                CGCC CG GT  CCGTCGCCGC
                                  _ _ ____
GAM2547 MAML1   5' GCGGAGCGGGCTCGCGCGCGGC 31286       C  A  _  A
           G                     GCGGAGCG GC CG GC GCGGCG
                                |||||||| || || || ||||||
                                CGCCTCGC CG GC CG CGCCGC
                                    C  A  G  _
GAM2547 MAP3K5  5' CGGGCAGCAACGGCGGCGGCG 25440    A  C  _   A
                                CGG GCG GCA CGGC GCGGCG
                                ||| ||| ||| |||| ||||||
                                GCC CGT CGT GCCG CGCCGC
                                  _  _  T   C
GAM2547 MAPK8IP1 5' GCGGAGCGCGGCGCGGAGGAGG 24158         _ A  CA___
           CGGCG                 GCGGAGCGCG C CGG    GCGGCG
                                |||||||||| | |||    ||||||
                                CGCCTCGCGC G GCC    CGCCGC
                                     C C  TCCTC
GAM2547 MAPT    5' GGGCGGTGGCAGCGGCG    32583   A  CGCAC
                                GG GCG    GGCAGCGGCG
                                || |||    ||||||||||
                                CC CGC    CCGTCGCCGC
                                  _  CA___
GAM2547 MGAT3   5' GCGGCAGCAGCGGCGGCGGCG  14460     _   C  AC  A
                                GCGG AGCG GC  GGC GCGGCG
                                |||| |||| ||  ||| ||||||
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                                CGCC TCGT CG  CCG CGCCGC
                                  G   _ __  C
GAM2547 MME     5' ACGGGGCCGGGTGGCAGTGGCG 28609     A  G  CAC    C
                                GCGG GC CG   GGCAG GGCG
                                |||| || ||   ||||| ||||
                                TGCC CG GC   CCGTC CCGC
                                  C _ CCA    A
GAM2547 MSI1    5' GCGGGCAGCGGAGCGGCGGCGG 14643     A _  CA_   A
            CG                    GCGG GC GCG   CGGC GCGGCG
                                |||| || |||   |||| ||||||
                                CGCC CG CGC   GCCG CGCCGC
                                  _ T   CTC    C
GAM2547 MYO1D   5' GGGGCGCGCACGCCGCTCGGCG 43503    A       G AG__
                                GG GCGCGCACG C    CGGCG
                                || |||||||| |    |||||
                                CC CGCGCGTGC G    GCCGC
                                 C        _ GCGA
GAM2547 NAP1L3  5' GCGGAGGTGGCAGCGGC    21211       CGCGCAC
                                GCGGAG      GGCAGCGGC
                                ||||||      |||||||||
                                CGCCTC      CCGTCGCCG
                                   CA_____
GAM2547 NEK4    5' GGGATGCGGCGGCAGCGGCG  17191   C   GC   CA
                                G GGA  GCG  CGGCAGCGGCG
                                | |||  |||  ||||||||||
                                C CCT  CGC  GCCGTCGCCGC
                                 _  A_  C_
GAM2547 NFYC    5' ACGGAGCGCGCGCGAAGCG   30592          A   C
                                GCGGAGCGCGC CGG AGCG
                                |||||||||| ||| ||||
                                TGCCTCGCGCG GCT TCGC
                                      C  _
GAM2547 NORE1   5' GCGGCAGCTTTGGCAGCGGCG  36429     _  GCGCAC
                                GCGG AGC     GGCAGCGGCG
                                |||| |||     ||||||||||
                                CGCC TCG     CCGTCGCCGC
                                  G  AAA___
GAM2547 P3      5' GCAAACGCGCGGCGGCGGCG  33379     G     AC  A
                                GCG AGCGCGC  GGC GCGGCG
                                ||| |||||||  ||| ||||||
                                CGT TTGCGCG  CCG CGCCGC
                                  _     __  C
GAM2547 PIM1    5' GGGGCTCGTGCGGCAGCG    44970    A  G  CA
                                GG GC CG  CGGCAGCG
                                || || ||  ||||||||
                                CC CG GC  GCCGTCGC
                                 C  A  AC
GAM2547 PK428   5' GCAGCAGCTGCGGCGGCGGCG  18804     _  GC  AC  A
                                GCGG AGC  GC  GGC GCGGCG
                                |||| |||  ||  ||| ||||||
```

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                                CGTC TCG  CG  CCG CGCCGC
                                  G  A_ __  C
GAM2547  PNUTL1   5'  GCGGGGCGCGACAACAAGCGGC 15432     A    C    _
             G                    GCGG GCGCG ACGGCA GCGGCG
                                  |||| ||||| |||||| ||||||
                                  CGCC CGCGC TGTTGT CGCCGC
                                    C    _     T
GAM2547  POMZP3   5'  GGAGCGCGGCGCCGGGCG    29242        _ A_  CA
                                  GGAGCGCG C  CGG  GCG
                                  |||||||| |  |||  |||
                                  CCTCGCGC G  GCC  CGC
                                       C CG  __
GAM2547  PPIC     5'  GAGCGGTGGCAGCGGC      9606       CGCAC
                                  GAGCG    GGCAGCGGC
                                  |||||    |||||||||
                                  CTCGC    CCGTCGCCG
                                     CA___
GAM2547  PPP6C    5'  GCGGCAACAGCGGCGGCGGCG  15542     AGCGC  _   A
                                  GCGG    GCA CGGC GCGGCG
                                  ||||    ||| |||| ||||||
                                  CGCC    TGT GCCG CGCCGC
                                    GT___  C   C
GAM2547  PTMS     5'  GCGGCGGCGACACGGCAGCGGC 15888     A_  C
             G                    GCGG  GCG GCACGGCAGCGGCG
                                  |||| ||| |||||||||||||
                                  CGCC  CGC TGTGCCGTCGCCGC
                                    GC  _
GAM2547  PTPRJ    5'  CGGAGACATGGCAGCGGCG   15952      CGC  C
                                  CGGAG   GCA GGCAGCGGCG
                                  |||||   ||| ||||||||||
                                  GCCTC   TGT CCGTCGCCGC
                                     ___  A
GAM2547  RFP      5'  GCGGGGGCGCACGGGCA     27132      AGC      CA
                                  GCGG   GCGCACGG  GCG
                                  ||||   ||||||||  |||
                                  CGCC   CGCGTGCC  CGT
                                    CC_      __
GAM2547  RIMS1    5'  GGAGGAGCAGCGGCGGCGGCG  43734     CGC  _   A
                                  GGAG   GCA CGGC GCGGCG
                                  ||||   ||| |||| ||||||
                                  CCTC   CGT GCCG CGCCGC
                                    CT_  C   C
GAM2547  SLIT3    5'  GCGGGGCGCTCCGGGCGGCGGC 16871     A   GCA___   A
             GGCG                   GCGG GCGC     CGGC GCGGCG
                                  |||| ||||     |||| ||||||
```

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                                CGCC CGCG     GCCG CGCCGC
                                  C   AGGCCC   C
GAM2547 ST7     3' GGAGATGGTGGCAGCGGCG  30268     CGCGCAC
                                GGAG     GGCAGCGGCG
                                ||||     ||||||||||
                                CCTC     CCGTCGCCGC
                                  TACCA__
GAM2547 TFDP1   5' GCGGGGCGGCGCGGAGAGGCG 28281     A  C A  C C
                                GCGG GCG GC CGG AG GGCG
                                |||| ||| || ||| || ||||
                                CGCC CGC CG GCC TC CCGC
                                  C  _ C  _ T
GAM2547 TFDP1   5' GCGGAGCGCGGGGCGGC    28280        CAC  CA
                                GCGGAGCGCG  GG  GCGGC
                                ||||||||||  ||  |||||
                                CGCCTCGCGC  CC  CGCCG
                                      ___ __
GAM2547 TMEFF2  5' GCGGCAGCAGAGGCGGCGGCG 32104     _   CGCAC  A
                                GCGG AGCG    GGC GCGGCG
                                |||| ||||    ||| ||||||
                                CGCC TCGT    CCG CGCCGC
                                  G   CT___  C
GAM2547 TMEPAI  5' GCGGGGCGCGCGCTGC     33611     A    ACG  A
                                GCGG GCGCGC  GC GC
                                |||| ||||||  || ||
                                CGCC CGCGCG  CG CG
                                  C    ___ A
GAM2547 TP53BP2 5' GCGGCGGCGGCGGCAGCGGCG 24061     AGC  CA
                                GCGG  GCG  CGGCAGCGGCG
                                ||||  |||  ||||||||||
                                CGCC  CGC  GCCGTCGCCGC
                                  GC_  C_
GAM2547 TPM1    5' GCGAGCGCGCGGTCGGC    7486     G     AC  CAG
                                GCG AGCGCGC  GG  CGGC
                                ||| |||||||  ||  ||||
                                CGC TCGCGCG  CC  GCCG
                                  _     __ A__
GAM2547 UBTF    5' GCGGAGCGCGGCGCG      30613        GCAC  A
                                GCGGAGCGC   GGC GCG
                                |||||||||   ||| |||
                                CGCCTCGCG   CCG CGC
                                     ____  _
GAM2547 USP13   5' GCGGGGTCTGCCGGCGGCGGCG 19482     AGCGC  A  A
                                GCGG    GC CGGC GCGGCG
                                ||||    || |||| ||||||
                                CGCC    CG GCCG CGCCGC
                                  CCAGA  _   C
GAM2547 WEE1    5' GCGGACGGTGGCGGCAGCGGCG 18097      G  CGCA
                                GCGGA CG   CGGCAGCGGCG
                                |||||  ||  ||||||||||
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                                CGCCT GC   GCCGTCGCCGC
                                  _ CACC
GAM2547 WNT6    5' GCGAGCGCAACGGCGGCG   27182    G    C    A
                                GCG AGCGCG ACGGC GCG
                                ||| |||||| ||||| |||
                                CGC TCGCGT TGCCG CGC
                                  _    _   C
GAM2547 WT1     5' GCGGAGCGTGTGCTGAGACG  35962       CGCACG  AGC
                                GCGGAGCG    GC  GGCG
                                ||||||||    ||  ||||
                                CGCCTCGC    CG  CTGC
                                    ACA___ ACT
GAM2547 YWHAB   5' GTGGCTGCAGCGGCGGCGGCG 18187  GA  GC  _   A
                                G  GC  GCA CGGC GCGGCG
                                |  ||  ||| |||| ||||||
                                C  CG  CGT GCCG CGCCGC
                                 AC  A_  C   C
GAM2547 ZNF10   5' GCGGAGCGCGAAGAGCGGCG  31737        CAC  C
                                GCGGAGCGCG  GG AGCGGCG
                                ||||||||||  || |||||||
                                CGCCTCGCGC  TC TCGCCGC
                                     T__ _
GAM2547 ZNF219  5' GCGGGCGGCGGCGGCGGCG   32329    A  C  AC  A
                                GCGG GCG GC  GGC GCGGCG
                                |||| ||| ||  ||| ||||||
                                CGCC CGC CG  CCG CGCCGC
                                  _  _ __  C
GAM2547 ZNF219  5' GCGGAGCGGGCGGCGGCGGCG 32328       C  AC  A
                                GCGGAGCG GC  GGC GCGGCG
                                |||||||| ||  ||| ||||||
                                CGCCTCGC CG  CCG CGCCGC
                                    C __  C
GAM2547 ZNF278  5' GCGGGGCGCGCACGGGGGCGG 36799    A       CA
                                GCGG GCGCGCACGG  GCGG
                                |||| ||||||||||  ||||
                                CGCC CGCGCGTGCC  CGCC
                                  C        CC
GAM2547 AVPR1A  5' CTCGCAGCTTGCCGGGCT   8726        CA_ AGAT
                                CTCGCAGCT   CG   GGCT
                                |||||||||   ||   ||||
                                GAGCGTCGA   GC   CCGA
                                    ACG ____
GAM2547 BACE    5' CTCGCAGCTCCCGGGCGGGC  39959        A  AGAT
                                CTCGCAGCTC CG   GGC
                                |||||||||| ||   |||
                                GAGCGTCGAG GC   CCG
                                     G  CCGC
GAM2547 DNASE1L1 5' CTCAGCTTCTCATGGGATGGCT 27492    _ AG   CGA
          G                    CTC GC  CTCA  GATGGCTG
                               ||| ||  ||||  ||||||||
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                                GAG CG  GAGT   CTACCGAC
                                  T  AA    ACC
GAM2547  PCDH7    5'  ACTCACAGTTCACGGGACACTG 37107        C    A   G
                C                  ACTCGCAG TCACG GATG CTGC
                                   |||||||| ||||| |||| ||||
                                   TGAGTGTC AGTGC CTGT GACG
                                       A    C   _
GAM2547  PPT2     3'  CTCGCAGCTCGTGAATCTCCTG 39918          AC   ATGG
                C                  CTCGCAGCTC  GAG   CTGC
                                   ||||||||||  |||   ||||
                                   GAGCGTCGAG  CTT   GACG
                                         CA   AGAG
GAM2547  RHO      3'  GCTGCTCCTGGTGGGATGGCTG 8063     A    ACGA___
                                   GC GCTC      GATGGCTG
                                   || ||||      ||||||||
                                   CG CGAG      CTACCGAC
                                    A   GACCACC
GAM2547  SLC5A1   3'  CTCCAGTAGGTACAGATGGCTG 7361      G   CTC__  G
                                   CTC CAG    AC AGATGGCTG
                                   ||| |||    || |||||||||
                                   GAG GTC    TG TCTACCGAC
                                    _   ATCCA  _
GAM2548  ARSD     3'  GTGCAGCTGCAGAACGTGA   11697         CGC    C C
                                   GTGCAGCTGC   AGAGC G GA
                                   ||||||||||   ||||| | ||
                                   CACGTCGACG   TCTTG C CT
                                          ___    _ A
GAM2548  HLX1     5'  GCGCGGCTGCCGCAGTCCAGCC 34987      A        ___    C
                GGA                   GTGC GCTGCCGCAG   AGCCG GA
                                   |||| ||||||||||   ||||| ||
                                   CGCG CGACGGCGTC   TCGGC CT
                                     C        AGG    _
GAM2548  IHPK1    3'  GTGCAGCTTTGCTCGCTGTGAG 45495        __ _  A__
                                   GTGCAGCT  GC CGC   GAG
                                   ||||||||  || |||   |||
                                   CACGTCGA  CG GCG   CTC
                                        AA  A   ACA
GAM2548  KCNN2    5'  GCGCAGCTGTTGCACCGGA   34667         CC  AGA   C
                                   GTGCAGCTG  GC   GCCG GA
                                   |||||||||  ||   |||| ||
                                   CGCGTCGAC  CG   TGGC CT
                                        AA  ____   _
GAM2548  LEF1     5'  GCAGCTGCCGCGGCGCCCGAA  32208          AGA   G
                                   GCAGCTGCCGC   GCC CGAA
                                   ||||||||||   ||| ||||
                                   CGTCGACGGCG   CGG GCTT
                                         CCG   _
GAM2548  LTK      5'  GTGTGCTGCCGCTGGCGA    14266     CA      AGAGCC
                                   GTG  GCTGCCGC     GCGA
                                   |||  ||||||||     ||||
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                                CAC  CGACGGCG     CGCT
                                  A_       AC____
GAM2548  MUC4     3'  GTGCAGCTGTCTCTGAGCGTGA 39672         CCGCA    C C
                A                  GTGCAGCTG     GAGC G GAA
                                   |||||||||     |||| | |||
                                   CACGTCGAC     CTCG C CTT
                                         AGAGA    _ A
GAM2548  PYGB     5'  GTGCAGCTGCTCTGGCGCG    16050          CGCAGA  C
                                   GTGCAGCTGC      GC GCG
                                   ||||||||||      || |||
                                   CACGTCGACG      CG CGC
                                         AGAC__  _
GAM2548  RAGE     3'  GCAGCTGCGCGGGCCGCG    30603         C  AGA
                                   GCAGCTGC GC   GCCGCG
                                   ||||||||  ||   ||||||
                                   CGTCGACG CG   CGGCGC
                                        _  CC_
GAM2548  TNFRSF7  3'  GTGCAGCTACCGCAGGTGC    10305             A_
                                   GTGCAGCTGCCGCAG  GC
                                   ||||||||||||||  ||
                                   CACGTCGATGGCGTC  CG
                                            CA
GAM2548  DSC2     5'  GTGCTTTTCTTAGCTTCTCTG  35939       CCACGCGC
                                   GTGCT       AGCTTCTCTG
                                   |||||       ||||||||||
                                   CACGA       TCGAAGAGAC
                                      AAAGAA__
GAM2548  SLC22A3  3'  GTGCACCTGACAGCTTCT    35053      T  ACGC
                                   GTGC CC    GCAGCTTCT
                                   ||||  ||    |||||||||
                                   CACG GG    TGTCGAAGA
                                     T  AC__
GAM2549  GNPAT    5'  GCCGTGGTGGTGCTCCTGCTGG 30623        TAGCG  _  G
                                   GCCGTG     GG GC CCTGCTGG
                                   ||||||     || || ||||||||
                                   CGGCAC     CC CG GGACGACC
                                      CA___  A  A
GAM2549  WIF1     3'  GCCTGAGCTGGGCGCCTGCTGG 41167     G  T   G
                                   GCC TG AGC GGGCGCCTGCTGG
                                   ||| || ||| ||||||||||||
                                   CGG AC TCG CCCGCGGACGACC
                                     _  _   A
GAM2550  CHD2     3'  TAATATAGGTGTAATGAGAATC 10450           TTTGCGCA
                TC                   TAATATAGGTGTA       CTC
                                     ||||||||||||        |||
                                     ATTATATCCACAT       GAG
                                           TACTCTTA
GAM2550  STARD4   3'  AATATAGAATCCTTTGTGCATT 40121         TGTA   C   C
                C                    AATATAGG    TTTG GCA TC
                                     ||||||||    |||| ||| ||
```

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                                TTATATCT    AAAC CGT AG
                                    TAGG    A   A
GAM2551  DSC2     3'  GCAAGAATGCAGTCTAC     35938      AT  CTCA
                                GCAA  GT    CAGTCTAC
                                ||||  ||    ||||||||
                                CGTT  TA    GTCAGATG
                                  CT  C___
GAM2551  EDNRA    3'  TGCTGTACTCACAGTCT     42002      AAA  _
                                TGC   TGT CTCACAGTCT
                                |||   ||| ||||||||||
                                ACG   ACA GAGTGTCAGA
                                  ___   T
GAM2551  ENPP2    3'  CAATGCAAATATCAAATCT    26302            TCAC
                                CAATGCAAATGTC    AGTCT
                                ||||||||||||    |||||
                                GTTACGTTTATAG    TTAGA
                                       T___
GAM2551  HERC2    3'  GCAGCCTACAGTCTA       21692      AAT    C
                                GCA   GTCT ACAGTCTA
                                |||   |||| ||||||||
                                CGT   CGGA TGTCAGAT
                                  ___   _
GAM2551  HMG20A   3'  ATGCAAATGTTTCAAGTC    32865          C   C
                                ATGCAAATGT TCA AGTC
                                |||||||||| ||| ||||
                                TACGTTTACA AGT TCAG
                                      A   _
GAM2551  NOV      3'  GCAATGTGAAACAGTCTA    14809      A   CTC
                                GCAA TGT   ACAGTCTA
                                |||| |||   ||||||||
                                CGTT ACA   TGTCAGAT
                                  _   CTT
GAM2551  PDE6D    3'  ATGTAATAATATCACAGTCTA  15159     CAAAT  C
                                ATG    GT TCACAGTCTA
                                |||    || ||||||||||
                                TAC    TA AGTGTCAGAT
                                  ATTAT  T
GAM2551  RALBP1   3'  AATGCAAATGTCTGTCAAT    27694            CA
                                AATGCAAATGTCT  CAGT
                                ||||||||||||  ||||
                                TTACGTTTACAGA  GTTA
                                       CA
GAM2551  RNF26    3'  TGAAATGTGCACAGTCT     36756    C     CT
                                TG AAATGT  CACAGTCT
                                ||  ||||||  ||||||||
                                AC TTTACA  GTGTCAGA
                                  _     C_
GAM2551  RRM2B    3'  CAAATGTCTCTCTA        42711          ACAG
                                CAAATGTCTC    TCTA
                                ||||||||||    ||||
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                              GTTTACAGAG   AGAT
                                    ____
GAM2551  SLC6A4   3'  GCTGTGTCACAGTCTA     9821     AAA  C
                              GC  TGT TCACAGTCTA
                              ||  ||| ||||||||||
                              CG  ACA AGTGTCAGAT
                               ___  C
GAM2552  CARKL    3'  TCAGGAATGTTAATCAGGTAAA 30003       C  C  C
                              TCAGGAA TG TAA CAGGTAAA
                              ||||||| || ||| ||||||||
                              AGTCCTT AC ATT GTCCATTT
                                  _ A  A
GAM2552  EGLN3    3'  TTCAGGAACCGTTACTAA    35213         ___
                              TTCAGGAACT  GCTAA
                              ||||||||||  |||||
                              AAGTCCTTGG  TGATT
                                    CAA
GAM2552  GYS1     5'  GGAATGCACCAGGTA      44789     C  TA
                              GGAA TGC  ACCAGGTA
                              |||| |||  ||||||||
                              CCTT ACG  TGGTCCAT
                                _  __
GAM2552  MTR      3'  GGAACTTATCACCAGGTAA   7018       GCTA
                              GGAACT   ACCAGGTAA
                              ||||||   |||||||||
                              CCTTGA   TGGTCCATT
                                 ATAG
GAM2552  MYD88    3'  TCCAGGAATTGAGAGGTAA   14720       C  CTAACC
                              TTCAGGAA TG     AGGTAA
                              |||||||| ||     ||||||
                              AGGTCCTT AC     TCCATT
                                   A  TC____
GAM2552  PPGB     3'  TTCAGGAACTGCTGCGG     7177           AACCA
                              TTCAGGAACTGCT    GG
                              ||||||||||||    ||
                              AAGTCCTTGACGA    CC
                                     CG___
GAM2552  SELL     3'  AGGAACTGTTGGTCAGGTA   8508        CTAAC
                              AGGAACTG    CAGGTA
                              ||||||||    ||||||
                              TCCTTGAC    GTCCAT
                                   AACCA
GAM2552  TXNRD1   3'  TTCAAGAACTGCTGGCAGG   17774          AAC
                              TTCAGGAACTGCT  CAGG
                              ||||||||||||  ||||
                              AAGTTCTTGACGA  GTCC
                                     CC_
GAM2552  TYROBP   3'  TTCAGGAATGGCTGGATCCAGG 17776       CT  AA__
                              TTCAGGAA  GCT   CCAGG
                              ||||||||  |||   |||||
```

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                                AAGTCCTT  CGA   GGTCC
                                    AC   CCTA
GAM2553  FSTL1    3'  GCTATGTATCTAGAGG     28218     AGA
                                GTTA   GTATCTAGAGG
                                ||||   ||||||||||
                                CGAT   CATAGATCTCC
                                  A__
GAM2553  GABPB1   3'  TATACAGTATAGATAACCTAGA 23527        TA   GT
            GG                    TATACAGT  AGA  ATCTAGAGG
                                ||||||||  |||  |||||||||
                                ATATGTCA  TCT  TGGATCTCC
                                    TA   AT
GAM2553  MPP1     3'  TATACAGTTGAAGGCAAAGGAG 14625         _   A   TCTA
            G                     TATACAGTT AAG GTA    GAGG
                                |||||||||| ||| |||    ||||
                                ATATGTCAA TTC CGT    CTCC
                                    C   _   TTC_
GAM2553  FGA      3'  TATTTATTGAGTCATGGC    34839       GC       C
                                TATTTA  TGAGTCAT GGT
                                ||||||  |||||||| |||
                                ATAAAT  ACTCAGTA CCG
                                  A_       _
GAM2553  TERF1    3'  TTAGCTGAGTATAC       32746          CATCG
                                TTAGCTGAGT    GTAC
                                ||||||||||    ||||
                                AATCGACTCA    TATG
                                    _____
GAM2553  ZNF26    5'  TTTAGCTGGTCAAGT      43807         A    TC
                                TTTAGCTG GTCA  GGT
                                |||||||| ||||  |||
                                AAATCGAC CAGT  TCA
                                    _   __
GAM2554  KCNJ8    5'  TGGGGGCTGCGTGTCCTAAGGA 22545    A           CTA
            G                     TG GGGCTGCGTGTTCTA   GAG
                                || ||||||||||||||   |||
                                AC CCCGACGCACAGGAT   CTC
                                 C            TC_
GAM2554  NDRG2    3'  TGAGGGCTGGGTCCCACTCTAG 32197         CGT       AG
                                TGAGGGCTG   GTTCTACT  AG
                                |||||||||   ||||||||  ||
                                ACTCCCGAC   CAGGGTGA  TC
                                    C__       GA
GAM2554  APLP2    3'  CAGTTCTACAGTAGTACT    44918         A  AAG  G
                                CAGTTCTG CA   AG ACT
                                |||||||| ||   || |||
                                GTCAAGAT GT   TC TGA
                                    _ CA_  A
GAM2554  BRCA1    3'  TAAGTTCTCTTCTGAGGACTCT 28640    C     GACAAA
                                A AGTTCT     GAGGACTCT
                                | ||||||     |||||||||
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```
                                A TCAAGA     CTCCTGAGA
                                 T     GAAGA_
GAM2554 ELOVL4   3' AGTTCTGACTACTCT      35537         AAAGAGG
                                AGTTCTGAC      ACTCT
                                |||||||||      |||||
                                TCAAGACTG      TGAGA
                                     A_______
GAM2554 KAI1     5' CACAGCAGCAGGGAGGACTCT  13785       TCTGA  AA
                                TACAGT    CA  GAGGACTCT
                                ||||||    ||  |||||||||
                                GTGTCG    GT  CTCCTGAGA
                                   TC____  CC
GAM2554 SLC21A2  3' AGGAACTGTGGGGAGGACTCT  24794    TT_   ACAAA
                                AG   CTG    GAGGACTCT
                                ||   |||    |||||||||
                                TC   GAC    CTCCTGAGA
                                 CTT   ACCC_
GAM2554 TIMM23   3' AGCTCTGACAGAGACT      26748         AA   G
                                AGTTCTGACA  GAG ACT
                                ||||||||||  ||| |||
                                TCGAGACTGT  CTC TGA
                                      __   _
GAM2555 SIAT7D   3' TAAATGTTTTTGTGGAGTGT   30833         AGACT
                                TAAATGTTT    TGGAGTGT
                                |||||||||    ||||||||
                                ATTTACAAA    ACCTCACA
                                     AAC__
GAM2555 BNC      3' TGACATTTAGGTCATCACTTGT 11856            A  A_
            TCT                   TGACATTTAGGTCA CG  TGTTCT
                                |||||||||||||| ||  ||||||
                                ACTGTAAATCCAGT GT  ACAAGA
                                       A  GA
GAM2555 CALB1    3' ATTTAGGTCATATTC       22308          ACGA
                                ATTTAGGTCA    TGTTC
                                ||||||||||    |||||
                                TAAATCCAGT    ATAAG
                                      _____
GAM2555 IGF1     3' TGACATTTTGGTTGCTCC    8356         A   CAACGA
                                TGACATTT GGT     TGTTCT
                                |||||||| |||     ||||||
                                ACTGTAAA CCA     ACGAGG
                                     A  _______
GAM2556 MTMR8    3' CCATACAGTGCAATTTTATT   31751        A  AAT
                                CCATATA TG   GTTTTATT
                                ||||||| ||   ||||||||
                                GGTATGT AC   TAAAATAA
                                   C  GT_
GAM2556 TTR      3' CACAGGAATGTTTTATT     7496       TAAT
                                CATA    GAATGTTTTATT
                                ||||    ||||||||||||
```

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                                GTGT   CTTACAAAATAA
                                  C___
GAM2556 ZNF75   3' TACCCTTCCCAAATGTTTTATT 28326     ATATAA
            A                    TACC     TGAATGTTTTATTA
                                 ||||     ||||||||||||||
                                 ATGG     GTTTACAAAATAAT
                                   GAAGG_
GAM2557 ACTR1B  3' TGACACACCAGTGGGAGCTG  43347       _  TCT  AA
                                 TGACACAC AGT  GGA  CTG
                                 |||||||| |||  |||  |||
                                 ACTGTGTG TCA  CCT  GAC
                                      G  C__  C_
GAM2557 FLRT3   3' TATGAATGCAGTCCTGA    30007      CACA
                                 TATGA   CAGTTCTGG
                                 |||||   |||||||||
                                 ATACT   GTCAGGACT
                                   TAC_
GAM2557 FOXI1   3' CATGACATGCACACAGGAAACT 29150       __   GTTCT
            G                    TATGACA  CACA    GGAAACTG
                                 |||||||  ||||    ||||||||
                                 GTACTGT  GTGT    CCTTTGAC
                                    AC   GT___
GAM2557 PCSK1   3' TATGATCAATTCTGGAA    7753       CACA
                                 TATGA   CAGTTCTGGAA
                                 |||||   ||||||||||
                                 ATACT   GTTAAGACCTT
                                   A___
GAM2557 RALB    5' TGACACACAGATGACCCACTG  16148        TTC  AA_
                                 TGACACACAG   TGG   ACTG
                                 ||||||||||   |||   ||||
                                 ACTGTGTGTC   ACT   TGAC
                                      T__   GGG
GAM2557 RASA1   3' ATGACAAACTCTGGAAACTG  35486      C  AGT
                                 ATGACA AC   TCTGGAAACTG
                                 |||||| ||   ||||||||||
                                 TACTGT TG   AGACCTTTGAC
                                   T  ___
GAM2557 TARBP2  3' CATGACACACAGTGGCCGG   39528          T_
                                 TATGACACACAGT  CTGG
                                 ||||||||||||  ||||
                                 GTACTGTGTGTCA  GGCC
                                       CC
GAM2557 TRIM14  3' CATGACATTCTGGAGGCT    37697       CACAG     AA
                                 TATGACA    TTCTGGA  CT
                                 |||||||    |||||||  ||
                                 GTACTGT    AAGACCT  GA
                                    _____     CC
GAM2558 CDC42   3' CGTCCTAGAAAAGAGGAGGG  12157       C  TC   A
                                 CGTCCTA AA  AGAG AGGG
                                 ||||||| ||  |||| ||||
```

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                                GCAGGAT TT  TCTC TCCC
                                    C  T_   C
GAM2558  HTRA3    3'  TTCGTCCTGATCTCGGGGGG  44839        ACA   AGAGAA
                                TTCGTCCT   ATC     GGG
                                ||||||||   |||     |||
                                AAGCAGGA   TAG     CCC
                                    C__   AGCCC_
GAM2558  ITGAM    3'  TTCGTGCCTCATGGGAGAAGGG 43524      _   A  ATCA
            A                    TTCGT CCT CA    GAGAAGGGA
                                ||||| ||| ||    |||||||||
                                AAGCA GGA GT    CTCTTCCCT
                                  C   _  ACC_
GAM2558  MGP      5'  TTCGTCCTGCAGGTCAGTCTCA 9465         A  A_    AGA_
           GGG                    TTCGTCCT CA  TCAG    AGGG
                                ||||||||  ||  ||||    ||||
                                AAGCAGGA GT  AGTC    TCCC
                                    C  CC    AGAG
GAM2558  PKIA     3'  TTCATAAGCAATCAGAGAGGGG 27748      CCTA        A
                                TTCGT    CAATCAGAGA GGG
                                |||||    |||||||||| |||
                                AAGTA    GTTAGTCTCT CCC
                                  TTC_        C
GAM2558  PTPRA    5'  TTCATCTTTAGGAGAAGGG   38921       CTACAATCA
                                TTCGTC       GAGAAGGG
                                ||||||       ||||||||
                                AAGTAG       CTCTTCCC
                                   AAATC____
GAM2558  RERE     3'  GTCCTACAATTCTTGGGA    29033         CAGAGAA
                                GTCCTACAAT      GGGA
                                ||||||||||      ||||
                                CAGGATGTTA      CCCT
                                    AGAA___
GAM2559  NEBL     3'  GTGGAAAGTGGAAAAGTTG   26905        ____
                                GTGGAAA   AGAAGTTG
                                |||||||   ||||||||
                                CACCTTT   TTTTCAAC
                                    CACC
GAM2559  SIRT1    3'  TGTGGAAAAGATCAATGC    29256         AGT_
                                TGTGGAAAAGA   TGC
                                ||||||||||   |||
                                ACACCTTTTCT   ACG
                                    AGTT
GAM2559  ST7      3'  TATGGAAATATATAGTTGC   30272        AGA__
                                TGTGGAAA    AGTTGC
                                ||||||||    ||||||
                                ATACCTTT    TCAACG
                                    ATATA
GAM2559  TAL1     3'  TGGAAAAGAATAAAGGTTG   17292         _____
                                TGGAAAAGAA    GTTG
                                ||||||||||    ||||
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                                ACCTTTTCTT    CAAC
                                     ATTTC
GAM2559  EPS8    3'  AATTGTGTTTCCAAAAATAACA 20808      A       CTT_
             TTT                   AATTG GTTTCCAAA   ACATTT
                                |||||| |||||||||   ||||||
                                TTAAC CAAAGGTTT   TGTAAA
                                   A       TTAT
GAM2559  IMPG2   5'  AATTGAGTGTCCAAATCCT   32187        T    _
                                AATTGAGT TCCAAA CTT
                                |||||||| |||||| |||
                                TTAACTCA AGGTTT GGA
                                     C     A
GAM2559  LANCL1  3'  ATTGAGTTTCTTTTAAACATTT 25850         CAAACTT
                                ATTGAGTTTC      ACATTT
                                ||||||||||      ||||||
                                TAACTCAAAG      TGTAAA
                                     AAAATT_
GAM2559  PTPRF   3'  ATTGAGTTTCCCTGCATT    39028          AAACTTA
                                ATTGAGTTTCC      CATT
                                ||||||||||      ||||
                                TAACTCAAAGG      GTAA
                                     GAC____
GAM2559  RNMT    3'  AATTGAGTTTTAAACTT     19143          CC
                                AATTGAGTTT  AAACTT
                                |||||||||  ||||||
                                TTAACTCAAA  TTTGAA
                                     A_
GAM2560  FZD10   3'  TGTGGAAATCATTTGTT     28463         T  AAA
                                TGTGGAAAT CA   TTGTT
                                ||||||||| ||   |||||
                                ACACCTTTA GT   AACAA
                                     _  A__
GAM2560  RDS     3'  TGTGGACAATTAGTGTTGTCC  7248        AATTCAAAAT
                                TGTGGA         TGTTGTCC
                                ||||||         ||||||||
                                ACACCT         ACAACAGG
                                   GTTAATC___
GAM2560  SRRM1   3'  TGTGGTAGTTCAAAACAGTGGT 25194       AAA       T  T
             C                   TGTGG   TTCAAAAT GT GTC
                                |||||   |||||||| || |||
                                ACACC   AAGTTTTG CA CAG
                                   ATC       T  C
GAM2560  TGFB3   5'  TGTAGCGCTGGGATTGTTGTCC 17463       AAATTCAAA
                                TGTGG        ATTGTTGTCC
                                |||||        ||||||||||
                                ACATC        TAACAACAGG
                                   GCGACCC__
GAM2560  IRTA1   3'  TCTCAGTTTATGTTTTGCT   36356         TG    TC
                                TCTCAGTTT  GTTTT  GCT
                                |||||||||  |||||  |||
```

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                                AGAGTCAAA  CAAAA  CGA
                                     TA    __
GAM2560  ITGA4    5'  CGTCCAGTTCTTTCG      9424      T     TGGTT
                                CGTC CAGTTT    TTTCG
                                |||| ||||||    |||||
                                GCAG GTCAAG    AAAGC
                                  _    _____
GAM2560  KERA     5'  GTCTCAGTCTGAGGTTTGCTA  28154         T_    TTC
                                GTCTCAGTTT  GGTTT   GCTA
                                ||||||||||  |||||  ||||
                                CAGAGTCAGA  CCAAA   CGAT
                                     CT    ___
GAM2560  NCALD    3'  GTCTTAGGTTAATTCGCT    36770      _   T_
                                GTTTT GGTT  TTCGCT
                                ||||| ||||  ||||||
                                CAGAA CCAA  AAGCGA
                                   T   TT
GAM2560  PHYH     3'  CGTTTGGTTTTGGTTTTC    26315     CTCA
                                CGT   GTTTTGGTTTTT
                                |||   ||||||||||||
                                GCA   CAAAACCAAAAG
                                  AAC_
GAM2561  PLS3     3'  TAAGGTACATTTTTCTTCTA  22760         _      CA
                                TAAGGTAC TTTTTCT  TA
                                |||||||| |||||||  ||
                                ATTCCATG AAAAAGA  AT
                                     T      AG
GAM2562  CASP7    3'  TTTAAAGCTATAACAGATT   10278         TA
                                TTTAAAGTT  AACAGATT
                                |||||||||  ||||||||
                                AAATTTCGA  TTGTCTAA
                                     TA
GAM2563  ADCY9    3'  GCGGGTGGGCAATGGGGGGTG  10020     T   T___
                                GTG GTGG   TGGGGGGTG
                                ||| ||||   |||||||||
                                CGC CACC   ACCCCCCAC
                                  C   CGTT
GAM2563  ADORA2A  3'  GAGAGTGGTGTGTGGGTGGC  8602     A   T  GT   G
                                GA AGTG GTG  TGGG GGT
                                || |||| |||  |||| |||
                                CT TCAC CAC  ACCC CCG
                                 C   _  AC   A
GAM2563  HHLA1    5'  GAAAATTTTTGGGGGGTG    25050       GTGTGG
                                GAAAGT     TTGGGGGGTG
                                ||||||     ||||||||||
                                CTTTTA     AACCCCCCAC
                                   AA____
GAM2563  LENG4    5'  GAAGGTGGGTGGGCTGGGTGGT 35885     A  T   _    G
                                GAA GTG GTGG TTGGG GGT
                                ||| ||| |||| ||||| |||
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                                CTT CAC CACC GACCC CCA
                                  C  C   C    A
GAM2563  RGS19IP1  3'  GAAAGTGGTGGAGGCGGGGGTG 41696       T   TTG_
                                GAAAGTG GTGG   GGGGGTG
                                ||||||| ||||   |||||||
                                CTTTCAC CACC   CCCCCAC
                                    _   TCCG
GAM2563  SORCS1   3'  GAAAGTGTTGCTTGGGTGGT  38099       G  G   G
                                GAAAGTGT TG TTGGG GGT
                                |||||||| || ||||| |||
                                CTTTCACA AC AACCC CCA
                                     _ G   A
GAM2563  DTNB     3'  GGGAAGACCTTGCCTTCGC   37607     TTTC      C
                                GGG   ACCTTGCC TCGC
                                |||   |||||||| ||||
                                CCC   TGGAACGG AGCG
                                  TTC_      A
GAM2563  ELAC2    5'  CCCGCGTTTCCCGTGCCCTCG  32853     G    A  T
                                CCCG GTTTC CC TGCCCTCG
                                |||| ||||| || ||||||||
                                GGGC CAAAG GG ACGGGAGC
                                  G    _ C
GAM2563  IGBP1    3'  AGCATCTTTGCCCTCG      11389     T  ACC
                                GGT TC   TTGCCCTCG
                                ||| ||   |||||||||
                                TCG AG   AACGGGAGC
                                  T  A__
GAM2563  PMP2     3'  GTTCCTACCTTGCCCTTGC   15422      _       C
                                GTTTC ACCTTGCCCT GC
                                ||||| |||||||||| ||
                                CAAGG TGGAACGGGA CG
                                   A        A
GAM2563  SCD      3'  GGGTTCTTGCCCTTGC      22831      TCAC      C
                                GGGTT   CTTGCCCT GC
                                |||||   |||||||| ||
                                CCCAA   GAACGGGA CG
                                   ____       A
GAM2563  SCG2     3'  ACCTGGTTTCATCTGCC     18444     CG     CC
                                ACC  GGTTTCA  TTGCC
                                |||  |||||||  |||||
                                TGG  CCAAAGT  GACGG
                                  A_     A_
GAM2563  TAL1     5'  ACCCGGGTCTTTGCTTTCCCCC 17276         CAC   G
                                ACCCGGGTTT   CTT CCCTC
                                ||||||||||   ||| |||||
                                TGGGCCCAGA   GAA GGGGG
                                      AAC   A
GAM2564  ARF3     3'  TGAAGATGGTGGGGAAGGAT   11678        A  AA  C_
                                TGAAGATG TG  GA  GAT
                                |||||||| ||  ||  |||
```

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                                ACTTCTAC AC  CT  CTA
                                     C  CC  TC
GAM2564 ATP8B2   5'  TGAGGATGATGATGTAGGACCA 42218     A       AGACGAT
                                TGA GATGATGA      GACCA
                                ||| ||||||||      |||||
                                ACT CTACTACT      CTGGT
                                  C       ACATC__
GAM2564 BCL2L2   3'  GATGATGAAGGAACAAGGCCA  19741          __    TGA
                                GATGATGAAG  ACGA   CCA
                                ||||||||||  ||||   |||
                                CTACTACTTC  TGTT   GGT
                                      CT    CC_
GAM2564 DDT      3'  TGAGGATGAAGAAGAGGAT   10672     A    T    C
                                TGA GATGA GAAGA GAT
                                ||| ||||| ||||| |||
                                ACT CTACT CTTCT CTA
                                  C    T    C
GAM2564 KCNS2    3'  TAAAGATGATGGAGAAGA    42837          A   C
                                TGAAGATGATG AGA GA
                                |||||||||||| ||| ||
                                ATTTCTACTAC TCT CT
                                      C   T
GAM2564 POU2F2   3'  TGAAGAGGATGAGGAGGAGAGG 15463       T    A  C  T  __
           CCA                    TGAAGA GATGA GA GA GA  CCA
                                ||||||  ||||| || || ||  |||
                                ACTTCT CTACT CT CT CT  GGT
                                   C    C  C  _  CC
GAM2564 PPP1R3D  3'  TGGAGGGTGGTGAAGAACAACC 26428    A  A_  A     CG TG
           A                     TG AG  TG TGAAGA  A  ACCA
                                || ||  || ||||||  |  ||||
                                AC TC  AC ACTTCT  T  TGGT
                                 C  CC  C     __ GT
GAM2564 UBE1     3'  GATGATGAGGGAACACCA    17781        AGAC  TG
                                GATGATGA   GA  ACCA
                                ||||||||   ||  ||||
                                CTACTACT   CT  TGGT
                                     CC__  TG
GAM2564 XRCC5    3'  TGAGGGTGCTGAAGACAGAGGT 34494     AGA  A     _  __
           GAC                    TGA   TG TGAAGAC GA  TGAC
                                |||   || |||||||  ||  ||||
                                ACT   AC ACTTCTG CT  ACTG
                                  CCC  G      T  CC
GAM2565 ATP11A   3'  ACGTTTGTAGTGAATG     44169    T    ATCTAT
                                AC TTTGT     GGTGAATG
                                || |||||     ||||||||
                                TG AAACA     TCACTTAC
                                 C    _______
GAM2565 CLCA3    3'  CTTTTGTATCGTCCATGT    22263          TATG  GA
                                CTTTTGTATC   GT  ATGT
                                ||||||||||   ||  ||||
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                                GAAAACATAG   CA  TACA
                                     ____ GG
GAM2566  DMD     5'  TTTTGCTGATTTCCCTGT    19701         C_   A
                                TTTTGCTGG  TCC TTGT
                                |||||||||  ||| ||||
                                AAAACGACT  AGG GACA
                                     AA   _
GAM2566  FABP2   3'  TTTTCTGGCTGAGCATATATTA 6590      G     CCATT
                                TTTT CTGGCT    GTATATTA
                                |||| ||||||    ||||||||
                                AAAA GACCGA    TATATAAT
                                  _    CTCG_
GAM2566  IFRD1   3'  TTTTGCTGTCTTCATAAATAAA 41110        G  C   T_   T
            TTA                   TTTTGCTG CT CAT  GTA ATTA
                                |||||||| || |||  ||| ||||
                                AAAACGAC GA GTA  TAT TAAT
                                     A  A   TT   T
GAM2567  GFRA1   3'  AATGTAGGCTGAAATTTATATC 23562       ATATAAT
            AT                    AATGTA      ATTTATATCAT
                                ||||||      ||||||||||
                                TTACAT      TAAATATAGTA
                                   CCGACTT
GAM2568  AXUD1   5'  CGTCCCGGCCGGGGACGCCCC  37488    AGGA
                                CG   GGCCGGGGACGCCCC
                                ||   ||||||||||||||
                                GC   CCGGCCCCTGCGGGG
                                 AGGG
GAM2568  COL6A2  5'  CCGAGGAGGCTCCGCTCC    38436         CGGGGA  _
                                CCGAGGAGGC     CGC CC
                                ||||||||||     ||| ||
                                GGCTCCTCCG     GCG GG
                                     AG____   A
GAM2568  COL9A3  3'  CCGAGGGGCAGCCAGGGGCGCT 12343       A__       A  _
            CC                    CCGAGG   GGCCGGGG CGC CC
                                ||||||   |||||||| ||| ||
                                GGCTCC   TCGGTCCC GCG GG
                                   CCG       C   A
GAM2568  DMD     5'  CGAGGAGGTCTAGGAGGCGCC  19703        CC__   A
                                CGAGGAGG    GGGG CGCC
                                ||||||||    |||| ||||
                                GCTCCTCC    CCTC GCGG
                                     AGAT    C
GAM2568  DUSP3   3'  GGAGCAAGGACGCCCC      19866      GC
                                GGAG  CGGGGACGCCCC
                                ||||  ||||||||||||
                                CCTC  GTTCCTGCGGGG
                                   __
GAM2568  EMX2    5'  CCGAGGAGCGGGCGCCC     44680        GC    GA
                                CCGAGGAG  CGGG  CGCCC
                                ||||||||  ||||  |||||
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                                GGCTCCTC  GCCC  GCGGG
                                   __   __
GAM2568  EN2      5'  GGTTCTCCGGGGACGCCC    10962    AGG_
                                GG   CCGGGGACGCCC
                                ||   ||||||||||||
                                CC   GGCCCCTGCGGG
                                 AAGA
GAM2568  ENG      3'  CCGAGGAGGCCGGGGCAGCC  6493             AC
                                CCGAGGAGGCCGGGG  GCC
                                |||||||||||||||  |||
                                GGCTCCTCCGGCCCC  CGG
                                       GT
GAM2568  EP300    5'  CACCGAGGAGGCCCCGCTCC  10973          GGGGA  _
                                TACCGAGGAGGCC    CGC CC
                                ||||||||||||     ||| ||
                                GTGGCTCCTCCGG    GCG GG
                                       G____  A
GAM2568  FCN2     3'  CCGGGGGGGCCAGGCCGACGTT 31889    A  A     __   CC
              CC                  CCG GG GGCCGGG  GACG  CC
                                ||| || |||||||  ||||  ||
                                GGC CC CCGGTCC  CTGC  GG
                                  C  C      GG   AA
GAM2568  LCN1     3'  GAGGAGCCAAGGTGTCCC    42019       G     ACG
                                GAGGAG CCGGGG   CCC
                                ||||||  ||||||   |||
                                CTCCTC GGTTCC   GGG
                                   _     ACA
GAM2568  LIMK1    5'  CCGGGCCGGGCCGGGGGCGCC  32529    A  A__      A
                                CCG GG   GGCCGGGG CGCC
                                ||| ||   |||||||| ||||
                                GGC CC   CCGGCCCC GCGG
                                  _ GGC       C
GAM2568  PRKCI    5'  CCGGGGGTGCGGGGGGCGC   15631    A  AG  C   A
                                CCG GG  GC GGGG CGC
                                ||| ||  ||  |||| |||
                                GGC CC  CG CCCC GCG
                                  C  CA  C   C
GAM2568  PTGS2    5'  GAGGAGTTCCTGGACGTGCTCC 9687       G_  GG   __  _
                                GAGGAG  CC  GGAC  GC CC
                                ||||||  ||  ||||  || ||
                                CTCCTC  GG  CCTG  CG GG
                                   AA  A_   CA  A
GAM2568  RAP1GA1  5'  CCTGGGCCGGGGGGCGTCC    16166    GAGGA      A  _
                                CC    GGCCGGGG CG CC
                                ||    |||||||| || ||
                                GG    CCGGCCCC GC GG
                                 AC___       C  A
GAM2568  SEPN1    3'  CCGGGGAAGCCACTGCCCC   42424    A      GGGAC
                                CCG GGAGGCCG    GCCCC
                                ||| ||||||||    |||||
```

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                                GGC CCTTCGGT    CGGGG
                                  C       GA___
GAM2568  TJP1     5'  CGAGGACGGGCTGGGGGTGTCC 17538       __   C    ACG_
                                CGAGGA  GGC GGGG    CC
                                ||||||  ||| ||||    ||
                                GCTCCT  CCG CCCC    GG
                                   GC   A    CACA
GAM2568  VGF      3'  CCGACGGGGACGTCC       17985      GGAGGC       _
                                CCGA     CGGGGACG CC
                                ||||     |||||||| ||
                                GGCT     GCCCCTGC GG
                                  _______      A
GAM2568  ABCD1    5'  CCTCTCCACCTTCTCCTCC    6195       C    C    A
                                CCTC CCGCC TCTCT CC
                                |||| ||||| ||||| ||
                                GGAG GGTGG AGAGG GG
                                  A    A    A
GAM2568  ADAMTS4  3'  CCTCCCTGCCTTCCCCCTCC   23004       C   __     A
                                CCTCCC GCC  CTCTCT CC
                                |||||| |||  |||||| ||
                                GGAGGG CGG  GGGGGA GG
                                   A   AA     _
GAM2568  ADCY8    5'  CCTTTTCGCCCTTCCTACC    10002     CCC     CT
                                CCT   CGCCCT  CTACC
                                |||   ||||||  |||||
                                GGA   GCGGGA  GATGG
                                  AAA     AG
GAM2568  APLP2    3'  CCTCCCCGTGTTCTCTCC     44919        CCC     A
                                CCTCCCCG   TCTCT CC
                                ||||||||   ||||| ||
                                GGAGGGGC   AGAGA GG
                                    ACA    _
GAM2568  ATP2B1   3'  CCTCCCTCTCTCTCCCATC    11747       CGCC     A
                                CCTCCC    CTCTCT CCTGTC
                                ||||||    |||||| ||||||
                                GGAGGG    GAGAGA GGGTAG
                                   A___     _
GAM2568  ATP8B2   5'  CCTCCTTTCTTCTTCTGTC    42204       CCGCC  C   AC
                                CCTCC     CT TCT  CTGTC
                                |||||     || |||  |||||
                                GGAGG     GA AGA  GACAG
                                  AAA__  _   A_
GAM2568  BCL2     3'  CCTTTCCATCCTCCACCAGT   8519      CC   C    CT   T
                                CCT  CCG CCTCT  ACC GT
                                |||  ||| |||||  ||| ||
                                GGA  GGT GGAGG  TGG CA
                                  AA   A    __   T
GAM2568  C18orf1  3'  CCTCCACTGTTCTCTGACTGTC 41221       CC  CC_    AC
              C                   CCTCC  GC   TCTCT  CTGTCC
                                  |||||  ||   |||||  ||||||
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                              GGAGG TG  AGAGA GACAGG
                                __ ACA   CT
GAM2568 CAPN1   5' CCTCCCCGCCCTCCTCC    23251          T A
                              CCTCCCCGCCCTC CT CC
                              |||||||||||| || ||
                              GGAGGGGCGGGAG GA GG
                                       _ _
GAM2568 CARPX   5' CTCCCCGCTCGCGTGTC    33568       CCTC TACC
                              CTCCCCGC  TC  TGTC
                              ||||||||  ||  ||||
                              GAGGGGCG  AG  ACAG
                                  _____ CGC_
GAM2568 CBFA2T3 3' CCCCCCCCGTTTTCTTTGTC  23261       CCC  CTACC
                              CCTCCCCG  TCT   TGTC
                              ||||||||  |||   ||||
                              GGGGGGGC  AGA   ACAG
                                  AAA  A____
GAM2568 CBS     3' CTCCCCGCCCCTTCCTG     6306         T CTA
                              CTCCCCGCCC CT  CCTG
                              |||||||||| ||  ||||
                              GAGGGGCGGG GA  GGAC
                                   _ A__
GAM2568 CD209L  3' CCTCCATGCCCTCTCTGGATGC 30683     CC       ACC
          C                    CCTCC GCCCTCTCT  TGTC
                              |||||  |||||||||  ||||
                              GGAGG CGGGAGAGA  ACGG
                                 TA       CCT
GAM2568 CD83    3' TCTTCTCCCTCTCTATGTCC  20142   CCCG      CC
                              TC  CCCTCTCTA TGTCC
                              ||  |||||||||  |||||
                              AG  GGGAGAGAT ACAGG
                               AAGA       __
GAM2568 CHST6   3' CCTCCCCAGCCTTCTCTCC   34677       _  C    A
                              CCTCCCC GCC TCTCT CC
                              ||||||| ||| ||||| ||
                              GGAGGGG CGG AGAGA GG
                                  T  A   _
GAM2568 CLTA    3' CCTCTTCCTCCTCTCCCTCC  28224     C_ G _    A
                              CCTC  CC CC CTCTCT CC
                              ||||  || || |||||| ||
                              GGAG  GG GG GAGGGA GG
                                AA  A  A    _
GAM2568 CLTA    3' CCTCCCCTTCCTCTTCCTCC  12297       GC   _ A
                              CCTCCCC  CCTCT CT CC
                              |||||||  ||||| || ||
                              GGAGGGG  GGAGA GG GG
                                  AA    A  A
GAM2568 CORO1C  3' CCTTTCCGCCCTCCCTAGGACC 30723     CC        ___
                              CCT  CCGCCCTCTCT  ACC
                              |||  ||||||||||  |||
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                                GGA  GGCGGGAGGGA   TGG
                                  AA         TCC
GAM2568  CRH     3'  CTCTCCCTCTCTCCCT      8895      CCCG       A
                                CTC    CCCTCTCT CCT
                                |||    |||||||| |||
                                GAG    GGGAGAGA GGA
                                  A___       G
GAM2568  CSF2RB   3'  CCTCTCCATCCCCTTGCCTGTC 7568       C   C    CTA
                                CCTC CCG CCTCT   CCTGTC
                                |||| ||| |||||   ||||||
                                GGAG GGT GGGGA   GGACAG
                                  A  A    AC_
GAM2568  CYBB     3'  CCTTCCCCTCTCTCTCC     44093     _   GCC     A
                                CCT CCCC   CTCTCT CC
                                ||| ||||   |||||| ||
                                GGA GGGG   GAGAGA GG
                                  A   A__     _
GAM2568  CYBB     3'  TCCCCTCTCTCTCCCT      44100      GCC     A
                                TCCCC   CTCTCT CCT
                                |||||   |||||| |||
                                AGGGG   GAGAGA GGA
                                   A__     G
GAM2568  DAP      3'  CCTCCCTCGGAGCTACCTGTC  43688       _  CCCTCT
                                CCTCCC CG     CTACCTGTC
                                |||||| ||     |||||||||
                                GGAGGG GC     GATGGACAG
                                   A  CTC___
GAM2568  DPYSL3   5'  CCTCCCTCCTTCTTCTGCTCC  10765       CGC   C   AC   _
                                CCTCCC   CCT TCT  CTG TCC
                                ||||||   ||| |||  ||| |||
                                GGAGGG   GGA AGA  GAC AGG
                                   A__   _   A_   G
GAM2568  EIF2C1   3'  TCCCCTCCCTTTCTTGGATGCC 29183       G    C   ACC_
                                TCCCC CCCT TCT    TGTC
                                ||||| |||| |||    ||||
                                AGGGG GGGA AGA    ACGG
                                   A    A   ACCT
GAM2568  EIF5A    3'  CCTCTCCTCCTCTTCCCT     12700      C  GC     CTA
                                CCTC CC  CCTCT   CCT
                                |||| ||  |||||   |||
                                GGAG GG  GGAGA   GGA
                                  A  A_    AG_
GAM2568  EMX2     3'  CCTCCCTCTTTCTCCT      44682       CGCC  C   A
                                CCTCCC    CT TCT CCT
                                ||||||    || ||| |||
                                GGAGGG    GA AGA GGA
                                   A___  A   _
GAM2568  EMX2     3'  CTCCTTCTCTCTGTGTC     44685      CCGCC     ACC
                                CTCC    CTCTCT   TGTC
                                ||||    ||||||   ||||
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                                GAGG    GAGAGA   ACAG
                                  AA___     C__
GAM2568  EMX2     3'  CTCCCTGTCTCTTTTGCTCC  44684      CGCCC    ACC  _
                                CTCCC    TCTCT   TG TCC
                                |||||    |||||   || |||
                                GAGGG    AGAGA   AC AGG
                                  AC___    AA_  G
GAM2568  EP300    5'  CTCTCGCCCTCTCTCC      10982     CC        A
                                CTC  CGCCCTCTCT CC
                                |||  |||||||||| ||
                                GAG  GCGGGAGAGA GG
                                  A_        _
GAM2568  EPB41    5'  TCCTCACCCTCTTCCT      20769     C       CTA
                                TCC CGCCCTCT   CCT
                                ||| ||||||||   |||
                                AGG GTGGGAGA   GGA
                                  A       A__
GAM2568  EPB49    5'  CTCTCCCTTTCTTCCTCCTGTC 12728     _   GCC  CT  A
                                CTC CCC   CT  CT CCTGTC
                                ||| |||   ||  || ||||||
                                GAG GGG   GA  GA GGACAG
                                  A   AAA  AG  _
GAM2568  FOSB     3'  TCCCCTCTCTCTCCT      27546       GCC     A
                                TCCCC   CTCTCT CCT
                                |||||   |||||| |||
                                AGGGG   GAGAGA GGA
                                  A__     _
GAM2568  FOSB     3'  CTCTCCTCCTTCTCCTCC    27537     C  G  C    A
                                CTC CC CC TCTCT CC
                                ||| || || ||||| ||
                                GAG GG GG AGAGG GG
                                  A  A  A     A
GAM2568  FOSB     3'  CCTTCCCACCCCCTGT      27536     C      TCTCTA
                                CCT CCCGCCC      CCTGT
                                ||| |||||||      |||||
                                GGA GGGTGGG      GGACA
                                  A      _______
GAM2568  FRAT2    3'  CTCCCTACACGTCCCTCTCTGC 28970       _____ _       A
            CTGT                  CTCCC    CG CCCTCTCT CCTGT
                                |||||    || |||||||| |||||
                                GAGGG    GC GGGAGAGA GGACA
                                  ATGT  A       C
GAM2568  GJA5     3'  CCTTCTTTCCCTCTACCCTGT  23580     CCCCG     CTA
                                CCT    CCCTCT   CCTGT
                                |||    ||||||   |||||
                                GGA    GGGAGA   GGACA
                                  AGAAA     TG_
GAM2568  GNB1     3'  CCTCCCTCTCTCTCCCTC    13203       CGCC     A   G
                                CCTCCC    CTCTCT CCT TC
                                ||||||    |||||| ||| ||
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                                GGAGGG   GAGAGA GGG AG
                                  A___    _  _
GAM2568  GPR62    5'  CCTCTGCTCCTCTTGTC    44873     CCC  _    CTACC
                                CCTC  GC CCTCT    TGTC
                                ||||  || |||||    ||||
                                GGAG  CG GGAGA    ACAG
                                  A__  A   _____
GAM2568  GRIA1    5'  TCCCCCCCTTTCCCT      9091       G   C  TA
                                TCCCC CCCT TC  CCT
                                ||||| |||| ||  |||
                                AGGGG GGGA AG  GGA
                                  _   A __
GAM2568  HNRPK    3'  CCTTCCCCCCCCCCAACCCTGT  36315    _   G    TCTA
                                CCT CCCC CCCTC   CCTGT
                                ||| |||| |||||   |||||
                                GGA GGGG GGGGG   GGACA
                                  A   _    TTG_
GAM2568  HOXC4    5'  CCTCTCTCCCTCTCTGCCT   31151     CCCG      A
                                CCTC   CCCTCTCT CCT
                                ||||   |||||||| |||
                                GGAG   GGGAGAGA GGA
                                  AGA_      C
GAM2568  HS2ST1   5'  CCTTCTCGCCTCTCCAGTC   29328    CCC   C    CCT
                                CCT  CGCC TCTCTA  GTC
                                |||  |||| ||||||  |||
                                GGA  GCGG AGAGGT  CAG
                                  AGA   _    ___
GAM2568  IL16     3'  CCTTCTGTCGGCACACCTGTCC 21094   GCC  C ____
                                CC  CT TC   TACCTGTCC
                                ||  || ||   |||||||||
                                GG  GA AG   GTGGACAGG
                                 AA_  C  CCGT
GAM2568  INHBB    3'  CCTCCCCGCCATTTCCTCC   13552        CTC  A
                                CCTCCCCGCC  TCT CC
                                ||||||||||  ||| ||
                                GGAGGGGCGG  AGG GG
                                      TAA  A
GAM2568  ITPR2    3'  CTCCCTGCCCTCTCCAGCCT  13677     C       _
                                CTCCC GCCCTCTCTA CCT
                                ||||| |||||||||| |||
                                GAGGG CGGGAGAGGT GGA
                                   A        C
GAM2568  ITPR2    5'  CCTCCTTCCCTCTCCGCTCC  13674     CCG      A__
                                CCTCC  CCCTCTCT  CC
                                |||||  ||||||||  ||
                                GGAGG  GGGAGAGG  GG
                                   AA_      CGA
GAM2568  ITPR2    5'  CCTCGCCGCCCTCTCTCC    13675     C        A
                                CCTC CCGCCCTCTCT CC
                                |||| |||||||||| ||
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                                GGAG GGCGGGAGAGA GG
                                  C        _
GAM2568 KCNA7    3' CCTCCCCCACTGGCTCTTTTTG 36648       _ CCT   ACC
             T                    CCTCCCC GC   CTCT   TGT
                                  ||||||| ||   ||||   |||
                                  GGAGGGG TG   GAGA   ACA
                                     G  ACC    AAA
GAM2568 KCNA7    3' CTCCCCACTCTGGATTTCTGT  36653        C  CTCTAC
                                  CTCCCCGC CT     CTGT
                                  |||||||| ||     ||||
                                  GAGGGGTG GA     GACA
                                       A  CCTAAA
GAM2568 KCNA7    3' CTCCCCCTCTCCCCT      36654       GCC     A
                                  CTCCCC   CTCTCT CCT
                                  ||||||   |||||| |||
                                  GAGGGG   GAGAGG GGA

                                     ___     _
GAM2568 KCNMB3   5' CCTTCTCCTCCTCTCTGGCC   30837     _ C  GC      A_
                                  CCT C CC  CCTCTCT  CC
                                  ||| | ||  |||||||  ||
                                  GGA G GG  GGAGAGA  GG
                                    A A  A_      CC
GAM2568 LASS2    3' CCTCCTCCCCCTCTGAGCTCTC 42670      _ G     ___ AC
             TGT                    CCTCC CC CCCTCT   CT  CTGT
                                  ||||| || ||||||   ||  ||||
                                  GGAGG GG GGGAGA   GA  GACA
                                     A  _     CTC  GA
GAM2568 LEP      3' CCCCTCTGCCCTCTCTGAAATC 6911       ___        ACCT
                                  CCCC   GCCCTCTCT    GTC
                                  ||||   |||||||||    |||
                                  GGGG   CGGGAGAGA    TAG
                                    AGA        CTT_
GAM2568 LIF      3' CCTCCCCATTCTCTCAGATCC  14142        CC    TACCT
                                  CCTCCCCG  CTCTC    GTCC
                                  ||||||||  |||||    ||||
                                  GGAGGGGT  GAGAG    TAGG
                                       AA    TC___
GAM2568 LPIN2    3' TCCCCTCCCTTTCTTACT    31219      G   C   AC
                                  TCCCC CCCT TCT  CT
                                  ||||| |||| |||  ||
                                  AGGGG GGGA AGA  GA
                                     A    A   AT
GAM2568 LRP1     5' CCTCGCTGCTCTTTCCCCCTCC 14210    C   C_   CTA   G
                                  CC CGC  CTCT   CCT TCC
                                  || |||  ||||   ||| |||
                                  GG GCG  GAGA   GGG AGG
                                   A  AC    AAG   G
GAM2568 MAB21L1  5' CCTCCCCCCCTCTGCTTGTC   24586       GC    _ ACC
                                  CCTCCCC  CCTCT CT   TGTC
                                  |||||||  ||||| ||   ||||
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                                GGAGGGG  GGAGA GA   ACAG
                                   __     C  ___
GAM2568  MBL2     3'  CCTCATCCTCTACCAGT     6960       CCCGCCC       T
                                CCTC       TCTCTACC GT
                                ||||       |||||||| ||
                                GGAG       GGAGATGG CA
                                  TA_____        T
GAM2568  MDFI     3'  CCTTCCCTTCCTTTCCCCT    24616     C   GC   C   A
                                CCT CCC  CCT TCT CCT
                                ||| |||  ||| ||| |||
                                GGA GGG  GGA AGG GGA
                                  A   AA   A   _
GAM2568  MDS1     5'  CTCCCTCCCTCTCTCC       22561       CG       A
                                CTCCC  CCCTCTCT CC
                                |||||  |||||||| ||
                                GAGGG  GGGAGAGA GG
                                   A_       _
GAM2568  MDS1     5'  CCTCCCTCTCTCTCCTGTC    22559       CGCC     A
                                CCTCCC    CTCTCT CCTGTC
                                ||||||    |||||| ||||||
                                GGAGGG    GAGAGA GGACAG
                                   A___      _
GAM2568  MGEA5    5'  CCTTCCCCTCCCCCTCTGTCC  29216     _   G       ACCT
                                CCT CCCC CCCTCTCT    GTCC
                                ||| |||| ||||||||    ||||
                                GGA GGGG GGGGGAGA    CAGG
                                  A   A       _____
GAM2568  MIA      5'  CCTCCCCTCCCTCTCTCC     27209        G       A
                                CCTCCCC CCCTCTCT CC
                                ||||||| |||||||| ||
                                GGAGGGG GGGAGAGA GG
                                    A       _
GAM2568  MKI67    3'  CCTCCCTGCCCCTTTCTA     14518        C     C_
                                CCTCCC GCCCT  TCTA
                                |||||| |||||  ||||
                                GGAGGG CGGGG  AGAT
                                   A     AA
GAM2568  MMP16    5'  CCTCTCTCCCTCTCCCTCC    35437      CCCG       A_
                                CCTC    CCCTCTCT  CC
                                ||||    ||||||||  ||
                                GGAG    GGGAGAGG  GG
                                  AGA_       GA
GAM2568  MYEOV    5'  CTCCCGCCCTCTGT        39874       C       CTACCT
                                CTCCC GCCCTCT      GT
                                ||||| |||||||      ||
                                GAGGG CGGGAGA      CA
                                   _     _______
GAM2568  OGG1     5'  CCTTTCCCCCTCCGGGATTGTC 32560     CC  G     CTACC
                                CCT  CC CCCTCT     TGTC
                                |||  || ||||||     ||||
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                                GGA  GG GGGAGG    ACAG
                                  AA  _     CCCTA
GAM2568  OPHN1    3'  CCTCCCTCCTTCAAATGT    14963       CGC   C  TACC
                                CCTCCC   CCT TC    TGT
                                ||||||   ||| ||    |||
                                GGAGGG   GGA AG    ACA
                                   A__   _  TTT_
GAM2568  PAPPA    5'  CTCCCCGCTCCTTTATCTGCC  15091         _  CTC  C
                                CTCCCCGC CCT   TA CTGTC
                                |||||||| |||   || |||||
                                GAGGGGCG GGA   AT GACGG
                                    A  A__  A
GAM2568  PEA15    3'  CTCTCTGCCCTCATCCCCATC  19077    CCC     TCTA
                                CTC   GCCCTC    CCTGTC
                                |||   ||||||    ||||||
                                GAG   CGGGAG    GGGTAG
                                  AGA     TAG_
GAM2568  PODXL    3'  CTCTTTGCCCTCTCTTGCCT   23971    CCC       A_
                                CTC   GCCCTCTCT  CCT
                                |||   |||||||||  |||
                                GAG   CGGGAGAGA  GGA
                                  AAA       AC
GAM2568  POLK     5'  TCTCCGCTCCTCCTGC      32139    C   _  CTCTA
                                TC CCGC CCT    CCTGT
                                || |||| |||    |||||
                                AG GGCG GGA    GGACG
                                 A   A  _____
GAM2568  POU2AF1  3'  CTCTTCGTCACTGGCCTGTCC  26368    CC  CCC  T  A_
                                CTC  CG   TC CT  CCTGTCC
                                |||  ||   || ||  |||||||
                                GAG  GC   AG GA  GGACAGG
                                  AA  ___  T  CC
GAM2568  POU3F2   5'  CCTCGCTCGCTCTTTCTGTC  24667    C   CCT    AC
                                CC CGC   CTCT  CTGTC
                                || |||   ||||  |||||
                                GG GCG   GAGA  GACAG
                                 A  AGC    AA
GAM2568  POU3F2   5'  CTCCTCGCTCGCTCTTTCTGTC 24669     C   CCT    AC
                                CTCC CGC   CTCT  CTGTC
                                |||| |||   ||||  |||||
                                GAGG GCG   GAGA  GACAG
                                  A  AGC    AA
GAM2568  POU5F1   3'  CCTCCCCTCCCCCTGT     15471       G   TCTCTA
                                CCTCCCC CCC     CCTGT
                                |||||||  |||     |||||
                                GGAGGGG GGG     GGACA
                                   A  _______
GAM2568  PPFIA3   3'  CCTCCCCGCTTCTTCCCCCTC  41417        CC   CTA   G
                                CCTCCCCGC  TCT   CCT TC
                                |||||||||  |||   ||| ||
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                                GGAGGGGCG  AGA   GGG AG
                                     A_   AG_   G
GAM2568  PPP5C    3'  CCTCCTTCCTCTCTGT     26487      CCGC      ACCT
                                CCTCC    CCTCTCT    GT
                                |||||    |||||||    ||
                                GGAGG    GGAGAGA    CA
                                  AA__      ____
GAM2568  PSME3    5'  CCTCCCTCTGTGCCTGTC    25123    G     CTA
                                CC CCCTCT   CCTGTC
                                || ||||||   ||||||
                                GG GGGAGA   GGACAG
                                 A     CAC
GAM2568  PXF      3'  CCTCCTCCTCTCTATCCTTGTC 16009      CCGC      _  _
             C                   CCTCC    CCTCTCTA CCT GTCC
                                |||||    |||||||| ||| ||||
                                GGAGG    GGAGAGAT GGA CAGG
                                  A___       A  A
GAM2568  RARG     3'  TCCCTTTGCCCTCTCTCC    9728      C__       A
                                TCCC   GCCCTCTCT CC
                                ||||   ||||||||| ||
                                AGGG   CGGGAGAGA GG
                                  AAA       _
GAM2568  RNF28    3'  CCTCCCCACCCTCTCCAGTC   37199              CCT
                                CCTCCCCGCCCTCTCTA   GTC
                                ||||||||||||||||   |||
                                GGAGGGGTGGGAGAGGT   CAG
                                                    ___
GAM2568  SGT      3'  CTCTTCCCCTCTCTCAGGCAGT 16611     CCCG      ACCT__
             CC                   CTC    CCCTCTCT     GTCC
                                |||    ||||||||     ||||
                                GAG    GGGAGAGA     CAGG
                                  AAG_       GTCCGT
GAM2568  SLC10A2  3'  CCTATCTTGCCTCACCTGTC   7814     CCCCGC    TCT
                                CCT     CCTC   ACCTGTC
                                |||     ||||   |||||||
                                GGA     GGAG   TGGACAG
                                  TAGAAC    ___
GAM2568  SLC20A2  3'  CTCCCTCCCTCTCATCC     27572      CG      TA
                                CTCCC  CCCTCTC  CC
                                |||||  |||||||  ||
                                GAGGG  GGGAGAG  GG
                                  A_      TA
GAM2568  SNRP70   5'  CCTCCTCGCTCTGGCGTCTGTC 44212       C   C  CTCTAC
             C                    CCTCC CGC CT     CTGTCC
                                ||||| ||| ||     ||||||
                                GGAGG GCG GA     GACAGG
                                  A  A  CCGCA_
GAM2568  SOX4     5'  CTCTCCCTCTCTCTCGC     16984     CCCG      ACC
                                CTC    CCCTCTCT   TGT
                                |||    ||||||||   |||
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                                GAG   GGGAGAGA  GCG
                                 A___      GA_
GAM2568 SSPN    3' TCCCCCACCTCCTGCCTGTC  22939     GC   T  A
                                TCCCC  CCTC CT CCTGTC
                                |||||  |||| || ||||||
                                AGGGG  GGAG GA GGACAG
                                   GT   _ C
GAM2568 STC1    3' CCTCCTCCCTCTCTTCCT    17173     CCG      A
                                CCTCC   CCCTCTCT CCT
                                |||||   |||||||| |||
                                GGAGG   GGGAGAGA GGA
                                   A__      A
GAM2568 SUPT5H  5' CCTCCCCAGTTTCCGAATCTGT 17218       CCC   CTAC
                                CCTCCCCG   TCT   CTGT
                                ||||||||   |||   ||||
                                GGAGGGGT   AGG   GACA
                                     CAA   CTTA
GAM2568 SYN2    3' CCTCCCCGCTTTCCTTTCGTTT 39458       ___   C  TACC
             GT                   CCTCCCCGC   CCT TC   TGT
                                |||||||||   ||| ||   |||
                                GGAGGGGCG   GGA AG   ACA
                                     AAA   A  CAA_
GAM2568 TBL2    3' CTCCTCTCCTCTCTACCATTC  29727     CCGC       TG
                                CTCC   CCTCTCTACC  TC
                                ||||   ||||||||||  ||
                                GAGG   GGAGAGATGG  AG
                                  AGA_       TA
GAM2568 TGFB3   3' CTCCCCTCTCTCTGTC     17460      GCCC    AC
                                CTCCCC   TCTCT  CTGTC
                                ||||||   |||||  |||||
                                GAGGGG   AGAGA  GACAG
                                   ____    __
GAM2568 TMPRSS3  5' CCTCCCCGTCTTTGCAATC   37060       CCC   CTACCT
                                CCTCCCCG   TCT    GTC
                                ||||||||   |||    |||
                                GGAGGGGC   AGA    TAG
                                     ___   AACGT_
GAM2568 TNFRSF6B 5' CCTCTCCTTCCTCTCCTGC   32351     C  GC    CTA
                                CCTC CC  CCTCT   CCTGT
                                ||||  ||  |||||   |||||
                                GGAG GG  GGAGA   GGACG
                                  A  AA    ___
GAM2568 TRPS1   5' CCTCCCCCCCCTTTCCCTCC   30460       G   __    A
                                CCTCCCC CCC  TCTCT CC
                                |||||||  |||  ||||| ||
                                GGAGGGG GGG  AGGGA GG
                                    G   AA    _
GAM2568 UBE2G2  3' CCTCTCCTCCCTCTCCCGATC  42119     C  G      TA  T
                                CCTC CC CCCTCTC  CC GTC
                                |||| || |||||||  || |||
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                                GGAG GG GGGAGAG  GG TAG
                                  A A      __ C
GAM2568  WDR10    5'  CCTACCCGCCTCAGCGTCTGTC 38154    C     C  TCTAC
                                CCT CCCGCC TC    CTGTC
                                ||| |||||| ||    |||||
                                GGA GGGCGG AG    GACAG
                                  T     _  TCGCA
GAM2569  MAP4K5   5'  CACCACGTTCCCCACCCG    27299         AT  A_
                                CACCGCGTTC  CA  CG
                                ||||||||||  ||  ||
                                GTGGTGCAAG  GT  GC
                                      GG  GG
GAM2569  COG3     3'  TTCACGTTTTAGCAAACCT   36420        TTAA   AT
                                TTCACGTTT   TAG  GACCT
                                |||||||||   |||  |||||
                                AAGTGCAAA   ATC  TTGGA
                                     ____   GT
GAM2569  GALNT7   3'  TTCACGTTTGTTAATAAAC   38364         _
                                TTCACGTTT TTAATAGAT
                                ||||||||| |||||||||
                                AAGTGCAAA AATTATTTG
                                     C
GAM2569  PCDHA9   3'  TTCATGTTTGCTAATGACCTC  36556     C    TTAATA
                                TTCA GTTT     GATGACCTC
                                |||| ||||     |||||||||
                                AAGT CAAA     TTACTGGAG
                                  A   CGA___
GAM2570  ABCB6    5'  TCACGTAGCCGCTGGGCG    25031          CGC
                                TCACGTAGTCGC   GCG
                                ||||||||||||   |||
                                AGTGCATCGGCG   CGC
                                       ACC
GAM2570  SCO2     5'  CGCGGCGGGGCCGCGCGTCAG  23103    TA  C__      C
                                CG  GT   GCCGCGCG CAG
                                ||  ||   |||||||| |||
                                GC  CG   CGGCGCGC GTC
                                 GC  CCC       A
GAM2570  NFATC1   5'  GCGCGCGTGGCGGGGCCCG   26076          C__
                                GCGCGCGTGGCG   CTCG
                                ||||||||||||   ||||
                                CGCGCGCACCGC   GGGC
                                       CCC
GAM2571  CAPN1    3'  TGGCAATGGGTGGGGCCCAG   23255        ACAA_  A
                                TGGCAATGG    GC TCAG
                                |||||||||    || ||||
                                ACCGTTACC    CG GGTC
                                     CACCC  _
GAM2571  EPHA8    3'  TGGAGGGAAGGCATCAGAG   33904     CAAT   CAA
                                TGG    GGA   GCATCAGAG
                                |||    |||   |||||||||
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                                ACC   CCT  CGTAGTCTC
                                  TC__  TC_
GAM2571  PAEP    3'  CATGGCAATGGTGCA      15066          ACAA
                                CATGGCAATGG   GCA
                                ||||||||||   |||
                                GTACCGTTACC   CGT
                                      A___
GAM2571  TNFAIP2  3'  GGCAGAAGTAGCATCAGAG   26639     AT  ACA
                                GGCA  GG   AGCATCAGAG
                                ||||  ||   ||||||||||
                                CCGT  TC   TCGTAGTCTC
                                  CT  A__
GAM2572  DPYSL3   3'  TTCTGGTGGAATGGTTCACT   10783     A  AT   C
                                TTC TG  TGGG ATGGTTCACT
                                ||| ||  |||| ||||||||||
                                AAG AC  ACCT TACCAAGTGA
                                  _ C_   _
GAM2572  MGAM     3'  TTCACGAAGCTTGATGGTTCAT 43660       TTG  ___      C
             TC                   TTCATGA   GGC   ATGGTTCA TC
                                |||||||   |||   |||||||| ||
                                AAGTGCT   TCG   TACCAAGT AG
                                    ___  AAC       A
GAM2572  NELL2    3'  TTCATAATTGAAAGTTCACTC  26052          CAT
                                TTCATGATTGGG   GGTTCACTC
                                ||||||||||||   |||||||||
                                AAGTATTAACTT   TCAAGTGAG
                                       ___
GAM2572  SEDL     3'  TTCATGGTTGGGCACGGTGGCT 31014       A         TCA
             C                    TTCATG TTGGGCATGGT   CTC
                                ||||||| ||||||||||   |||
                                AAGTAC AACCCGTGCCA   GAG
                                   C         CC_
GAM2572  ABCC2    3'  CCTTTTTTAAAACGTACA    7562       CGTC
                                CCTTT    GAACGTACA
                                |||||    |||||||||
                                GGAAA    TTTGCATGT
                                   AAAT
GAM2572  CREB1    5'  CGTCACTGCTTTCGTTCACG   39595    C  C_     CGA
                                CG CAC  CTTTCGT   ACG
                                || |||  |||||||   |||
                                GC GTG  GAAAGCA   TGC
                                 A  AC      AG_
GAM2572  NEO1     3'  GCTGTCCTCTCGTACTCTGTAC 14755    CAC      CGAAC
             A                    GC   CCTTTCGT    GTACA
                                ||   ||||||||    |||||
                                CG   GGAGAGCA    CATGT
                                 ACA       TGAGA
GAM2572  WDR10    5'  CGTTACCCCTGGCAACGTACA  38144    CC     TC  CG
                                CG  ACCCTT  GT  AACGTACA
                                ||  ||||||  ||  ||||||||
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                              GC  TGGGGA  CG  TTGCATGT
                               AA     C_  __
GAM2573  HUNK     3'  GGTTGGGTTGTGCAGGCTTTGG 31075        AGC_   C    C
                GT                 GGTTGGGT    CAG CTTT GGGT
                                   ||||||||    ||| |||| ||||
                                   CCAACCCA    GTC GAAA CCCA
                                       ACAC   C    _
GAM2573  SLC9A1   3'  GGTTGGGTGGTGGCCAGGG   43239        AGCCA   TTTC
                                   GGTTGGGT    GCC    GGG
                                   ||||||||    |||    |||
                                   CCAACCCA    CGG    CCC
                                       CCAC_   T___
GAM2574  LHX2     5'  CTAATGATACATGCTACA    21982          CA
                                   TTAATGATACA  CTACA
                                   ||||||||||  |||||
                                   GATTACTATGT  GATGT
                                         AC
GAM2574  MS4A1    3'  TTAATGATACAATACTGC    6605           CACTAC
                                   TTAATGATACA     ACTGT
                                   ||||||||||      |||||
                                   AATTACTATGT     TGACG
                                         TA____
GAM2575  AQP7     3'  GGACAAGCCTTGCTTTATT   10119        G   A_
                                   GGACAAGC TTG  TTATT
                                   ||||||| |||  |||||
                                   CCTGTTCG AAC  AATAA
                                       G   GA
GAM2575  FGF23    3'  GGAGAGTTGGAATTTATTTCCA 33955    A  C    A___
                TT                   C AG GTTG    TTATTTCCATT
                                     | || ||||    ||||||||||
                                     C TC CAAC    AATAAAGGTAA
                                      C  T    CTTA
GAM2575  PDK4     3'  GGCCAATGTAGATTATTTC    15205    A   GC  T
                                   GG CAA  GT GATTATTTC
                                   || |||  || |||||||||
                                   CC GTT  CA CTAATAAAG
                                    G   A_  T
GAM2575  ASTN     3'  GAAATATTTGCCCCTTGA    42946            CTA
                                   GAAATATTTGTCTTT   TGA
                                   ||||||||||||||   |||
                                   CTTTATAAACGGGGA   ACT
                                                     ___
GAM2575  ATP2B4   3'  ATATTTGTCTCCCTCTGAA   43196         TT  A
                                   ATATTTGTCT  CT TGAA
                                   ||||||||||  || ||||
                                   TATAAACAGA  GA ACTT
                                         GG  G
GAM2575  BNC      3'  GAAACAGAAACATTTCTATG   11852       TTT TC
                                   GAAATA   G  TTTCTATG
                                   ||||||   |  ||||||||
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                                CTTTGT   T  AAAGATAC
                                   CTT GT
GAM2575 GRINL1A  3' GAAATAAGTCATTTTCTATG  42998      TTT  __
                                GAAATA  GTC  TTTCTATG
                                ||||||  |||  ||||||||
                                CTTTAT  CAG  AAAGATAC
                                   T__  TA
GAM2575 HSPA8    5' GAAATGTTTGTCTTTTCT    27325      A      _
                                GAAAT TTTGTCTTT CT
                                ||||| ||||||||| ||
                                CTTTA AAACAGAAA GA
                                   C       A
GAM2575 MMP13    3' AATATTTGTCTTATATGA    14552          TC
                                AATATTTGTCTT  TATGA
                                ||||||||||||  |||||
                                TTATAAACAGAA  ATACT
                                      T_
GAM2575 MTMR7    3' GAAATATTTGTATTGCACTGAA 42904          CTTTCTA
                                GAAATATTTGT      TGAA
                                ||||||||||       ||||
                                CTTTATAAACA      ACTT
                                      TAACGTG
GAM2575 NOVA1    3' GAAAAAATTCTTTCTATGAA  27059     TATTTG
                                GAAA     TCTTTCTATGAA
                                ||||     ||||||||||||
                                CTTT     AGAAAGATACTT
                                  TTTA__
GAM2576 POU4F1   3' TACCCTATACTCCAATCC    26396        G G_
                                TACCTTATA C  TAATCC
                                |||||||| |  ||||||
                                ATGGGATAT G  GTTAGG
                                     _ AG
GAM2576 RNF6     3' TACCTTATTTAATAATCC    25580        AGC
                                TACCTTAT   GTAATCC
                                ||||||||   |||||||
                                ATGGAATA   TATTAGG
                                     AAT
GAM2577 AIRE     3' TTTTGTTTTTGAGACGGAG   8531         C_ _
                                TTTTGTTT  GA ACGGAG
                                ||||||||  || ||||||
                                AAAACAAA  CT TGCCTC
                                     AA  C
GAM2577 ALDH3A2  3' TTTGTTTCGGAGACAG     42925        GAAC   _
                                TTTGTTTC    GGAG CAG
                                ||||||||    |||| |||
                                AAACAAAG    CCTC GTC
                                     ____    T
GAM2577 BCL7A    3' TTTTGCTTCACAGCAGA     34227        GAAC G
                                TTTTGTTTC    G AGCAGA
                                |||||||||    | ||||||
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                                AAAACGAAG   T TCGTCT
                                     ____ G
GAM2577 CNTNAP2  3' TATTTTGTTTTGATACAGAA  30494        C _
                                TATTTTGTTT GA ACGGAG
                                |||||||||| || ||||||
                                ATAAAACAAA CT TGTCTT
                                     A  A
GAM2577 CYB5     3' TTTTGTTTCTAATGTCGGAA  12538       GAA___
                                TTTTGTTTC    CGGAG
                                |||||||||    |||||
                                AAAACAAAG    GCCTT
                                     ATTACA
GAM2577 GABRE    3' TGTTTGGGGAATGGGGCAG   35081     C__  C  A
                                TGTTT  GAA GG GCAG
                                |||||  ||| || ||||
                                ACAAA  CTT CC CGTC
                                   CCC  A  C
GAM2577 NR5A2    3' TTTTGTTTTGAAAGCAGA    19240       C  ACG
                                TTTTGTTT GA  GAGCAGA
                                |||||||| ||  |||||||
                                AAAACAAA CT  TTCGTCT
                                     A ___
GAM2577 RAD51L1  3' TATTTTGTTTCTGTGGCAGAA 39454         GAACGGA
                                TATTTTGTTTC     GCAGAA
                                ||||||||||      ||||||
                                ATAAAACAAAG     CGTCTT
                                     ACAC___
GAM2577 ABCA3    3' CCTGTCCCTGCCTGATGGC   9901     T   C  CGTC
                                CCTG TCCC GTT   GGC
                                |||| |||| |||   |||
                                GGAC AGGG CGG   CCG
                                  _   A  ACTA
GAM2577 BBS2     5' CCTGCTCCTCCTGCGGC    36637       _ GTTCGT
                                CCTGTTCC CC    CGGC
                                |||||||| ||    ||||
                                GGACGAGG GG    GCCG
                                     A  AC____
GAM2577 BSG      5' CCTATTCCTCGCCGG      11903       CCGT
                                CCTGTTCC   TCGTCGG
                                |||||||    |||||||
                                GGATAAGG   AGCGGCC
                                     _____
GAM2577 CAPN10   5' CCCGTTCCCCGCCCGGC    35782         TCG
                                CCTGTTCCCCGT  TCGGC
                                ||||||||||||  |||||
                                GGGCAAGGGGCG  GGCCG
                                     ___
GAM2577 CDH23    5' CTGCTCTCCGCCGGATCGGC  38075     C   C_
                                CTGTTC CCGTT  GTCGGC
                                ||||||  |||||  ||||||
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                                GACGAG GGCGG  TAGCCG
                                   A    CC
GAM2577  CDH6    3'  CCTGTCCTCCCCTCCGGC    22326       _  G  CGT
                                CCTGTTC CCC TT   CGGC
                                ||||||| ||| ||   ||||
                                GGACAGG GGG AG   GCCG
                                   A  G  ___
GAM2577  CDS2    3'  CTGTTCCTGTTCTCCTGGC   19213       CC   GT _
                                CTGTTCC  GTTC  C GGC
                                |||||||  ||||  | |||
                                GACAAGG  CAAG  G CCG
                                   A_   AG A
GAM2577  CERD4   3'  CTGTTCCCTTTCCTGGC    28948       CG   GTC
                                CTGTTCCC  TTC   GGC
                                ||||||||  |||   |||
                                GACAAGGG  AGG   CCG
                                    AA   A__
GAM2577  CHRNB2  3'  CCTGTCCCCTTCCTGGC    8857      T   G   GTC
                                CCTGT CCCC TTC   GGC
                                ||||| |||| |||   |||
                                GGACA GGGG AAG   CCG
                                  _   _  GA_
GAM2577  CKAP1   5'  CCTGTTCCCAGCGTGGC    43879       CGTT   C
                                CCTGTTCCC   CGT GGC
                                |||||||||   ||| |||
                                GGACAAGGG   GCA CCG
                                     TC__   _
GAM2577  CLCA3   3'  CCAGTTCTTCGTCAG      22261    T   CCCG
                                CC GTTC   TTCGTCGG
                                || ||||   ||||||||
                                GG CAAG   AAGCAGTC
                                 T   _____
GAM2577  DAP3    5'  CCTTTCCCTCAGCGG      21573    G   CGT   T
                                CCT TTCCC   TCG CGG
                                ||| |||||   ||| |||
                                GGA AAGGG   AGT GCC
                                  _   ___   C
GAM2577  DTR     3'  CCTGTTCCTTCTCAG      12611       CCG   G
                                CCTGTTCC   TTC TCGG
                                ||||||||   ||| ||||
                                GGACAAGG   AAG AGTC
                                     ___   _
GAM2577  E4F1    3'  CCTGTCCCTGCCCGG      20694     T   C  TCG
                                CCTGT CCC GT   TCGG
                                ||||| ||| ||   ||||
                                GGACA GGG CG   GGCC
                                  _   A  ___
GAM2577  ENPP1   5'  CCGTTCCCCGCCGGG      26297         T  TC
                                CTGTTCCCCGT CG  GG
                                |||||||||| ||  ||
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                              GGCAAGGGGCG GC  CC
                                        _ __
GAM2577  EPHA2    3'  CTGTCCCCAGCCCTGGC     20735        C    GTC
                              CTGTTCCC GTTC   GGC
                              |||||||| ||||   |||
                              GACAGGGG CGGG   CCG
                                   T    A__
GAM2577  ETV3     5'  CCTGCTCTTCCCGG       23476        CCCG   G
                              CCTGTTC    TTC TCGG
                              |||||||    ||| ||||
                              GGACGAG    AAG GGCC
                                   ____   _
GAM2577  GCK      3'  CTGTTCCCCAGCGG       37925         TTC T
                              CTGTTCCCCG   G CGG
                              ||||||||||   | |||
                              GACAAGGGGT   C GCC
                                   ___ _
GAM2577  HAP1     3'  CCTGTTCCCTGCTCAGGGC   19498         C     TC
                              CCTGTTCCC GTTCG  GGC
                              ||||||||| |||||  |||
                              GGACAAGGG CGAGT  CCG
                                   A    C_
GAM2577  HIVEP2   3'  CCTGTTCCCATGTAAACCGGC 27551         C_  TCG
                              CCTGTTCCC  GT   TCGGC
                              |||||||||  ||   |||||
                              GGACAAGGG  CA   GGCCG
                                   TA  TTT
GAM2577  L1CAM    3'  CTGTTCCCAGTCCCAGC     35800         C    GT
                              CTGTTCCC GTTC  CGGC
                              |||||||| ||||  ||||
                              GACAAGGG CAGG  GTCG
                                   T   __
GAM2577  LMO2     5'  CCTGTTCCTTCTCGGGAGGC  24538         CCG    TC_
                              CCTGTTCC   TTCG   GGC
                              ||||||||   ||||   |||
                              GGACAAGG   GAGC   CCG
                                   AA_    CCT
GAM2577  LTB      3'  CCTGTTCCTTCGTCG       14251         CCG
                              CCTGTTCC   TTCGTCG
                              ||||||||   |||||||
                              GGACAAGG   AAGCAGC
                                   ____
GAM2577  LTC4S    3'  CTTTCCCGGCTCCGTCGGC   9461     G    C   _
                              CT TTCCC GTTC GTCGGC
                              || ||||| |||| ||||||
                              GA AAGGG CGAG CAGCCG
                               _    C   G
GAM2577  MFAP4    3'  CTGCTCCCTCATGTGGC     42909         _  TC  C
                              CTGTTCCC CGT  GT GGC
                              |||||||| |||  || |||
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                                GACGAGGG GTA  CA CCG
                                    A  __ _
GAM2577  MPDU1    3'  CTGTTCCCCTCACTGC     22177        GT   TCG
                                CTGTTCCCC  TCG   GC
                                |||||||||  |||   ||
                                GACAAGGGG  AGT   CG
                                    __  GA_
GAM2577  MSF      3'  CCTGTCCCCGCATCTGGC    44724      T     TC  _
                                CCTGT CCCCGT  GTC GGC
                                ||||| ||||||  ||| |||
                                GGACA GGGGCG  TAG CCG
                                  _    __  A
GAM2577  MTA1L1   3'  CTGTCCTCCATCGG       21886       CCCG
                                CTGTTC   TTCGTCGG
                                ||||||   ||||||||
                                GACAGG   AGGTAGCC

                                ____
GAM2577  OGDH     3'  CCTGCTCCCCCCGG        45011         GTTCG
                                CCTGTTCCCC    TCGG
                                ||||||||||    ||||
                                GGACGAGGGG    GGCC

                                _____
GAM2577  OSR1     5'  CCTGCTCCTCCGAGTCCGGC  23035        _  TTCG
                                CCTGTTCC CCG   TCGGC
                                |||||||| |||   |||||
                                GGACGAGG GGC   GGCCG
                                    A  TCA_
GAM2577  PBX2     3'  CTTTTCCCCACATCTGGC    15104    G     TT   _
                                CT TTCCCCG  CGTC GGC
                                || |||||||  |||| |||
                                GA AAGGGGT  GTAG CCG
                                 A      __   A
GAM2577  PDE6D    3'  CCTGTCCCCTGCCCTGG     15160        C   GTC
                                CCTGTTCCC GTTC  GG
                                ||||||||| ||||  ||
                                GGACAGGGG CGGG  CC
                                    A   A__
GAM2577  PET112L  3'  CCTGTTCCCAGTCAGGC     21281        CGTTC  _
                                CCTGTTCCC    GTC GGC
                                |||||||||    ||| |||
                                GGACAAGGG    CAG CCG
                                    T____  T
GAM2577  PLSCR1   5'  CCGGTTCCCCGCGCTGGC    34409    T      TT  C
                                CC GTTCCCCG  CGT GGC
                                || ||||||||  ||| |||
                                GG CAAGGGGC  GCG CCG
                                 C      __  A
GAM2577  PTPN11   5'  CCTGCTTCCCGTCAG       38755       C  GTTC
                                CCTGTT CCC   GTCGG
                                |||||| |||   |||||
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                                GGACGA GGG   CAGTC
                                   A  ____
GAM2577 RAD51L3  3' CCTGCTCCCTCGATGG     39466        CGT  TC
                                CCTGTTCCC  TCG  GG
                                |||||||||  |||  ||
                                GGACGAGGG  AGC  CC
                                     ___  TA
GAM2577 RECQL5   3' CCTGTTCCCTTGCCTGGC    20166        CGTTC  _
                                CCTGTTCCC    GTC GGC
                                |||||||||    ||| |||
                                GGACAAGGG    CGG CCG
                                     AA___  A
GAM2577 RERE     3' CCTGCTCCCTCTGCGGC     29025        CGT  GT
                                CCTGTTCCC  TC  CGGC
                                |||||||||  ||  ||||
                                GGACGAGGG  AG  GCCG
                                     ___ AC
GAM2577 RPL8     5' CCTGTTCACCAGCGCGGC    9734        C  TT  T
                                CCTGTTC CCG  CG CGGC
                                |||||||  |||  ||  ||||
                                GGACAAG GGT  GC GCCG
                                    T  C_  _
GAM2577 SIRT2    5' CTGCTTCTCCACCAGCGGC   36145      _ C   TC T
                                CTGTT C CCGT  G CGGC
                                |||||  |  ||||  |  ||||
                                GACGA G GGTG  C GCCG
                                   A A   GT _
GAM2577 TGFBR1   3' CTGTTCCCTCTCAG       21435        CGT  G
                                CTGTTCCC  TC TCGG
                                ||||||||  ||  ||||
                                GACAAGGG  AG AGTC
                                     ___  _
GAM2577 TGIF     5' CCTGCTCCTGCTCGG       17500        CC  TCG
                                CCTGTTCC  GT  TCGG
                                ||||||||  ||  ||||
                                GGACGAGG  CG  AGCC
                                    A_  ___
GAM2577 WRN      5' CCTTTCCCCGCCCCCGGC    8137     G       G
                                CCT TTCCCCGTTC TCGGC
                                |||  ||||||||||  |||||
                                GGA AAGGGGCGGG GGCCG
                                  _       _
GAM2578 GRM6     3' TACTATACAGAAGCTCT     9175         C  TACC
                                TACTATACG GAA   CTCT
                                |||||||||  |||   ||||
                                ATGATATGT CTT   GAGA
                                     _  C___
GAM2579 ACTN2    3' AGCAAAAAGAAAGAATGAACA  9938             __
                                GGCAAAAAGAAAGAA  AACA
                                ||||||||||||||  ||||
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                                TCGTTTTTCTTTCTT  TTGT
                                        AC
GAM2579  ADAM28   3'  AGATGAAAAGAAAAAGACACCC 34740     CA        AA
              A                  AGG  AAAAGAAAGA  ACACCCA
                                 |||  ||||||||||  |||||||
                                 TCT  TTTTCTTTTT  TGTGGGT
                                   AC         C_
GAM2579  ANGPT1   3'  AGGCAAAAAGGGGTAGAATACA 10083          AA__    A
                                 AGGCAAAAAG    AGAA ACA
                                 ||||||||||    |||| |||
                                 TCCGTTTTTC    TCTT TGT
                                       CCCA    A
GAM2579  CHD2     3'  AGGCAAAAGGAAAGTGACA    10439         A     AAA
                                 AGGCAAAA GAAAG   ACA
                                 ||||||||| |||||   |||
                                 TCCGTTTT CTTTC   TGT
                                      C     AC_
GAM2579  CNGA3    3'  AGGAAGAAGAAAGAAAA     10534     C  A
                                 AGG AA AAGAAAGAAAA
                                 ||| || ||||||||||
                                 TCC TT TTCTTTCTTTT
                                   _  C
GAM2579  COL19A1  3'  AGGCAAAAAGATAAACAACC   12370          AAGA    C
                                 AGGCAAAAAGA    AAACA CC
                                 ||||||||||    ||||| ||
                                 TCCGTTTTTCT    TTTGT GG
                                       A___     T
GAM2579  CTBP2    3'  AGCAAAAAGAGGTCACCC     10623          AAGAAAA
                                 GGCAAAAAGA      CACCC
                                 ||||||||||      |||||
                                 TCGTTTTTCT      GTGGG
                                       CCA_____
GAM2579  CYP1B1   3'  AGGCAAAAGGATAAATCCACCC 6443          A  A   AAA
              A                   AGGCAAAA GA AGA   CACCCA
                                  ||||||| || |||   ||||||
                                  TCCGTTTT CT TTT   GTGGGT
                                       C  A   AG_
GAM2579  DDEF2    3'  AGGCAAATTCCAAAACACC    19314        AAGAAAG
                                 AGGCAAA      AAAACACC
                                 |||||||      ||||||||
                                 TCCGTTT      TTTTGTGG
                                     AAGG___
GAM2579  DDX3     3'  GGCCAGAAGAAAACA       35823     AAAA    A
                                 GGC    AGAA GAAAACA
                                 |||    |||| |||||||
                                 CCG    TCTT CTTTTGT
                                   G___    _
GAM2579  DVL3     3'  AGGCAGGTGCCAAAACACCCA  20670       AAAAGAAAG
                                 AGGCA        AAAACACCCA
                                 |||||        ||||||||||
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                                TCCGT       TTTTGTGGGT
                                  CCACGG___
GAM2579  DVL3     3'  AGGAAAAAAGAAAGAAAA    20669     C
                                AGG AAAAAGAAAGAAAA
                                ||| ||||||||||||||
                                TCC TTTTTCTTTCTTTT
                                  T
GAM2579  DXS1283E 3'  AGCTAAGTCACGGAAACACCCA 43351     AAA   AAAGA_
                                GGC   AAG     AAACACCCA
                                |||   |||     |||||||||
                                TCG   TTC     TTTGTGGGT
                                  A__   AGTGCC
GAM2579  EGFL5    5'  AGGAAAGAAAGAAACA      44516     CAA         A
                                AGG   AAAGAAAGAAA CA
                                |||   |||||||||| ||
                                TCC   TTTCTTTCTTT GT
                                  ___         _
GAM2579  FOXD2    5'  AGGGAGAAAGAACTCACCC    20952     CAAAA       AA
                                AGG    AGAAAGAA  CACCC
                                |||    ||||||||  |||||
                                TCC    TCTTTCTT  GTGGG
                                  C____       GA
GAM2579  FUT8     3'  GGCAAAGTAGAAAACAACC    20996       AAGAA       C
                                GGCAAA     AGAAAACA CC
                                ||||||     |||||||| ||
                                CCGTTT     TCTTTTGT GG
                                   CA___       T
GAM2579  GNAI3    3'  AGGCAAAAGGAAACAGAAGACA 27095         A   __    A
                                AGGCAAAA GAA  AGAA ACA
                                |||||||| |||  |||| |||
                                TCCGTTTT CTT  TCTT TGT
                                     C   TG    C
GAM2579  GYPA     3'  GCAAAATAGAAAACA       44623       AGAA
                                GCAAAA    AGAAAACA
                                ||||||    ||||||||
                                CGTTTT    TCTTTTGT
                                   A___
GAM2579  HMG20A   5'  GGCCAAAAGAAAGTCCC     32869     A       AAAACA
                                GGC AAAAGAAAG     CCC
                                ||| |||||||||     |||
                                CCG TTTTCTTTC     GGG
                                  G       A_____
GAM2579  ITPR1    5'  AGGATGGAAGCGGAACACCCA  13662     CAAA   AAA  AA
                                AGG    AAG   GA  ACACCCA
                                |||    |||   ||  |||||||
                                TCC    TTC   CT  TGTGGGT
                                  TACC   GC_  __
GAM2579  LUZP1    3'  GGCAAAAGAAAGTGTCAC    37962        A    AAAA
                                GGCAAAA GAAAG    CAC
                                |||||||  |||||    |||
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                                CCGTTTT CTTTC   GTG
                                   _    ACA_
GAM2579 LZTS1    3' GGCAGGAAAGAACACCC    34272     AAAA    AA
                                GGCA   GAAAGA  ACACCC
                                ||||   ||||||  ||||||
                                CCGT   CTTTCT  TGTGGG
                                  C___     __
GAM2579 MME      3' AGGCTGAGAGAAAGAAGCCA  28594     AAAA      AA
                                AGGC   AGAAAGAA  CA
                                ||||   ||||||||  ||
                                TCCG   TCTTTCTT  GT
                                  ACTC       CG
GAM2579 MPP2     3' AGGAAAAAGAAAGAAAAC    40791     C
                                AGG AAAAAGAAAGAAAAC
                                ||| ||||||||||||||
                                TCC TTTTTCTTTCTTTTG
                                 _
GAM2579 NOTCH2   3' GGAGTCAAAGAAAGAAAGCA  35910    CAA_        A
                                GG   AAAGAAAGAAA CA
                                ||   |||||||||||  ||
                                CC   TTTCTTTCTTT GT
                                 TCAG         C
GAM2579 NSD1     3' AGGGGGAAAGAAAGAAAA    35359     CAA
                                AGG   AAAGAAAGAAAA
                                |||   ||||||||||||
                                TCC   TTTCTTTCTTTT
                                  CCC
GAM2579 NSEP1    3' GGCAAAAAGCAAGCAC      43998         A   AAAA
                                GGCAAAAAG AAG   CAC
                                |||||||||  |||   |||
                                CCGTTTTTC TTC   GTG
                                     G  ____
GAM2579 P2RY1    3' AGGCAAAAGAGAAAGTAAA   15004        _     A
                                AGGCAAAA AGAAAG AAA
                                ||||||||  ||||||  |||
                                TCCGTTTT TCTTTC TTT
                                     C     A
GAM2579 PARG     3' GGCAGGAAGAAAGAGACCC   18856     AA       AAAC
                                GGCA  AAGAAAGA   ACCC
                                ||||  ||||||||   ||||
                                CCGT  TTCTTTCT   TGGG
                                  CC       C___
GAM2579 PPP2R2B  5' AGGCGGAGAGAAAAAAAA    21326     AAAA
                                AGGC   AGAAAGAAAA
                                ||||   ||||||||||
                                TCCG   TCTTTTTTTT
                                  CCTC
GAM2579 PPP2R5C  3' AGCAGAAAGAAAAC        15520     AAAA
                                GGCA   GAAAGAAAAC
                                ||||   ||||||||||
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                                TCGT    CTTTCTTTTG
                                  ____
GAM2579  PPP2R5C  3'  GGCAAAAAGAGAGTCTTCCCA  15524          A  AAAACA
                                GGCAAAAAGA AG     CCCA
                                |||||||||| ||     ||||
                                CCGTTTTTCT TC     GGGT
                                     C  AGAA__
GAM2579  PROX1    3'  AGGCAGAAAGAAAACAACC   15720      AAAA         C
                                AGGCA   GAAAGAAAACA CC
                                |||||   |||||||||| ||
                                TCCGT   CTTTCTTTTGT GG
                                  ____         T
GAM2579  RAI14    3'  AGGCAGATGGGAAGAAAACA  31798      AAAAGA
                                AGGCA     AAGAAAACA
                                |||||     |||||||||
                                TCCGT     TTCTTTTGT
                                   CTACCC
GAM2579  RALB     3'  AGGGGAGAAGAAAGAAATTCCA 16143     CAAA         ACAC
                                AGG   AAGAAAGAAA   CCA
                                |||   ||||||||||   |||
                                TCC   TTCTTTCTTT   GGT
                                  CCTC        AA__
GAM2579  RHEB2    5'  AGGCAAAAAAAAGGGGACGCC  24713           AGAAA  A
                                AGGCAAAAAGAA    AC CC
                                ||||||||||||    || ||
                                TCCGTTTTTTTT    TG GG
                                      CCCC_  C
GAM2579  RNMT     3'  GGCGGGGAATGAAAACAC    19152     AAAAA  A
                                GGC    GAA GAAAACAC
                                |||    ||| ||||||||
                                CCG    CTT CTTTTGTG
                                  CCC__   A
GAM2579  RP42     3'  GGCAAAAAGGAAACTGTACC  33986         AAA   AC__
                                GGCAAAAAG  GAAA   ACC
                                |||||||||  ||||   |||
                                CCGTTTTTC  CTTT   TGG
                                     ___   GACA
GAM2579  RPL36A   5'  GGCGCGGAAAGAAAGAAACC  34293     AA__         AAC
                                GGC   AAAGAAAGAA  ACC
                                |||   ||||||||||  |||
                                CCG   TTTCTTTCTT  TGG
                                  CGCC        ___
GAM2579  S100A4   3'  GGAAAAAAAAAAGTGCCCA   33326    C         AAAACA
                                GG AAAAAGAAAG     CCCA
                                || ||||||||||     ||||
                                CC TTTTTTTTTC     GGGT
                                  T        AC____
GAM2579  SELE     3'  GGCAAAAGAAAGAAAGCC    7805         A       ACAC
                                GGCAAAA GAAAGAAA   CC
                                ||||||| ||||||||   ||
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                                CCGTTTT CTTTCTTT   GG
                                   _      C___
GAM2579 SFPQ    5' AGGCAAAAGCGAAGAAGAC   22857       A_  A  A
                                AGGCAAAA  GAA GAA AC
                                ||||||||  ||| ||| ||
                                TCCGTTTT  CTT CTT TG
                                    CG  _  C
GAM2579 SFRS2IP  5' AAGCAAAAGGAGAGAGAAAA  21790       __  A
                                AGGCAAAA  AGA AGAAAA
                                ||||||||  ||| ||||||
                                TTCGTTTT  TCT TCTTTT
                                    CC  C
GAM2579 SMARCD2  3' GGCTGGGAAGAAAGATCCC   16920    AAA_     AAACA
                                GGC   AAGAAAGA   CCC
                                |||   ||||||||   |||
                                CCG   TTCTTTCT   GGG
                                  ACCC      A____
GAM2579 SMCY    3' GGCAAAAATAAAGGTACGCAC  21639       G   AAAA_
                                GGCAAAAA AAAG    CAC
                                |||||||| ||||    |||
                                CCGTTTTT TTTC    GTG
                                    A   CATGC
GAM2579 STIM1   3' AGGGAAGGAGAGACAGAACACC 41121    C  AA  AAGAA
           CA                     AGG AA  AGA    AACACCCA
                                ||| ||  |||    ||||||||
                                TCC TT  TCT    TTGTGGGT
                                  C  CC  CTGTC
GAM2579 SURF4   3' AGGAGAAACAGGAACACCC   37650    CAAAA   GAA_
                                AGG   AGAAA   AACACCC
                                |||   |||||   |||||||
                                TCC   TCTTT   TTGTGGG
                                  _____   GTCC
GAM2579 TEC     3' AGGCAAAAAGGAAGGCCC    17382        A  AAAACA
                                AGGCAAAAAG AAG    CCC
                                |||||||||| |||    |||
                                TCCGTTTTTC TTC    GGG
                                    C  C_____
GAM2579 TFDP1   3' GGCAAAAATGAACTCTGCAC  28282       _  AGAAAA
                                GGCAAAAA GAA    CAC
                                |||||||| |||    |||
                                CCGTTTTT CTT    GTG
                                    A  GAGAC_
GAM2579 TLL2    3' GGCAGAGAGAAAGAAAATGATT 29753    AAA      CAC__
           CCA                   GGCA  AGAAAGAAAA   CCA
                                ||||  ||||||||||   |||
                                CCGT  TCTTTCTTTT   GGT
                                  CTC       ACTAA
GAM2579 TLR4    3' AGGAAAAAGTGAACACCC   17562    CAAAA    AA
                                AGG   AGAAAG  AACACCC
                                |||   ||||||  |||||||
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                                TCC    TTTTTC  TTGTGGG
                                 _____     AC
GAM2579  TRPC5    3'  AAGCAAAAAGGTTAAGCACCCA 29763          AAAGAAAA
                                AGGCAAAAAG       CACCCA
                                ||||||||||       ||||||
                                TTCGTTTTTC       GTGGGT
                                     CAATTC__
GAM2579  UBL3     3'  AGGTTGCAGAAAGAAAAC    28263     CAAAA
                                AGG    AGAAAGAAAAC
                                |||    ||||||||||
                                TCC    TCTTTCTTTTG
                                 AACG_
GAM2579  WNT11    3'  AAGCAAAAAACAAAAGAAAACA 21530          __
                                AGGCAAAAA  GAAAGAAAACA
                                |||||||||  ||||||||||
                                TTCGTTTTT  TTTTCTTTTGT
                                     TG
GAM2579  ABCB9    3'  CGGGTCCTCTGCCCCACCG   33354     C         __
                                CGG GTCCTCTGTCCC  CG
                                ||| ||||||||||||  ||
                                GCC CAGGAGACGGGG  GC
                                 _         TG
GAM2579  ADAM23   5'  CGGCGCCCCCTTTCCCG     19203          GTC
                                CGGCGTCCTCT   CCCG
                                ||||||||||   ||||
                                GCCGCGGGGGA   GGGC
                                      AA_
GAM2579  ADCY9    3'  CGGCTCTGAGACCCCCGA    10018     GTCC   ___
                                CGGC   TCTG   TCCCCGA
                                ||||   ||||   |||||||
                                GCCG   AGAC   GGGGGCT
                                  _____   TCT
GAM2579  ADRA2A   5'  GGGTCCTCCTCTTCCTCCG   8639     C      G__  _
                                GG GTCCTCT   TCC CCG
                                || |||||||   ||| |||
                                CC CAGGAGG   AGG GGC
                                 _     AGA   A
GAM2579  APAF1    5'  CGGCGGCTGCACCCCG      29818      TCCT   _
                                CGGCG   CTGT CCCCG
                                |||||   |||| |||||
                                GCCGC   GACG GGGGC
                                   C___   T
GAM2579  APAF1    5'  GGCGCCCTTCCCCCGA      29823        CTG
                                GGCGTCCT   TCCCCGA
                                ||||||||   |||||||
                                CCGCGGGA   GGGGGCT
                                     A__
GAM2579  ATP2B2   5'  CGGCTCCTCTGCCGCG      11757      G      T  C
                                CGGC TCCTCTG CC CG
                                |||| ||||||| || ||
```

```
                                GCCG AGGAGAC GG GC
                                  _      _ C
GAM2579  AXIN1    3'  GGCTTCCTCGTCCCCGA     41385     G    T
                                GGC TCCTC GTCCCCGA
                                ||| ||||| ||||||||
                                CCG AGGAG CAGGGGCT
                                  A    _
GAM2579  BLVRB    5'  CGGTGCTCTCTGCCCCCA    8738      C TC
                                CGG G  CTCTGTCCCCG
                                ||| |  ||||||||||
                                GCC C  GAGACGGGGGT
                                  A GA
GAM2579  CA12     3'  GTCCCCATTTGTCCCCGA    10248       ___
                                GTCCTC   TGTCCCCGA
                                ||||||   |||||||||
                                CAGGGG   ACAGGGGCT
                                    TAA
GAM2579  CABC1    5'  GGCGACCTCTGCCAGTGCCCCG 33686      T      _____     III
                AT                GGCG CCTCTGT    CCCCGA   T
                                |||| |||||||    ||||||  |
                                CCGC GGAGACG    GGGGCT   A
                                  T      GTCAC     III
GAM2579  CD2AP    5'  CGACGTCCGCTCCTCCCG    29070        T  G  _
                                CGGCGTCC CT TC CCCG
                                |||||||| || || ||||
                                GCTGCAGG GA GG GGGC
                                     C  _  A
GAM2579  CDKN2D   5'  CGGCTCCCCAGCCCGA     12213     G    TGTC
                                CGGC TCCTC    CCCGA
                                |||| |||||    |||||
                                GCCG AGGGG    GGGCT
                                  _     TC__
GAM2579  CHST6    5'  GGCGGCTCTGCCCGA      34680     TC    TC
                                GGCG  CTCTG  CCCGA
                                ||||  |||||  |||||
                                CCGC  GAGAC  GGGCT
                                  C_    __
GAM2579  CRY2     3'  GGCAGTCCCCATCCCTGA    43583     _   T     C
                                GGC GTCC CTGTCCC GA
                                ||| |||| ||||||| ||
                                CCG CAGG GGTAGGG CT
                                  T   _      A
GAM2579  CTSG     3'  GGCCTGTGTCCCCGA       12533     GTC  C
                                GGC   CT TGTCCCCGA
                                |||   || |||||||||
                                CCG   GA ACAGGGGCT
                                  ____ C
GAM2579  DDX11    3'  GCCCCCGTTTGTCCCTGA    20577       ___     C
                                GTCCTC   TGTCCC GA
                                ||||||   |||||| ||
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                                CGGGGG  ACAGGG CT
                                   CAA    A
GAM2579 DGCR2   3' GGAGTCCATCCCCGA     23097   C   TCT
                                GG GTCC  GTCCCCGA
                                || ||||  ||||||||
                                CC CAGG  TAGGGGCT
                                 T  ___
GAM2579 DLG1    5' CGGCGTCCCGCAGTTCCGA  19865       CT_ CC
                                CGGCGTCCT  GT  CCGA
                                |||||||||  ||  ||||
                                GCCGCAGGG  CA  GGCT
                                     CGT  A_
GAM2579 DXYS155E 3' CGGCTCCGCTCCCTCCG    22952    G  T  G  _
                                CGGC TCC CT TCC CCG
                                |||| ||| || ||| |||
                                GCCG AGG GA GGG GGC
                                  _  C  _  A
GAM2579 EPO     3' AGCATGGCTCTGTCCCTGA  9028     C_      C
                                GGCGT  CTCTGTCCC GA
                                |||||  ||||||||| ||
                                TCGTA  GAGACAGGG CT
                                   CC       A
GAM2579 EPO     3' GGTCATCCTGTCCCTGA    9035    _    CT   C
                                GG CGTCCT  GTCCC GA
                                || ||||||  ||||| ||
                                CC GTAGGA  CAGGG CT
                                 A    __    A
GAM2579 FADD    5' CGTGCGCCCTCTGTCCTCG  19245   _        C
                                CG GCGTCCTCTGTCC CG
                                || |||||||||||| ||
                                GC CGCGGGAGACAGG GC
                                 A          A
GAM2579 FCN2    3' GGCGTCCTGACCCTGA     31891       CT T  C
                                GGCGTCCT  G CCC GA
                                ||||||||  | ||| ||
                                CCGCAGGA  C GGG CT
                                     __T  A
GAM2579 FE65L2  5' GGCGTCTGGATCCCCGA    39320      CTCT
                                GGCGTC   GTCCCCGA
                                ||||||   ||||||||
                                CCGCAG   TAGGGGCT
                                   ACC_
GAM2579 FMR2    5' GGCGCCTGTCCCTGA      12972     CCT    C
                                GGCGT  CTGTCCC GA
                                |||||  ||||||| ||
                                CCGCG  GACAGGG CT
                                   ___     A
GAM2579 FOLR2   5' CCACAGCCTCTGTCTTCG   9038   G  T     CC
                                C GCG CCTCTGTC  CG
                                | ||| ||||||||  ||
```

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                                G TGT GGAGACAG  GC
                                 G   C       AA
GAM2579  GPC1     3'  CGGGGTCCTCCAACAGCCC   13243     C       TC__
                                CGG GTCCTCTG    CCC
                                ||| ||||||||    |||
                                GCC CAGGAGGT    GGG
                                  C       TGTC
GAM2579  GTF2IRD1  5'  CGGCGGCCCCCACCCCCG    32256      T    TG
                                CGGCG CCTC  TCCCCG
                                ||||| ||||  ||||||
                                GCCGC GGGG  GGGGGC
                                   C    GT
GAM2579  GTF2IRD1  5'  CGGCGCCCCGGCCCCG      32255         CT T
                                CGGCGTCCT  G CCCCG
                                |||||||||  | |||||
                                GCCGCGGGG  C GGGGC
                                      C_ _
GAM2579  HCN4     3'  GGCGTCCTCTTCCCTGA     24230          G    C
                                GGCGTCCTCT TCCC GA
                                |||||||||| |||| ||
                                CCGCAGGAGA AGGG CT
                                      _    A
GAM2579  HOXB6    3'  GGCTCCCCCACCCGA       40824     G     GTC
                                GGC TCCTCT   CCCGA
                                ||| ||||||   |||||
                                CCG AGGGGG   GGGCT
                                  _      T__
GAM2579  LAMA5    5'  CGGGCCGCGTCCCCGA      24498     C   CTC
                                CGG GTC   TGTCCCCGA
                                ||| |||   |||||||||
                                GCC CGG   GCAGGGGCT
                                  _   C__
GAM2579  LAMP1    3'  CGGCATTCCACCCCTCG     24506       CC  TG   _
                                CGGCGT  TC  TCCC CG
                                ||||||  ||  |||| ||
                                GCCGTA  AG  GGGG GC
                                   __  GT    A
GAM2579  LASS1    3'  CGGGGCCGGTGTCCCCG     34601     C T  TC
                                CGG G CC  TGTCCCCG
                                ||| | ||  ||||||||
                                GCC C GG  ACAGGGGC
                                  C _  CC
GAM2579  LIMD1    3'  CGGCTCCTGTGTCCCCG     30628      G    C
                                CGGC TCCT TGTCCCCG
                                |||| |||| ||||||||
                                GCCG AGGA ACAGGGGC
                                  _    C
GAM2579  MAN2A2   5'  CGGCCTCCGCGCCGCTCCG   25945      G   T__    CC
                                CGGC TCC   CTGT  CCG
                                |||| |||   ||||  |||
```

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                                GCCG AGG   GGCG  GGC
                                  G  CGC    A_
GAM2579  MAP3K5   5'  CGGCGCCCTCTCCCCCGA    25438          G
                                CGGCGTCCTCT TCCCCGA
                                |||||||||| |||||||
                                GCCGCGGGAGA GGGGGCT
                                          _
GAM2579  MAPK3    5'  CGGCGGCCCCGCCCGA      43840      T   TGTC
                                CGGCG CCTC    CCCGA
                                ||||| ||||   |||||
                                GCCGC GGGG    GGGCT
                                  C   C___
GAM2579  MAPK9    5'  CAGCGTCCTGCAATATCCC   40076        C___
                                CGGCGTCCT   TGTCCC
                                |||||||||   ||||||
                                GTCGCAGGA   ATAGGG
                                     CGTT
GAM2579  MGAT1    5'  CGACGTCCTGGCCCCGA     14430        CT T
                                CGGCGTCCT  G CCCCGA
                                |||||||||  | ||||||
                                GCTGCAGGA  C GGGGCT
                                     C_ _
GAM2579  MN1      5'  CGGTGCCGGCCCCCGA      14577     C  CTCT
                                CGG GTC    GTCCCCGA
                                ||| |||    ||||||||
                                GCC CGG    CGGGGGCT
                                  A  C___
GAM2579  MX2      3'  CGGCATCCTGCACCGA      14695        CT  CC
                                CGGCGTCCT  GT  CCGA
                                |||||||||  ||  ||||
                                GCCGTAGGA  CG  GGCT
                                     __  T_
GAM2579  NRCAM    5'  CGGTGTCCTCCGTTCTCGA   22690     C       CCC
                                CGG GTCCTCTGT   CGA
                                ||| |||||||||   |||
                                GCC CAGGAGGCA   GCT
                                  A        AGA
GAM2579  NRG1     5'  CGGCGCCCTCGCAACCCGA   30341         T  C_
                                CGGCGTCCTC GT  CCCGA
                                |||||||||| ||  |||||
                                GCCGCGGGAG CG  GGGCT
                                     _  TT
GAM2579  NRGN     3'  CGGCATCCATCTCTCCTCG   26125        _  G   C
                                CGGCGTCC TCT TCC CG
                                |||||||| ||| ||| ||
                                GCCGTAGG AGA AGG GC
                                     T  G   A
GAM2579  PARG     5'  CAGCGCACTGTCCCCG      18854       CCT
                                CGGCGT   CTGTCCCCG
                                ||||||   |||||||||
```

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                                GTCGCG  GACAGGGGC
                                   T__
GAM2579 PCDH11X  5' CGGCTCCTCCCGCCCCGA   37324     G    GT
                                CGGC TCCTCT  CCCCGA
                                |||| ||||||  ||||||
                                GCCG AGGAGG  GGGGCT
                                  _     GC
GAM2579 PCDH7    5' CGGCGCCCCCCTCCTCCG    37114         G  _
                                CGGCGTCCTCT TCC CCG
                                |||||||||| ||| |||
                                GCCGCGGGGGG AGG GGC
                                      _  A
GAM2579 PDGFB    5' CGGCGCCGCCGCCCCCG     15174      T  T
                                CGGCG CC CTGTCCCCG
                                ||||| || |||||||||
                                GCCGC GG GGCGGGGGC
                                  _ C
GAM2579 PDPK1    5' CAGCGTCCTCCTCCCCGA    15209         G
                                CGGCGTCCTCT TCCCCGA
                                |||||||||| |||||||
                                GTCGCAGGAGG AGGGGCT
                                      _
GAM2579 PLA2G10  5' CGGCTCCGCCCCCG       18673     GTCC
                                CGGC   TCTGTCCCCG
                                ||||   ||||||||||
                                GCCG   AGGCGGGGGC
                                     ____
GAM2579 PLCB4    5' CAGTGTCCTCTGTTCCCA    9582     C       C
                                CGG GTCCTCTGT CCCG
                                ||| ||||||||| ||||
                                GTC CAGGAGACA GGGT
                                  A       A
GAM2579 POU3F2   5' CGACGCCTTCTGTTCCCG    24668       C    C
                                CGGCGTC TCTGT CCCG
                                ||||||| ||||| ||||
                                GCTGCGG AGACA GGGC
                                    A    A
GAM2579 PPARG    5' CGGTGTCCTCGAGGCCGA    39815    C    T TCC
                                CGG GTCCTC G   CCGA
                                ||| |||||| |   ||||
                                GCC CAGGAG C   GGCT
                                  A     _ TCC
GAM2579 ROR2     5' CGTCGTCCTCTTCTCCG     21259    G      G  C
                                CG CGTCCTCT TC CCG
                                || |||||||| || |||
                                GC GCAGGAGA AG GGC
                                 A       _ A
GAM2579 RPL5     5' CGGCGTCCGCTGCTCGA     9733         T   CCC
                                CGGCGTCC CTGT   CGA
                                |||||||| ||||   |||
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                                GCCGCAGG GACG   GCT
                                     C    A__
GAM2579  SFRP5    5'  CGGCGTGCGCCCCCG       16593       CCTC
                                CGGCGT    TGTCCCCG
                                ||||||    ||||||||
                                GCCGCA    GCGGGGGC
                                   C___
GAM2579  SIAH2    5'  CGGCGTCCCGGGCCCCGA    22863         CT T
                                CGGCGTCCT  G CCCCGA
                                |||||||||  | ||||||
                                GCCGCAGGG  C GGGGCT
                                     CC _
GAM2579  SNX15    5'  CGCCGTCCCCACCCCTCCG   43934    G      TG  _
                                CG CGTCCTC  TCC CCG
                                || |||||||  ||| |||
                                GC GCAGGGG  GGG GGC
                                 G      TG   A
GAM2579  SPTBN2   3'  GGCGGTGGCTGTCCCCGA    28071     TCCT
                                GGCG    CTGTCCCCGA
                                ||||    ||||||||||
                                CCGC    GACAGGGGCT
                                  CACC
GAM2579  UMPS     5'  CGGCGTCCGGCGCCCCGA    7501         TC  T
                                CGGCGTCC  TG CCCCGA
                                ||||||||  || ||||||
                                GCCGCAGG  GC GGGGCT
                                     CC  _
GAM2579  VDR      3'  GGTGTCTCTGTCCCTGA     7526     C  C      C
                                GG GTC TCTGTCCC GA
                                || ||| |||||||| ||
                                CC CAG AGACAGGG CT
                                 A  _       A
GAM2579  VIPR1    3'  GGCAGGCCTCTGTCCCCG    21511      T_
                                GGCG  CCTCTGTCCCCG
                                ||||  ||||||||||||
                                CCGT  GGAGACAGGGGC
                                  CC
GAM2579  ZNF134   5'  CGGTCGTCCGTCCCCG      18325     _    TCT
                                CGG CGTCC   GTCCCCG
                                ||| |||||   |||||||
                                GCC GCAGG   CAGGGGC
                                 A    ____
GAM2580  AGA      3'  TGTAGAGTTGTCATACAGAGAG 6187        ATG       CC
           TT                    TGTAGA   GTCATATGG  AGTT
                                ||||||   |||||||||  ||||
                                ACATCT   CAGTATGTC  TCAA
                                   CAA       TC
GAM2580  CUTL1    3'  TAGGGTGGTCCACAGCCAGTT  12535     AA    A
                                TAG  TGGTC TATGGCCAGTT
                                |||  ||||| ||||||||||
```

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                                ATC  ACCAG GTGTCGGTCAA
                                  CC    _
GAM2580  VHL     3'  TGTAGAATGTCAATCCTAGTT  8122         G   TATGG  _
                                TGTAGAATG TCA    CC AGTT
                                ||||||||| |||    || ||||
                                ACATCTTAC AGT    GG TCAA
                                      _  TA___  A
GAM2580  CACNB2   5'  ACTGCTTCTTAGCACGCT    8789          TACTAA   A
                                ACTGCTTTTT     CAC CT
                                ||||||||||     ||| ||
                                TGACGAAGAA     GTG GA
                                      TC____   C
GAM2580  HDAC8    3'  AACTGCTTGCATAAACACGCT  32968        TTTTACT    A
                                AACTGCTT      AACAC CT
                                ||||||||      ||||| ||
                                TTGACGAA      TTGTG GA
                                     CGTAT__    C
GAM2580  NCAM2    3'  AACTGCTTTGTTTGTTTAGACA 21221         TTTACTAAC_
              CTA                   AACTGCTTT        ACACTA
                                ||||||||||        ||||||
                                TTGACGAAA         TGTGAT
                                     CAAACAAATC
GAM2580  NEFH     3'  TGCCCTCTCTTGCTAACA    34348         A__
                                TGCTTTTTT   CTAACA
                                |||||||||   ||||||
                                ACGGGAGAG   GATTGT
                                     AAC
GAM2580  NTSR1    3'  AACTGCCTTTTGCCGCACACTA 14869          TACTAA
                                AACTGCTTTTT     CACACTA
                                ||||||||||     |||||||
                                TTGACGGAAAA     GTGTGAT
                                      CGGC__
GAM2580  TCF2     3'  GCATGTTACTCTGACACACTA  27026    TTTT    A__
                                GC    TTACT   ACACACTA
                                ||    |||||   ||||||||
                                CG    AATGA   TGTGTGAT
                                 TAC_    GAC
GAM2580  TRIM34   5'  CTGCTTTTTCCTCCCATGCT   38972         A  AA  CA
                                CTGCTTTTTT CT  CA  CT
                                |||||||||| ||  ||  ||
                                GACGAAAAAG GA  GT  GA
                                      _  GG  AC
GAM2581  APPBP2   3'  ATGTGCACAAAACCAAAAAATA 26874        G    ATGTGT
                                ATGTGCA AAAA     AAATA
                                ||||||| ||||     |||||
                                TACACGT TTTT     TTTAT
                                    G   GGTTT_
GAM2581  ARG2     3'  TGTGAGAATGTGTAAAT     10123      C   AAA
                                TGTG AGA   ATGTGTAAAT
                                |||| |||   ||||||||||
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                                ACAC TCT   TACACATTTA
                                  _  ___
GAM2581  ATRX     5'  CATGTGCACAAGGAATCAAATA 39605        G  AAATGTG
                                CATGTGCA AA      TAAATA
                                |||||||| ||      ||||||
                                GTACACGT TT      GTTTAT
                                    G  CCTTA__
GAM2581  BID      3'  ATGTGCAGATTCATGTGT    10177         AAA
                                ATGTGCAGA   ATGTGT
                                |||||||||   ||||||
                                TACACGTCT   TACACA
                                     AAG
GAM2581  CAPZA1   3'  CATGTGCAGGGAATGTG     43711         AAA
                                CATGTGCAG   AATGTG
                                |||||||||   ||||||
                                GTACACGTC   TTACAC
                                     CC_
GAM2581  CD5L     3'  GTGTAAATGTGTAAAT      25318     CAGAA
                                GTG    AAATGTGTAAAT
                                |||    ||||||||||||
                                CAC    TTTACACATTTA
                                 A____
GAM2581  CHST1    3'  TGTGCGTGTGTGGATGTGTAAA 18916       AGAAAA__
            T                    TGTGC       ATGTGTAAAT
                                |||||       ||||||||||
                                ACACG       TACACATTTA
                                   CACACACC
GAM2581  CYP3A4   3'  ATGTGCAGGAAAGCATCTG    32711         _  A_  G
                                ATGTGCAG AAA  AT TG
                                |||||||| |||  || ||
                                TACACGTC TTT  TA AC
                                     C   CG  G
GAM2581  EGFL3    3'  CATGTGCAGTGGCCCATAAATA 41704         AAAAATGT
                                CATGTGCAG       GTAAATA
                                |||||||||       |||||||
                                GTACACGTC       TATTTAT
                                     ACCGGG__
GAM2581  EIF1A    3'  ATGTACAGAAGCCTAAAT    44805          AAAT  G
                                ATGTGCAGAA    GT TAAAT
                                ||||||||||    || |||||
                                TACATGTCTT    CG ATTTA
                                      ____  G
GAM2581  F3       3'  ATGTGCAAAAGGTGC       42549          AAAT
                                ATGTGCAGAA    GTGT
                                ||||||||||    ||||
                                TACACGTTTT    CACG
                                     C___
GAM2581  FCAR     3'  ATGTGCAGAAAGGTGGGT    39334          AA  T
                                ATGTGCAGAAA  TG GT
                                ||||||||||  || ||
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                                TACACGTCTTT  AC CA
                                      CC  C
GAM2581  GPR48    3'  TATCAGATGTGTAAATA     32990     G    AAAA
                                TGT CAGA    TGTGTAAATA
                                ||| ||||    ||||||||||
                                ATA GTCT    ACACATTTAT
                                  _   ____
GAM2581  HBE1     3'  CATGTGCAGAAGGAGGGTG    23725          AAAT_
                                CATGTGCAGAA     GTG
                                ||||||||||     |||
                                GTACACGTCTT     CAC
                                      CCTCC
GAM2581  MANBA    3'  CATGTACAGAAAAATACCCA   25385             TG
                                CATGTGCAGAAAAATG  TA
                                ||||||||||||||||  ||
                                GTACATGTCTTTTTAT  GT
                                         GG
GAM2581  PREP     3'  TGCAGAAAGGTGAAAT      15556        AAT   T
                                TGCAGAAA   GTG AAAT
                                ||||||||   ||| ||||
                                ACGTCTTT   CAC TTTA
                                     C__   _
GAM2581  SSX2     3'  TGTGCGTGTGTGTGTAAAT   45531       AGAAAAA
                                TGTGC      TGTGTAAAT
                                |||||      |||||||||
                                ACACG      ACACATTTA
                                   CACAC__
GAM2581  STK10    3'  CATGTGCAGGAAGGGGGACGCG 25617         AAAA____
                                CATGTGCAG       ATGTG
                                |||||||||       |||||
                                GTACACGTC       TGCGC
                                      CTTCCCCC
GAM2581  WASF3    3'  CATGTGCAGAGGTAATGAAAT  27377          AAAAT   T
                                CATGTGCAGA     GTG AAAT
                                ||||||||||     ||| ||||
                                GTACACGTCT     TAC TTTA
                                      CCAT_   _
GAM2581  ZNF141   3'  CATGTGCAAAAAGATGAGCA   18346           A   T
                                CATGTGCAGAAA ATG GTA
                                |||||||||||| ||| |||
                                GTACACGTTTTT TAC CGT
                                       C   T
GAM2581  MCC      3'  ACATGTGTTTACACGCT     14378       T  TA
                                ATATGT TT  TATACGCT
                                |||||| ||  ||||||||
                                TGTACA AA  ATGTGCGA
                                   C  __
GAM2582  BCRP2    3'  TCTCTGGAGATGAGGGTGG   41653    C     T    ACTA  _
                                TC CTGGAG ATGAG    GG GG
                                || |||||| |||||    || ||
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```
                                AG GACCTC TACTC    CC CC
                                 A     _    ____  A
GAM2582  FVT1     3'  CTGGACTTAATCTCTAGGGGG  13029      GTA   GA_
                                CTGGA   TGA   CTAGGGGG
                                |||||   |||   ||||||||
                                GACCT   ATT   GATCCCCC
                                   GA_   AGA
GAM2582  G6PT1    3'  TCCCTGGAGTCTGAGGTATTGG 11167          A    ACTAG
                                TCCCTGGAGT TGAG    GG
                                |||||||||| ||||    ||
                                AGGGACCTCA ACTC    CC
                                      G    CATAA
GAM2582  JUP      3'  TCCCTGGGGAGTGAGGG     13782        AGTAT   ACT
                                TCCCTGG    GAG   AGGG
                                |||||||    |||   ||||
                                AGGGACC    CTC   TCCC
                                    C____   AC_
GAM2582  NT5C3    3'  GGGAGTTATTTTTCTAATTTTG 32409      A          CC
                                GGGA TTATTTTTCTAA  TTG
                                |||| ||||||||||||  |||
                                CCCT AATAAAAAGATT  AAC
                                  C          AA
GAM2583  CHN1     3'  TATAAAACATTCCTTCATCT   12247           AGCA
                                TATAAAGCATTT    CATCT
                                ||||||||||||    |||||
                                ATATTTTGTAAG    GTAGA
                                      GAA_
GAM2583  MAP3K7IP2 3'  TAAAGCATTTAAACTTCT    31523           C  A
                                TAAAGCATTTAG AC TCT
                                |||||||||||| || |||
                                ATTTCGTAAATT TG AGA
                                      _  A
GAM2583  RTDR1    3'  TAAAGAGACTTAGCACAT    30883       C_
                                TAAAG  ATTTAGCACAT
                                |||||  ||||||||||
                                ATTTC  TGAATCGTGTA
                                   TC
GAM2583  STAU2    3'  TATAAAGCATTTCATTATTCT  30804           AGCACA
                                TATAAAGCATTT      TCT
                                ||||||||||||      |||
                                ATATTTCGTAAA      AGA
                                      GTAATA
GAM2583  ABH      3'  CATTAAAAAGCCAACAGG    40738         T  TTTCG
                                CATTAAAA GT    CAACAGG
                                |||||||| ||    |||||||
                                GTAATTTT CG    GTTGTCC
                                    T  _____
GAM2583  BCL2     3'  CATTAAAATGATTTTGGCA   8518           _   C
                                CATTAAAATG TTTT GCA
                                |||||||||| |||| |||
```

```
                                GTAATTTTAC AAAA CGT
                                     T   C
GAM2583  CBS     3'  AAATGTCCAGAACAGGG     6305         TCGC
                                AAATGTTT   AACAGGG
                                ||||||||   |||||||
                                TTTACAGG   TTGTCCC
                                    TC__
GAM2583  TCF21   3'  TAAAGTGTTCTCGCGG      17350      A       AACA
                                TAAA TGTTTTCGC   GG
                                |||| |||||||||   ||
                                ATTT ACAAGAGCG   CC
                                  C       _____
GAM2583  UGT1A1  3'  ATTAAAACTGCCATTTGCAGTA 7864         _   TTC_  AC
            GGG                   ATTAAAA TGTT   GCA  AGGG
                                ||||||| ||||   |||  ||||
                                TAATTTT ACGG   CGT  TCCC
                                    G   TAAA   CA
GAM2583  UGT1A4  3'  ATTAAAACTGCCATTTGCAGTA 28293        _   TTC_  AC
            GGG                   ATTAAAA TGTT   GCA  AGGG
                                ||||||| ||||   |||  ||||
                                TAATTTT ACGG   CGT  TCCC
                                    G   TAAA   CA
GAM2583  UGT1A9  3'  ATTAAAACTGCCATTTGCAGTA 34287        _   TTC_  AC
            GGG                   ATTAAAA TGTT   GCA  AGGG
                                ||||||| ||||   |||  ||||
                                TAATTTT ACGG   CGT  TCCC
                                    G   TAAA   CA
GAM2584  PCDHB13  3'  CTGGGTTAAAGAATGAATTGT  33185       CATTTA
                                CTGGGT     GATGAATTGT
                                ||||||     ||||||||||
                                GACCCA     TTACTTAACA
                                   ATTTC_
GAM2584  TGFA    3'  CACGGGTCATAGAATT      17441     T     TTAGAT
                                CAC GGGTCAT     GAATT
                                ||| |||||||     |||||
                                GTG CCCAGTA     CTTAA
                                  _      T_____
GAM2584  ZNF20   3'  GGCTATAGGTGAATTGT     41821     CATT   A
                                GGT   TAG TGAATTGT
                                |||   ||| ||||||||
                                CCG   ATC ACTTAACA
                                  AT__   C
GAM2584  DDX24   3'  ATTGTTTTTAATTTATGAAAT  33826          AAAC
                                GTTGTTTTTAA   TATGAAAT
                                ||||||||||   ||||||||
                                TAACAAAAATT   ATACTTTA
                                      AA__
GAM2584  KCNK10  3'  AGTTGTTTATGGCACAGTGAAA 39680        TTAAAA  TA
            T                  AGTTGTTT     AC  TGAAAT
                                ||||||||     ||  ||||||
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                                TCAACAAA     TG  ACTTTA
                                     TACCG_  TC
GAM2584  PRKAA2    3'  AGCTGTTTTTAAGAAACCTGAA 26500           _     A
              A                   AGTTGTTTTTAA AAACT TGAAA
                                  |||||||||||| ||||| |||||
                                  TCGACAAAAATT TTTGG ACTTT
                                        C    _
GAM2584  TGFB2     5'  AGTTGTTTTTAAAAGTCAGAA  17453            ACTAT
                                  AGTTGTTTTTAAAA    GAA
                                  ||||||||||||||    |||
                                  TCAACAAAAATTTT    CTT
                                        CAGT_
GAM2585  ARHGEF12  3'  GTACACCACCCCTGTGCC    31642       A      C  TCGA
                                  GTACA CCACCCC GT    CC
                                  ||||| ||||||| ||    ||
                                  CATGT GGTGGGG CA    GG
                                     _      A  C___
GAM2585  CCNG1     5'  AACCACCCTCCCCGGGCC    19766         _ GT   A_
                                  AACCACCC CC  TCG  CC
                                  |||||||| ||  |||  ||
                                  TTGGTGGG GG  GGC  GG
                                       A  __   CC
GAM2585  ENC1      3'  CGTACAACCATTCACACACGTC 18861          CCCC____
              C                    CGTACAACCA       CGTTC
                                   ||||||||||       |||||
                                   GCATGTTGGT       GCAGG
                                         AAGTGTGT
GAM2585  ITPR3     3'  CGTACAACTCTTCCCCAGGAAG 13686         CAC_    TTCGA
              CC                     CGTACAAC    CCCCG    CC
                                     ||||||||    |||||    ||
                                     GCATGTTG    GGGGT    GG
                                         AGAA     CCTTC
GAM2585  NRAP      3'  GTAGGCCACCCCGCTC      40197      CAA      C
                                  GTA   CCACCCC GTTC
                                  |||   ||||||| ||||
                                  CAT   GGTGGGG CGAG
                                    CC_      _
GAM2585  OAS2      3'  GTGCAACCACCTCCACAGTCA  32553     A       _ _  T
                                  GT CAACCACC CC CG TCG
                                  || |||||||| || || |||
                                  CA GTTGGTGG GG GT AGT
                                   C       A  T  C
GAM2585  PTS       3'  CGTACAACAATCACGTGTTGAC 7225          ___   CCCC   C
              C                    CGTACAAC   CAC    GTT GACC
                                   ||||||||   |||    ||| ||||
                                   GCATGTTG   GTG    CAA CTGG
                                        TTA   CA__   _
GAM2585  RNF4      3'  CGTTAGCCACCCCCCAGGCC    16352      ACAA       TTCGA
                                  CGT    CCACCCCCG    CC
                                  |||    |||||||||    ||
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                                GCA   GGTGGGGGT    GG
                                  ATC_       CC___
GAM2585 SACM1L   5' GCACAACCACCTCCTTC    30426          C  G
                                GTACAACCACC CC TTC
                                |||||||||| || |||
                                CGTGTTGGTGG GG AAG
                                       A  _
GAM2585 UPK1B    3' GTAAATCACCCCATTC     28083     C  C     C
                                GTA AA CACCCC GTTC
                                ||| || |||||| ||||
                                CAT TT GTGGGG TAAG
                                  _ A     _
GAM2586 ATP8A2   3' TCCCTATAGTGAGACGAACC   45267           A  T
                                TCCCTATAGTGA AC GATT
                                |||||||||||| || ||||
                                AGGGATATCACT TG TTGG
                                       C  C
GAM2586 CRIM1    3' TCCAGGAGCTGATTAGT     32384     CTAT  T  AA
                                TCC    AG GA  CTGATTAGT
                                |||    || ||  |||||||||
                                AGG    TC CT  GACTAATCA
                                  _____  _  C_
GAM2586 FOP      3' TCCCTGTAATGAAACTGA    28189       A
                                TCCCT TAGTGAAACTGA
                                ||||| ||||||||||||
                                AGGGA ATTACTTTGACT
                                   C
GAM2586 AP1B1    3' ACAGGGGCTCTGGGAGCT    10032       A  C    GT
                                ACAGG GC CTGGG  CT
                                ||||| || |||||  ||
                                TGTCC CG GACCC  GA
                                   C  A    TC
GAM2586 ARF3     5' GGGCAGTGGCAGTCTGGT    11674    A  CC  _
                                GG GC  TGG GGTCTGGT
                                || ||  ||| ||||||||
                                CC CG  ACC TCAGACCA
                                 _ TC   G
GAM2586 ARHC     5' GGAGCCCCATCCTGGTT     23171        GGGG
                                GGAGCCCT    TCTGGTT
                                ||||||||    |||||||
                                CCTCGGGG    GGACCAA
                                     TA__
GAM2586 ASCL1    5' GGAGCCCTGACGGAAGTT    43746          _ TCT
                                GGAGCCCTGG GG   GGTT
                                |||||||||| ||   ||||
                                CCTCGGGACT CC   TCAA
                                      G  T__
GAM2586 CACNA2D2 3' CAGGAGCCCATGGGGGCT    25705          _    T
                                CAGGAGCCC TGGGG CT
                                ||||||||| ||||| ||
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                                GTCCTCGGG ACCCC GA
                                     T    C
GAM2586 CLC     3' CAGGGCCTTGGGGAGC     29894     A  C    TCT
                                CAGG GCC TGGGG   GGT
                                |||| ||| |||||   |||
                                GTCC CGG ACCCC   TCG
                                  _  A    ___
GAM2586 EBAF    3' AACAGGGGCCTAGGTATGTT  42258      A  C   GTCTG
                                AACAGG GCC TGGG    GTT
                                |||||| ||| ||||    |||
                                TTGTCC CGG ATCC    CAA
                                   C  _   ATA__
GAM2586 ETF1    3' AGGGCTGGGTCTGGTT     21829     A  CCTG
                                AGG GC    GGGTCTGGTT
                                ||| ||   ||||||||||
                                TCC CG    CCCAGACCAA
                                  _ A___
GAM2586 GABPB1  3' AAACAGTGGCTTATTCTGGTT 23521      GA  CCTGGGG
                                AAACAG  GC     TCTGGTT
                                ||||||  ||     |||||||
                                TTTGTC  CG     AGACCAA
                                   AC  AATA___
GAM2586 GIPR    5' GGCGGCGAAGGGTCTGGT    6726     A_  CCT
                                GG  GC   GGGGTCTGGT
                                ||  ||   ||||||||||
                                CC  CG   TCCCAGACCA
                                 GC  CT_
GAM2586 LASS1   3' CAGGGGTCCTGGGGGGC    34593     AGC     TCT
                                CAGG   CCTGGGG   GGT
                                ||||   |||||||   |||
                                GTCC   GGACCCC   CCG
                                  CCA     ___
GAM2586 MYLK2   3' GGGGCCCCGAGTGGTT     37529    A      GTC
                                GG GCCCTGGG   TGGTT
                                || ||||||||   |||||
                                CC CGGGGCTC   ACCAA
                                 C      ___
GAM2586 PTMA    3' CAGGGCCTTGGAAGTTTTGGTT 15865     A  C   _  C_
                                CAGG GCC TGGG GT  TGGTT
                                |||| ||| |||| ||  |||||
                                GTCC CGG ACCT CA  ACCAA
                                  _  A   T  AA
GAM2586 RERE    5' CAGGAGCCCAGGATCATGTCTG 29023        T  ____
            GTT                   CAGGAGCCC GGG   GTCTGGTT
                                |||||||| |||   ||||||||
                                GTCCTCGGG CCT   CAGACCAA
                                     T  AGTA
GAM2586 TCF21   5' GGAGTTGGGGTCTGGTT    17349     CCC
                                GGAG   TGGGGTCTGGTT
                                ||||   ||||||||||||
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                                CCTC   ACCCCAGACCAA
                                  A__
GAM2586  TNP2     5'  AGGAGCCCTTGGGTCAGATT   24053         G    T
                                AGGAGCCCT GGGTC GGTT
                                ||||||||| ||||| ||||
                                TCCTCGGGA CCCAG CTAA
                                    A    T
GAM2587  AMFR     3'  AGTTCTTTTTTATTTCTTTAAT 39934        ___
              A                  GGTTCTT   TATTTCTTTAATA
                                |||||||   ||||||||||||||
                                TCAAGAA   ATAAAGAAATTAT
                                   AAA
GAM2587  CD8A     3'  AGTGGTTCTTATTTCCTTA   12088    C      T
                                AG GGTTCTT ATTTCTTTA
                                || ||||||| |||||||||
                                TC CCAAGAA TAAAGGAAT
                                 A      _
GAM2587  NXF5     5'  ACGGCATTATTTCTTTAAT   37617      TCT
                                GCGGT   TTATTTCTTTAAT
                                |||||   ||||||||||||||
                                TGCCG   AATAAAGAAATTA
                                  T__
GAM2587  B4GALT2  3'  GCAATGTACAAACACAA     36140      TATGAA
                                GCAAT     ATAAACACAA
                                |||||     ||||||||||
                                CGTTA     TGTTTGTGTT
                                  CA_____
GAM2587  DDX5     3'  GCAATTATGAAAAACA      20535          TA
                                GCAATTATGAAA  AACA
                                ||||||||||||  ||||
                                CGTTAATACTTT  TTGT
                                       __
GAM2587  GPR48    3'  GCTCACTAAGAAATAAACA   32988    A_   T
                                GC  ATTA GAAATAAACA
                                ||  |||| ||||||||||
                                CG  TGAT CTTTATTTGT
                                 AG    T
GAM2587  SNAI2    3'  TATAAAAATAAACACAAA    16885        _
                                TATGAAA TAAACACAAA
                                ||||||| ||||||||||
                                ATATTTT ATTTGTGTTT
                                    T
GAM2587  SPARC    3'  ACCCTGAAATGAAATGAACACA 17063    AATT__      A
              AA                  GC      ATGAAAT AACACAAA
                                ||      ||||||| ||||||||
                                TG      TACTTTA TTGTGTTT
                                 GGACTT      C
GAM2588  ACN      5'  CCTGGTATAACCATAATCGGAG 31409    GC  CTT__       A
              ATG                  CC  GG    CTATAATC GAGATG
                                ||  ||    |||||||| ||||||
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                                GG  CC    GGTATTAG CTCTAC
                                 A_  ATATT       C
GAM2588  BMPR1B   3'  GGCTTTCTGCAGAGATG     10206      _  ATAAT
                                GGCTT CT    CAGAGATG
                                ||||| ||    ||||||||
                                CCGAA GA    GTCTCTAC
                                   A  C____
GAM2588  CERD4    3'  GGCTTCTTAGCAGAGATG    28952       ATAAT
                                GGCTTCT    CAGAGATG
                                |||||||    ||||||||
                                CCGAAGA    GTCTCTAC
                                    ATC__
GAM2588  EGLN1    5'  CCTCGGCTTCTGCCTCGGAG   35163    G       ATAA  A
                                CC CGGCTTCT    TC GAG
                                || ||||||||    || |||
                                GG GCCGAAGA    AG CTC
                                 A       CGG_  C
GAM2588  FREB     3'  CCTGGCTTCTATTTACTGGATG 37223    GC        AATCAGA
                                CC  GGCTTCTAT      GATG
                                ||  |||||||||      ||||
                                GG  CCGAAGATA      CTAC
                                 A_       AATGAC_
GAM2589  IL1RAP   3'  TAAGTAATTAATGAATGAT   13504          AG  A
                                TAAGTAATTAAT  AT GAT
                                ||||||||||||  || |||
                                ATTCATTAATTA  TA CTA
                                       CT  _
GAM2590  BACH1    3'  TAAGCTATAGCAAACTGTTAAA 10148     AA    T
              AA                  TAG  TATA CAAACTGTTAAAAA
                                |||  |||| ||||||||||||||
                                ATT  ATAT GTTTGACAATTTTT
                                  CG   C
GAM2590  CDH6     3'  TAGGATATAACAAACTAT    22331     A     T
                                TAG ATATA CAAACTGT
                                ||| ||||| ||||||||
                                ATC TATAT GTTTGATA
                                  C    T
GAM2590  HHIP     3'  TAGAATATTCAAACAGTC    35414        A     T
                                TAGAATAT TCAAAC GTT
                                ||||||||  ||||||  |||
                                ATCTTATA AGTTTG CAG
                                     _     T
GAM2590  MAN1A2   5'  TAGAATACATTGAACTGTC   27457         CA
                                TAGAATATAT  AACTGTT
                                ||||||||||  |||||||
                                ATCTTATGTA  TTGACAG
                                      AC
GAM2590  MSX2     3'  TAAAATATATCAAATTGT    42300            C
                                TAGAATATATCAAA TGT
                                |||||||||||||| |||
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                                ATTTTATATAGTTT ACA
                                       A
GAM2590  SUDD     3'  TAAAATATGTCAAACATGGTTA 19261         A     T__
              AA                  TAGAATAT TCAAAC   GTTAAA
                                  |||||||| ||||||   ||||||
                                  ATTTTATA AGTTTG   CAATTT
                                      C     TAC
GAM2590  ADRA2A   3'  AAAATGGACAGAAATCTTTTC  8622        ACT    A
                                  AGAGTG   GACA AAATCTTTTC
                                  ||||||   |||| ||||||||||
                                  TTTTAC   CTGT TTTAGAAAAG
                                     ___    C
GAM2590  C18orf1  3'  GTGACAGGTGGAAATCTTTT   41224       TGACAA
                                  GTGAC     AAATCTTTT
                                  |||||     |||||||||
                                  CACTG     TTTAGAAAA
                                     TCCACC
GAM2590  FOXO1A   3'  AGGATCTGAAAATCTTTT    12882    T _   CAA
                                  AG GA CTGA   AAATCTTTT
                                  || || ||||   |||||||||
                                  TC CT GACT   TTTAGAAAA
                                   _ A   ____
GAM2590  GRINL1A  3'  GAGTGCTGGCAAGACCTC    42999      A   A   AA
                                  GAGTG CTG CAA  ATCTT
                                  ||||| ||| |||  |||||
                                  CTCAC GAC GTT  TGGAG
                                     _  C   C_
GAM2590  MADH6    3'  GAGTGACTGGTATTAGCTTTT  24599         ACAAAAAT
                                  GAGTGACTG       CTTTT
                                  |||||||||       |||||
                                  CTCACTGAC       GAAAA
                                       CATAATC_
GAM2590  MSMB     3'  AGTGTTTGCTCAAAAATCTTTT 39791      AC  A_
                                  AGTG  TG  CAAAAATCTTTT
                                  ||||  ||  ||||||||||||
                                  TCAC  AC  GTTTTTAGAAAA
                                    AA  GA
GAM2590  NP       3'  AGGTGAAGGACAGGAATCTTTT 7075     A    CT    AA
              C                    AG GTGA  GACA  AATCTTTTC
                                  || ||||  ||||  |||||||||
                                  TC CACT  CTGT  TTAGAAAAG
                                   _   TC    CC
GAM2590  SP3      5'  GTGGCTGACAAAACCTC     44380     A       A
                                  GTG CTGACAAAA TCTT
                                  ||| ||||||||| ||||
                                  CAC GACTGTTTT GGAG
                                    C       _
GAM2590  UC28     3'  GAGTGATGAGAATCTTTT    34689       C   CAAA
                                  GAGTGA TGA    AATCTTTT
                                  |||||| |||    ||||||||
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                                CTCACT ACT    TTAGAAAA
                                   _  C___
GAM2590  ZNF274   3'  AAGTGAATGGGAAATCTTTT  32244       C  ACAA
                                GAGTGA TG    AAATCTTTT
                                |||||| ||    |||||||||
                                TTCACT AC    TTTAGAAAA
                                   T  CC__
GAM2591  IGF1     3'  TAAATGATGCCATTGCA     8347          GCGTT
                                TGAATGATGC    TATTGCA
                                ||||||||||    |||||||
                                ATTTACTACG    GTAACGT
                                      _____
GAM2591  NFIC     3'  TGAGTGTGTGCGTCTAT     24645     A  A  C
                                TGA TG TG GCGTTTAT
                                ||| || || ||||||||
                                ACT AC AC CGCAGATA
                                  C  _  A
GAM2591  TFRC     3'  TGAAGATGTCATTGCA      17436      T    CGCGT
                                TGAA GATG    TTATTGCA
                                |||| ||||    ||||||||
                                ACTT CTAC    AGTAACGT
                                   _   _____
GAM2592  GNAZ     3'  GACACCCCGTGGGTT       13180       T      TTTGCG
                                GACAC CCCGTGG     GTT
                                ||||| |||||||     |||
                                CTGTG GGGCACC     CAA
                                   _     _______
GAM2592  MASP2    3'  CACTCTCGTGGTTTATGTC   40175       C        CG
                                CACTC CGTGGTTTG  GTT
                                ||||| |||||||||  |||
                                GTGAG GCACCAAAT  CAG
                                   A        A_
GAM2593  AMPH     3'  ACAAACACAGATACTGTTGA  11595          C   TAT
                                ACAAACACAGA ATT   TTGA
                                |||||||||| |||   ||||
                                TGTTTGTGTCT TGA   AACT
                                      A  C__
GAM2593  ASB2     5'  TGACAGACACAGGGCTCTG   32055      A     ACATTTA
                                TGACA ACACAG      TTTG
                                ||||| ||||||      ||||
                                ACTGT TGTGTC      AGAC
                                   C     CCG____
GAM2593  RET      3'  TGATGGACACAGACCAACACT 33941     CAA       ATT
                                TGA   ACACAGAC   TATT
                                |||   ||||||||   ||||
                                ACT   TGTGTCTG   GTGA
                                  ACC       GTT
GAM2593  TEM7     3'  TGACAACCGCAGACATCT    33814       ACA
                                TGACAA   CAGACATTT
                                ||||||   |||||||||
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                                ACTGTT  GTCTGTAGA
                                   GGC
GAM2593 YWHAG    3' TGACAAACACCAGACATT    29801          _
                                TGACAAACAC AGACATT
                                |||||||||| |||||||
                                ACTGTTTGTG TCTGTAA
                                      G
GAM2594 AOC3     3' CAGCCTCCCAAACAGGCT    19013     ACAATG
                                CAGC     CTAAACAGGCT
                                ||||     ||||||||||
                                GTCG     GGTTTGTCCGA
                                  GAG___
GAM2594 CNTN2    3' GCACAGTGTCAGGCCACC    22910      A  CTAAA
                                GCACA TG    CAGGCTATT
                                ||||| ||    |||||||||
                                CGTGT AC    GTCCGGTGG
                                   C  A____
GAM2594 EIF5A2   3' CAGCACAATCTGAAAACAA   33786        G __
                                CAGCACAAT CT  AAACAG
                                ||||||||| ||  ||||||
                                GTCGTGTTA GA  TTTGTT
                                      _ CT
GAM2594 ITK      3' CAACACAATGCTGCC       24441          AAACAG
                                CAGCACAATGCT     GCT
                                ||||||||||||     |||
                                GTTGTGTTACGA     CGG
                                                 _______
GAM2594 MSL3L1   3' AGCATAGGCTAAACAACCA   38597     CAAT       G
                                AGCA    GCTAAACAG CTA
                                ||||    ||||||||| |||
                                TCGT    CGATTTGTT GGT
                                  ATC_       _
GAM2594 MYH11    3' AGACAATGCTAAGTACAG    35624    C        __
                                AG ACAATGCTAA  ACAG
                                || ||||||||||  ||||
                                TC TGTTACGATT  TGTC
                                 _        CA
GAM2594 ZNF236   3' CAGCTACCTGGTAGGCTAT   28859     ACAA    AAAC
                                CAGC    TGCT    AGGCTAT
                                ||||    ||||    |||||||
                                GTCG    ATGG    TCCGATA
                                  _____    ACCA
GAM2595 BSN      3' GGGCCTTTTACTGCCTGCCCTG 18405     ACCC   GCAC
                                GGGC    TGC    CCTGCCCTG
                                ||||    |||    |||||||||
                                CCCG    ATG    GGACGGGAC
                                  GAAA   AC__
GAM2595 CEBPD    3' GGGCACCCGGCGGCC       45519        T   CACCCT  C
                                GGGCACCC GCG     GC C
                                |||||||| |||     || |
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                                CCCGTGGG CGC     CG G
                                    C  ______  A
GAM2595  DUSP7    5'  GGGCCGGGCAGCCCTGCCCTG  42276     ACCC  C  _
                                GGGC   TG GCA CCCTGCCCTG
                                ||||   || ||| ||||||||||
                                CCCG   GC CGT GGGACGGGAC
                                  ____  C  C
GAM2595  GALNT2   3'  GGGCTACGCACACCCTGCTCTG 21008     ACCC         C
                                GGGC   TGCGCACCCTGC CTG
                                ||||   |||||||||||| |||
                                CCCG   GCGTGTGGGACG GAC
                                  AT__          A
GAM2595  HCK      3'  GGGCACCCCCTGGCCCTGCCCT 40941        GCGCA
             G                   GGGCACCCT    CCCTGCCCTG
                                |||||||||    ||||||||||
                                CCCGTGGGG    GGGACGGGAC
                                     GACC_
GAM2595  HM13     3'  GGTATCCTGCTGCCCCCTGCCC 43110    GCAC   _  A
             TG                   GG   CCTGC GC CCCTGCCCTG
                                ||   ||||| || ||||||||||
                                CC   GGACG CG GGGACGGGAC
                                 ATA_    A  G
GAM2595  KCNA7    5'  GGACGCCCGCCCTGCCCT    36660     A  TGCGCA
                                GGGC CCC     CCCTGCCCT
                                |||| |||     |||||||||
                                CCTG GGG     GGGACGGGA
                                  C  C_____
GAM2595  MRPS12   3'  GGGCACCCTTTGCACCCC    37891        GC
                                GGGCACCCT  GCACCCT
                                |||||||||  |||||||
                                CCCGTGGGA  CGTGGGG
                                     AA
GAM2595  NRL      3'  GAGCACCCTGTGCAGGTCTG   26135        C  CC_
                                GGGCACCCTG GCA   CTG
                                |||||||||| |||   |||
                                CTCGTGGGAC CGT   GAC
                                      A   CCA
GAM2595  OVOL1    3'  GGGACCTGCAGCCCCTGCCCTG 21275     CAC    _  A
                                GGG   CCTGC GC CCCTGCCCTG
                                |||   ||||| || ||||||||||
                                CCC   GGACG CG GGGACGGGAC
                                  T__     T  _
GAM2595  PACE     3'  AGGCACCTGCCTTGCC      15028        C  GCAC C
                                GGGCACC TGC    C TGCC
                                ||||||| |||    | ||||
                                TCCGTGG ACG    G ACGG
                                    _  _____ A
GAM2595  PIG3     3'  GGCCGCGTCCTGTCCT     22196     ACCC   CAC   C
                                GGC    TGCG   CCTG CCT
                                |||    ||||   |||| |||
```

```
                                CCG   GCGC   GGAC GGA
                                 _____   A__   A
GAM2595  PROK1    3'  GGGCTCCCTACACCTGCC    37100      A      CAC
                                GGGC CCCTGCG   CCTGCC
                                |||| |||||||   ||||||
                                CCCG GGGATGT   GGACGG
                                  A     ___
GAM2595  RARA     3'  GGGCCCTTGCTCTGCCCT    9711       A  C   GCACC
                                GGGC CC TGC    CTGCCCT
                                |||| || |||    |||||||
                                CCCG GG ACG    GACGGGA
                                  _ A   A____
GAM2595  SREBF2   3'  GGGCTGCCCAGTTTCTGCCCTG 21405      ACCC   G  CC__
                                GGGC   TGC CA   CTGCCCTG
                                ||||   ||| ||   ||||||||
                                CCCG   ACG GT   GACGGGAC
                                  _____  G  CAAA
GAM2595  TCIRG1   5'  GGGCTGCTCCAACCTCCTGCCC 25690      ACC  G  _ AC
             TG                   GGGC   CT CG C  CCTGCCCTG
                                ||||   || || |  |||||||||
                                CCCG   GA GT G  GGACGGGAC
                                  AC_  G  T GA
GAM2595  VEGF     3'  GGGCACGTGGATCCTGCCCTG  17959       CC  CGCAC
                                GGGCAC  TG    CCTGCCCTG
                                ||||||  ||    |||||||||
                                CCCGTG  AC    GGACGGGAC
                                   C_  CTA__
GAM2595  WBSCR5   3'  GGGACCTACTCTGCCCT    37127     CAC    GCACC
                                GGG   CCTGC    CTGCCCT
                                |||   |||||    |||||||
                                CCC   GGATG    GACGGGA
                                  T__    A____
GAM2595  ZNF147   3'  GGGAGTAGGTCACCCTGCCCTG 22930     CACCCTGCG
                                GGG        CACCCTGCCCTG
                                |||        ||||||||||||
                                CCC        GTGGGACGGGAC
                                  TCATCCA__
GAM2596  ABCA3    5'  CTAGAGAAGTAGGTGGTCT   9902           T  AT
                                CTAGAGAAGTAG GT  GTCT
                                |||||||||||| ||  ||||
                                GATCTCTTCATC CA  CAGA
                                       _  C_
GAM2596  BACH2    3'  TCACTAGAGGTGCCATGTC   34806         AAGTA   _
                                TCACTAGAG    GTGT ATGTC
                                |||||||||    |||| |||||
                                AGTGATCTC    CACG TACAG
                                     _____   G
GAM2596  CACNG1   3'  TCACCAGAGAGGGTGTGT    8804          A_  A
                                TCACTAGAGA  GT GTGT
                                ||||||||||  || ||||
```

```
                                AGTGGTCTCT  CA CACA
                                      CC  _
GAM2597  EXTL3    3'  TAAGTACGGAGGCAAGCCT   11037       GA  ATA T
                                TAAGTA  GA   G GTAAGCCT
                                ||||||  ||   | ||||||||
                                ATTCAT  CT   C CGTTCGGA
                                   GC  ___ _
GAM2597  MBNL     5'  TAAGTAGAAATGGGGGTGT   34318         ATA__
                                TAAGTAGAGA    GTGT
                                ||||||||||    ||||
                                ATTCATCTTT    CACA
                                      ACCCC
GAM2597  TCTA     3'  AGTGGGGAGGAGCTGAGCCTG  35277    A__   AAT   GTA
                                AGT   GAG   AGT   AGCCTG
                                |||   |||   |||   ||||||
                                TCA   CTC   TCG   TCGGAC
                                  CCC   C__   AC_
GAM2597  CASP7    3'  AGGCAGCCCCCACCAT     10272    A      T  T
                                AG CAGCCCTT AC CAT
                                || |||||||| || |||
                                TC GTCGGGGG TG GTA
                                 C       _ _
GAM2597  CYP8B1   5'  TCAGACAGCTCTTGCACC    20509         C  _
                                TCAGACAGC CTT TACT
                                ||||||||| ||| ||||
                                AGTCTGTCG GAA GTGG
                                      A   C
GAM2597  KCNJ16   3'  TCAGTGGTAGCCCTCATAATT  33018     AC__    TTTAC
                                TCAG    AGCCC    TCATAATT
                                ||||    |||||    ||||||||
                                AGTC    TCGGG    AGTATTAA
                                  ACCA    _____
GAM2598  CASP8    3'  AAGCTCTTCAAAGGTCGT    37865           _
                                AAGCTCTTCAAAG TCGT
                                |||||||||||| ||||
                                TTCGAGAAGTTTC AGCA
                                        C
GAM2598  COG6     3'  AAAAAATTCTTCAAACCTTTCA 43763       C       GTCG
           TA                     AAAAAG TCTTCAAA    TCATA
                                ||||||  ||||||||    |||||
                                TTTTTT AGAAGTTT    AGTAT
                                   A       GGAA
GAM2598  EPB41    3'  AAAAAGCTCTTCAAAAGGATCA 20761              TC
                                AAAAAGCTCTTCAAAG  GTCA
                                ||||||||||||||||  ||||
                                TTTTTCGAGAAGTTTT  TAGT
                                        CC
GAM2598  F3       3'  AAAAAGCTTTTCAAAAGTC   42546         C     _
                                AAAAAGCT TTCAAA GTC
                                ||||||||  ||||||  |||
```

```
                                TTTTTCGA AAGTTT CAG
                                    A     T
GAM2598 GALE     3'  GGAAAGCTCTTTCAGAGC    41800   A       _ A
                                A AAAGCTCTT CA AGT
                                | ||||||||| || |||
                                C TTTCGAGAA GT TCG
                                 C        A  C
GAM2598 LAMB2    3'  AGCTCTTCAGTGCAT       14070         AA  C T
                                AGCTCTTCA  GT G CAT
                                |||||||||  || | |||
                                TCGAGAAGT  CA C GTA
                                    __ _ _
GAM2598 MTIF2    5'  AAAAAGCTTCTCCAATGTCAT  14684        _     A
                                AAAAAGCT CTTCAA GTCGT
                                |||||||| |||||| |||||
                                TTTTTCGA GAGGTT CAGTA
                                    A     A
GAM2598 NFATC3   3'  GCCCTTCAAATGACCATA    21250         GTCG
                                GCTCTTCAAA    TCATA
                                ||||||||||    |||||
                                CGGGAAGTTT    GGTAT
                                     ACT_
GAM2598 OAS3     3'  GCTCTTCAATAGCCCACATA   26181         _   GT
                                GCTCTTCAA AGTC  CATA
                                ||||||||| ||||  ||||
                                CGAGAAGTT TCGG  GTAT
                                     A    GT
GAM2598 P53AIP1  3'  AAAAGGCTCCTCAAGGTCA   35227     A       A
                                AAAA GCTCTTCAA GTCG
                                |||| ||||||||| ||||
                                TTTT CGAGGAGTT CAGT
                                  C        C
GAM2598 PPP1R2   3'  AAAAAGCTCTATAATATC    26414         TC  A
                                AAAAAGCTCT  AA GTC
                                ||||||||||  || |||
                                TTTTTCGAGA  TT TAG
                                     TA  A
GAM2598 RAG1     3'  AAAAAGCTCTTTTGAATC    7781          CAA
                                AAAAAGCTCTT   AGTC
                                ||||||||||   ||||
                                TTTTTCGAGAA   TTAG
                                     AAC
GAM2598 S100A12  3'  AAAAAGCCTTCAGAGAGC    24735       T    A  TC
                                AAAAAGC CTTCA AG  GT
                                ||||||| ||||| ||  ||
                                TTTTTCG GAAGT TC  CG
                                    _    C  T_
GAM2598 CEACAM6  3'  TAGAAGAATTCAGGGTT     14733         AAAAGTAA   G
                                TAGAAGAATT       GGT T
                                ||||||||||       ||| |
```

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                                ATCTTCTTAA       CCA A
                                      GTC_____   G
GAM2598  CENPF    3'  TAGAAGAATAAAATG       32282        ATTAAAA
                                TAGAAGA      GTAAGGTG
                                |||||||      ||||||||
                                ATCTTCT      TATTTTAC
                                       ________
GAM2598  GDI1     3'  CAGAAGAATTAGGGGTG     41012          AAAGTAA
                                TAGAAGAATTA      GGTG
                                ||||||||||       ||||
                                GTCTTCTTAAT      CCAC
                                      CC_____
GAM2598  HAS2     3'  TAGAGGAACTAAGGTGT     23721      A   TAAAAG
                                TAGA GAAT     TAAGGTGT
                                |||| ||||     ||||||||
                                ATCT CTTG     ATTCCACA
                                  C   _______
GAM2598  STAM     3'  GAAGAATTAAAGGATACAATGT 18459          A_   AG
                 G                 GAAGAATTAAA  GTA  GTGTG
                                |||||||||||  |||  |||||
                                CTTCTTAATTT  TAT  TACAC
                                      CC   GT
GAM2599  NRAP     3'  GCAGTGCATATAGCTGTT    40194       A  __
                                GTAGT GCA  TAGCTGTT
                                |||||| |||  ||||||||
                                CGTCA CGT  ATCGACAA
                                   _  AT
GAM2599  SLC22A1LS 5'  TGTGCAGTCAGCTGT       28259     C    AGCA
                                TG GTAGT    TAGCTGT
                                || |||||    |||||||
                                AC CGTCA    GTCGACA
                                 A    _____
GAM2599  VNN1     3'  TGCACAGTGCATGGCTGTT    21689         A   A
                                TGCGTAGT GCAT GCTGTT
                                |||||||| |||| ||||||
                                ACGTGTCA CGTA CGACAA
                                      _    C
GAM2599  AVPR1A   5'  TCAGGCAATTTTACAAGGA    8734      C       TAGGT
                                TCA GCAATTTT     CAAGGA
                                ||| ||||||||     ||||||
                                AGT CGTTAAAA     GTTCCT
                                  C       T_____
GAM2599  COL7A1   3'  TCATCACAGGCTTGGGTCAAGG 6426      _   ATT   A
                                TCA CGCA   TTT GGTCAAGG
                                ||| ||||   ||| ||||||||
                                AGT GTGT   GAA CCAGTTCC
                                  A   CC_   C
GAM2599  EBAG9    5'  TCACGCAAATTTCCCTGAGGAA 20119         T   AGGTCA
                                TCACGCAA TTTT      AGGAA
                                ||||||||| ||||      |||||
```

```
                                AGTGCGTT AAAG     TCCTT
                                    T   GGAC__
GAM2599  FCMD    3'  TCATGCAATCTTTTGAGTAAAG 27524     C       A_  C
              GAA                   TCA GCAATTTTT  GGT AAGGAA
                                ||| |||||||||  ||| ||||||
                                AGT CGTTAGAAA  TCA TTCCTT
                                  A       AC   T
GAM2599  FGF1    3'  CGCAGCCAATGGTCAAGG    37568     A  TTTA
                                CGCA TT    GGTCAAGG
                                |||| ||    ||||||||
                                GCGT GG    CCAGTTCC
                                  C  TTA_
GAM2599  GATM    3'  TCATGCACTTTTTAAAGCAGGA 11233     C   A       TCA
                                TCA GCA TTTTTAGG   AGGA
                                ||| ||| ||||||||   ||||
                                AGT CGT AAAAATTT   TCCT
                                  A   G       CG_
GAM2599  HTR6    5'  TCGCGCTAGGTCAGGG      9313     A   AATTTT      A
                                TC CGC     TAGGTCA GG
                                || |||     ||||||| ||
                                AG GCG     ATCCAGT CC
                                 C  _______      C
GAM2599  MAP4    3'  GCCAGTTTTTAGGTTATTAGAA 36273     AA_       CAA_
                                GC   TTTTTAGGT    GGAA
                                ||   |||||||||    ||||
                                CG   AAAAATCCA    TCTT
                                 GTC        ATAA
GAM2599  MCL1    3'  TCAGCAATTTCAAGG       35001     C     TTTAGG
                                TCA GCAATT     TCAAGG
                                ||| ||||||     ||||||
                                AGT CGTTAA     AGTTCC
                                  _     _______
GAM2599  PHB     3'  GCAATTTTTGGTAGGGA     15264          A   CAA
                                GCAATTTTT GGT   GGA
                                ||||||||| |||   |||
                                CGTTAAAAA CCA   CCT
                                     _  TC_
GAM2599  PPARBP  3'  TCATGCAAATGCATCAAGGAA  21933     C    TTTTTAG
                                TCA GCAA      GTCAAGGAA
                                ||| ||||      |||||||||
                                AGT CGTT      TAGTTCCTT
                                  A   TACG___
GAM2599  STC1    3'  TCATGCAATTTTCTTTAAGG   17183     C       AGGTC
                                TCA GCAATTTTT    AAGG
                                ||| |||||||||    ||||
                                AGT CGTTAAAAG    TTCC
                                  A       AAA__
GAM2599  UBL1    3'  CACGTAATTTTTAAAAAGGA   17839     C        TC
                                CACG AATTTTTAGG  AAGGA
                                |||| ||||||||||  |||||
```

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                                GTGC TTAAAAATTT  TTCCT
                                  A       __
GAM2600  ABCC8    5'  CCGCCGCCCGGCCCGGCC    7397          AACCC   C
                                CCGCCGCCCG    CCC GCC
                                ||||||||||    ||| |||
                                GGCGGCGGGC    GGG CGG
                                    C____   C
GAM2600  ABL1     5'  CCGCCGCCCGCCGCC      28707          AACCCCC
                                CCGCCGCCCG     CCGCC
                                ||||||||||     |||||
                                GGCGGCGGGC     GGCGG
                                    ________
GAM2600  ABL1     5'  CCGCCGCCCGCGCCCGCCCA  28708          AACCCC
                                CCGCCGCCCG     CCCGCCCA
                                ||||||||||     ||||||||
                                GGCGGCGGGC     GGGCGGGT
                                    GC____
GAM2600  ACCN2    5'  CCCCGCCCGGCCCCGC     33437    G     AACCC
                                CC CCGCCCG    CCCCGC
                                || |||||||    ||||||
                                GG GGCGGGC    GGGGCG
                                 _     C____
GAM2600  ADAM10   5'  CCGCGCCCCTACCTCCCGCCCA 9969      C   GA   CC
                                CCGC GCCC  ACC  CCCGCCCA
                                |||| ||||  |||  ||||||||
                                GGCG CGGG  TGG  GGGCGGGT
                                  _   GA   A_
GAM2600  ADRBK1   5'  CCGCCGCCGCCGCCGCTCC   11526        CGAACC  C   _
                                CCGCCGCC     CC CCGC CC
                                ||||||||     || |||| ||
                                GGCGGCGG     GG GGCG GG
                                    C_____  C    A
GAM2600  AKR1B1   5'  CGCTCCCCAGACCCCCGCCCA  11569     CG    AACC
                                CGC  CCCG   CCCCCGCCCA
                                |||  ||||   ||||||||||
                                GCG  GGGT   GGGGGCGGGT
                                  AG   CT__
GAM2600  ANK1     5'  CCGCCCAAGTGCCCTTCTGCCC 33855        A__   CCCC
            A                    CCGCCCGA   CCC   GCCCA
                                 ||||||||   |||   |||||
                                 GGCGGGTT   GGG   CGGGT
                                     CAC   AAGA
GAM2600  AP2A1    5'  CCGCCCCCTGCCCCTCCCCTCC 30539      ____   GAA   C
            GCCC                   CCGCC   GCCC   CCCC CCGCCC
                                   |||||   ||||   |||| ||||||
                                   GGCGG   CGGG   GGGG GGCGGG
                                     GGGA   GA_   A
GAM2600  ATP6V0A4 5'  GCCACCCGGGCCACCC     33944        AACCCCC
                                GCCGCCCG     CCGCCC
                                ||||||||     ||||||
```

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                                CGGTGGGC      GGTGGG
                                    CC_____
GAM2600 ATSV     3' CCGCTCCCTCCTGGTCCCCGCC 20225     CG   GAACCC_
             CA                   CCGC  CCC      CCCCGCCCA
                                  ||||  |||      |||||||||
                                  GGCG  GGG      GGGGCGGGT
                                    A_   AGGACCA
GAM2600 B4GALT5  5' CCACCGCCTGGGCCTCGGCCA 21937        CGAACCC  C  C
                                  CCGCCGCC      CC CG CCA
                                  ||||||||      || || |||
                                  GGTGGCGG      GG GC GGT
                                      ACCC___  A  C
GAM2600 BCL11B   5' CCGCCGCCGCACCTCCTCCTCT 39747        CGA  _  _  C__
             GCCC                   CCGCCGCC   ACC CC CC   GCCC
                                  ||||||||   ||| || ||   ||||
                                  GGCGGCGG   TGG GG GG   CGGG
                                      CG_   A  A  AGA
GAM2600 BCL7A    3' CCGCCGCCCGAACCAAACCA   34204           CCC
                                  CCGCCGCCCGAACC   CCG
                                  ||||||||||||||   |||
                                  GGCGGCGGGCTTGG   GGT
                                         TTT
GAM2600 BIN1     5' CCGCGGTCGGCGCCCCCCGCCC 40294     C CC  AAC
                                  CCGC G  CG   CCCCCCGCCC
                                  |||| |  ||   ||||||||||
                                  GGCG C  GC   GGGGGGCGGG
                                    _ CA  CGC
GAM2600 BIN2     5' CCGCCGCCCTGGCCCCGC    32224         GAACCC
                                  CCGCCGCCC     CCCCGC
                                  |||||||||     ||||||
                                  GGCGGCGGG     GGGGCG
                                      ACC___
GAM2600 BYSL     5' CCGCTTCTCCCGGACCCCCGCC 19755     CG__    AACC
             C                    CCGC    CCCG    CCCCCGCCC
                                  ||||    ||||    |||||||||
                                  GGCG    GGGC    GGGGGCGGG
                                    AAGA    CT__
GAM2600 CACNG3   5' CCGCCGCCCGGGCTAGAAACCC 27231          AACCCCCCC
                                  CCGCCGCCCG        GCCC
                                  ||||||||||        ||||
                                  GGCGGCGGGC        TGGG
                                       CCGATCTT_
GAM2600 CALM1    5' CCGCCGCCTGCGCCGCCGCC   27855        CGAACC  C
                                  CCGCCGCC     CC CCGCC
                                  ||||||||     || |||||
                                  GGCGGCGG     GG GGCGG
                                      ACGC__  C
GAM2600 CAPN10   5' CCGCCCCGCCCGTTCCCCGCCC 35783       __    AACCC
                                  CCGCC  GCCCG    CCCCGCCC
                                  |||||  |||||    ||||||||
```

```
                              GGCGG  CGGGC    GGGGCGGG
                                GG    AA___
GAM2600  CAPN10   5'  CCGCCTCCGGCCCGCCCCGCCC 35768      GC   AA  _
                              CCGCC  CCG  CCC CCCCGCCC
                              |||||  |||  ||| ||||||||
                              GGCGG  GGC  GGG GGGGCGGG
                                A_   C_   C
GAM2600  CDKN2D   5'  GCCGCCCGCGGGGCCCTGCCC  38612        AACCC   C
                              GCCGCCCG    CCC GCCC
                              ||||||||    ||| ||||
                              CGGCGGGC    GGG CGGG
                                  GCCCC   A
GAM2600  CDR2     5'  CCGCCGCCCAGACTCCGC    44020          A  CCCC
                              CCGCCGCCCG AC    CCGC
                              |||||||||| ||    ||||
                              GGCGGCGGGT TG    GGCG
                                    C  A___
GAM2600  CELSR3   5'  CCGCCGCCCCGGGCCCCCGCCC 10834         GAACC
                              CCGCCGCCC    CCCCCGCCC
                              |||||||||    |||||||||
                              GGCGGCGGG    GGGGGCGGG
                                   GCCC_
GAM2600  CEP2     3'  CCGCCGCCAGGGCCGGGTCCA  27687        CGAACCCCC   C__
                              CCGCCGCC       CCG   CCA
                              ||||||||       |||   |||
                              GGCGGCGG       GGC   GGT
                                  TCCC_____   CCA
GAM2600  CHN2     5'  CCGCCGCCGCTGCCCTCGCCC  19807        C AACC   C
                              CCGCCGCC G    CCC CGCCC
                              |||||||| |    ||| |||||
                              GGCGGCGG C    GGG GCGGG
                                  _ GAC_   A
GAM2600  CHRNA4   5'  CCCCGCCCGGCCCTGCCC    8847     G     AACCC   C
                              CC CCGCCCG    CCC GCCC
                              || |||||||    ||| ||||
                              GG GGCGGGC    GGG CGGG
                               _      C_____   A
GAM2600  CLCN7    3'  CCGCGCCTGCCGCCTGCCC    10514     C   CGAAC  C  C
                              CCGC GCC    CC CC GCCC
                              |||| |||    || || ||||
                              GGCG CGG    GG GG CGGG
                                _   AC___  C  A
GAM2600  CXCL16   5'  CCGCCCGCCTGGCCCGTCC    35195       AA  CC_   C
                              CCGCCCG  CC   CCCG CC
                              |||||||  ||   |||| ||
                              GGCGGGC  GG   GGGC GG
                                  __ ACC    A
GAM2600  DBN1     5'  CCCCGCCCCGTCCCCGCCC    20532    G     GAACCC
                              CC CCGCCC     CCCCGCCC
                              || ||||||     ||||||||
```

```
                                GG GGCGGG     GGGGCGGG
                                 _     GCA___
GAM2600  DBN1     5'  CCCCGCCCGGACCTCGCCC   38926    G      A   CCCC
                                CC CCGCCCG ACC    CGCCC
                                || ||||||| |||    |||||
                                GG GGCGGGC TGG    GCGGG
                                 _      C   A___
GAM2600  DDX26    5'  CCGCCTCCGCCTCCTCCTGCC  29088      GC   AA  _  _  C
                                CCGCC  CCG  CC CC CC GCC
                                |||||  |||  || || || |||
                                GGCGG  GGC  GG GG GG CGG
                                   A_   __  A  A  A
GAM2600  DLG3     5'  CCGCGGCTCGGACCCCCC    34430      C  C  A
                                CCGC GC CG ACCCCCC
                                |||| || || |||||||
                                GGCG CG GC TGGGGGG
                                  C  A  C
GAM2600  DSCAM    5'  CGCCCCCCGCGCTCCGCCC   10797     G    AACCCCC
                                CGCC CCCG      CCGCCC
                                |||| ||||      ||||||
                                GCGG GGGC      GGCGGG
                                  G   GCGA___
GAM2600  DUSP7    5'  CCGCCGCCCCGGCCTCCCG   42265         GAAC  C
                                CCGCCGCCC   CC CCCG
                                |||||||||   || ||||
                                GGCGGCGGG   GG GGGC
                                     GCC_  A
GAM2600  DVL1     5'  CCGCCCGCCTGCGCCCCGCCC  40406       AACCC_
                                CCGCCCG     CCCCGCCC
                                |||||||     ||||||||
                                GGCGGGC     GGGGCGGG
                                   GGACGC
GAM2600  EN2      5'  CCGCCGCCCGGCCGTCCCCGCC 10937          AA  C_
              C                  CCGCCGCCCG  CC  CCCCGCCC
                                |||||||||  ||  ||||||||
                                GGCGGCGGGC  GG  GGGGCGGG
                                     C_  CA
GAM2600  EN2      5'  CCGCCGCCTGGGCCGCCC    10938        CGAACCCCC
                                CCGCCGCC       CCGCCC
                                ||||||||       ||||||
                                GGCGGCGG       GGCGGG
                                    ACCC_____
GAM2600  EN2      5'  CGCCGCCTCGGCCTCCG     10941        _  AACC  C
                                CGCCGCC CG    CC CCG
                                ||||||| ||    || |||
                                GCGGCGG GC    GG GGC
                                   A  C___  A
GAM2600  ENO1     5'  CGCCGCCCGCGCCGACTTCCTG 10971          AA  CC___  C
              CC                  CGCCGCCCG  CC    CC GCC
                                |||||||||  ||    || |||
```

```
                                GCGGCGGGC  GG    GG CGG
                                     GC  CTGAA  A
GAM2600  ESD     5'  CCTCGCCTCAGCCCCGCCC   45071    GC   _  AACCC
                                CC  CGCC CG    CCCCGCCC
                                ||  |||| ||    ||||||||
                                GG  GCGG GT    GGGGCGGG
                                 A_   A  C____
GAM2600  FBXL7    5'  CCGCCGCCGGGTCCCCATCCGC 29397       CGAA   C_
              CC                  CCGCCGCC   CCCC  CCGCCC
                                ||||||||   ||||  ||||||
                                GGCGGCGG   GGGG  GGCGGG
                                     CCCA   TA
GAM2600  FMR1     5'  CCGCCGCCCGCGCTCGCC    12938        AACCCCCC
                                CCGCCGCCCG      CGCC
                                ||||||||||      ||||
                                GGCGGCGGGC      GCGG
                                     GCGA____
GAM2600  FUT4     5'  CCACCGCCCTGGCCCTCGCTCA 13016        GAACC   C   C
                                CCGCCGCCC    CCC CGC CA
                                |||||||||    ||| ||| ||
                                GGTGGCGGG    GGG GCG GT
                                     ACC__   A   A
GAM2600  FZD10    5'  CCCCTGCTCGGGCCCCCGCCCA 28448    G  _  C  AACC
                                CC CC GC CG    CCCCCGCCCA
                                || || || ||    ||||||||||
                                GG GG CG GC    GGGGGCGGGT
                                 _  A  A  CC__
GAM2600  GNAQ     5'  CCGCCGCCCGGTCGCGCGTCC  13175        AACCCCCC  __
                                CCGCCGCCCG      CGC  CC
                                ||||||||||      |||  ||
                                GGCGGCGGGC      GCG  GG
                                     CAGC____   CA
GAM2600  GNB1     5'  CCGCCGCCGCCGCCGCCTCCGT 13200       CGAA  _  C   C
              CC                  CCGCCGCC   CC CC CCG CC
                                ||||||||   || || ||| ||
                                GGCGGCGG   GG GG GGC GG
                                     CGGC  C  A   A
GAM2600  GNB1     5'  CCGCCGCCTCGGCCGCCGC   13201        _  AACC  C
                                CCGCCGCC CG    CC CCGC
                                |||||||| ||    || ||||
                                GGCGGCGG GC    GG GGCG
                                     A  C___  C
GAM2600  HUNK     5'  CCGCCGCCCTGGGCCCAGCCCC 31063        GAA_  __
              GCC                   CCGCCGCCC   CCC  CCCCGCC
                                |||||||||   |||  |||||||
                                GGCGGCGGG   GGG  GGGGCGG
                                     ACCC   TC
GAM2600  IDS      5'  CCGCCGCCCGGGCCCGC     25960          AACCCC
                                CCGCCGCCCG     CCCGC
                                ||||||||||     |||||
```

```
                                GGCGGCGGGC     GGGCG
                                      CC____
GAM2600  INHBB    5'  CCGCGCCCGCGCCCGCCC    13549      C    AACCCC
                                CCGC GCCCG     CCCGCCC
                                |||| |||||     |||||||
                                GGCG CGGGC     GGGCGGG
                                  _    GC____
GAM2600  INHBB    5'  CCCGCCCCGCCCCCGCCC    13545      AA  _
                                CCCG  CC CCCCCGCCC
                                ||||  || |||||||||
                                GGGC  GG GGGGGCGGG
                                  GG  C
GAM2600  IRAK1    5'  CCGCCGCCGGGCCGGGACC    11471         C AA  CCCCC
                                CCGCCGCC G  CC    GCC
                                |||||||| |  ||    |||
                                GGCGGCGG C  GG    TGG
                                    _ CC  CCC__
GAM2600  JAG2     5'  CCGCCGCCCGCGCCCGGCTCCC 13708          AA   CCCCG
              A                  CCGCCGCCCG  CCC    CCCA
                                |||||||||  |||    ||||
                                GGCGGCGGGC  GGG    GGGT
                                    GC   CCGA_
GAM2600  JUN      5'  GCCGCCCGGACTCCGACGAC   13742        A  C  CC  _
                                GCCGCCCG AC CC  CG C
                                |||||||| || ||  || |
                                CGGCGGGC TG GG  GC G
                                    C  A  CT  T
GAM2600  KCNA7    5'  CCGCCGCCCGCGCC        36646          AACCCCCC
                                CCGCCGCCCG       CGCC
                                ||||||||||       ||||
                                GGCGGCGGGC       GCGG
                                      _________
GAM2600  KCNA7    5'  CCGCCGCCCCAGCCCGGTGTCC 36645          GAA   CCCCG
                                CCGCCGCCC   CCC    CC
                                |||||||||   |||    ||
                                GGCGGCGGG   GGG    GG
                                    GTC   CCACA
GAM2600  KCNK1    5'  CCGCCGCCCCCGCCCCCGCCC  13885         GAA  _
                                CCGCCGCCC   CC CCCCCGCCC
                                |||||||||   || |||||||||
                                GGCGGCGGG   GG GGGGGCGGG
                                      ___  C
GAM2600  KCNK1    5'  CCCCCGCCCGGGCCTGGCTCCC 13881    G      AA  CC___
              GCCC                  CC CCGCCCG  CC    CCCGCCC
                                || |||||||  ||    |||||||
                                GG GGCGGGC  GG    GGGCGGG
                                 G      CC  ACCGA
GAM2600  KCNMB4   5'  CCGCCGCCTGGGCCCCGC    30942         CGAACCC
                                CCGCCGCC      CCCCGC
                                ||||||||      ||||||
```

```
                                GGCGGCGG     GGGGCG
                                   ACCC___
GAM2600 KIF5C    5' CCCTGCCCCGCCCCTGCCC   21146    GAA  _   _
                                CCC  CCC CCCC GCCC
                                |||  ||| |||| ||||
                                GGG  GGG GGGG CGGG
                                  ACG  C   A
GAM2600 KIFC3    3' CCACCCCCGCCTTTCCGCCCA 24454     G   AA  CCC
                                CCGCC CCCG  CC  CCGCCCA
                                ||||| ||||  ||  |||||||
                                GGTGG GGGC  GG  GGCGGGT
                                  _   __ AAA
GAM2600 KPNA1    5' CGCCGCCCCGCCCCGCC    44316       GAAC C
                                CGCCGCCC   C CCCCGCC
                                ||||||||   | |||||||
                                GCGGCGGG   G GGGGCGG
                                   _____ C
GAM2600 LMO2     5' CGCCGCCGCTCCTGCCTCCGC 24539      C AA  C_ _
                                CGCCGCC G  CC  CC CCGC
                                ||||||| |  ||  || ||||
                                GCGGCGG C  GG  GG GGCG
                                   _ GA  AC  A
GAM2600 MAD1L1   5' CCGCCGCTCGGATCTCCCTCCG 44669      C  AACC_  _
                                CCGCCGC CG    CCC CCG
                                ||||||| ||    ||| |||
                                GGCGGCG GC    GGG GGC
                                   A  CTAGA   A
GAM2600 MAP3K1   5' CCGCCGCCGCCAGTCCGCCC  42703      CGAA  CCC
                                CCGCCGCC   CC   CCGCCC
                                ||||||||   ||   ||||||
                                GGCGGCGG   GG   GGCGGG
                                   C___  TCA
GAM2600 MAP3K1   5' CCGCCAGTCCGCCCGC     42700      C_  AACCCC
                                CCGCCG  CCG    CCCGC
                                ||||||  |||    |||||
                                GGCGGT  GGC    GGGCG
                                   CA  _______
GAM2600 MBNL     5' CGCGGCCCCTCCCCCGCCC   34310    C   GAACC
                                CGC GCCC    CCCCCGCCC
                                ||| ||||    |||||||||
                                GCG CGGG    GGGGGCGGG
                                  C   GA___
GAM2600 MLLT1    5' CCGCCCCCGGGCCCCGC     25480     G   AACCC
                                CCGCC CCCG    CCCCGC
                                ||||| ||||    ||||||
                                GGCGG GGGC    GGGGCG
                                   _   CC___
GAM2600 MLLT1    5' CCGGCCGCCCGCTCGCCC    25483    _     AACCCCCC
                                CCG CCGCCCG      CGCCC
                                ||| |||||||      |||||
```

```
                                GGC GGCGGGC       GCGGG
                                  C      GA_____
GAM2600  MTCP1    5'  CCGCCGCCCGGCCTGACGCCC  30574          AAC  CCC
                                CCGCCGCCCG   CC   CGCCC
                                ||||||||||   ||   |||||
                                GGCGGCGGGC   GG   GCGGG
                                     C__  ACT
GAM2600  MYO5A    5'  CCGCGCGCCTACGCCCCCCGCC 40754      _   CGA  _
                                CCGC CGCC   AC CCCCCCGCC
                                |||| ||||   || |||||||||
                                GGCG GCGG   TG GGGGGGCGG
                                  C   A__  C
GAM2600  NCOA6IP  5'  CCCCTGCCCCTGCCCCCGCC   36048    G  _   GAACC
                                CC CC GCCC    CCCCCGCC
                                || || ||||    ||||||||
                                GG GG CGGG    GGGGGCGG
                                 _ A   GAC__
GAM2600  NRXN2    5'  CCTCGCGCCTCTCTCCCCGCCC 31481    GC  _  GAACCC
                                CC  CGC CC    CCCCGCCC
                                ||  ||| ||    ||||||||
                                GG  GCG GG    GGGGCGGG
                                 A_  C  AGAGA_
GAM2600  NUP214   5'  GCCACCCACGCCTTGCCCA   22932        AA  CCCCC
                                GCCGCCCG  CC    GCCCA
                                ||||||||  ||    |||||
                                CGGTGGGT  GG    CGGGT
                                     GC  AA___
GAM2600  OPRD1    5'  CGCCGCCCGCACCGGCCC    9515         A   CCCCC
                                CGCCGCCCG ACC    GCCC
                                ||||||||| |||    ||||
                                GCGGCGGGC TGG    CGGG
                                     G   C____
GAM2600  OSBP     5'  CGCCGCCCGGAGCGCCCCA   14986         AACCC
                                CGCCGCCCG    CCCCG
                                |||||||||    |||||
                                GCGGCGGGC    GGGGT
                                     CTCGC
GAM2600  PDE5A    5'  CACCCCAGCTTCCCCGCCCA  37903      GAACCC
                                CGCCC     CCCCGCCCA
                                |||||     |||||||||
                                GTGGG     GGGGCGGGT
                                   GTCGAA
GAM2600  PK428    5'  GCCGCCCGAGCCCACTCCA   18805         ACCCC   _
                                GCCGCCCGA    CCCGC CCA
                                |||||||||    ||||| |||
                                CGGCGGGCT    GGGTG GGT
                                     C____    A
GAM2600  PLCG2    5'  GCCGCCCGGGCACAGCTGCCC  43675        A__  CCCCCC
                                GCCGCCCG   AC     GCCC
                                ||||||||   ||     ||||
```

```
                                CGGCGGGC  TG    CGGG
                                    CCG  TCGA__
GAM2600  POLR2E   5'  CCGCCGCTCGCACCCCTTCTCC 40917       C  A    CCCG
                                CCGCCGC CG ACCCC   CC
                                ||||||| || |||||   ||
                                GGCGGCG GC TGGGG   GG
                                    A  G    AAGA
GAM2600  PPFIA3   3'  CCTCGGCGCGAGCTCCCCCGCC 41418   GCC  C   ACC
            C                    CC   GC CGA   CCCCCGCCC
                                ||   || |||   |||||||||
                                GG   CG GCT   GGGGGCGGG
                                 AGC  C   CGA
GAM2600  PPID     5'  GCCGCCCGGGCCGCCC     44615        AACCCCC
                                GCCGCCCG     CCGCCC
                                ||||||||     ||||||
                                CGGCGGGC     GGCGGG
                                    CC_____
GAM2600  PTEN     5'  CACCGCCCGCCGGCCTGCCC   7203         AA  CC  C
                                CGCCGCCCG  CC  CC GCCC
                                |||||||||  ||  || ||||
                                GTGGCGGGC  GG  GG CGGG
                                    __  CC  A
GAM2600  PTPRA    5'  CCGCCGCCCGGCCCGCGGCTCC 38909         AAC   CCC  _
                                CCGCCGCCCG   CCC   GC CC
                                ||||||||||   |||   || ||
                                GGCGGCGGGC   GGG   CG GG
                                    C__   CGC  A
GAM2600  PTPRE    5'  CCGCCGCCTCGGCTCCAGCTCC 38983        _  AACCCC  C  _
                                CCGCCGCC CG     CC GC CC
                                |||||||| ||     || || ||
                                GGCGGCGG GC     GG CG GG
                                    A  CGA___  T  A
GAM2600  PURA     5'  CCGCCGCCTGCCGCTCCGCCC  25205        CGAA  CCC
                                CCGCCGCC   CC   CCGCCC
                                ||||||||   ||   ||||||
                                GGCGGCGG   GG   GGCGGG
                                    AC__  CGA
GAM2600  RAB1A    5'  CCGCCGCCCTGACTCTCCG   43186         GA  CCCC
                                CCGCCGCCC  AC   CCG
                                |||||||||  ||   |||
                                GGCGGCGGG  TG   GGC
                                    AC  AGA_
GAM2600  RAI14    5'  GCTGCTCCACCCCGCCC     31803    C  _  AACCC
                                GC GC CCG    CCCCGCCC
                                || || |||    ||||||||
                                CG CG GGT    GGGGCGGG
                                 A  A  _____
GAM2600  RALB     5'  CCGCCGTCCGCACCCGGCCC   16146       C  A   CCCC
                                CCGCCG CCG ACCC   GCCC
                                |||||| ||| ||||   ||||
```

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                                GGCGGC GGC TGGG   CGGG
                                   A  G   C___
GAM2600 RENT1   5' GCCGCCGAGCCCCTCCG    16254      C A   C
                                GCCGCC GA CCCC CCG
                                |||||| || |||| |||
                                CGGCGG CT GGGG GGC
                                   _ C   A
GAM2600 RET     5' GCCGCCCCATCCCCGCCC   33935      GAACCC
                                GCCGCCC    CCCCGCCC
                                |||||||    ||||||||
                                CGGCGGG    GGGGCGGG
                                   GTA___
GAM2600 ROCK2   5' CCGCGGCCCGGACCGCCCCG  42354    C    A  C
                                CCGC GCCCG ACC CCCCG
                                |||| ||||| ||| |||||
                                GGCG CGGGC TGG GGGGC
                                  C    C  C
GAM2600 SFRP5   5' CCGCCGCCGCGGAGGTCGCCCA 16591       _ AACCCCCC
                                CCGCCGCC CG      CGCCCA
                                |||||||| ||      ||||||
                                GGCGGCGG GC      GCGGGT
                                    C  CTCCA___
GAM2600 SGCB    5' CCGCCGCCGCCGAGCTCCCCGC 6927        __  ACCC
            CC                  CCGCCGCC  CGA   CCCCGCCC
                                |||||||  |||   ||||||||
                                GGCGGCGG  GCT   GGGGCGGG
                                    CG   CGA_
GAM2600 SIRT3   5' CCGCCCCCGGCGCCCCGCCC  29260     G   AACCC
                                CCGCC CCCG    CCCCGCCC
                                ||||| ||||    ||||||||
                                GGCGG GGGC    GGGGCGGG
                                  _   CGC__
GAM2600 SLC18A3 5' CCGCCCGCTTGCCCGCCC   16826      AACCCC
                                CCGCCCG    CCCGCCC
                                |||||||    |||||||
                                GGCGGGC    GGGCGGG
                                   GAAC__
GAM2600 SLC18A3 5' CCGCCCGCCCGCTTGCCC   16825      AA  CCCC
                                CCGCCCG  CCC   GCCC
                                |||||||  |||   ||||
                                GGCGGGC  GGG   CGGG
                                   __  CGAA
GAM2600 SLC22A3 5' CCGCCGCCCGCCGCC      35048        AACCCCC
                                CCGCCGCCCG     CCGCC
                                ||||||||||     |||||
                                GGCGGCGGGC     GGCGG
                                               _______
GAM2600 SLC30A4 5' CCGCCTCTCCCCGCCCTGCCC 30012     CGAA  _  _
                                CCGCC   CCCC CCC GCCC
                                |||||   |||| ||| ||||
```

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                                GGCGG   GGGG GGG CGGG
                                  AGA_   C   A
GAM2600 SMARCC1  5' GCCGCTTCCCGGCCCCGCCCA 16903     CCGAA  __
                                GCCGC   CCC  CCCCGCCCA
                                |||||    |||  |||||||||
                                CGGCG   GGG  GGGGCGGGT
                                  AA___  CC
GAM2600 SMG1    5' CCGCCGCCCGAACCGGCCG   31506          CCC
                                CCGCCGCCCGAACC  CCG
                                ||||||||||||||  |||
                                GGCGGCGGGCTTGG  GGC
                                       CC_
GAM2600 SNX3    5' CCGCCGCCGCGGGCTCCCTCCT 19137       _ AAC_  _ _
           CG                    CCGCCGCC CG   CCC CC CG
                                |||||||| ||   ||| || ||
                                GGCGGCGG GC   GGG GG GC
                                    C  CCGA  A  A
GAM2600 SORT1   5' GCCGCCCGGCGCGCCCGCCCA 16440       AACCCC
                                GCCGCCCG    CCCGCCCA
                                ||||||||    ||||||||
                                CGGCGGGC    GGGCGGGT
                                    CGCGC_
GAM2600 SUV39H2  5' CCGCCGCCCGGGCCTTGGGAGC 36011        AA  CCCCC_
                                CCGCCGCCCG  CC    GC
                                ||||||||||  ||    ||
                                GGCGGCGGGC  GG    CG
                                      CC  AACCCT
GAM2600 TBL3    5' CCGCCGCTCCAGCTGAAACC  26986      _ _____
                                CCGCCGC CC    GAACC
                                |||||||  ||    |||||
                                GGCGGCG GG    TTTGG
                                    A  TCGAC
GAM2600 TCOF1   5' CCCCGCCTTAGTCCCCGCCC  7408    G   CGAACCC
                                CC CCGCC     CCCCGCCC
                                || |||||     ||||||||
                                GG GGCGG     GGGGCGGG
                                 _    AATCA__
GAM2600 THOP1   5' CCGCCGCCCGCGCTCCCG   43830        AACCCC
                                CCGCCGCCCG    CCCG
                                ||||||||||    ||||
                                GGCGGCGGGC    GGGC
                                      GCGA__
GAM2600 THOP1   5' CCGCCGCCACGGCCGCC    43829       _ AACCCCC
                                CCGCCGCC CG     CCGCC
                                ||||||||  ||     |||||
                                GGCGGCGG GC     GGCGG
                                    T  C_______
GAM2600 UBE2B   5' CCGCCTCCGGATCCCTCCGCCC 17791     GC  AAC  C
                                CCGCC  CCG  CCC CCGCCC
                                |||||  |||  ||| ||||||
```

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                                GGCGG  GGC   GGG GGCGGG
                                  A_   CTA   A
GAM2600  UBE2E3   5'  CCGCCCGCCCGGCCGC      26817        AA   CC
                                CCGCCCG  CCC  CCGC
                                |||||||  |||  ||||
                                GGCGGGC  GGG  GGCG
                                   __   CC
GAM2600  VAMP5    5'  CCGCCGCCGCCTCGCC      40463        CGAACCC  C
                                CCGCCGCC      CC CGCC
                                ||||||||      || ||||
                                GGCGGCGG      GG GCGG
                                    C_______ A
GAM2600  WEE1     5'  CGCCGCCCGAACACCGCCC    18089          CCCC
                                CGCCGCCCGAAC    CCGCCC
                                ||||||||||||    ||||||
                                GCGGCGGGCTTG    GGCGGG
                                      T___
GAM2600  WIG1     5'  CCGCCGCCGAGCCCCCTCCG   45385        C  A    _
                                CCGCCGCC GA CCCCC CCG
                                |||||||| || ||||| |||
                                GGCGGCGG CT GGGGG GGC
                                    _ C    A
GAM2600  WNT2     5'  CGCCGCGCCCCCGCCCCCCGC  18104       _  GAAC
                                CGCCGC CC    CCCCCCGC
                                |||||| ||    ||||||||
                                GCGGCG GG    GGGGGGCG
                                   C  GGGC
GAM2600  WT1      5'  GCCGCCCGGGTCCCGGACTCCC 35961         AA_   CCCCG
                                GCCGCCCG   CCC    CCC
                                ||||||||   |||    |||
                                CGGCGGGC   GGG    GGG
                                     CCA   CCTGA
GAM2600  WTAP     5'  CCGCCGCCGAACCCCGCC    22226        C      CCC
                                CCGCCGCC GAACCCC   GCC
                                |||||||| |||||||   |||
                                GGCGGCGG CTTGGGG   CGG
                                   _     ____
GAM2601  PART1    3'  AGCCAGTTAGACTTGTTATG   32456         TTT  G
                                AGCCGGTTA   AC TTGTTATG
                                |||||||||   || ||||||||
                                TCGGTCAAT   TG AACAATAC
                                    C__  _
GAM2601  TEM6     3'  TTCATAATTTTATTATACTCTG 35566        ATATTT
              A                  TTCATAA     TTATACTCTGA
                                 |||||||     ||||||||||
                                 AAGTATT     AATATGAGACT
                                    AAAAT_
GAM2602  ACN      5'  GGGTGTTTGGGGCGG       31411    T      GGAGA
                                GG TGTTTGGG    GCGG
                                || ||||||||    ||||
```

```
                                CC ACAAACCC    CGCC
                                 C      _____
GAM2602  ADD2    3'  GGTTGTTTCGGGCTCTGTGGT  32731       G  GAGAGC
                                GGTTGTTT GGG     GGT
                                |||||||| |||     |||
                                CCAACAAA CCC     CCA
                                     G  GAGACA
GAM2602  BMP6    3'  GGTTTTTGGGGGAGGAGGGT  11868     G       _ C
                                GGTT TTTGGGGGAG AG GGT
                                |||| |||||||||| || |||
                                CCAA AAACCCCCTC TC CCA
                                  _       C _
GAM2602  EPB42   3'  AGGGTTGGCAGGAGAGTGGT  6513     TTGT   _     C
                                AGG   TTGG GGGAGAG GGT
                                |||   |||| ||||||| |||
                                TCC   AACC TCCTCTC CCA
                                  C___   G      A
GAM2602  KCNK3   3'  GGGTGCTGGGGGAGAGTGGT  13911    T   T       C
                                GG TGTT GGGGGAGAG GGT
                                || |||| ||||||||| |||
                                CC ACGA CCCCCTCTC CCA
                                 C   _       A
GAM2602  MAGEC1  3'  TGTTTTTACAAAATATCAAACT 24168        CAGCGCT
           G                     TGTTTTTAC      TCAAACTG
                                |||||||||      ||||||||
                                ACAAAAATG      AGTTTGAC
                                     TTTTAT_
GAM2602  ROBO1   3'  TGTTTCTACCCCATTC      39491         AG  C
                                TGTTTTTACC  CG TTC
                                ||||||||||  || |||
                                ACAAAGATGG  GT AAG
                                     G_  _
GAM2603  IGF1    3'  TGCTGAATATCTGTTTTAGA  8357        CTAAATA
                                TGCTGGAT      TTTTAGA
                                ||||||||      |||||||
                                ACGACTTA      AAAATCT
                                     TAGAC__
GAM2603  TGFA    3'  TGCTGGACCTAGGAACTAGAAC 17449         AATATT
                                TGCTGGATCTA     TTAGAAC
                                ||||||||||      |||||||
                                ACGACCTGGAT     GATCTTG
                                     CCTT__
GAM2603  WASF3   3'  CTGGATTTAAATTTCAGAA   27383      C    AT
                                CTGGAT TAAAT  TTTAGAA
                                |||||| |||||  |||||||
                                GACCTA ATTTA  AAGTCTT
                                   A    __
GAM2603  ELMO2   3'  TATGGGCCAGAGAGATCTGGT  35222     ATAATA      A
                                TATG     AGAGATCT GT
                                ||||     |||||||| ||
```

```
                                ATAC     TCTCTAGA CA
                                  CCGGTC       C
GAM2603  RFP      3'  TGACTGGTAAGGGATCTAGTAA 27134      AA_    A
                C                  TGAT   TAAG GATCTAGTAAC
                                   ||||   |||| ||||||||||
                                   ACTG   ATTC CTAGATCATTG
                                     ACC    C
GAM2604  ANKH     3'  GCGGAAGGGAAATTTAAGA   38318    A    T    A
                                   GC GAAG GAAA TTTGGGA
                                   || |||| |||| |||||||
                                   CG CTTC CTTT AAATTCT
                                    C    C    _
GAM2604  AP1B1    3'  GCAGAAGTGGGGAGTTGGG    10035          AAAAT
                                   GCAGAAGTG     TTGGG
                                   |||||||||     |||||
                                   CGTCTTCAC     AACCC
                                         CCCTC
GAM2604  BACH2    3'  GCAGAAGTTAGGTTGGGGGAAG 34789         GAAAATTT
                                   GCAGAAGT       GGGAAG
                                   ||||||||       ||||||
                                   CGTCTTCA       CCCTTC
                                        ATCCAACC
GAM2604  CA12     3'  TAGCAGAAGGAAATCAGAGGGA 10249          T    ATTT_
                                   TAGCAGAAG GAAA     GGGA
                                   ||||||||| ||||     ||||
                                   ATCGTCTTC CTTT     CCCT
                                         _    AGTCT
GAM2604  CACNA1C  3'  GCAAAAGTGAAAACAGG     8754             TT
                                   GCAGAAGTGAAAAT  GGG
                                   |||||||||||||  |||
                                   CGTTTTCACTTTTG  TCC
                                                ___
GAM2604  CLECSF12 3'  GCAGAATGAAAATTCAAG    44123        G        TG
                                   GCAGAA TGAAAATT  GG
                                   |||||| ||||||||  ||
                                   CGTCTT ACTTTTAA  TC
                                        _       GT
GAM2604  COX11    3'  TAGAGGAGTGAAAATCTCTAGG 20419     C  A         ___
                                   TAG AG AGTGAAAATT  TGGG
                                   ||| || ||||||||||  ||||
                                   ATC TC TCACTTTTAG  ATCC
                                     _ C         AG
GAM2604  DDX26    5'  ACAGGAGTGGGGACCTGGGA   29084      A    AAA
                                   GCAG AGTG   ATTTGGGA
                                   |||| ||||   ||||||||
                                   TGTC TCAC   TGGACCCT
                                     C    CCC
GAM2604  FBLN5    3'  ACAGGTGAGAGTCAGGAAG    26753      AA    AAAT TG
                                   GCAG  GTGA    T  GGAAG
                                   ||||  ||||    |  |||||
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                                TGTC  CACT    A  CCTTC
                                  __    CTC_ GT
GAM2604  GAB2     3'  GCAGAAGTGGAGCTGGAA    29380         AAAAT
                                GCAGAAGTG    TTGGGA
                                |||||||||    ||||||
                                CGTCTTCAC    GACCTT
                                     CTC__
GAM2604  GALNT2   3'  GCAGAAGTGAAAGCTGGAA   21005           AT
                                GCAGAAGTGAAA  TTGGGA
                                ||||||||||||  ||||||
                                CGTCTTCACTTT  GACCTT
                                       C_
GAM2604  GPR84    3'  AGAGACTTGATTTGGGA     33779    C   AG   AAA
                                AG AGA  TGA   TTTGGGA
                                || |||  |||   |||||||
                                TC TCT  ACT   AAACCCT
                                 _   GA   ___
GAM2604  KIF3C    3'  GCAGAAAGCAGAGTTTGGGAAG 13952       _ _  AAA
                                GCAGAA GT GA   TTTGGGAAG
                                |||||| || ||   |||||||||
                                CGTCTT CG CT   AAACCCTTC
                                    T  T  C__
GAM2604  MLF2     3'  GCAGAATGAAAAATCAAG    24144       G     T TG
                                GCAGAA TGAAAA T  GG
                                |||||| |||||| |  ||
                                CGTCTT ACTTTT A  TC
                                   _     T GT
GAM2604  PIK3C2B  3'  ACAGAAATGGAGTTTGGGA   15286         AAAA
                                GCAGAAGTG    TTTGGGA
                                |||||||||    |||||||
                                TGTCTTTAC    AAACCCT
                                     CTC_
GAM2604  PRKACA   3'  GCAGAAGTGGGCTGGGA     15578         AAAAT
                                GCAGAAGTG    TTGGGA
                                |||||||||    ||||||
                                CGTCTTCAC    GACCCT
                                     CC___
GAM2604  PSMD9    3'  TAGCGAAGTGAAAGGA      15847      A       AATTT
                                TAGC GAAGTGAA    GGGA
                                |||| ||||||||    ||||
                                ATCG CTTCACTT    TCCT
                                  _      ______
GAM2604  PXF      3'  TAGCAGAAGTGAGAATCTGTAA 16011           A     _
            AAG                   TAGCAGAAGTGA AATTTG GGAAG
                                |||||||||||| |||||| |||||
                                ATCGTCTTCACT TTAGAC TTTTC
                                       C     A
GAM2604  SLC22A2  5'  CAGGGGTGAAGCCCAGGAAG  40519     AA    AA  TG
                                CAG  GTGAA  TT  GGAAG
                                |||  |||||  ||  |||||
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```
                                GTC  CACTT  GG  CCTTC
                                  CC    C_  GT
GAM2604  SLC31A1   3'  AGAAAAAACAATTTGGGA    12394      TGAA
                                AGAAG   AATTTGGGA
                                |||||   |||||||||
                                TCTTT   TTAAACCCT
                                   TTTG
GAM2604  SLC7A8    3'  CAGCAGGAGTGGCTGGGAA   29281       A   AAAAT
                                TAGCAG AGTG    TTGGGAA
                                |||||| ||||    |||||||
                                GTCGTC TCAC    GACCCTT
                                   C   C____
GAM2604  SOX13     3'  GCAGAGATGAAAACAGCAAG  25013      AG     TT  G
                                GCAGA  TGAAAAT  GG AAG
                                |||||  |||||||  || |||
                                CGTCT  ACTTTTG  TC TTC
                                   CT      __  G
GAM2604  TXNRD1    3'  TAGCAGGAATGAAAAAGAA   17772      A      TTTG
                                TAGCAG AGTGAAAA   GGAA
                                |||||| ||||||||   ||||
                                ATCGTC TTACTTTT   TCTT
                                   C      ____
GAM2604  DSC1      3'  TCTTTCATGGAAATCTTCTCA  35934     G   A_
                                TCTTT CGT  AAATCTTCTCA
                                |||||  |||  ||||||||||
                                AGAAA GTA  TTTAGAAGAGT
                                   _  CC
GAM2604  NOTCH2    3'  GCTAGTGTAGAATCTTCTCA   35909    CTTTGC   A
                                GCT     GTA AATCTTCTCA
                                |||     ||| ||||||||||
                                CGA     CAT TTAGAAGAGT
                                  TCA___   C
GAM2604  PPP1R3C   3'  GCCCTTTGTGTATACTTTTCAC 23988       C   AAAT   C
                                GCTCTTTG GTA   CTT TCAC
                                |||||||| |||   ||| ||||
                                CGGGAAAC CAT   GAA AGTG
                                     A  AT__   A
GAM2604  SCA1      5'  TCCTTGCAGCAGATCTTTTCAC 7290       _  AA    C
                                TCTTTGC GTA  ATCTT TCAC
                                |||||||  |||  |||||  ||||
                                AGGAACG CGT  TAGAA AGTG
                                     T  C_    A
GAM2604  ZNF10     3'  GCTCTTTGTGAAAAATTCCCA  31738       CGT    CT
                                GCTCTTTG   AAAAT  TCTCA
                                ||||||||   |||||  |||||
                                CGAGAAAC   TTTTA  AGGGT
                                     ACT    __
GAM2604  ZNF138    3'  CTCTTTACTATGAATTTTCT   44342       GTAA   C
                                CTCTTTGC    AAT TTCT
                                ||||||||    ||| ||||
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                                GAGAAATG   TTA AAGA
                                    ATAC   A
GAM2604 ZNF76    3' TCTTGCTGTCTTCTCAC     18313     T  GTAAAA
                                TCTT GC     TCTTCTCAC
                                |||| ||     |||||||||
                                AGAA CG     AGAAGAGTG
                                  _ AC____
GAM2605 BAT2     3' TACTCTTTTTTAACAAACAGC  21582         CCT  C
                                TACTCTTTTT   CA ACAGC
                                ||||||||||   || |||||
                                ATGAGAAAAA   GT TGTCG
                                     ATT  T
GAM2605 COL19A1  3' TGATACTCCCTTTTCATGCAG  12386   A        CC   CA
                                C GTACTCTTTTT  TCA  CAG
                                | ||||||||||  |||  |||
                                A TATGAGGGAAA  AGT  GTC
                                 C          __   AC
GAM2605 GALNT3   3' ATGCTCTTTTTCGTACAG    21015    A       CTCAC
                                GT CTCTTTTTC    ACAG
                                || |||||||||    ||||
                                TA GAGAAAAAG    TGTC
                                 C        CA___
GAM2605 HSPA1L   5' CAGTAATCTTTTTCCAAAC   45118      C       TC
                                CAGTA TCTTTTTCC  AC
                                ||||| |||||||||  ||
                                GTCAT AGAAAAAGG  TG
                                   T        TT
GAM2605 NEU3     3' CAGTGCTCTTTCCACTGCA   27400     A     TC _
                                CAGT CTCTTTT  CT CA
                                |||| |||||||  || ||
                                GTCA GAGAAAG  GA GT
                                  C      GT  C
GAM2605 SH2D1A   3' AGTGCTTGTTTTAGCACACAG  14288     A  CT   CCT
                                AGT CT  TTTT   CACACAG
                                ||| ||  ||||   |||||||
                                TCA GA  AAAA   GTGTGTC
                                  C  AC   TC_
GAM2605 SLC4A4   3' AGTATTCATTTCACACAG    19061     C  TTTTTCC
                                AGTA TC      TCACACAG
                                |||| ||      ||||||||
                                TCAT AG      AGTGTGTC
                                  A  TAA____
GAM2606 BCL11B   3' CACACCAACAGGATAGTATC   35647      GT_   T   AC
                                CACAC   CGG GATA  ATC
                                |||||   ||| ||||  |||
                                GTGTG   GTC CTAT  TAG
                                   GTT   _    CA
GAM2606 MTCP1    5' CAGCCGATGATGTCC       30573    C       AACA
                                CA GTCGGTGAT    TCC
                                || |||||||||    |||
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                                GT CGGCTACTA    AGG
                                 _       C___
GAM2606  SHOC2    5'  CAGCATGGAGTAACATCCA   28891    _  C  TGA
                                CA CGT GG   TAACATCCA
                                || ||| ||   |||||||||
                                GT GTA CC   ATTGTAGGT
                                 C   _  TC_
GAM2606  IGFBP4   5'  GGAAGTTAGCAGGCGTGCC   11403        _ TTGAC   A__
                                GGAAGTTA CA    GGT   CC
                                |||||||| ||    |||   ||
                                CCTTCAAT GT    CCG   GG
                                     C _____   CAC
GAM2606  IL12RB2  3'  AGGAAGTTCTGTTGAACAGTAC 11421         ACA   _
                                AGGAAGTT   TTGA CGGTAC
                                ||||||||   |||| ||||||
                                TCCTTCAA   AACT GTCATG
                                     GAC    T
GAM2606  IRTA2    3'  AGAAGTTACCTTGGTGT     36336         A   ACG
                                GGAAGTTAC TTG   GT
                                ||||||||| |||   ||
                                TCTTCAATG AAC   CA
                                     G   CA_
GAM2606  LMAN1    3'  AGGAAGTTGCATTAAGAT    24527         A     C
                                AGGAAGTT CATTGA GGT
                                |||||||| |||||| |||
                                TCCTTCAA GTAATT CTA
                                     C     _
GAM2606  MYO7A    3'  AGGAAGTTGCATGGT       7025          A   TGAC
                                AGGAAGTT CAT    GGT
                                |||||||| |||    |||
                                TCCTTCAA GTA    CCA
                                     C   ____
GAM2606  NAPB     3'  AGGAAGTTTCGTTACC      43167         ACATTGA  G
                                AGGAAGTT      CG TACC
                                ||||||||      || ||||
                                TCCTTCAA      GC ATGG
                                     A_______  A
GAM2606  PKHD1    3'  AGGAAGTTGCCTTGTGGT    39801         ACA   AC
                                AGGAAGTT   TTG  GGT
                                ||||||||   |||  |||
                                TCCTTCAA   AAC  CCA
                                     CGG   A_
GAM2606  PRKG2    3'  AGGAGGTTCTGTTGGCTACCA  26520      A   ACA   AC  _
                                AGGA GTT   TTG  GGT ACCA
                                |||| |||   |||  ||| ||||
                                TCCT CAA   GAC  CCG TGGT
                                  C  ___   AA   A
GAM2606  RALBP1   3'  AGCAAGAGTGACGGTACC    27696    G   TTACAT
                                AG AAG     TGACGGTACC
                                || |||     ||||||||||
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                                TC TTC     ACTGCCATGG
                                 G  TC____
GAM2606 VCAM1    3' AAGAAGTTGCATTTTTAGGC  9887        A   GAC_
                                AGGAAGTT CATT   GGT
                                |||||||| ||||   |||
                                TTCTTCAA GTAA   CCG
                                    C   AAAT
GAM2606 ZNF217   5' AGGAAGCTCAGTGATGGT   27189       A T  C
                                AGGAAGTT CA TGA GGT
                                |||||||| || ||| |||
                                TCCTTCGA GT ACT CCA
                                    _ C  A
GAM2607 COL6A2   3' GAATGGTCCTGGGGAAGGTGG 38440       T     CGTTT
                                GAATGGT CCTGGGG    TGG
                                ||||||| |||||||    |||
                                CTTACCA GGACCCC    ACC
                                   _     TTCC_
GAM2607 MSI1     3' ATGGTTCCAGGGGCTCGG    14636       T    GTT
                                ATGGTTCC GGGGC  TTGG
                                |||||||| |||||  ||||
                                TACCAAGG CCCCG  AGCC
                                    T   ____
GAM2607 SLC8A2   3' AGGATGGTTACTGGGGGT    42410   A    C    C
                                AG ATGGTT CTGGGG GT
                                || |||||| |||||| ||
                                TC TACCAA GACCCC CA
                                 C    T    _
GAM2608 ANXA11   5' CACTCGGGGCACTGGGGAGCCG 10104    _   TG CGCCA  AA
                                CAC CGGGG  T    GGA  CCG
                                ||| |||||  |    |||  |||
                                GTG GCCCC  G    CCT  GGC
                                  A    GT ACC__   C_
GAM2608 CLTC     5' CCGGGGACGCAGGAAAC     22149       TGT  C
                                CCGGGG   CGC AGGAAAC
                                ||||||   ||| |||||||
                                GGCCCC   GCG TCCTTTG
                                   T__   _
GAM2608 DGCR2    5' CCGGGGCGGCTGGGAGGCCG  23090       TC  CA  AA
                                CCGGGGTG  GC  GGA  CCG
                                ||||||||  ||  |||  |||
                                GGCCCCGC  CG  CCT  GGC
                                    __ AC  CC
GAM2608 DKK1     5' CCTGGGTCCCCAGGAAACC   29269    GG  T  G
                                CC  GG GTC CCAGGAAACC
                                ||  || ||| ||||||||||
                                GG  CC CAG GGTCCTTTGG
                                 A_  _  G
GAM2608 DNMT3B   5' CCGACCGCCAGGGAGCCG    27870     GGTG      AAA
                                CCGG   TCGCCAGG  CCG
                                ||||   ||||||||  |||
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                                GGCT   GGCGGTCC  GGC
                                  ____      CTC
GAM2608 DRD2    3' CCGGGGTGAAGAGGAGGCCG  9012       TCGCC   AA
                                CCGGGGTG   AGGA CCG
                                ||||||||   |||| |||
                                GGCCCCAC   TCCT GGC
                                    TTC__   CC
GAM2608 ESRRA   5' CCGGAGTGAGCCGGGGGCCG  20827       TC  A AAA
                                CCGGGGTG GCC GG  CCG
                                |||||||| ||| ||  |||
                                GGCCTCAC CGG CC  GGC
                                    T_  C CC_
GAM2608 FGFR1   3' CACCGGGGTATGGGGAGCC   31930        CGCCA  AA
                                CACCGGGGTGT   GGA CC
                                ||||||||||   ||| ||
                                GTGGCCCCATA   CCT GG
                                     CC___  C_
GAM2608 GALC    5' GGCGTTGCCAGGAAGCCG   6675      C      A
                                GGTGT GCCAGGAA CCG
                                ||||| |||||||| |||
                                CCGCA CGGTCCTT GGC
                                  A       C
GAM2608 GARS    5' CGGGGCGCAGGAGGCC     13056      TCGC    AA
                                CGGGGTG   CAGGA CC
                                |||||||   ||||| ||
                                GCCCCGC   GTCCT GG
                                   ____   CC
GAM2608 HDAC4   5' CGCCGGGGGCCCAGG     25755   A    T CG
                                C CCGGGG GT  CCAGG
                                | |||||| ||  |||||
                                G GGCCCC CG  GGTCC
                                 C     _ __
GAM2608 HDAC7A  3' CACCAGGGCATCGCCAGGA  32467
                                CACCGGGGTGTCGCCAGGA
                                ||||||||||||||||||
                                GTGGTCCCGTAGCGGTCCT

GAM2608 IL12RB2 5' CCGGGGTGGGCGCGGGGA   11426       T_  CA
                                CCGGGGTG CGC GGA
                                |||||||| ||| |||
                                GGCCCCAC GCG CCT
                                    CC  CC
GAM2608 IRS2    5' CGTCGCGCTCCGGGAAGCC  40702   GG   CG A   A
                                CG GTGT CC GGAA CC
                                || |||| || |||| ||
                                GC CGCG GG CCTT GG
                                 AG   A_ C   C
GAM2608 PTBP1   3' GGGGTGTCGCAGCC       15852         C GAAA
                                GGGGTGTCGC AG   CC
                                |||||||||| ||   ||
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                                CCCCACAGCG TC    GG
                                          _ _____
GAM2608 TPTE     5' CCGGGGGTCCCTAGAGCCG   30021       T  G  A   AA
                                CCGGGG GTC CC GGA  CCG
                                |||||| ||| || |||  |||
                                GGCCCC CAG GG TCT  GGC
                                   _  _ A   C_
GAM2609 H4F2     3' TGGGAGCTGACAGAATTT    18642     A     GT
                                TGG AGCTGGC  GGAATTT
                                ||| |||||||  |||||||
                                ACC TCGACTG  TCTTAAA
                                  C      __
GAM2609 PAX9     3' CTGCTGGAGACGGAAT      26204        AGCT  GT
                                CTGCTGGA    GGC  GGAAT
                                ||||||||    |||  |||||
                                GACGACCT    CTG  CCTTA
                                          _____  __
GAM2610 ASCL1    3' TGATGGGAGTTACTATAAC   43749   T      AAA  A
                                A ATGGGAGT   GC TATAAC
                                | ||||||||   || ||||||
                                A TACCCTCA   TG ATATTG
                                 C       A__  _
GAM2611 F2R      3' TGACATTCATTTATTACTGTA  12799   T         ___
                                A ACATTCATTTAT   TGTA
                                | ||||||||||||   ||||
                                A TGTAAGTAAATA   ACAT
                                 C           ATG
GAM2611 ITGA1    3' TATACATTCATTCATTGC    41853
                                TATACATTCATTTATTGT
                                ||||||||||||||||||
                                ATATGTAAGTAAGTAACG

GAM2611 TNF      3' ATACATTCATCTGTAAATAA  44978          TAT
                                ATACATTCATT   TGTAAATAA
                                ||||||||||   |||||||||
                                TATGTAAGTAG   ACATTTATT
                                          ___
GAM2612 ABL1     3' GCCCTTGCAGACCTGCC     28715        TC   GC
                                GTCCTTGCA  GGC  GCC
                                |||||||||  |||  |||
                                CGGGAACGT  CTG  CGG
                                     __   GA
GAM2612 ATP10C   3' AGTCCTTGTACTTGGTGC    35976       C  C_  C
                                AGTCCTTG AT  GG GC
                                |||||||| ||  || ||
                                TCAGGAAC TG  CC CG
                                     A  AA  A
GAM2612 CDC20    5' GTCCTTGCAGTTGGTGCCTACG 10364         TC_  C  GCC
                                GTCCTTGCA   GG GC   CG
                                |||||||||   || ||   ||
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                                CAGGAACGT  CC CG  GC
                                     CAA  A  GAT
GAM2612  CNTN2    3'  GTCCTTGCTGCTGCTCGA   22915       ATCG  GC  C
                                GTCCTTGC   GC  GC CGA
                                ||||||||   ||  || |||
                                CAGGAACG   CG  CG GCT
                                    A___  A_  A
GAM2612  DMRT2    3'  AGTCCTTGCTTGGTGGTTCCA 27258        ATC  CGCGC
                                AGTCCTTGC  GG   CCG
                                |||||||||  ||   |||
                                TCAGGAACG  CC   GGT
                                     AA_  ACCAA
GAM2612  HIRA     5'  GTCCCTCAGCGCGCCCG    17742      TGCA
                                GTCCT   TCGGCGCGCCCG
                                |||||   ||||||||||||
                                CAGGG   AGTCGCGCGGGC
                                  _____
GAM2612  KCNN2    5'  GCTCTCGCGGCGCGCC     34668   TC    ATC
                                G  CTTGC   GGCGCGCC
                                |  |||||   ||||||||
                                C  GAGCG   CCGCGCGG
                                 GA    ___
GAM2612  NFATC2   5'  GTCCTGGACGCGCCCG     29591      T CATC
                                GTCCT G    GGCGCGCCCG
                                ||||| |    ||||||||||
                                CAGGA C    CTGCGCGGGC
                                  _ _____
GAM2612  PIWIL1   5'  GTCCTTGCACCTCAGCCCGAG  43754         GG  C
                                GTCCTTGCATC  CG GCCCGAG
                                ||||||||||  || |||||||
                                CAGGAACGTGG  GT CGGGCTC
                                      A_  _
GAM2613  ALDH1B1  3'  AGAAGGATGTTTTCAGGG    8667        ATTCAGAGA
                                AGAGGGAT       TCAGGG
                                ||||||||       ||||||
                                TCTTCCTA       AGTCCC
                                    CAAA_____
GAM2613  DAG1     3'  AAAGGGATGGGGTGGGTCGGGG 20514       ATTCAGAGA  A
           C                     AGAGGGAT       TC GGGC
                                 ||||||||       || ||||
                                 TTTCCCTA       AG CCCG
                                     CCCCACCC_  C
GAM2613  FXR2     3'  GGGGGTGTTCAGAGAGAGATTG 22167     ATA_      TCA____
           GGGC                    GGG   TTCAGAGA      GGGC
                                   |||   ||||||||      ||||
                                   CCC   AAGTCTCT      CCCG
                                     CCAC       CTCTAAC
GAM2613  HTRA3    3'  AGATGGGTGTTCACAGGGG   44823     _   ATA   G  ATCA
                                AGA GGG   TTCA AG    GGG
                                ||| |||   |||| ||    |||
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                                TCT CCC   AAGT TC    CCC
                                  A   AC_   G  ____
GAM2613  NRAP     3'  GGGATGGTCGGGGATCAGGG   40195      AT  AGA
                                GGGAT  TC   GATCAGGG
                                |||||  ||   ||||||||
                                CCCTA  AG   CTAGTCCC
                                   CC  CCC
GAM2613  PTPRA    3'  GAGGGATATTTACAGG      38912         CAGAGAT   G
                                GAGGGATATT      CAG G
                                ||||||||||      ||| |
                                CTCCCTATAA      GTC C
                                      AT_____   A
GAM2613  PYGM     5'  AGAGGGATGCTCAGGTTACTGG 24694        A    AGATCAG
             C                   AGAGGGAT TTCAG      GGC
                                ||||||||| |||||      |||
                                TCTCCCTA GAGTC      CCG
                                    C    CAATGA_
GAM2613  RAP1GA1  3'  AGAGGGATGCTCAGGG      16157        A    AGATCA
                                AGAGGGAT TTCAG     GG
                                |||||||| |||||     ||
                                TCTCCCTA GAGTC     CC
                                    C    _______
GAM2613  RENT1    3'  GAGGTGTTCGGATCAGGG    16252     GATA   AGA
                                GAGG   TTC   GATCAGGG
                                ||||   |||   ||||||||
                                CTCC   AAG   CTAGTCCC
                                  AC__   C__
GAM2613  SCG3     5'  AAGGGATAAGCAGGGTTGGGGC 29878        TT   AGATCA
                                GAGGGATA  CAG     GGGC
                                ||||||||  |||     ||||
                                TTCCCTAT  GTC     CCCG
                                    TC   CCAAC_
GAM2613  WWOX     3'  GAGGGACATTTGGAAGGGGC   39115         CA   ATCA
                                GAGGGATATT  GAG   GGGC
                                ||||||||||  |||   ||||
                                CTCCCTGTAA  CTT   CCCG
                                     AC   C___
GAM2614  PCSK1    5'  AGCGCTCAGTGAAGCGCT    7750         ATA  TGCCA
                                AGCGTTCA   GT    CGCT
                                ||||||||   ||    ||||
                                TCGCGAGT   CA    GCGA
                                    ___  CTTC_
GAM2615  PPP4R1   3'  AAGGAAAATGCTCTGCCAAT   23074        _   AAG
                                AAGGAAA TGT   TCTGCCAAT
                                ||||||| |||   |||||||||
                                TTCCTTT ACG   AGACGGTTA
                                    T  ___
GAM2615  PRKY     3'  AAGAAAATACTGCCAA      15681          TAAGT
                                AAGGAAATG    CTGCCAA
                                |||||||||    |||||||
```

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                              TTCTTTTAT    GACGGTT
                                           _____
GAM2615 SLC5A2   3' TCATGGGAAGTGACTGCCAAT 16778    A_   A TAAGT
                              TCA  GGAA TG    CTGCCAAT
                              |||  |||| ||    ||||||||
                              AGT  CCTT AC    GACGGTTA
                                AC    C  T____
GAM2615 TTC3     5' AGGGTAAGTCTGCCAA     17713     AAAT
                              AGG   GTAAGTCTGCCAA
                              |||   ||||||||||||
                              TCC   CATTCAGACGGTT
                                    ____
GAM2615 YWHAG    3' TCAGGTTCTAAGTCTGTCA   29799    A  AAATG      C
                              TCA GG    TAAGTCTG CA
                              ||| ||    |||||||| ||
                              AGT CC    ATTCAGAC GT
                                _ AAG__      A
GAM2616 ALX3     3' TGAGCCAAGTAAGCTG     27069       AATGA
                              TGAGCCA    GGTGAGTTG
                              |||||||    |||||||||
                              ACTCGGT    TCATTCGAC
                                         _____
GAM2616 B4GALT1  3' TGAGCCAAGGGGAGCTG    11290       AATG  T
                              TGAGCCA    AGG GAGTTG
                              |||||||    ||| ||||||
                              ACTCGGT    TCC CTCGAC
                                   ____  C
GAM2616 BRCA1    5' TGAGCTGGCATGAGTATTTGT 28652     CAA_    GTGAG
                              TGAGC    ATGAG    TTGT
                              |||||    |||||    ||||
                              ACTCG    TACTC    AACA
                                 ACCG    ATA__
GAM2616 BRCA1    3' TGAGCTGGCATGAGTATTTGT 28652     CAA_    GTGAG
                              TGAGC    ATGAG    TTGT
                              |||||    |||||    ||||
                              ACTCG    TACTC    AACA
                                 ACCG    ATA__
GAM2616 CASP7    3' TGATTGAATGGATAAATTGT  10277    GCCA   A
                              TGA   AATG GGTGAGTTGT
                              |||   |||| ||||||||||
                              ACT   TTAC CTATTTAACA
                                AAC_   _
GAM2616 CERD4    3' TGGGCCAAATGGAGATATTGT 28956    A      _   GA
                              TG GCCAAATG AGGT  GTTGT
                              || |||||||| ||||  |||||
                              AC CGGTTTAC TCTA  TAACA
                               C       C   __
GAM2616 CKTSF1B1 3' TGAGCCGGGGTGAGGTGGGTT 30091       AAA_     A
                              TGAGCC   TGAGGTG GTT
                              ||||||   ||||||| |||
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                                ACTCGG   ACTCCAC CAA
                                   CCCC      C
GAM2616 CNGB3    3' TGAGCCAGATGAGTTA     33311       AATGA
                                TGAGCCA    GGTGAGTTG
                                |||||||    |||||||||
                                ACTCGGT    CTACTCAAT
                                   _____
GAM2616 COL4A2   3' GAGTTGAACAATGTGAGTTGT 12315     CCA  TG G
                                GAG   AA  A GTGAGTTGT
                                |||   ||  | |||||||||
                                CTC   TT  T CACTCAACA
                                  AAC  GT A
GAM2616 EIF2C1   3' TGAGTCACATGAGACACCTGT 29187     C  A    GT AG
                                TGAG CA ATGAG  G  TTGT
                                |||| || |||||  |  ||||
                                ACTC GT TACTC  T  GACA
                                   A  G    TG G_
GAM2616 GORASP1  3' TGAGCCAAGTGTAGCATTGT  36708       A  A   GA
                                TGAGCCAA TG GGT  GTTGT
                                |||||||| || |||  |||||
                                ACTCGGTT AC TCG  TAACA
                                     C  A  __
GAM2616 HUS1     3' TGAGCCAAGGAGGTCAAT    45004       AT    G
                                TGAGCCAA  GAGGT AGT
                                ||||||||  ||||| |||
                                ACTCGGTT  CTCCA TTA
                                     C_    G
GAM2616 LYAAT1   3' TGAGTTGGGCGAGGTG     38529     CCAAA  A     T
                                TGAG    TG GGTGAG TG
                                ||||    || |||||| ||
                                ACTC    AC CCGCTC AC
                                  A____  _     C
GAM2616 MSN      3' TGAGTTAGGTGAGTTA     41249     CCAAATG
                                TGAG      AGGTGAGTTG
                                ||||      ||||||||||
                                ACTC      TCCACTCAAT
                                  AA_____
GAM2616 PACE4    5' TGGACCAAATGGGGTCG     15063    AG      A  TGA
                                TG  CCAAATG GG   GTTG
                                ||  ||||||| ||   ||||
                                AC  GGTTTAC CC   CAGC
                                 CT      _ ___
GAM2616 RFXAP    3' TGAGCTAGATGAGTCA      8057       CAAATG
                                TGAGC     AGGTGAGTTG
                                |||||     ||||||||||
                                ACTCG     TCTACTCAGT
                                  A_____
GAM2616 RPL10    3' TGAGCAGGGCTGAGTTG     25672      CAAATG  __
                                TGAGC     AGG  TGAGTTG
                                |||||     |||  |||||||
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                                ACTCG     TCC  ACTCAAC
                                  _______  CG
GAM2616 SCA1     3'  TGAGTCCACATGAGTTG     7296       _  AATGAG
                                TGAG CCA     GTGAGTTG
                                |||| |||     ||||||||
                                ACTC GGT     TACTCAAC
                                  A  G_____
GAM2616 SERPINB3 3'  TGAGCCAAGAGAATCTGTTGT  27947        AT   TGA_
                                TGAGCCAA  GAGG   GTTGT
                                ||||||||  ||||   |||||
                                ACTCGGTT  CTCT   CAACA
                                    __   TAGA
GAM2616 SERPINB4 3'  TGAGCCAAGAGAATCTGTTGT  42228        AT   TGA_
                                TGAGCCAA  GAGG   GTTGT
                                ||||||||  ||||   |||||
                                ACTCGGTT  CTCT   CAACA
                                    __   TAGA
GAM2616 TACR1    3'  AGCCAGGCTGAGTTG      31858      AATGA  _
                                AGCCA    GG TGAGTTG
                                |||||    || |||||||
                                TCGGT    CC ACTCAAC
                                  _____ G
GAM2616 WFDC1    3'  TGAGCTGAATGTGAACTGT   34526      CAAA   _   GT
                                TGAGC   TGAG GTGA  TGT
                                |||||   |||| ||||  |||
                                ACTCG   ACTT CACT  ACA
                                  _____  A   TG
GAM2616 ZNF179   3'  TGAGCCAGGTGGGGAG     28378       AA  A  T
                                TGAGCCA  TG GG GAG
                                |||||||  || || |||
                                ACTCGGT  AC CC CTC
                                   CC  _ _
GAM2616 QPCT     3'  AACCAAAGACACATAA      29674      CGCCC
                                AACCG    GACACATAA
                                |||||    |||||||||
                                TTGGT    CTGTGTATT
                                  TT___
GAM2616 WDR1     5'  TACCGCGCCGCGCTCGCCGA  32751      AA_    ___
                                TACC   CCGCGC   CCGA
                                ||||   ||||||   ||||
                                ATGG   GGCGCG   GGCT
                                  CGC     AGC
GAM2617 MSN      3'  CAGTTGACATCCTGGA      41240        CT     T
                                CAGTTGAC  GTTTTG GA
                                ||||||||  |||||| ||
                                GTCAACTG  TAGGAC CT
                                    __    _
GAM2617 TCFL4    3'  AACCAGCTGACCAGTGTGA   41823          TGTTT
                                AACCAGTTGACC    TGTGA
                                ||||||||||||    |||||
```

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                                TTGGTCGACTGG    ACACT
                                      TC___
GAM2618 C18orf1  3' GGTGGAAATCTTTTTC     41223      CCTC
                                GGTGGA   GTCTTTTTC
                                ||||||   |||||||||
                                CCACCT   TAGAAAAAG
                                   T___
GAM2618 MGAT3    3' GGTGGGCTTTTTCC       14465      ACCTC T
                                GGTGG    G CTTTTTCC
                                |||||    | ||||||||
                                CCACC    C GAAAAAGG
                                  _____ _
GAM2618 MUCDHL   3' ACGGTGGAGTTCACTTTC    34927       CC   T
                                ACGGTGGA  TCG CTTTT
                                ||||||||  ||| |||||
                                TGCCACCT  AGT GAAAG
                                     CA  _
GAM2618 APP      5' CGCGCCGCCACCGCCGCCGT   7915     ACA  A      CCCA
                                CG   CC CCACCGTC    CCGT
                                ||   || ||||||||    ||||
                                GC   GG GGTGGCGG    GGCA
                                 GC_  C       C___
GAM2618 APP      5' CGCCACCGCCGCCGTCTCC    7914     A    A  A    C
                                CG CACC CC CCGTC CC
                                || |||| || ||||| ||
                                GC GTGG GG GGCAG GG
                                 G    C  C     A
GAM2618 AQP6     5' GACACCACACCGTGCCC      38244        C    C
                                GACACCAC ACCGT CCC
                                |||||||| ||||| |||
                                CTGTGGTG TGGCA GGG
                                     _    C
GAM2618 BDKRB2   5' GATGTCCCCACCGTCAGGACCG 8403     CA_  A      CCC
           T                     GA   CC CCACCGTC   ACCGT
                                ||   || ||||||||   |||||
                                CT   GG GGTGGCAG   TGGCA
                                 ACA  _       TCC
GAM2618 EDG8     3' GACCACCATCACCATCTCTGTC 44205     _   C      CCCAC
           GT                     GAC ACCA CACCGTC     CGT
                                ||| |||| |||||||     |||
                                CTG TGGT GTGGTAG     GCA
                                 G    A      AGACA
GAM2618 KCNS2    3' CCACACCACCATCGTGCAC    42821    G       C   CCC
                                C ACACCACCA CGT   CAC
                                | |||||||||  |||   |||
                                G TGTGGTGGT GCA   GTG
                                 G        A  C__
GAM2619 COG7     3' TCAGATAGTCGATGTCAGT    42659     A      GCC  C
                                TCA ATAGTCGA   TC GT
                                ||| ||||||||   || ||
```

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                                AGT TATCAGCT   AG CA
                                  C       AC_  T
GAM2619  ABCC4    5'  GCGGCGGTGGCCGC       25196         ACCCC T
                                GCGGCGGTG    G CCGC
                                |||||||||    | ||||
                                CGCCGCCAC    C GGCG
                                     _____ _
GAM2619  ADARB1   5'  GCGTGGCCGTGGCCTCGCGCGG 9975     C   G   A  C  TC
                                GCG GGC GTG CC CG  CGCGG
                                ||| ||| ||| || ||  |||||
                                CGC CCG CAC GG GC  GCGCC
                                  A   G   C A __
GAM2619  FHL1     5'  GCGCGGCGGTGGCGGC      11095          ACCC  TCC
                                GCGCGGCGGTG   CG   GC
                                ||||||||||    ||   ||
                                CGCGCCGCCAC   GC   CG
                                      C___  ___
GAM2619  FOXE1    5'  GCAGCGGCGGTGGCCTCGTGAC 20944    _       A  C  __
              CG                  GC GCGGCGGTG CC CGT  CCG
                                || |||||||| || |||  |||
                                CG CGCCGCCAC GG GCA  GGC
                                 T       C  A   CT
GAM2619  FTH1     5'  GCGGCGGCGGTGGCTGCGCGG  42787    _      ACCCC  C_
                                GCG CGGCGGTG    GT  CGCGG
                                ||| ||||||||    ||  |||||
                                CGC GCCGCCAC    CG  GCGCC
                                  C       _____  AC
GAM2619  HNRPDL   5'  GCGCGGCGGGGCCTCCCG    24176        TGACC  G   G
                                GCGCGGCGG    CC TCC CG
                                |||||||||    || ||| ||
                                CGCGCCGCC    GG AGG GC
                                     CC___  _  _
GAM2619  ID4      5'  GCTCCGGGCCCCGTCCGCG   11383    GG   TGA
                                GC  CGG   CCCCGTCCGCG
                                ||  |||   ||||||||||
                                CG  GCC   GGGGCAGGCGC
                                 AG   C__
GAM2619  MAF      5'  GCGGCGGTGGTGGCTGCG    23832         ACCCC  CC
                                GCGGCGGTG    GT  GCG
                                |||||||||    ||  |||
                                CGCCGCCAC    CG  CGC
                                     CAC__  A_
GAM2619  PCTK1    5'  GCGGCGGCGGTGGCTGAGGCGG 37474    _      ACCCCGTCC
                                GCG CGGCGGTG        GCGG
                                ||| ||||||||        ||||
                                CGC GCCGCCAC        CGCC
                                  C       CGACTC___
GAM2619  PLCD1    5'  GCGCGGCGGGAGGGGCACCGCG 26343         T  CCCCGT
              G                   GCGCGGCGG GA     CCGCGG
                                ||||||||| ||     ||||||
```

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                                CGCGCCGCC CT     GGCGCC
                                     _ CCCCGT
GAM2619 PTMA     5' GCGCGGCGGAGGCGGCTGCGG 15868        TGACCC TCC
                                GCGCGGCGG     CG  GCGG
                                |||||||||     ||  ||||
                                CGCGCCGCC     GC  CGCC
                                     TCC___ CGA
GAM2619 RPS28    5' GCGCGGCGGCGGTCTGGCG   9752         ACCCC  C_
                                GCGCGGCGGTG    GTC GCG
                                ||||||||||    ||| |||
                                CGCGCCGCCGC    CAG CGC
                                      _____ AC
GAM2619 SH3GL1   3' GCGCGGCTGTGGTCCCGT    16670       G  AC
                                GCGCGGC GTG  CCCGT
                                ||||||| |||  |||||
                                CGCGCCG CAC  GGGCA
                                    A  CA
GAM2619 USP14    5' GCGCGGTGGTGGCGGC     23113      C   ACCC TCC
                                GCGCGG GGTG   CG  GC
                                |||||| ||||   ||  ||
                                CGCGCC CCAC   GC  CG
                                   A  C___ ___
GAM2619 VGF      3' GCGCGGCGGGGGGCGCGCG    17993        TGACCCC C
                                GCGCGGCGG     GT CGCG
                                |||||||||     || ||||
                                CGCGCCGCC     CG GCGC
                                     CC_____ C
GAM2619 WEE1     5' GCGCGGCGGCGGCCTGCG    18096         ACCCC  C
                                GCGCGGCGGTG    GTC GCG
                                ||||||||||    ||| |||
                                CGCGCCGCCGC    CGG CGC
                                      _____ A
GAM2619 WEE1     5' GCCGACCTTGTCCGCG     18094    GG    CC
                                GC  TGACC  GTCCGCG
                                ||  |||||  |||||||
                                CG  GCTGG  CAGGCGC
                                 __    AA
GAM2620 ABR      3' GGCAGCCGGCTTTGTACAAGG  35013       A  CC  _
                                GGCGGCCG CT  GT CGAGG
                                |||||||| ||  || |||||
                                CCGTCGGC GA  CA GTTCC
                                     C  AA  T
GAM2620 ACHE     5' AGGCGGCCGATGTTCCCCGGCG 8559         ____    T
                                AGGCGGCCGA    CTCCG CG
                                ||||||||||    ||||| ||
                                TCCGCCGGCT    GGGGC GC
                                      ACAA    C
GAM2620 ADAM17   3' AGGCGGCCTGGAGTCTGGGGCG 34828        GACTCC  GA_
                                AGGCGGCC     GTC  GGCG
                                ||||||||     |||  ||||
```

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                                TCCGCCGG    CAG  CCGC
                                    ACCT__  ACC
GAM2620 ADARB1   3' AGGGGCTGACTCCATTAGCG  31868    C  C      CGA
                                AGG GGC GACTCCGT  GGCG
                                ||| ||| ||||||||  ||||
                                TCC CCG CTGAGGTA  TCGC
                                  _  A      A__
GAM2620 BTAF1    5' AGCGGCCGGTGCGGCGTGGGGC 43663       ACTC  T  A__
           G                     GGCGGCCG   CG CG  GGCG
                                ||||||||   || ||  ||||
                                TCGCCGGC   GC GC  CCGC
                                    CAC_  C  ACC
GAM2620 COL6A2   3' AGGCGGCCGGGTCCTGCG   38434        AC  GT
                                AGGCGGCCG  TCC  CG
                                |||||||||  |||  ||
                                TCCGCCGGC  AGG  GC
                                     CC   AC
GAM2620 CYP26A1  5' AGGTGTGCTGAGCTCCGAGGCG 38403    CG_  C  _   GTC
                                AGG  GC GA CTCC  GAGGCG
                                |||  || || ||||  ||||||
                                TCC  CG CT GAGG  CTCCGC
                                 ACA  A  C   ___
GAM2620 EMP3     3' GGCAGCCGAGCGAGGC     10904        CTCC T
                                GGCGGCCGA   G CGAGGC
                                |||||||||   | ||||||
                                CCGTCGGCT   C GCTCCG
                                      ____ _
GAM2620 EP300    5' GGCGGCCGGCGGAGGC     10989        ACTCC  C
                                GGCGGCCG    GT GAGGC
                                ||||||||    || |||||
                                CCGCCGGC    CG CTCCG
                                    _____  C
GAM2620 FTH1     5' GGCGGCCGGCCGGGG      42788        ACTCC   A
                                GGCGGCCG    GTCG GG
                                ||||||||    |||| ||
                                CCGCCGGC    CGGC CC
                                    _____   C
GAM2620 GLS      5' GGCGGCCGGTTTCCTCGGG   31378        AC_  G  A
                                GGCGGCCG   TCC TCG GG
                                |||||||   ||| ||| ||
                                CCGCCGGC   AGG AGC CC
                                    CAA  _  _
GAM2620 GMDS     3' GGCGGGCCGGGCTCCGAGGCG 11300      _  A_  GTC
                                GGCGG CCG  CTCC  GAGGCG
                                ||||| |||  ||||  ||||||
                                CCGCC GGC  GAGG  CTCCGC
                                  C  CC   ___
GAM2620 GNA11    5' GGCGGCCGAGGCGGGGCG   44048        CTCC T  A
                                GGCGGCCGA   G CG GGCG
                                |||||||||   | || ||||
```

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                                CCGCCGGCT   C GC CCGC
                                    C___ _  C
GAM2620  GNA11    5'  AGGCGGCGGCCGAGG      44025       CGACTCC
                                AGGCGGC     GTCGAGG
                                |||||||     |||||||
                                TCCGCCG     CGGCTCC
                                   C_______
GAM2620  GRB14    5'  AGCGGCCGGTGGGTGGGGCG  21026       ACTCC  CGA
                                GGCGGCCG    GT  GGCG
                                ||||||||    ||  ||||
                                TCGCCGGC    CA  CCGC
                                    CACC_  CC_
GAM2620  KRT16    5'  AGGCGGTCACCGAGG      45447       C  ACTCCG
                                AGGCGG CG    TCGAGG
                                |||||| ||    ||||||
                                TCCGCC GT    GGCTCC
                                   A _______
GAM2620  LMO1     5'  GGCGCCGACTCGGGGC     14184     G     CGTC A
                                GGCG CCGACTC   G GGC
                                |||| |||||||   | |||
                                CCGC GGCTGAG   C CCG
                                  _     _____ C
GAM2620  RBM3     5'  AGGCGGCCAGGCTCTGTC    43251       A_  C
                                AGGCGGCCG  CTC GTC
                                |||||||||  ||| |||
                                TCCGCCGGT  GAG CAG
                                     CC   A
GAM2620  RFNG     3'  AGGCAGCCCTGGGTCGGGG   44766       GA  CC   A
                                AGGCGGCC  CT  GTCG GG
                                ||||||||  ||  |||| ||
                                TCCGTCGG  GA  CAGC CC
                                    __  CC   C
GAM2620  RNF6     5'  GGCGGCCGTTCTCTCGGG    25577       A_  CG  A
                                GGCGGCCG  CTC  TCG GG
                                ||||||||  |||  ||| ||
                                CCGCCGGC  GAG  AGC CC
                                    AA  __  _
GAM2620  SUPT6H   5'  AGGCGGTCATCAAAAGAGG   41285      C  AC  CGTC
                                AGGCGG CG  TC   GAGG
                                |||||| ||  ||   ||||
                                TCCGCC GT  AG   CTCC
                                   A __ TTTT
GAM2620  TSG      5'  GGTCGGCCGAGCCCGGGGCG  34007   _     CT  TCGA
                                GG CGGCCGA  CCG   GGCG
                                || |||||||  |||   ||||
                                CC GCCGGCT  GGC   CCGC
                                 A     CG  C___
GAM2620  ABL1     5'  CCGCTGGCCGGGACGCGCC   28709    G GA
                                CCG C  GTCGGGACGCGCC
                                ||| |  ||||||||||||
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                                GGC G  CGGCCCTGCGCGG
                                  _ AC
GAM2620  ARCN1    5'  CGGTGGTGGGGCGCGCCC    11651     CGA  C   A
                                CGG   GT GGG CGCGCCC
                                |||   || ||| |||||||
                                GCC   CA CCC GCGCGGG
                                  AC_  C   _
GAM2620  ARNTL    5'  CCGGGAGCGCCCGCGCCCG   10133      C   T  GGA
                                CCGG GAG CG   CGCGCCCG
                                |||| ||| ||   ||||||||
                                GGCC CTC GC   GCGCGGGC
                                  _   _  GG_
GAM2620  CDK2     5'  CCAGCGAGTCGGGTCAGCCCG  12200           A  C
                                CCGGCGAGTCGGG CG GCCCG
                                |||||||||||| || |||||
                                GGTCGCTCAGCCC GT CGGGC
                                        A  _
GAM2620  CHAD     5'  CAGCGGCGAGTCCTAGGCGCTC 10412    C       G_  AC    C
              G                  CA CGGCGAGTC  GG  GCGC CG
                                 || |||||||||  ||  |||| ||
                                 GT GCCGCTCAG  TC  CGCG GC
                                  C        GA  __    A
GAM2620  DNCI1    5'  GGTTTCCTGGACGCGCTCG    44991    CGAG  G_      C
                                 GG    TC  GGACGCGC CG
                                 ||    ||  |||||||| ||
                                 CC    AG  CCTGCGCG GC
                                  AA__  GA       A
GAM2620  DUSP4    5'  CCAGCGAAGGAAGGCGCGCCCG 38411        _ TC   A
                                 CCGGCGA G  GGG CGCGCCCG
                                 ||||||| |  ||| ||||||||
                                 GGTCGCT C  TCC GCGCGGGC
                                     T CT   _
GAM2620  ECGF1    5'  CCCGCGGGTCGGGACCG     12639    G   A      G
                                 CC GCG GTCGGGAC CG
                                 || ||| |||||||| ||
                                 GG CGC CAGCCCTG GC
                                  G   C       _
GAM2620  EN2      5'  CCCGCGGTCAGCGCGCCCG    10932    G   A    GA
                                 CC GCG GTCGG  CGCGCCCG
                                 || ||| |||||  ||||||||
                                 GG CGC CAGTC  GCGCGGGC
                                  G   _    __
GAM2620  GAN      5'  GAGCCCCCGGGACGTGCC     35146      ___      C
                                 GAGT   CGGGACG GCC
                                 ||||   ||||||| |||
                                 CTCG   GCCCTGC CGG
                                   GGG      A
GAM2620  HK2      5'  ACCGGCGAGGGTGCGCCC     6784          GTC   AC
                                 ACCGGCGA   GGG  GCGCCC
                                 ||||||||   |||  ||||||
```

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                                TGGCCGCT   CCC  CGCGGG
                                   ___   A_
GAM2620  HSF2BP   5'  CCGGGGGTCGGGAACG      28144      CGA      C
                                CCGG   GTCGGGA GCG
                                ||||   ||||||| |||
                                GGCC   CAGCCCT TGC
                                  CC_      _
GAM2620  IRS2     5'  CCGGGAAGCCGGGGTGCGCCCG 40696      C       AC
                                CCGG GAGTCGGG  GCGCCCG
                                |||| ||||||||  |||||||
                                GGCC TTCGGCCC  CGCGGGC
                                  C       CA
GAM2620  IRS2     5'  CCGGGGGACGCGCC        40697      CGAGTC       C
                                CCGG     GGGACGCGC C
                                ||||     ||||||||| |
                                GGCC     CCCTGCGCG G
                                  _______        A
GAM2620  MADH1    5'  CACCGGGTTGGCGGCGCGCCCG 25336       CGAGT   GA
                                CACCGG    CGG  CGCGCCCG
                                ||||||    |||  ||||||||
                                GTGGCC    GCC  GCGCGGGC
                                   CAACC   __
GAM2620  NFATC1   5'  CCGGCGAGTTCGGAGCC     26071          _   ACGC
                                CCGGCGAGT CGGG    GCC
                                ||||||||| ||||    |||
                                GGCCGCTCA GCCT    CGG
                                    A   _____
GAM2620  OSBP     5'  CCTGGGGTGGGACGCGTCC    14985    _ CGA  C      C
                                CC GG   GT GGGACGCG CC
                                || ||   || |||||||| ||
                                GG CC   CA CCCTGCGC GG
                                 A  C__  _       A
GAM2620  POU3F1   3'  GCGGGCGGGCTGCGCGCCCG   40374     A T    A__
                                GCG G CGGG   CGCGCCCG
                                ||| | ||||   ||||||||
                                CGC C GCCC   GCGCGGGC
                                  C _    GAC
GAM2620  TBL1X    5'  GGCGGCGCCGCGCGCCCG    24890      A_    GGA
                                GGCG  GTCG   CGCGCCCG
                                ||||  ||||   ||||||||
                                CCGC  CGGC   GCGCGGGC
                                  CG    ___
GAM2620  TRPM7    5'  GACTGGCCACAGGGACGCGCCC 41619     GA   ___
              G                  GGC  GTC   GGGACGCGCCCG
                                 |||  |||   ||||||||||||
                                 CTG  CGG   CCCTGCGCGGGC
                                   AC   TGT
GAM2620  WNT11    5'  CGCGCGGCGGGCGCGCCCG   21531    _   A T    A
                                CG GCG G CGGG CGCGCCCG
                                || ||| | |||| ||||||||
```

```
                                GC CGC C GCCC GCGCGGGC
                                 G  _ _  _
GAM2621  TCEA1    3'  ACTCAAGTTGCTTTAAAAATTT 44323    GG  C   C
                                GC  GGG TGCT TAAAAATTT
                                ||  ||| |||| |||||||||
                                TG  TTC ACGA ATTTTTAAA
                                 AG  A   A
GAM2621  ATBF1    5'  GGCACTTGCAGGTCCGGGGGCC 27850          A   TAA
                                GGCACTTGCAG TTTG  GGCC
                                |||||||||| ||||  ||||
                                CCGTGAACGTC AGGC  CCGG
                                      C   CC_
GAM2621  COL5A3   3'  GGGATTTGCAGAGCTGGGC   31853    CAC     T  TAA
                                GGG  TTGCAGA TTG  GGC
                                |||  ||||||| |||  |||
                                CCC  AACGTCT GAC  CCG
                                  TA_     C  ___
GAM2621  DLEC1    3'  GGCCACTTGCAGTCCCTGGGGC 28831    G       A_   TAA
                                GG CACTTGCAG  TTTG  GGC
                                || |||||||||  ||||  |||
                                CC GTGAACGTC  GGAC  CCG
                                 G       AG   C__
GAM2621  FOS      3'  GGCACTTGTGGGTGCCGGC   23517        CAGATT  AA
                                GGCACTTG     TGT  GGC
                                ||||||||     |||  |||
                                CCGTGAAC     ACG  CCG
                                     ACCC__  G_
GAM2621  GJA5     3'  AGGCATTTGTAAAGC      23577      CTTGCAGA
                                GGGCA       TTTGTAAGGC
                                |||||       ||||||||||
                                TCCGT       AAACATTTCG
                                  _________
GAM2621  ITGA5    3'  GGGCATTTCAGGATCTGAGG  41500      C  G  _    TA
                                GGGCA TT CAG ATTTG  AGG
                                ||||| || ||| |||||  |||
                                CCCGT AA GTC TAGAC  TCC
                                   A  _  C    __
GAM2621  LFG      3'  GGGAACTTGCAGGAGCTAAGGC 44143    C       ATTTG
              C                  GGG ACTTGCAG    TAAGGCC
                                 ||| ||||||||    |||||||
                                 CCC TGAACGTC    ATTCCGG
                                   T       CTCG_
GAM2621  MAPK8IP1 3'  GGGCACTTGCAGGTGGCACAGG 24159          ATTT  _
              C                  GGGCACTTGCAG   GTA AGGC
                                 ||||||||||||   ||| ||||
                                 CCCGTGAACGTC   CGT TCCG
                                        CAC_  G
GAM2621  PRY      3'  GGACACTTTTGTAAGG      41256         GCAGAT
                                GGGCACTT     TTGTAAGG
                                ||||||||     ||||||||
```

```
                                CCTGTGAA     AACATTCC
                                         _______
GAM2621  SLC7A6   3'  GGGCACCTGGCATGTGAGG   19594        _ GATT   A
                                GGGCACTTG CA    TGT AGG
                                ||||||||| ||    ||| |||
                                CCCGTGGAC GT    ACA TCC
                                     C _____   C
GAM2621  STAT6    5'  GGGCACTTCCAGGCCCCATAGG 17156       G   A_  TG  A
                                GGGCACTT CAG  TT  TA GG
                                |||||||| |||  ||  || ||
                                CCCGTGAA GTC  GG  AT CC
                                     G   CG  GT  _
GAM2621  ZNF205   5'  GGGCACCTGCGGCAGTGGGGGC 18383         AGATT  TAA
              C                   GGGCACTTGC    TG   GGCC
                                  ||||||||||    ||   ||||
                                  CCCGTGGACG    AC   CCGG
                                       CCGTC  CC_
GAM2622  GFRA2    3'  AGGGCCCACGGTGCTGCAGAC  11263       T    CCA_
                                AGGGCCC ACGGT    CAGAC
                                ||||||| |||||    |||||
                                TCCCGGG TGCCA    GTCTG
                                   _    CGAC
GAM2622  HMMR     3'  TTAAAGGCCAATCCACAGA    29809         CTAC
                                TTAAGGGCC    GGTCCACAGA
                                |||||||||    ||||||||||
                                AATTTCCGG    TTAGGTGTCT
                                         _____
GAM2622  LPIN2    3'  TTAAGGGCTCGTGGAGTTGTCA 31227        CCTAC_   C__
              CAGA                  TTAAGGGC     GGT   CACAGA
                                    ||||||||     |||   ||||||
                                    AATTCCCG     TCA   GTGTCT
                                         AGCACC   ACA
GAM2622  ZNF289   3'  AAGGGCTCAGTCCACAG     42253       CCTA
                                AAGGGC    CGGTCCACAG
                                ||||||    ||||||||||
                                TTCCCG    GTCAGGTGTC
                                   A___
GAM2622  AIM1     5'  GCCCTTGGGGGGCTGGCTGC   45083        A__  GACC   A
                                GCCCTTGG   GC    GGC GC
                                ||||||||   ||    ||| ||
                                CGGGAACC   CG    CCG CG
                                     CCC  A___   A
GAM2622  AIM1     5'  ACCCTTGGGGCGGGC       45073         A   ACC
                                GCCCTTGG GCG   GGC
                                |||||||| |||   |||
                                TGGGAACC CGC   CCG
                                     C  ___
GAM2622  ALDH3B2  5'  GCCCTGGAGCTGCGCAGC    8682        T    GACCG
                                GCCCT GGAGC    GCAGC
                                ||||| |||||    |||||
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```
                                CGGGA CCTCG    CGTCG
                                  _    ACG__
GAM2622  AOC3    3'  GCCCTGGAGCCCTTGGC    19018     T    GA  __
                                GCCCT GGAGC  CC  GGC
                                ||||| |||||  ||  |||
                                CGGGA CCTCG  GG  CCG
                                  _    __  AA
GAM2622  AQP3    3'  GCCCTTGGACAGTCAG     40583       GCGAC  _
                                GCCCTTGGA    CGG CAG
                                |||||||||    ||| |||
                                CGGGAACCT    GTC GTC
                                     _____  A
GAM2622  ARHC    5'  GCTTCTGGAGCGGCGGC    23170    CC      AC
                                GC  TTGGAGCG  CGGC
                                ||  ||||||||  ||||
                                CG  GACCTCGC  GCCG
                                 AA       C_
GAM2622  ARVCF   5'  GCTCCTGGAGCGCAGC     11703    C       AC
                                GC CTTGGAGCG  CGGC
                                || |||||||||  ||||
                                CG GGACCTCGC  GTCG
                                 A        __
GAM2622  ASB2    5'  GCCCTTGGAGGAAGC      32051         C  CC
                                GCCCTTGGAG GA  GGC
                                |||||||||| ||  |||
                                CGGGAACCTC CT  TCG
                                     _ __
GAM2622  BMP6    5'  GCCCTTGGCGTGAGCAG    11865       GA   ACC
                                GCCCTTG  GCG   GGCAG
                                |||||||  |||   |||||
                                CGGGAAC  CGC   TCGTC
                                   __   AC_
GAM2622  CASP2   3'  CCTCTTGGAGCTGGAGCAG  37398    _      GACC
                                CC CTTGGAGC    GGCAG
                                || ||||||||    |||||
                                GG GAACCTCG    TCGTC
                                 A       ACC_
GAM2622  CDH12   5'  GCTCTCGGAGCGGCTGGAGC  19776    C       ACC  C
                                GC CTTGGAGCG   GG AGC
                                || |||||||||   || |||
                                CG GAGCCTCGC   CC TCG
                                 A        CGA  _
GAM2622  CDK2    5'  GCCCTGGAGCGGGGGC     12204      T     ACC
                                GCCCT GGAGCG   GGC
                                ||||| ||||||   |||
                                CGGGA CCTCGC   CCG
                                  _     CC_
GAM2622  CDKN2C  5'  GCCCTGGAGCAGAGCCTGGCAG 38563      T    _ _ _
              C                  GCCCT GGAGC GA CC GGCAGC
                                 ||||| ||||| || || ||||||
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                                CGGGA CCTCG CT GG CCGTCG
                                  _    T  C  A
GAM2622  CDS2    5'  GCCCTGGAGCTCGGC      19214      T    GAC
                                GCCCT GGAGC  CGGC
                                ||||| |||||  ||||
                                CGGGA CCTCG  GCCG
                                  _    A__
GAM2622  CELL    3'  CCTGTCTTGGGGCCGGTAGC  12224   ___    A  GAC  C
                                CC  CTTGG GC  CGG AGC
                                ||  ||||| ||  ||| |||
                                GG  GAACC CG  GCC TCG
                                 ACA   C ___  A
GAM2622  CENPB   5'  GCCCTTGACCGGCAG      43014      GGAGC
                                GCCCTT    GACCGGCAG
                                ||||||    |||||||||
                                CGGGAA    CTGGCCGTC

                                  _____
GAM2622  CEP2    5'  GCCGGACCCGACCGGC     28438    CTT  G_
                                GCC  GGA  CGACCGGC
                                |||  |||  ||||||||
                                CGG  CCT  GCTGGCCG
                                  ___  GG
GAM2622  CHAD    5'  GCCCTGACCGCAGCCGGCAGC  10413     T  A_  A
                                GCCCT GG  GCG CCGGCAGC
                                ||||| ||  ||| ||||||||
                                CGGGA CT  CGT GGCCGTCG
                                  _ GG  C
GAM2622  CISH    5'  GCTTTGGAGCGCAGC      40358    CC      AC
                                GC  TTGGAGCG  CGGC
                                ||  ||||||||  ||||
                                CG  AACCTCGC  GTCG
                                 A_      __
GAM2622  CLCN4   5'  GCCCTCGGGGGCGAGGC     12285       A   CC
                                GCCCTTGG GCGA  GGC
                                |||||||| ||||  |||
                                CGGGAGCC CGCT  CCG
                                    C   __
GAM2622  CLCN7   3'  GCCCTCGGGGGCAGCAG     10517       A  GACC
                                GCCCTTGG GC   GGCAG
                                |||||||| ||   |||||
                                CGGGAGCC CG   TCGTC
                                    C  ____
GAM2622  CLNS1A  5'  GCCCTGGAAGAGGCAG     10526     T   C  CC
                                GCCCT GGAG GA  GGCAG
                                ||||| |||| ||  |||||
                                CGGGA CCTT CT  CCGTC
                                  _   _ __
GAM2622  CNN2    3'  ACCCTTGGTTGACTGGCAGC  20402       AGC  C
                                GCCCTTGG   GAC GGCAGC
                                ||||||||   ||| ||||||
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                                TGGGAACC   CTG CCGTCG
                                    AA_   A
GAM2622  CUL3     5'  GCCCCTGGGCAGCCGCGGCGGC 18735        A   A __   A
                                GCCCTTGG GCG CC  GGC GC
                                |||||||| ||| ||  ||| ||
                                CGGGGACC CGT GG  CCG CG
                                    _  C  CG   C
GAM2622  CYP1B1   5'  GCCCTTGGGGACCTGGC     6449         AGC   _
                                GCCCTTGG   GACC GGC
                                ||||||||   |||| |||
                                CGGGAACC   CTGG CCG
                                    C__    A
GAM2622  DDX3     5'  GCTCTGGAGCGCACCGCGCGGC 35821    CC      _   _ A
                                GC  TTGGAGCG ACCG GC GC
                                ||  |||||||| |||| || ||
                                CG  GACCTCGC TGGC CG CG
                                 A_      G   G  C
GAM2622  DGKQ     3'  GCCCTTGGGCTGCCCCAGC   10664        A  GA__
                                GCCCTTGG GC    CCGGC
                                |||||||| ||    |||||
                                CGGGAACC CG    GGTCG
                                    _ ACGG
GAM2622  DMPK     5'  GCCCTGGAGCCCTGGC      20614      T    GA  _
                                GCCCT GGAGC  CC GGC
                                ||||| |||||  || |||
                                CGGGA CCTCG  GG CCG
                                   _    ___ A
GAM2622  EIF4G2   3'  GCCTATGATAACTGGCAGC   10875     CT   AGC   C
                                GCC  TGG   GAC GGCAGC
                                |||  |||   ||| ||||||
                                CGG  ACT   TTG CCGTCG
                                  AT   A__   A
GAM2622  ENG      5'  GCTGTGGTATGACCGGCAGC   6500     CCT   AGC
                                GC   TGG   GACCGGCAGC
                                ||   |||   ||||||||||
                                CG   ACC   CTGGCCGTCG
                                 AC_   ATA
GAM2622  EPS8     5'  GCCCTCGGGGCCACGGC     20811        A  G  C
                                GCCCTTGG GC AC GGC
                                |||||||| || || |||
                                CGGGAGCC CG TG CCG
                                    C  G  _
GAM2622  FGFR4    3'  GCCCTTGGACACGGC       35654         G  AC
                                GCCCTTGGA CG  CGGC
                                ||||||||| ||  ||||
                                CGGGAACCT GT  GCCG
                                    _ __
GAM2622  FZD10    5'  CTTGGAGCGCCCAGGTGGC   28453         A ____
                                CTTGGAGCG CC    GGC
                                ||||||||| ||    |||
```

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                                GAACCTCGC GG   CCG
                                     G  TCCA
GAM2622  GAB2    3'  GCCCTTGGGCCTAGAGTGGC  38680       A ___  CC
                                GCCCTTGG GC  GA  GGC
                                |||||||| ||  ||  |||
                                CGGGAACC CG  CT  CCG
                                     _  GAT  CA
GAM2622  GGT2    5'  CCTTGGAGGCCGAGGGCAGC  43924       __  CC
                                CCTTGGAG  CGA  GGCAGC
                                ||||||||  |||  ||||||
                                GGAACCTC  GCT  CCGTCG
                                     CG   C_
GAM2622  GPC1    3'  GCTTTTGGGCACACTGGC   13251   CC   A  _  C
                                GC  TTGG GCG AC GGC
                                ||  |||| ||| || |||
                                CG  AACC CGT TG CCG
                                 AA   _  G  A
GAM2622  GRP     5'  GCCCTTGGAGCGCGC      13300          ACCG
                                GCCCTTGGAGCG   GC
                                ||||||||||||   ||
                                CGGGAACCTCGC   CG
                                       G___
GAM2622  GTF2I   5'  GCGGGGGGGCGACCGGTGGC  37445   CCTT  A      CA
                                GC   GG GCGACCGG  GC
                                ||   || ||||||||  ||
                                CG   CC CGCTGGCC  CG
                                 CCCC  _      AC
GAM2622  HPN     3'  GCCCTGGAGGCTGCGCAGC   13458     T   _ GACCG
                                GCCCT GGAG C    GCAGC
                                ||||| |||| |    |||||
                                CGGGA CCTC G    CGTCG
                                   _   C ACG__
GAM2622  HYOU1   3'  CTTGGAGCTGAGGCAGC    40633       GACC
                                CTTGGAGC   GGCAGC
                                ||||||||   ||||||
                                GAACCTCG   CCGTCG
                                     ACT_
GAM2622  IHPK1   3'  GCCCTGGGAGGAGCAGC    45490     T   C  C
                                GCCCT GGAG GA CGGC
                                ||||| |||| || ||||
                                CGGGA CCTC CT GTCG
                                   C   _  C
GAM2622  IHPK3   3'  GCCCTTGGAGCGAGCAG    38371          CCG
                                GCCCTTGGAGCGA  GCAG
                                ||||||||||||  ||||
                                CGGGAACCTCGCT  CGTC
                                        ___
GAM2622  ITPKB   3'  ACCCTTGGAGCTCAGC     13641          GAC
                                GCCCTTGGAGC  CGGC
                                ||||||||||  ||||
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                                TGGGAACCTCG   GTCG
                                      A__
GAM2622 JUP     3'  GCCCTGGGGGCTTAGGGCAG  13776      T  A  GACC
                                GCCCT GG GC    GGCAG
                                ||||| || ||    |||||
                                CGGGA CC CG    CCGTC
                                   C  C  AATC
GAM2622 KCND3    5'  GCTCTTGGGCCGGCAGC     22534    C     A  GAC
                                GC CTTGG GC   CGGCAGC
                                || ||||| ||   |||||||
                                CG GAACC CG   GCCGTCG
                                 A    _ ___
GAM2622 LEF1     5'  GCCGCCGGCCGGCAG       32210     C    AGCGA
                                GCC TTGG    CCGGCAG
                                ||| ||||    |||||||
                                CGG GGCC    GGCCGTC
                                  C   _____
GAM2622 LGMN     3'  GCCCTGGAGCGGGGGC      24685      T     ACC
                                GCCCT GGAGCG   GGC
                                ||||| ||||||   |||
                                CGGGA CCTCGC   CCG
                                   _     CC_
GAM2622 LILRA1   5'  GCCCTCGGTGCATGGCAG    27799        A   ACC
                                GCCCTTGG GCG   GGCAG
                                |||||||| |||   |||||
                                CGGGAGCC CGT   CCGTC
                                     A   A__
GAM2622 LILRB1   5'  GCCCTCGGTGCATGGCAG    27427        A   ACC
                                GCCCTTGG GCG   GGCAG
                                |||||||| |||   |||||
                                CGGGAGCC CGT   CCGTC
                                     A   A__
GAM2622 LILRB2   5'  GCCCTCGGTGCATGGCAG    25244        A   ACC
                                GCCCTTGG GCG   GGCAG
                                |||||||| |||   |||||
                                CGGGAGCC CGT   CCGTC
                                     A   A__
GAM2622 LPHH1    3'  GCCCTTGGAATTCCTTAGC    29388         CGA  __
                                GCCCTTGGAG   CC  GGC
                                |||||||||   ||  |||
                                CGGGAACCTT   GG  TCG
                                      AA_  AA
GAM2622 LY6E     3'  GCCCTTGAAGTGCATGCAGC   14278         CGACCG
                                GCCCTTGGAG     GCAGC
                                ||||||||||     |||||
                                CGGGAACTTC     CGTCG
                                      ACGTA_
GAM2622 MAD1L1   5'  GCCCTGGAAGCCTGGCAG    44670      T    GACC
                                GCCCT GGAGC    GGCAG
                                ||||| |||||    |||||
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                                CGGGA CTTCG    CCGTC
                                  C    GA__
GAM2622  MAN2A2   3'  GCCCTTGGGGACAGCAGC    25950        AGC   C
                                GCCCTTGG   GAC GGCAGC
                                ||||||||   ||| ||||||
                                CGGGAACC   CTG TCGTCG
                                    C__   _
GAM2622  MFAP3    5'  CCCTGGAGCCCAGGGCAG    25453        GA  __
                                CCTTGGAGC  CC  GGCAG
                                |||||||||  ||  |||||
                                GGGACCTCG  GG  CCGTC
                                     __ TC
GAM2622  MGAT5    5'  GCCCTTGACCAGGCAG      14474       GGAGC   _
                                GCCCTT    GACC GGCAG
                                ||||||    |||| |||||
                                CGGGAA    CTGG CCGTC
                                  _____   T
GAM2622  MMP19    5'  GCCCTTAGAGCGTGGCAGC    35588          ACC
                                GCCCTTGGAGCG   GGCAGC
                                ||||||||||||   ||||||
                                CGGGAATCTCGC   CCGTCG
                                      A__
GAM2622  MNT      3'  CTTGGAGCATGAACAGC     33713         ACC
                                CTTGGAGCG   GGCAGC
                                |||||||||   ||||||
                                GAACCTCGT   TTGTCG
                                    AC_
GAM2622  NRG2     5'  GCCCTCCACCGGCAG       30365       GGAG G
                                GCCCTT    C ACCGGCAG
                                ||||||    | ||||||||
                                CGGGAG    G TGGCCGTC
                                  ____ _
GAM2622  NT5M     3'  GCCCCTGGGCTTCTGGCAGC   33651        A  GACC
                                GCCCTTGG GC    GGCAGC
                                |||||||| ||    ||||||
                                CGGGGACC CG    CCGTCG
                                    _  AAGA
GAM2622  OLIG2    3'  GCCCCTGAAATCGGCAG     25147         CGAC
                                GCCCTTGGAG    CGGCAG
                                ||||||||||    ||||||
                                CGGGGACTTT    GCCGTC
                                    A___
GAM2622  OPCML    3'  GCCATTGGAGAAGCAG      14952     C     CGACC
                                GCC TTGGAG    GGCAG
                                ||| ||||||    |||||
                                CGG AACCTC    TCGTC
                                  T     T____
GAM2622  PACSIN1  3'  GCCCTGGAGTGGGCAG      45150       T   CGACC
                                GCCCT GGAG    GGCAG
                                ||||| ||||    |||||
```

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                                CGGGA CCTC    CCGTC
                                  _   AC___
GAM2622  PCM1    5'  GCCCTCGGAGACCGCAGC   26226        GC    G
                                GCCCTTGGA  GACCG CAGC
                                |||||||||  ||||| ||||
                                CGGGAGCCT  CTGGC GTCG
                                     __    _
GAM2622  PEX10   3'  GCCCTCGGGGAGAGCAGC   15220        AGC  CC
                                GCCCTTGG   GA  GGCAGC
                                ||||||||   ||  ||||||
                                CGGGAGCC   CT  TCGTCG
                                    C__  C_
GAM2622  PML     3'  CCCTTGGAGGAGCAG      37751         C  CCG
                                CCCTTGGAG GA   GCAG
                                |||||||||  ||   ||||
                                GGGAACCTC CT   CGTC
                                    _  ___
GAM2622  PMP22   3'  CCTTGGAGGCACAGAACAGC  7161         _  ACC
                                CCTTGGAG CG   GGCAGC
                                ||||||||  ||   ||||||
                                GGAACCTC GT   TTGTCG
                                    C  GTC
GAM2622  PRKCQ   5'  GCCCTGGAGCGAGC       26512       T     CCG
                                GCCCT GGAGCGA   GC
                                |||||  |||||||   ||
                                CGGGA CCTCGCT   CG
                                  _     ___
GAM2622  PSCD3   3'  GCTCTGGAGCAGCAG      20128    CC     GACC
                                GC  TTGGAGC    GGCAG
                                ||  |||||||    |||||
                                CG  GACCTCG    TCGTC
                                 A_     ____
GAM2622  RENT1   3'  GCCCTCGGAGAACACAGGCAGC 16253          C  _ _
                                GCCCTTGGAG GAC C GGCAGC
                                |||||||||| ||| | ||||||
                                CGGGAGCCTC TTG G CCGTCG
                                     _   T T
GAM2622  RGS2    3'  GCTTTTGGACCAACAG     16315    CC    GCGA
                                GC  TTGGA    CCGGCAG
                                ||  |||||    |||||||
                                CG  AACCT    GGTTGTC
                                 AA    ____
GAM2622  RPLP1   5'  GCACCTTGGCGGCAG      9744    _     AGCGAC
                                GC CCTTGG     CGGCAG
                                || ||||||     ||||||
                                CG GGAACC     GCCGTC
                                 T    _______
GAM2622  RUNX1   3'  CCTTGGAGTGACCCTCAG    12019        C    GG
                                CCTTGGAG GACC  CAG
                                |||||||| ||||  |||
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                                GGAACCTC CTGG  GTC
                                    A    GA
GAM2622  SFN     3'  CCCTTTGGAGCAAGAACAGC   43965      _      CC
                                CCCTT GGAGCGA  GGCAGC
                                ||||| |||||||  ||||||
                                GGGAA CCTCGTT  TTGTCG
                                   A      C_
GAM2622  SLN     3'  GCCCTTGGGAGCAGC       16878         _  GACC
                                GCCCTTGG AGC    GGC
                                |||||||| |||    |||
                                CGGGAACC TCG    TCG
                                    C  ____
GAM2622  SMP1    3'  GCCCTTGGAATGAGAGGC    30716          C  CC
                                GCCCTTGGAG GA  GGC
                                |||||||||| ||  |||
                                CGGGAACCTT CT  CCG
                                     A  CT
GAM2622  SNL     3'  GCCCTGGAGCCCACCTGGC   16940      T    G_  _
                                GCCCT GGAGC  ACC GGC
                                ||||| |||||  ||| |||
                                CGGGA CCTCG  TGG CCG
                                   _    GG   A
GAM2622  SPO11    5'  GCCCTTGGGGCGTGGC     29708        A   ACC
                                GCCCTTGG GCG   GGC
                                |||||||| |||   |||
                                CGGGAACC CGC   CCG
                                    C   A__
GAM2622  SSPN     5'  GCCCTGGAGCGCGGC      22935      T     AC
                                GCCCT GGAGCG  CGGC
                                ||||| ||||||  ||||
                                CGGGA CCTCGC  GCCG
                                   _     __
GAM2622  TBX1     3'  GCCCTTGGGGCAGGGTGGC   38769        A   ACC_
                                GCCCTTGG GCG    GGC
                                |||||||| |||    |||
                                CGGGAACC CGT    CCG
                                    C   CCCA
GAM2622  TBX6     5'  GCCCTGGAGGGAAGCAGC    38857      T   C  CC
                                GCCCT GGAG GA  GGCAGC
                                ||||| |||| ||  ||||||
                                CGGGA CCTC CT  TCGTCG
                                   _   C  __
GAM2622  TCF2     3'  GCCCCTGGAAAGAGGCAG    27027          C  CC
                                GCCCTTGGAG GA  GGCAG
                                |||||||||| ||  |||||
                                CGGGGACCTT CT  CCGTC
                                     T  __
GAM2622  TGM2     3'  GCCCCTGGAGCTGGGTGCAG  21439           GACCG
                                GCCCTTGGAGC    GCAG
                                ||||||||||     ||||
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                                CGGGGACCTCG    CGTC
                                      ACCCA
GAM2622  TUBB    5'  GCCCTCGGAGCGGTGCGCGGC  9886          AC___
                                GCCCTTGGAGCG    CGGC
                                ||||||||||||    ||||
                                CGGGAGCCTCGC    GCCG
                                      CACGC
GAM2622  VAV1    5'  GCCTGTGGAGCGACAGC    24072    CT       C
                                GCC  TGGAGCGAC GGC
                                |||  ||||||||| |||
                                CGG  ACCTCGCTG TCG
                                  AC       _
GAM2622  VDR     3'  GCCCTGGAGGAGCAGC      7520       T   C  C
                                GCCCT GGAG GA CGGC
                                ||||| |||| || ||||
                                CGGGA CCTC CT GTCG
                                  _   _ C
GAM2622  VIPR1   3'  GCCTTTGGAGGAGGAG     21509    C    C  CC  C
                                GCC TTGGAG GA  GG AG
                                ||| ||||||  ||  || ||
                                CGG AACCTC CT  CC TC
                                  A     _ __ _
GAM2622  WISP1   3'  GCCCCTGGAGTCCCACAGC   38901         CGA  G
                                GCCCTTGGAG   CC GCAGC
                                ||||||||||   || |||||
                                CGGGGACCTC   GG TGTCG
                                      A__  G
GAM2622  ZNF76   3'  GCCCTTGGGGGCAAGAGTGGC  18308        A_   CC__
                                GCCCTTGG  GCGA   GGC
                                ||||||||  ||||   |||
                                CGGGAACC  CGTT   CCG
                                     CC   CTCA
GAM2623  CENTD1  5'  CTTGCGCTCGGGTCGCGG    40139         AT   T
                                CTTGCGCTCG  GTCG CGG
                                ||||||||||  |||| |||
                                GAACGCGAGC  CAGC GCC
                                      C_   _
GAM2624  CHST1   3'  AGACGTAGTGCAAATTTC    18901    T       TTGAA
                                AG CGTAGTGTAA    ATTTC
                                || ||||||||||    |||||
                                TC GCATCACGTT    TAAAG
                                  T       ______
GAM2624  MAP3K5  3'  AGATGTAGTTAGGAAATTTCA 25434    TC    GTAATT
                                AG  GTAGT     GAAATTTCA
                                ||  |||||     |||||||||
                                TC  CATCA     CTTTAAAGT
                                  TA    ATC___
GAM2625  AP3S1   3'  TATCAGGCAAACAGAAAGGTGC 10506      AA       TCATA
                                TATCA  CAAACAGGA    TGC
                                |||||  |||||||||    |||
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                                ATAGT  GTTTGTCTT    ACG
                                  CC       TCC__
GAM2625  BAZ2A    3'  TATCAAACAATACAGGGTC   30314         _    A
                                TATCAAACAA ACAGG TC
                                |||||||||| ||||| ||
                                ATAGTTTGTT TGTCC AG
                                     A    C
GAM2625  MCL1     3'  CAAACAAGGGATCAAATG    34996       ACA     T
                                CAAACAA   GGATCA ATG
                                |||||||   |||||| |||
                                GTTTGTT   CCTAGT TAC
                                    C__     T
GAM2625  SLC21A3  5'  TCAAGCAAACAAAAAAATATG  39578     A       TC
                                TCAA CAAACAGGA  ATATG
                                |||| |||||||||  |||||
                                AGTT GTTTGTTTT  TATAC
                                  C       TT
GAM2626  AP2B1    3'  GACACACTTTTCCTTCT     10483    A       CTCAA
                                GA CACACTTTT    CCTTCT
                                || |||||||||    ||||||
                                CT GTGTGAAAA    GGAAGA
                                 _       _____
GAM2626  CRIM1    3'  GAACACCTTTTTCTTTTTCT   32372       AC     CAACC
                                GAACAC  TTTTCT    TTCT
                                ||||||  ||||||    ||||
                                CTTGTG  AAAAGA    AAGA
                                   GA     AA___
GAM2626  MICB     3'  CCCTCAGCAAACCTTCTG    25475       ____
                                TTCTCA    ACCTTCTG
                                ||||||    ||||||||
                                GGGAGT    TGGAAGAC
                                   CGTT
GAM2626  SNK      3'  GAATGCACTTTTCCAGCC    27361     CA       T  A
                                GAA  CACTTTTC CA CC
                                |||  |||||||| || ||
                                CTT  GTGAAAAG GT GG
                                  AC       _  C
GAM2626  TNFSF4   3'  AAACACACACACAATCTTCTG  17746        TTTTCT   C
                                GAACACAC     CAA CTTCTG
                                ||||||||     ||| ||||||
                                TTTGTGTG     GTT GAAGAC
                                     TGT___   A
GAM2626  USP11    5'  ACACTTCGACCTTCTG      21626        TCTCA
                                ACACTTT    ACCTTCTG
                                |||||||    ||||||||
                                TGTGAAG    TGGAAGAC
                                   C____
GAM2626  VENTX2   3'  CACTTCCAGACCTTCT      30911      TT   CA
                                CACT  TCT  ACCTTCT
                                ||||  |||  |||||||
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                                GTGA  AGG  TGGAAGA
                                  __   TC
GAM2627  GPR30    3'  GAGCGCTGCTGCTCCTCGTGGG 11309    A         ATAC
                                GA CGTTGCTGCTT    CGTGGG
                                || ||||||||||    ||||||
                                CT GCGACGACGAG    GCACCC
                                 C         GA__
GAM2627  HUNK     3'  TTGCTGCTTACTTGG       31091           ACCG
                                TTGCTGCTTAT    TGG
                                ||||||||||    |||
                                AACGACGAATG    ACC
                                      A___
GAM2628  OLFM1    5'  CTCCGGCGGCGGCGCCTGGCTC 26771         AAAA_  __    C
              GTGTC                 CTCCGGCG    GCC  GCTCG GTC
                                ||||||||    |||  ||||| |||
                                GAGGCCGC    CGG  CGAGC CAG
                                     CGCCG   AC    A
GAM2630  DAZL     3'  CACAGGTACTTGTTGGAGAAGT 42774          ATTAAAAT
                                CACAGGTATT       GAGT
                                ||||||||||       ||||
                                GTGTCCATGA       TTCA
                                      ACAACCTC
GAM2630  PDE7A    3'  ACAGGCACATATTAAAATGAGT 42284         _
              AT                  ACAGGTAT TATTAAAATGAGTAT
                                ||||||||| ||||||||||||||
                                TGTCCGTG ATAATTTTACTCATA
                                     T
GAM2630  PPEF1    5'  CACAGGTCTTATTGAAGAG    26409        A    AAAAT
                                CACAGGT TTATT    GAG
                                ||||||| |||||    |||
                                GTGTCCA AATAA    CTC
                                    G    CTT__
GAM2630  RAP1GA1  3'  CACAGGGGCTTCCAAAATGGGT 16162        TA  A       A
              AT                  CACAGG  TT TTAAAATG GTAT
                                ||||||  || ||||||||| ||||
                                GTGTCC  GA GGTTTTAC CATA
                                   CC  A       C
GAM2630  TNFSF6   3'  CAGGCACTAAGATGAGT     8473          TTAAA
                                CAGGTATTA    ATGAGT
                                |||||||||    ||||||
                                GTCCGTGAT    TACTCA
                                      TC___
GAM2631  GLDC     3'  TCAAGATGCTTTTATTAGAATA 42027      T   ACGTG
              C                   TCAA GAT    TATTAGAATAC
                                |||| |||    ||||||||||
                                AGTT CTA    ATAATCTTATG
                                  _  CGAAA
GAM2631  HLCS     5'  TCACTGATACGTCGTCCAG   7647      A       _  A
                                TCA TGATACGT GT TTAG
                                ||| |||||||| || ||||
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                                AGT ACTATGCA CA GGTC
                                  G       G  _
GAM2631  PPP2R5E   3'  TCAATGATATATGCAACTAATA 26476         CG    TTAG
              C                   TCAATGATA  TGTA    AATAC
                                  |||||||||  ||||    |||||
                                  AGTTACTAT  ACGT    TTATG
                                       AT    TGA_
GAM2632  BCL11A    3'  TTAATTGTCCTATCTGAGC    39723           A  G   AT
                                  TTAATTGTCCTA TC TGA  GC
                                  ||||||||||||  ||  |||  ||
                                  AATTAACAGGAT AG ACT  CG
                                                _  _  __
GAM2632  F2RL3     3'  ATTGCACAGTATCGTGAATG   19510       CCTA_
                                  ATTGT    ATCGTGAATG
                                  |||||    ||||||||||
                                  TAACG    TAGCACTTAC
                                     TGTCA
GAM2632  PACE      3'  ATTGTCCTAATGGGAGGGGTGC 15030          CGT  A___
              A                    ATTGTCCTAAT   GA    TGCA
                                   ||||||||||   ||    ||||
                                   TAACAGGATTA   CT    ACGT
                                         CC_  CCCC
GAM2632  SRGAP2    3'  TTAATTGTCCTTGTTTGC    43992          AATCG  AA
                                  TTAATTGTCCT    TG  TGC
                                  ||||||||||     ||  |||
                                  AATTAACAGGA    AC  ACG
                                         _____  AA
GAM2632  TDG       3'  TTAATTGCTCCTAATCCCTGAT 17360        _      _ G   A
              GCA                    TTAATTG TCCTAAT C TGA TGCA
                                     ||||||| ||||||| | ||| ||||
                                     AATTAAC AGGATTA G ACT ACGT
                                        G      G G   _
GAM2633  SMURF1    3'  GTTCTTTGGGGTGG       45198         CCC   A
                                  GTTCTTTG   GGG TGG
                                  ||||||||   ||| |||
                                  CAAGAAAC   CCC ACC
                                         ___   _
GAM2633  TCF8      3'  ATGATCTTTGCCTGGGAT    36230     T       C
                                  ATG TCTTTGCC GGGAT
                                  ||| ||||||||  |||||
                                  TAC AGAAACGG CCCTA
                                    T       A
GAM2633  TNFRSF6   3'  GTTCTTTAGGTGGT       6221         GCCC   A
                                  GTTCTTT    GGG TGGT
                                  |||||||    ||| ||||
                                  CAAGAAA    TCC ACCA
                                         _____  _
GAM2634  ADAMTS8   3'  AGGGGTTGCGGCAATGGG    28159         AA   CA
                                  AGGGGTTGC  CAA  GG
                                  |||||||||  |||  ||
```

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                                TCCCCAACG  GTT  CC
                                     CC   AC
GAM2634  ADCY6    5'  AGAGGTTGCAGTGAGCAAAGAT 34162          A____   C
                C                    AGGGGTTGCA     CAA AGGTC
                                     ||||||||||     ||| |||||
                                     TCTCCAACGT     GTT TCTAG
                                          CACTC  _
GAM2634  AHR      3'  AGAGGTTGCAGTGAGCCA     11543          ACAACA
                                     AGGGGTTGCA     GGTCA
                                     ||||||||||     |||||
                                     TCTCCAACGT     TCGGT
                                          CAC___
GAM2634  ARHGAP6  5'  AAGGGTTGCGGTGGGGTCA   30206          AACAACA
                                     AGGGGTTGC      GGTCA
                                     |||||||||      |||||
                                     TTCCCAACG      CCAGT
                                          CCACC__
GAM2634  CLTCL1   3'  AAGCACCAGCAGCAGGTCAT   41879      TG  A  A
                                     GGGT  CA CA CAGGTCAT
                                     ||||  || || ||||||||
                                     TTCG  GT GT GTCCAGTA
                                       TG  C  C
GAM2634  CXCL16   3'  GGGGTTGCAGTGAGCCGAGATC 35202          ACAAC___
                A                    GGGGTTGCA       AGGTCA
                                     |||||||||       ||||||
                                     CCCCAACGT       TCTAGT
                                          CACTCGGC
GAM2634  CYP2B6   3'  AGAGGTTGCAGTGAACAAA   8920           AC_
                                     AGGGGTTGCA   AACAGG
                                     ||||||||||   ||||||
                                     TCTCCAACGT   TTGTTT
                                          CAC
GAM2634  CYP8B1   3'  AGAGGTTGTAGTGAGCCAAGAT 20501          CAACAA__  _
                CA                     AGGGGTTG       CA GGTCA
                                     ||||||||       || |||||
                                     TCTCCAAC       GT CTAGT
                                          ATCACTCG  T
GAM2634  DFFB     3'  GAGGTTGCAGTGAGCCA     44600          ACAACA
                                     GGGGTTGCA      GGTCA
                                     |||||||||      |||||
                                     CTCCAACGT      TCGGT
                                          CAC___
GAM2634  FEZ1     3'  GAGGTTGCAGTGAGCCA     35421          ACAACA
                                     GGGGTTGCA      GGTCA
                                     |||||||||      |||||
                                     CTCCAACGT      TCGGT
                                          CAC___
GAM2634  G6PC     3'  AGAGGTTGCAGTGAGCCAAGAT 6658           ACAA__  _
                C                    AGGGGTTGCA     CA GGTC
                                     ||||||||||     || ||||
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                                TCTCCAACGT     GT CTAG
                                     CACTCG  T
GAM2634  KCNK4    5'  AGGGGTTGCAGCAGGGGCCA  37824          A  ACA
                                AGGGGTTGCA CA   GGTCA
                                |||||||||| ||   |||||
                                TCCCCAACGT GT   CCGGT
                                     C  CC_
GAM2634  LCP1     3'  AGGGGCTTGCAACAGATCA   14102        GCAA
                                AGGGGTT   CAACAGGTCA
                                |||||||   ||||||||||
                                TCCCCGA   GTTGTCTAGT
                                   AC__
GAM2634  LILRA3   3'  GAGGTTGCAGTGAGCCCAGAT  27803         ACAA___
                                GGGGTTGCA      CAGGT
                                |||||||||      |||||
                                CTCCAACGT      GTCTA
                                     CACTCGG
GAM2634  LNK      3'  GAGGTTGCAGTGAGCCA     24202          ACAACA
                                GGGGTTGCA     GGTCA
                                |||||||||     |||||
                                CTCCAACGT     TCGGT
                                     CAC___
GAM2634  MEFV     3'  GAGGTTGCAGTGAGCCA     6969           ACAACA
                                GGGGTTGCA     GGTCA
                                |||||||||     |||||
                                CTCCAACGT     TCGGT
                                     CAC___
GAM2634  MEN1     3'  AGGGGTTGTGTATGACGATGAT 39149         CAACAACA   C
              C                  AGGGGTTG       GGT ATC
                                |||||||||       ||| |||
                                TCCCCAAC       CTA TAG
                                   ACATACTG   C
GAM2634  MHC2TA   3'  GAGGTTGCAGTGAACCCAGATC 6983          ACAA___
                                GGGGTTGCA      CAGGTC
                                |||||||||      ||||||
                                CTCCAACGT      GTCTAG
                                     CACTTGG
GAM2634  PCDHB16  3'  AGAGGTTGCAGTGAGCCA    34139          ACAACA
                                AGGGGTTGCA     GGTCA
                                ||||||||||     |||||
                                TCTCCAACGT     TCGGT
                                     CAC___
GAM2634  PRKWNK3  3'  GAGGTTGCAGCAGTGAGCCA  41537          A  ACA
                                GGGGTTGCA CA   GGTCA
                                ||||||||| ||   |||||
                                CTCCAACGT GT   TCGGT
                                     C  CAC
GAM2634  PSMB2    3'  GAGGTTGCAGTGAGCCA     15819          ACAACA
                                GGGGTTGCA     GGTCA
                                |||||||||     |||||
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                                CTCCAACGT     TCGGT
                                     CAC___
GAM2634  RAB5C    3'  AGGGGTTGTGGGCAATGGGT  40806        CAA_  CA
                                AGGGGTTG   CAA  GGT
                                ||||||||   |||  |||
                                TCCCCAAC   GTT  CCA
                                    ACCC   AC
GAM2634  SEDL     3'  GAGGTTGCAGTGAGCCAAGATC 31006        ACAA__ _
                                GGGGTTGCA     CA GGTC
                                |||||||||     || ||||
                                CTCCAACGT     GT CTAG
                                     CACTCG  T
GAM2634  SEDL     3'  GAGGTTGCAGTGAGCCA     31005        ACAACA
                                GGGGTTGCA     GGTCA
                                |||||||||     |||||
                                CTCCAACGT     TCGGT
                                     CAC___
GAM2634  SEPN1    3'  GAGGTTGCAGTGAGCCAAGATC 42425        ACAA__ _
                                GGGGTTGCA     CA GGTC
                                |||||||||     || ||||
                                CTCCAACGT     GT CTAG
                                     CACTCG  T
GAM2634  SERPINB9 3'  GAGGTTGCAGTGAGCCCAGATC 19995        ACAA___
           A                     GGGGTTGCA      CAGGTCA
                                |||||||||      |||||||
                                CTCCAACGT      GTCTAGT
                                     CACTCGG
GAM2634  SLC7A6   5'  GAGGTTGCAGTGAGCCAAGATC 19593        ACAA__ _
           A                     GGGGTTGCA     CA GGTCA
                                |||||||||     || |||||
                                CTCCAACGT     GT CTAGT
                                     CACTCG  T
GAM2634  SNAP23   3'  GAGGTTGCAGTGAGCCCAGATC 19251        ACAA___
                                GGGGTTGCA      CAGGTC
                                |||||||||      ||||||
                                CTCCAACGT      GTCTAG
                                     CACTCGG
GAM2634  TAPBP    3'  GAGGTTGCAGTAAGCCAAGATC 17302        ACAA__ _
           A                     GGGGTTGCA     CA GGTCA
                                |||||||||     || |||||
                                CTCCAACGT     GT CTAGT
                                     CATTCG  T
GAM2634  TDGF1    3'  GAGGTTGCAGTGAACCAAGATC 17363        AC_  __
                                GGGGTTGCA   AAC  AGGTC
                                |||||||||   |||  |||||
                                CTCCAACGT   TTG  TCTAG
                                     CAC   GT
GAM2634  TRPM6    3'  AGAGGTTGCAGTGAGATC    32782        ACAAC
                                AGGGGTTGCA    AGGTC
                                ||||||||||    |||||
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                                TCTCCAACGT    TCTAG
                                     CAC__
GAM2634  TRPV1    3'  AGAGGTTGCAGTGAGCCAAGAT 38790          ACAA__ _
                CA                  AGGGGTTGCA     CA GGTCA
                                    ||||||||||     || |||||
                                    TCTCCAACGT     GT CTAGT
                                         CACTCG  T
GAM2634  ZNF264   3'  GAGGTTGCAGTGAGCCAAGATC 18272         ACAA__ _
                                    GGGGTTGCA     CA GGTC
                                    |||||||||     || ||||
                                    CTCCAACGT     GT CTAG
                                         CACTCG  T
GAM2635  BHLHB3   3'  TAGTGTGTGGAGGGTGGGGTGG 36259     C       CGATCCT
                TG                  TAG GTGTGGAG      TGGTG
                                    ||| ||||||||      |||||
                                    ATC CACACCTC      ACCAC
                                      A       CCACCCC
GAM2635  LARGE    3'  GTGGTGGGCTTCTTGGT     21865     _   A  GATC
                                    GTG TGG GC    CTTGGT
                                    ||| ||| ||    ||||||
                                    CAC ACC CG    GAACCA
                                      C   _  AA__
GAM2635  PPP1R12B 3'  GTGTGAACCTTGGT       36958       GCGAT
                                    GTGTGGA    CCTTGGT
                                    |||||||    |||||||
                                    CACACTT    GGAACCA
                                         _____
GAM2635  APPBP2   3'  AGGAGCAACATCTT       26871       CGTT
                                    AGGAGCA    ATATCTT
                                    |||||||    |||||||
                                    TCCTCGT    TGTAGAA
                                         ____
GAM2635  BPAG1    3'  GGAACGAATTTATATCTTT   31781      ACG_
                                    GGAGC    TTATATCTTT
                                    |||||    ||||||||||
                                    CCTTG    AATATAGAAA
                                       CTTA
GAM2635  BTC      5'  AGGAGTTATATCTT       45538      GCAC
                                    AGGA    GTTATATCTT
                                    ||||    ||||||||||
                                    TCCT    CAATATAGAA
                                         ____
GAM2635  CHD1     3'  GAAGATCTGTTTATATCTTT  10433      GCACG
                                    GAGGA    TTATATCTTT
                                    |||||    ||||||||||
                                    CTTCT    AATATAGAAA
                                       AGACA
GAM2635  DLST     3'  GAGAAGCAAAATCATCTTT   12572       CGTTA
                                    GAGGAGCA    TATCTTT
                                    ||||||||    |||||||
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                              CTCTTCGT    GTAGAAA
                                  TTTA_
GAM2635 EFG2    3' AAGCTTAAGTTATATCTTT  37031     AC__
                              GAGC   GTTATATCTTT
                              ||||   ||||||||||
                              TTCG   CAATATAGAAA
                                AATT
GAM2635 ITGB1   3' GAGGAACATACATCTTT    38048       CGT
                              GAGGAGCA  TATATCTTT
                              ||||||||  |||||||||
                              CTCCTTGT  ATGTAGAAA
                                  ___
GAM2635 KNSL3   5' GAAGGCCAGTATATCTTT   36149     A A T
                              GAGG GC CG TATATCTTT
                              |||| || || |||||||||
                              CTTC CG GT ATATAGAAA
                                _ _ C
GAM2635 OLR1    3' GAGGAGCATTGTGACACTTT  14940       C_ T  T
                              GAGGAGCA  GT ATA CTTT
                              ||||||||  || ||| ||||
                              CTCCTCGT  CA TGT GAAA
                                  AA  C  _
GAM2635 PART1   3' GAAGAGCAGTGCTGGTCTTT  32458       C_  ATA
                              GAGGAGCA  GTT  TCTTT
                              ||||||||  |||  |||||
                              CTTCTCGT  CGA  AGAAA
                                  CA  CC_
GAM2635 PIN4    3' AAGGAGCATCCAATATCTTT  26327       CGTT
                              GAGGAGCA   ATATCTTT
                              ||||||||   ||||||||
                              TTCCTCGT   TATAGAAA
                                  AGGT
GAM2635 PRKAR2A 3' AAGGAGCATGTTTATACTTT  20004       CG_   T
                              GAGGAGCA  TTATA CTTT
                              ||||||||  ||||| ||||
                              TTCCTCGT  AATAT GAAA
                                  ACA   _
GAM2635 RECK    3' GAGGAGCATTCTGCACTTT   34415       CG  A  T
                              GAGGAGCA  TT TA CTTT
                              ||||||||  || || ||||
                              CTCCTCGT  GA GT GAAA
                                  AA  C  _
GAM2635 RELN    3' AAGGAGATACAATATCTTT   45352      CACGTT
                              GAGGAG    ATATCTTT
                              ||||||    ||||||||
                              TTCCTC    TATAGAAA
                                 TATGT_
GAM2635 SNX6    3' GAGGAGCAGTTCATTCTTT   34563       C  ATA
                              GAGGAGCA GTT  TCTTT
                              |||||||| |||  |||||
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                                CTCCTCGT CAA   AGAAA
                                     _  GTA
GAM2636 AKAP13   3' GGACACAGCCAGTGGGGGGT  40351   A    AA_  ACT
                                A ACGCA   AG   TGGGGGGT
                                | |||||   ||   ||||||||
                                C TGTGT   TC   ACCCCCCA
                                 C    CGG  ___
GAM2636 AQP8    3' GCAGTGGAAGCAGGGGGTCG  10117    AAA  CT
                                GCA   GA  TGGGGGGTCG
                                |||   ||  ||||||||||
                                CGT   CT  GTCCCCCAGC
                                  CAC  TC
GAM2636 CD14    3' GCAAAGGGTTGAATTGGTCG  42461     A AC    GG_
                                GCAAA G  TTGG   GGTCG
                                ||||| |  ||||   |||||
                                CGTTT C  AACT   CCAGC
                                   _ CC    TAA
GAM2636 CYP4F3   3' AACGCAGGAGGCGGAGG    9448       AAA  CT
                                AACGCA   GA  TGGGGG
                                ||||||   ||  ||||||
                                TTGCGT   CT  GCCTCC
                                    C__  CC
GAM2636 DSP     5' GCGGAAGGCTCGCGAGGTCG  20644    AA   A    G
                                GC  AAG CTTG GGGGTCG
                                ||  ||| |||| |||||||
                                CG  TTC GAGC CTCCAGC
                                 CC   C    G
GAM2636 EPB49    3' GCAAAAGGCTTGGAAGCTCG  12731       A      G
                                GCAAAAG CTTGGGGG TCG
                                ||||||| |||||||| |||
                                CGTTTTC GAACCTTC AGC
                                    C       G
GAM2636 IGFBP1   3' ACGCAGGAGCTTTGGAAG    8242       AA  AC
                                ACGCA  AG  TTGGGGG
                                |||||  ||  |||||||
                                TGCGT  TC  AACCTTC
                                   CC  GA
GAM2636 PFKFB4   3' GGACACAAAGGACTTGGG    21292   A      A
                                A ACGCAAA GACTTGGG
                                | ||||||| ||||||||
                                C TGTGTTT CTGAACCC
                                 C      C
GAM2636 PKD2     3' GCAGAAGATTAGCAATCG    41072     A   CTTG  G
                                GCA AAGA    GG GGTCG
                                ||| ||||    || |||||
                                CGT TTCT    TC TTAGC
                                  C    AA__  G
GAM2636 POMC     3' GCAAGGGGCTTTGGGGTCG   9601      AAGA   GG
                                GCAA    CTT  GGGGTCG
                                ||||    |||  |||||||
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                                CGTT   GAA  CCCCAGC
                                  CCCC   A_
GAM2636  TERF2    3'  GCCCGGGAGACGGAGGTCG   24909    AAA__   TTG
                                GC    AGAC   GGGGGTCG
                                ||    ||||  ||||||||
                                CG    TCTG   CCTCCAGC
                                 GGCCC   ___
GAM2636  TESK1    3'  AACGCGAGCCGGGGGGTCG   26610      AAAA  C
                                AACGC   GA TTGGGGGGTCG
                                |||||   || ||||||||||
                                TTGCG   CT GGCCCCCCAGC
                                   _____ C
GAM2636  TRAF5    5'  GGACGCGCAGGAAGGGGTC   21472   A   AAA  ACTT
                                A ACGC   AG   GGGGGGTC
                                | ||||  ||   ||||||||
                                C TGCG   TC   TTCCCCAG
                                 C   CG_  C___
GAM2636  ZFP103   5'  ACGGGAGAGAGAAGGGTCG   24955    CAAA   CTT
                                ACG   AGA   GGGGGGTCG
                                |||   |||  |||||||||
                                TGC   TCT   CTTCCCAGC
                                  CC__   CT_
GAM2637  IL8      3'  TAGCAGACTAGGGTTGCCAGAT 45391          _______
            T                    TAGCAGACTA      TAGATT
                                ||||||||||      ||||||
                                ATCGTCTGAT      GTCTAA
                                     CCCAACG
GAM2638  COL4A5   3'  CCCGGGATACAGCAGGATTAG  37897     AA      TACT
                                TCC  GATACAGT   ATTAG
                                |||  ||||||||   |||||
                                GGG  CTATGTCG   TAATC
                                  CC       TCC_
GAM2638  FLRT2    5'  ACTTCAGGCTACAGTTACTAT  29835     C  AGA
                                ACT CA   TACAGTTACTAT
                                ||| ||   ||||||||||||
                                TGA GT   ATGTCAATGATA
                                  A  CCG
GAM2638  NPY1R    3'  CAAGATACATGAAATTAG    9482          GTTACT
                                CAAGATACA     ATTAG
                                |||||||||     |||||
                                GTTCTATGT     TAATC
                                     ACTT__
GAM2639  CCK      3'  CTTCCGTTGGGCTGAT      8807          ACCCAA
                                CTTCCGTTG     CTGAT
                                |||||||||     |||||
                                GAAGGCAAC     GACTA
                                     CC_____
GAM2639  DGKA     5'  CTTCCGTTGCTTGGACCTCTTC 10646         ACCCA   GATA
            A                    CTTCCGTTG    ACT    TCA
                                |||||||||    |||   |||
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                                GAAGGCAAC    TGG   AGT
                                     GAACC  AGA_
GAM2639  PIGR     5'  CTCCCGTTGATCTGACTTC   43703         CCCAA    A
                                CTTCCGTTGA    CTGAT TC
                                ||||||||||    ||||| ||
                                GAGGGCAACT    GACTG AG
                                     A____    A
GAM2640  AGL      3'  ATATTATAATAAATGAGAT   8486           _
                                ATATTATAATAAATG GAT
                                ||||||||||||||| |||
                                TATAATATTATTTAC CTA
                                         T
GAM2641  BAAT     3'  TATCAGGTTTTTACCCT    11791        G
                                TATCAGGT TTTTATTTT
                                |||||||| |||||||||
                                ATAGTCCA AAAATGGGA

                                _
GAM2641  C18orf1  3'  CAGGTGGAAATCTTTTTCT   41214       TTTTA
                                CAGGTG    TTTTTTCT
                                ||||||    ||||||||
                                GTCCAC    GAAAAAGA
                                   CTTTA
GAM2642  ANKH     3'  AGGGAACAAAATACGATG    38310    T        AGCG
                                AG GGAACAAAATAT    GATG
                                || ||||||||||||    ||||
                                TC CCTTGTTTTATG    CTAC

                                _       _____
GAM2642  CHD2     3'  AGAGGAACAAAGATAAGGATGA 10438    T      AT   C
                                AG GGAACAAA  ATAG GGATGA
                                || ||||||||  |||| ||||||
                                TC CCTTGTTT  TATT CCTACT
                                 T       C_   _
GAM2642  D12S2489E 3'  AGTGGGACAAACATAGGATG   28883      A    A   GC
                                AGTGG ACAAA TATA  GGATG
                                ||||| ||||| ||||  |||||
                                TCACC TGTTT GTAT  CCTAC
                                   C    _   __
GAM2642  DDX24    3'  GTGGAGTGAAACACAAGGGTG  33827      ACA      C  A
                                GTGGA   AAATATAG GG TG
                                |||||   |||||||| || ||
                                CACCT   TTTGTGTT CC AC
                                   CAC       C  _
GAM2642  IL8      3'  AGTGGAACAAGGAC       45389          AATATAGC
                                AGTGGAACAA       GGAT
                                ||||||||||       ||||
                                TCACCTTGTT       CCTG

                                          _________
GAM2642  KRT6B    3'  AGTGGAACAGGTATTGATG   24479         AAATA  GCG
                                AGTGGAACA    TA   GATG
                                |||||||||    ||   ||||
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                                TCACCTTGT    AT   CTAC
                                     CC___  AA_
GAM2642  MAP4K2   3'  GTGGAACAAAATGGAATGGATG 21356          AT  C
                                GTGGAACAAAAT  AG GGATG
                                ||||||||||||  || |||||
                                CACCTTGTTTTA  TT CCTAC
                                      CC  A
GAM2642  MDM1     3'  AGTGGAACAGAATGGA      33514         A   ATAGC
                                AGTGGAACA AAT    GGA
                                |||||||||| |||    |||
                                TCACCTTGT TTA    CCT
                                     C  _____
GAM2642  PUM1     3'  AGTGAACAAAATATGTGG    31229      G        AGC
                                AGTG AACAAAATAT   GG
                                |||| ||||||||||   ||
                                TCAC TTGTTTTATA   CC
                                  _        CA_
GAM2642  RAD54B   3'  AGTTGAACAAAAGGCAGGGGTG 39582     G       TA   C  A
              A                  AGT GAACAAAA  TAG GG TGA
                                 ||| ||||||||  ||| || |||
                                 TCA CTTGTTTT  GTC CC ACT
                                   A       CC   _  C
GAM2642  ROR2     3'  AGTGGGCAAAATACACATGG   21257      AA       GC_
                                AGTGG  CAAAATATA   GG
                                |||||  |||||||||   ||
                                TCACC  GTTTTATGT   CC
                                   C_       GTA
GAM2642  SLC19A2  3'  GTGGAACAAAGAGGCTATGA   42891         ATATA  GG
                                GTGGAACAAA    GC  ATGA
                                ||||||||||    ||  ||||
                                CACCTTGTTT    CG  TACT
                                      CTC__  A_
GAM2642  SYN3     3'  GTGGAACAGAATGGGTACAG   39495        A   ATA_
                                GTGGAACA AAT    GCGG
                                |||||||| |||    ||||
                                CACCTTGT TTA    TGTC
                                     C   CCCA
GAM2642  TGFBR3   3'  GTGGGGTGAATACAACGGGTGA 17492      AACAA        A
                                GTGG    AATATAGCGG TGA
                                ||||    |||||||||| |||
                                CACC    TTATGTTGCC ACT
                                  CCAC_         C
GAM2643  EDAR     3'  TGACACTGGCTGGCCTTAC    35312         ATTA  A  C
                                TGATACTGGC    GG CC TAC
                                ||||||||||    || || |||
                                ACTGTGACCG    CC GG ATG
                                      A___  _  A
GAM2643  SLC13A4  3'  GATACTGGCAGCTCCT      29725          TTAG AC
                                GATACTGGCA    G  CCT
                                ||||||||||    |  |||
```

```
                                CTATGACCGT   C  GGA
                                     ____ GA
GAM2643  SLC1A4   3'  TGTACTGGCAAGAAAGGGCTCT 16761    A      TT__   ACC
             A                    TG TACTGGCA   AGG   CTA
                                  || ||||||||   |||  |||
                                  AC ATGACCGT   TCC   GAT
                                   _      TCTT   CGA
GAM2644  ASGR2    5'  GGTGGTGGCCTGGGTAGGATCT 38955       AG  TAC   C
             G                    GGTGGTGG  TG   AGGA CTG
                                  ||||||||  ||   |||| |||
                                  CCACCACC  AC   TCCT GAC
                                       GG  CCA   A
GAM2644  CAPNS1   3'  GGTGTGTGCAGGGCCT     11979     GA   TA   A
                                  GGTG  GTG  CAGG CCT
                                  ||||  |||  |||| |||
                                  CCAC  CAC  GTCC GGA
                                    A_  __   C
GAM2644  DHCR24   3'  TGGTGGCTGGGGTGGGCCT   31302      _  A   TACA  A
                                  TGGTGG TGG GTG   GG CCT
                                  |||||| ||| |||   || |||
                                  ACCACC ACC CAC   CC GGA
                                     G   C  ____ _
GAM2644  DIA1     3'  TGGGGTGGGCCCTGGGACCTG  28797    T    A  GTACA
                                  TGG GGTGG GT    GGACCTG
                                  ||| ||||| ||    |||||||
                                  ACC CCACC CG    CCTGGAC
                                    _    _ GGAC_
GAM2644  DISC1    3'  TGATGGTGGGGTGAATAGG   33053        A   TAC
                                  TGGTGGTGG GTG   AGG
                                  |||||||||| |||   |||
                                  ACTACCACC CAC   TCC
                                       C   TTA
GAM2644  DNAJB1   3'  GGAGGAGTGTACAGGGTCTG   26031    T         AC
                                  GG GGAGTGTACAGG  CTG
                                  || ||||||||||||  |||
                                  CC CCTCACATGTCC  GAC
                                   T          CA
GAM2644  HDAC7A   5'  TGGTGTGTCTGCACAGGGCCTG 32478      G  GAG      A
                                  TGGTG TG   TGTACAGG CCTG
                                  ||||| ||   |||||||| ||||
                                  ACCAC AC   ACGTGTCC GGAC
                                     _ AG_       C
GAM2644  IHPK3    5'  TGGTGGTGGGGGGGTCCCT    38379        AGTGTACA  A_
                                  TGGTGGTGG       GG  CCT
                                  |||||||||       ||  |||
                                  ACCACCACC       CC  GGA
                                       CC_______  AG
GAM2644  MSF      3'  GGTGGTGGGAGGGCC       44740        _  TGTACA  A
                                  GGTGGTGG AG     GG CC
                                  |||||||| ||     || ||
```

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                                CCACCACC TC     CC GG
                                    C _______ _
GAM2644 SLC4A1   3' TGGTGGGGGAGGGTCTAGGGCC 7360       T   T AC  A
            TG                   TGGTGG GGAG GT  AGG CCTG
                                 |||||| |||| ||  ||| ||||
                                 ACCACC CCTC CA  TCC GGAC
                                    C   C  GA  C
GAM2644 SORCS2   3' TGGGGCGGCCGTGTGTGGGGTC 34068    T    A_   ACA  AC
            TG                   TGG GGTGG  GTGT   GG  CTG
                                 ||| |||||  ||||   ||  |||
                                 ACC CCGCC  CACA   CC  GAC
                                  _    GG   CAC  CA
GAM2645 CDH5     3' GGGCTGCAGGGGGTTTG     12189      ATTGA  __
                                 GGGCT    GTA  GGGTTTG
                                 |||||    |||  |||||||
                                 CCCGA    CGT  CCCAAAC
                                   ______  CC
GAM2645 DTR      3' TGAGGGGAAGTGGGGTTTG   12619   T   CTATT   A
                                 C AGGG    GAGT GGGTTTG
                                 | ||||    |||| |||||||
                                 A TCCC    TTCA CCCAAAC
                                  C   C____   C
GAM2645 EPM2A    3' CAGGGTTGTTGGGTAGAGAAGG 24967      CTA  A    TTT
                                 TAGGG   TTG GTAGGG   GG
                                 |||||   ||| ||||||   ||
                                 GTCCC   AAC CATCTC   CC
                                    AAC   C     TT_
GAM2645 GATA2    3' GGGCTGCTAAGGGTTTG     13088      A   AGT
                                 GGGCT TTG   AGGGTTTG
                                 ||||| |||   ||||||||
                                 CCCGA GAT   TCCCAAAC
                                    C  ___
GAM2645 NDUFV3   5' CTGGGGCTATTGGCTATCCCCG 34340    A       A  AGGG
            G                    CT GGGCTATTG GT    TTTGG
                                 || |||||||| ||    |||||
                                 GA CCCGATAAC CG    GGGCC
                                  C        _ ATAG
GAM2645 PIGR     3' CAGGGGTTGTGAGGGTTTG   43701      CTA   AGT
                                 TAGGG   TTG   AGGGTTTG
                                 |||||   |||   ||||||||
                                 GTCCC   AAC   TCCCAAAC
                                    C__   AC_
GAM2646 PTPN7    5' TTGGAGCTGGTTGGGCAGC   38722          A_   AGTTC
                                 TTGGAGCTGGT  GGCG    GC
                                 ||||||||||  ||||    ||
                                 AACCTCGACCA  CCGT    CG
                                        AC   ______
GAM2646 SOLH     3' TTGGGGCTGGCAGGTGAGCGGG 24834      A       C   TC_
            GC                   TTGG GCTGGTAGG GAGT   GC
                                 |||| ||||||||| ||||   ||
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                                AACC CGACCGTCC CTCG   CG
                                  C       A   CCC
GAM2646 TIMM17B  5' TTGGAGCTGGAGGAAGTGC   25180         T  C   TC
                                TTGGAGCTGG AGG GAGT  GC
                                |||||||||| ||| ||||  ||
                                AACCTCGACC TCC TTCA  CG
                                      _  _   __
GAM2647 MLLT2    3' AAAATACCTTACATCCGTT   25488        _ TC
                                AAAATACCT AT  CCGTT
                                ||||||||| ||  |||||
                                TTTTATGGA TG  GGCAA
                                     A  TA
GAM2648 PCDH15   3' TCTTATCAGAAAACAGATG   37510     T   TAACC
                                TCTT ATC    GAACAGATG
                                |||| |||    |||||||||
                                AGAA TAG    TTTGTCTAC
                                  _  TCT__
GAM2648 PDK4     3' TATTCTTATCAAAAACAGATG  45546    CT    TAACC
                                TAT  TTATC    GAACAGATG
                                |||  |||||    |||||||||
                                ATA  AATAG    TTTGTCTAC
                                  AG    TT___
GAM2649 ADD1     3' GCTCTGAGCCCTTTTCCAGCC  30522    AAGC      C
                                GC    AGCCCTTT CCAGCC
                                ||    |||||||| ||||||
                                CG    TCGGGAAA GGTCGG
                                 AGAC       A
GAM2649 ARVCF    3' TCCAAGTTCTTTCCCAGCCC   11711    G   CAGCC
                                TC CAAG    CTTTCCCAGCCC
                                || ||||    ||||||||||||
                                AG GTTC    GAAAGGGTCGGG
                                 _   AA___
GAM2649 B3GAT1   3' GCCCCCTCTTTCCCAGCCC   33003    AG  _
                                GC  CC CTTTCCCAGCCC
                                ||  || ||||||||||||
                                CG  GG GAAAGGGTCGGG
                                 GG  A
GAM2649 CENTD2   5' TCGCAAACAGCCTGGCCC    40132          CTTT
                                TCGCAAGCAGCC   CCC
                                ||||||||||||   |||
                                AGCGTTTGTCGG   GGG
                                       ACC_
GAM2649 EFEMP2   3' TCGTGGTGCAGAGCTCCCAGC  32622    CAA_   CCCT
                                TCG   GCAG   TTCCCAGC
                                |||   ||||   ||||||||
                                AGC   CGTC   GAGGGTCG
                                  ACCA   TC__
GAM2649 EFNB2    3' GCAGCCAGCCCTTTCCCCAGCC 19882     AG         _
             C                   GCA  CAGCCCTTTCCC AGCCC
                                |||  |||||||||||| |||||
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                                CGT  GTCGGGAAAGGG TCGGG
                                  CG          G
GAM2649  ERBB2IP   5'  GCAGGAGTTTCCCAGCCC    33099      CCC
                                GCAG   TTTCCCAGCCC
                                ||||   ||||||||||
                                CGTC   AAAGGGTCGGG
                                  CTC
GAM2649  EXTL1     3'  TCGCAAGCCAGTCCTGGGGCC  20873         _  C   TTCCCA
                                TCGCAAGC AG CCT     GCC
                                |||||||| || |||     |||
                                AGCGTTCG TC GGA     CGG
                                     G  A   CCC___
GAM2649  GBF1      3'  GCAGTCCCCCACCCAGCCC    20077      _    TT
                                GCAG CCCT  CCCAGCCC
                                |||| ||||  ||||||||
                                CGTC GGGG  GGGTCGGG
                                  A    GT
GAM2649  GNAT1     5'  TCCCAGGCACCCTTCTGGCCC  6742     G  A   G     CCCA
                                TC CA GCA CCCTTT    GCCC
                                || || ||| ||||||    ||||
                                AG GT CGT GGGAAG    CGGG
                                 G  C   _      AC__
GAM2649  ICA1      3'  TCGAAGAAATTTTCCCAG    22470     C   CAGCCC
                                TCG AAG     TTTCCCAG
                                ||| |||     ||||||||
                                AGC TTC     AAAGGGTC
                                  _   TTTA__
GAM2649  KCND2     5'  TCCAAGTAGCCCTTCCC     29368    G    C
                                TC CAAG AGCCCTTTCC
                                || |||| ||||||||||
                                AG GTTC TCGGGAAGGG
                                 _    A
GAM2649  MGA       3'  GCAAACAGCTCTTTCGC     41724         C     CCA
                                GCAAGCAGC CTTTC   GC
                                ||||||||| |||||   ||
                                CGTTTGTCG GAAAG   CG
                                     A    ___
GAM2649  MSH2      3'  GCAAACAGTCCTCAGTTACAGC 7004         C    TCC__
                                GCAAGCAG CCTT     CAGC
                                |||||||| ||||     ||||
                                CGTTTGTC GGAG     GTCG
                                     A    TCAAT
GAM2649  MSR1      3'  AGCAGCCCTCCAGTCC      14655         TTC   _
                                AGCAGCCCT   CCAG CC
                                |||||||||   |||| ||
                                TCGTCGGGA   GGTC GG
                                     ___    A
GAM2649  RANBP3    3'  TCTGAGCAGCCCCCGGCC    28780    GCA      TTTC  A
                                TC   AGCAGCCC    CC GCC
                                ||   ||||||||    || |||
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                                AG   TCGTCGGG    GG CGG
                                 AC_       _____  C
GAM2649  RGS16    3'  TCGAAGCAGCCTCTCCCCCCAG 16328     C       _  TT   _
                C                 TCG AAGCAGCC CT  CCC AGC
                                  ||| |||||||| ||  ||| |||
                                  AGC TTCGTCGG GA  GGG TCG
                                    _       A  GG   G
GAM2649  RLBP1    3'  TCTCAAGCAGCCCTTTCCTAGC 7258     G            C
                C                 TC CAAGCAGCCCTTTCC AGCC
                                  || ||||||||||||||| ||||
                                  AG GTTCGTCGGGAAAGG TCGG
                                   A             A
GAM2649  RPP20    5'  GCAAGCAGCCAGCCAGC     25185          CTTTC
                                  GCAAGCAGCC     CCAGC
                                  ||||||||||     |||||
                                  CGTTCGTCGG     GGTCG
                                        TC___
GAM2649  RPS6KA5  3'  ACAAGCAGCTCAAATCTAGCCC 21912          CCTT_  CC
                                  GCAAGCAGC     TC  AGCCC
                                  |||||||||     ||  |||||
                                  TGTTCGTCG     AG  TCGGG
                                       AGTTT  A_
GAM2649  SCNN1G   3'  TCACAAGCGGCTCCAGC     9791          A  CCTTTC
                                  TCGCAAGC GC     CCAGC
                                  |||||||| ||     |||||
                                  AGTGTTCG CG     GGTCG
                                       C  A_____
GAM2649  SLC7A6   3'  AAGCAGCTTTCCTCCCAG     19583        CC_
                                  AAGCAGC   TTTCCCAG
                                  |||||||   ||||||||
                                  TTCGTCG   GGAGGGTC
                                      AAA
GAM2649  SMURF1   3'  TCCCAGGCAGCCTCAGC     45200    G  A     CTTTCC
                                  TC CA GCAGCC     CAGC
                                  || || ||||||     ||||
                                  AG GT CGTCGG     GTCG
                                   G  C     A_____
GAM2649  STAT6    5'  AAGCAGTGGCTGCCCCAGCCC  17147       CC_  T
                                  AAGCAG   CT TCCCAGCCC
                                  ||||||   || |||||||||
                                  TTCGTC   GA GGGGTCGGG
                                     ACC  C
GAM2649  STK18    5'  TCCAAGCAGCCAGCCGGCC   30686    G       CTTTC  A
                                  TC CAAGCAGCC     CC GCC
                                  || |||||||||     || |||
                                  AG GTTCGTCGG     GG CGG
                                    _       TC___  C
GAM2649  SYNJ1    5'  TCGGAGGCAGCCCTCTTCCTCC 19350     CAA        C  AG
                                  TCG   GCAGCCCTTT CC  CC
                                  |||   |||||||||| ||  ||
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                                AGC  CGTCGGGAGA GG  GG
                                  CTC        A  A_
GAM2649  TAL1     5'  TCGCAAACAGCTTTCCGCC   17290          CC    CA
                                TCGCAAGCAGC  TTTCC  GCC
                                ||||||||||  |||||  |||
                                AGCGTTTGTCG  AAAGG  CGG
                                          __    __
GAM2649  ZNF2     5'  TCTCAGGCTTAGTTTCCCAG  34386    G  A  AGCCC
                                TC CA GC    TTTCCCAG
                                || || ||    ||||||||
                                AG GT CG    AAAGGGTC
                                 A  C  AATC_
GAM2649  ZNF205   3'  CCGCTCCCCCTTTCCTGGCC  18378     AAGCAG      CA
                                TCGC     CCCTTTCC  GCC
                                ||||     ||||||||  |||
                                GGCG     GGGAAAGG  CGG
                                   AGG___       AC
GAM2649  CHGA     5'  GGCTGGGGGCGCAGTGCCTCG  10471     AGAA      CGA
                                GGC   GGCGCAGT   TCTCG
                                |||   ||||||||   |||||
                                CCG   CCGCGTCA   GGAGC
                                  ACCC       C__
GAM2649  MPP1     5'  AGGCGGGAGACGCGGTGCG   14623     AGA     A  _
                                AGGC   AGGCGC GT CG
                                ||||   ||||||  || ||
                                TCCG   TCTGCG CA GC
                                   CCC     C  C
GAM2649  PHEMX    3'  GGCAGAGGCGCAGCATC     40022       A       CG
                                GGCAGA GGCGCAGT  ATC
                                ||||||  ||||||||  |||
                                CCGTCT CCGCGTCG  TAG
                                          _      __
GAM2649  PRX      3'  AGGCAGAAGGTACGCTCG    34101          CG AG
                                AGGCAGAAGG  C  TCG
                                ||||||||||  |  |||
                                TCCGTCTTCC  G  AGC
                                      AT CG
GAM2649  PTMS     3'  GGTGGAGGGCGCAGTGTCT   15898    CA  A       CGA
                                GG  GA GGCGCAGT   TCT
                                ||  ||  ||||||||   |||
                                CC  CT CCGCGTCA   AGA
                                 AC  C       C__
GAM2649  RPA1     3'  AGGCAGAGGGAGTGAC      16367        A  CGC   C
                                AGGCAGA GG   AGT GAT
                                |||||||  ||   |||  |||
                                TCCGTCT CC   TCA CTG
                                    C  ___   _
GAM2649  SPTBN2   3'  AGGCAGAAGGCGAGTGCCCTCG  28065           C   CGA
                                AGGCAGAAGGCG AGT   TCTCG
                                ||||||||||||  |||   |||||
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                                TCCGTCTTCCGC TCA   GGAGC
                                      _  CG_
GAM2649  TIMM23   3'  GGCAGAGGCTGCAATCTC    26751       A   GCAGT
                                GGCAGA GGC    CGATCTC
                                |||||| |||    |||||||
                                CCGTCT CCG    GTTAGAG
                                   _  AC___
GAM2649  TNFRSF1A  3'  GGTTGGAAGGCGATCTC    9869     CA_     GCAGTC
                                GG   GAAGGC    GATCTC
                                ||   ||||||    ||||||
                                CC   CTTCCG    CTAGAG
                                 AAC    _______
GAM2650  DPYD     3'  ACTACTTATAGATTCATA    41290    A  C_
                                AC GC  GTAGATTCATA
                                || ||  ||||||||||
                                TG TG  TATCTAAGTAT
                                 A  AA
GAM2650  DSCAM    3'  TACAACCGCTGTCCAGTCATGC 10808       A  C  AGAT   A
              TG                  TACAAC GC GT    TCAT CTG
                                |||||| || ||    |||| |||
                                ATGTTG CG CA    AGTA GAC
                                   G  A  GGTC    C
GAM2650  USP9Y    5'  ACAGCAGTTATCATACT     41955      C  AGAT
                                ACAGC GT    TCATACT
                                |||||  ||    |||||||
                                TGTCG CA    AGTATGA
                                  T  AT__
GAM2651  BCL7A    3'  CACCTGCAAACCAGGTG     34201     G  G  CG
                                CAC TG TG  TCAGGTG
                                ||| || ||  |||||||
                                GTG AC GT  GGTCCAC
                                 G  _  TT
GAM2651  BTEB1    3'  CGAGTATGGGTCAGGTGA    10214    TG_  C
                                CG   GTG GTCAGGTGA
                                ||   ||| |||||||||
                                GC   TAC CAGTCCACT
                                 TCA   C
GAM2651  C20orf1  3'  CACTGGTGCAGTTGGTGA    29055     G      TCA
                                CAC TGGTGCG   GGTGA
                                ||| |||||||   |||||
                                GTG ACCACGT   CCACT
                                  _      CAA
GAM2651  COL5A1   3'  CGTAGATGAAGTCAGGTG    6415       _  C_
                                CGTGG TG  GTCAGGTG
                                |||||  ||  ||||||||
                                GCATC AC  CAGTCCAC
                                  T  TT
GAM2651  CPNE6    3'  CACCTGGTCCAAGAGGTG    25731     G   G  TC
                                CAC TGGT CG  AGGTG
                                ||| |||| ||  |||||
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                                GTG ACCA GT  TCCAC
                                  G   G  TC
GAM2651  CX3CR1   3'  CACATGGTAAGGGTGA     43293        CGTCA
                                CACGTGGTG    GGTGA
                                |||||||||    |||||
                                GTGTACCAT    CCACT
                                     TC___
GAM2651  DFFB     3'  CACGTGGTTCAACGTGA     44595       GCG  _
                                CACGTGGT   TCAG GTGA
                                ||||||||   |||| ||||
                                GTGCACCA   AGTT CACT
                                    ___   G
GAM2651  ENO1     3'  CACTTGGTGGAAAGTGA     10970     G    CGTC
                                CAC TGGTG    AGGTGA
                                ||| |||||    ||||||
                                GTG ACCAC    TTCACT
                                  A    CT__
GAM2651  EPB72    3'  CAGCGGTGTCAGGTG       19897    C    GC
                                CA GTGGT  GTCAGGTG
                                || |||||  ||||||||
                                GT CGCCA  CAGTCCAC
                                 _    __
GAM2651  ETV5     3'  CACATGGCCGGGTG        20844        G  TCA
                                CACGTGGT CG   GGTG
                                |||||||| ||   ||||
                                GTGTACCG GC   CCAC
                                   _  ____
GAM2651  FLT1     3'  ACGTGATGCATTGGGTGA    12902          CA
                                ACGTGGTGCGT  GGTGA
                                ||||||||||  |||||
                                TGCACTACGTA  CCACT
                                      AC
GAM2651  FUT6     5'  CACCTGTCATCAGGTGA     6650      G  GTG
                                CAC TG   CGTCAGGTGA
                                ||| ||   ||||||||||
                                GTG AC   GTAGTCCACT
                                  G  A__
GAM2651  GCG      3'  CACGTGGCTAGCAGGTGA    13116        GCGT
                                CACGTGGT    CAGGTGA
                                ||||||||    |||||||
                                GTGCACCG    GTCCACT
                                     ATC_
GAM2651  GFI1     3'  ACTTGGTAGCCGGTGA      23549    G    C   A
                                AC TGGTG GTC GGTGA
                                || ||||| ||| |||||
                                TG ACCAT CGG CCACT
                                 A    _  _
GAM2651  GRM6     3'  CACAGTGGACCACAGGTGA   9167      _    T  GT
                                CAC GTGG GC  CAGGTGA
                                ||| |||| ||  |||||||
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                                GTG CACC TG  GTCCACT
                                  T   _ GT
GAM2651  HDAC4    3'  CACGTGGCTGCAGTG      25748        GC  CA
                                CACGTGGT  GT  GGTG
                                ||||||||  ||  ||||
                                GTGCACCG  CG  TCAC
                                    A_  __
GAM2651  HPSE     3'  ACATCACTCAGGTGA      27414     GG   G
                                ACGT  TGC TCAGGTGA
                                ||||  ||| ||||||||
                                TGTA  GTG AGTCCACT
                                  __  _
GAM2651  HS3ST3B1 5'  CACGCTGGACGCCCGGGTG   25793     _  T    A_
                                CACG TGG GCGTC  GGTG
                                |||| ||| |||||  ||||
                                GTGC ACC TGCGG  CCAC
                                  G  _    GC
GAM2651  HSF2BP   3'  CACATGGTACATGGTGA     28142          CA
                                CACGTGGTGCGT  GGTGA
                                ||||||||||||  |||||
                                GTGTACCATGTA  CCACT
                                      __
GAM2651  ITGAM    3'  CACTGGAAACGAGGGTGA    8438     G   T_  TCA
                                CAC TGG  GCG   GGTGA
                                ||| |||  |||   |||||
                                GTG ACC  TGC   CCACT
                                  _  TT   TC_
GAM2651  ITPKA    3'  CACATGTCAGGTGA       13636      GGTGC
                                CACGT    GTCAGGTGA
                                |||||    |||||||||
                                GTGTA    CAGTCCACT
                                  _____
GAM2651  JAM3     3'  CACATGGTGCTGTCGTG     37259         _  AG
                                CACGTGGTGC GTC  GTG
                                |||||||||| |||  |||
                                GTGTACCACG CAG  CAC
                                    A  __
GAM2651  KCNK5    5'  CACGCGGCCCGGGGTG      19029        G  TCA
                                CACGTGGT CG   GGTG
                                |||||||| ||   ||||
                                GTGCGCCG GC   CCAC
                                    G  C__
GAM2651  LIF      3'  CACGTGGGCGGGACTGA     14138       T   TCA  __
                                CACGTGG GCG   GG  TGA
                                ||||||| |||   ||  |||
                                GTGCACC CGC   CC  ACT
                                    _  ____  TG
GAM2651  LILRB3   3'  CATCTTTGAGTCAGGTGA    27800     GG_  C
                                CGT   TG GTCAGGTGA
                                |||   || |||||||||
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                                GTA   AC CAGTCCACT
                                  GAA  T
GAM2651  LOXL2    3'  CACATGGTGCTCAGTGA     14193          G    G
                                CACGTGGTGC TCAG TGA
                                |||||||||| |||| |||
                                GTGTACCACG AGTC ACT
                                        _   _
GAM2651  NARS     3'  CACTTGATGTTCAGGTGA    21217     G    CG
                                CAC TGGTG  TCAGGTGA
                                ||| |||||  ||||||||
                                GTG ACTAC  AGTCCACT
                                  A    A_
GAM2651  P23      3'  GTTTCTACAGTCAGGTGA    27346    GG_  _
                                GT   TGC GTCAGGTGA
                                ||   ||| |||||||||
                                CA   ATG CAGTCCACT
                                  AAG   T
GAM2651  PDE1B    3'  CAGTGGGTGTCAGGTG      9562     C    TGC
                                CA GTGG   GTCAGGTG
                                || ||||   ||||||||
                                GT CACC   CAGTCCAC
                                  _    CA_
GAM2651  POLR2J   3'  CACGTCGGTGTCAGGGTGA   26357       _  GC     _
                                CACGT GGT  GTCAGG TGA
                                ||||| |||  |||||| |||
                                GTGCA CCA  CAGTCC ACT
                                   G   __     C
GAM2651  PTGFR    3'  CACATGGCCAGGGTGA      9658          GCGT   _
                                CACGTGGT    CAGG TGA
                                ||||||||    |||| |||
                                GTGTACCG    GTCC ACT
                                      _____   C
GAM2651  PTPN2    3'  CAATGTTGGTCAGGTGA     15910   C   G  C
                                A GTG TG GTCAGGTGA
                                | ||| || |||||||||
                                G TAC AC CAGTCCACT
                                 T   A  _
GAM2651  SLC2A2   3'  CGCTATATGATCAGGTGA    7346      G__   C
                                CGT   GTG GTCAGGTGA
                                |||   ||| |||||||||
                                GCG   TAC TAGTCCACT
                                  ATA   _
GAM2651  SMG1     3'  CACAGGGTCAGGTG        31505      T  TGC
                                CACG GG   GTCAGGTG
                                |||| ||   ||||||||
                                GTGT CC   CAGTCCAC
                                        _ ___
GAM2651  STK10    3'  ACATTAGGTTCAGGTGA     25612      __   GCG
                                ACGT  GGT   TCAGGTGA
                                ||||  |||   ||||||||
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                                TGTA  CCA   AGTCCACT
                                  AT   ___
GAM2651  TARBP2   3'  CACAGTGGCCGGCTGGGTG   39525    _    GC  CA
                                CAC GTGGT  GT  GGTG
                                ||| |||||  ||  ||||
                                GTG CACCG  CG  CCAC
                                  T    GC  AC
GAM2651  TNFRSF8  3'  CACGTGGCTGCCCGATGA    10313        GC   A
                                CACGTGGT  GTC GGTGA
                                ||||||||  ||| |||||
                                GTGCACCG  CGG CTACT
                                    A_   G
GAM2651  UBE2L6   3'  CACCTGTGGCCAGGTGA     20121     G  G  C
                                CAC TG TG GTCAGGTGA
                                ||| || || |||||||||
                                GTG AC AC CGGTCCACT
                                  G  _  _
GAM2651  USP11    3'  CACTCTGTGTTCAGGTGA    21627     GTG   CG
                                CAC   GTG  TCAGGTGA
                                |||   |||  ||||||||
                                GTG   CAC  AGTCCACT
                                  AGA   A_
GAM2651  VANGL2   3'  CACGTGGTTGCCTATG      43453        GC   AG
                                CACGTGGT  GTC  GTG
                                ||||||||  |||  |||
                                GTGCACCA  CGG  TAC
                                    A_   A_
GAM2651  ZNF157   3'  CACTGTGGTGCCCTGGTGA   18353     _     G  A
                                CAC GTGGTGC TC GGTGA
                                ||| ||||||| || |||||
                                GTG CACCACG GG CCACT
                                  A      _  A
GAM2652  ATP11A   3'  TGGCACATGTGTGTATATG   44189         C  TAG_
                                TGGCACATG GT    ATG
                                ||||||||| ||    |||
                                ACCGTGTAC CA    TAC
                                     A  CATA
GAM2652  UBE2I    3'  TGGCGCAGAACCGAGATGCTGC 17819      A  T_  GTT
                                TGGC CA  GC   AGATGCTGC
                                |||| ||  ||   |||||||||
                                ACCG GT  TG   TCTACGACG
                                  C  CT  GC_
GAM2652  IRS2     3'  ACATAACATTTATACATTTT   40692     CG  TA_
                                ACA  GC   TATACATTTT
                                |||  ||   ||||||||||
                                TGT  TG   ATATGTAAAA
                                  AT  TAA
GAM2652  MYCN     3'  CAGCACTAAATATATACATTTT 23915    _  GGC_
                                CA CAC    TATATACATTTT
                                || |||    ||||||||||||
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                              GT GTG    ATATATGTAAAA
                               C   ATTT
GAM2652  PPARGC1   3'  CACAGCTTACATTTT      29949       ATA
                              CACGGCT   TACATTTT
                              |||||||   ||||||||
                              GTGTCGA   ATGTAAAA
                                  ___
GAM2652  RP1       3'  ACAGTCAATATACATTTTA   26552     CT_
                              ACGG   ATATACATTTTA
                              ||||   ||||||||||||
                              TGTC   TATATGTAAAAT
                                AGT
GAM2652  TM4SF4    3'  ACATGTGACTTTATACATTTTA 21454     CAC    A
                              ACA   GGCT TATACATTTTA
                              |||   |||| ||||||||||
                              TGT   CTGA ATATGTAAAAT
                                ACA    A
GAM2652  ZNF216    3'  CACATGGGAACTACATTTT   25652     C  CTATA
                              CACA GG     TACATTTT
                              |||| ||     ||||||||
                              GTGT CC     ATGTAAAA
                                A  CTTG_
GAM2653  ABCD4     3'  AGACTGAACACTGGGAGA    33739        A  G  A_
                              AGACTGAG CG TG  AGA
                              |||||||| || ||  |||
                              TCTGACTT GT AC  TCT
                                   _  G  CC
GAM2653  CCNDBP1   5'  GGAAGCTGAGAGAAGAC     29102    T    A     CGGT
                              G GAAG CTGAGA    GAAGAC
                              | |||| ||||||    ||||||
                              C CTTC GACTCT    CTTCTG
                               _   _    _____
GAM2653  GA        3'  GTGAAGAGCTGGGATGGT    29971        _   A  C
                              GTGAAGA CTG GA GGT
                              ||||||| ||| || |||
                              CACTTCT GAC CT CCA
                                   C   C  A
GAM2653  HLA-DOB   3'  TGAAGACTGTGGAGA       13385         AGAC  TGA
                              TGAAGACTG    GG   AGA
                              |||||||||    ||   |||
                              ACTTCTGAC    CC   TCT
                                   A___  ___
GAM2653  IL1RAP    3'  ATGAAGACTGGGGGGA      13498          AGAC  TGAA
                              GTGAAGACTG    GG    GA
                              ||||||||||    ||    ||
                              TACTTCTGAC    CC    CT
                                    _____  CC__
GAM2653  LPIN2     3'  GTGAGGACTAAGAAATTAAG   31216      A      C   G
                              GTGA GACTGAGA GGT AAG
                              |||| |||||||| ||| |||
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                                CACT CTGATTCT TTA TTC
                                  C       _  A
GAM2653  MYO1E    5'  GTGAGGGCGAGACGGCGGCGAC 22657      A AC         AA
                T                  GTGA G  TGAGACGGTG  GACT
                                   |||| |  ||||||||||  ||||
                                   CACT C  GCTCTGCCGC  CTGA
                                     _ CC         CG
GAM2653  NDUFV3   3'  GTGAAGACGGTGGAAG      34341      AGACTG       _
                                   GTGA     AGACGGTG AAG
                                   ||||     |||||||| |||
                                   CACT     TCTGCCAC TTC
                                     _______       C
GAM2653  NRAS     3'  GTGAAGACTAGGATAGAC    14851          AGAC  TGA
                                   GTGAAGACTG    GG   AGAC
                                   ||||||||||    ||   ||||
                                   CACTTCTGAT    CC   TCTG
                                         _____  TA_
GAM2653  PTHR2    3'  GTGAAGACCTGAGGTCTGGC   22784         _    AC__
                                   GTGAAGAC TGAG    GGT
                                   |||||||| ||||    |||
                                   CACTTCTG ACTC    CCG
                                        G    CAGA
GAM2653  TEM5     3'  GTGAAGACTGGGAGGGAACCCT 37241          A  C  T   GA
                                   GTGAAGACTG GA GG GAA  CT
                                   |||||||||| || || |||  ||
                                   CACTTCTGAC CT CC CTT  GA
                                         C  _  _   GG
GAM2653  TNR      3'  ATGGAGACTGAGGGTCAGGCT  17621     A       AC   GA  A
                                   GTG AGACTGAG  GGT  AG CT
                                   ||| ||||||||  |||  || ||
                                   TAC TCTGACTC  CCA  TC GA
                                     C       __   G_  C
GAM2653  TYRO3    3'  GAATCAGAAAGATGGTGAAGA  26653     GACT_   C
                                   GAA     GAGA GGTGAAGA
                                   |||     |||| ||||||||
                                   CTT     TTCT CCACTTCT
                                     AGTCT    A
GAM2653  ZNF255   3'  ATGAAGACTGAGTGAAGAC    25100          GACG
                                   GTGAAGACTGA    GTGAAGAC
                                   ||||||||||    ||||||||
                                   TACTTCTGACT    CACTTCTG
                                                 ____
GAM2653  ADAMTS5  3'  CCACTGTCACGTGAAGCAG   28177      C  ACTAA
                                   CCGC GT     TGAAGCAG
                                   |||| ||     ||||||||
                                   GGTG CA     ACTTCGTC
                                     A  GTGC_
GAM2653  ATP5B    5'  GGACCGCCGTCGGAGCG     40649    A       ACTAA  A   A
                                   C ACCGCCGT     TG AGC G
                                   | ||||||||     || ||| |
```

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                                C TGGCGGCA    GC TCG C
                                 C      _____ C  C
GAM2653 BLK     3' GCCCTCTACAAATGAAGCGGC 11846    G__  T     A
                                GCC  TAC AATGAAGC GC
                                |||  ||| |||||||| ||
                                CGG  ATG TTACTTCG CG
                                  GAG  T      C
GAM2653 BUB3    3' AACCTCCTCATGAAGCAG   21800     G GTACTA
                                AACC CC    ATGAAGCAG
                                |||| ||     |||||||||
                                TTGG GG    TACTTCGTC
                                  A AG____
GAM2653 KCNA3   3' CACCTGTTTCAGTATGAAGCAG 13792     _ ACTA__
             C                   CGCC GT    ATGAAGCAGC
                                |||| ||     ||||||||||
                                GTGG CA    TACTTCGTCG
                                  A AAGTCA
GAM2653 PPT2    3' CCTGCCGTATTAAAACAA   39917   _    CTAA
                                CC GCCGTA   TGAAGCAG
                                || ||||||   ||||||||
                                GG CGGCAT   ATTTTGTT
                                 A    A___
GAM2653 RAB4A   5' CAACCGCCGGTCTCCCAGCGGC 21344        TA AATGA  A
                                CAACCGCCG CT    AGC GC
                                |||||||||  ||    ||| ||
                                GTTGGCGGC GA    TCG CG
                                     CA GGG__  C
GAM2654 ALPI    3' TAAGACGGTGGGGCACGCGGT 11582        AAGACTGAGA
                                TGAGACGGTG       CGGT
                                ||||||||||       ||||
                                ATTCTGCCAC       GCCA
                                     CCCGTGC___
GAM2654 CNGA1   5' TGGGAGGTGAAGACTGCAG   40495   A C       AGA
                                TG GA GGTGAAGACTG  CGG
                                || || ||||||||||  |||
                                AC CT CCACTTCTGAC  GTC
                                 C _        ___
GAM2654 HDAC4   5' CGGGACGGTGAGGGCTGGG   25762   A     AGA  AGAC
                                TG GACGGTGA  CTG   GG
                                || ||||||||  |||   ||
                                GC CTGCCACT  GAC   CC
                                 C      CCC  ____
GAM2654 PKD1    3' TGAGACGGTGCAGGGAGTACGG 7143         A ACT  _
             T                   TGAGACGGTG AG  GAG ACGGT
                                |||||||||| ||  ||| |||||
                                ACTCTGCCAC TC  CTC TGCCA
                                     G  C__  A
GAM2655 CHI3L1  3' CCCGAGTCTTACATTGCGATG 10474     TA   _     A
                                CCTG  GGTCT ACATTGC ATG
                                ||||  ||||| ||||||| |||
```

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                                GGGC  TCAGA TGTAACG TAC
                                  __    A      C
GAM2655  EYA1     5'  CCTTGTAGGTCTGCCCAT    7988     C       ACATT  A_
                                CC TGTAGGTCT    GC  AT
                                || |||||||||    ||  ||
                                GG ACATCCAGA    CG  TA
                                 A       _____  GG
GAM2655  MAP4     3'  CCTGTAGGTCTCAATCTGCA  36271          ACA_
                                CCTGTAGGTCT   TTGCA
                                ||||||||||   |||||
                                GGACATCCAGA   GACGT
                                      GTTA
GAM2655  MKPX     3'  ACTCTGTGGGTTTGCAAT   33630   C   A  CTACA
                                AC CTGT GGT    TTGCAAT
                                || |||| |||    |||||||
                                TG GACA CCA    AACGTTA
                                 A   C  _____
GAM2655  MUC4     3'  ACACTGGCTCTCTGCATTGCAA 39654   C   TAGG   A
              TG                  AC CTG    TCT CATTGCAATG
                                || |||    ||| ||||||||||
                                TG GAC    AGA GTAACGTTAC
                                 T   CGAG   C
GAM2655  RGL      5'  CTGCAGATCCCGTTGCGATG  31540         ACA    A
                                CTGTAGGTCT   TTGC ATG
                                ||||||||||   |||| |||
                                GACGTCTAGG   AACG TAC
                                      GC_    C
GAM2656  DLEC1    3'  TGCAGATGGGGTGAGTC     28840     CAA   A
                                TGC   ATG GGTGAGTT
                                |||   ||| ||||||||
                                ACG   TAC CCACTCAG
                                  TC_   C
GAM2656  FCGR2A   3'  GCCAGGTGGTTTTGTTTG    44278     AATGA   AG_
                                GCCA    GGTG   TTGTTTG
                                ||||    ||||   |||||||
                                CGGT    CCAC   AACAAAC
                                  _____    CAA
GAM2656  GAS7     3'  TGCCGAATGAGGTAGTT     25287      A      G
                                TGCC AATGAGGT AGTT
                                |||| |||||||| ||||
                                ACGG TTACTCCA TCAA
                                  C       _
GAM2656  PRKACB   3'  TGCTGAATGAGACACGTTTG   15597     CA     GT AGT
                                TGC  AATGAG  G   TGTTTG
                                |||  ||||||  |   ||||||
                                ACG  TTACTC  T   GCAAAC
                                  AC     TG ___
GAM2657  MTAP     3'  TCTTTGTATGCATCTCTGATA  14681     G     __    A
                                TCT TTGTAT  ATCT CTGATA
                                |||  ||||||  ||||  ||||||
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                                AGA AACATA  TAGA GACTAT
                                  _     CG   _
GAM2657  NUMB     3'  CTCTGCTGGGCAGTTGCTGATA 19050        TA  TCTA
                                CTCTGTTG  TA    CTGATA
                                ||||||||  ||    ||||||
                                GAGACGAC  GT    GACTAT
                                    CC  CAAC
GAM2657  AGTR1    5'  GACTTGTGATTCATTTTCTT   28912    AA  _       C
                                GG  TG GATTCATT TCTT
                                ||  || |||||||| ||||
                                CT  AC CTAAGTAA AGAA
                                 GA  A       A
GAM2657  DPP6     3'  TGTACAGAAAAGCGTTTTCT   39136         T  ATTCA
                                TGTACGGAA GG     TTCT
                                |||||||||  ||     ||||
                                ACATGTCTT TC     AAGA
                                      T  GCAA_
GAM2658  AGRN     3'  ATTGTTTGGAAGTCACAGTAT  44247        AACTTTTA
                                ATTGTTT       CACAGTAT
                                |||||||       ||||||||
                                TAACAAA       GTGTCATA
                                   CCTTCA__
GAM2658  CNTN3    3'  GATTGTTTCAATATATACAGTA 42481         AACTTT  C
            T                    GATTGTTT     TA ACAGTAT
                                ||||||||     ||  |||||||
                                CTAACAAA     AT TGTCATA
                                     GTTAT_  A
GAM2658  GABPB1   3'  AATTGCTTTTTTATACAGTAT  23524         AAC     C
                                GATTGTTT   TTTTA ACAGTAT
                                ||||||||   |||||  |||||||
                                TTAACGAA   AAAAT TGTCATA
                                     ___     A
GAM2659  BCL10    3'  TGTTCAAATAGCATTAAAAA   19409     _  T
                                TGT CA ATAGCATTAAAAA
                                |||  ||  ||||||||||||
                                ACA GT TATCGTAATTTTT
                                  A  T
GAM2659  DIAPH2   3'  TCCTTGTCATATAGTGGCAAAA 28682      A         CAT
            A                    TCCT TGTCATATAG   TAAAAA
                                ||||  ||||||||||   ||||||
                                AGGA ACAGTATATC   GTTTTT
                                  _         ACC
GAM2659  DSCR3    3'  CTTGGCAAATAGCATTAA    25825    A  T  T
                                CT TG CA ATAGCATTAA
                                ||  ||  ||  ||||||||||
                                GA AC GT TATCGTAATT
                                 _  C  T
GAM2659  RDS      3'  CCTGTCAATCTTGGCATTAAAA 7243      AT    TATA__
            A                    CCT  GTCA     GCATTAAAAA
                                |||  ||||     ||||||||||
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                                GGA  CAGT     CGTAATTTTT
                                  __    TAGAAC
GAM2659  RLN1     3'  GTTAACAGCATTAAAAA     27917    CAT
                                GT   ATAGCATTAAAAA
                                ||   ||||||||||||
                                CA   TGTCGTAATTTTT
                                 AT_
GAM2659  SUSP1    3'  TCCTGTGTTTACACAGATTAAA 31796      A   C_     C
              AA                  TCCT TGT  ATATAG ATTAAAAA
                                |||| |||  |||||| ||||||||
                                AGGA ACA  TGTGTC TAATTTTT
                                  C   AA     _
GAM2659  TAF4     3'  CTATGTCATGTGCCAAAA    17260          ATA  ATT
                                CTATGTCAT   GC   AAA
                                |||||||||   ||   |||
                                GATACAGTA   CG   TTT
                                     CA_  GT_
GAM2659  YWHAG    3'  TCCTATGCTTTTTTCATTAAAA 29800         CATATAG
              A                   TCCTATGT      CATTAAAAA
                                |||||||||      |||||||||
                                AGGATACG      GTAATTTTT
                                     AAAAAA_
GAM2660  TRAM     3'  TGGTCCCTAAACTATTTT    30704       AGCG
                                TGGTT    TAAACTATTTT
                                |||||    ||||||||||||
                                ACCAG    ATTTGATAAAA
                                   GG__
GAM2661  AXL      3'  TGAATCTAGACTCTTTAAA   34889         GT    G
                                TGGATCTA  GATT TTTAAA
                                ||||||||  |||| ||||||
                                ACTTAGAT  CTGA AAATTT
                                     __    G
GAM2661  CELSR3   3'  CTGGATCTGCTGTT       10838         A  GAT
                                CTGGATCT GT   TGTT
                                |||||||| ||   ||||
                                GACCTAGA CG   ACAA
                                     _  ____
GAM2661  ENAM     3'  CTAGATCTGGTGATCCCC    36674         A     G
                                CTGGATCT GTGATT TT
                                |||||||| |||||| ||
                                GATCTAGA CACTAG GG
                                     C     G
GAM2661  ITGA5    3'  CTGGATCTGGCCCCATTT    41497         A  GA TG
                                CTGGATCT GT  T  TTT
                                |||||||| ||  |  |||
                                GACCTAGA CG  G  AAA
                                     C  G_ GT
GAM2661  MTMR3    3'  GGAAGAGATTGTTTA       34396     TCT  T
                                GGA   AG GATTGTTTA
                                |||   || |||||||||
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                                CCT   TC CTAACAAAT
                                  ___  T
GAM2661  PLAG1    3'  TGGATGTGAATGTTTAAA    15360      CTA    T
                                TGGAT   GTGA TGTTTAAA
                                |||||   |||| ||||||||
                                ACCTA   CACT ACAAATTT
                                   ___    T
GAM2661  RRM2     3'  TGGATCATTTTGTTTAA     9763       TAGTGA
                                TGGATC     TTGTTTAA
                                ||||||     ||||||||
                                ACCTAG     AACAAATT
                                   TAA___
GAM2661  SCG3     3'  TGGATCTAATCTAGTTTA    29892         GATT
                                TGGATCTAGT    GTTTA
                                ||||||||||    |||||
                                ACCTAGATTA    CAAAT
                                      GAT_
GAM2661  SLC2A2   3'  CTGACTCATGATTGTTT     7348     GA  TA
                                CTG  TC  GTGATTGTTT
                                |||  ||  ||||||||||
                                GAC  AG  TACTAACAAA
                                  TG  __
GAM2662  GNB1     3'  TATTTTCAAAACATTGATTTG  13209       AA       C
                                TATTTT  CAAAGCAT GATTTG
                                ||||||  |||||||| ||||||
                                ATAAAA  GTTTTGTA CTAAAC
                                   __       A
GAM2662  MSL3L1   3'  TTTTAAAAAAGCACCTGATTT  38596       C       _
                                TTTTAA AAAGCATC GATTT
                                ||||||| |||||||| |||||
                                AAAATT TTTCGTGG CTAAA
                                   T       A
GAM2662  SET      3'  TATTGTAACAAAGCAACTTG   16562      T        TCG
                                TATT TAACAAAGCA   ATTTG
                                |||| ||||||||||   |||||
                                ATAA ATTGTTTCGT   TGAAC
                                  C        ___
GAM2663  EPS15    3'  TCTCTAAATCCAGATAAA    12748          __
                                TCTCTAAGTT  GATAAA
                                ||||||||||  ||||||
                                AGAGATTTAG  CTATTT
                                      GT
GAM2664  CRI1     3'  GTTGATAGAATAACTGTTCATA 30734       C  TTT
                                GTTGA AG   TAACTGTTCATA
                                ||||| ||   ||||||||||||
                                CAACT TC   ATTGACAAGTAT
                                   A  TT_
GAM2664  CSNK1A1  3'  GCTGAAGACTGTTCAT      12464       C  TTTTA
                                GTTGA AG    ACTGTTCAT
                                ||||| ||    |||||||||
```

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                                CGACT TC    TGACAAGTA
                                  _ _____
GAM2664  DXF68S1E  3'  TGTTACAGTTGTGTTCAT    41041      A    TTAAC
                                TGTTG CAGTT    TGTTCAT
                                ||||| |||||    |||||||
                                ACAAT GTCAA    ACAAGTA
                                  _    C____
GAM2664  FBXL5     5'  TTGCATAATTTAACTGTTCATA 37952     A  GT_
                                TTG CA   TTTAACTGTTCATA
                                ||| ||   ||||||||||||||
                                AAC GT   AAATTGACAAGTAT
                                  _ ATT
GAM2664  GALC      3'  TGTAGACAGTTTTAATTGT    6677      T        C
                                TGT GACAGTTTTAA TGT
                                ||| ||||||||||| |||
                                ACA CTGTCAAAATT ACA
                                  T         A
GAM2664  IL22RA2   3'  TGTTGATAGTTTTAATTCA    38135       C      ACT
                                TGTTGA AGTTTTA   GTTCA
                                |||||| |||||||   |||||
                                ACAACT TCAAAAT   TAAGT
                                   A      ___
GAM2664  MADH3     3'  TTGGCAGACACAGCTGTTCATA 25354     A   TTT  A
                                TTG CAG   TA CTGTTCATA
                                ||| |||   || |||||||||
                                AAC GTC   GT GACAAGTAT
                                  C   TGT  C
GAM2664  RORB      5'  TGTTAACAGTTTTGATGTT    27925           AAC
                                TGTTGACAGTTTT   TGTT
                                ||||||||||||   ||||
                                ACAATTGTCAAAA   ACAA
                                        CT_
GAM2664  TCTE1L    3'  TGTTGATAGCTTTAAAGC    43375       C       CT
                                TGTTGA AGTTTTAA  GT
                                |||||| ||||||||  ||
                                ACAACT TCGAAATT  CG
                                   A       T_
GAM2665  HK1       3'  TCCAGCCAATAAATAAC     37920      A       CA
                                TCCA CCGATAAAT  AGC
                                |||| |||||||||  |||
                                AGGT GGTTATTTA  TTG
                                  C        __
GAM2665  ACTB      3'  GGGGGAAGGGGGGGGCACG    9928       A    AA  A
                                GGGG AAGGG  GG ACG
                                |||| |||||  || |||
                                CCCC TTCCC  CC TGC
                                  C    CC  G
GAM2665  CARPX     5'  GGGGGAAGGGGGGGAGCCCGA  33577      A    AA   AC
                                GGGG AAGGG  GGA  GCCCGA
                                |||| |||||  |||  ||||||
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                                CCCC TTCCC  CCT  CGGGCT
                                  C    C_  __
GAM2665  CELSR2   3'  TGGGGAAGGGAAGGGAGCCTCG 10861       A     AAC  _
                                TGGGGAA GGGAAGG  GCC CG
                                ||||||| |||||||  ||| ||
                                ACCCCTT CCCTTCC  CGG GC
                                   _     CT_  A
GAM2665  EIF4EBP1 3'  TGGGGAAGGAGGGGGAGG    19888       __   A_
                                TGGGGAA  AGGG  AGG
                                |||||||  ||||  |||
                                ACCCCTT  TCCC  TCC
                                    CC   CC
GAM2665  EPHB1    3'  TGGGAGAAGGGAGGGGAC    20780     GA    A  A
                                TGGG  AAGGGA GG AC
                                ||||  |||||| || ||
                                ACCC  TTCCCT CC TG
                                  TC     C  C
GAM2665  GFAP     3'  TGGGGAGAGGGAAGGACCC   13128      A      AAC
                                TGGGGA AGGGAAGG  GCCC
                                |||||| ||||||||  ||||
                                ACCCCT TCCCTTCC  TGGG
                                   C      ___
GAM2665  GPR4     5'  TGGGGGCAGGGGAGGGAC    40895     AA   A  A
                                TGGGG  AGGG AGG AC
                                |||||  |||| ||| ||
                                ACCCC  TCCC TCC TG
                                  CG   C  C
GAM2665  HHIP     5'  AGGGAAGGGGAGGGGGCG    35402      A   A  AA
                                GGGGAA GGGA GG  CG
                                |||||| |||| ||  ||
                                TCCCTT CCCT CC  GC
                                   C   C  CC
GAM2665  HOXB3    3'  GGGGGAAGGGAAGGAGC     13441     A       AC
                                GGGG AAGGGAAGGA  GC
                                |||| ||||||||||  ||
                                CCCC TTCCCTTCCT  CG
                                  C       __
GAM2665  KCNQ3    5'  GGGAAGAAGGGGCGCTCG    21128     AAG    AA  C
                                GGGA  GGAAGG  CGC CG
                                ||||  ||||||  ||| ||
                                CCCT  TCTTCC  GCG GC
                                  ___    CC  A
GAM2665  LAD1     3'  TGGGGAAGGAGGGTAGGCC   24494      AA   A  AAC
                                TGGGGA  GGGA GG  GCC
                                ||||||  |||| ||  |||
                                ACCCCT  TCCT CC  CGG
                                   __   C  ATC
GAM2665  LMO4     5'  GGCTTCCAGGGAAGGGGCGCC  27659    AA___      AA
                                GG    AGGGAAGG  CGCC
                                ||    ||||||||  ||||
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                                CC    TCCCTTCC  GCGG
                                 GAAGG       CC
GAM2665  MAPK4    3'  TGGGGGAAGAGAAGGAGC    15671      A        AC
                                TGGGG AAGGGAAGGA  GC
                                ||||| ||||||||||  ||
                                ACCCC TTCTCTTCCT  CG
                                   C         __
GAM2665  MUCDHL   3'  GGTCAGGGAGGAACGCC     34943    GAA    A
                                GG   AGGGA GGAACGCC
                                ||   ||||| ||||||||
                                CC   TCCCT CCTTGCGG
                                 AG_    _
GAM2665  NRCAM    3'  TGGGGGGAGGGGGGAACCCA   22694      AA   AA   AC
                                TGGGG  AGGG  GGA  GCCCG
                                |||||  ||||  |||  |||||
                                ACCCC  TCCC  CCT  TGGGT
                                   CC   C_  __
GAM2665  NRGN     3'  TGGGGAAAGGGGAGGGAACG   26131          AA_
                                TGGGGAAAGGG   GGAACG
                                ||||||||||   ||||||
                                ACCCCTTTCCC   CCTTGC
                                      CTC
GAM2665  NT5M     3'  TGGGGAAGGGAAGGGACA    33656       A      A
                                TGGGGAA GGGAAGG ACG
                                ||||||| ||||||| |||
                                ACCCCTT CCCTTCC TGT
                                   _      C
GAM2665  OTP      3'  TGGGGAAAGAGGGGACCG    37007          AA   ACGC
                                TGGGGAAAGGG  GGA    CCG
                                ||||||||||  |||    |||
                                ACCCCTTTCTC  CCT    GGC
                                      C_  ____
GAM2665  PAK1     5'  TGGGGGGGCGGGAGGGAGCG   15088      AAA_   A   A
                                TGGGG    GGGA GGA CG
                                |||||    |||| ||| ||
                                ACCCC    CCCT CCT GC
                                   CCCG    C   C
GAM2665  RAD21    5'  TGGGGAAAGGGGGGGAGCC    26533          AA   AC
                                TGGGGAAAGGG  GGA  GCC
                                ||||||||||  |||  |||
                                ACCCCTTTCCC  CCT  CGG
                                      C_  __
GAM2665  SPF30    5'  GGGGGAAGGGAGGAACGCC    25239     A     A
                                GGGG AAGGGA GGAACGCC
                                |||| |||||| ||||||||
                                CCCC TTCCCT CCTTGCGG
                                   C     _
GAM2665  SPN      3'  TGGTGAGAGGGAAGGTGC     17091     G  A       AAC
                                TGG GA AGGGAAGG   GC
                                ||| || ||||||||   ||
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                                ACC CT TCCCTTCC   CG
                                  A  C       A__
GAM2665  TNFSF5   3'  TGGGGGAGGGAAGAGAC     6333       AA      GA
                                TGGGG  AGGGAAG  AC
                                |||||  |||||||  ||
                                ACCCC  TCCCTTC  TG
                                   C_      TC
GAM2665  USP11    3'  TGAGGAGAGGGAAGGGCACGA  21635       A       AAC  C
                                TGGGGA AGGGAAGG   GC CGA
                                ||||||| ||||||||   || |||
                                ACTCCT TCCCTTCC   CG GCT
                                   C       ___  T
GAM2666  ALDH1B1  3'  GCAAGCATTGGTCAAGGTGG   8669         A___
                                GCAAGCAT    TAGGGTGG
                                ||||||||    ||||||||
                                CGTTCGTA    GTTCCACC
                                     ACCA
GAM2666  AMPH     3'  AGCAATGCATGTATCAATGACA 11596      _   A  G_   GT
             A                   AGCAA GCAT TA  GGTG  AA
                                ||||| |||| ||  ||||  ||
                                TCGTT CGTA AT  TTAC  TT
                                   A    C  AG    TG
GAM2666  ATP6V1G2 3'  AGTGAGCAGGTGGTGGTAA   39625    CA    TATAG
                                AG  AGCA    GGTGGTAA
                                ||  ||||    ||||||||
                                TC  TCGT    CCACCATT
                                 AC    CCA__
GAM2666  BACE2    3'  AGTAAGCATATGTGATA     39986    C       AGG
                                AG AAGCATAT   GTGGTA
                                || ||||||||   ||||||
                                TC TTCGTATA   CACTAT
                                 A       ___
GAM2666  BCL7A    3'  AGAAAGCAGTGATGGGGGTGGT 34198    C     TATA___
                                AG AAGCA      GGGTGGT
                                || |||||      |||||||
                                TC TTCGT      CCCACCA
                                 T    CACTACC
GAM2666  BIN1     3'  GCAAGCATGGTGGC        40295         ATAG
                                GCAAGCAT    GGTGGT
                                ||||||||    ||||||
                                CGTTCGTA    CCACCG
                                     _____
GAM2666  C18orf1  3'  AGGAAGCAATGATGTGGTAACA 41206    C     TATAGG
             A                   AG AAGCA     GTGGTAACAA
                                || |||||     ||||||||||
                                TC TTCGT     CACCATTGTT
                                 C    TACTA_
GAM2666  CAPG     3'  AGCAAGCAGGCAGGTGGT    11958         TATA
                                AGCAAGCA    GGGTGGT
                                ||||||||    |||||||
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                                TCGTTCGT   TCCACCA
                                    CCG_
GAM2666 CD4     3' AGTAAGCAAATGGGGAGCCCCA 8323    C   T A  TG AA
                                AG AAGCA AT GGG  GT  CA
                                || ||||| || |||  ||  ||
                                TC TTCGT TA CCC  CG  GT
                                 A    T _  CT  GG
GAM2666 CDH2    3' AGCAAGCACTGTGCTAGTAG  12165       ATAG__
                                AGCAAGCAT    GGTGG
                                |||||||||    |||||
                                TCGTTCGTG    TCATC
                                     ACACGA
GAM2666 CDKN1B  5' GCAAGCGGAGAGGGTGGCAA  19799      ATAT
                                GCAAGC   AGGGTGGTAA
                                ||||||   ||||||||||
                                CGTTCG   TCCCACCGTT
                                   CCTC
GAM2666 CEP2    5' GCAAGCGGGCCCCGGGTAACAA 28437     ATATA  ____
                                GCAAGC   GGGT   GGTAACAA
                                ||||||   ||||   ||||||||
                                CGTTCG   CCCG   CCATTGTT
                                   _____  GGGC
GAM2666 CRHR1   3' GCAGGGCATTGCTGGTGGCA  20441    A_  ATAG
                                GCA GCAT   GGTGGTA
                                |||  ||||   |||||||
                                CGT CGTA   CCACCGT
                                  CC   ACGA
GAM2666 DPYSL2  3' AGAGAGACAAGGGTGGT    10742    CA C  T
                                AG  AG ATA AGGGTGGT
                                ||  || ||| ||||||||
                                TC  TC TGT TCCCACCA
                                 TC  _  _
GAM2666 DVL3    3' GCAGGCATGGGGCAGGGGTA  20681    A   ATA  ___
                                GCA GCAT   GGGT   GGTA
                                ||| ||||   ||||   ||||
                                CGT CGTA   CCCG   CCAT
                                  C   C__   TCC
GAM2666 EGFL5   5' AGCAAGCACTGTGGTTTAACAA 44512       ATAG  GG
                                AGCAAGCAT   GGT  TAACAA
                                |||||||||   |||  ||||||
                                TCGTTCGTG   CCA  ATTGTT
                                     ACA_   A_
GAM2666 EPHB2   3' GCAGGCCTGGTGGTGACAA   32670    A  ATATAG    A
                                GCA GC     GGTGGT ACAA
                                ||| ||     |||||| ||||
                                CGT CG     CCACCA TGTT
                                  C  GA____     C
GAM2666 ERBB2IP 3' AGCAAATGTATAGTCAATGG  33095      CA   __
                                AGCAAG  TATAG  GGTGG
                                ||||||  |||||  |||||
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                                TCGTTT  ATATC  TTACC
                                   AC    AG
GAM2666  GABRE    3'  AGCAAGTGATAGAACTCCGACA 35073       CAT    GG GGTA
                                AGCAAG   ATAG  T    ACA
                                ||||||   ||||  |    |||
                                TCGTTC   TATC  G    TGT
                                   AC_    TT AGGC
GAM2666  GFI1     3'  AGGGAGCAGAGTGGTGGCAA   23550    CA    TAT  _
                                AG  AGCA   AG GGTGGTAA
                                ||  ||||   || ||||||||
                                TC  TCGT   TC CCACCGTT
                                 CC    C__  A
GAM2666  HLA-DRA  3'  GCATTGCATGGTGATAA     33315     A_    ATAG
                                GCA  GCAT    GGTGGTAA
                                |||  ||||    ||||||||
                                CGT  CGTA    CCACTATT
                                  AA   _____
GAM2666  HSPA5    3'  AGCCGAGCATGGTGGTAACAA  23787     A_     ATAG
                                AGC  AGCAT    GGTGGTAACAA
                                |||  |||||    ||||||||||
                                TCG  TCGTA    CCACCATTGTT
                                  GC    _____
GAM2666  IFI16    3'  AGCTAGTATATATGGTGG    43410     A  C    G
                                AGC AG ATATA GGTGG
                                ||| ||  ||||| |||||
                                TCG TC TATAT CCACC
                                  A  A    A
GAM2666  IGF1R    3'  GCAGCGTTAAAATGGTAACA   9329      A  ATA
                                GCA GC   TAGGGTGGTAACA
                                ||| ||   ||||||||||||
                                CGT CG   ATTTTACCATTGT
                                  _  CA_
GAM2666  JAG1     3'  GCAGGCAGTGTACTCTATGGCA 6856      A   ___   AGG
              A                  GCA GCA   TAT   GTGGTAA
                                |||  |||   |||   |||||||
                                CGT CGT   ATG   TACCGTT
                                  C   CAC   AGA
GAM2666  JUP      3'  GCAGCTGTGTGGGTGGGACA   13773     A  ATATA     TA
                                GCA GC    GGGTGG  ACA
                                |||  ||    ||||||  |||
                                CGT CG    CCCACC  TGT
                                  _  ACACA     C_
GAM2666  KCNJ16   3'  ACAAGCATGTAAGATAATAA   33013        A
                                GCAAGCAT TAGGGTGGTAA
                                ||||||||  ||||||||||
                                TGTTCGTA ATTCTATTATT
                                     C
GAM2666  KIF5C    3'  AGCAGGTATATTGGGCTGG   21143      AGC    A   _
                                AGCA   ATAT GGG TGG
                                ||||   |||| ||| |||
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                                TCGT   TATA CCC ACC
                                  CCA    A   G
GAM2666  M11S1    3'  AGCAATTGAAAAGGGTGGTAGC 25325       GCATAT        A
             A                    AGCAA      AGGGTGGTA CA
                                  |||||      ||||||||| ||
                                  TCGTT      TCCCACCAT GT
                                     AACTTT        C
GAM2666  MASP1    3'  GCAAGTTGCACGGTGGCAA   40100       CATA  G
                                  GCAAG    TA GGTGGTAA
                                  |||||    || ||||||||
                                  CGTTC    GT CCACCGTT
                                     AAC_  G
GAM2666  MLLT4    3'  GCAAGTCATTCTTGGTAACA   25525       _   ATAGGG
                                  GCAAG CAT     TGGTAACA
                                  ||||| |||     ||||||||
                                  CGTTC GTA     ACCATTGT
                                     A   AGA___
GAM2666  MTA1L1   3'  GCAAGCATGGAGGCA       21888         ATAG  T
                                  GCAAGCAT    GG GGTA
                                  ||||||||    || ||||
                                  CGTTCGTA    CC CCGT
                                        _____  T
GAM2666  MYD88    3'  GCCAGCATGTAGTCCAGCAA   14717    A    A   GG
                                  GC AGCAT TAG  TGGTAA
                                  || ||||| |||  ||||||
                                  CG TCGTA ATC  GTCGTT
                                   G    C   AG
GAM2666  NEBL     3'  GCAAGTGTGTAAACAATAACAA 26903       CATATA   TG
                                  GCAAG     GGG  GTAACAA
                                  |||||     |||  |||||||
                                  CGTTC     TTT  TATTGTT
                                     ACACA_   GT
GAM2666  PER2     3'  AGTGAGCACATATTAAATGATA 19347    CA       __
             A                     AG  AGCATATA  GGGTGGTAA
                                   ||  ||||||||  |||||||||
                                   TC  TCGTGTAT  TTTACTATT
                                    AC       AA
GAM2666  PIK3C2B  3'  AGCATATAGGTCATAATAA    15288          __
                                  AGCATATAGG  GTGGTAA
                                  ||||||||||  |||||||
                                  TCGTATATCC  TATTATT
                                        AG
GAM2666  PTPN18   3'  GCAGGCTGTGTGAATAGTAA   30767     A  ATATA
                                  GCA GC     GGGTGGTAA
                                  ||| ||     |||||||||
                                  CGT CG     CTTATCATT
                                    C  ACACA
GAM2666  RECK     3'  GCAATTATATAAGTAGCA    34416      GC      G
                                  GCAA  ATATAGG TGGTA
                                  ||||  ||||||| |||||
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                                CGTT  TATATTC ATCGT
                                  AA     _
GAM2666 SDPR     3' AGCAAGCTTATGGAATGACAA 21650       A  A    GT
                                AGCAAGC TAT GGGTG  AA
                                ||||||| ||| |||||  ||
                                TCGTTCG ATA CTTAC  TT
                                    A  C    TG
GAM2666 SERPINE1 3' GCAGGCAGTACAAGAGTGAT  8289     A  _    _
                                GCA GCA TATAGG GTGGT
                                ||| ||| |||||| |||||
                                CGT CGT ATGTTC CACTA
                                  C  C     T
GAM2666 SLC16A2  3' AACAAGTGTGCTGGTGGCAA  27146      CATATAG
                                AGCAAG      GGTGGTAA
                                ||||||      ||||||||
                                TTGTTC      CCACCGTT
                                   ACACGA_
GAM2666 SLC21A3  3' AGCAAATGTATGAGTAATAA  39570      CA  A
                                AGCAAG  TAT GGGTGGTAA
                                ||||||  ||| |||||||||
                                TCGTTT  ATA CTCATTATT
                                   AC  _
GAM2666 SLC25A1  3' AGTAAGCACATGGACAA     25599    C      A  TG
                                AG AAGCATAT GGG  G
                                || |||||||| |||  |
                                TC TTCGTGTA CCT  T
                                 A       _  GT
GAM2666 ST7      3' AGCAGGGTGGTGACA       30264     TATA     A
                                AGCA   GGGTGGT ACA
                                ||||   ||||||| |||
                                TCGT   CCCACCA TGT
                                  ____      C
GAM2666 TEM5     3' AGCAAGCATAAATAAC      37228         TAGGGT
                                AGCAAGCATA     GGTAAC
                                ||||||||||     ||||||
                                TCGTTCGTAT     TTATTG
                                     ______
GAM2666 TIMP4    3' AGCAAGAGGTCAGGTGGTAA  17528      CATATA
                                AGCAAG     GGGTGGTAA
                                ||||||     |||||||||
                                TCGTTC     TCCACCATT
                                   TCCAG_
GAM2667 ANGPT2   3' CTTGGTTGTGACAGCAGCGT  10087   G  A       A
                                CT TGG TGTGACAGCA CGT
                                || ||| |||||||||| |||
                                GA ACC ACACTGTCGT GCA
                                 _  A        C
GAM2667 CHAC     3' TTGCTGTGTGTCTTCAGGCA  37820       GA  GA_  _
                                TTGCTGTG  TGT   CAG CA
                                ||||||||  |||   ||| ||
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                                AACGACAC  ACA   GTC GT
                                    __   GAA   C
GAM2667  HYAL1    3'  TTGCTGTGCAACCTTGGGCAAC 37647        _   G_  ACA
              GT                  TTGCTGTG GAT  TG   GCAACGT
                                  |||||||| |||  ||   |||||||
                                  AACGACAC TTG  AC   CGTTGCA
                                      G   GA  C__
GAM2667  ADAM19   3'  TCGCAACCTTTGGCATCA    37778    A      AAAACAA
                                  TC CAACCTTT      CATTA
                                  || ||||||||      |||||
                                  AG GTTGGAAA      GTAGT
                                   C       CC_____
GAM2667  EWSR1    3'  TCACAACCATGAACATT     23483        TTTAAAAC
                                  TCACAACC       AACATT
                                  ||||||||       ||||||
                                  AGTGTTGG       TTGTAA
                                      TAC_____
GAM2667  FAP      3'  ACAGCCTTTAGAACAACATT   20891     A     A
                                  ACA CCTTTA AACAACATT
                                  ||| |||||| |||||||||
                                  TGT GGAAAT TTGTTGTAA
                                    C     C
GAM2667  MID1     3'  TCACAACCTTTCTTTCCAACAT 7540           AAAA_
              TA                  TCACAACCTTT    CAACATTA
                                  ||||||||||    ||||||||
                                  AGTGTTGGAAA    GTTGTAAT
                                       GAAAG
GAM2667  UBL3     3'  TCAAGACCTTTAAAATTAC   28269     CA        CA
                                  TCA  ACCTTTAAAA  AC
                                  |||  ||||||||||  ||
                                  AGT  TGGAAATTTT  TG
                                    TC         AA
GAM2668  YWHAZ    3'  TTAATGCTACCCAATGTCA   18207      A       AA
                                  TTAGT CTACCCAAT  TCA
                                  ||||| |||||||||  |||
                                  AATTA GATGGGTTA  AGT
                                     C        C_
GAM2668  LAMP2    3'  TATAACTCAGTTATATGGT   30388       AA_
                                  TATAATT   TTATATGGT
                                  |||||||   |||||||||
                                  ATATTGA   AATATACCA
                                      GTC
GAM2669  ADAMTS8  3'  TGGGTGGGCCGTGCTGCCTTG 28168    AGAGAC   CAAA
                                  TGG     GCT    CTGCCTTG
                                  |||     |||   ||||||||
                                  ACC     CGG    GACGGAAC
                                    CACC__   CAC_
GAM2669  CD244    5'  TGGGGAGCAGAACTGCCTTG   32298    A   A  CTCA
                                  TGG GAG CG    AACTGCCTTG
                                  ||| ||| ||    ||||||||||
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                                ACC CTC GT    TTGACGGAAC
                                  C   _ C___
GAM2669  CELSR3   3'  TGGGGAGCAGGAGGCTGCCTTG 10842     A   A  CTCAAA
                                TGG GAG CG     CTGCCTTG
                                ||| ||| ||     ||||||||
                                ACC CTC GT     GACGGAAC
                                  C   _ CCTCC_
GAM2669  GPC6     5'  TGGGAAGGCTGCTGCCTT    25047     AG  AC   CAAA
                                TGG  AG  GCT    CTGCCTT
                                |||  ||  |||    |||||||
                                ACC  TC  CGA    GACGGAA
                                  CT  __   C___
GAM2669  GPR45    5'  TGGAGAGACCCTTGGAGCTG   28520         G  CAAA_
                                TGGAGAGAC CT     CTG
                                ||||||||| ||     |||
                                ACCTCTCTG GA     GAC
                                      G  ACCTC
GAM2669  TSTA3    3'  TGGAAAGATGCTTGGGGCTG   17706         C   CAAA_
                                TGGAGAGA GCT     CTG
                                |||||||| |||     |||
                                ACCTTTCT CGA     GAC
                                     A   ACCCC
GAM2669  DFFB     3'  TGGGCATTTAGAAGAGTCAAGA 44605     A  TCTATT
              G                  TG GC      GAAGAGTCAAGAG
                                 || ||      ||||||||||||||
                                 AC CG      CTTCTCAGTTCTC
                                  C  TAAAT_
GAM2669  ITGA1    3'  GCGGATGTGGAGAGTCAAGAG  41845     TCTAT  A
                                GC     TG AGAGTCAAGAG
                                ||     || ||||||||||
                                CG     AC TCTCAGTTCTC
                                 CCTAC  C
GAM2669  MTCP1    3'  TGGCCTGAAGAGTCAGGA    30587     A   CTAT        A
                                TG GCT    TGAAGAGTCA GA
                                || |||    |||||||||| ||
                                AC CGG    ACTTCTCAGT CT
                                 _  _____         C
GAM2670  SDC2     3'  GCGCATAAAAGTTTAAA     42568     AGT
                                GTG   TAAAAGTTTAAA
                                |||   ||||||||||||
                                CGC   ATTTTCAAATTT
                                  GT_
GAM2670  DIO1     3'  AATTCTGTTATTAGTTT     9000        AC
                                AATTC  GTTATTAGTTT
                                |||||  ||||||||||
                                TTAAG  CAATAATCAAA
                                   A_
GAM2671  ENPP2    3'  ACTAACATTTTTAATGTC    26301            TA
                                ACTAACATTTTTA  GTT
                                ||||||||||||  |||
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                                TGATTGTAAAAAT  CAG
                                       TA
GAM2671  FGF2     3'  ACATTTTTACATAAAATCATT  12825          GTT_
                                ACATTTTTATA   ATCATT
                                ||||||||||   ||||||
                                TGTAAAAATGT   TAGTAA
                                      ATTT
GAM2671  GPR48    3'  TAACACTTTTATATATC     32989           GT
                                TAACATTTTTATA  TATC
                                ||||||||||||  ||||
                                ATTGTGAAAATAT  ATAG
                                       __
GAM2671  PCDHA9   3'  ACTGGCATTTTCATAGTTAT   36535     AA
                                ACT  CATTTTTATAGTTAT
                                |||  ||||||||||||||
                                TGA  GTAAAAGTATCAATA
                                  CC
GAM2671  XRCC2    3'  CTGACATTTTTATAATAGCCAT 24093    A          TA
            T                    CT ACATTTTTATAGT  TCATT
                                || ||||||||||||  |||||
                                GA TGTAAAAATATTA  GGTAA
                                 C          TC
GAM2671  HUS1     3'  TGTGTTGTTGAATCAACTTTTA 45006     ATAA    AG
            GT                    TGT   TTGAA  AACTTTTAGT
                                |||   |||||  ||||||||||
                                ACA   AACTT  TTGAAAATCA
                                  CAAC    AG
GAM2671  MTMR8    3'  TGTATATTGCACATACTTTTAG 31760       A   AAAGA
            T                    TGTATA TTG    ACTTTTAGT
                                ||||||| |||    |||||||||
                                ACATAT AAC    TGAAAATCA
                                   _  GTGTA
GAM2672  TEM7     3'  CCTCAGACAGTAGATAAAAAT  33805       T  A  A
                                CCTCAG TAG TA ATAAAAAT
                                |||||| ||| || ||||||||
                                GGAGTC GTC AT TATTTTTA
                                   T  _  C
GAM2672  GALNT7   3'  TTTCTCAACTGTGAACACCTT  38367        C  ATT  _
                                TTTCTCAAC TG   AAC CCTT
                                |||||||||  ||   ||| ||||
                                AAAGAGTTG AC   TTG GGAA
                                      _  AC_   T
GAM2672  HSPD1    3'  TTTCTCAACTATCGAAGATCCT 41155        C__   TTAAC
            TCA                   TTTCTCAAC   TGA    CCTTCA
                                |||||||||   |||    ||||||
                                AAAGAGTTG   GCT    GGAAGT
                                      ATA   TCTA_
GAM2672  IMMP2L   5'  TTTCTCAACCTAGTTAGCC   37184          A   A
                                TTTCTCAACCTG TTA CC
                                |||||||||||| ||| ||
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                                AAAGAGTTGGAT AAT GG
                                      C   C
GAM2672  MME      3'  TTTCATCAGCTCCCAACCCTT  28617      _   AC  GA
                                TTTC TCA  CT  TTAACCCTT
                                |||| |||  ||  |||||||||
                                AAAG AGT  GA  GGTTGGGAA
                                  T   C_  G_
GAM2672  PKIA     3'  TTTCTCCACCTGATTCAGCTT  27749        A       AACC
                                TTTCTC ACCTGATT    CTT
                                ||||||| ||||||||    |||
                                AAAGAG TGGACTAA    GAA
                                   G       GTC_
GAM2672  PPP1R3C  3'  TCAACCTGTTACTTGATCCTTC 23990         A   AC____
              A                  TCAACCTG TTA     CCTTCA
                                ||||||||| |||     ||||||
                                AGTTGGAC AAT     GGAAGT
                                     _   GAACTA
GAM2672  SEL1L    3'  TCTCTTGGTGACTAACTCTTC  22850      AACC       C
                                TCTC    TGATTAAC CTTC
                                ||||    |||||||| ||||
                                AGAG    ACTGATTG GAAG
                                  AACC       A
GAM2672  SYT4     3'  TTCTCAACTCAGCCCTT     41665         CTGA   A
                                TTCTCAAC    TTA CCCTT
                                ||||||||    ||| |||||
                                AAGAGTTG    AGT GGGAA
                                     ____   C
GAM2673  AMFR     3'  GTTTTACAATAAAAACA     10079     A
                                GTT TTACAATAAAAATG
                                ||| ||||||||||||||
                                CAA AATGTTATTTTTGT
                                 _
GAM2673  DNMT2    3'  GTTGCTACAATAAAGAACAACT 20629     A         AAT TG
                                GTT TTACAATAAA   G  ACT
                                ||| ||||||||||   |  |||
                                CAA GATGTTATTT   T  TGA
                                  C         CT_ GT
GAM2673  FACL2    3'  GTTATTACAATGAC        34436          ATAAAAAT
                                GTTATTACA       GTGAC
                                |||||||||       |||||
                                CAATAATGT       TACTG
                                          _________
GAM2673  PVT1     3'  ATTATGGCAATAAAAATGTGGC 42306       TA          A
              T                   GTTAT  CAATAAAAATGTG CT
                                |||||  |||||||||||||| ||
                                TAATA  GTTATTTTTACAC GA
                                   CC           C
GAM2673  SPAG6    3'  CCTTAAATACCTGAAAATGTGA 29701    G   T_   AATA
              CT                   C TTA  TAC    AAAATGTGACT
                                | |||  |||    ||||||||||
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                                G AAT  ATG   TTTTACACTGA
                                 G  TT  GAC_
GAM2674  CAMLG    5'  CGGTGATGTTGGCCGCCGCTGC 11953    CAACA    AT
              G                   CGG    TTGGC  CCGCTGCG
                                  |||    |||||  ||||||||
                                  GCC    AACCG  GGCGACGC
                                    ACTAC    GC
GAM2674  PLA2G5   5'  TCGGAACATTGGTATCCA    9578      C      C
                                  TCGG AACATTGG ATCCG
                                  |||| |||||||| |||||
                                  AGCC TTGTAACC TAGGT
                                    _      A
GAM2674  PTPRJ    3'  TCGGGGCATGTGCCTTCGCTG  15962     CAA   TG  ATC
                                  TCGG   CAT  GC   CGCTG
                                  ||||   |||  ||   |||||
                                  AGCC   GTA  CG   GCGAC
                                    CC_   CA  GAA
GAM2675  CCNT2    3'  TCAAATCACAGTAATCC     38494      CTAAG
                                  TCAAA    ACAGTAATCC
                                  |||||    ||||||||||
                                  AGTTT    TGTCATTAGG
                                     AG___
GAM2675  CTNS     5'  TCTCACAAAACACAGTAATCC  22350      AACT  G
                                  TCTCA    AA ACAGTAATCC
                                  |||||    || ||||||||||
                                  AGAGT    TT TGTCATTAGG
                                     GTT_  G
GAM2675  DMP1     3'  CAAACTAAGTATTGAATCC   20600        ACAGT
                                  CAAACTAAG    AATCC
                                  |||||||||    |||||
                                  GTTTGATTC    TTAGG
                                       ATAAC
GAM2675  EIF4G2   3'  TCTCTCAAAACTGATCAGT   10879        _  AA  _
                                  TCTCTCAAA CT  GA CAGT
                                  ||||||||| ||  || ||||
                                  AGAGAGTTT GA  CT GTCA
                                       T  __  A
GAM2675  EMS1     5'  TCTGTTTAAAACACAGTAATCC 23428    CAAACT  G
                                  TCT     AA ACAGTAATCC
                                  |||     || ||||||||||
                                  AGA     TT TGTCATTAGG
                                    CAAATT  G
GAM2675  FKBP1A   3'  TCTCTCAACTTGGAGAGTAAT  38283       A  AA  C
                                  TCTCTCAA CT  GA AGTAAT
                                  |||||||| ||  || ||||||
                                  AGAGAGTT GA  CT TCATTA
                                       _  AC  C
GAM2675  GALR1    3'  CTTCCACTGTTAAGACAGTGGT 11200    CT  AAC_      AA
              C                   CT  CA   TAAGACAGT  TC
                                  ||  ||   |||||||||  ||
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                                GA  GT    ATTCTGTCA  AG
                                 AG  GACA        CC
GAM2675  MADH5    3'  TCTCTAAAATTAAAACAAGTCC 25357       C   C       TAA
                                TCTCT AAA TAAGACAG   TCC
                                ||||| ||| ||||||||   |||
                                AGAGA TTT ATTTTGTT   AGG
                                   T   A       C__
GAM2675  MSL3L1   3'  TCTTTCAAACAAGACAG     38603     C     T
                                TCT TCAAAC AAGACAG
                                ||| |||||| |||||||
                                AGA AGTTTG TTCTGTC
                                  A     _
GAM2675  MTL5     3'  TCTAGACTAAGACAAAATC    22272     CAA        T
                                TCT   ACTAAGACAG AATC
                                |||   |||||||||| ||||
                                AGA   TGATTCTGTT TTAG
                                  TC_         _
GAM2675  PPIG     3'  TCTCTCAAACTTAAAATC     21992           A   CAGTA
                                TCTCTCAAACT AGA     ATC
                                |||||||||| |||     |||
                                AGAGAGTTTGA TTT     TAG
                                      A  _____
GAM2675  RFXAP    3'  TCTTCAAACTCACAGTAATC   8056      C      AAG
                                TCT TCAAACT   ACAGTAATC
                                ||| |||||||   |||||||||
                                AGA AGTTTGA   TGTCATTAG
                                  _      G__
GAM2676  RYR3     3'  GGAAGTTGACTGTCCAGAATTG 9773            CAA  TC
                                GGAGGTTGACTG   CC  AATTG
                                ||||||||||||   ||  |||||
                                CCTTCAACTGAC   GG  TTAAC
                                      A__  TC
GAM2677  ACP2     3'  CATCTGGCTGGGGT        11505          AAGAT   A
                                TATCTGGCT    GGG GT
                                |||||||||    ||| ||
                                GTAGACCGA    CCC CA
                                     _____   _
GAM2677  ADRBK1   3'  TCAGGGAAGTGGGAGTG     11540    T  CT   A
                                TC GG  AAG TGGGAGTG
                                || ||  ||| ||||||||
                                AG CC  TTC ACCCTCAC
                                 T  C_   _
GAM2677  ATP2B4   5'  TCTGGCTAAGGCCGGGGAGTG  43201          AT__
                                TCTGGCTAAG    GGGAGTG
                                ||||||||||    |||||||
                                AGACCGATTC    CCCTCAC
                                      CGGC
GAM2677  CACNA1S  3'  TCCTGCAGGTGGGAGTG     6304      G  TA  A
                                TCT GC  AG TGGGAGTG
                                ||| ||  || ||||||||
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                                AGG CG  TC ACCCTCAC
                                  A  __  C
GAM2677  CELL    3'  TCGGGGGAGATGGGAGTG    12230    T  CTA
                                TC GG   AGATGGGAGTG
                                || ||   ||||||||||
                                AG CC   TCTACCCTCAC
                                 C  CC_
GAM2677  DDEF2   3'  TATCTGGCAAGAGT       19325        TAAGAT
                                TATCTGGC     GGGAGT
                                ||||||||     ||||||
                                ATAGACCG     TTCTCA
                                   _______
GAM2677  DGKB    3'  TCATAAAGATGGGAGTG     45212    TGGCT
                                TC     AAGATGGGAGTG
                                ||     ||||||||||||
                                AG     TTCTACCCTCAC
                                 TAT__
GAM2677  HPS4    3'  TACCTGCGGCGTGGGAGTG   35217      __  TAAGA
                                TATCT  GGC    TGGGAGTG
                                |||||  |||    ||||||||
                                ATGGA  CCG    ACCCTCAC
                                   CG   C____
GAM2677  ICAM1   3'  TATCTGACTGAGGACAATG   43434        AA  T  G
                                TATCTGGCT  GA GG AGTG
                                |||||||||  || || ||||
                                ATAGACTGA  CT CT TTAC
                                     __  C  G
GAM2677  ITPR3   3'  TCTGGCAGAGTGGGAGTG    13692       TA  A
                                TCTGGC  AG TGGGAGTG
                                ||||||  || ||||||||
                                AGACCG  TC ACCCTCAC
                                   TC  _
GAM2677  KCNK3   3'  CATCTGTAAAATGGGAGTG   13898       GC
                                TATCTG  TAAGATGGGAGTG
                                ||||||  ||||||||||||
                                GTAGAC  ATTTTACCCTCAC
                                   __
GAM2677  MAML1   3'  CATCTGACATGGGAGTG     31278        TAAG
                                TATCTGGC   ATGGGAGTG
                                ||||||||   |||||||||
                                GTAGACTG   TACCCTCAC
                                   _____
GAM2677  MCL1    3'  TCTGGCTAGGTTGCTAGGGTG  35002        AGA___   A
                                TCTGGCTA     TGGG GTG
                                ||||||||     |||| |||
                                AGACCGAT     ATCC CAC
                                     CCAACG   _
GAM2677  NR1I2   3'  TCTTGGCCCGGGAGTG      35109    _   AAGA
                                TCT GGCT   TGGGAGTG
                                ||| ||||   ||||||||
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                                AGA CCGG   GCCCTCAC
                                  A  ____
GAM2677 EHHADH   3' TCATTAGCTATTATGGT    12684   CC       AA
                                TC  TAGCTATTAT  GGT
                                ||  ||||||||||  |||
                                AG  ATCGATAATA  CCA
                                 TA       __
GAM2677 LECT2    5' CCTAGCTATTTAGCC      14128         ATAA
                                CCTAGCTATT   GGTT
                                ||||||||||   ||||
                                GGATCGATAA   TCGG
                                      A___
GAM2678 CDYL     3' GGGTAAGAACTGGACGTATTT 22087    C      AC  _
                                GGG AAGAATTG  CG ATTT
                                ||| ||||||||  || ||||
                                CCC TTCTTGAC  GC TAAA
                                  A       CT  A
GAM2678 EXTL2    5' GGGCCAGCCGATTTAT     11020     A  AATTGA
                                GGGC AG     CCGATTTAT
                                |||| ||     |||||||||
                                CCCG TC     GGCTAAATA
                                  G _______
GAM2678 IGFBP5   5' GGGAGAGAAAAATGGATTTATC 8273     CA    TTGACC
           T                     GGG  AGAA     GATTTATCT
                                |||  ||||     |||||||||
                                CCC  TCTT     CTAAATAGA
                                  TC    TTTAC_
GAM2678 AXL      3' GGTGGGATAGGTAGGAAG    34887      A   CC  C
                                GGTGG GGT  GG AGGAAG
                                ||||| |||  || ||||||
                                CCACC CTA  CC TCCTTC
                                   _  T_  A
GAM2678 C1QG     3' GGTGGGTCCATGCAGGAAG   41691      AG    _
                                GGTGG  GTCCG GCAGGAAG
                                |||||  ||||| ||||||||
                                CCACC  CAGGT CGTCCTTC
                                   __     A
GAM2678 CFL1     3' CAGCCCCTCCGGTCTGGCAGGA 24284     GGA___    C
           AG                     CGGT     GGTC GGCAGGAAG
                                ||||     |||| |||||||||
                                GTCG     CCAG CCGTCCTTC
                                  GGGAGG    A
GAM2678 CIT      3' ACGCTGGGGGGGTGGGGAAG   43036    G   A  TCC  CA
                                ACG TGG GG   GG  GGAAG
                                ||| ||| ||   ||  |||||
                                TGC ACC CC   CC  CCTTC
                                  G   _  CCA  __
GAM2678 DAPK1    3' GGCTGTGGGTGCAGGAA     22359    _  GA   CCG
                                GG TG  GGT   GCAGGAA
                                || ||  |||   |||||||
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                                CC AC  CCA   CGTCCTT
                                 G  AC   ___
GAM2678  DBP      3'  TAACGGAGGCGGTGGGAGG   10667       T  A   CC  C
                                TAACGG GG GGT  GG AGG
                                |||||| || |||  || |||
                                ATTGCC CC CCA  CC TCC
                                   T  G   __  C
GAM2678  FGFR1    3'  ACGGTGGAGTCTGGGGA     31926         G  C  CA
                                ACGGTGGAG TC GG  GGA
                                ||||||||| || ||  |||
                                TGCCACCTC AG CC  CCT
                                     _  A  __
GAM2678  GSTM5    3'  GATGGAGGACAGTGGGGA    9206         TC   CA_
                                GGTGGAGG  CGG   GGA
                                ||||||||  |||   |||
                                CTACCTCC  GTC   CCT
                                     T_   ACC
GAM2678  HLCS     3'  GGTGGGGGTGGGGACAGGAAG  7645        A   CC_
                                GGTGG GGT   GGCAGGAAG
                                |||||| |||   |||||||||
                                CCACC CCA   CTGTCCTTC
                                   C   CCC
GAM2678  HMGA2    5'  CGGTGGAGGTGGAGG       18510         CC  C
                                CGGTGGAGGT  GG AGG
                                ||||||||||  || |||
                                GCCACCTCCA  CC TCC
                                     __  _
GAM2678  HMGA2    5'  GGTGGAGGTAGCAAGA      18527         CC
                                GGTGGAGGT  GGCAGGA
                                |||||||||  |||||||
                                CCACCTCCA  TCGTTCT
                                     __
GAM2678  HOXB9    3'  GGTGGGAGGTGGGGA       35845       _   CC  CA
                                GGTGG AGGT  GG  GGA
                                ||||| ||||  ||  |||
                                CCACC TCCA  CC  CCT
                                   C   __  __
GAM2678  KCNK2    3'  GGTGGGGGGCAGGGAA      30566       A  TCCG   _
                                GGTGG GG    GCAGG AA
                                ||||| ||    ||||| ||
                                CCACC CC    CGTCC TT
                                     _ ____    C
GAM2678  LMO1     3'  CGGTGGTGGAGGAGGA      14180        A  TCC  C
                                CGGTGG GG   GG AGGA
                                |||||| ||   || ||||
                                GCCACC CC   CC TCCT
                                   A  T__  _
GAM2678  MAZ      5'  CGGCGGAGGCGGGGGG      43850         TC   CA
                                CGGTGGAGG  CGG  GG
                                |||||||||  |||  ||
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                                GCCGCCTCC  GCC  CC
                                     __  CC
GAM2678  NHLH1    3'  GGTGGAGGGAGTTGAGGAAG  24655       TCCGGC
                                GGTGGAGG    AGGAAG
                                ||||||||    ||||||
                                CCACCTCC    TCCTTC
                                    CTCAAC
GAM2678  NTSR1    3'  GGCAAAGTTTGGCAGGAAG   14885   TG  GTCC
                                GG  GAG   GGCAGGAAG
                                ||  |||   |||||||||
                                CC  TTC   CCGTCCTTC
                                 GT  AAA_
GAM2678  PIN1     3'  ACGGTGGCAGGGAGTGGGGGG  26320      _  TCC_  CA
                                ACGGTGG AGG   GG  GG
                                |||||||  |||   ||  ||
                                TGCCACC TCC   CC  CC
                                    G  CTCA  CC
GAM2678  PMCHL1   3'  GATGGAGGTAAACCAAGGA   36669       ___  GC
                                GGTGGAGGT  CCG  AGGA
                                |||||||||  |||  ||||
                                CTACCTCCA  GGT  TCCT
                                     TTT  __
GAM2678  PSMB2    3'  AATGGAGGGCGGAGCAGGAAG  15816      TCC_
                                GGTGGAGG   GGCAGGAAG
                                ||||||||   |||||||||
                                TTACCTCC   TCGTCCTTC
                                    CGCC
GAM2678  PSMC4    3'  GGTGGAGGGAAGGGAA     27104       TCC  CA
                                GGTGGAGG  GG  GGAA
                                ||||||||  ||  ||||
                                CCACCTCC  CT  CCTT
                                    ___  TC
GAM2678  RIMS1    5'  AGCGGCGGCGGCAGGA     43727      A  TC
                                GGTGG GG  CGGCAGGA
                                |||||  ||  ||||||||
                                TCGCC CC  GCCGTCCT
                                   G  __
GAM2678  RXRA     3'  ACGGTGGATCGGGCAGG     16407       GG  C
                                ACGGTGGA  TC GGCAGG
                                ||||||||  || ||||||
                                TGCCACCT  AG CCGTCC
                                    __  C
GAM2678  SNAI2    5'  GATAACGGTCCGGCGGGA    16881      A      A
                                GGTGG GGTCCGGC GGA
                                |||||  |||||||| |||
                                CTATT CCAGGCCG CCT
                                   G       C
GAM2678  SP4      5'  GGTGGGGGCGAGGCGGGA    17051      A  CC  A
                                GGTGG GGT  GGC GGA
                                |||||  |||  ||| |||
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                                CCACC CCG  CCG CCT
                                  C   CT   C
GAM2678  TAF4     3'  ATGGCTTGTTTGGCAGGAAG   17258      AG_  CC
                                GTGG   GT  GGCAGGAAG
                                ||||   ||  |||||||||
                                TACC   CA  CCGTCCTTC
                                  GAA  AA
GAM2678  TCF3     3'  TAACGGTGGGAGTCTCAGGA   43328         AG   CGG
                                TAACGGTGG  GTC   CAGGA
                                |||||||||  |||   |||||
                                ATTGCCACC  CAG   GTCCT
                                     CT   A__
GAM2678  TEM8     3'  GGTGGAGTAGAGGCAGGAAG   38187        GTCC
                                GGTGGAG    GGCAGGAAG
                                |||||||    |||||||||
                                CCACCTC    CCGTCCTTC
                                    ATCT
GAM2678  VAPB     5'  CGGCGGAGCACCTTTGGCGGGG 21873         GT  ___   A_
              A                  CGGTGGAG  CC   GGC  GGA
                                |||||||| ||   |||  |||
                                GCCGCCTC  GG   CCG  CCT
                                    GT  AAA   CC
GAM2679  ADH5     3'  GTCTTAGGTAACACGCAG    8583      GT_   T
                                GTC   GGT GACACGCAG
                                |||   ||| |||||||||
                                CAG   CCA TTGTGCGTC
                                  AAT  _
GAM2679  CRAT     5'  GTCCGCGGACACGCAG      19667     _    TTG
                                GTC GTGG   ACACGCAG
                                ||| ||||   ||||||||
                                CAG CGCC   TGTGCGTC
                                  G   ___
GAM2679  DCLRE1C  3'  GTCATGGCTCACTGCAG     35417         G  AC
                                GTCGTGGTT AC  GCAG
                                ||||||||| ||  ||||
                                CAGTACCGA TG  CGTC
                                     G  A_
GAM2679  IDH3G    5'  GTCCCGACACGCAG        19979     GTGG
                                GTC    TTGACACGCAG
                                |||    ||||||||||
                                CAG    GGCTGTGCGTC
                                       _____
GAM2679  IFNA2    3'  GTCATGGTCATAGCAG      8294          ACAC
                                GTCGTGGTTG   GCAG
                                ||||||||||   ||||
                                CAGTACCAGT   CGTC
                                     AT__
GAM2679  KCNK6    3'  GTCATGGTTAAGGGCAG     22084          CAC
                                GTCGTGGTTGA  GCAG
                                ||||||||||   ||||
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                                CAGTACCAATT  CGTC
                                     CC_
GAM2679  MAN2A2   3'  GCCTTCAGTGACACGCAG    25951    GT_  T
                                GTC  GGT GACACGCAG
                                |||  ||| |||||||||
                                CGG  TCA CTGTGCGTC
                                  AAG  _
GAM2679  MYD88    3'  GTCGTGGTCACAGCAG     14719       G  C
                                GTCGTGGTT ACA GCAG
                                ||||||||| ||| ||||
                                CAGCACCAG TGT CGTC
                                      _  _
GAM2679  NMI      3'  GTAGTTGAAAACATGCAG   21721       ___  C
                                GTGGTTGA  CA GCAG
                                ||||||||  || ||||
                                CATCAACT  GT CGTC
                                     TTT  A
GAM2679  P4HB     3'  GTCATGGCGACACTGCAG   9549        T   _
                                GTCGTGGT GACAC GCAG
                                |||||||| ||||| ||||
                                CAGTACCG CTGTG CGTC
                                     _    A
GAM2679  PMM2     3'  ATCAAGGTGACATGCAG    43549     T  T  C
                                GTCG GGT GACA GCAG
                                |||| ||| |||| ||||
                                TAGT CCA CTGT CGTC
                                  T  _   A
GAM2679  PRY      3'  ATCGTGGTTCCACTCAG    41255       GA  G
                                GTCGTGGTT  CAC CAG
                                |||||||||  ||| |||
                                TAGCACCAA  GTG GTC
                                     G_  A
GAM2679  RASD1    5'  GTCGCTGGGGTGGCACGC   32013     __  T  A
                                GTCGT  GG TG CACGC
                                |||||  || || |||||
                                CAGCG  CC AC GTGCG
                                   AC  C  C
GAM2679  RNMT     3'  ATCGTGGTGAGGTGCAG    19147       T  CAC
                                GTCGTGGT GA  GCAG
                                |||||||| ||  ||||
                                TAGCACCA CT  CGTC
                                     _ CCA
GAM2679  SOX11    3'  GTCGTGGTGATTTTGCAG   17034       T  CAC_
                                GTCGTGGT GA   GCAG
                                |||||||| ||   ||||
                                CAGCACCA CT   CGTC
                                     _ AAAA
GAM2679  SYNGR1   3'  GTCTGTGGGACACGCAG    21768    _   TT
                                GTC GTGG  GACACGCAG
                                ||| ||||  |||||||||
```

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                                CAG CACC  CTGTGCGTC
                                  A   __
GAM2679  ZNF140   3'  GTCCTGGTTGACAGATGC    18342     G       C__
                                GTC TGGTTGACA   GC
                                ||| |||||||||   ||
                                CAG ACCAACTGT   CG
                                  G        CTA
GAM2679  ATP1B1   3'  TCAAGACTAGTAGG       11734          C  AATC
                                TCAAGACTAG TG    GG
                                |||||||||| ||    ||
                                AGTTCTGATC AT    CC
                                      _ _____
GAM2680  GUCY1A3  5'  TCAGGCAGCTCAGGCGACAGGG 41838      A       AG   GA
             TG                   TTAG CAGCTCAG  GAT  GGTG
                                |||| ||||||||  |||  ||||
                                AGTC GTCGAGTC  CTG  CCAC
                                  C       CG   TC
GAM2680  UNRIP    3'  TTAGATGTTCAGAGGCAGT   28425      CAGC      ATGA
                                TTAGA    TCAGAGG    GGT
                                |||||    |||||||    |||
                                AATCT    AGTCTCC    TCA
                                   ACA_      G___
GAM2680  ATM      3'  CTCGAACTCCTGACCTTGT   39633    G  TC       C
                                CT GA  CTCCTGACC TGT
                                || ||  ||||||||| |||
                                GA CT  GAGGACTGG ACA
                                 G  T_       A
GAM2680  BAZ2A    5'  TGGATCCTCCCAAACTGT    30316          TG CC
                                TGGATCCTCC  A  CTGT
                                ||||||||||  |  ||||
                                ACCTAGGAGG  T  GACA
                                      GT T_
GAM2680  CDK10    5'  GCTGGATCCTCTGCTTGT    38149           C  ACCC
                                GCTGGATCCTC TG    TGT
                                |||||||||| ||    |||
                                CGACCTAGGAG AC    ACA
                                      _  GA__
GAM2680  EGFL5    3'  CTCGAACTCCTGACCTTGT   44523    G  TC       C
                                CT GA  CTCCTGACC TGT
                                || ||  ||||||||| |||
                                GA CT  GAGGACTGG ACA
                                 G  T_       A
GAM2680  FANCD2   3'  CTTGAACTCCTGACCTTGT   37512    G  TC       C
                                CT GA  CTCCTGACC TGT
                                || ||  ||||||||| |||
                                GA CT  GAGGACTGG ACA
                                 A  T_       A
GAM2680  FUT6     3'  GGTCTCGATCTCCTGACCTTGT 6654    AG  G   C      C
                                G  CT GATC TCCTGACC TGT
                                |  || |||| |||||||| |||
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                                C  GA CTAG AGGACTGG ACA
                                 CA  G   _      A
GAM2680  IAPP     3'  CTCGAACTCCTGACCTTGT   7663     G  TC       C
                                CT GA  CTCCTGACC TGT
                                || ||  ||||||||| |||
                                GA CT  GAGGACTGG ACA
                                 G  T_       A
GAM2680  KCNA6    3'  AGACATTCCTCCTGGCTCTGT  13805     ___      ACC
                                GGA   TCCTCCTG   CTGT
                                |||   ||||||||   ||||
                                TCT   AGGAGGAC   GACA
                                  GTA       CGA
GAM2680  LUZP1    3'  CTTGAACTCCTGACCTTGT   37959    G  TC       C
                                CT GA  CTCCTGACC TGT
                                || ||  ||||||||| |||
                                GA CT  GAGGACTGG ACA
                                 A  T_       A
GAM2680  RAD50    3'  GAGCAGGCCTTGACTCTGT   39436     T  AT   CC   C
                                GAGC GG  CCT  TGAC CTGT
                                |||| ||  |||  |||| ||||
                                CTCG CC  GGA  ACTG GACA
                                  T __  __   A
GAM2680  RXRA     3'  GCTGGGGCCCGAAGACCCTGTA 16428      AT   CCT
                                GCTGG  CCT   GACCCTGTA
                                |||||  |||   |||||||||
                                CGACC  GGG   CTGGGACAT
                                   CC   CTT
GAM2680  SLC1A4   3'  GGCTGGGTCAACTCTGT    16750   A    A  CTCCT   C
                                G GCTGG TC    GAC CTGT
                                | ||||| ||    ||| ||||
                                C CGACC AG    TTG GACA
                                 _    C _____   A
GAM2680  UBE2G2   3'  GGTCTCAATTTCCTGACCTTGT 42124   AG  G   CC      C
                                G  CT GAT  TCCTGACC TGT
                                |  || |||  |||||||| |||
                                C  GA TTA  AGGACTGG ACA
                                 CA  G   A_       A
GAM2681  COL1A1   3'  CTGAGGGTGGGGGCCACTTGGG 6373     A      T  TG___
             T                   CT AGGGTGGG GT     GGGT
                                || |||||||| ||     ||||
                                GA TCCCACCC CG     CCCA
                                 C       C  GTGAA
GAM2681  DES      3'  CTGAGGCTGGGTGTGGTGT   43564    A   G      T  G
                                CT AGG TGGGTGT GG GT
                                || ||| ||||||| || ||
                                GA TCC ACCCACA CC CA
                                 C   G      _ A
GAM2681  EEF1A1   3'  TAAGAGTGGGGTGGCAGGTAT  10822          T  T  __
                                TAAGGGTGGG GT GG  GGTAT
                                |||||||||| || ||  |||||
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                                ATTCTCACCC CA CC  CCATA
                                      _ _ GT
GAM2681  JAM2     5'  GGGTGGGGGGATTGGGTGT   34550       T__     _
                                GGGTGGG   GTTGGG GT
                                |||||||   |||||| ||
                                CCCACCC   TAACCC CA
                                    CCC     A
GAM2681  KIF2     3'  CTAGGAGTGGGCAAGGTAT   21134     A      GTT
                                CTA GGGTGGGT   GGGGTAT
                                ||| ||||||||   |||||||
                                GAT CTCACCCG   TTCCATA
                                  C      ___
GAM2681  LASS1    3'  CTGAGGGCGGGGCCGGTGT   34605    A      T    G
                                CT AGGGTGGG GTTGG GT
                                || |||||||| ||||| ||
                                GA TCCCGCCC CGGCC CA
                                 C      _    A
GAM2681  PMM2     3'  GGGTGGGTGAGCAC       43555         TTGG
                                GGGTGGGTG    GGTAT
                                |||||||||    |||||
                                CCCACCCAC    TCGTG
                                      _____
GAM2681  SLC7A8   3'  GGGTGGGTGCAGGTAT     29294          TG
                                GGGTGGGTGT  GGGTAT
                                ||||||||||  ||||||
                                CCCACCCACG  TCCATA
                                      __
GAM2681  ADD2     5'  GTTTTGTTATTTTATGGG    32732     C        G
                                GTTT TGTTATTTTA GGG
                                |||| |||||||||| |||
                                CAAA ACAATAAAAT CCC
                                  _        A
GAM2681  CLECSF11 3'  TGCTGAAACATTTTAGGGGCAT 39044      TCTGT
            T                    TGTT    TATTTTAGGGGCATT
                                ||||    ||||||||||||||||
                                ACGA    GTAAAATCCCCGTAA
                                  CTTT_
GAM2681  IMMP2L   3'  TCTGCATATTTTGGGGGCATT  37182      _     A
                                TCTGT TATTTT GGGGCATT
                                ||||| |||||| ||||||||
                                AGACG ATAAAA CCCCGTAA
                                   T     C
GAM2681  STK24    3'  TGTTCTGTAAGAGAGGGGCATT 18710     T    TATTTT
                                TGTT CTGT     AGGGGCATT
                                |||| ||||     |||||||||
                                ACAA GACA     TCCCCGTAA
                                  _   TTCTC_
GAM2682  CPD      3'  TAAAGCTTTATGTCGATTCTGA 10559        CAAATTCA_
            C                    TAAAGCTT       TCTGAC
                                ||||||||       ||||||
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                                ATTTCGAA       AGACTG
                                     ATACAGCTA
GAM2682 MBP     3' TAAAGCTTTGATTCATAGAC  44892       CAA     CT
                                TAAAGCTT  ATTCAT  GAC
                                ||||||||  ||||||  |||
                                ATTTCGAA  TAAGTA  CTG
                                     AC_     T_
GAM2682 MS4A4A   5' TAAAGCTCCAAGTATATTTGAC 35851          ATTC  C
                                TAAAGCTTCAA   AT TGAC
                                ||||||||||    || ||||
                                ATTTCGAGGTT   TA ACTG
                                      CATA  A
GAM2682 NKX3A   3' AAACTTCAAGTCACAGAC   26108        AT   CT
                                AAGCTTCAA  TCAT  GAC
                                |||||||||  ||||  |||
                                TTTGAAGTT  AGTG  CTG
                                     C_   T_
GAM2682 TIMELESS 3' TAAAGCTCCCCATCTG     19397        AAAT
                                TAAAGCTTC   TCATCTG
                                |||||||||   |||||||
                                ATTTCGAGG   GGTAGAC
                                      ____
GAM2682 ATP6V1E1 3' TGGAGGTGGGTCCTGATCA   11788   A  G  C  A
                                TG AGG GGG CCT ATCA
                                || ||| ||| ||| ||||
                                AC TCC CCC GGA TAGT
                                 C  A  A  C
GAM2682 MAN2A1   5' GAAGGGGGGCCCCCACAAACTT 14333          A  C
                                GAAGGGGGGCCCT AT AACTT
                                |||||||||||| || |||||
                                CTTCCCCCCGGGG TG TTGAA
                                       G  T
GAM2682 MUCDHL   3' TGGAGGGGGGCTCCTGTTCGGA 34948    A     _  AA ___
           AACTT                TG AGGGGGGC CCT  TC   AACTT
                                || ||||||| |||  ||  |||||
                                AC TCCCCCCG GGA  AG   TTGAA
                                 C      A  CA  CCT
GAM2683 APTX    5' TTCGCTGGTGCCGGCTGTCCTG 32812    A   ATATATTG
           T                    TTC CTGG      TGTCCTGT
                                |||  ||||      ||||||||
                                AAG GACC      ACAGGACA
                                  C   ACGGCCG_
GAM2683 GPLD1   3' TCCACTGGATGTGCCACT   45116        TATAT    _
                                TTCACTGGA    TGTGTC CT
                                |||||||||    |||||| ||
                                AGGTGACCT    ACACGG GA
                                      _____     T
GAM2683 NCOA6IP  3' TTCACTGATATTTAAGTCCTGT 36055       G   A  T
                                TTCACTG ATAT TTG GTCCTGT
                                ||||||| |||| ||| |||||||
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                                AAGTGAC TATA AAT CAGGACA
                                   _  _  T
GAM2683  EPB72    3'  GTACAGGGAAGGACATCCAT  19901     CA   CA
                                GTGCA  GGAA  GACATCCAT
                                |||||  ||||  |||||||||
                                CATGT  CCTT  CTGTAGGTA
                                  C_   C_
GAM2683  EPHB4    3'  TGCGGGAACGCACCCATCA  20792    ACA   AGA
                                TGC  GGAAC  CATCCATCA
                                |||  |||||  |||||||||
                                ACG  CCTTG  GTGGGTAGT
                                  C__    C__
GAM2683  PYGO2    3'  GTGTTAGGGGCATCCATC   41953    CAC  AACAGA
                                GTG  AGG    CATCCATC
                                |||  |||    ||||||||
                                CAC  TCC    GTAGGTAG
                                  AA_  CC____
GAM2683  SOCS5    3'  GCATAGGAACAGATCCA    30422    C      CA
                                GCA AGGAACAGA  TCCA
                                ||| |||||||||  ||||
                                CGT TCCTTGTCT  AGGT
                                  A      __
GAM2683  TLR5     5'  GTGCCAGGAACATGAACATC  17569    A      __
                                GTGC CAGGAACA  GACATC
                                |||| ||||||||  ||||||
                                CACG GTCCTTGT  TTGTAG
                                  _      AC
GAM2684  STMN2    3'  GCAGGGGGATTTACTATT   45407     TGTTA
                                GCAGG    GATTTACTATT
                                |||||    ||||||||||
                                CGTCC    CTAAATGATAA
                                  CC___
GAM2684  NRXN1    3'  AGACTATTTCTATACAA    39836    C    CC
                                AG ACTAT  CTATACAA
                                || |||||  ||||||||
                                TC TGATA  GATATGTT
                                 _    AA
GAM2684  PLCD1    3'  AGCCCTGTCCCCACATGTGGAC 26342    A  A      CAATA
           A                     AGC CT TCCCTATA    GACA
                                |||  || ||||||||    ||||
                                TCG GA AGGGGTGT    CTGT
                                  G  C       ACAC_
GAM2685  SOX12    3'  GGATCGCTCTACACTCGCCCCC 28045    CCACA      A
                                GGA    CTACACTC TTTTT
                                |||    |||||||| |||||
                                CCT    GATGTGAG GGGGG
                                  AGCGA      C
GAM2685  VIPR2    3'  GGAACAAGACATTCATTTTTAA 18019    CC   CT   C
                                GGA  ACA  ACA TCATTTTTAA
                                |||  |||  ||| ||||||||||
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                                CCT  TGT  TGT AGTAAAAATT
                                  __  TC   A
GAM2685  ACTN2    3'  TCTGATGGGATGAGTGA     9952          T  A
                                TTTGATGGGATG AG TGG
                                |||||||||||| || |||
                                AGACTACCCTAC TC ACT
                                      _  _
GAM2685  CLCA2    3'  TTTGATGGGAGTAGAAAC    27226         T    T
                                TTTGATGGGA GTAGA GGC
                                |||||||||| ||||| |||
                                AAACTACCCT CATCT TTG
                                      _    _
GAM2685  NDST1    3'  TGGTGGGATGTCCTAGC     11374    A      AGA
                                TG TGGGATGT   TGGC
                                || ||||||||   ||||
                                AC ACCCTACA   ATCG
                                 C       GG_
GAM2685  RAB30    5'  TTTGATGGGTGTGTACAGC    30937         A   AG
                                TTTGATGGG TGT  ATGGC
                                ||||||||| |||  |||||
                                AAACTACCC ACA  TGTCG
                                     _  CA
GAM2686  ALDH2    3'  TTTCTTGGTTTTGTTGC     40689          CTTAT
                                TTTCTTGGTTT    TTGT
                                ||||||||||    ||||
                                AAAGAACCAAA    AACG
                                      AC___
GAM2686  DNASE1   5'  TTTCTTGGTTCTTTTGT     23361         T   AT
                                TTTCTTGGTT CTT  TTGT
                                |||||||||| |||  ||||
                                AAAGAACCAA GAA  AACA
                                      _  __
GAM2686  KRT10    3'  TTTCTTGGTTTCTGATTCA   7681           T
                                TTTCTTGGTTTCT ATTTG
                                |||||||||||| |||||
                                AAAGAACCAAAGA TAAGT
                                       C
GAM2686  TNC      3'  TTTCTGGTTTCTGTTGTAT   13475      T     TAT
                                TTTCT GGTTTCT   TTGTAT
                                ||||| |||||||   ||||||
                                AAAGA CCAAAGA   AACATA
                                   _      C__
GAM2686  IRTA2    3'  GTGATGGATATCATAAAAGCG  36346    A    C      TA
                                GT ATGGA ATCATAGG  CG
                                || ||||| ||||||||  ||
                                CA TACCT TAGTATTT  GC
                                 C    A       TC
GAM2686  RNASE4   3'  GTAGTGACATCATTATAAGT   16345    ATG     ___
                                GTA   GACATCA   TAGGT
                                |||   |||||||   |||||
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                                CAT   CTGTAGT   ATTCA
                                  CA_      AAT
GAM2687  APAF1    3'  TATAATACAAAAAAATACA   29827          CAAGC
                                TATAATGCAAAA    AATACA
                                ||||||||||||    ||||||
                                ATATTATGTTTT    TTATGT
                                       T____
GAM2687  CSF2RB   3'  ATAATGCAGAACCTACAA    7567        A   AA
                                ATAATGCA AAC  GCAA
                                |||||||| |||  ||||
                                TATTACGT TTG  TGTT
                                     C   GA
GAM2687  E2F3     3'  TAATGCAAACAAAATACA    12629        A   GC
                                TAATGCAAA CAA  AATACA
                                ||||||||| |||  ||||||
                                ATTACGTTT GTT  TTATGT
                                       _  __
GAM2687  KLHL1    3'  TATAATACAAAACAAATTAC  34082            CAA
                                TATAATGCAAAACAAG   TAC
                                ||||||||||||||||   |||
                                ATATTATGTTTTGTTT   ATG
                                          A__
GAM2687  LIG4     5'  ACGCAGGTAAAGCAGGCAATAC 14163      ___  _  A
              A                  ATGCA   AAA CA GCAATACA
                                 |||||   ||| || ||||||||
                                 TGCGT   TTT GT CGTTATGT
                                    CCA   C  C
GAM2687  PSAP     3'  TAGTGCAAAACAAAAATCAC  42970    A        CAA
                                TA TGCAAAACAAG   TAC
                                || ||||||||||   |||
                                AT ACGTTTTGTTT   GTG
                                  C         TTA
GAM2687  PUM2     3'  TATAAGCAAAACAAAATACAA  31665      T       GC
                                TATAA GCAAAACAA  AATACAA
                                ||||| |||||||||  |||||||
                                ATATT CGTTTTGTT  TTATGTT
                                       _      __
GAM2687  EPHA3    3'  TTTGCAGCATTATTTTATCC  23447       T      AAA
                                TTTGCAG CATTATT   GTCT
                                ||||||| |||||||   ||||
                                AAACGTC GTAATAA   TAGG
                                    _      AA_
GAM2688  ECM1     5'  TCAGGCAAGTCTGGATG     20695       _ _  CTCGCCA
                                TCAGGCA G CTG      GATG
                                ||||||| | |||      ||||
                                AGTCCGT C GAC      CTAC
                                    T A  ________
GAM2688  KIF3C    3'  TCAGGGGCTGCTCGCCA     13957      CA
                                TCAGG  GCTGCTCGCCA
                                |||||  ||||||||||
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                                AGTCC  CGACGAGCGGT
                                  C_
GAM2688  MFI2     3'  TCAGGAGGCTGAGATG     25471      CA   CTCGCC
                                TCAGG  GCTG     AGATG
                                |||||  ||||     |||||
                                AGTCC  CGAC     TCTAC
                                  TC   _______
GAM2688  MIC2     3'  TCAGGCAGCTGTTCTAACC   14509          C __
                                TCAGGCAGCTG TC  GCC
                                |||||||||||  ||  |||
                                AGTCCGTCGAC AG  TGG
                                      A  AT
GAM2688  MYOZ1    5'  TCAGCCGGCTGCTCGGGCAG  34556      G A_      C_
                                TCAG C  GCTGCTCG  CAG
                                ||||  |  ||||||||  |||
                                AGTC G  CGACGAGC  GTC
                                  _ GC       CC
GAM2688  SCNN1G   3'  TCAGGTGGCCAGATG      9792       CAGC  CTC
                                TCAGG   TG   GCCAGATG
                                |||||   ||   ||||||||
                                AGTCC   AC   CGGTCTAC
                                  _____ ____
GAM2688  VENTX2   3'  CCAGGTAGGAGCCAGGTGCG  30913      C  CTGCTC    A
                                TCAGG AG     GCCAG TGCG
                                ||||| ||     ||||| ||||
                                GGTCC TC     CGGTC ACGC
                                  A  CT_____    C
GAM2688  BRCA1    3'  TAAGTTATCTGAAATCAGATA  28639        G  CC
                                TGAGTTAT TG  AAATCAGATA
                                ||||||||  ||  ||||||||||
                                ATTCAATA AC  TTTAGTCTAT
                                     G  __
GAM2688  ITPR1    3'  TGGTTCAAGTGCAAATCAG   13670    A   AT_   C
                                TG GTT   GTGC AAATCAG
                                || |||   ||||  |||||||
                                AC CAA   CACG TTTAGTC
                                 _   GTT   _
GAM2689  AASS     3'  AACAAAATATAATTCCC     25096       GTATC
                                AACAAAA    TATAATTCCC
                                |||||||    ||||||||||
                                TTGTTTT    ATATTAAGGG
                                  _____
GAM2689  ATRX     3'  ACAAAAGTATTTCATAACT   39600         C_
                                ACAAAAGTAT  TATAATT
                                ||||||||||  |||||||
                                TGTTTTCATA  GTATTGA
                                      AA
GAM2689  CELSR1   3'  AAAAGTATCTCCACCTTTCCCA 30647          ATAA__
                                AAAAGTATCT     TTCCCA
                                ||||||||||     ||||||
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                                TTTTCATAGA     AAGGGT
                                      GGTGGA
GAM2689  CMAR     3'  AAAGTATCTCAACAATTCTCA  23290         __      C
                                AAAGTATCT  ATAATTC CA
                                |||||||||  |||||||  ||
                                TTTCATAGA  TGTTAAG GT
                                     GT       A
GAM2689  GCH1     3'  CAAAAGTATCTACACTC      6700             A
                                CAAAAGTATCTATA TTC
                                |||||||||||||| |||
                                GTTTTCATAGATGT GAG
                                          _
GAM2689  HCS      3'  CAAAAGCACCATTCCC       33220          TATA
                                CAAAAGTATC    ATTCCC
                                ||||||||||    ||||||
                                GTTTTCGTGG    TAAGGG
                                          ____
GAM2689  HIVEP2   3'  TAACAAAAGTATATATAAT    27553           C
                                TAACAAAAGTAT TATAAT
                                |||||||||||| ||||||
                                ATTGTTTTCATA ATATTA
                                       T
GAM2689  IMMP2L   3'  ACAAATCACAATGTAATTCCCA 37179       AGTATCTA
                                ACAAA       TAATTCCCA
                                |||||       |||||||||
                                TGTTT       ATTAAGGGT
                                   AGTGTTAC
GAM2689  PXMP3    3'  ACAAAAGCTGTCCATTATTC   7227         A_    A
                                ACAAAAGT  TCTAT ATTC
                                ||||||||  ||||| ||||
                                TGTTTTCG  AGGTA TAAG
                                     AC    A
GAM2689  PYCS     5'  TAACCAAAGTATCTTCCC     16038      A       ATAAT  _
                                TAAC AAAGTATCT     TCC C
                                |||| |||||||||     ||| |
                                ATTG TTTCATAGA     AGG G
                                  G        _____  A
GAM2689  SPG7     3'  AAAGTATCTCAACAATTCTCA  17071         __      C
                                AAAGTATCT  ATAATTC CA
                                |||||||||  |||||||  ||
                                TTTCATAGA  TGTTAAG GT
                                     GT       A
GAM2690  CLECSF12 3'  CATCATCAGATTTTATGT     44120        __
                                CATCATT  ATTTTATGT
                                |||||||  |||||||||
                                GTAGTAG  TAAAATACA
                                     TC
GAM2690  HTR2C    3'  TATTACATCTCATTATCCT    9291         CCA
                                TATTACA   TCATTATTTT
                                |||||||   ||||||||||
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                                ATAATGT   AGTAATAGGA
                                   AG_
GAM2691  APP     3'  TCGATTCTTAAAGCATATGT   7921       CAT   TT   C
                                TCGAT   TCTT  AGCA ATGT
                                |||||   ||||  |||| ||||
                                AGCTA   AGAA  TCGT TACA
                                   ___    TT    A
GAM2691  APPBP2   3'  TCAATCATGTTTTGGCATGTGT 26883        TC    A   CA
                                TCGATCAT  TTTT GCA  TGT
                                ||||||||  |||| |||  |||
                                AGTTAGTA  AAAA CGT  ACA
                                     C_    C   AC
GAM2691  CCR2    3'  GATTATTCCCTGAGCACATGT  8499      C      T
                                GAT ATTCTTT AGCACATGT
                                ||| ||||||| |||||||||
                                CTA TAAGGGA TCGTGTACA
                                  A      C
GAM2691  UFD1L   3'  TCATTCTAACATTCACATGT   43825       TTTAG_
                                TCATTCT     CACATGT
                                |||||||     |||||||
                                AGTAAGA     GTGTACA
                                   TTGTAA
GAM2692  AQP6    5'  CTTCTTGATTCTTCCT      38243    C       AGCA
                                CT CTTGATTTT    TCCT
                                || |||||||||    ||||
                                GA GAACTAAGA    AGGA
                                 A       ____
GAM2692  ATF2    3'  TCCTTGATTTCCCT       12436          AGCAT
                                TCCTTGATTTT    CCT
                                ||||||||||     |||
                                AGGAACTAAAG    GGA
                                          _____
GAM2692  BIN1    3'  TCCTCTTGATTTCCCT      40302       C       AGCAT
                                TCCTC TTGATTTT    CCT
                                ||||| ||||||||    |||
                                AGGAG AACTAAAG    GGA
                                   _      _____
GAM2692  BRCA1   3'  TCCTTGATTTTCTTCCT     28645          AGCA
                                TCCTTGATTTT    TCCT
                                ||||||||||    ||||
                                AGGAACTAAAA    AGGA
                                      GA__
GAM2692  FGF1    3'  TCCTTCTGAAATCATCCTC   37573     CC    TTTTAG
                                TCCT  TTGA     CATCCTC
                                ||||  ||||     |||||||
                                AGGA  GACT     GTAGGAG
                                  A_    TTA___
GAM2692  HDAC7A  3'  TCCTCCATGTCTGTATCTTCT  32475       T  A   TAGC   C
                                TCCTCC TG TTT    ATC TCT
                                |||||| || |||    ||| |||
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                                AGGAGG AC AGA   TAG AGA
                                   T  _  CA__  A
GAM2692 LIMK1   3' CCTCCTTGAGGAACGTCCTCT 32530       TTTT  A
                                CCTCCTTGA   AGC TCCTCT
                                |||||||||   ||| ||||||
                                GGAGGAACT   TTG AGGAGA
                                     CC__  C
GAM2692 MAPK14  3' TTGATTTTCAGCATTTCT   40019      _    CC
                                TTGATTT TAGCAT  TCT
                                ||||||| ||||||  |||
                                AACTAAA GTCGTA  AGA
                                    A     A_
GAM2692 MYO10   3' TCCTTTTTTAAGGCATGTGTCC 29577     GATTTTA  ____
           TCT                    TCCTT     GCA   TCCTCT
                                |||||     |||   ||||||
                                AGGAA     CGT   AGGAGA
                                   AAAATTC  ACAC
GAM2692 PAX3    3' TTGATTCCTAGTGTCCTCT  30329      _  CA
                                TTGATTT TAG  TCCTCT
                                ||||||| |||  ||||||
                                AACTAAG ATC  AGGAGA
                                    G  AC
GAM2692 VIPR2   3' TCCTCCTTGGCTCCCCT    18028       ATTTTA  A
                                TCCTCCTTG    GC TCCTCT
                                |||||||||    || ||||||
                                AGGAGGAAC    CG AGGGGA
                                      _______ _
GAM2693 DBT     3' TATCCATAATTACTATTAGAC 12553     T   AATTT
                                TATCC ATAA    TTATTAGAC
                                ||||| ||||    |||||||||
                                ATAGG TATT    GATAATCTG
                                   _   AAT__
GAM2693 RP42    3' TATCCTAAAAAATTTTCAT  33994      T
                                TATCCTA AAAATTTTTAT
                                ||||||| ||||||||||
                                ATAGGAT TTTTAAAAGTA
                                    T
GAM2693 SIP     3' TCCTATAAACATTTTTAT   30846       _
                                TCCTATAAA ATTTTTAT
                                ||||||||| ||||||||
                                AGGATATTT TAAAAATA
                                     G
GAM2693 ZNF214  3' TCCTATCTTTTATTAG     29912      AAAA
                                TCCTAT   TTTTTATTAG
                                ||||||   ||||||||||
                                AGGATA   GAAAATAATC
                                     ____
GAM2693 GCH1    3' TTTAAATAGGACCAACTT   6709         GA
                                TTTAAATAGGA  GATTT
                                ||||||||||  |||||
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                                AAATTTATCCT  TTGAA
                                      GG
GAM2693  ITPR2    3'  AACAATTTGAATAAGAGA    13672        TA
                                AACAATTT  AATAGGAGA
                                ||||||||  |||||||||
                                TTGTTAAA  TTATTCTCT
                                    C_
GAM2693  MLLT2    3'  AACAATTTTAATAATACCAAGA 25489          A   GA__
              TTT                 AACAATTTTAA TAG    GAGATTT
                                ||||||||||| |||    |||||||
                                TTGTTAAAATT ATT    TTCTAAA
                                      _  ATGG
GAM2693  ZNF10    3'  AACAATTTAGAATAGGAAAG   31729        TA
                                AACAATTT  AATAGGAGAG
                                ||||||||  ||||||||||
                                TTGTTAAA  TTATCCTTTC
                                    TC
GAM2694  DSC2     3'  AATGTGCATTTGACCAAAGA   35935      A    AGA
                                AATGT CATTT   GATTAGAGA
                                ||||| |||||   |||||||||
                                TTACA GTAAA   CTGGTTTCT
                                  C    ___
GAM2694  MBL2     3'  ATGAACATTGATTAGAG     6958      T    TAGA
                                ATG ACATT    GATTAGAG
                                ||| |||||    ||||||||
                                TAC TGTAA    CTAATCTC
                                  T    _____
GAM2694  PSG4     3'  CAATGTGCATTTAAAGGAG    15798       A       ATTA
                                TAATGT CATTTAGAG    GAG
                                |||||| |||||||||    |||
                                GTTACA GTAAATTTC    CTC
                                   C        _____
GAM2694  SLC9A6   3'  TGTACACAGATTAGAG      26834        TTAG
                                TGTACAT    AGATTAGAG
                                |||||||    |||||||||
                                ACATGTG    TCTAATCTC
                                           _____
GAM2694  ASPA     3'  TAAGACACCGTGTAAGATGTAA 6254          AA    TATTTG
                                TAAGACAC  TGTA     GTAA
                                ||||||||  ||||     ||||
                                ATTCTGTG  ACAT     CATT
                                    GC    TCTA__
GAM2694  NRXN1    3'  TAAGATACATATGTATATATG  39848      C  _      T
                                TAAGA ACA ATGTATAT TG
                                ||||| ||| |||||||| ||
                                ATTCT TGT TACATATA AC
                                   A  A       T
GAM2694  PHKA2    3'  AGACACAAGTGTTCTATTTGGT 7116          _  A_
                                AGACACAA TGT  TATTTGGT
                                |||||||| |||  ||||||||
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                                TCTGTGTT ACA  ATAAACCA
                                    C   AG
GAM2694  PRPS2    3'  GACCAATGTATTTGGT     15731     A       AT
                                GAC CAATGTAT  TTGGT
                                ||| ||||||||  |||||
                                CTG GTTACATA  AACCA
                                  _       __
GAM2694  PTPRZ1   3'  GAACAATGTTTGGT       15985    C      ATAT
                                GA ACAATGT    TTGGT
                                || |||||||    |||||
                                CT TGTTACA    AACCA
                                  _     _____
GAM2694  SLC30A3  3'  AGACACAAGTTTATTGGT    18426        T  A    T
                                AGACACAA GT TATT GGT
                                |||||||| || |||| |||
                                TCTGTGTT CA ATAA CCA
                                    _ A   _
GAM2694  TCEA1    3'  ACACACCATATTTGGTAA    44322      ATG
                                ACACA   TATATTTGGTAA
                                |||||   ||||||||||||
                                TGTGT   GTATAAACCATT
                                  G__
GAM2695  GAD1     3'  AGTTGTTGGACAAGCTGGTT  9050     CA       G  CA
                                GGT  TTGGACGGG TG  GTT
                                |||  ||||||||| ||  |||
                                TCA  AACCTGTTC AC  CAA
                                  AC       G  __
GAM2695  ITGA5    3'  GGTGATTGGTGGTGCAGTT   41501    C    ACGG
                                GGT ATTGG    GGTGCAGTT
                                ||| |||||    |||||||||
                                CCA TAACC    CCACGTCAA
                                  C    A___
GAM2695  EFNA3    3'  GCCCGGGACCCATGGC      22400           AA
                                GCCCGGGACCCATG  GC
                                ||||||||||||||  ||
                                CGGGCCCTGGGTAC  CG
                                                __
GAM2695  M17S2    5'  TGCCCGAGACTCGTGGGGC   36591         CCA  AA
                                TGCCCGGGAC   TG  GC
                                |||||||||    ||  ||
                                ACGGGCTCTG   AC  CG
                                     AGC  CC
GAM2695  SCA1     3'  TGCTTGTGGTTCATGAAACA  7298     CCG_ ACC
                                TGC    GG   CATGAAGCA
                                |||    ||   |||||||||
                                ACG    CC   GTACTTTGT
                                  AACA  AA_
GAM2695  TACSTD1  5'  GCCCGGGACTCGCGGGAGGGCG 14299         CCAT__  A_  A
            TGCG                  GCCCGGGAC     GA  GC TGCG
                                |||||||||     ||  || ||||
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                                CGGGCCCTG     CT  CG ACGC
                                      AGCGCC  CC  C
GAM2695  ZNF2     5'  TGCTCGGGACCCGGGAAGACG  34387     C       AT    C
                                TGC CGGGACCC  GAAG ATG
                                ||| ||||||||  |||| |||
                                ACG GCCCTGGG  CTTC TGC
                                  A       CC   _
GAM2696  GRM8     3'  TAGTTTTCCTTTTGTGA     9192       CCGTG  G
                                TAGTT     TT CTTTTGTGA
                                |||||     || |||||||||
                                ATCAA     AA GAAAACACT
                                   _____  G
GAM2696  NELL2    3'  GTAATTTTCCTTTTGTGA    26049       CCGTG  G
                                GTAGTT     TT CTTTTGTGA
                                ||||||     || |||||||||
                                CATTAA     AA GAAAACACT
                                   _____  G
GAM2696  ARF3     3'  GTGGACAGGAAAAAGGAGG   11677     AAGA  A  C
                                GTG    AG GA AGAGGAGG
                                |||    || || ||||||||
                                CAC    TC CT TTTCCTCC
                                  CTG_  _  T
GAM2696  BCL10    5'  AATGGGGAAGAAGGAGAGGAGG 19401      AA     AC
                                AGTG  GAAGAG  AGAGGAGG
                                ||||  ||||||  ||||||||
                                TTAC  CTTCTT  TCTCCTCC
                                  CC     CC
GAM2696  CBFA2T3  3'  GAGGAGAGAGGTAGAGGAGG  23263    A  _   AC
                                GA GA AGAG  AGAGGAGG
                                || || ||||  ||||||||
                                CT CT TCTC  TCTCCTCC
                                 C  C    CA
GAM2696  CHRNB4   3'  AGGGAAGGCCTCTCAGAGGAGG 8867     T    AAGAGA
                                AG GAAG     CAGAGGAGG
                                || ||||     |||||||||
                                TC CTTC     GTCTCCTCC
                                 C    CGGAGA
GAM2696  CKTSF1B1 3'  AGGAGGAGGAGGAAAGGAGG   30080    T  A  A   AC
                                AG GA GA GAG  AGAGGAGG
                                || || || |||  ||||||||
                                TC CT CT CTC  TTTCCTCC
                                 _  C  C   C_
GAM2696  CNGA3    3'  TAAGTGAAGGATGGAATTTGAG 10538         AA__   ACA
            G                    TAAGTGAAG    GAG   GAGG
                                |||||||||    |||   ||||
                                ATTCACTTC    CTT   CTCC
                                      CTAC   AAA
GAM2696  CSNK1E   5'  ATGGAGAGGCAGAGGAG     12471     AAGA   A
                                GTG    AGAG CAGAGGAG
                                |||    |||| ||||||||
```

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                                TAC    TCTC GTCTCCTC
                                  C___    C
GAM2696  DPYSL3   3'  TAAGTGAAGAAAGAGAGG    10776          A    CA
                                TAAGTGAAGA GAGA  GAGG
                                |||||||||| ||||  ||||
                                ATTCACTTCT TTCT  CTCC
                                        _   __
GAM2696  EIF5A    3'  GTGAGGGGAGAAGAGGAGG   12701      A AA    C
                                GTGA G  GAGA AGAGGAGG
                                |||| |  |||| ||||||||
                                CACT C  CTCT TCTCCTCC
                                  _ CC   _
GAM2696  FAT2     3'  AGTGGAGAGGAGGCAATGG   11071      A   A   A   A
                                AGTG AGA GAG CAG GG
                                |||| ||| ||| ||| ||
                                TCAC TCT CTC GTT CC
                                  C   C   C   A
GAM2696  FGFR1    3'  GTGGAGAGGAGGTGGAGG    31950     A   A   ACAGA
                                GTG AGA GAG     GGAGG
                                ||| ||| |||     |||||
                                CAC TCT CTC     CCTCC
                                  C   C   CA___
GAM2696  FMO4     3'  TGATGGAGAGCAGAGGAG    12926     AGA    A
                                TGA   AGAG CAGAGGAG
                                |||   |||| ||||||||
                                ACT   TCTC GTCTCCTC
                                  ACC   _
GAM2696  GAS7     3'  AGTGGAGGTAGAAAGGAGG   25263      A  AAG   CA
                                AGTG AG   AGA  GAGGAGG
                                |||| ||   |||  |||||||
                                TCAC TC   TCT  TTCCTCC
                                  C  CA_  __
GAM2696  GLP1R    3'  TGAGAGAAGACAGGGGAG    13143     A  AG     A
                                TGA GA  AGACAG GGAG
                                ||| ||  |||||| ||||
                                ACT CT  TCTGTC CCTC
                                  _ CT     C
GAM2696  GNRHR    5'  TAAGTGAAGAAGGATAG     7617           A  C
                                TAAGTGAAGAAG GA AG
                                |||||||||||| || ||
                                ATTCACTTCTTC CT TC
                                        _ A
GAM2696  GTF2H1   3'  GTGAAGAATGAAGGATGGAGGA 23692        _ __  CA
            GG                    GTGAAGAA GA  GA  GAGGAGG
                                |||||||| ||  ||  |||||||
                                CACTTCTT CT  CT  CTCCTCC
                                     A  TC  AC
GAM2696  HLF      3'  AGTGAAGGAGGGAGGG      13386        AA   ACA    A
                                AGTGAAG  GAG   GAGG G
                                |||||||  |||   |||| |
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                                TCACTTC  CTC   CTCC C
                                   __   C__   _
GAM2696  IL1F8    5'  AAGTGAAGGAGAGGTGAG    30893        A   ACA
                                AAGTGAAG AGAG   GAG
                                |||||||| ||||   |||
                                TTCACTTC TCTC   CTC
                                    C    CA_
GAM2696  KCNK4    5'  GTGAGGAAAGAGAGGAGG    37839     AGAA   C
                                GTGA    GAGA AGAGGAGG
                                ||||    |||| ||||||||
                                CACT    CTTT TCTCCTCC
                                  C___    C
GAM2696  KHK      3'  GTGGGCAGGGCAGAGGAGG   6894     AAGA  AGA
                                GTG    AG   CAGAGGAGG
                                |||    ||   |||||||||
                                CAC    TC   GTCTCCTCC
                                  CCG_  CC_
GAM2696  KRT15    3'  GTGGGGAGAGGCAGAGGGG   14013    AA  A   A     A
                                GTG  GA GAG CAGAGG GG
                                |||  || ||| |||||| ||
                                CAC  CT CTC GTCTCC CC
                                  CC  _   C     _
GAM2696  LAMC2    3'  GTGGAGGAAAGAGAGAGG    33118    A  A    C
                                GTG AG AGAGA AGAGG
                                ||| || ||||| |||||
                                CAC TC TTTCT TCTCC
                                  C  C    C
GAM2696  MGAT5    5'  GTGGGGAGGAGACAGAAG    14477    AA  A
                                GTG  GA GAGACAGAGG
                                |||  || ||||||||||
                                CAC  CT CTCTGTCTTC
                                  CC  C
GAM2696  MYO1D    3'  TAAGTGGAAGGAGAGAGG    43505      AA    A  C
                                TAAGTG  GAAG GA AGAGG
                                ||||||  |||| || |||||
                                ATTCAC  CTTC CT TCTCC
                                    __    _  C
GAM2696  NAV2     3'  AGGAAGAGAGAGAGAGGAGG  41140    T    A    C
                                AG GAAGA GAGA AGAGGAGG
                                || ||||| |||| ||||||||
                                TC CTTCT CTCT TCTCCTCC
                                  _    _    C
GAM2696  NAV2     3'  GCGGTGAGGAGAAGAGGAGG  41144    AA  A   C
                                GTG  GA GAGA AGAGGAGG
                                |||  || |||| ||||||||
                                CGC  CT CTCT TCTCCTCC
                                  CA  C   _
GAM2696  NFIA     5'  GTGAGAGAGGAGAAAGAGG   43222      _  A   C
                                GTGA AGA GAGA AGAGG
                                |||| ||| |||| |||||
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                                CACT TCT CTCT TCTCC
                                  C   C    T
GAM2696  NLGN2    3'  TGAGGAAGAGGAGGGA      44763     A     AC  A
                                TGA GAAGAG  AG GGA
                                ||| ||||||  || |||
                                ACT CTTCTC  TC CCT
                                  C     C_  _
GAM2696  NTSR1    3'  AAAGAGGAGATGGGGGAGG   14868      A   CAGA
                                GAAGA GAGA    GGAGG
                                ||||| ||||    |||||
                                TTTCT CTCT    CCTCC
                                   C    ACCC
GAM2696  PCM1     5'  GTGGAGAAGAGGGCGGGG    26228     A      ACAGA  A
                                GTG AGAAGAG     GG GG
                                ||| |||||||     || ||
                                CAC TCTTCTC     CC CC
                                  C      CCG__  _
GAM2696  PMX1     3'  TAAGTGAAGAACGGATAG    35515          GA  C
                                TAAGTGAAGAA  GA AG
                                ||||||||||  || ||
                                ATTCACTTCTT  CT TC
                                       GC  A
GAM2696  PPP4C    3'  CAAGTGGGGAGAGAGGAG    15529       AAGAA    CA
                                TAAGTG    GAGA  GAGGAG
                                ||||||    ||||  ||||||
                                GTTCAC    CTCT  CTCCTC
                                   CC___   __
GAM2696  PXN      3'  TGATGAAGAAGAGATACAAAAG 16033    A          __
                                A GTGAAGAAGAGA  CAGAGG
                                | ||||||||||||  ||||||
                                A TACTTCTTCTCT  GTTTTC
                                 C           AT
GAM2696  PYGB     5'  AGGAAAAGAGATGGAGGAGG   16042    T    A    CA
                                AG GAAGA GAGA  GAGGAGG
                                || ||||| ||||  |||||||
                                TC CTTTT CTCT  CTCCTCC
                                 _    _    AC
GAM2696  SC5DL    3'  AAGTGAGGGGAGAAGAGGAGG  44911       A AA    C
                                AAGTGA G  GAGA AGAGGAGG
                                |||||| |  |||| ||||||||
                                TTCACT C  CTCT TCTCCTCC
                                   _ CC    _
GAM2696  SMARCA2  3'  GTAGAAATGAGACAGGGGAGG  16893     A   A      A
                                GTG AGA GAGACAG GGAGG
                                ||| ||| ||||||| |||||
                                CAT TTT CTCTGTC CCTCC
                                  C   A      C
GAM2696  SMCX     3'  AGGAAAGGAGACAGGGGAGG   20066    TG   AA      A
                                AG  AAG  GAGACAG GGAGG
                                ||  |||  ||||||| |||||
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                                TC  TTC  CTCTGTC CCTCC
                                 CT   __      C
GAM2696  ST7      5'  AGAGAGGAGGAGACGGAGGAGG 30263    T  A  A     A      III
                C                 AG GA GA GAGAC GAGGAGG   C
                                  || || || ||||| |||||||   |
                                  TC CT CT CTCTG CTCCTCC   G
                                   T  C  C    C      III
GAM2696  TRPC5    5'  GTGGGGAGGGGAAAATCAAGGA 29769     AA  A__    CA_
                GG                 GTG  GA   GAGA   GAGGAGG
                                  |||  ||   ||||   |||||||
                                  CAC  CT   CTTT   TTCCTCC
                                    CC  CCC    TAG
GAM2696  UBTF     3'  AAGTGGGGGAGGCCAGGGGG  30606      AAGAA   A_   A  A
                                  AAGTG    GAG  CAG GG GG
                                  |||||    |||  ||| || ||
                                  TTCAC    CTC  GTC CC CC
                                     CCC__   CG   _  _
GAM2696  UGCG     5'  GTGGGGAGAGGAAAGGGCGGAG 17879     A__   A    CAGA
                G                  GTG   AGA GAGA    GGAGG
                                  |||   ||| ||||    |||||
                                  CAC   TCT CTTT    CCTCC
                                    CCC   C    CCCG
GAM2696  VDR      3'  AGGGGAGGTGGCAGAGGAGG   7511     AA   A___
                                  AG  GAG    CAGAGGAGG
                                  ||  |||    |||||||||
                                  TC  CTC    GTCTCCTCC
                                   CC   CACC
GAM2696  VIPR1    3'  GTGAAGGGCAGACAGAGGAGG  21515       AAG
                                  GTGAAG   AGACAGAGGAGG
                                  ||||||   ||||||||||||
                                  CACTTC   TCTGTCTCCTCC
                                     CCG
GAM2697  ANXA3    3'  TTCATTTATGAGCTGCTAC    23104         ACGT   T
                                  TTCGTTTAT    GCT GCTAC
                                  |||||||||    ||| |||||
                                  AAGTAAATA    CGA CGATG
                                       CT__   _
GAM2697  COL4A6   3'  TTCATTTATTTTATTTGCTA   37979         ACG  C
                                  TTCGTTTAT   TG TTGCTA
                                  |||||||||   || ||||||
                                  AAGTAAATA   AT AACGAT
                                       AA_  A
GAM2697  CPA3     3'  ACTTCGTTATGGTGCTAC    12415         TATAC    T
                                  ACTTCGTT    GTGCT GC
                                  ||||||||    ||||| ||
                                  TGAAGCAA    CACGA TG
                                       TAC__    _
GAM2697  OSBP     5'  TTCAGTTTATGCGCCTG     14991     _     AC
                                  TTC GTTTAT  GTGCTTG
                                  ||| ||||||  |||||||
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                                AAG CAAATA  CGCGGAC
                                  T     __
GAM2697  OXTR     3'  ACTTCGTTTTCATATTGTTTGT 9518         __    C_  GC_
              TGC                   ACTTCGT  TTATA  GT   TTGC
                                |||||||  |||||  ||   ||||
                                TGAAGCA  AGTAT  CA   AACG
                                    AA    AA  AAC
GAM2697  WASF3    3'  GTTTATACAAAAGGTGCTA   27388         TGCT_
                                GTTTATACG    TGCTA
                                |||||||||    |||||
                                CAAATATGT    ACGAT
                                     TTTCC
GAM2697  ABCE1    3'  GCCATCTGGGGACTTTTGC   40502    G  ACA_  A
                                GC CA    GG ACTTTTGC
                                || ||    || ||||||||
                                CG GT    CC TGAAAACG
                                 _  AGAC  C
GAM2697  AS3      3'  ACAAATTTAGGAACTTTTGC  31979     C___
                                GCAA    AGGAACTTTTGC
                                ||||    ||||||||||||
                                TGTT    TCCTTGAAAACG
                                  TAAA
GAM2697  BACH2    3'  GAGGCATGCAGGACTTTTGC  34788     C   A_    A
                                GAG GCA  CAGGA CTTTTGC
                                ||| |||  ||||| |||||||
                                CTC CGT  GTCCT GAAAACG
                                  _   AC    _
GAM2697  DAZ      3'  CGAGCACATAACTTTTG     19849         ACAGG
                                CGAGCGCA    AACTTTTG
                                ||||||||    ||||||||
                                GCTCGTGT    TTGAAAAC
                                     A____
GAM2697  DRPLA    5'  GCACCTGGAACTTTTGC     12586      AACA
                                GCGC    GGAACTTTTGC
                                ||||    ||||||||||
                                CGTG    CCTTGAAAACG
                                  GA__
GAM2697  EPM2A    3'  AGTGCAACAGGAAAGTGC    24965    C        CTTT
                                AG GCAACAGGAA    TGC
                                || ||||||||||    |||
                                TC CGTTGTCCTT    ACG
                                 A         TC__
GAM2697  ERBB2IP  3'  GAGTCCAACTCACTTTTGC   33098     CG    AGGA
                                GAG  CAAC    ACTTTTGC
                                |||  ||||    ||||||||
                                CTC  GTTG    TGAAAACG
                                  AG    AG__
GAM2697  PCTK1    5'  GCAAACGGGACTTTTGC     37473     C   A   A
                                GCG AAC GGA CTTTTGC
                                ||| ||| ||| |||||||
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                                CGT TTG CCT GAAAACG
                                  _  C  _
GAM2697  SNRP70   5'  CGAGCGCACCAGGCCGCTGC  44213        A   AA  T
                                CGAGCGCA CAGG  CT TTGC
                                |||||||| ||||  || ||||
                                GCTCGCGT GTCC  GG GACG
                                    G   __ C
GAM2697  TGFB2    5'  GATGCGAAACTTTTG      17454    GC  AACA
                                GA  GC   GGAACTTTTG
                                ||  ||   ||||||||||
                                CT  CG   CTTTGAAAAC
                                 A_ ____
GAM2698  CRY2     3'  CACTGTGGTGCCTTG      43577        TTTCGC   CA
                                CATTGTGGT    GCCT  G
                                |||||||||    ||||  |
                                GTGACACCA    CGGA  C
                                     _______   AC
GAM2699  ABCD2    3'  ACTATGATTCTCAGAATCC   23148     CAT      _
                                ACTA   TTCTCAGAA CC
                                ||||   ||||||||| ||
                                TGAT   AAGAGTCTT GG
                                  ACT       A
GAM2699  CTGF     3'  ACCACATTTCCTACC       12499         CAGA
                                ACTACATTTCT   ACC
                                ||||||||||    |||
                                TGGTGTAAAGG   TGG
                                      A___
GAM2699  CYP1B1   3'  CACATTTCTCAATCTAAAAAA  6446          AACC
                                TACATTTCTCAG   AAAAA
                                ||||||||||||   |||||
                                GTGTAAAGAGTT   TTTTT
                                       AGAT
GAM2699  GAC1     3'  CACATTTCTCCACAAA      26793         AGAAC
                                TACATTTCTC    CAAA
                                ||||||||||    ||||
                                GTGTAAAGAG    GTTT
                                      GT___
GAM2699  GRAF     3'  CTGCATTTCTCAGTGGCAAA  31444    A       AAC
                                CT CATTTCTCAG  CAAA
                                || ||||||||||  ||||
                                GA GTAAAGAGTC  GTTT
                                 C        ACC
GAM2699  MMP8     3'  CTACATTTCTTTCCAA      14545         CAGAA
                                CTACATTTCT    CCAA
                                ||||||||||    ||||
                                GATGTAAAGA    GGTT
                                      AA___
GAM2699  RAD23B   3'  CTGCATTTCTCCATTGGCCCCA 16137    A      AGAA____
            AAA                   CT CATTTCTC       CCAAAA
                                || ||||||||       ||||||
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                                GA GTAAAGAG       GGTTTT
                                 C       GTAACCGG
GAM2699  RSN      3'  TACATTTATAACCAAAAAT   16403        CTCAG
                                TACATTT     AACCAAAAAT
                                |||||||     ||||||||||
                                ATGTAAA     TTGGTTTTTA
                                    TA___
GAM2699  WHSC1L1  3'  ACTACACTTCTTGAAATTCCTA 32817           CA  __ _
            AAAAT                   ACTACATTTCT  GAA  CC AAAAAT
                                |||||||||||  |||  || ||||||
                                TGATGTGAAGA  TTT  GG TTTTTA
                                      AC   AA  A
GAM2699  ZNF144   3'  ACTTGCTCCTCAGAACCA    28334     ACA
                                ACT   TTTCTCAGAACCA
                                |||   ||||||||||||
                                TGA   GAGGAGTCTTGGT
                                  AC_
GAM2699  ZNF36    3'  TTTCTCAGAGCAACAAAA    45298         AC__
                                TTTCTCAGA    CAAAA
                                |||||||||    |||||
                                AAAGAGTCT    GTTTT
                                     CGTT
GAM2700  COL16A1  3'  AAAGGGCAGATAGTTTTG    12362         _  _
                                AAAGGGCA ATA TTTTG
                                |||||||| ||| |||||
                                TTTCCCGT TAT AAAAC
                                     C   C
GAM2700  FZD8     3'  AGGGCAATGGTTAAATCATTT  36610         ATT   C
                                AGGGCAAT   TTG GTCATTT
                                ||||||||   ||| |||||||
                                TCCCGTTA   AAT TAGTAAA
                                     CC_   T
GAM2700  RAD1     3'  GGAGTGCAATGGCGTCATT    39344    A  G    ATTTT
                                A AG GCAAT    GCGTCATT
                                | || |||||    ||||||||
                                C TC CGTTA    CGCAGTAA
                                 C  A    C_____
GAM2701  C14orf1  3'  TAAGTTTCATAGTTCAC     28418           A
                                TAAGTTTCATA GTTTAT
                                |||||||||||  ||||||
                                ATTCAAAGTAT CAAGTG
                                                _
GAM2701  HSPA4    3'  CAAGTTTAAGACAGGTTTATTT 44847         C__   A
            TATT                   TAAGTTT   ATA GTTTATTTTATT
                                |||||||   ||| ||||||||||||
                                GTTCAAA   TGT CAAATAAAATAA
                                     TTC   C
GAM2702  MAPK10   5'  TAAGTAAAGATATGAGTGACT  39982         C    AAC_
                                TAAGTAAAG ATAT    GACT
                                |||||||||  ||||    ||||
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                                ATTCATTTC TATA   CTGA
                                    _   CTCA
GAM2702  TP63     3'  AATAAAGCATATAAAAC     18990           C
                                AGTAAAGCATATAA GAC
                                |||||||||||||| |||
                                TTATTTCGTATATT TTG
                                    _
GAM2703  CHRNB3   5'  AGCATTTCCATTGGAAAAGGGG 8864          CAACTGCT__
              GTT                 AGCATTTCCA       GGGTT
                                |||||||||         |||||
                                TCGTAAAGGT        CCCAA
                                    AACCTTTTCC
GAM2703  GALNT7   3'  AAGCTTTTCAGCTGCTGGGTT  38348     A   CACAA
                                AAGC TTTC    CTGCTGGGTT
                                |||| ||||    ||||||||||
                                TTCG AAAG    GACGACCCAA
                                  A   TC___
GAM2703  GNB1     3'  AGCATTTCTACAGCATGCGATT 13196       C   ACT  _  _
                                AGCATTTC ACA   GC TG GGTT
                                |||||||| |||   || || ||||
                                TCGTAAAG TGT   CG AC CTAA
                                    A   ___  T  G
GAM2703  OGDH     5'  AAGTTTTTCACAACTGCC    45007     CA    C
                                AAG  TTTC ACAACTGCT
                                |||  |||| |||||||||
                                TTC  AAAG TGTTGACGG
                                  AA   _
GAM2703  PCDH9    5'  GCATTTCCAGCAGTGTC     44400        CAACT  TGG
                                GCATTTCCA    GC   GTT
                                |||||||||    ||   |||
                                CGTAAAGGT    CG   CAG
                                    _____  TCA
GAM2703  RERE     3'  TTTCCACAGCCAGCGTT     29040        ACT  TG _
                                TTTCCACA   GC  G GTT
                                ||||||||   ||  | |||
                                AAAGGTGT   CG  C CAA
                                    ___  GT G
GAM2703  TH1L     3'  TTTCCACAACGGGT       32312          TGCT
                                TTTCCACAAC    GGGT
                                |||||||||    ||||
                                AAAGGTGTTG    CCCA
                                    _____
GAM2704  CR1L     5'  TCATCAGTTAGGTTGGT     44867      G        A
                                TCGT CAGTTAGGTT GT
                                |||| |||||||||| ||
                                AGTA GTCAATCCAA CA
                                  _        C
GAM2704  HYAL1    3'  TCGTGCAGGGCTGGT       37645        TTA    A
                                TCGTGCAG   GGTT GT
                                ||||||||   |||| ||
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                                AGCACGTC  CCGA CA
                                    ___   C
GAM2704 TLL2    5' TCGTGAGACAGGTTAGT    29757     C  T
                                TCGTG AG TAGGTTAGT
                                ||||| || |||||||||
                                AGCAC TC GTCCAATCA
                                  _  T
GAM2705 NAV2    3' GTCCAGTTGGGTTGTCAGC  41151       A  C  G
                                GTCCAGTT GG TG CGGT
                                |||||||| || || ||||
                                CAGGTCAA CC AC GTCG
                                    C  A  A
GAM2706 ATP1A2  3' GAGTGTAATGGCACGATC   8705        AGAAT  C
                                GAGTGTAAT   CAC GTC
                                |||||||||   ||| |||
                                CTCACATTA   GTG TAG
                                     CC___  C
GAM2706 CRHR1   3' GAGTGTAAGCAGCACGTTGTC 20440       _  AAT  C__
                                GAGTGTAA TAG  CAC  GTC
                                |||||||| |||  |||  |||
                                CTCACATT GTC  GTG  CAG
                                    C  ___  CAA
GAM2706 DNMT2   3' TAGGGGCAAGAATCACCGTC  20630    AGT  AT
                                TAG  GTA  AGAATCACCGTC
                                |||  |||  ||||||||||||
                                ATC  CGT  TCTTAGTGGCAG
                                  CC_  __
GAM2706 HSPA9B  3' TGTTAGAATCACTGTC     19976    AA      C
                                TGT  TAGAATCAC GTC
                                |||  ||||||||| |||
                                ACA  ATCTTAGTG CAG
                                  __       A
GAM2706 LTB     3' TAGAGGTAATAGAGGCCGTC  14252     T      ATCA
                                TAGAG GTAATAGA   CCGTC
                                ||||| ||||||||   |||||
                                ATCTC CATTATCT   GGCAG
                                   _      CC__
GAM2706 HIP1    3' TGGTAATTGGGAACATATGAG 23761    CG  CAAAA  C
                                TGG  AT   GG GCGTATGAG
                                |||  ||   || |||||||||
                                ACC  TA   CC TGTATACTC
                                  AT  AC___  T
GAM2707 GM2A    3' TCAGAAGTTGTTATGATG   42690       AC__
                                TCGGAAGTT   TGATG
                                |||||||||   |||||
                                AGTCTTCAA   ACTAC
                                     CAAT
GAM2707 S100A5  5' TCTGAAATCTGATGGAACAA  16445   G   TA
                                TC GAAGT  CTGATGGAACAA
                                || |||||  ||||||||||||
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                                AG CTTTA  GACTACCTTGTT
                                 A    __
GAM2707  TMEM2    3'  TCGGGGGTTTAGAACAAC    30154     AA   ACTGA
                                TCGG  GTT    TGGAACAAC
                                ||||  |||    |||||||||
                                AGCC  CAA    ATCTTGTTG
                                  CC  _____
GAM2707  CCR2     3'  TTCACCTCCAGCTGGCC     8505      AA      CGA
                                TTCA  TTTCCAGC   CC
                                ||||  ||||||||   ||
                                AAGT  GGAGGTCG   GG
                                  __       ACC
GAM2707  CD83     3'  CAGCATTTCCAGCCGGCC    20134    A_        A
                                CA  ATTTCCAGCCG CC
                                ||  ||||||||||| ||
                                GT  TAAAGGTCGGC GG
                                 CG          C
GAM2707  FGFR4    5'  CTCCCAGCTCCAGCCGGCC   12865     AAAT       A
                                TTC    TTCCAGCCG CC
                                |||    ||||||||| ||
                                GAG    GAGGTCGGC GG
                                  GGTC        C
GAM2707  GPX4     5'  TCCCCTCGTCCAGCCGACC   13283     AAATT
                                TTC    TCCAGCCGACC
                                |||    ||||||||||
                                AGG    AGGTCGGCTGG
                                  GGAGC
GAM2707  HADHB    3'  TCCAAATCTCAGTTGACC    6770          C  CC
                                TTCAAATTTC AG  GACC
                                |||||||||| ||  ||||
                                AGGTTTAGAG TC  CTGG
                                      _  AA
GAM2707  NDUFA5   3'  TTCAAATCTTCCCATGGCC   22668         __   __
                                TTCAAATT  TCCA  GCC
                                ||||||||  ||||  |||
                                AAGTTTAG  GGGT  CGG
                                     AA    AC
GAM2707  NFIA     5'  TTCACATTTCCAAGTCGAC   43226      A      _ C
                                TTCA ATTTCCA G CGAC
                                |||| ||||||| | ||||
                                AAGT TAAAGGT C GCTG
                                  G      T A
GAM2707  PIK3R2   5'  TTCAAATTATTCCATGACC   22754         __   GCC
                                TTCAAATT  TCCA   GACC
                                ||||||||  ||||   ||||
                                AAGTTTAA  AGGT   CTGG
                                     TA    A__
GAM2707  PTP4A2   3'  TTCACATTTCCAGGTACC    38646      A      CCG
                                TTCA ATTTCCAG   ACC
                                |||| ||||||||   |||
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                                AAGT TAAAGGTC   TGG
                                  G       CA_
GAM2707  WHSC1    3'  TTCAAATCCAACTTGAC     39396       TT     C_
                                TTCAAA  TCCAGC  GAC
                                ||||||  ||||||  |||
                                AAGTTT  AGGTTG  CTG
                                   __      AA
GAM2707  XPA      3'  CTCAAATTTGTAGCTGACC   7538         CC   C
                                TTCAAATTT  AGC GACC
                                |||||||||  ||| ||||
                                GAGTTTAAA  TCG CTGG
                                     CA   A
GAM2707  ZNF151   5'  CTCAGATTTCCAGACAGCC   18351      A       C  A
                                TTCA ATTTCCAG CG CC
                                |||| |||||||| || ||
                                GAGT TAAAGGTC GT GG
                                  C       T  C
GAM2708  COX7C    3'  TAGTATGGCATATGAGTTCTAG 12414         TTTTCTC    C
           T                     TAGTATGGC      GTTC AGT
                                 |||||||||      |||| |||
                                 ATCATACCG      CAAG TCA
                                      TATACT_    A
GAM2708  DNMT3L   5'  TGGGTTCAAGGTTCCAGT    30075     C   TCTC
                                TGG TTT    GTTCCAGT
                                ||| |||    ||||||||
                                ACC AAG    CAAGGTCA
                                  C   TTC_
GAM2708  GABPB1   3'  TGGGAGAAATACCTATGT    23529       T       ATTA
                                TGGGA GAAATATT    TATGT
                                ||||| ||||||||    |||||
                                ACCCT CTTTATGG    ATACA
                                   _       ____
GAM2709  DGKG     5'  TCTCAGAAGATGAGACAAGATC 10658         AAC    G   CT
           T                     TCTCAGAA   GAGA TGA  TCT
                                 ||||||||   |||| |||  |||
                                 AGAGTCTT   CTCT GTT  AGA
                                      CTA    _   CT
GAM2709  DLD      3'  TCAGGAATGTGACTTC      6467       AAAAC   A
                                TCAG     GAG GTGACTTC
                                ||||     ||| ||||||||
                                AGTC     CTT CACTGAAG
                                   _____   A
GAM2709  ENPP1    3'  TCTCAGAAGTATTTTGGCTTCT 26300         AACGAGAG  A
                                TCTCAGAA       TG CTTCT
                                ||||||||       || |||||
                                AGAGTCTT       AC GAAGA
                                      CATAAA__  C
GAM2709  FBXW7    3'  CCAGAAAAATGACTT       37968        AACGA
                                TCAGAA     GAGTGACTT
                                ||||||     |||||||||
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                                GGTCTT    TTTACTGAA
                                      _____
GAM2709 KIR2DS1  3' TCTCAGAAGGGCGAGTGA    30954       AACGA
                                TCTCAGAA    GAGTGA
                                ||||||||    ||||||
                                AGAGTCTT    CTCACT
                                     CCCG_
GAM2709 KIR2DS2  3' TCTCAGAAGGGCGAGTGATTTC 29480       AACGA     C
             T                   TCTCAGAA    GAGTGA TTCT
                                ||||||||    |||||| ||||
                                AGAGTCTT    CTCACT AAGA
                                     CCCG_     A
GAM2709 KIR2DS4  3' TCTCAGAAGGGCGAGTGA    29485       AACGA
                                TCTCAGAA    GAGTGA
                                ||||||||    ||||||
                                AGAGTCTT    CTCACT
                                     CCCG_
GAM2709 POLR2C   3' TCTCAGAAACGAGAAGAGTCT  15455       A     T  CT
                                TCTCAGAAA CGAGAG GA  TCT
                                ||||||||| |||||| ||  |||
                                AGAGTCTTT GCTCTT CT  AGA
                                     _     _ C_
GAM2709 PPBP     3' TCTCAGAATAAAATGTGA    15490       AAC   _
                                TCTCAGAA   GAGA GTGA
                                ||||||||   |||| ||||
                                AGAGTCTT   TTTT CACT
                                     A__    A
GAM2710 MLC1     3' TAAGAAAATAAGAAAGTGCA   40153           ___
                                TAAGAAAATAAGAA   GCA
                                ||||||||||||||   |||
                                ATTCTTTTATTCTT   CGT
                                       TCA
GAM2710 PTPRK    3' AAGAAAATAAGCCAGTTA    15963       AGA   A
                                AAGAAAATA   AGC CAGTTA
                                |||||||||   ||| ||||||
                                TTCTTTTAT   TCG GTCAAT
                                     ___  _
GAM2710 RRM2B    3' GAAAAAATGAAAACACAGTT   42720     TAA_
                                GAAAA    GAAGCACAGTT
                                |||||    ||||||||||||
                                CTTTT    TTTTGTGTCAA
                                   TTAC
GAM2711 AVPR2    5' GCAGATGCCTGTTGGCGT    6286       GGT   ACA_
                                GCAGATGT   CTG    CGT
                                ||||||||   |||    |||
                                CGTCTACG   GAC    GCA
                                     ___   AACC
GAM2711 CLECSF2  3' TATGTGTAGCCTGACACGT   23062     CAGA
                                TATG    TGTGGTCTGACACGT
                                ||||    ||||||||||||||
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                                ATAC    ACATCGGACTGTGCA
                                  ____
GAM2711  JAM3     3'  GCAACTATGGTCTGATGTGTA  37264      A        CAC
                                GCAG TGTGGTCTGA   GTA
                                |||| ||||||||||   |||
                                CGTT ATACCAGACT   CAT
                                  G         ACA
GAM2711  ALPI     3'  AGTCTCTGGGGTTGGG      11575      G     CATGTA
                                AGTCT TGGGGT     TGGG
                                ||||| ||||||     ||||
                                TCAGA ACCCCA     ACCC
                                  G    _______
GAM2711  ASTN     3'  GTCTTGGGGACATGGGA     42950      G    T  TGTA
                                GTCT TGGGG CA    TGGGA
                                |||| ||||| ||    |||||
                                CAGA ACCCC GT    ACCCT
                                  _     T  ____
GAM2711  LAIR1    3'  AGTCTCTGGGGTCACTGGA    14051      G       GTA
                                AGTCT TGGGGTCAT   TGGG
                                ||||| |||||||||   ||||
                                TCAGA ACCCCAGTG   ACCT
                                  G        ___
GAM2711  NRGN     5'  GTCTGTGTGGTGCCGGGTGGG  26130       G   CA  TA
                                GTCTGTG GGT  TG  TGGG
                                ||||||| |||  ||  ||||
                                CAGACAC CCA  GC  ACCC
                                    A   CG  CC
GAM2711  POR      3'  AGTCTGTGGGGTGGGTGGG    45299          CAT TA
                                AGTCTGTGGGGT   G  TGGG
                                ||||||||||||   |  ||||
                                TCAGACACCCCA   C  ACCC
                                       ___ CC
GAM2711  SOLH     3'  CTGTGGGGTTCAGGGA      24829          _  TGTAT
                                CTGTGGGGT CA    GGGA
                                ||||||||| ||    ||||
                                GACACCCCA GT    CCCT
                                    A  _____
GAM2712  ADK      3'  GGAAATAAACATCATTTTT    27483      C    T
                                GGAAA AAAT ATCATTTTT
                                ||||| |||| |||||||||
                                CCTTT TTTG TAGTAAAAA
                                  A   _
GAM2712  COL4A3   3'  GGAAACAAATTGAAACTTT    36381          ATC
                                GGAAACAAATT   ATTTT
                                ||||||||||   |||||
                                CCTTTGTTTAA   TGAAA
                                      CTT
GAM2712  COX15    3'  TTTAGGGTAACCACACTTAA   38520        T   TTTA
                                TTTAGGGT ACC    TTAA
                                |||||||| |||    ||||
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                                AAATCCCA TGG    AATT
                                     T   TGTG
GAM2712  DBN1     3'  GGATTTCTTTATTAACA     38936       AC
                                GGGTT  CTTTATTAACA
                                |||||  ||||||||||
                                CCTAA  GAAATAATTGT
                                   A_
GAM2712  FCMD     3'  TTCAATTCTCCTTTATTAACA  27527       GG  A
                                TTTAG  TT CCTTTATTAACA
                                |||||  ||  ||||||||||||
                                AAGTT  GA GGAAATAATTGT
                                   AA  _
GAM2712  HCS      3'  TTTAGGGCTGCTGCACTGACA  33239         AC  T    A
                                TTTAGGGTT  CT TATT ACA
                                |||||||||  ||  |||| |||
                                AAATCCCGA  GA GTGA TGT
                                      C_  C    C
GAM2712  SMP1     3'  GGGTTAATTTTATTGACA     30717       CC      A
                                GGGTTA  TTTATT ACA
                                ||||||  |||||| |||
                                CCCAAT  AAATAA TGT
                                    TA     C
GAM2713  CORO1C   3'  TCGCTGGTTGACAAATCT    30725    ACA      T   T
                                TC   TGGTTGG CAG TCT
                                ||   ||||||| ||| |||
                                AG   ACCAACT GTT AGA
                                 CG_      _   T
GAM2713  DIO1     3'  TCCCATAATTGGTTCTAAA    9003     A        CAGT
                                TC CATGGTTGGT    TCTAAA
                                || ||||||||||    ||||||
                                AG GTATTAACCA    AGATTT
                                 G        ____
GAM2713  DUSP11   3'  TCAATGCTTCAGTTCTAAA    18722     C   G TGG
                                TCA ATG T   TCAGTTCTAAA
                                ||| ||| |   ||||||||||
                                AGT TAC A   AGTCAAGATTT
                                  _   G ___
GAM2713  GPR62    3'  CCACATGCCAGTTCT       44872       GGTTG
                                TCACAT    GTCAGTTCT
                                ||||||    |||||||||
                                GGTGTA    CGGTCAAGA
                                     _____
GAM2713  GRM1     3'  TCACATGGTTTGTTCT      9142          GGTCA
                                TCACATGGTT    GTTCT
                                ||||||||||    |||||
                                AGTGTACCAA    CAAGA
                                      A____
GAM2713  WNT6     3'  TCCTGTGGCCAGCAGTTCT   27186    ACA    TG T
                                TC   TGGT  G CAGTTCT
                                ||   ||||  | |||||||
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                                AG   ACCG  C GTCAAGA
                                 GAC    GT _
GAM2713  ZNF2     3'  TCATATGGTTGGTGACAG    34385     C       __
                                TCA ATGGTTGGT  CAG
                                ||| |||||||||  |||
                                AGT TACCAACCA  GTC
                                  A        CT
GAM2713  ZNFN2A1  3'  TGGATGGTACACAGTTCTA   41367     T   ___
                                TGG TGGT   CAGTTCTA
                                ||| ||||   ||||||||
                                ACC ACCA   GTCAAGAT
                                  T    TGT
GAM2713  CTPS     3'  GTAAGTGACCCCTTGATG    44799         G___
                                GTAAGTGAC    TGATG
                                |||||||||    |||||
                                CATTCACTG    ACTAC
                                      GGGA
GAM2713  NEBL     3'  GTCAGTGACATATAGATGC    26904    A       AT  C
                                GT AGTGACGTG  GA GC
                                || |||||||||  || ||
                                CA TCACTGTAT  CT CG
                                 G        AT  A
GAM2713  PRPS2    3'  TTCAGGTAAGTGACAGTTATG  15734     C       _  G
                                TTCA GTAAGTGAC GT ATG
                                |||| ||||||||| || |||
                                AAGT CATTCACTG CA TAC
                                  C        T  A
GAM2713  SLC16A1  5'  GTGCGTGACGTGGTGGCG    16814    AA      A  A
                                GT  GTGACGTG TG CG
                                ||  |||||||| || ||
                                CA  CACTGCAC AC GC
                                 CG       C  C
GAM2714  ACE2     3'  TGCTCAGCACTGCTCAAACA   34763     AG   _  A T
                                TGC  TCAG AC G CTCAAACA
                                |||  |||| || | ||||||||
                                ACG  AGTC TG C GAGTTTGT
                                  __    G  A _
GAM2714  COG3     3'  TCTGCAGTCAGCACTGAGC    36418          _  __
                                TCTGCAGTCAG AC  AGT
                                ||||||||||| ||  |||
                                AGACGTCAGTC TG  TCG
                                       G  AC
GAM2714  DDIT3    5'  TCTGCAGTTGGATCAGTCT    19858         CA  _
                                TCTGCAGT  GA CAGTCT
                                ||||||||  || ||||||
                                AGACGTCA  CT GTCAGA
                                     AC  A
GAM2714  LYPLA1   3'  TCTACAGTAGTTGGTTTCAAAC 26761         C  ACA  C
                                TCTGCAGT AG   GT TCAAAC
                                |||||||| ||   || ||||||
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                                AGATGTCA TC   CA AGTTTG
                                    _ AAC  A
GAM2714  NESH     3'  TCTGCAGCAGGCCTC      32344        T   ACA
                                TCTGCAG CAG   GTCTC
                                ||||||| |||   |||||
                                AGACGTC GTC   CGGAG
                                   _  ____
GAM2714  RGL      3'  TCTGCATTTTAGTCTCAAA   31546       GTCAGAC
                                TCTGCA      AGTCTCAAA
                                ||||||      |||||||||
                                AGACGT      TCAGAGTTT
                                   AAAA___
GAM2714  RPA1     3'  TCTGCAGTTAGGGTCAGT    16373        C  A__
                                TCTGCAGT AG   CAGT
                                |||||||| ||   ||||
                                AGACGTCA TC   GTCA
                                     A  CCA
GAM2714  SLC4A4   3'  TCAGCAGTCAATACATTTCAA  19064    T      _   GTC
                                TC GCAGTCAG ACA   TCAA
                                || ||||||||| |||   ||||
                                AG CGTCAGTT TGT   AGTT
                                 T       A   AA_
GAM2714  SS18     3'  ACAGGACAGTCTCAAA      24838      TCA
                                GCAG   GACAGTCTCAAA
                                ||||   ||||||||||||
                                TGTC   CTGTCAGAGTTT
                                  ___
GAM2715  ACK1     5'  TCCCCGCACTCTTCTGCGCCCG 25118       _   C    TA  A
            ACT                    TCCCCG ACTC TCTG  CT GACT
                                |||||| |||| ||||  || ||||
                                AGGGGC TGAG AGAC  GG CTGA
                                   G    A    GC  G
GAM2715  HKE4     3'  TCCCCGACTCCTCCTGTTACC  28094           _   _
                                TCCCCGACTCCTC TGT ACT
                                |||||||||||| ||| |||
                                AGGGGCTGAGGAG ACA TGG
                                       G   A
GAM2716  GBAS     3'  TGCTATTCAAGGTGTTCATTT  11238     A     TTTTA
                                TGC TATTTA    TGTTCATTT
                                ||| ||||||    |||||||||
                                ACG ATAAGT    ACAAGTAAA
                                  _     TCC__
GAM2716  NT5C3    3'  TGCATATTATTTCACCATT    32411        T      GTT
                                TGCATATT ATTTTAT   CATT
                                |||||||| |||||||   ||||
                                ACGTATAA TAAAGTG   GTAA
                                   _     ___
GAM2716  PACSIN1  3'  TGCATACTTTGTTTTGTTC    45165         AT   A
                                TGCATATTT  TTT TGTTC
                                |||||||||  ||| |||||
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                                ACGTATGAA  AAA ACAAG
                                     AC  _
GAM2717 NR1I2    3' TCCTTGTGCTGCTTTTG    35108    C    AGG  GACTC
                                TCC TGTGC  TGC    TTG
                                ||| |||||  |||    |||
                                AGG ACACG  ACG    AAC
                                  A   ___  AA___
GAM2717 XK      3' TCCCTGTGTAGGGCTCATTATT 34370       C  T  GACTC__
             TGT                  TCCCTGTG AGG GC      TTGT
                                ||||||||| ||| ||      ||||
                                AGGGACAC TCC CG      AACA
                                     A  _ AGTAATA
GAM2717 ZNF75    3' CCTTATGTATCAACTCTTGT  28325    GTGCAG  _
                                CCT     GTG CGACTCTTGT
                                |||     ||| ||||||||||
                                GGA     CAT GTTGAGAACA
                                  ATA___  A
GAM2718 AGM1     3' TTTATAAAGAATTATTC     31819          CA
                                TTTATAAAGAAT  TATTC
                                ||||||||||||  |||||
                                AAATATTTCTTA  ATAAG
                                          __
GAM2718 BCL10    3' TTTATAAAAAGTCATATTC   19410          A
                                TTTATAAAGA TCATATTC
                                |||||||||| ||||||||
                                AAATATTTTT AGTATAAG
                                      C
GAM2719 DDX20    3' TTGCTTTTATTGTTTTTA    28508        A
                                TTGCTTT ATTGTTTTTG
                                ||||||| ||||||||||
                                AACGAAA TAACAAAAAT
                                    A
GAM2719 DHFR     3' TTGCTTTAAGTGTTTGGCA   8998         T    TT
                                TTGCTTTAA TGTTT  GTA
                                ||||||||| |||||  |||
                                AACGAAATT ACAAA  CGT
                                     C    C_
GAM2719 DSG1     3' TTGCTTCAATTCGAGAAGTAAA 12604          GTTTTT
             CT                   TTGCTTTAATT     GTAAACT
                                ||||||||||     |||||||
                                AACGAAGTTAA     CATTTGA
                                      GCTCTT
GAM2719 EBI2     3' TTGCTTTATGTTGTTCTC    22395        A_
                                TTGCTTTA  TTGTTTTT
                                ||||||||  ||||||||
                                AACGAAAT  AACAAGAG
                                     AC
GAM2719 GYPA     3' TTGCTTTTATTAAAAATGTAAA 44632        A   TTTT
                                TTGCTTT ATTG   TGTAAA
                                ||||||| ||||   ||||||
```

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                                AACGAAA TAAT    ACATTT
                                    A    TTTT
GAM2719  HTR2A    3'  TTGTTTTAATTATTTTTATA   8391      C
                                TTG TTTAATTGTTTTTGTA
                                ||| ||||||||||||||||
                                AAC AAATTAATAAAAATAT
                                  A
GAM2719  MGA      3'  CTGCTTTAATTGTTTTAAC    41723              TGTA
                                TTGCTTTAATTGTTTT    AAC
                                ||||||||||||||||    |||
                                GACGAAATTAACAAAA    TTG
                                                    ____
GAM2719  OPA1     3'  TTACTTTAATTGTTGAAATAA  39273             TTT
                                TTGCTTTAATTGTT   GTAA
                                ||||||||||||||   ||||
                                AATGAAATTAACAA   TATT
                                         CTT
GAM2719  XYLB     3'  TTGCTTTGTTTGTTTTGC    23031        AA      T
                                TTGCTTT  TTGTTTT GT
                                |||||||  ||||||| ||
                                AACGAAA  AACAAAA CG
                                    CA      _
GAM2720  ARCN1    3'  GGTAGCAACAGCAGCAGACATG 11657    C   T       T__
                                GG AGC ACAGCAGC   TATG
                                || ||| ||||||||   ||||
                                CC TCG TGTCGTCG   GTAC
                                 A   T       TCT
GAM2720  CDK3     3'  AGGCAGCTGGGGCAGCAGCT   10378        A___
                                AGGCAGCT    CAGCAGCT
                                ||||||||    ||||||||
                                TCCGTCGA    GTCGTCGA
                                    CCCC
GAM2720  CELSR1   3'  AGGCAGCTGTAGGGCTTCTAG  30648         AC  CA    A
                                AGGCAGCT  AG  GCTT TGG
                                |||||||  ||  |||| |||
                                TCCGTCGA  TC  CGAA ATC
                                    CA  C_    G
GAM2720  DNM2     3'  AGGCACTTACAGTGGT      22376       GC    CAGCTTA
                                AGGCA  TACAG      TGGT
                                |||||  |||||      ||||
                                TCCGT  ATGTC      ACCA
                                  GA    ________
GAM2720  EGFL4    3'  AGGCAGCTGGAGCAGCAGT   41557         AC     TTAT
                                AGGCAGCT  AGCAGC    GGT
                                ||||||||  ||||||    |||
                                TCCGTCGA  TCGTCG    TCA
                                    CC     _____
GAM2720  HRMT1L1  3'  GGTGGCCACGGCAGCTCCTG  42182    CA    A      A
                                GG  GCTAC GCAGCTT TG
                                ||  ||||| ||||||| ||
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                                CC  CGGTG CGTCGAG AC
                                 AC    C      G
GAM2720  HTR4     3'  AGACGGCTATAGCAGCATAC  9298      A   C     T
                                AGGC GCTA AGCAGC TAT
                                |||| |||| ||||||| |||
                                TCTG CGAT TCGTCG ATG
                                  C   A     T
GAM2720  KCNK3    3'  GGTAATTATCAGCAATTATGGT 13912    C  C  _     C
            G                    GG AG TA CAGCAG TTATGGTG
                                || || || ||||||| ||||||||
                                CC TT AT GTCGTT AATACCAC
                                 A  A  A     _
GAM2720  LAMA5    3'  AGGCAGCTGCAGGGGCCT    24496        A   CA
                                AGGCAGCT CAG  GCTT
                                |||||||| |||  ||||
                                TCCGTCGA GTC  CGGA
                                     C   CC
GAM2720  MTMR3    3'  AGGCAGCTCGGCAGTTACAGTG 34390        ACA   C
                                AGGCAGCT   GCAG TTATGGTG
                                ||||||||   |||| ||||||||
                                TCCGTCGA   CGTC AATGTCAC
                                     GC_   _
GAM2720  NOV      3'  GGCGCAGCAGCTACAGGTG   14811     A  TAC      TAT
                                GGC GC   AGCAGCT   GGTG
                                ||| ||   |||||||   ||||
                                CCG CG   TCGTCGA   CCAC
                                  _ ____      TGT
GAM2720  RAGE     3'  AGGCAGCTGCGCGGGCCGCGGG 30601        ACA  A_   TAT
            TG                    AGGCAGCT   GC  GCT   GGTG
                                |||||||   ||  |||   ||||
                                TCCGTCGA   CG  CGG   CCAC
                                     CG_  CC   CGC
GAM2720  SLC5A2   3'  GGCAACTGCAGCGGG      16777        ACA    TTAT
                                GGCAGCT   GCAGC   GG
                                |||||||   |||||   ||
                                CCGTTGA   CGTCG   CC
                                     ____    C___
GAM2720  THBS1    3'  AGGTACTACAGTAGCTT     17509     CA      C
                                AGG  GCTACAG AGCTT
                                |||  ||||||| |||||
                                TCC  TGATGTC TCGAA
                                  A_      A
GAM2720  YWHAG    3'  AGGGAGCTGCAGCAGCTT    29787     C    A
                                AGG AGCT CAGCAGCTT
                                ||| |||| |||||||||
                                TCC TCGA GTCGTCGAA
                                  C   C
GAM2721  ARHG     3'  ACAAGGCACCAAGGCACAACTG 44114      T   A   A_
                                ACAAG GTA CAA  CACAACTG
                                ||||| ||| |||  ||||||||
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                                TGTTC CGT GTT  GTGTTGAC
                                  _  G  CC
GAM2721  C14orf2   3'  ACAAGTGTACAGTGACT     22204         A  AACACA
                                ACAAGTGTA CA     ACT
                                ||||||||| ||     |||
                                TGTTCACAT GT     TGA
                                     _ CAC___
GAM2721  CRMP1     3'  AGCATGAACACAACTG      10591       AACA
                                AGTGT   AACACAACTG
                                |||||   ||||||||||
                                TCGTA   TTGTGTTGAC
                                  C___
GAM2721  NUP62     3'  TAACAAATGTGACAGGGACCGG 29603          A  A__  ACAA
            GCTG                  TAACAAGTGT ACA  AC   CTG
                                |||||||||| |||  ||   |||
                                ATTGTTTACA TGT  TG   GAC
                                      C  CCC  GCCC
GAM2721  TSN       3'  CAACAAGCCAGCAACAAACACA 21490        __
            ACTG                  TAACAAGT  GTAACAAACACAACTG
                                ||||||||  ||||||||||||||||
                                GTTGTTCG  CGTTGTTTGTGTTGAC
                                     GT
GAM2721  OGN       3'  GAGTTTAAAACTTTTTTT    37458      __
                                GAGT  AAAACTTTTTTT
                                ||||  ||||||||||||
                                CTCA  TTTTGAAAAAAA
                                  AA
GAM2721  PART1     3'  TGAATTAAAGCATTTTTTT   32461           AAAC
                                TGAATTAGAGTA   TTTTTTT
                                ||||||||||||   |||||||
                                ACTTAATTTCGT   AAAAAAA
                                       _____
GAM2722  GABPB1    3'  TGGCTGTACCTTTGTTGT    23528      TGTTA       A
                                TGGT    TGTGCCTTT TTGT
                                ||||    ||||||||| ||||
                                ACCG    ACATGGAAA AACA
                                  _____       C
GAM2723  ATP11A    3'  TGGTATGTGTACACGTGCATG  44191    A     C  _
                                TG TATGTG AC CGTGTGTG
                                || |||||| || ||||||||
                                AC ATACAC TG GCACGTAC
                                 C     A  T
GAM2723  ATP8B2    3'  TGATATGTGTGTGTGT      42219         CACC
                                TGATATGTG   GTGTGT
                                |||||||||   ||||||
                                ACTATACAC   CACACA
                                     A___
GAM2723  KCNJ1     5'  TGATAGTGGAGTCGTGTGATTT 6890        T   CACCG
                                TGATA GTG    TGTGTGATTT
                                ||||| |||    ||||||||||
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                                ACTAT CAC    GCACACTAAA
                                   _  CTCA_
GAM2723 NAPB    3' TGATATGTGTGTGTGTG    43180        CACC
                                TGATATGTG   GTGTGTG
                                |||||||||   |||||||
                                ACTATACAC   CACACAC
                                     A___
GAM2723 PATE    3' TGTGTGTGTGTGTGATTT    39648     CACC
                                TGTG   GTGTGTGATTT
                                ||||   ||||||||||
                                ACAC   CACACACTAAA
                                  ACA_
GAM2723 SVIL    3' TGACATGTGTACTGTTTGT   34738        C C G
                                TGATATGTG AC GT TGT
                                ||||||||| || || |||
                                ACTGTACAC TG CA ACA
                                     A A A
GAM2723 ATP11A  3' AGCCTGCGCATGTGTTTGTG  44170   G  GA  A
                                AG CTG  CAT TGTTTGTG
                                || |||  ||| ||||||||
                                TC GAC  GTA ACAAACAC
                                 G  GC  C
GAM2723 CASP4   3' GAGGGCTGGGCTGCTTGTG   10269   A    ACATA
                                GA GGCTGG    TGTTTGTG
                                || ||||||    ||||||||
                                CT CCGACC    ACGAACAC
                                 C    CG___
GAM2723 FHL1    5' CAAAGGCTGGATATGGTTG   11092         CA   T
                                CGAAGGCTGGA  TATG TTG
                                ||||||||||  |||| |||
                                GTTTCCGACCT  ATAC AAC
                                      __   C
GAM2723 GLTSCR1 3' ACGGAGCTGGACGTGCGGATG 31830    AA     ATA  TT
                                ACG  GGCTGGAC   TGT  GTG
                                |||  ||||||||   |||  |||
                                TGC  TCGACCTG   ACG  TAC
                                  C_      C__   CC
GAM2723 ITGB4   3' ACAAAGGCTGGGTCCTTGT   6843         ACATATG
                                ACGAAGGCTGG     TTTGT
                                ||||||||||      |||||
                                TGTTTCCGACC     GAACA
                                     CAG____
GAM2723 MEF2D   3' GAAGGCTGGACGTGCT     25418         ATA
                                GAAGGCTGGAC   TGTT
                                ||||||||||   ||||
                                CTTCCGACCTG   ACGA
                                     C__
GAM2723 MX1     3' ACGGGGCTGGACAGAGTGT   14688    AA      TA_
                                ACG  GGCTGGACA   TGT
                                |||  |||||||||   |||
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                                TGC  CCGACCTGT   ACA
                                  C_       CTC
GAM2723  PPL      3'  CGAGGGCTGGACACTTGT    15492     A        A
                                CGA GGCTGGACAT TGT
                                ||| |||||||||| |||
                                GCT CCGACCTGTG ACA
                                  C         A
GAM2723  STXBP1   3'  AGAGATGATATATGTTTGTG   17201     CTG  C
                                AGG   GA ATATGTTTGTG
                                |||   || ||||||||||
                                TCT   CT TATACAAACAC
                                  CTA  A
GAM2724  APAF1    5'  GACAAGACTGGGAGACTC    29820        C___
                                GACAAGAC    GGATTC
                                ||||||||    ||||||
                                CTGTTCTG    TCTGAG
                                     ACCC
GAM2724  COMT     5'  TGCAGGATGAACTCGTTC    28696    A  A  CC
                                TG CA GA  GGATTCGTTC
                                || || ||  ||||||||||
                                AC GT CT  CTTGAGCAAG
                                 _  C  A_
GAM2724  DLX4     3'  TGGCAAGACCAAGGGTTC    39624    A      __ A
                                TG CAAGACC  GG TTC
                                || |||||||  || |||
                                AC GTTCTGG  CC AAG
                                 C      TT  C
GAM2724  NRCAM    5'  ACAAAGATTCGTTC       22686      GACC
                                ACAA    GGATTCGTTC
                                ||||    ||||||||||
                                TGTT    TCTAAGCAAG
                                  _____
GAM2724  PTGFR    3'  TGACAAGAATGGGCCCATTC  9662         CC  AT
                                TGACAAGA  GG  TCGTTC
                                ||||||||  ||  ||||||
                                ACTGTTCT  CC  GGTAAG
                                     TA  CG
GAM2724  WHSC1    3'  TGACAGACCCAGCACTTGTTC 39406      A   _ _  C
                                TGACA GACC GG ATT GTTC
                                ||||| |||| || ||| ||||
                                ACTGT CTGG TC TGA CAAG
                                   _   G  G   A
GAM2725  CDY1     3'  TGATCGTCAGTGGATTTTG   41260      AGCCT   A
                                TGATC    TCAG GGATTTTG
                                |||||    |||| ||||||||
                                ACTAG    AGTC CCTAAAAC
                                   C_____   A
GAM2725  PIP5K1B  3'  TGATCAGCCTTAAGTTTG    18669          C  AGGAT
                                TGATCAGCCTT AG    TTTG
                                |||||||||| ||    ||||
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                                ACTAGTCGGAA TC    AAAC
                                      T _____
GAM2726 MKPX    3' AACATGACTACGTATATAT   33629        __
                                AACATGAT  TGTATATAT
                                ||||||||  |||||||||
                                TTGTACTG  GCATATATA
                                    AT
GAM2727 EPB41   5' TCTGTTTTGAGTTCCGGTTCA 20771       ATAT  GAG
                                TCTGTTTT   AGT  GGTTCA
                                ||||||||   |||  ||||||
                                AGACAAAA   TCA  CCAAGT
                                    C___  AGG
GAM2727 GPR30   5' TCTGTTTTAAATGGTGAATCCA 11319       T A   GG
                                TCTGTTTTA AT GTGA  GTTCA
                                ||||||||| || ||||  |||||
                                AGACAAAAT TA CACT  TAGGT
                                     T C   __
GAM2727 PMCHL1  3' TGTCTTATATGCTTTAGGTT  36670       A  GA_
                                TGTTTTATAT GT  GGGTT
                                |||||||||| ||  |||||
                                ACAGAATATA CG  TCCAA
                                     _ AAA
GAM2727 TRIM14  3' TCAGTTTTATATGGTT     37707    T      AGTGAG
                                TC GTTTTATAT     GGTT
                                || |||||||||     ||||
                                AG CAAAATATA     CCAA
                                 T       _______
GAM2728 A1BG    3' TCCTGGGAGGAATGAGGGA   39095    G    A  CG
                                TCC TGGGA GA  ATGGGGGA
                                ||| ||||| ||  ||||||||
                                AGG ACCCT CT  TACTCCCT
                                  _    C __
GAM2728 ABCC1   3' TCCGTGGGAAGCACCAGGAAA 33408         A G  G
                                TCCGTGGGAAG C AT GGGGAA
                                |||||||||| | || ||||||
                                AGGCACCCTTC G TG TCCTTT
                                     _ _ G
GAM2728 ATP1B2  3' TGGGAAGGCGAATGGGGGAA  11740       A  _
                                TGGGAAG CGA TGGGGGAA
                                ||||||| ||| ||||||||
                                ACCCTTC GCT ACCCCCTT
                                    C  T
GAM2728 C18orf2 3' TCCATGGGAAGGTGAAGGGAG 36408         AC  T
                                TCCGTGGGAAG  GA GGGGG
                                ||||||||||  || |||||
                                AGGTACCCTTC  CT CCCTC
                                     CA  T
GAM2728 CALCR   3' TCCTGGGAGGATGGAGA    11946    G    AGAC
                                TCC TGGGA   GATGGGGG
                                ||| |||||   ||||||||
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                              AGG ACCCT   CTACCTCT
                                _   C___
GAM2728 CELSR2   3' TCTTTGGGAAGGGAAAGGGGA 10856   CG     AC  T
                              TC  TGGGAAG  GA GGGGGA
                              ||  |||||||  || ||||||
                              AG  ACCCTTC  CT TCCCCT
                               AA      C_  T
GAM2728 CLN5     3' GTGGGAAGAGGGAGA      27085        CGAT
                              GTGGGAAGA   GGGGGA
                              |||||||||   ||||||
                              CACCCTTCT   CCCTCT
                                   ____
GAM2728 COL1A2   3' TGGGGGAGCGGGGGAA     6388      AA  CGA
                              TGGG  GA   TGGGGGAA
                              ||||  ||   ||||||||
                              ACCC  CT   GCCCCCTT
                                C_  C__
GAM2728 CUL4B    3' GTGGGAAAAATGAGGGA     18725        CG
                              GTGGGAAGA  ATGGGGGA
                              |||||||||  ||||||||
                              CACCCTTTT  TACTCCCT
                                   __
GAM2728 CYLN2    3' TGGTCCACTGATGGGGGA    18073     GAAG  _
                              TGG    AC GATGGGGGA
                              |||    || |||||||||
                              ACC    TG CTACCCCCT
                                AGG_  A
GAM2728 DLG4     3' GTGGGAGAGGATGGGGGA    10709       A  C
                              GTGGGA GA GATGGGGGA
                              |||||| || |||||||||
                              CACCCT CT CTACCCCCT
                                 _  C
GAM2728 DPP6     3' TCCGAGGGAAGAGGGAG     39134      T      CGAT
                              TCCG GGGAAGA    GGGGG
                              |||| |||||||    |||||
                              AGGC CCCTTCT    CCCTC
                                T      _____
GAM2728 EFNA3    3' TCTCTGGGGGGACAAAGGGAGA 22403    CG    AA    T
                              TC  TGGG  GACGA GGGGGA
                              ||  ||||  ||||| ||||||
                              AG  ACCC  CTGTT CCCTCT
                               AG    CC    T
GAM2728 FBXL11   3' TCGGTGGGGAGTCAGGGGAA  29441    C    A  ACGA
                              TC GTGGG AG    TGGGGGAA
                              || ||||| ||    ||||||||
                              AG CACCC TC    GTCCCCTT
                               C    C  A___
GAM2728 GATA3    5' TCGGTGGGGGGATGGGAA    13099    C    AAGAC
                              TC GTGGG    GATGGGGG
                              || |||||    ||||||||
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                                AG CACCC    CTACCCTT
                                 C    CC___
GAM2728  HAS3    3'  CGTGGGAGATGAAGGAA    39772       AGAC
                                CGTGGGA   GATGGGGGAA
                                |||||||   ||||||||||
                                GCACCCT   CTACTTCCTT
                                    ____
GAM2728  HOXB9   3'  GTTGGAAGGAGAGGGAAA   35846   G    AC  T
                                GT GGAAG  GA GGGGGAAA
                                || |||||  || ||||||||
                                CA CCTTC  CT CTCCCTTT
                                 A    __ _
GAM2728  JPH3    3'  TCCCTGGGGTCTGGTGGGGGAA 34025    G   AAGACGA
            A                    TCC TGGG      TGGGGGAAA
                                ||| ||||      |||||||||
                                AGG ACCC      ACCCCCTTT
                                  G   CAGACC_
GAM2728  LCP1    3'  TCCTGGGAGGCGGAGGGGGGAA 14109    G    AGAC  T
                                TCC TGGGA   GA GGGGGAA
                                ||| |||||   || |||||||
                                AGG ACCCT   CT CCCCCTT
                                  _    CCGC  C
GAM2728  MAPK4   3'  TCTTTGGGAGTGTTGGGGGAA  15668   CG    AGACGA
                                TC  TGGGA     TGGGGGAA
                                ||  |||||     ||||||||
                                AG  ACCCT     ACCCCCTT
                                 AA    CACA__
GAM2728  MEN1    3'  GTGGGAAGGGAGGCTGGGGG   39196       ACGA__
                                GTGGGAAG     TGGGGG
                                ||||||||     ||||||
                                CACCCTTC     ACCCCC
                                    CCTCCG
GAM2728  MYO1D   3'  GTGGCAGGACGGGAA      43504     GA  AC
                                GTGG  AG  GATGGGGG
                                ||||  ||  ||||||||
                                CACC  TC  CTGCCCTT
                                  G_  __
GAM2728  NPHP1   3'  TCCGTGGGAAGCTGAGGG    41683         ACGA
                                TCCGTGGGAAG   TGGGGG
                                ||||||||||   ||||||
                                AGGCACCCTTC   ACTCCC
                                      G___
GAM2728  PAK1    5'  TCCGCGGGGGGGCAAGGGGGGA 15085       AAGA  T
                                TCCGTGGG   CGA GGGGGA
                                ||||||||   ||| ||||||
                                AGGCGCCC   GTT CCCCCT
                                    CCCC  C
GAM2728  PBX2    3'  GTGGGAAGAAGGGGGA     15108        CGAT
                                GTGGGAAGA   GGGGGA
                                |||||||||   ||||||
```

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                                CACCCTTCT   CCCCCT
                                     T___
GAM2728 PEA15   3' TCCTGGAGGATGGGGGAA   19083    G   AAGAC
                                TCC TGGG    GATGGGGGAA
                                ||| ||||    ||||||||||
                                AGG ACCT    CTACCCCCTT
                                  _   C____
GAM2728 PTGFRN  3' GTGGGGGAGCAGGGGGAAA  42594     A_  ACGAT
                                GTGGG  AG    GGGGGAAA
                                |||||  ||    ||||||||
                                CACCC  TC    CCCCCTTT
                                   CC  GT___
GAM2728 STC1    3' CGTGGGGAGAAAAGGGGGG  17175     A   C  T
                                CGTGGG AGA GA GGGGG
                                |||||| ||| || |||||
                                GCACCC TCT TT CCCCC
                                    C   T  C
GAM2728 TEM8    3' GTGGGAGCCTGGGGGAA    38188      A ACGA
                                GTGGGA G    TGGGGGAA
                                ||||||| |   ||||||||
                                CACCCT C    ACCCCCTT
                                   _ GG__
GAM2728 TFG     5' CGTGGCAGGTGGGGGAA    25871     GA  ACGA
                                CGTGG  AG   TGGGGGAA
                                |||||  ||   ||||||||
                                GCACC  TC   ACCCCCTT
                                   G_  C___
GAM2728 TM6SF2  3' TCCATGGGGGGATGATGGG  43662       AA  C
                                TCCGTGGG  GA GATGGG
                                ||||||||  || ||||||
                                AGGTACCC  CT CTACCC
                                     CC  A
GAM2728 YWHAB   5' CCGTGGGAGGGCTGCAGGGAA 18185       AGACGA  _
                                CCGTGGGA     TG GGGGAA
                                ||||||||     || ||||||
                                GGCACCCT     AC TCCCTT
                                     CCCG__  G
GAM2728 YWHAB   5' CCCGTGGGAGGGCTGCAGGGAA 18184       AGACGA  _
                                TCCGTGGGA     TG GGGGAA
                                |||||||||     || ||||||
                                GGGCACCCT     AC TCCCTT
                                     CCCG__  G
GAM2729 CFTR    3' TGTAATATATGTTTGAAACATT 7959      C    CA
            A                    TGTA ATATA  TTTGGAACATTA
                                ||||| |||||  ||||||||||||
                                ACAT TATAT  AAACTTTGTAAT
                                  _    AC
GAM2729 DISC1   3' TACATATACAAGAAGGCATT  33048        TTT_  AA
                                TACATATACA   GG  CATT
                                ||||||||||   ||  ||||
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                                ATGTATATGT   CC  GTAA
                                     TCTT  __
GAM2729  MADH6    3'  TGTCCATATACACACATT    24609     A       TTGGA
                                TGT CATATACAT    ACATT
                                ||| |||||||||    |||||
                                ACA GTATATGTG    TGTAA
                                  G       _____
GAM2729  RECK     3'  TGTGCATACACACAAGAA    34418     A       TT
                                TGT CATATACAT  GGA
                                ||| |||||||||  |||
                                ACA GTATGTGTG  CTT
                                  C       TT
GAM2729  SOS2     3'  TGTACATACATGGCATATT   42855         CATT   AAC
                                TGTACATATA   TGG   ATT
                                ||||||||||   |||   |||
                                ACATGTATGT   ACC   TAA
                                     ____  GTA
GAM2729  MGST2    3'  TATTTAACAAATGATACCA   14496      TT__
                                TGTTT   AATGATACCA
                                |||||   ||||||||||
                                ATAAA   TTACTATGGT
                                   TTGT
GAM2729  SP3      3'  TAGTGTTTTATTAACTACCACA 44381     T    TAATGA
           C                     TAGT GTTTT     TACCACAC
                                ||||| |||||     ||||||||
                                ATCA CAAAA     ATGGTGTG
                                  _    TAATTG
GAM2729  UC28     3'  GTAGTTTTTAATGGCCCAC   34692    T       ATA
                                GT GTTTTTAATG   CCAC
                                || ||||||||||   ||||
                                CA CAAAAATTAC   GGTG
                                 T        CG_
GAM2729  ZNF10    3'  GTTGTTTTTAATTGTACTACA  31739          GA   C
                                GTTGTTTTTAAT  TAC ACA
                                ||||||||||||  ||| |||
                                CAACAAAAATTA  ATG TGT
                                      AC   A
GAM2730  ARCN1    3'  GAAAGGAGGGGACTGATGA   11652     CTAT   A_
                                GAAA   GAGG  ACTGATGA
                                ||||   ||||  ||||||||
                                CTTT   CTCC  TGACTACT
                                  C___    CC
GAM2730  CALU     3'  TGTGAGGTATGAGGATCCCTG  10266      AAC      A  GA
                                TGTGA   TATGAGGA CT  TG
                                |||||   |||||||| ||  ||
                                ACACT   ATACTCCT GG  AC
                                  CC_       A  G_
GAM2730  CD3E     3'  TGTGAGGGTGTGACTACTGATG 8815       AACTA   GGA
           A                     TGTGA    TGA   ACTGATGA
                                |||||    |||   ||||||||
```

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                                ACACT    ACT   TGACTACT
                                  CCCAC   GA_
GAM2730  CTSB     3'  TGGAGGTACTGGGGGAACTGAT 42109    T  AACTA  A_
             G                   TG GA    TG  GGAACTGATG
                                 || ||    ||  ||||||||||
                                 AC CT    AC  CCTTGACTAC
                                  _  CCATG  CC
GAM2730  INPP5B   3'  GTGGGTTGCAGAGGAACTGGTG 45473     AAACTAT       A
             A                   GTG      GAGGAACTG TGA
                                 |||      ||||||||| |||
                                 CAC      CTCCTTGAC ACT
                                   CCAACGT       C
GAM2730  TRRAP    3'  GTGAAACTATGGGGCTTCTGTG 18592          A  AA_  A
             A                   GTGAAACTATG GG   CTG TGA
                                 |||||||||| ||   ||| |||
                                 CACTTTGATAC CC   GAC ACT
                                       C  GAA  _
GAM2731  ADARB1   3'  CAGCGTGGGGATGATAAAAA  31870       AA   TA
                                 TAGCGTG  GGA  TGATAAAAA
                                 |||||||  |||  |||||||||
                                 GTCGCAC  CCT  ACTATTTTT
                                    C_  __
GAM2731  ANKRD3   3'  GCGTGTGGAGATAAAAA    33967      AA   TAT
                                 GCGTG  GGA   GATAAAAA
                                 |||||  |||   ||||||||
                                 CGCAC  CCT   CTATTTTT
                                   A_  ____
GAM2731  SIM2     3'  TAGTGTGAAGAAAATTGA    22881     C      TA_
                                 TAG GTGAAGGA   TGA
                                 ||| ||||||||   |||
                                 ATC CACTTCTT   ACT
                                   A       TTA
GAM2732  TREM1    3'  ACATTCTCGTGGGTTCGT    32998        __
                                 ACATTCTC  GGGTTCGT
                                 ||||||||  ||||||||
                                 TGTAAGAG  CCCAAGCA
                                      CA
GAM2733  ATP11B   3'  TTGTATATATGATATACC    44314         AAC
                                 TTGTATATAT   GTACC
                                 ||||||||||   |||||
                                 AACATATATA   TATGG
                                       CTA
GAM2733  GALNT7   3'  TTGTAATGATACCATGAT    38365      TATATAAC
                                 TTGTA       GTACCATGAT
                                 |||||       ||||||||||
                                 AACAT       TATGGTACTA
                                   TAC_____
GAM2733  MYO1E    3'  TTATATATACAGTATATGATC  22660          AC   CC
                                 TTGTATATATA  GTA  ATGATC
                                 ||||||||||  |||  ||||||
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                                AATATATATGT  CAT  TACTAG
                                      __  A_
GAM2734 ATP1A2   3'  TTAGATAGGGAGTAAGGGA   8716          C
                                TTGGATAGGGGG AAGGGA
                                |||||||||||| ||||||
                                AATCTATCCCTC TTCCCT
                                       A
GAM2734 B3GALT5  3'  CATTGATCAAAAACAAGGGA  37680      ATA
                                CATTGG  GGGGGCAAGGGA
                                ||||||  ||||||||||||
                                GTAACT  TTTTTGTTCCCT
                                   AG_
GAM2734 B4GALT5  3'  TGGGGTAGGAGATGGGGA   21947    A_     CAA
                                TGG  TAGGGGG  GGGA
                                |||  |||||||  ||||
                                ACC  ATCCTCT  CCCT
                                  CC     AC_
GAM2734 B4GALT5  3'  TGGAAAACAAGGGCGGGGGA  21945    TA__    AA
                                TGGA   GGGGGC  GGGA
                                ||||   ||||||  ||||
                                ACCT   TTCCCG  CCCT
                                  TTTG    CC
GAM2734 C1QB     3'  CATTGGCTGGGCAAGGG     7944       ATAGG
                                CATTGG    GGGCAAGGG
                                ||||||    |||||||||
                                GTAACC    CCCGTTCCC
                                   GA___
GAM2734 CAPG     3'  ATTGAACATCTGCAGGGG    11961       GGGG  A
                                ATTGGATA   GCA GGG
                                ||||||||   ||| |||
                                TAACTTGT   CGT CCC
                                     AGA_  C
GAM2734 CSF3     3'  CATGGGATGGGGAGGG      8900     T   A   GCA
                                CAT GGAT GGGG  AGGG
                                ||| |||| ||||  ||||
                                GTA CCTA CCCC  TCCC
                                  C   _   ___
GAM2734 CSF3R    3'  CATTGGGTGGGGCTGGA     8905       ATAG   AAG
                                CATTGG   GGGGC  GGA
                                ||||||   |||||  |||
                                GTAACC   CCCCG  CCT
                                   CA__    A__
GAM2734 CXCL16   3'  CACTGGGGTAGGCAAGGGA   35194      ATA _
                                CATTGG  GG GGGCAAGGGA
                                ||||||  || ||||||||||
                                GTGACC  CC TCCGTTCCCT
                                   ___ A
GAM2734 CYFIP1   3'  TGGTAACTGGCAAGGGA     42459    A  GG
                                TGG TAG  GGCAAGGGA
                                ||| |||  |||||||||
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                                ACC ATT  CCGTTCCCT
                                  _  GA
GAM2734  EFNB1    3'  TGGCAAGGGGGGCGAGGGA   20729     ATA_     A
                                TGG    GGGGGC AGGGA
                                |||    |||||| |||||
                                ACC    CCCCCG TCCCT
                                  GTTC     C
GAM2734  GRB7     3'  CACTGGATGGGTGGAGGG    23639        A  _  CA
                                CATTGGAT GGG GG  AGGG
                                |||||||| ||| ||  ||||
                                GTGACCTA CCC CC  TCCC
                                     _  A  __
GAM2734  ISLR     3'  CATTGGTAGGGGCAAGGG    24432       ATA
                                CATTGG   GGGGGCAAGGG
                                ||||||   ||||||||||
                                GTAACC   TCCCCGTTCCC
                                   A__
GAM2734  JAG1     3'  TTGAATAACAAGGG        6861         GGGG
                                TTGGATA    GCAAGGG
                                |||||||    |||||||
                                AACTTAT    TGTTCCC
                                     _____
GAM2734  KRT4     3'  CATTGGACTGGGAAGGGA    14002         A    GCA
                                CATTGGAT GGGG   AGGGA
                                |||||||| ||||   |||||
                                GTAACCTG CCCT   TCCCT
                                     A   ___
GAM2734  MASP1    3'  TGGATAGGCCGAAGGAGGG   40114         _____   CA
                                TGGATAGG    GGG  AGGG
                                ||||||||    |||  ||||
                                ACCTATCC    TCC  TCCC
                                     GGCT  __
GAM2734  MEN1     3'  ATTGGATAGGAGATTCAGA   39160           CAA
                                ATTGGATAGGGGG   GGG
                                ||||||||||||   |||
                                TAACCTATCCTCT   TCT
                                       AAG
GAM2734  PDE4A    3'  ATTGGGTAGGGGGCAGG     26253       A        A
                                ATTGG TAGGGGGCA GG
                                ||||| |||||||| ||
                                TAACC ATCCCCCGT CC
                                   C       _
GAM2734  PPP1R14B 3'  ACTGAGGGGGCAGGGGA     39792      GAT       A
                                ATTG   AGGGGGCA GGGA
                                ||||   |||||||| ||||
                                TGAC   TCCCCCGT CCCT
                                   ___       C
GAM2734  PPP2R2B  5'  GGAGAGGGGGGCAGGGGA    21334     TA_      A
                                GGA   GGGGGCA GGGA
                                |||   ||||||| ||||
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                                CCT   CCCCCGT CCCT
                                  CTC      C
GAM2734  PYGB     3'  CATTGGATGGCTACAAAGG   16046        A  GG
                                CATTGGAT GG  GCAAGGG
                                |||||||| ||  |||||||
                                GTAACCTA CC  TGTTTCC
                                     _  GA
GAM2734  RARG     3'  CATTGGAAGGGGTGGGGA    9722         T    GCAA
                                CATTGGA AGGGG   GGGA
                                ||||||| |||||   ||||
                                GTAACCT TCCCC   CCCT
                                     _    AC__
GAM2734  RDX      3'  TGGAAAGGGCAAGGGA      16238      TA
                                TGGA  GGGGGGCAAGGGA
                                ||||  ||||||||||||
                                ACCT  TTCCCGTTCCCT

                                  __
GAM2734  RFX1     3'  TTGAGCTTGGGGGGCAAGGGA   16302     _ ATA
                                TTG G   GGGGGGCAAGGGA
                                ||| |   ||||||||||||
                                AAC C   CCCCCGTTCCCT
                                  T GAA
GAM2734  RPA3     5'  TTGGATAGGGGCGG        16388          G AAG
                                TTGGATAGGGG C   GG
                                |||||||||| |   ||
                                AACCTATCCCC G   CC

                                   _ ___
GAM2734  SLC38A3  3'  CACTGGATGGGAGCAGGGG   27758         A      A
                                CATTGGAT GGGGGCA GGG
                                |||||||| ||||||| |||
                                GTGACCTA CCCTCGT CCC
                                     _      C
GAM2734  SLC7A5   3'  CACTGGATGGTGAGGGG     18541         A  _   CAA
                                CATTGGAT GG GGG   GGG
                                |||||||| || |||   |||
                                GTGACCTA CC CTC   CCC
                                     _  A   ___
GAM2734  SOX10    3'  CACTGGGAGGCAAGGG      27996       ATAG
                                CATTGG   GGGGCAAGGG
                                ||||||   ||||||||||
                                GTGACC   CTCCGTTCCC

                                   ____
GAM2734  TNS      3'  CACTGGCCCTGGGCAAGGG   35466       ATAGG
                                CATTGG    GGGCAAGGG
                                ||||||    |||||||||
                                GTGACC    CCCGTTCCC
                                   GGGA_
GAM2734  TTC3     5'  TTCAATGGGGGGCAAGGG    17724    G   A
                                TT GAT GGGGGCAAGGG
                                || ||| ||||||||||
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                                AA TTA CCCCCGTTCCC
                                 G   C
GAM2734  UBTF     3'  GGCCAGGGGGGCAAGGGA    30614    ATA_
                                GG    GGGGGCAAGGGA
                                ||    ||||||||||||
                                CC    CCCCCGTTCCCT
                                 GGTC
GAM2734  UNC13    3'  CAGTGGATTCTACTCAAGGGA  26861    T    AGGGGG
                                CA TGGAT     CAAGGGA
                                || |||||     |||||||
                                GT ACCTA     GTTCCCT
                                 C    AGATGA
GAM2734  VTN      3'  ATTGGGCTGGGGGAAGGA    8467       ATA    C
                                ATTGG   GGGGG AAGGG
                                |||||   ||||| |||||
                                TAACC   CCCCC TTCCT
                                   CGA    _
GAM2734  TCFL4    3'  TTAATTTTATATAAAAATATTT 41832       CA
                                TTAATT  TTGTATGAAAATATTT
                                ||||||  ||||||||||||||||
                                AATTAA  AATATATTTTTATAAA
                                   __
GAM2735  ATP8B2   3'  ACCAACCACAACATAAAA    42198    A     CCA
                                ACC AGCCAT   AACATAAAA
                                ||| ||||||   |||||||||
                                TGG TTGGTG   TTGTATTTT
                                  _    ____
GAM2735  COX7A2L  3'  AAGCCATCCAAGTAAAAA    21789          ACA
                                AAGCCATCCAA   TAAAAA
                                ||||||||||   ||||||
                                TTCGGTAGGTT   ATTTTT
                                      C__
GAM2735  CYP19    3'  GCCCCAGACATAAAAA     36305    AT   A
                                GCC  CCA ACATAAAAA
                                |||  ||| |||||||||
                                CGG  GGT TGTATTTTT
                                  __   C
GAM2735  EIF5A2   3'  CAAAGTCCTCACATAAAAAC  33785     CCA   AA
                                CAAG   TCC  ACATAAAAAC
                                ||||   |||  ||||||||||
                                GTTT   AGG  TGTATTTTTG
                                  C__   AG
GAM2735  FBXL11   3'  CCAAAAAACAAACATAAAAAC 29426      CCATC
                                CCAAG    CAAACATAAAAAC
                                |||||    ||||||||||||
                                GGTTT    GTTTGTATTTTTG
                                   TTT__
GAM2735  FOXO1A   3'  ACCAAGCCATTTAAACATAA  12880         CC
                                ACCAAGCCAT  AAACATAA
                                ||||||||||  ||||||||
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                                TGGTTCGGTA  TTTGTATT
                                      AA
GAM2735  KCNA5    3'  AGCCACTTACCAGGCATAAAAA 40681       ___  AA
                                AGCCAT   CCA  CATAAAAA
                                ||||||   |||  ||||||||
                                TCGGTG   GGT  GTATTTTT
                                   AAT   CC
GAM2735  SLC6A3   3'  GCCATTCGCAAACATAAAAAC  9812       _ _
                                GCCAT C CAAACATAAAAAC
                                ||||| | ||||||||||||
                                CGGTA G GTTTGTATTTTTG
                                  A C
GAM2735  SMURF1   3'  CAAGCCACTTTAAGATAAAA   45184        CCAAAC
                                CAAGCCAT     ATAAAA
                                ||||||||     ||||||
                                GTTCGGTG     TATTTT
                                     AAATTC
GAM2735  TAL1     3'  ACCGTGCCGTCTTCACAAAAA  17277     AA   A  CAAA
                                ACC  GCC TC    CATAAAAA
                                |||  ||| ||    ||||||||
                                TGG  CGG AG    GTGTTTTT
                                  CA   C  AA__
GAM2735  TGFBR2   5'  ACCAAGTAATTCAACACAAA   17468       CCATCCA
                                ACCAAG      AACATAAA
                                ||||||      ||||||||
                                TGGTTC      TTGTGTTT
                                   ATTAAG_
GAM2735  TP63     3'  CAAGCCATCCAAAACAA     18994            C
                                CAAGCCATCCAAA ATAA
                                |||||||||||| ||||
                                GTTCGGTAGGTTT TGTT
                                          _
GAM2735  UBE4A    3'  CCATAGCCATTCATAAAAA   21970     _     CCAAA
                                CCA AGCCAT    CATAAAAA
                                ||| ||||||    ||||||||
                                GGT TCGGTA    GTATTTTT
                                  A     A____
GAM2735  WNT1     3'  ACCAAGTCATCGATAAAAA   24075       C    CAAAC
                                ACCAAG CATC    ATAAAAA
                                |||||| ||||    |||||||
                                TGGTTC GTAG    TATTTTT
                                   A   C____
GAM2735  ACHE     3'  TCGGGGTGGGGTGGGGATGGG  31865      A       AT  T
                                TTGG GTGGGGTGG  GG GTGGG
                                |||| |||||||||  || |||||
                                AGCC CACCCCACC  CC TACCC
                                  C       __  _
GAM2735  EMX2     5'  TTGGGGTGGGGGTGGGGGTGGG 44709      A     _   AT  T
                                TTGG GTGGGG TGG  GG GTGGG
                                |||| |||||| |||  || |||||
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                                AACC CACCCC ACC  CC CACCC
                                  C     C  __ _
GAM2735  FASN     3'  TGGGGTGGGGGTGGGGTGGG   19949     A       AT    T
                                TGG GTGGGGTGG  GGTG GG
                                ||| |||||||||  |||| ||
                                ACC CACCCCACC  CCAC CC
                                  C       __   _
GAM2735  FLOT1    3'  TTGAGGTGGGGTGGAGTGG   25136     GA        TGGT
                                TTG  GTGGGGTGGA   GTGG
                                |||  ||||||||||   ||||
                                AAC  CACCCCACCT   CACC
                                  TC       _____
GAM2735  HSF4     5'  TGGGGTGGGGTGGAGTGG    40774     A        TGGT
                                TGG GTGGGGTGGA   GTGG
                                ||| ||||||||||   ||||
                                ACC CACCCCACCT   CACC
                                  C       _____
GAM2735  HSF4     5'  TGGAGTGGGGTGGGGTGGG   40773           AT    T
                                TGGAGTGGGGTGG  GGTG GG
                                ||||||||||||  |||| ||
                                ACCTCACCCCACC  CCAC CC
                                              __   _
GAM2735  ID3      3'  GGGGTGGGGTGGGAGCAGGG   44274    A       AT    T
                                GG GTGGGGTGG  GGTG GGG
                                || |||||||||  |||| |||
                                CC CACCCCACC  TCGT CCC
                                  C       C_   _
GAM2735  LASS1    3'  TTGGAGGGGGTGGAGGG     34621       T       T
                                TTGGAG GGGGTGGA GG
                                ||||||| |||||||| ||
                                AACCTC CCCCACCT CC
                                    _       C
GAM2735  MECP2    3'  TTGGATTGGGGCTGGTGTGGG  22625      G     GGA
                                TTGGA TGGGGT   TGGTGTGGG
                                ||||| ||||||   |||||||||
                                AACCT ACCCCG   ACCACACCC
                                   A     ___
GAM2735  REQ      3'  CTGGGGTGGGGTGGAATGG    26544     A        TGGT
                                TTGG GTGGGGTGGA   GTGG
                                |||| ||||||||||   ||||
                                GACC CACCCCACCT   TACC
                                  C       _____
GAM2735  S100A1   3'  GGGGTGGGGTGGGCAAGGGTGG 26562    A       AT__  T
              G                  GG GTGGGGTGG   GG GTGGG
                                || |||||||||   || |||||
                                CC CACCCCACC   CC CACCC
                                  C       CGTT  _
GAM2735  SEPN1    3'  GGAGTGGGGTGGGAGTGGG   42428           ATG T
                                GGAGTGGGGTGG   G GTGGG
                                ||||||||||||   | |||||
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                                CCTCACCCCACC  C CACCC
                                      ___ T
GAM2735 SLC12A7  3' GTGGGGTGGGGTGGG     27332       AT   T
                                GTGGGGTGG  GGTG GG
                                |||||||||  |||| ||
                                CACCCCACC  CCAC CC
                                      __   _
GAM2735 SLC12A7  3' CTGGGGTGGGGTGGGGTGGG  27329     A      AT   T
                                TTGG GTGGGGTGG  GGTG GG
                                |||| |||||||||  |||| ||
                                GACC CACCCCACC  CCAC CC
                                  C      __   _
GAM2735 SLC6A9   5' CTGGAGTGGGGTGTGTGG    27986         GGATG
                                TTGGAGTGGGGT    GTGTGG
                                ||||||||||||    ||||||
                                GACCTCACCCCA    CACACC
                                      _____
GAM2735 TBX6     5' TTGGGCTGGGGTGGAGACCCCT 38866     AG       TGGTG_
           GGG                    TTGG  TGGGGTGGA     TGGG
                                ||||  |||||||||     ||||
                                AACC  ACCCCACCT     ACCC
                                  CG       CTGGGG
GAM2735 WDR1     3' TTGTGGTGGGGTGGGGGCATGG 23047     GA       AT
           G                     TTG  GTGGGGTGG  GGTGTGGG
                                |||  |||||||||  ||||||||
                                AAC  CACCCCACC  CCGTACCC
                                  AC       C_
GAM2735 ZNF278   3' TTGGAGTGGGGTTGGGGG    36814         GGA   TGT
                                TTGGAGTGGGGT   TGG   GG
                                ||||||||||||  |||  ||
                                AACCTCACCCCA   ACC   CC
                                      ___  C__
GAM2736 ABCG1    3' GATCAGAAGAGTCTCTGTGTC  22253       AAA   CATAA_
                                GATCAGG   AGAG     TGTC
                                |||||||   ||||     ||||
                                CTAGTCT   TCTC     ACAG
                                    ___   AGAGAC
GAM2736 ALS2     3' GATGAGGAAGAGCACCTATGT  34093     C   AA     A_
                                GAT AGGA  AGAGCAT  ATGT
                                ||| ||||  |||||||  ||||
                                CTA TCCT  TCTCGTG  TACA
                                  C   __      GA
GAM2736 DLG1     5' AATCAGGAAGAGGGCACA     19864        A  A
                                GATCAGGAA AG GCATA
                                ||||||||| || |||||
                                TTAGTCCTT TC CGTGT
                                     C  C
GAM2736 FGF5     3' AGGATTCCACATAATGTCA    37578      AAAGA
                                AGGA    GCATAATGTCA
                                ||||    ||||||||||
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                                TCCT    TGTATTACAGT
                                  AAGG_
GAM2736 LAMC2    3' GATCAGGAATGGGGTCAGGTCA 33114        AAGAG_ TAAT
                                GATCAGGAA     CA   GTCA
                                |||||||||     ||   ||||
                                CTAGTCCTT     GT   CAGT
                                     ACCCCA  C___
GAM2736 NCOA6    3' GACTAGGAAAAGGGCCACAT  30436    C      A  ATA
                                GAT AGGAAAAG GC   AT
                                ||| |||||||| ||   ||
                                CTG TCCTTTTC CG   TA
                                  A       C  GTG
GAM2736 PIK3R3   3' TCAGAAAAGATACTGTC    41448     G    GCATAA
                                TCAG AAAAGA     TGTC
                                |||| ||||||     ||||
                                AGTC TTTTCT     ACAG
                                  _     ATG___
GAM2736 PTPRE    3' AATTAGGGAAGATATTAATGTC 38980    C   AA   GCA
              A                  GAT AGG  AAGA   TAATGTCA
                                ||| |||  ||||   ||||||||
                                TTA TCC  TTCT   ATTACAGT
                                  A  C_   ATA
GAM2736 RARG     3' GATCAGGAAGGGGATGAACA  9723         AA____
                                GATCAGGAA     GAGCA
                                |||||||||     |||||
                                CTAGTCCTT     CTTGT
                                     CCCCTA
GAM2736 SULT2A1  3' GACAGGAGAATCAATGTC    43472    T    AAA   CA
                                GA CAGGA   GAG  TAATGTC
                                || |||||   |||  |||||||
                                CT GTCCT   CTT  GTTACAG
                                 _    ___   A_
GAM2737 FKBP1A   3' CCATATGGACTCATGTGC    38276        _     C
                                TCATATGG TTTATG GC
                                |||||||| |||||| ||
                                GGTATACC GAGTAC CG
                                     T     A
GAM2737 HBZ      3' TCATTGGTTTATTGGCGC    23733      A      __
                                TCAT TGGTTTAT  GCGC
                                |||| ||||||||  ||||
                                AGTA ACCAAATA  CGCG
                                  _       AC
GAM2737 MEF2B    5' TCATATGGTCCCGGATGC    25412          ___
                                TCATATGGTTT   ATGC
                                ||||||||||   ||||
                                AGTATACCAGG   TACG
                                       GCC
GAM2737 PLA2G2D  3' TCACATGGCCAGACTGTGC   29638          TA__  C
                                TCATATGGTT    TG GC
                                ||||||||||    || ||
```

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                                AGTGTACCGG   AC CG
                                     TCTG  A
GAM2737  RERE    3'  TCAAATGGTTTACCAGTGC   29035    T     ____
                                TCA ATGGTTTA   TGC
                                ||| ||||||||   |||
                                AGT TACCAAAT   ACG
                                  T      GGTC
GAM2738  ABCB10  3'  CCTTTTTAAAGTTGTCATTTGA 28989     C   A      AT
           CA                     TCTTT TAAA TTGTCATTT  CA
                                ||||| |||| |||||||||  ||
                                GGAAA ATTT AACAGTAAA  GT
                                   A   C       CT
GAM2738  LECT2   3'  TCTTTCTTGCATTTAT     14129       AAAAT  T
                                TCTTTCT    TG CATTTAT
                                |||||||    || |||||||
                                AGAAAGA    AC GTAAATA
                                     _____  _
GAM2738  PARK2   3'  TCTTTCTAAAGTTGCAAATCA  30376        A   CATTT
                                TCTTTCTAAA TTGT    ATCA
                                |||||||||| ||||    ||||
                                AGAAAGATTT AACG    TAGT
                                     C   TT___
GAM2738  PIK3C2B 3'  TTTCTCAAATGTCATTTAT   15299     AAAAT
                                TTTCT    TGTCATTTAT
                                |||||    ||||||||||
                                AAAGA    ACAGTAAATA
                                   GTTT_
GAM2739  BMP1    3'  TTTGTGGGGAAGTGGCT    26000     T   CTTCTT
                                TTTGT GGGAA     TGGCT
                                ||||| |||||     |||||
                                AAACA CCCTT     ACCGA
                                   C    C_____
GAM2739  EHD2    3'  TTGGGAAGAAGCCTTGGCTT  31141      CTT_
                                TTGGGAA   CTTTGGCTT
                                |||||||   |||||||||
                                AACCCTT   GGAACCGAA
                                    CTTC
GAM2739  FACL4   5'  CTTGTTATTCTTTGGCTT   35678      GGAAC
                                TTTGTTG    TTCTTTGGCTT
                                |||||||    ||||||||||
                                GAACAAT    AAGAAACCGAA
                                     _____
GAM2740  FMO4    3'  TAATAGCAGTTATGATGGAG  12925       CAC  CA_
                                TAATAGCAG  ATG  GAG
                                |||||||||  |||  |||
                                ATTATCGTC  TAC  CTC
                                     AA_  TAC
GAM2740  FMR2    3'  TAGACATGTTGCACATGCAG  12980     ATAGCA
                                TAGATA    GCACATGCAG
                                ||||||    ||||||||||
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                                ATCTGT     CGTGTACGTC
                                   ACAA__
GAM2740  FPGS     3'  GATGGCAGCAGCCTCACGGAG  22430     AA      A_   C
                                GAT  TAGCAGC  CATG AG
                                |||  |||||||  |||| ||
                                CTA  GTCGTCG  GTGC TC
                                  CC      GA    C
GAM2740  GHRHR    3'  GATGAGAGCAGACACAGAG   9066      AAT    C  AT
                                GAT   AGCAG AC  GCAGAG
                                |||   ||||| ||  ||||||
                                CTA   TCGTC TG  TGTCTC
                                  CTC    _ __
GAM2740  GRM1     3'  GATAATAGTAGGCATTCAGAG  9134         C  CA   G
                                GATAATAG AG  CAT CAGAG
                                ||||||||  ||  ||| |||||
                                CTATTATC TC  GTA GTCTC
                                     A  C_   A
GAM2740  HUNK     5'  TAGACAATAGCGGCTGCCCAG  31080           A  ACA   AG
                                TAGATAATAGC GC   TGC  AG
                                ||||||||||| ||   |||  ||
                                ATCTGTTATCG CG   ACG  TC
                                      C ___   GG
GAM2740  KCNH3    3'  TAGAGGCAGGGGCACATGCAG  42089      TAA   CA
                                TAGA   TAG  GCACATGCAG
                                ||||   |||  ||||||||||
                                ATCT   GTC  CGTGTACGTC
                                  CC_   CC
GAM2740  MAP1A    3'  CAGATGACCACATGCAGA    14340       A  AGCAG
                                TAGAT AT    CACATGCAGA
                                |||||  ||    ||||||||||
                                GTCTA TG    GTGTACGTCT
                                   C _____
GAM2741  CAPN10   3'  CTGTTGGTAGAGTTTCAG    35770     G       G_
                                CTG TGGTAGAGT  CAG
                                |||  |||||||||  |||
                                GAC ACCATCTCA  GTC
                                  A        AA
GAM2741  EGFL4    5'  GTGGAAGCTGCAGCCAC     41582      T  AG
                                GTGG AG  TGCAGCCAC
                                ||||  ||  |||||||||
                                CACC TC  ACGTCGGTG
                                   T  G_
GAM2741  HADH2    3'  CGACTGGTAGGCAGTTAC    21053         _    AG
                                CGACTGGT GGTAG  TGC
                                ||||||||  |||||  |||
                                GCTGACCA CCGTC  ATG
                                     T    A_
GAM2741  HD       3'  GACTGGTGGGTGGAGAACGACA 13350          T____     _
            G                    GACTGGTGG    AGAGTG CAG
                                |||||||||    ||||||  |||
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                                CTGACCACC    TCTTGC GTC
                                     CACC      T
GAM2741  MCCC2    3'  GAATGGTGGTAATGGCTGC   35250    C       AGT  A
                                GA TGGTGGTAG   GC GC
                                || |||||||||   || ||
                                CT ACCACCATT   CG CG
                                 T        AC_  A
GAM2741  MS4A1    3'  GACTGGTGGTAAAATATTTGC  6598              CA_
                                GACTGGTGGTAGAGTG   GC
                                ||||||||||||||||   ||
                                CTGACCACCATTTTAT   CG
                                          AAA
GAM2741  OBP2A    3'  CTGGTGGTAGGGTGGGC     31039          A   CA
                                CTGGTGGTAG GTG  GC
                                |||||||||| |||  ||
                                GACCACCATC CAC  CG
                                      C   C_
GAM2741  OBP2B    3'  CTGGTGGTAGGGTGGGC     31034          A   CA
                                CTGGTGGTAG GTG  GC
                                |||||||||| |||  ||
                                GACCACCATC CAC  CG
                                      C   C_
GAM2741  ORM1     5'  CTGGTGGCTGCAGGGTGCAGTC 8298          ___  A     C
                AC                  CTGGTGGT   AG GTGCAG CAC
                                |||||||||   || ||||||  |||
                                GACCACCG   TC CACGTC GTG
                                     ACG  C     A
GAM2741  PLA2G4C  3'  ACTGGCTAGAAGTGCAGTCA  43857       GGTA       C
                                ACTGGT    GAGTGCAG CA
                                ||||||    |||||||| ||
                                TGACCG    TTCACGTC GT
                                   ATC_       A
GAM2741  SFRS2    3'  GACTGGAAGTGCAG        42175       TGGTA
                                GACTGG    GAGTGCAG
                                ||||||    ||||||||
                                CTGACC    TTCACGTC
                                     ______
GAM2741  SLC2A6   3'  CTGGTGGCAGGGATGACTGC  32769          A_   _ A
                                CTGGTGGTAG  GTG C GC
                                ||||||||||  ||| | ||
                                GACCACCGTC  TAC G CG
                                      CC   T A
GAM2741  TERF1    3'  CTGGTGGTGTGTGCC       32740        AGA   CA
                                CTGGTGGT   GTG  GCC
                                ||||||||   |||  |||
                                GACCACCA   CAC  CGG
                                     ___   A_
GAM2742  HIS1     3'  GTTAACCAAAATGACAGG     26994       A      TC
                                GTTAA CCAAAAT  GCAGG
                                ||||| |||||||  |||||
```

```
                                CAATT GGTTTTA  TGTCC
                                  _      C_
GAM2742  WNT5A    5'  CAAGTTAAACCAGGGGAGCATC 18113          AAATTC  __
              GGG                  TAAGTTAAACCA     GCA  GGG
                                   ||||||||||||     |||  |||
                                   GTTCAATTTGGT     CGT  CCC
                                         CCCCT_   AG
GAM2743  DLEC1    3'  TCGCTATGCACTGAGC      28852        A   C   III
                                   TTGCTAT CAC GAG   C
                                   |||||||  ||| |||   |
                                   AGCGATA GTG CTC   G
                                       C   A   III
GAM2743  DUT      3'  TATTGCTACTTCACTGAG    12625         A_  C
                                   TGTTGCTAT  CAC GAG
                                   |||||||||  ||| |||
                                   ATAACGATG  GTG CTC
                                         AA   A
GAM2743  LRP4     3'  TGTTACTAACACACTTGAG   42070         _    C_
                                   TGTTGCTA TACAC  GAG
                                   ||||||||  |||||  |||
                                   ACAATGAT GTGTG  CTC
                                        T     AA
GAM2744  BDKRB2   3'  TGGGCAGGGCAGGAAT      8408     T       TGCGG
                                   TG GCAGGGCA    GGAAT
                                   ||  ||||||||    |||||
                                   AC CGTCCCGT    CCTTA
                                    C       ______
GAM2744  BIRC7    3'  GGGCGGTGGTCGGGGAATCAG  40254      ATG___
                                   GGGC     CGGGGAATCAG
                                   ||||     ||||||||||||
                                   CCCG     GCCCCTTAGTC
                                     CCACCA
GAM2744  CACNA1D  5'  TGTGCAGGGCACTGTGCTGG   8771           ___   G
                                   TGTGCAGGGCA   TGC GG
                                   ||||||||||||   ||| ||
                                   ACACGTCCCGT   ACG CC
                                         GAC   A
GAM2744  DVL1     3'  TGTGCAGGAGGTGGGGGTCAG  40419         CA  C    AA
                                   TGTGCAGGG  TG GGGG  TCAG
                                   |||||||||  ||  ||||  ||||
                                   ACACGTCCT  AC CCCC  AGTC
                                        CC  _    __
GAM2744  FBXL7    3'  TGTGCAAGGCGAGGGATCA   29418          ATGC    A
                                   TGTGCAGGGC    GGGGA TCA
                                   ||||||||||    ||||| |||
                                   ACACGTTCCG    TCCCT AGT
                                         C___    _
GAM2744  G6PD     3'  TGGCAGGGCATTGAGG      7612     T       GC
                                   TG GCAGGGCAT  GGGG
                                   ||  |||||||||  ||||
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```
                                AC CGTCCCGTA  CTCC
                                 _       A_
GAM2744 HDAC7A   3' TATGTGGGGTGGGAATCA    32473     CA   CATGCG
                                TGTG  GGG     GGGAATCA
                                ||||  |||     ||||||||
                                ATAC  CCC     CCCTTAGT
                                  A_   CA____
GAM2744 PIK3R2   3' TGGGCAGGGCAGAGGGTCA   22753    T      TGC    AA
                                TG GCAGGGCA   GGGG  TCA
                                || ||||||||   ||||  |||
                                AC CGTCCCGT   TCCC  AGT
                                 C       C__   __
GAM2745 ACTN1    3' CTTTGTGCTTGGTTATT     9932     GTG    TT
                                CT   GTGT  TTGGTTATT
                                ||   ||||  |||||||||
                                GA   CACG  AACCAATAA
                                 AA_    __
GAM2745 DNLC2A   3' TAGCATTTTGGTTATTT     30508         T
                                TGGTGTTTT GGTTATTT
                                ||||||||| ||||||||
                                ATCGTAAAA CCAATAAA
                                      _
GAM2745 FKBP1A   3' CCTTGTGGTGTTTTTTGTT   9037     C         G
                                CC TGTGGTGTTTTT GTT
                                || ||||||||||| |||
                                GG ACACCACAAAAA CAA
                                 A          A
GAM2745 GNAI3    3' TGGATTATTGGTTATTT     27099     T   T
                                TGG GTT TTGGTTATTT
                                ||| ||| ||||||||||
                                ACC TAA AACCAATAAA
                                  _   T
GAM2745 ZFH4     5' TGGGGTGTTTTTCGGGTT    36024    T       __
                                TG GGTGTTTTT  GGTT
                                || |||||||||  ||||
                                AC CCACAAAAA  CCAA
                                 C        GC
GAM2746 BLAME    3' TGAGCAGGCCAGGCAGGGAG   33498    T   A   ACCTTT
                                TG AGCA GCCA     GGAG
                                || |||| ||||     ||||
                                AC TCGT CGGT     CCTC
                                 _   C    CCGTC_
GAM2746 EHD3     3' TGAAGCAAGCCAGGGGAG    31116    T       ACCTTT
                                TG AGCAAGCCA     GGAG
                                || |||||||||     ||||
                                AC TCGTTCGGT     CCTC
                                 T       CC____
GAM2746 FRK      5' TGCAGCAAGTCCTACCTGGAGA 13015         _ A    TT
             G                   TGTAGCAAG CC ACCT  GGAGAG
                                 |||||||||  || ||||  ||||||
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                                ACGTCGTTC GG TGGA  CCTCTC
                                    A  A   __
GAM2746  HKE4     3'  TGTAGCAACTTGGTTCTCCGAG 28095        GCCAACC   G
                                TGTAGCAA      TTT GAG
                                ||||||||      ||| |||
                                ACATCGTT      GAG CTC
                                    GAACCAA   G
GAM2746  ITPKB    3'  TAGCAAGTCGGCCCACACAGGA 13654        CCAA   TT___
              G                  TAGCAAG   CCT    GGAG
                                |||||||   |||    ||||
                                ATCGTTC   GGG    CCTC
                                   AGCC   TGTGT
GAM2746  LRP1     5'  GTAGGGGAGCCTTTGGAG    14225      CA_   AACC
                                GTAG   AGCC   TTTGGAG
                                ||||   ||||   |||||||
                                CATC   TCGG   AAACCTC
                                  CCC   _____
GAM2746  PDE4B    3'  TGTAGCAACTCCTGTGG     15157        G CAA   T
                                TGTAGCAA C   CCT TGG
                                |||||||| |   ||| |||
                                ACATCGTT G   GGA ACC
                                    _ A__   C
GAM2746  PYGM     5'  TGAAGTGACCTTTTGGAGA   24701   C   CCA    _
                                G AAG   ACCTTT GGAGA
                                | |||   |||||| |||||
                                A TTC   TGGAAA CCTCT
                                 C   AC_     A
GAM2746  TNFRSF7  5'  GTGGCAAGCCAACCTTTG    10306    A
                                GT GCAAGCCAACCTTTG
                                || ||||||||||||||
                                CA CGTTCGGTTGGAAAC
                                 C
GAM2747  ADK      5'  TCACACACCCCGCGCGGCCGG  27484      G    GT
                                TCACA CGCTC  CGCGCGGCCGG
                                ||||| |||||  ||||||||||
                                AGTGT GTGGG  GCGCGCCGGCC
                                   _    ___
GAM2747  CDH4     3'  GCGCGGTGCTGGGCAGCGGCCG 12177      TC_  C__  _
              G                  GCGC   GT   GC GCGGCCGG
                                ||||   ||   || ||||||||
                                CGCG   CG   CG CGCCGGCC
                                  CCA  ACC  T
GAM2747  DUSP7    5'  TCGAAGAGCTCGTGCGGCCGG  42277    AC  C     CGC
                                TC  AG GCTCGT   GCGGCCGG
                                ||  || ||||||   ||||||||
                                AG  TC CGAGCA   CGCCGGCC
                                 CT  T     ____
GAM2747  FXYD6    3'  TCACAGCGCACGGTTTGG    35123         TCGTCGC    CC_
                                TCACAGCGC      GCGG   GG
                                |||||||||      ||||   ||
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                                AGTGTCGCG     TGCC  CC
                                      _______  AAA
GAM2747 GAS1    5' GCAGATCCGTTGTGCGGCCGG 13067    C__   CGC
                                GCG  TCGT  GCGGCCGG
                                |||  ||||  ||||||||
                                CGT  GGCA  CGCCGGCC
                                  CTA   ACA
GAM2747 ITM2B   5' CAGCCTCTACGGCCG      35092     G  GTCGC
                                CAGC CTC    GCGGCCG
                                |||| |||    |||||||
                                GTCG GAG    TGCCGGC
                                  _  A____
GAM2747 KIF5B   5' TCGCAGCCGGGGCCGCGGCCGG 21141    A   GCT  TC  _
                                TC CAGC   CG  GC GCGGCCGG
                                || ||||   ||  || ||||||||
                                AG GTCG   GC  CG CGCCGGCC
                                 C   ___  CC  G
GAM2747 LASS1   3' GCGTCGCGCCGCGGCCGG    34608    C  T  _
                                GCG TCG CGC GCGGCCGG
                                ||| ||| ||| ||||||||
                                CGC AGC GCG CGCCGGCC
                                  _  _  G
GAM2747 MFRP    3' CGCCCGGCGGCCGG       36424       TCGC
                                CGCTCG   GCGGCCGG
                                ||||||   ||||||||
                                GCGGGC   CGCCGGCC
                                      ____
GAM2747 PIK3C2B  3' TCACAGCGCTCTCCTTTGG   15295          GT GCGC
                                TCACAGCGCTC  C   GG
                                ||||||||||  |   ||
                                AGTGTCGCGAG  G   CC
                                      AG AAA_
GAM2747 RAD17   5' GCGGTCAGGGCGCGCGGCCGG  39411    C  T__
                                GCG TCG   CGCGCGGCCGG
                                ||| |||   ||||||||||
                                CGC AGT   GCGCGCCGGCC
                                  C   CCC
GAM2747 VGF     3' TCACAGCGACTTGGAGAGGCTG 17996        _ CGTCGCGC   C
            G                    TCACAGCG CT       GGC GG
                                ||||||| ||       ||| ||
                                AGTGTCGC GA       CCG CC
                                    T  ACCTCT__   A
GAM2748 LRRC2   3' TATATAGCTCCAGAGAATAGTG 35998       AC   CCAC
            AG                    TATATAG  CCA   ATAGTGAG
                                |||||||  |||   ||||||||
                                ATATATC  GGT   TATCACTC
                                    GA   CTCT
GAM2748 NEU3    5' TACATAGATTTGTCACATAG   27406       CCCAC
                                TATATAGA    CACATAG
                                ||||||||    |||||||
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                                ATGTATCT    GTGTATC
                                    AAACA
GAM2748 UBE2E3   3'  TATAAAGATTTGCAGCACAGTG 26820     T  CCCAC  _
          AG                     TATA AGA    CA CATAGTGAG
                                 |||| |||    || |||||||||
                                 ATAT TCT    GT GTGTCACTC
                                   T  AAAC_  C
GAM2749 BRF1    5'  TCGCCGCGCGCGCCCG      11340        GA   AGCAG
                                 TCGCCGCG  CGCG    CCG
                                 ||||||||  ||||    |||
                                 AGCGGCGC  GCGC    GGC
                                     __   G____
GAM2749 CAPN5   5'  CCGCCGCGGGTCCAGCCGG   44926         ACGCGAG
                                 TCGCCGCGG      CAGCCGG
                                 |||||||||      |||||||
                                 GGCGGCGCC      GTCGGCC
                                      CAG____
GAM2749 DLK1    5'  GCGGACGCGAAAGGG       19265          C  CC
                                 GCGGACGCGAG AG  GG
                                 ||||||||||| ||  ||
                                 CGCCTGCGCTT TC  CC
                                       _ __
GAM2749 FGF2    5'  TCTCCGCGGACGCCGCCTGG   12845    G        GAGCA  _
                                 TC CCGCGGACGC    GCC GG
                                 || ||||||||||    ||| ||
                                 AG GGCGCCTGCG    CGG CC
                                  A        G____  A
GAM2749 MID2    5'  CGCCGCGCAGCAGCCGG     38056       GGAC  G
                                 CGCCGC   GC AGCAGCCGG
                                 ||||||   || |||||||||
                                 GCGGCG   CG TCGTCGGCC
                                     ____ _
GAM2749 NKX2H   5'  TCGCCATGCGCTGGCAGCCGG  30761       CGGA  GA
                                 TCGCCG   CGC  GCAGCCGG
                                 ||||||   |||  ||||||||
                                 AGCGGT   GCG  CGTCGGCC
                                    AC__  AC
GAM2749 NPY2R   5'  CGCCGCGCGGGCGGGCAGCCGG 9492        GAC  A
          A                      CGCCGCG  GCG GCAGCCGGA
                                 |||||||  ||| |||||||||
                                 GCGGCGC  CGC CGTCGGCCT
                                     GCC  C
GAM2749 PACE4   5'  CCGCCGCGGGCGGGAGCCGG  15046        AC  AGC
                                 TCGCCGCGG GCG  AGCCGG
                                 |||||||||  |||  ||||||
                                 GGCGGCGCC  CGC  TCGGCC
                                      __  CC_
GAM2749 PCDH11X 5'  CGCAGTCCGCAGAGCAGCCGGA 37301      A_  _
                                 CGCGG  CGC GAGCAGCCGGA
                                 |||||  ||| ||||||||||
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                                GCGTC  GCG CTCGTCGGCCT
                                  AG   T
GAM2749  PCDH11Y   5'  CGCAGTCCGCAGAGCAGCCGGA 37340      A_  _
                                CGCGG  CGC GAGCAGCCGGA
                                ||||| ||| ||||||||||
                                GCGTC  GCG CTCGTCGGCCT
                                  AG   T
GAM2749  PRKCI     5'  TCGCCTCGCCGGAGCAGCCGGA 15635      G  GA  C
                                TCGCC CG  CG GAGCAGCCGGA
                                ||||| ||  || ||||||||||
                                AGCGG GC  GC CTCGTCGGCCT
                                  A  G_  _
GAM2749  SIAT8E    5'  CGCCGCGGGCGCGGGGTACGG  40833       A   AGCAGC
                                CGCCGCGG CGCG     CGG
                                |||||||| ||||     |||
                                GCGGCGCC GCGC     GCC
                                    C    CCCAT_
GAM2749  ZNF7      5'  CCGCCGCGGGGGAGGGTGGCTG 18261        ACGC   CA__  C
           G                     TCGCCGCGG    GAG    GC GG
                                |||||||||    |||    || ||
                                GGCGGCGCC    CTC    CG CC
                                     CC__   CCAC  A
GAM2750  CIT       5'  TTGGTTGTTGAGTTCAGCGTTG 43066        _ ATAA   ATCG_
           TCC                    TTGGTTGT GA    AGT    CC
                                |||||||| ||    |||    ||
                                AACCAACA CT    TCG    GG
                                     A  CAAG   CAACA
GAM2750  EPHB2     3'  TTGGTTGTTGAGTGAGGCC   32686       GAATAA   ATC
                                TTGGTTGT     AGT   GCC
                                ||||||||     |||   |||
                                AACCAACA     TCA   CGG
                                     AC_____   CTC
GAM2750  TEGT      3'  CTGGTTGTGAATAGGGAGAGCC 42095          AAGTATC
                                TTGGTTGTGAATA      GCC
                                |||||||||||||      |||
                                GACCAACACTTAT      CGG
                                       CCCTCT_
GAM2751  ALDH1A3   3'  AGCAGCAAAGGTAACCTC    8677         ACAC  A
                                AGCGGCAAA    AC CTC
                                |||||||||    || |||
                                TCGTCGTTT    TG GAG
                                     CCAT  _
GAM2751  ANK3      3'  CAGCGAACACACACACACT    10093       _ AA
                                CAGCGG CA  ACACACACT
                                |||||| ||  |||||||||
                                GTCGCT GT  TGTGTGTGA
                                  T  G_
GAM2751  ASB1      3'  CAGCAGCAGCACAGCACTC   32029        AAA   _
                                CAGCGGCA   CACA CACTC
                                ||||||||   |||| |||||
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                                GTCGTCGT  GTGT GTGAG
                                    C__   C
GAM2751  ATP8A2   3'  ACAAACACAAACACACACT   45247     _ _
                                GCGG CA AAACACACACT
                                |||| || ||||||||||
                                TGTT GT TTTGTGTGTGA
                                  T  G
GAM2751  C18orf1  3'  CAACAACAAAAATGTGCACT  41210         CACA_
                                CAGCGGCAAAA    CACT
                                ||||||||||    ||||
                                GTTGTTGTTTT    GTGA
                                      TACAC
GAM2751  CALM3    3'  CAACGGCAAAGGGCATGCTC  23228         ACA  CA
                                CAGCGGCAAA  CA  CTC
                                |||||||||  ||  |||
                                GTTGCCGTTT  GT  GAG
                                      CCC  AC
GAM2751  CDC6     5'  CAGCGGCAGCAGCAAACTC   10361        AAA  _  C
                                CAGCGGCA  CA CA ACTC
                                ||||||||  || || ||||
                                GTCGCCGT  GT GT TGAG
                                    C__  C  T
GAM2751  CLN5     5'  GCCCCAAACACACACTC    27083    GGCA
                                GC   AAACACACACTC
                                ||   ||||||||||||
                                CG   TTTGTGTGTGAG
                                 GGG_
GAM2751  CREBL2   3'  CAGCGACAGAGAACACAACTC  10577        A__     C
                                CAGCGGCA  AACACA ACTC
                                ||||||||  |||||| ||||
                                GTCGCTGT  TTGTGT TGAG
                                    CTC    _
GAM2751  DLG5     5'  CAGCGGCAGCATACACTC    44446        AAA  C
                                CAGCGGCA  CA ACACTC
                                ||||||||  || ||||||
                                GTCGCCGT  GT TGTGAG
                                    C__  A
GAM2751  DSCR3    5'  CAGCGGCGTCGCACACACTC  25819        AAAA
                                CAGCGGC   CACACACTC
                                |||||||   |||||||||
                                GTCGCCG   GTGTGTGAG
                                    CAGC
GAM2751  E2F1     3'  ACATGCTCACACACATTC    44482    _  AAA     C
                                GCG GC  ACACACA TC
                                ||| ||  ||||||| ||
                                TGT CG  TGTGTGT AG
                                  A  AG_     A
GAM2751  EBI3     3'  CAGCAGCAAAGCAAGGACTC  25094         A  CAC
                                CAGCGGCAAA CA  ACTC
                                |||||||||| ||  ||||
```

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                                GTCGTCGTTT GT   TGAG
                                      C  TCC
GAM2751  EGR3     3'  GCGAGCACGCACACACTC    40547     _  AAA
                                GCG GCA   CACACACTC
                                ||| |||   |||||||||
                                CGC CGT   GTGTGTGAG
                                  T  GC_
GAM2751  EGR3     3'  GCGCGCACACACACACACTC   40548     _  AA_
                                GCG GCA   ACACACACTC
                                ||| |||   ||||||||||
                                CGC CGT   TGTGTGTGAG
                                  G  GTG
GAM2751  EPB49    3'  GCGGCAAACATGAACTC     12732        A  CAC
                                GCGGCAAA CA   ACTC
                                |||||||| ||   ||||
                                CGCCGTTT GT   TGAG
                                     _  ACT
GAM2751  EXTL3    3'  AGCGCCACACACCACACTC   11024      G  AA_  A
                                AGCG CA   AC CACACTC
                                |||| ||   || |||||||
                                TCGC GT   TG GTGTGAG
                                  G  GTG  _
GAM2751  FEZ1     3'  CAACGGCAAAGGACCCC     35420         ACAC  A
                                CAGCGGCAAA    AC CTC
                                ||||||||||    || |||
                                GTTGCCGTTT    TG GGG
                                      CC__  _
GAM2751  HLF      3'  CAGTGCAAAAACACACTC    13387     CG     C
                                CAG  GCAAAA ACACACTC
                                |||  |||||| ||||||||
                                GTC  CGTTTT TGTGTGAG
                                  A_     _
GAM2751  IHPK1    3'  CAGTATGCACACACACT     45483     CG_  AAA
                                CAG   GC   ACACACACT
                                |||   ||   |||||||||
                                GTC   CG   TGTGTGTGA
                                  ATA  ____
GAM2751  IL13     3'  CAACGGTGACAAACACACTC  13524       CAAAAC
                                CAGCGG     ACACACTC
                                ||||||     ||||||||
                                GTTGCC     TGTGTGAG
                                   ACTGTT
GAM2751  IL17R    3'  ACGTGCACACACACTC      30737     _  AAA
                                GCG GC   ACACACACTC
                                ||| ||   ||||||||||
                                TGC CG   TGTGTGTGAG
                                  A  ____
GAM2751  LHX1     5'  AGAGGACACACACTC       24522     C  CAAA
                                AG GG    ACACACACTC
                                || ||    ||||||||||
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                                TC CC    TGTGTGTGAG
                                 T _____
GAM2751  LILRB4   3'  CAGAGCAGTATACACACTC   27774     C    AAAC
                                CAG GGCA    ACACACTC
                                ||| ||||    ||||||||
                                GTC TCGT    TGTGTGAG
                                  _    CATA
GAM2751  MECP2    3'  CAAGACAACACACACT      22575     C    AA
                                CAG GGCA  ACACACACT
                                ||| ||||  |||||||||
                                GTT CTGT  TGTGTGTGA
                                  _   __
GAM2751  MPO      3'  CAGCACAAACACACACTC    7000       _
                                CGGCA AAACACACACTC
                                ||||| ||||||||||||
                                GTCGT TTTGTGTGTGAG
                                   G
GAM2751  MUC4     3'  CAGCGGCAGCACCAGCTC    39664        AAA   A  _
                                CAGCGGCA   CAC CA CTC
                                ||||||||   ||| || |||
                                GTCGCCGT   GTG GT GAG
                                     C__   _  C
GAM2751  NFYC     3'  AGCATTGGACACACACTC    30593      GCAAA
                                AGCG     ACACACACTC
                                ||||     ||||||||||
                                TCGT     TGTGTGTGAG
                                  AACC_
GAM2751  ROBO1     5'  CAGCAGCAGGACCGCGGACACT 39480         AA  AC___
              C                  CAGCGGCA  AC     ACACTC
                                ||||||||  ||    ||||||
                                GTCGTCGT  TG    TGTGAG
                                     CC  GCGCC
GAM2751  ROCK2    3'  GCAGTATAAAACACACACT    42357      C__
                                GCGG   AAAACACACACT
                                ||||   ||||||||||||
                                CGTC   TTTTGTGTGTGA
                                  ATA
GAM2751  SDC2     5'  CAGGGCAAAACGAAGCCTC    42559     C       ACACA
                                CAG GGCAAAAC     CTC
                                ||| ||||||||     |||
                                GTC CCGTTTTG     GAG
                                  _       CTTCG
GAM2751  SOS2     3'  CAGCAGCAAATACCGGCA     42852          _  ACA
                                CAGCGGCAAA AC   CA
                                |||||||||| ||   ||
                                GTCGTCGTTT TG   GT
                                      A  GCC
GAM2751  SS18     3'  AACACACAAACACACACTC    24837      G  _
                                AGCG CA AAACACACACTC
                                |||| || ||||||||||||
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                                TTGT GT TTTGTGTGTGAG
                                  _ G
GAM2751  STAT5B   3'  ACACACACAAACACATACTC  29716    _  _     C
                                GCG GCA AAACACA ACTC
                                ||| ||| ||||||| ||||
                                TGT TGT TTTGTGT TGAG
                                  G  G     A
GAM2751  TFDP1    3'  CAGGGGCAAAAATGAACTC   28275    C     CACAC
                                CAG GGCAAAA    ACTC
                                ||| |||||||    ||||
                                GTC CCGTTTT    TGAG
                                  C     TACT_
GAM2751  VAX2     3'  CAGTGAGAGACACACACACTC  29778    C  CAAA_
                                CAG GG    ACACACACTC
                                ||| ||    ||||||||||
                                GTC CT    TGTGTGTGAG
                                  A  CTCTG
GAM2751  WHSC1    3'  GCATCAGTAAACACACACT   39365    G  __
                                GCG CA  AAACACACACT
                                ||| ||  ||||||||||
                                CGT GT  TTTGTGTGTGA
                                  A  CA
GAM2751  ZNF184   5'  AGCGATCCACACACTC     45131     CAAAA
                                AGCGG    CACACACTC
                                |||||    |||||||||
                                TCGCT    GTGTGTGAG
                                   AG___
GAM2752  APOB48R  3'  GGCATTGGAGCAAGCCTTCT  33090    ACTGAAA   __
                                GG     GGAG  GGCCTTCT
                                ||     ||||  ||||||||
                                CC     CCTC  TCGGAAGA
                                 GTAA___   GT
GAM2752  HNRPA1   5'  ACGGGCAGAAAGGAGCAAGC  36291     ACT     __
                                ACGG   GAAAGGAG  GGC
                                ||||   ||||||||  |||
                                TGCC   CTTTCCTC  TCG
                                  CGT      GT
GAM2752  HS3ST2   3'  GGGCAGAAAGGAGAATGATTCT 25814    ACT       CC_
                                GG   GAAAGGAGGG   TTCT
                                ||   ||||||||||   ||||
                                CC   CTTTCCTCTT   AAGA
                                 CGT        ACT
GAM2752  PKD2     3'  GGGTAGAAAGGAGGAATTCT  41075    ACT       CC
                                GG   GAAAGGAGGG  TTCT
                                ||   ||||||||||  ||||
                                CC   CTTTCCTCCT  AAGA
                                 CAT        T_
GAM2752  PLD2     3'  GGGCTGGGAGGGCCCT     15383    A   AAA
                                GG CTG   GGAGGGCCTT
                                || |||   ||||||||||
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```
                                CC GAC   CCTCCCGGGA
                                 C  ___
GAM2752  TBL1X    3'  GGACTGAAAATCTTCCTTCT  24888         GAGGG
                                GGACTGAAAG    CCTTCT
                                ||||||||||    ||||||
                                CCTGACTTTT    GGAAGA
                                     AGAA_
GAM2752  TRIM14   3'  GGACTGAAACTGCCGCTTTCT  37702         GGAGG  ___
                                GGACTGAAA    GCC   TTCT
                                |||||||||    |||  ||||
                                CCTGACTTT    CGG   AAGA
                                     GA___   CGA
GAM2753  AKAP13   3'  CAAGGGCCAGACAGCTGCT   28471        ACT   A
                                TAAGGGC   GGA CAGCTGCT
                                |||||||   ||| ||||||||
                                GTTCCCG   TCT GTCGACGA
                                    G__   _
GAM2753  CDY1     5'  AGACACGGGATTGGAACAGTTG 21714       _____      C
              CT                  GGGCAC    TGGAACAG TGCT
                                |||||||    |||||||| ||||
                                TCTGTG    ACCTTGTC ACGA
                                   CCCTA       A
GAM2753  CDY2     5'  AGACACGGGATTGGAACAGTTG 22089       _____      C
              CT                  GGGCAC    TGGAACAG TGCT
                                |||||||    |||||||| ||||
                                TCTGTG    ACCTTGTC ACGA
                                   CCCTA       A
GAM2753  CLTB     3'  GGGTAGCAGCTGCT       28227     CAC   AA
                                GGG   TGG  CAGCTGCT
                                |||   |||  ||||||||
                                CCC   ATC  GTCGACGA
                                 ___   __
GAM2753  DNMT3B   5'  GAGCCGGGAGCAGCTGCT    27874      ACT   A
                                GGGC   GGA CAGCTGCT
                                ||||   ||| ||||||||
                                CTCG   CCT GTCGACGA
                                  GC_   C
GAM2753  DYRK1A   5'  CAAGGGCACTGGGGCCGCTGC  10816          AACA
                                TAAGGGCACTGG    GCTGC
                                ||||||||||||    |||||
                                GTTCCCGTGACC    CGACG
                                      CCGG
GAM2753  EDN3     5'  AAGGGCACTGGGGCCG      6480          AACA
                                AAGGGCACTGG    GCTG
                                ||||||||||||    ||||
                                TTCCCGTGACC    CGGC
                                      C___
GAM2753  GRLF1    3'  AGGGCACTGGAGCCATTGC   44221          A_  GC
                                AGGGCACTGGA  CA  TGC
                                ||||||||||  ||  |||
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                                TCCCGTGACCT  GT  ACG
                                      CG  A_
GAM2753  MLLT7    3'  AAGGGCACTGGGGGAAGGGCTG 25526          AACA___
              C                    AAGGGCACTGG      GCTGC
                                   ||||||||||       |||||
                                   TTCCCGTGACC      CGACG
                                      CCCTTCC
GAM2753  NR3C2    3'  AGGGCTCAGAGGCAGCTGCT   9467       ACT   A_
                                   AGGGC   GGA  CAGCTGCT
                                   |||||   |||  ||||||||
                                   TCCCG   TCT  GTCGACGA
                                     AG_   CC
GAM2753  PTGFRN   3'  AAGGGCACTGGCTGTTA     42580         GAACA   C
                                   AAGGGCACTG    GCTG TA
                                   ||||||||||    |||| ||
                                   TTCCCGTGAC    CGAC AT
                                         _____   A
GAM2753  PTPRO    5'  AGGGACACTGGGGCTG      36221      _     AACA
                                   AGGG CACTGG   GCTG
                                   |||| ||||||   ||||
                                   TCCC GTGACC   CGAC
                                     T     C___
GAM2753  SLC7A5   3'  GGGCACCAGCTGCT        18552       TGGAA
                                   GGGCAC    CAGCTGCT
                                   ||||||    ||||||||
                                   CCCGTG    GTCGACGA
                                        _____
GAM2753  TARBP2   3'  GGGGTAGCAGCTGCT       39534     CAC   AA
                                   GGG   TGG  CAGCTGCT
                                   |||   |||  ||||||||
                                   CCC   ATC  GTCGACGA
                                     C__   __
GAM2754  C6       3'  CTACATATTTTACCTGTT    45401           G
                                   CTACATATTTTACT TGTT
                                   |||||||||||||| ||||
                                   GATGTATAAAATGG ACAA
                                                  _
GAM2754  CD2AP    3'  TACATATTTTATATGTGCT   29072          C_
                                   TACATATTTTA  TGTGTT
                                   ||||||||||  ||||||
                                   ATGTATAAAAT  ACACGA
                                         AT
GAM2754  CDK7     3'  TACATATTTTACATGTGT    12210          _
                                   TACATATTTTAC TGTGT
                                   ||||||||||| |||||
                                   ATGTATAAAATG ACACA
                                          T
GAM2754  ERBB2IP  3'  TACATATTTTATTGCATT    33100          C
                                   TACATATTTTA TGTGTT
                                   |||||||||| ||||||
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                                ATGTATAAAAT ACGTAA
                                      A
GAM2754 F8      3' TACATTTTTGTTGTGTTATTT 6566       A   AC
                                TACAT TTTT  TGTGTTATTT
                                ||||| ||||  ||||||||||
                                ATGTA AAAA  ACACAATAAA
                                   _   CA
GAM2754 HD      3' TACATTCACAGTGTTATTT   13358      ATT   T
                                TACAT   TTAC GTGTTATTT
                                |||||   |||| |||||||||
                                ATGTA   AGTG CACAATAAA
                                   ___   T
GAM2754 KCNJ16  3' CCTATATATTTTACTTGTATT 33016     C       _
                                TCTA ATATTTTACT GTGTT
                                |||| |||||||||| |||||
                                GGAT TATAAAATGA CATAA
                                  A       A
GAM2754 MAGEB4  3' TCTACCTATTTTACTGTGGAGT 14327      A        ___
             TATTT                  TCTAC TATTTTACTGT   GTTATTT
                                |||||| ||||||||||   |||||||
                                AGATG ATAAAATGACA   CAATAAA
                                   G         CCT
GAM2754 PDX1    3' TACATATTTTAGCTATAGTT   18490          _   _
                                TACATATTTTA CTGT GTT
                                |||||||||| |||| |||
                                ATGTATAAAAT GATA CAA
                                      C   T
GAM2755 CPS1    3' CCAAAACTGGGGGAGAGTG   12421         CC__  C
                                CCGGAGCTG   AG GTG
                                |||||||||   || |||
                                GGTTTTGAC   TC CAC
                                     CCCC  T
GAM2755 MBP     3' CCCAGTGTTGAACCCCAGCGTG 44885     ACACCG    G
                                TCCA     GAGCT CCAGCGTG
                                ||||     ||||| ||||||||
                                GGGT     CTTGG GGTCGCAC
                                  CACAA_    _
GAM2756 PPP2R2B 3' TTAGCTGGCAGCTTTCAATTC 21343     ATA   C
                                TTAG   GTA GCTTTCAATTC
                                ||||   ||| ||||||||||
                                AATC   CGT CGAAAGTTAAG
                                  GAC  _
GAM2757 ETV5    3' GTCACATCATGTCCCGT    20853       GC   ATAG  TA
                                GTCACA  CAT   GT  CGT
                                ||||||  |||   ||  |||
                                CAGTGT  GTA   CA  GCA
                                   A_  ____  GG
GAM2757 FST     3' ACAGCCATATTACAGCGTT   30175         AGGTTA
                                ACAGCCATAT     CGTT
                                ||||||||||     ||||
```

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                                TGTCGGTATA     GCAA
                                     ATGTC_
GAM2758 BRCA1    3' TCCTTCACCACAGA       28644        AAATATC
                                TCCTTCACC      GCAGA
                                |||||||||      |||||
                                AGGAAGTGG      TGTCT
                                _______
GAM2758 CHGA     3' TTCACCAAAAGGTCAGAAG   10473        TATCG
                                TTCACCAAA    CAGAAG
                                |||||||||    ||||||
                                AAGTGGTTT    GTCTTC
                                     TCCA_
GAM2758 CRTL1    5' CTCACCAAGAGCAGAAG     12448        ATATC
                                TTCACCAA    GCAGAAG
                                ||||||||    |||||||
                                GAGTGGTT    CGTCTTC
                                    CT___
GAM2758 EIF4E    3' TCCTTCACCAATGTTACATGA 12696         ATATC  _
                                TCCTTCACCAA    GCA GA
                                ||||||||||    ||| ||
                                AGGAAGTGGTT    TGT CT
                                     ACAA_  A
GAM2758 FMR2     3' TCCTTCACCAAAAATATCAG  12983         TATCG
                                TCCTTCACCAAA    CAG
                                ||||||||||||    |||
                                AGGAAGTGGTTT    GTC
                                      TTATA
GAM2758 MAPK1    3' TCTCTCACCAAATGTCGAG   39932   C       A  C
                                TC TTCACCAAAT TCG AG
                                || ||||||||| ||| ||
                                AG GAGTGGTTTA AGC TC
                                 A        C  _
GAM2758 MUCDHL   3' CCCTTCACCAGCAGA      34933        AATATC
                                TCCTTCACCA     GCAGA
                                |||||||||      |||||
                                GGGAAGTGGT     CGTCT
                                _______
GAM2758 RAP1A    5' TCCTTCACCCACGTGGAA    16152        AAATAT  CA
                                TCCTTCACC     CG  GAA
                                |||||||||     ||  |||
                                AGGAAGTGG     GC  CTT
                                    GT____  AC
GAM2758 SLC25A11 3' TCCTTTACCGCAGA       18679      CACCAAA
                                TCCTT      TATCGCAGA
                                |||||      |||||||||
                                AGGAA      ATGGCGTCT
                                _______
GAM2759 ARHI     3' TTTGTTCTTTTCAAAACATTTT 21702         ATGTT
                                TTTGTTCTTTT    TATTTT
                                ||||||||||    ||||||
```

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                                AAACAAGAAAA    GTAAAA
                                     GTTTT
GAM2759  FMN2     3'  TCTTTATTCTTTTATTATTCAT 44288            _
              TTT                  TCTTTGTTCTTTTAT GTTTATTTT
                                   ||||||||||||||| |||||||||
                                   AGAAATAAGAAAATA TAAGTAAAA
                                         A
GAM2759  MME      3'  TCTTGGTTCACAACTGTTTATT 28604     T   TTTTA
              TT                   TCTT GTTC    TGTTTATTTT
                                   |||| ||||    ||||||||||
                                   AGAA CAAG    ACAAATAAAA
                                     C   TGTTG
GAM2759  TYROBP   3'  TTTGTGCTTCATGTTTATTTT  17778      T   T
                                   TTTGT CTTT ATGTTTATTTT
                                   ||||| |||| ||||||||||
                                   AAACA GAAG TACAAATAAAA
                                      C   _
GAM2760  ABCG5    3'  TTTCAGACGTTCAGA       35332      T     GC
                                   TTTC AGACGTT  CAGA
                                   |||| |||||||  ||||
                                   AAAG TCTGCAA  GTCT
                                     _     __
GAM2760  AKAP13   3'  TTTCTAAACTCCCTCCCAG   40355        GT__ G
                                   TTTCTAGAC   T CCAG
                                   |||||||||   | ||||
                                   AAAGATTTG   A GGTC
                                        AGGG G
GAM2760  ANXA2    3'  TTTCTAGACCTGTTAGCTGGA  19720         __  _ CA
                                   TTTCTAGAC  GTT GC  GA
                                   |||||||||  ||| ||  ||
                                   AAAGATCTG  CAA CG  CT
                                        GA   T  AC
GAM2760  BMP6     3'  TTTCTGCAGTTACCAGA     11872       AGAC
                                   TTTCT    GTTGCCAGA
                                   |||||    |||||||||
                                   AAAGA    CAATGGTCT
                                      CGT_
GAM2760  CUL3     3'  TCTCTAGAAATAACTCAGA    18746        C  T  _
                                   TTTCTAGA GT GC CAGA
                                   |||||||| || || ||||
                                   AGAGATCT TA TG GTCT
                                        T  T  A
GAM2760  DAAM2    3'  TCTCTGGAACCTACCAGA    45181       A  CG
                                   TTTCT GA  TTGCCAGA
                                   ||||| ||  ||||||||
                                   AGAGA CT  GATGGTCT
                                      C  TG
GAM2760  ESR1     3'  TTTCCAAAGTTGCTGGA     6543         C     CA
                                   TTTCTAGA GTTGC  GA
                                   |||||||| |||||  ||
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                                AAAGGTTT CAACG  CT
                                    _    AC
GAM2760  FOXO1A   3'  TTTCCAGACAGACCAGA    12896         TT
                                TTTCTAGACG  GCCAGA
                                ||||||||||  ||||||
                                AAAGGTCTGT  TGGTCT
                                   C_
GAM2760  FUT1     3'  CTTCTAGAGTAGACCAGA    6632        C  T_
                                TTTCTAGA GT  GCCAGA
                                ||||||||  ||  ||||||
                                GAAGATCT CA  TGGTCT
                                    _  TC
GAM2760  GPR85    3'  TTTCTAAAATACCAGA      33264        CGT
                                TTTCTAGA   TGCCAGA
                                ||||||||   |||||||
                                AAAGATTT   ATGGTCT
                                    T__
GAM2760  HHEX     3'  TTTCCAGAATACCAGA      15568        CGT
                                TTTCTAGA   TGCCAGA
                                ||||||||   |||||||
                                AAAGGTCT   ATGGTCT
                                    T__
GAM2760  ITGA7    5'  TTTCAGACGTCTCCCAGA    13611      T      G_
                                TTTC AGACGTT  CCAGA
                                ||||  |||||||  |||||
                                AAAG TCTGCAG  GGTCT
                                  _      AG
GAM2760  ITK      3'  TTTCTAGACTGAATGTTCCAGA 24452          _____   G
                                TTTCTAGAC    GTT CCAGA
                                |||||||||    ||| |||||
                                AAAGATCTG    CAA GGTCT
                                     ACTTA  _
GAM2760  NUMB     3'  TCTCTGTTGCCAGA        19053       AGAC
                                TTTCT    GTTGCCAGA
                                |||||    |||||||||
                                AGAGA    CAACGGTCT
                                    ____
GAM2760  PDE4D    3'  TTTCTAGACTTCACTCAG    43906         G TG _
                                TTTCTAGAC T  C CAG
                                |||||||| |  | |||
                                AAAGATCTG A  G GTC
                                     A GT A
GAM2760  PUM2     3'  TTTCTGTACATTGCCAGA    31669       AG
                                TTTCT  ACGTTGCCAGA
                                |||||  ||||||||||
                                AAAGA  TGTAACGGTCT
                                  CA
GAM2760  RBL2     3'  TTTCTAAAAGCTTTGCCAGA  24706         C  __
                                TTTCTAGA GT  TGCCAGA
                                |||||||| ||  |||||||
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                                AAAGATTT CG  ACGGTCT
                                     T  AA
GAM2760  SEL1L    3'  TTCTAATGACTTGCCAGA    22854      __  G
                                TTCTA  GAC TTGCCAGA
                                |||||  ||| ||||||||
                                AAGAT  CTG AACGGTCT
                                   TA  _
GAM2760  SHANK2   3'  TTCCTAGACACCCAGA     29476         TTG
                                TTTCTAGACG   CCAGA
                                ||||||||||   |||||
                                AAGGATCTGT   GGTCT
                                     G__
GAM2760  SMARCD2  3'  TTTCCAAACCTGCCAGA     16924         G
                                TTTCTAGAC TTGCCAGA
                                ||||||||| ||||||||
                                AAAGGTTTG GACGGTCT
                                          _
GAM2760  TLR4     5'  TCTCTAGAGATGCTAGA     17566        CGT   C
                                TTTCTAGA   TGC AGA
                                ||||||||   ||| |||
                                AGAGATCT   ACG TCT
                                     CT_   A
GAM2760  TNFRSF6  3'  TCTCTAGAATTATCAGA     6225         C   C
                                TTTCTAGA GTTG CAGA
                                |||||||| |||| ||||
                                AGAGATCT TAAT GTCT
                                     _    A
GAM2760  WFS1     3'  TTTCCAGACACCGGA       25646        GTT   A
                                TTTCTAGAC   GCC GA
                                |||||||||   ||| ||
                                AAAGGTCTG   TGG CT
                                     ___   C
GAM2761  CAPZB    3'  AACGAGTGCACGGCGTGTC   22315         CCTTCAA
                                AGCGAGTGC      GCGTGTC
                                |||||||||      |||||||
                                TTGCTCACG      CGCACAG
                                     TGC____
GAM2761  HSF4     5'  AGCGGGTGGGGCGTGTC     40759      A  CCCTTCAA
                                AGCG GTG       GCGTGTC
                                |||| |||       |||||||
                                TCGC CAC       CGCACAG
                                  C   CC_______
GAM2761  LDB3     3'  AGCGAGTGCTGTTTGGCACTTC 44107         CCTTCAA   TG
                                AGCGAGTGC      GCG  TC
                                |||||||||      |||  ||
                                TCGCTCACG      CGT  AG
                                     ACAAAC_   GA
GAM2761  MTNR1A   3'  AGCGAGGCCTTGCGCAGCGTGT 25547       T   CTTCA_
              CC                   AGCGAG GCC     AGCGTGTCC
                                |||||| |||     |||||||||
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                                TCGCTC CGG     TCGCACAGG
                                   _  AACGCG
GAM2761  RBP3     3'  AGGAGTGCCCTTGGTGTGTGTC 16183    C        CAAGC
              C                    AG GAGTGCCCTT     GTGTCC
                                   || ||||||||||     ||||||
                                   TC CTCACGGGAA     CACAGG
                                   _         CCACA
GAM2761  SLC1A4   3'  GCAGTGCCCTGTGT       16749    G      TCAAGC
                                   GC AGTGCCCT     GTGT
                                   || ||||||||     ||||
                                   CG TCACGGGA     CACA
                                   _      _______
GAM2761  WHSC1    3'  GCGAGTGCCCCTCAGAGGC   39368            _  C
                                   GCGAGTGCCCTTCA AG GT
                                   |||||||||||||| || ||
                                   CGCTCACGGGGAGT TC CG
                                            C  _
GAM2762  CAPZB    3'  ACAAAAACCACACGGTCTCTAT 22316         _    AGA
              G                    ACAAAAAT ATGC   TCTCTATG
                                   |||||||| ||||   ||||||||
                                   TGTTTTTG TGTG   AGAGATAC
                                       G    CC_
GAM2762  SERPINE2 3'  ACAAAAATATTTAACAGAACTA 44000          ___     TCT
              TG                     ACAAAAATAT   GCAGA   CTATG
                                   ||||||||||   |||||   |||||
                                   TGTTTTTATA   TGTCT   GATAC
                                        AAT     T__
GAM2763  BCL2L2   3'  TCAGTGGTTTTCCAACT     19748        C
                                   TCAGTGG TTTTCTAACT
                                   ||||||| ||||||||||
                                   AGTCACC AAAAGGTTGA
                                      _
GAM2763  BLAME    3'  CGGTGTCTACAACTGCAA    33486     CT   C
                                   TGG  TTT TAACTGCAA
                                   |||  ||| |||||||||
                                   GCC  AGA GTTGACGTT
                                     AC   T
GAM2763  ID4      3'  CCGGTGGCTTTTTTTCTCTAAC 11380    A     _____
              T                    TC GTGGCT     TTTCTAACT
                                   || ||||||     |||||||||
                                   GG CACCGA     AGAGATTGA
                                    C     AAAAA
GAM2763  IPP      3'  TCATTGGCTTTCTCTGTGGC  25323     G     _   AACT
                                   TCA TGGCTT TTCT    GC
                                   ||| |||||| ||||    ||
                                   AGT ACCGAA GAGA    CG
                                     A     A   CAC_
GAM2763  SP1      3'  CCAGTGGCAGCAAACTGCA   41477         TTTTCT
                                   TCAGTGGC     AACTGCA
                                   ||||||||     |||||||
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                                GGTCACCG     TTGACGT
                                     TCGT__
GAM2763  THBS1    3'  ATGGCTTTCTTTGCAA      17510        T  AAC
                                GTGGCTTT CT   TGCAA
                                |||||||| ||   |||||
                                TACCGAAA GA   ACGTT
                                     _  A__
GAM2764  ADM      3'  TCCGGGGGTCTCAGCATTCATT 10029      TAA    TTTA
              T                  TCCG   GTCTT   GTTCATTT
                                 ||||   |||||   ||||||||
                                 AGGC   CAGAG   TAAGTAAA
                                   CCC    TCG_
GAM2764  GATM     3'  TAAGTCTTTCTCTCATTT    11230          AG
                                 TAAGTCTTTTT  TTCATTT
                                 ||||||||||  |||||||
                                 ATTCAGAAAGA  GAGTAAA

                                      __
GAM2764  VTN      5'  AGTCTTAGTTCATTT      8466       TTT
                                 AGTCT   TAGTTCATTT
                                 |||||   ||||||||||
                                 TCAGA   ATCAAGTAAA

                                     ___
GAM2765  SIGLEC6  3'  TGGGCTATATAATATTG     40936        GCCGG
                                 TGGGCTATG    AATATTG
                                 |||||||||    |||||||
                                 ACCCGATAT    TTATAAC
                                      A____
GAM2766  ANGPT1   3'  GACACATAAATATAAAAAA    40240      TG
                                 GATAT  ATAAATATAAAAAA
                                 |||||  ||||||||||||||
                                 CTGTG  TATTTATATTTTTT

                                     __
GAM2766  ITGA9    3'  ATAATATCGATACAAATATAAA 13612          __
              A                   ATGATATTGATA  AATATAAAA
                                  ||||||||||||  |||||||||
                                  TATTATAGCTAT  TTATATTTT
                                        GT
GAM2766  MAN1A1   3'  ATGATATTGAAAAACAGAAA   45092         T    T
                                 ATGATATTGA AAATA AAA
                                 |||||||||| ||||| |||
                                 TACTATAACT TTTGT TTT
                                      T    C
GAM2766  ROBO1    3'  ATGATATTCATAAAATGACAAA 39479        G    T__
              AAA                   ATGATATT ATAAA   ATAAAAAA
                                    |||||||| |||||   ||||||||
                                    TACTATAA TATTT   TGTTTTTT
                                       G    TAC
GAM2767  CTNNB1   3'  TAAAAATTAGAAATTGCTGTA  12519      T      AATC
                                 TGAAA GTTGGAGA   GCTGTA
                                 ||||| ||||||||   ||||||
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                                ATTTT TAATCTTT   CGACAT
                                  _      AA__
GAM2767  DDX3    3'  TGAAAGAGGAATTGCTGT   35825   TT   A  C
                                TG  GGAG AAT GCTGT
                                ||  |||| ||| |||||
                                AC  TCTC TTA CGACA
                                 TT   C   A
GAM2767  HIVEP3  5'  TGAAGGTTGGAGACATCTGT  35992    AT     AATCG
                                TGAA  GTTGGAGA   CTGT
                                ||||  ||||||||   ||||
                                ACTT  CAACCTCT   GACA
                                  C_      GTA__
GAM2767  MOCS1   5'  TGCAATGTTGGGGAAGCTG   45126   A      A  ATC
                                TG AATGTTGG GAA  GCTG
                                || |||||||| |||  ||||
                                AC TTACAACC CTT  CGAC
                                 G      C  ___
GAM2767  RGS6    3'  TGTTGGAATACAACTGTA   20191       AA  C
                                TGTTGGAG  AT GCTGTA
                                ||||||||  || ||||||
                                ACAACCTT  TG TGACAT
                                     A_  T
GAM2768  MLLT4   3'  ATATCATTTAAGTACAATTT  25523
                                ATATCATTTAAGTATAGTTT
                                ||||||||||||||||||
                                TATAGTAAATTCATGTTAAA

GAM2769  CXCL16  5'  GACCGTGCGCTCAGTACTCGGC 35197       A _____   CC
           C                     GACCGTGC CT   ACTC  GCC
                                ||||||||  ||   ||||  |||
                                CTGGCACG GA   TGAG  CGG
                                     C  GTCA   C_
GAM2769  LAMC1   5'  GACCGCGCTGCTCGCCGAC   14085       ACTA   CC
                                GACCGTGC   CTC  GCCGAC
                                ||||||||   |||  ||||||
                                CTGGCGCG   GAG  CGGCTG
                                     AC__   __
GAM2769  MYCL1   5'  GACCGGCTCCCCGCCG     23889      T  ACTAC
                                GACCG GC    TCCCGCCG
                                |||||  ||   ||||||||
                                CTGGC CG    GGGGCGGC
                                  _  A_____
GAM2769  SLC7A5  3'  CGTGCGTGGGCCCCGCCGGCC  18545      ACTAC      A
                                CGTGC    TCCCGCCG CC
                                |||||    |||||||| ||
                                GCACG    GGGGCGGC GG
                                   CACCC      C
GAM2770  CALB2   3'  GACCTTTCCATTTTATTG    11936         CAGCAC
                                GACCTTTTCA     TTTATTG
                                ||||||||||     |||||||
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                                CTGGAAAGGT     AAATAAC
                                    A_____
GAM2770  CD36    3'  CTTTGGCACAGTGCTTTATTGT 6313      T_    CA
                                CTTT  CACAG  CTTTATTGT
                                ||||  |||||  |||||||||
                                GAAA  GTGTC  GAAATAACA
                                  CC    AC
GAM2770  GLRX    3'  GACCTTTCACAGAATT      13149       T    CACTTT
                                GACCTTT CACAG     ATT
                                ||||||| |||||     |||
                                CTGGAAA GTGTC     TAA
                                    _    T_____
GAM2770  HAT1    3'  TTTTCACAGCACATTG      18882           TTT
                                TTTTCACAGCAC   ATTG
                                ||||||||||||  ||||
                                AAAAGTGTCGTG   TAAC
                                      ___
GAM2770  PPIL1   3'  AACCATCAATGGCATTTTATTG 31996     TTT   CA_   C
           T                     GACC   TCA   GCA TTTATTGT
                                ||||   |||   ||| ||||||||
                                TTGG   AGT   CGT AAATAACA
                                  T__   TAC   A
GAM2770  RDX     3'  GAGCTTTTGTCACTTTATTGT  16236    C    CACAG
                                GA CTTTT    CACTTTATTGT
                                || |||||    ||||||||||
                                CT GAAAA    GTGAAATAACA
                                 C    CA___
GAM2771  EVI2B   5'  TCTAACTGGACATTTTGGTGAT 27093          TTAACAAC
                                TCTAATTGGAT       GAT
                                ||||||||||       |||
                                AGATTGACCTG       CTA
                                      TAAAACCA
GAM2772  SCN3A   3'  TTAATAGAAGTTGTTTATCAGG 27956       TTATA
                                TTAATA    TTGTTTATCAGG
                                ||||||    ||||||||||||
                                AATTAT    AACAAATAGTCC
                                   CTTC_
GAM2772  VCL     3'  TTAATATTGCATTTATATCAGG 30410        A   GTT
                                TTAATATT TATT   TATCAGG
                                |||||||| ||||  |||||||
                                AATTATAA GTAA   ATAGTCC
                                    C   AT_
GAM2773  PFKFB1  3'  CACTGGAAGTGGGGTGCCT   15228     C       AAC
                                CAC GGAAGTGG   GCCT
                                ||| ||||||||  ||||
                                GTG CCTTCACC   CGGA
                                  A       CCA
GAM2774  COX11   3'  TAGCTAGGCATATGAGTTTC  20420         CACT  C
                                TAGCTGGGCA    TG GGTTTC
                                ||||||||||    || ||||||
```

```
                                ATCGATCCGT   AC TCAAAG
                                     AT__ _
GAM2774 GPR44   3' TAGCTGGGCACCTCACTGTTCC 21959         A  TG G
                                TAGCTGGGCAC CT  C GTTTC
                                |||||||||||  ||  | |||||
                                ATCGACCCGTG GA  G CAAGG
                                     _ GT A
GAM2774 HLA-DQA1 3' TAGCTGGGTGGCTTACTC   45568       CACA   GGTT
                                TAGCTGGG   CTTGC   TC
                                ||||||||   |||||   ||
                                ATCGACCC   GAATG   AG
                                    ACC_   _____
GAM2774 PIGB    5' GGCCTCCTTGCGGTTTCC   22142    ACA
                                GGC   CTTGCGGTTTCC
                                |||   ||||||||||||
                                CCG   GAACGCCAAAGG
                                  GAG
GAM2774 PPL     3' GCTGGACACTTGTGGTTTC   15495     GC     C
                                GCTGG  ACACTTG GGTTTC
                                |||||  ||||||| ||||||
                                CGACC  TGTGAAC CCAAAG
                                   __     A
GAM2774 TRIM14  3' CAGCTGGGCACTCTGGGTTTCC 37696         A  T C
                                TAGCTGGGCAC CT G GGTTTCC
                                |||||||||||  || | |||||||
                                GTCGACCCGTG GA C CCAAAGG
                                     A _ _
GAM2775 EPS8    3' TACATAACATCTGTTTTA   20812        __
                                TACGTAGCG  TGTTTTA
                                |||||||||  |||||||
                                ATGTATTGT  ACAAAAT
                                     AG
GAM2776 CASP10  5' GAAGAGACTTCAAGACTTGC  37384       GCAGTCA
                                GAAGAGAC      ACTTGC
                                ||||||||      ||||||
                                CTTCTCTG      TGAACG
                                    AAGTTC_
GAM2776 FSTL1   3' GAAGAATAAAGTCAACTTGCC  28216      ACGC
                                GAAGAG   AGTCAACTTGCC
                                ||||||   ||||||||||||
                                CTTCTT   TCAGTTGAACGG
                                   ATT_
GAM2776 IL1F5   5' TAGGGAGGGGCCCTGAAACTTG 29357    AA   AC  AGTC_
            CC                   TAG  GAG  GC    AACTTGCC
                                ||| |||  ||    ||||||||
                                ATC  CTC  CG    TTGAACGG
                                  C_   CC  GGACT
GAM2776 LFG     3' TAGAAGAGATGTGGACTGTGCC 44146        CGCA  CA  _
                                TAGAAGAGA   GT  ACT TGCC
                                |||||||||   ||  ||| ||||
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                                ATCTTCTCT   CA  TGA ACGG
                                     A___  CC   C
GAM2776 NEBL    3' TAGAATAGGCAGCAACTTGC  26908      G  AC   T
                                TAGAA AG  GCAG CAACTTGC
                                ||||| ||  |||| ||||||||
                                ATCTT TC  CGTC GTTGAACG
                                   A __   _
GAM2776 P2RY6   5' GAGAGGAAGTAACTTGCC    19991     CGC   C
                                GAGA   AGT AACTTGCC
                                ||||   ||| ||||||||
                                CTCT   TCA TTGAACGG
                                  CCT   _
GAM2776 RANBP2  3' AAAGGAAATAGTCAACTTG   26535     A  CGC
                                GAAG GA   AGTCAACTTG
                                |||| ||   ||||||||||
                                TTTC CT   TCAGTTGAAC
                                  _  TTA
GAM2776 SVIL    5' GAGGACGCAGTCAGAGC     34729     _       ACTT
                                GAG ACGCAGTCA   GC
                                ||| |||||||||   ||
                                CTC TGCGTCAGT   CG
                                  C       CT__
GAM2776 UBE2V1  3' AAAGACGCAGCAATTTGCC   35338         T   C
                                AGAGACGCAG CAA TTGCC
                                |||||||||| ||| |||||
                                TTTCTGCGTC GTT AACGG
                                      _  A
GAM2777 FZD6    3' CAGTGTAACACAAATTTGCTT 18625          T   A
                                TAGTGTAATATA ATTT CTT
                                |||||||||||| |||| |||
                                GTCACATTGTGT TAAA GAA
                                       T   C
GAM2777 NRCAM   3' ATAGAATATATATTTACTT   22687     T
                                GTG AATATATATTTACTT
                                ||| ||||||||||||||
                                TAT TTATATATAAATGAA
                                  C
GAM2777 SHANK2  3' TAGTGCAATAGTATATTTA   29468         _
                                TAGTGTAATA TATATTTA
                                |||||||||| ||||||||
                                ATCACGTTAT ATATAAAT
                                      C
GAM2778 CNN1    3' TGTGAGGGAGTGGGGGGAC   10543    CA      A__
                                TG  AGGGAGTG   GGAC
                                ||  ||||||||   ||||
                                AC  TCCCTCAC   CCTG
                                 AC       CCC
GAM2778 GYG     3' TCTGAAGGGAGTGACTGA    19970     C       G_
                                TCTG AAGGGAGTGA  GA
                                |||| ||||||||||  ||
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                                AGAC TTCCCTCACT  CT
                                  _        GA
GAM2778  SCD      3'  TCTGCAGAGGGAGTGAGGGC   22834       _         AC
                                TCTGCA AGGGAGTGAGG  GC
                                |||||| ||||||||||  ||
                                AGACGT TCCCTCACTCC  CG
                                   C         __
GAM2779  NPHP1    3'  TTATTAGCTGTGACCTTA    41685     C    C
                                TTA TAGC GTGACCTTG
                                ||| |||| |||||||||
                                AAT ATCG CACTGGAAT
                                  A    A
GAM2780  C4orf1   3'  TCCAGTAAATAAACATTATG   40492            ACTT
                                TCCAGTAAATAAA    TTATG
                                ||||||||||||    |||||
                                AGGTCATTTATTT    AATAC
                                        GT__
GAM2780  C8orf1   3'  CCAGTGTCTCAAATTTTTATGA 20271       AAATA   C
                                CCAGT     AAA TTTTATGA
                                |||||     ||| ||||||||
                                GGTCA     TTT AAAATACT
                                   CAGAG   A
GAM2780  CASP10   3'  TCCAGTAAATGAGGACTGTGA  37391          AAA_   TTTA
                                TCCAGTAAAT    ACT    TGA
                                ||||||||||    |||    |||
                                AGGTCATTTA    TGA    ACT
                                      CTCC   C___
GAM2780  PPARGC1  3'  TCCAGTGTATAAAACTTC    29967       AA
                                TCCAGT  ATAAAACTTT
                                ||||||  ||||||||||
                                AGGTCA  TATTTTGAAG
                                   CA
GAM2781  CDH1     3'  ACAATACCTAGTCAAGAT    20357      CA  A
                                ACAA  AC TAGTCAAGAT
                                ||||  ||  ||||||||||
                                TGTT  TG ATCAGTTCTA
                                  A_  G
GAM2781  EPM2A    3'  AAAAACAACAACAAATGAGAGA 24964             TAGTCA
            T                    AAAAACAACAACA      AGAT
                                ||||||||||||      ||||
                                TTTTTGTTGTTGT     TCTA
                                      TTACTC
GAM2781  JJAZ1    3'  TAAAAACAAAAACATAAT    31693          C
                                TAAAAACAA AACATAGT
                                ||||||||| ||||||||
                                ATTTTTGTT TTGTATTA
                                      T
GAM2781  PRPS2    3'  AAACACCAAATAGTCAAG    15728       A   C
                                AAACA CAA ATAGTCAAG
                                ||||| ||| |||||||||
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                                TTTGT GTT TATCAGTTC
                                   G  _
GAM2781  TSN      3'  AACAACATAATAGTCAGGAT   21488        AC      A
                                AACAACA  ATAGTCA GAT
                                |||||||  ||||||| |||
                                TTGTTGT  TATCAGT CTA
                                    AT      C
GAM2782  FKRP     3'  TCTAGTGGCGGAAGCAACCCCT 35899      A         TG  A_
              G                  TCTA TGGTGGAAGCG  GC  CTG
                                |||| ||||||||||  ||  |||
                                AGAT ACCGCCTTCGT  TG  GAC
                                  C          __  GG
GAM2782  PRKRA    3'  TGATGTGCATGGCACT      18974       GAA
                                TGGTG   GCGTGGCACT
                                |||||   ||||||||||
                                ACTAC   CGTACCGTGA
                                   A__
GAM2782  EHHADH   3'  ATCATTTTTATTGATGT     12681           A
                                ATCATTTTTATT GATGT
                                |||||||||||| |||||
                                TAGTAAAAATAA CTACA
                                                _
GAM2782  RNTRE    3'  ATCATTTTTATAATTTTAACAT 31247           TAGATG
                                ATCATTTTTAT     TAACAT
                                ||||||||||      ||||||
                                TAGTAAAAATA     ATTGTA
                                      TTAAA_
GAM2783  AP1B1    3'  GTGGGCGCTGGCCGG       10040        TGT
                                GTGGGTG   CTGGCCGG
                                |||||||   ||||||||
                                CACCCGC   GACCGGCC
                                   ___
GAM2783  CD5      5'  GTGAGGGTGTCTGGCCGG    30546       T
                                GTGGG GTGTCTGGCCGG
                                ||||| ||||||||||||
                                CACTC CACAGACCGGCC
                                   C
GAM2783  CFTR     3'  TAAGAGGCTGTGTCTGGCTGG  7956    T  T  G        C
                                A AG GG TGTGTCTGGC GG
                                | || || |||||||||| ||
                                A TC CC ACACAGACCG CC
                                 T  T  G         A
GAM2783  FCN1     3'  ATGGGAGTGTGTCTGGCTGG   12817      __        C
                                GTGGG  TGTGTCTGGC GG
                                |||||  |||||||||| ||
                                TACCC  ACACAGACCG CC
                                   TC         A
GAM2783  LAMC2    3'  TATAGTGAGTGTTCTGG     33120           G
                                TATAGTGGGTGT TCTGG
                                |||||||||||| |||||
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                                ATATCACTCACA AGACC
                                           _
GAM2783 LY64     3' TAGTGGGGGTGGGTAGTGG   24570       T  TC  CC
                                TAGTGGG GTG  TGG  GG
                                ||||||| |||  |||  ||
                                ATCACCC CAC  ATC  CC
                                    C  CC  A_
GAM2783 MHC2TA   3' GTCAAGGTGTCTGGTCGG    6987     G  T      C
                                GT GG GTGTCTGG CGG
                                || || |||||||| |||
                                CA TT CACAGACC GCC
                                 G  C       A
GAM2783 NUFIP1   3' TATGGTGGGTACAAGGCTGG   29594     A      TGTCT   C
                                TAT GTGGGTG     GGC GG
                                ||| |||||||     ||| ||
                                ATA CACCCAT     CCG CC
                                  C      GTT__   A
GAM2783 SH3GL1   3' GTGGGTGTGGGTGGCTGG    16675         TC    C
                                GTGGGTGTG  TGGC GG
                                |||||||||  |||| ||
                                CACCCACAC  ACCG CC
                                     CC    A
GAM2783 TBL2     3' GTGTTGTTCATCTGGTTGG   29729     GG  __     CC
                                GTG  TGT  GTCTGG  GG
                                |||  |||  ||||||  ||
                                CAC  ACA  TAGACC  CC
                                  A_  AG     AA
GAM2783 TEL2     3' GTGGGTACAGAGTCTGGCTGG  32045       T___      C
                                GTGGGTG    GTCTGGC GG
                                |||||||    ||||||| ||
                                CACCCAT    CAGACCG CC
                                    GTCT      A
GAM2783 VEGF     3' GTGGGTGTGTCTACAGG     17961           G C
                                GTGGGTGTGTCTG C GG
                                |||||||||||| | ||
                                CACCCACACAGAT G CC
                                       _ T
GAM2784 CDC23    3' TAGCATCTACTGTGCAAATATA 21668         ATA_   T
             TT                   TAGCATCTAC    CAA ATATGTT
                                |||||||||    ||| |||||||
                                ATCGTAGATG    GTT TATATAA
                                     ACAC   _
GAM2784 DAAM1    3' ACATTTACATACACACGT    31429      C      ATA
                                GCAT TACATACA   TATGT
                                |||| ||||||||   |||||
                                TGTA ATGTATGT   GTGCA
                                  A       ____
GAM2784 PPAT     3' ACATCTACATGTATATATGTT  15479          ACA
                                GCATCTACAT   ATATATGTT
                                |||||||||   |||||||||
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                                TGTAGATGTA   TATATACAA
                                     CA_
GAM2785 AOX1     3'  TAGAAGCCAAGTAGGAGC    10109        ATTA    A  C
                                TGGAAGCCA    AGTAG AG C
                                |||||||||    ||||| || |
                                ATCTTCGGT    TCATC TC G
                                     ____    C  A
GAM2785 C9       3'  TGGAGCTCAGAGAAGC      11932      A  CAATTA  T
                                TGGA GC     AG AGAAGC
                                |||| ||     || ||||||
                                ACCT CG     TC TCTTCG
                                  _ AG____  _
GAM2785 CAPN10   3'  TGGAAGCCGATGGGGTGGAA   35779        A  TAA  A
                                TGGAAGCC AT   GT GAA
                                |||||||| ||   || |||
                                ACCTTCGG TA   CA CTT
                                     C  CCC  C
GAM2785 CAPN9    3'  GAAGGTCAAGGTCCAGAAGCCA 27357      CCAA    ___
                                GAAG    TTAAG   TAGAAGCCA
                                ||||    |||||   |||||||||
                                CTTC    AGTTC   GTCTTCGGT
                                  C___    CAG
GAM2785 DVL1     3'  TGGGGGCCAGAGAAGCC     40418     AA    ATTAA T
                                TGG  GCCA    G AGAAGCC
                                |||  ||||    | |||||||
                                ACC  CGGT    C TCTTCGG
                                  CC   _____ _
GAM2785 EDN1     3'  TGGAAGCCAGTGAAG       12643         ATTAA  A
                                TGGAAGCCA    GT GAAG
                                |||||||||    || ||||
                                ACCTTCGGT    CA CTTC
                                     _____  _
GAM2785 GOT1     3'  TGGGGCCGGTTTAAACAGAGGC 13227     AA   AA_       A
                                TGG  GCC   TTAAGTAGA GC
                                |||  |||   ||||||||| ||
                                ACC  CGG   AATTTGTCT CG
                                  C_   CCA       C
GAM2785 HTR6     5'  GGAAGTCAAGCAGA        9308       CCAA
                                GGAAG    TTAAGTAGA
                                |||||    |||||||||
                                CCTTC    AGTTCGTCT
                                     ____
GAM2785 KRT9     3'  TGGAAGCCAATGGAAAGCC    44064          TAAGTA
                                TGGAAGCCAAT     GAAGCC
                                ||||||||||     ||||||
                                ACCTTCGGTTA     TTTCGG
                                     CC____
GAM2785 KRTHA8   3'  TGGAAGCCATATGTAAGAGGC  27671         AT  A   _  A
                                TGGAAGCCA  TA GTA GA GC
                                |||||||||  || ||| || ||
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                                ACCTTCGGT  AT CAT CT CG
                                    __ A   T  C
GAM2785  MBL2     3'  TGGAAGCCACTTAAGTGCC   6967          A     AGAA
                                TGGAAGCCA TTAAGT    GCC
                                ||||||||| ||||||    |||
                                ACCTTCGGT AATTCA    CGG
                                   G     _____
GAM2785  SEPP1    3'  TGGAAGCCAATTCAGTAG    24000           A
                                TGGAAGCCAATT AGTAG
                                |||||||||||| |||||
                                ACCTTCGGTTAA TCATC
                                     G
GAM2785  SPTBN2   3'  TGGAAGCCATTGAGAGCAGC  28076         A  A  T  A
                                TGGAAGCCA TT AG AG AGC
                                ||||||||| || || || |||
                                ACCTTCGGT AA TC TC TCG
                                    _  C  _  G
GAM2785  TCF2     3'  TGGAAGCCGAGTGAGCC     27032        AATTA   A  A
                                TGGAAGCC     AGT GA GCC
                                ||||||||     ||| || |||
                                ACCTTCGG     TCA CT CGG
                                    C_____   _  _
GAM2785  TCL1A    3'  TAGAAGCTGATTGCGCACGAAG 35029        CA   AA   _
                                TGGAAGC  ATT  GTA GAAG
                                |||||||  |||  ||| ||||
                                ATCTTCG  TAA  CGT CTTC
                                   AC   CG   G
GAM2785  UBE2I    5'  TGGGGTTGGGATCAAAGAAGCC 17820     AAGCCA_    GT
            A                    TGG      ATTAA  AGAAGCCA
                                |||      |||||  ||||||||
                                ACC      TAGTT  TCTTCGGT
                                  CCAACCC    __
GAM2785  ARF3     3'  AGTGGAAAATCCTAAGTAG    11665        CCAA
                                AGTGGAAG    TTAAGTAG
                                ||||||||    ||||||||
                                TCACCTTT    GATTCATC
                                    TAG_
GAM2785  EPB72    3'  AGTGGAAGTCAAAACAAG     19896        C   T_
                                AGTGGAAG CAA  TAAG
                                |||||||| |||  ||||
                                TCACCTTC GTT  GTTC
                                    A   TT
GAM2785  HPSE     3'  TAAGTGGAAGCTTAGCTGTAG  27418          CAATTAA
                                TAAGTGGAAGC      GTAG
                                ||||||||||       ||||
                                ATTCACCTTCG      CATC
                                     AATCGA_
GAM2785  LDLR     3'  AAGTGGAAGCACTAGGT     8020          CA   A
                                AAGTGGAAGC  ATTA GT
                                ||||||||||  |||| ||
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                                TTCACCTTCG  TGAT CA
                                    __    C
GAM2785  RGR      3'  TAAGTGGGAGCTAAATAA    16304        A   CAAT
                                TAAGTGG AGC    TAAGTAG
                                ||||||| |||    |||||||
                                ATTCACC TCG    ATTTATT
                                   C  ____
GAM2785  RUNX1    3'  GTGGGGGCTGGCTTAAATAG   12027      AA  CAA_
                                GTGG  GC    TTAAGTAG
                                ||||  ||    ||||||||
                                CACC  CG    AATTTATC
                                  CC  ACCG
GAM2785  SERPINA5 3'  GTGGAAGCAATCATCATAG   8415         C    A_
                                GTGGAAGC AATTA  GTAG
                                |||||||| |||||  ||||
                                CACCTTCG TTAGT  TATC
                                   _    AG
GAM2785  SERPINB13 5'  AAGCATAAGTCAATTAAGTAG  29618       G   C
                                AAGTG AAG CAATTAAGTAG
                                ||||| ||| ||||||||||
                                TTCGT TTC GTTAATTCATC
                                  A   A
GAM2785  TBL1X    3'  CAAGTGGAGGCCAATCAA    24872         A
                                TAAGTGGA GCCAATTAA
                                |||||||| |||||||||
                                GTTCACCT CGGTTAGTT
                                   C
GAM2786  ATP6V1A1  3'  AACTTGTTTAATTGGCT     11774       CTAC
                                GGCTT    TTAATTGGCT
                                |||||    ||||||||||
                                TTGAA    AATTAACCGA
                                  CA__
GAM2786  BRCA1    3'  TTCTACCTAGTTCTGCTT    28657         A  G_
                                TTCTACTTA TT  GCTT
                                ||||||||| ||  ||||
                                AAGATGGAT AA  CGAA
                                     C  GA
GAM2786  EHD2     3'  TTCTACGTAGGGGCTCCACTTA 31140       T  ATT    T
                                TTCTAC TA   GGCT CCACTTA
                                |||||| ||   |||| |||||||
                                AAGATG AT   CCGA GGTGAAT
                                   C  CC_   _
GAM2786  KIF3B    3'  TTCTCTTGCTTTCCACTT    22047      A   AATTG   _
                                TTCT CTT    GCTT CCACTT
                                |||| |||    |||| ||||||
                                AAGA GAA    CGAA GGTGAA
                                  _  _____   A
GAM2787  EDN3     3'  TGTTCGTGACTTATTTTG    6486          GTC_
                                TGTTCGTGAC    TTTG
                                ||||||||||   ||||
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                                ACAAGCACTG   AAAC
                                     AATA
GAM2787 HGF     3' TGTTCGTGTACCAGTAT    45326       ACGT  TT
                                TGTTCGTG   CT  GTAT
                                ||||||||   ||  ||||
                                ACAAGCAC   GG  CATA
                                    AT__  T_
GAM2787 MAPK14  3' TATACATCCACCTGTTCCTC  40015      CAC   CCCG_
                                TATACAT  CCACC   CTC
                                |||||||  |||||   |||
                                ATATGTA  GGTGG   GAG
                                   ___   ACAAG
GAM2787 OGT     3' TATATATCACCCATCTGCAACA 18785     C      CCCCC  T_
                                TATA ATCACCCA    GC  CA
                                |||| ||||||||    ||  ||
                                ATAT TAGTGGGT    CG  GT
                                  A      AGA__  TT
GAM2788 NEU3    3' GCATTGAGATTCTCATTG    27402        __   C
                                GCATTGGGA  CTCG TG
                                |||||||||  |||| ||
                                CGTAACTCT  GAGT AC
                                     AA   A
GAM2788 PPP1R12B 5' ACTGTTGGGGCTCGAGTT   36955   A_   A   CT
                                GC  TTGGG CTCG  GTT
                                ||  ||||| ||||  |||
                                TG  AACCC GAGC  CAA
                                 AC    C   T_
GAM2788 SLC24A1  3' TACCATTGGGATTCACAGTT  21820   G      C   T
                                TA CATTGGGA TCGC GTT
                                || |||||||| |||| |||
                                AT GTAACCCT AGTG CAA
                                 G      A   T
GAM2789 CHAC    3' TTGATTTCTTACCCA      37818       GAAA
                                TTGATTTC   TTACCCA
                                ||||||||   |||||||
                                AACTAAAG   AATGGGT
                                    ____
GAM2789 LCP1    3' CTTGATTCCGATTCCA     14106         AATTAC
                                CTTGATTTCGA    CCA
                                ||||||||||     |||
                                GAACTAAGGCT    GGT
                                     AA____
GAM2790 COX10   3' TAGCTATTGGTATTGT     10555     CCTCT  GTG
                                TAGC    TA  GGTATTGT
                                ||||    ||  ||||||||
                                ATCG    AT  CCATAACA
                                  _____ AA_
GAM2790 FZD10   3' CCTCTTAGTTCTTTTGTTA  28450       GGGTA
                                CCTCTTAGT    TTGTTA
                                |||||||||    ||||||
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                                GGAGAATCA    AACAAT
                                     AGAA_
GAM2791  AHR     3'  TGTAATTTTGATACCATTTTTA 11552      CTCCA
                                TGTGA    ATACCATTTTTA
                                |||||    ||||||||||||
                                ACATT    TATGGTAAAAAT
                                   AAAAC
GAM2791  RAD1    5'  TGTTACTTTGATACCATTTTTA 15997    G  CCA
                                TGT ACT  ATACCATTTTTA
                                ||| |||  ||||||||||||
                                ACA TGA  TATGGTAAAAAT
                                  A  AAC
GAM2791  TRO     3'  TGTAACTCTGATACCAAAATAT 32073       CA     TTTT
             G                   TGTGACTC  ATACCA   TATG
                                ||||||||  ||||||   ||||
                                ACATTGAG  TATGGT   ATAC
                                     AC     TTT_
GAM2792  LPIN1   3'  GATCCAAACATAAAATTGCA  42638      TTT  C
                                GATCCG   TA AAAATTGCA
                                ||||||   || |||||||||
                                CTAGGT   GT TTTTAACGT
                                   TT_  A
GAM2792  NQO1    3'  AGAAATTTACACAAAATTGCA  9475       CCGTTT
                                AGAGAT     TACAAAATTGCA
                                ||||||     ||||||||||||
                                TCTTTA     GTGTTTTAACGT
                                   AAT___
GAM2792  PPP1R12B  5'  GAGCCCATTTTATGAGATTG  36974    A       CAAA
                                GAG TCCGTTTTA    ATTG
                                ||| |||||||||    ||||
                                CTC GGGTAAAAT    TAAC
                                  _       ACTC
GAM2792  UBE2A   3'  GTACATTTTTTTTTACATGGG  17787         CGTCAG  C
                                GTACATTTTTT     ACA GGG
                                ||||||||||      ||| |||
                                CATGTAAAAAA     TGT CCC
                                      AAA___   A
GAM2793  CDH13   3'  TTTCTCTGCTCTCCCTCTCTG  10376        G  GG  GC
                                TTTCTCTGCT TCC  TC  CTG
                                |||||||||| |||  ||  |||
                                AAAGAGACGA AGG  AG  GAC
                                     G  G_  A_
GAM2793  EPHA3   3'  TTCCTCTGTGTTGCT      23445        C  CCGGTC  C
                                TTTCTCTG TGT     GC T
                                |||||||| |||     || |
                                AAGGAGAC ACA     CG A
                                     _  A_____  A
GAM2793  HRC     5'  TTTCTCTGTGTCTCTCCT    13462        C   CGG  G
                                TTTCTCTG TGTC   TC CCT
                                |||||||| ||||   || |||
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                                AAAGAGAC ACAG   AG GGA
                                  _   ___  A
GAM2793  PML      3'  TTTCTCTGCTGTTCCACACTGC 37749          CCGG   _
                                TTTCTCTGCTGT   TCGC CTGC
                                ||||||||||||   |||| ||||
                                AAAGAGACGACA   GGTG GACG
                                      A___   T
GAM2793  SKIV2L   5'  TTTCTCTGTTCTTCCTCTTTGC 27973        CTG_  GG  GCC
                                TTTCTCTG   TCC  TC   TGC
                                ||||||||   |||  ||   |||
                                AAAGAGAC   AGG  AG   ACG
                                    AAGA   __  AA_
GAM2793  SMG1     3'  TTTCTCTGTTTCTGAGTGGGGT 31515        ___   TCC__
                                TTTCTCTG   CTG    GGT
                                ||||||||   |||    |||
                                AAAGAGAC   GAC    CCA
                                    AAA   TCACC
GAM2793  ADARB1   3'  CAGTTGTAACGTGTGGTGT   31873     C   _  CGG
                                CGG TGTA CG   GGTGT
                                |||  |||| ||   |||||
                                GTC ACAT GC   CCACA
                                  A   T  ACA
GAM2793  ALEX2    5'  ACGGCTGTGTGGGCCGGAGGTG 31324        AC__  _  _
            T                    ACGGCTGT    GC GG GGTGT
                                ||||||||    || || |||||
                                TGCCGACA    CG CC CCACA
                                    CACC  G  T
GAM2793  ARHGEF6  3'  ACGGCTGTGTGTGGTTGGCTGA 42795        ACGC  __  G
            TGT                   ACGGCTGT    GG  GGT TGATGT
                                ||||||||    ||  ||| ||||||
                                TGCCGACA    CC  CCG ACTACA
                                    CACA  AA  _
GAM2793  DGSI     3'  GGCCCTGGGGTGTGGTG     35532      GTACGC       A
                                GGCT     GGGGTGTG TG
                                ||||     |||||||| ||
                                CCGG     CCCCACAC AC
                                  GA____       C
GAM2794  IL18R1   3'  TCTATTTTGATTATATATGT   19297           ___
                                TCTATTTTGATT   TATGT
                                ||||||||||||   |||||
                                AGATAAAACTAA   ATACA
                                      TAT
GAM2794  MMP20    3'  TCTAATTTGATTTGAAGGCCT  21925      T       AT__
                                TCTA TTTGATTT    GTCT
                                ||||  ||||||||    ||||
                                AGAT AAACTAAA    CGGA
                                  T       CTTC
GAM2794  SLC26A2  3'  TCTTTTTGACTCTGTCCA    6471      A        A
                                TCT TTTTGATTT TGTCTA
                                |||  ||||||||| ||||||
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                                AGA AAAACTGAG ACAGGT
                                  _       _
GAM2795 ADAM19   3' TACTCTGGTCACACTCCT    37774         C  GA
                                TACTCTGGTC CG  CCT
                                |||||||||| ||  |||
                                ATGAGACCAG GT  GGA
                                     T  GA
GAM2795 AQP6     5' CTCTGGTCTCTGATCTCC    38241        CCG  C  A
                                CTCTGGTC   GA CT CC
                                ||||||||   || || ||
                                GAGACCAG   CT GA GG
                                    AGA  A  _
GAM2795 CASP7    5' CTCTGATCTCATTGATCT    10274        C  __  C
                                CTCTGGTC CG  GA CT
                                |||||||| ||  || ||
                                GAGACTAG GT  CT GA
                                    A  AA  A
GAM2795 GCNT1    3' CTCTGGCCTCAAGGCTACC   11247        C   AC
                                CTCTGGTC CGG  CTACC
                                |||||||| |||  |||||
                                GAGACCGG GTT  GATGG
                                    A   CC
GAM2795 GM2A     3' CACTCTGGTTCCCATTCCT   42685         _   GA
                                TACTCTGGT CCCG  CCT
                                ||||||||| ||||  |||
                                GTGAGACCA GGGT  GGA
                                     A    AA
GAM2795 LDLR     3' CCTGGTCCCCCCGGGCCT    8024         ___  A
                                TCTGGTCCC   GG CCT
                                |||||||||   || |||
                                GGACCAGGG   CC GGA
                                     GGG  C
GAM2795 NUMB     3' TACTCTGGGCCTGGACTTGTTC 19052       T  C   CTACC
           CT                     TACTCTGG CC GGAC    CCT
                                |||||||| || ||||    |||
                                ATGAGACC GG CCTG    GGA
                                    C  A   AACAA
GAM2795 RAG1     3' CTCTGGTCCCCTGCAGTTACTC 7785         GGACC__  C
           CT                     CTCTGGTCCC      TAC CCT
                                ||||||||||      ||| |||
                                GAGACCAGGG      ATG GGA
                                     GACGTCA   A
GAM2795 SRGAP2   3' TCTGGTCCTGATACTCC     43986        CG  CC   C
                                TCTGGTCC  GA  TAC CC
                                ||||||||  ||  ||| ||
                                AGACCAGG  CT  ATG GG
                                    A_  __   A
GAM2795 TEAD2    3' TACTCCGGAGTGATCTGTCC   18769        TCCCG  C  AC
                                TACTCTGG    GA CT  CC
                                ||||||||    || ||  ||
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                                ATGAGGCC    CT GA  GG
                                    TCA__  A  CA
GAM2795  TUFT1    3'  TACTCTGATGCCTATCTACTTC 33509        C  GGAC   CC
             T                   TACTCTGGT CC   CTAC  CT
                                 ||||||||| ||   ||||  ||
                                 ATGAGACTA GG   GATG  GA
                                     C  ATA_   AA
GAM2795  WNT5B    5'  CTCTGGTCCTGCAGTTCCT   37212        __  A_
                                 CTCTGGTCC  CGG  CCT
                                 |||||||||  |||  |||
                                 GAGACCAGG  GTC  GGA
                                     AC   AA
GAM2796  ADCY7    3'  GGTAAGAAAAGTAAGATACA  9989     A  A       C
                                 GG AA AAAGGTGGG ATACA
                                 || || ||||||||| |||||
                                 CC TT TTTTCATTC TATGT
                                  A  C       _
GAM2796  ADORA1   3'  TGGGACAGCGGGCAT      8597       AAAAAA
                                 TGGGA     GGTGGGCAT
                                 |||||     |||||||||
                                 ACCCT     TCGCCCGTA
                                    G_____
GAM2796  APPL     3'  GGGGAAAAAAGATCAATGCA  29010     A       GG__
                                 GGG AAAAAAGGT    GCA
                                 ||| |||||||||    |||
                                 CCC TTTTTTCTA    CGT
                                   C        GTTA
GAM2796  AQP6     3'  GGGAAGAAGGTGGAACACA   38253      AAA      C
                                 GGGAA   AAGGTGGG ATACA
                                 |||||   |||||||| |||||
                                 CCCTT   TTCCACCT TGTGT
                                    C__      _
GAM2796  ATP6V1G2 3'  TGGGAAAGTAAGGTGTCA    39630       AA     GG
                                 TGGGAAA  AAGGTG  CA
                                 |||||||  ||||||  ||
                                 ACCCTTT  TTCCAC  GT
                                     CA     A_
GAM2796  BRCA1    3'  TGGGAAAAAGTGGTGGTATAC  28656        AA    GC
                                 TGGGAAAAA  GGTGG  ATAC
                                 |||||||||  |||||  ||||
                                 ACCCTTTTT  CCACC  TATG
                                      CA    A_
GAM2796  BSN      3'  TGGAGAAGGGGGGTGAGCA    18421     _  AAAAA
                                 TGG GAA    GGTGGGCA
                                 ||| |||    ||||||||
                                 ACC CTT    CCACTCGT
                                   T  CCC__
GAM2796  CLASP2   3'  TGGGAAGACAAAGTACAAACAT 42082       AA_   _ TG
                                 TGGGAA   AAAG G  GGCAT
                                 ||||||   |||| |  |||||
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                              ACCCTT  TTTC T  TTGTA
                                 CTG   A GT
GAM2796 COL15A1  3' TGGAAAAAAAATCCAATTATAC 12359        GG  GC
           AA                  TGGGAAAAAAA TGG  ATACAA
                               ||||||||||  |||  ||||||
                               ACCTTTTTTTT GTT  TATGTT
                                    AG  AA
GAM2796 DHCR24   3' TGGGAAAGATGAGGCCTGCA  31300      AAAA   _  ATA
                               TGGGAA   AGGTG GGC  CA
                               ||||||   ||||| |||  ||
                               ACCCTT   TCTAC CCG  GT
                                  ____   T  GAC
GAM2796 EFNB1    3' GGGAAAAAGGGGGAT      20723       AA  T  C
                               GGGAAAA  AGG GGG AT
                               |||||||  ||| ||| ||
                               CCCTTTT  TCC CCC TA
                                  __  _  _
GAM2796 EGFL5    3' GGAAGAGAGGACACACA    44529     AAAA  T
                               GGAA   AGG GGGCATACA
                               ||||   ||| |||||||||
                               CCTT   TCT CCTGTGTGT
                                 C___  _
GAM2796 EGLN1    5' GGAGGAGCGCAGGGCATAC   35170    AAAAA _ _
                               GGA    AG GT GGGCATAC
                               |||    || || ||||||||
                               CCT    TC CG CCCGTATG
                                 CC___  G  T
GAM2796 ENTPD1   5' TAGGAGAAAAGGCATACA   12127     A  AAGGT
                               TGGGA AAA    GGGCATACA
                               ||||| |||    |||||||||
                               ATCCT TTT    TCCGTATGT
                                 C  _____
GAM2796 FGFR1    3' TGGGACAAAGAGGTAAACA   31961     A  A
                               TGGGA AAA AGGTGGGCA
                               ||||| ||| |||||||||
                               ACCCT TTT TCCATTTGT
                                  G  C
GAM2796 FUT1     3' TGGGAAGAGCAGGTGGGCAC  6635      AAAA
                               TGGGAA   AGGTGGGCAT
                               ||||||   ||||||||||
                               ACCCTT   TCCACCCGTG
                                  CTCG
GAM2796 FUT5     3' TGGGAAAGTGAGGTCCCTGGCA 13024      AAA   G___
                               TGGGAAA  AGGT   GGCA
                               |||||||  ||||   ||||
                               ACCCTTT  TCCA   CCGT
                                   CAC   GGGA
GAM2796 FY       5' AGGAGGAAAAGGAAGAGATA  13033    AA    T_  C
                               GGGA  AAAAGG  GGG ATA
                               ||||  ||||||  ||| |||
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                                TCCT  TTTTCC  CTC TAT
                                  CC     TT  _
GAM2796  FZD3     3'  TGGGAAAAGATGGCTACA    32637        AAA     G A
                                TGGGAAA   AGGTGG C TACA
                                |||||||   ||||||  | ||||
                                ACCCTTT   TCTACC G ATGT
                                    ___     _ _
GAM2796  GAS7     3'  TGGGAAAAGGTGGTGGC     25290        AAA     __
                                TGGGAAA   AGGTGG  GC
                                |||||||   ||||||  ||
                                ACCCTTT   TCCACC  CG
                                    ___     AC
GAM2796  GPC4     3'  TGAGAAAAAAAACATAC      11087          AGGTGG
                                TGGGAAAAAA     GCATAC
                                ||||||||||     ||||||
                                ACTCTTTTTT     TGTATG
                                    _______
GAM2796  GRLF1    3'  TGGGAAAGACGGGGACA     44236        AAAA  T
                                TGGGAAA    GG GGGCA
                                |||||||    || |||||
                                ACCCTTT    CC CCTGT
                                    CTG_  _
GAM2796  ITGAM    3'  TGGTGAAAAAAAGCAAGATACA 43522     GA       TG  C
                                TGG  AAAAAAGG  GG ATACA
                                |||  ||||||||  || |||||
                                ACC  TTTTTTTC  TC TATGT
                                  AC       GT  _
GAM2796  KCNK5    3'  TGGGAGGGGAAGGCGGGCA   19040      AAAA
                                TGGGA    AAGGTGGGCA
                                |||||    ||||||||||
                                ACCCT    TTCCGCCCGT
                                   CCCC
GAM2796  KIF3B    3'  TGGGAAAAGATGGTGACA    22045        AAA     G
                                TGGGAAAA   GGTGG CA
                                ||||||||   ||||| ||
                                ACCCTTTT   CCACT GT
                                     CTA    _
GAM2796  MASP1    3'  TGGCAAAAAAGCATAC      40115     G    AAGGTG
                                TGG AAAAA     GGCATAC
                                ||| |||||     |||||||
                                ACC TTTTT     TCGTATG
                                  G    _______
GAM2796  MGP      3'  GGGAAAAAGGGGTGCA      9463         AA   T  _
                                GGGAAAA  AGG GG GCA
                                |||||||  ||| || |||
                                CCCTTTT  TCC CC CGT
                                    __  _  A
GAM2796  MLLT2    3'  GGGGAAAAAAGGTACTGC    25502     A        G_
                                GGG AAAAAAGGTG  GC
                                ||| ||||||||||  ||
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                                CCC TTTTTTCCAT  CG
                                  C        GA
GAM2796  MSX2     3'  TGGGAAGGTGAGATA      42303      AAAAA     C
                                TGGGA    AGGTGGG ATA
                                |||||    ||||||| |||
                                ACCCT    TCCACTC TAT
                                  _____     _
GAM2796  MYBBP1A  3'  TGGGGGCAAAGAGGTGGCA   30957     AA_  A    G
                                TGGG   AAA AGGTGG CA
                                ||||   ||| |||||| ||
                                ACCC   TTT TCCACC GT
                                  CCG   C    _
GAM2796  NPR1     3'  TGGTAGAAGCAAGGCATACA  44592     GAAAAA  GT
                                TGG     AAG  GGGCATACA
                                |||     |||  |||||||||
                                ACC     TTC  TCCGTATGT
                                  ATC___   GT
GAM2796  NRCAM    3'  TGGGGGGAGGGGGGAACCCAA 22695     AAAAAA  T   C TA
                                TGGG     AGG GGG A  CAA
                                ||||     ||| ||| |  |||
                                ACCC     TCC CCC T  GTT
                                  CCC___   C   T GG
GAM2796  NRXN2    3'  GGGAAGGAGGGTGGGGACA   31486      AAAAA     C
                                GGGAA    GGTGGG ATA
                                |||||    |||||| |||
                                CCCTT    CCACCC TGT
                                   CCTC_    C
GAM2796  OPA3     3'  GGGAGAAAAGGCCACTGCA   36071     AA     GG__
                                GGGA  AAAAGGT   GCA
                                ||||  |||||||   |||
                                CCCT  TTTTCCG   CGT
                                  C_     GTGA
GAM2796  PCSK2    3'  TGGGAAAGGCGGATGTGCA   15137      AAAA    ____
                                TGGGAA   AGGTGG   GCA
                                ||||||   ||||||   |||
                                ACCCTT   TCCGCC   CGT
                                   _____     TACA
GAM2796  PDE6H    3'  TAGGAAAAGGTGGTCA      26282       AAA     G
                                TGGGAAA   AGGTGG CA
                                |||||||   |||||| ||
                                ATCCTTT   TCCACC GT
                                   ___     A
GAM2796  PHLDA3   3'  TGGGGGAAAAGTGTGCA     29616     AAAA     G
                                TGGG   AAAGGTG GCA
                                ||||   ||||||| |||
                                ACCC   TTTTCAC CGT
                                  CC__     A
GAM2796  PKD2     3'  TGGGAAAAAGAATATGCA    41081        AA   G
                                TGGGAAAAA  GGTG GCA
                                |||||||||  |||| |||
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                                ACCCTTTTT  TTAT CGT
                                     C_    A
GAM2796  PLTP     3'  TGGGAAAAGAGGGGC       26349         AAA  T
                                TGGGAAAA   GG GGGC
                                ||||||||   || ||||
                                ACCCTTTT   TC CCCG
                                     C__  _
GAM2796  POU1F1   3'  GGGAGAAAAAGGCTATTATACA 7166       A       GGGC
              A                  GGGA AAAAAGGT    ATACAA
                                ||||  ||||||||    ||||||
                                CCCT TTTTTCCG    TATGTT
                                  C       ATAA
GAM2796  PTK2B    3'  TGAGAAAAGAAGGGTGCA     19925         A    TGG
                                TGGGAAAA AAGG   GCA
                                |||||||| ||||   |||
                                ACTCTTTT TTCC   CGT
                                     C    CA_
GAM2796  PYGB     3'  TGGGGAAAAAAGGAGGTGCA   16051      A       T  _
                                TGGG AAAAAAGG GG GCA
                                |||| |||||||| || |||
                                ACCC TTTTTTCC CC CGT
                                  C       T  A
GAM2796  RHEB2    5'  GGGAGAGAGCGGCATACA     24719      AAAAAA     G
                                GGGA     GGTGG CATACA
                                ||||     ||||| ||||||
                                CCCT     TCGCC GTATGT
                                  CTC____    _
GAM2796  SPOCK    3'  GGGAAAAAGTACAGTGTGG    41737         AA__    _
                                GGGAAAAA    GGTG GG
                                ||||||||    |||| ||
                                CCCTTTTT    TCAC CC
                                     CATG    A
GAM2796  STK24    3'  TGGGAAAGATGATATGCA     18709        AAAA    G
                                TGGGAAA    GGTG GCA
                                |||||||    |||| |||
                                ACCCTTT    CTAT CGT
                                     CTA_    A
GAM2796  TFDP1    3'  GGGAGAGAAAAGAGTGTACA   28283      AA_    _  GG
                                GGGA   AAAAG GTG  CA
                                ||||   ||||| |||  ||
                                CCCT   TTTTC CAC  GT
                                  CTC    T   AT
GAM2796  VANGL2   3'  TGGGAAAAAGACGTGTCA    43464         AAG   GG
                                TGGGAAAAA   GTG  CA
                                |||||||||   |||  ||
                                ACCCTTTTT   CAC  GT
                                     CTG  A_
GAM2796  ZNFN1A3  3'  TGGGAAAACAAAGGTTTCACA  41201         _     GGG
                                TGGGAAAA AAAGGT   CATA
                                |||||||| ||||||   ||||
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                                ACCCTTTT TTTCCA   GTGT
                                    G     AA_
GAM2796 ASTN     3'  TGTGTGTTCAGGCCACTGAG  42959       ACCTATTTT
                                TGTGTGT       CCACTGAG
                                |||||||       ||||||||
                                ACACACA       GGTGACTC
                                   AGTCC____
GAM2796 CSNK1G3  3'  TGTTGTATTATCCACTGA    20477     ACC    T
                                TGT   TATT TCCACTGA
                                |||   |||| ||||||||
                                ACA   ATAA AGGTGACT
                                  AC_    T
GAM2796 FGF5     3'  TGTGTGTACTATTTTCC     37597         C
                                TGTGTGTAC TATTTTCC
                                ||||||||| ||||||||
                                ACACACATG ATAAAAGG
                                          _
GAM2796 MUCDHL   3'  TGTGCTGTGCCCCCACTG    34950      _  A   ATTTT
                                TGTG TGT CCT     CCACTG
                                |||| ||| |||     ||||||
                                ACAC ACA GGG     GGTGAC
                                  G   C   _____
GAM2796 ROBO1    3'  TGTTTGGCTTTGTTTTCCACTG 39492     G  TACCTA
                                TGT TG     TTTTCCACTG
                                ||| ||     ||||||||||
                                ACA AC     AAAAGGTGAC
                                  A  CGAAAC
GAM2797 MLANA    3'  GAGCTAAATTGCCATAGGTACA 24299          TA   A___
             TT                   GAGCTAAATT  CTA    TACATT
                                |||||||||  |||    ||||||
                                CTCGATTTAA  GGT    ATGTAA
                                      C_   ATCC
GAM2798 ARNT2    3'  TCTGGAGAACATGTAGTCACAT 31366     AAT       AT   TC
                                TCT   GAACATGT  AGT  CAT
                                |||   ||||||||  |||  |||
                                AGA   CTTGTACA  TCA  GTA
                                  CCT       __   GT
GAM2798 CIS4     3'  TAATAATAATTCTAGTTCCAT  20131       ACATGTA
                                TAATGA      TAGTTCCAT
                                ||||||      |||||||||
                                ATTATT      ATCAAGGTA
                                   ATTAAG_
GAM2798 GNRH1    5'  TCTAATGAAATGTGTCTCCA   9078         C    ATAG
                                TCTAATGAA ATGT    TTCCA
                                ||||||||| ||||    |||||
                                AGATTACTT TACA    GAGGT
                                      _   CA__
GAM2798 HSPA1B   3'  TCTAATGAACATATCGGTT    23783           ATA
                                TCTAATGAACATGT   GTT
                                ||||||||||||||   |||
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                                AGATTACTTGTATA  CAA
                                      GC_
GAM2799 ATP2A3   3' ACATATAAAATCATCAGTCTG 23188     _     G_
                                ATATA AAAGTCA  AGTCTG
                                ||||| |||||||  ||||||
                                TGTAT TTTTAGT  TCAGAC
                                   A      AG
GAM2799 BCL2A1   3' TCACAATATGGAGTGTCCTTTC 19732       AAAA_  AGAG
           TG                  TCACAATAT    GTC   TCTG
                                |||||||||    |||   ||||
                                AGTGTTATA    CAG   AGAC
                                     CCTCA  GAA_
GAM2799 FRZB     3' TCACAATATACTTAAGAGTCTG 11155       AAAGTC
                                TCACAATATA     AGAGTCTG
                                ||||||||||     ||||||||
                                AGTGTTATAT     TCTCAGAC
                                     GAAT__
GAM2800 CDC2L2   5' CAACTCGAACCGCT       37935         CCCGT A
                                TAACTCGAACC    G CT
                                ||||||||||    | ||
                                GTTGAGCTTGG    C GA
                                      _____ _
GAM2800 CHST2    5' ACTCGGGCCGCGACTCC     41711      AACCC
                                ACTCG    CCGTGACTCC
                                |||||    ||||||||||
                                TGAGC    GGCGCTGAGG
                                   CC___
GAM2800 CHST6    3' TAACTCAACTTCCCTGTCC   34682       ACC  G  AC
                                TAACTCGA  CCC TG  TCC
                                ||||||||  ||| ||  |||
                                ATTGAGTT  GGG AC  AGG
                                     GAA  _ __
GAM2800 CUL3     5' CTCGGACTCTGGCGACTCC   18734     A  CCCC
                                CTCG AC   GTGACTCC
                                ||||  ||   ||||||||
                                GAGC TG   CGCTGAGG
                                   C  AGAC
GAM2800 MAP3K9   3' CTCGAACCAAGCCAGATTCC  41353       C__  T  C
                                CTCGAACC  CCG GA TCC
                                ||||||||  ||| || |||
                                GAGCTTGG  GGT CT AGG
                                     TTC  _  A
GAM2800 MYO15A   3' TAACTCCAACTCCTGCCTCC  32184      G  C  C  GA
                                TAACTC AAC CC GT  CTCC
                                |||||| ||| || ||  ||||
                                ATTGAG TTG GG CG  GAGG
                                   G  A A __
GAM2800 SORD     3' TAACTCAGCCCTCATTC     16968       AA  C  GAC
                                TAACTCG  CCC CGT  TC
                                |||||||  ||| |||  ||
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                                ATTGAGT  GGG GTA   AG
                                   C_   A   ___
GAM2800  SPG4     3'  TAACTCAAACCTTCAAACC    31400          CC  T
                                TAACTCGAACC  CG GACT
                                ||||||||||  || ||||
                                ATTGAGTTTGG  GT TTGG
                                      AA  _
GAM2800  TNXB     5'  TCGCTGTGGCCTCGTGACTCC  33313     AACC__  _
                                TCG      CC CGTGACTCC
                                |||      || |||||||||
                                AGC      GG GCACTGAGG
                                  GACACC  A
GAM2800  TYK2     5'  CTCGAACCCGGACCCC       40858          CC T
                                CTCGAACCC  G GACTCC
                                |||||||||  | ||||||
                                GAGCTTGGG  C CTGGGG
                                     __ _
GAM2801  ITGB1    3'  TATATTTAGGATGCTTTCTGT  38054        TTTGA        C
                                TATGTTT    GATGCTTTC GT
                                |||||||    ||||||||| ||
                                ATATAAA    CTACGAAAG CA
                                   TC___        A
GAM2802  CLCN4    3'  GATAATATGAATTTCGTTC    12283         AG      A
                                GATAATAT  ATTTTG TTC
                                ||||||||  |||||| |||
                                CTATTATA  TAAAGC AAG
                                    CT     _
GAM2802  EPHX2    3'  AATAATGTCAAATTTGATTCAC 41368        ATA  T
            T                    GATAAT   GA TTTGATTCACT
                                ||||||   || ||||||||||
                                TTATTA   TT AAACTAAGTGA
                                   CAG  T
GAM2802  MAN1A1   3'  ATATTGATTTTGATTTACTC   45089      A         C
                                ATAT GATTTTGATT ACTC
                                |||| |||||||||| ||||
                                TATA CTAAAACTAA TGAG
                                  A         A
GAM2802  NUMB     3'  GGAATATAGATTCTTGTTC    19051    T          GA
                                A AATATAGATTTT  TTC
                                | ||||||||||||  |||
                                C TTATATCTAAGA  AAG
                                 C           AC
GAM2802  P2RY1    3'  GAGAATATAGATTTTTTATTC  15008    T          G_
                                GA AATATAGATTTT  ATTC
                                || ||||||||||||  ||||
                                CT TTATATCTAAAA  TAAG
                                 C           AA
GAM2802  PIWIL1   3'  TAATATAGAGATTTACT     43755          TTTT   C
                                TAATATAGA    GATT ACT
                                |||||||||    |||| |||
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                                ATTATATCT   CTAA TGA
                                    ____   A
GAM2803  CD8A    3'  TCAGAGATTCAAGAGGGC    12092            T
                                TCAGAGATTCAAGAGG GT
                                |||||||||||||||| ||
                                AGTCTCTAAGTTCTCC CG
                                     _
GAM2803  DGKE    3'  TGTTGGAGATATAATGTGT   18891    CA    TCAAGA
                                TGT  GAGAT    GGTGTGT
                                |||  |||||    |||||||
                                ACA  CTCTA    TTACACA
                                  AC    TA____
GAM2803  HUNK    3'  TGTCAGAGATGTGAGG      31089         TCAA
                                TGTCAGAGAT   GAGG
                                ||||||||||   ||||
                                ACAGTCTCTA   CTCC
                                     CA__
GAM2803  NRAS    3'  TGGCAGAGGTGTGTTGAGGTGT 14854    T    ATTCAA_
                GT                TG CAGAG      GAGGTGTGT
                                || |||||      |||||||||
                                AC GTCTC      CTCCACACA
                                 C    CACACAA
GAM2803  RAD52   3'  TGTCAGAGGTCTGGGCTGGGTC 39563        AT  AAGA   GT_
                                TGTCAGAG  TC   GGT   GTC
                                ||||||||  ||   |||   |||
                                ACAGTCTC  AG   CCG   CAG
                                     C_  AC__   ACC
GAM2803  TBXA2R  3'  TGTTGGAGGTTCAAAAGGAAGC 9862     CA   A       T_
                                TGT  GAG TTCAAGAGG  GT
                                |||  ||| |||||||||  ||
                                ACA  CTC AAGTTTTCC  CG
                                  AC   C        TT
GAM2803  TMOD2   3'  TGTTAAAGATTCAATTTATGT  30970    C        GAG
                                TGT AGAGATTCAA   GTGT
                                ||| ||||||||||   ||||
                                ACA TTTCTAAGTT   TACA
                                  A         AAA
GAM2803  ZNF2    3'  TCAGACAAGAGGTGTGT     34384      GATT
                                TCAGA    CAAGAGGTGTGT
                                |||||    ||||||||||||
                                AGTCT    GTTCTCCACACA
                                     _____
GAM2804  ABCC8   3'  ATTTACAAGTGATTTACAG   7396         AAA   _
                                ATTTACA   AGTG TTTACAG
                                |||||||   |||| |||||||
                                TAAATGT   TCAC AAATGTC
                                     ___   T
GAM2804  AFP     3'  TAATTCACAAAAAGTGTTAAAT 10067              TA__
                CAG                  TAATTTACAAAAAGTGTT   CAG
                                ||||||||||||||||||   |||
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                                ATTAAGTGTTTTTCACAA   GTC
                                      TTTA
GAM2804 CALCRL   3' TTACAAAAAGGACTACGGC   25130        TGT   A
                                TTACAAAAAG   TTAC GC
                                ||||||||||   |||| ||
                                AATGTTTTTC   GATG CG
                                     CT_   C
GAM2804 CHD1     3' ATTTACAATAATTTACAG    10432       AAAGT
                                ATTTACAA    GTTTACAG
                                ||||||||    ||||||||
                                TAAATGTT    TAAATGTC
                                    AT___
GAM2804 ELMO2    3' TTTACAAGTGCTGCAG      35223       AAA     TA
                                TTTACA   AGTGTT  CAG
                                ||||||   ||||||  |||
                                AAATGT   TCACGA  GTC
                                   ___     C_
GAM2804 FGFR1    3' TAATTTAAAAAAATAAAACAGC 31953       C       TTT
                                TAATTTA AAAAAGTG   ACAGC
                                ||||||| ||||||||   |||||
                                ATTAAAT TTTTTTAT   TGTCG
                                   _       TT_
GAM2804 MASP2    3' TTTACAGAAATGCCAACAGC   40177       AA     TT
                                TTTACA  AAGTGT  ACAGC
                                ||||||  ||||||  |||||
                                AAATGT  TTTACG  TGTCG
                                   C_     GT
GAM2804 MTM1     3' TAATTTATGAAATATTTACAGC 7007        CAAA
                                TAATTTA    AAGTGTTTACAGC
                                |||||||    |||||||||||||
                                ATTAAAT    TTTATAAATGTCG
                                    AC__
GAM2804 PDE4A    3' TAATTTACAAACCAACCTTACA 26279         AAGTG
              G                  TAATTTACAAA     TTTACAG
                                 ||||||||||     |||||||
                                 ATTAAATGTTT     GAATGTC
                                       GGTTG
GAM2804 PDE4D    3' TAATTTACAATTAACATTACAG 43896         AA  TG  T
                                TAATTTACAA  AG  TT ACAG
                                ||||||||||  ||  || ||||
                                ATTAAATGTT  TT  AA TGTC
                                     AA  GT  _
GAM2804 PEX3     3' ATTCACTTCTGTTTACAGC   18848       AAAAAG
                                ATTTAC     TGTTTACAGC
                                ||||||     ||||||||||
                                TAAGTG     ACAAATGTCG
                                   AAG___
GAM2804 SLC19A2  3' ATTTACAAAACTGCATACAG  42885         AG   T
                                ATTTACAAAA  TGT TACAG
                                ||||||||||  ||| |||||
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                                TAAATGTTTT  ACG ATGTC
                                     G_   T
GAM2804  ZNF26    3'  TTTACAAAAACACAG       43806          GTGTT
                                TTTACAAAAA     TACAG
                                ||||||||||     |||||
                                AAATGTTTTT     GTGTC
                                      _____
GAM2805  CA14     5'  GTGTATTTATCTCTGCTTT    29059     C       AACA
                                GTG ATTTATCTC    GTTTT
                                ||| |||||||||    |||||
                                CAC TAAATAGAG    CGAAA
                                  A        A___
GAM2805  D1S155E  3'  GTGCATTCATTTTTTTTGTTTT 28390          CTCAACA
                                GTGCATTTAT       GTTTT
                                ||||||||||       |||||
                                CACGTAAGTA       CAAAA
                                     AAAAAAA
GAM2805  GAD1     3'  GCGTTTTGAAAAACAGTTTTCC 30291     A   ATCTC
                                GC TTT     AACAGTTTTCC
                                || |||     ||||||||||
                                CG AAA     TTGTCAAAAGG
                                 C   ACTTT
GAM2805  MADH1    3'  ATGCAAGGCTCAATAGTTTTCC 25335       TTTAT     C
                                GTGCA     CTCAA AGTTTTCC
                                |||||     ||||| ||||||||
                                TACGT     GAGTT TCAAAAGG
                                   TCC__     A
GAM2805  NOX4     3'  GTGCATCTAACAGTTTTC     32596          TCTCA
                                GTGCATTTA     ACAGTTTTC
                                |||||||||     |||||||||
                                CACGTAGAT     TGTCAAAAG
                                      _____
GAM2805  PAK1     3'  GTGCATTTATCTCACAG      15084             A
                                GTGCATTTATCTCA CAG
                                |||||||||||||| |||
                                CACGTAAATAGAGT GTC
                                      _
GAM2805  SHOC2    3'  GTGCATTTAGTTCAGCAGC    28894          TC   A
                                GTGCATTTA  TCA CAGT
                                |||||||||  ||| ||||
                                CACGTAAAT  AGT GTCG
                                     CA   C
GAM2806  CENPA    5'  TCCTGCTCGGGCTGCCGGGTCC 12232     C           C
            G                    TCC GCTCGGGCTGTCGG GTCCG
                                ||| ||||||||||||| |||||
                                AGG CGAGCCCGACGGCC CAGGC
                                  A          _
GAM2806  DLEC1    3'  GCTCAGGCTGTTTTGCGGACGC 28848          T________   CGT
            C                    GCTCGGGCTG       CGG   CC
                                ||||||||||       |||   ||
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                                CGAGTCCGAC      GCC   GG
                                      AAAACIII  TGC
GAM2806  SIAH2    5'  TCCTGCTCGGGCTGCGGGCCG  22868    C       T   C T
                                TCC GCTCGGGCTG CGG G CCG
                                ||| |||||||||| ||| | |||
                                AGG CGAGCCCGAC GCC C GGC
                                  A       _  _ _
GAM2806  TEM6     5'  TCCTGCTGGGGCTGTCGG    35561    C   C
                                TCC GCT GGGCTGTCGG
                                ||| ||| ||||||||||
                                AGG CGA CCCGACAGCC
                                  A  C
GAM2807  APAF1    5'  GACACAAAGGGAGGAGGTCTT  29821    _        A
                                GGC CGGAGGGAGGAG TCTT
                                ||| |||||||||||| ||||
                                CTG GTTTCCCTCCTC AGAA
                                  T          C
GAM2807  B3GAT1   3'  AGGGGCCGGAGGGGGGGAC   38292    A       A  A
                                AG GGCCGGAGGG GG GAT
                                || |||||||||| || |||
                                TC CCGGCCTCCC CC CTG
                                 C        _ C
GAM2807  B4GALT1  3'  AAGGGGGTGGGGGGAGGA    11273    A  CC  A
                                AAG GG  GG GGGAGGA
                                ||| ||  || |||||||
                                TTC CC  CC CCCTCCT
                                  C  CA  C
GAM2807  B4GALT1  3'  AAGGGGCCAGAGGGTGA     11272    A       AG
                                AAG GGCCGGAGGG  GA
                                ||| ||||||||||  ||
                                TTC CCGGTCTCCC  CT
                                  C        A_
GAM2807  B4GALT6  5'  AAGAGGTGGAGGGGGGAG    40842      CC    A
                                AAGAGG  GGAGGG GGAG
                                ||||||  |||||| ||||
                                TTCTCC  CCTCCC CCTC
                                    A_     C
GAM2807  FKBP1A   3'  AAGGGGCTGAGGGAGGAA    38274    A  CG
                                AAG GGC  GAGGGAGGAG
                                ||| |||  ||||||||||
                                TTC CCG  CTCCCTCCTT
                                  C  A_
GAM2807  GAB2     3'  AAGGGGCCAGAGGGAGGA    38671    A
                                AAG GGCCGGAGGGAGGA
                                ||| ||||||||||||||
                                TTC CCGGTCTCCCTCCT
                                  C
GAM2807  HOXB9    3'  GAGGACTGGGGGTAATCTT   35841     CCGGA  A  A
                                GAGG    GGG GG GATCTT
                                ||||    ||| || ||||||
```

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                                CTCC    CCC CC TTAGAA
                                  TGA__  _ A
GAM2807 KCNC3   3' AGGGCTTGGGGGGAGAT    22493   A  CGGA  A
                                AG GGC   GGG GGAGAT
                                || |||   ||| |||||||
                                TC CCG   CCC CCTCTA
                                 _  AAC_  _
GAM2807 MN1     3' AAGGGCCTGGTAGAGGAGGGGA 14567    A  _ _ _   A
           TCTT                  AAG GGCC GG AG GGAGG GATCTT
                                ||| |||| || || ||||| |||||||
                                TTC CCGG CC TC CCTCC CTAGAA
                                  _   A A T   C
GAM2807 NDRG1   3' AAGGGGCCGGGGAGGAG    40573    A    AG
                                AAG GGCCGG  GGAGGAG
                                ||| ||||||  |||||||
                                TTC CCGGCC  CCTCCTC
                                  C    __
GAM2807 NR1D1   3' GGCCAGAGGCTCATCTT    34702        GAGGAG
                                GGCCGGAGG     ATCTT
                                |||||||||     |||||
                                CCGGTCTCC     TAGAA
                                     GAG___
GAM2807 PRG2    3' GAGGTGGAGGGAGGGAT    15562     CC       A
                                GAGG  GGAGGGAGG GAT
                                ||||  ||||||||| |||
                                CTCC  CCTCCCTCC CTA
                                  A_       _
GAM2807 PRKRA   3' AAGGGGCCAGAGGGGAA    18971    A        A
                                AAG GGCCGGAGGG GGA
                                ||| |||||||||| |||
                                TTC CCGGTCTCCC CTT
                                  C        _
GAM2807 TCF7L2  5' GAGGGGAAGGGGGGGGAGATCT 36251     CC     A__
           T                     GAGG  GGAGGG   GGAGATCTT
                                ||||  ||||||   |||||||||
                                CTCC  CTTCCC   CCTCTAGAA
                                  C_     CCC
GAM2807 TIMP3   3' GAGGCTGGAGGAGTCTC    7453       CGGAG      A
                                GAGGC    GGAGGAG TCTT
                                |||||    ||||||| ||||
                                CTCCG    CCTCCTC AGAG
                                  A_____      _
GAM2808 AGA     3' TATGATGATTCCTTTTGGGT  6186          AAGA  A
                                TATGATGATTT   TTG GT
                                ||||||||||   ||| ||
                                ATACTACTAAG   AAC CA
                                      GAA_  C
GAM2808 EGFL5   5' ATGATGATGTTAAATTGGGTCC 44517        TTA    A
           A                     ATGATGAT   AGATTG GTCCA
                                ||||||||   |||||| |||||
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                                TACTACTA   TTTAAC CAGGT
                                     CAA     C
GAM2808  PCDH11X   3'  TATGAGGATTTAAGAACCTCCC 37310      T       TTGAG
                                TATGA GATTTAAGA     TCC
                                ||||| |||||||||     |||
                                ATACT CTAAATTCT     GGG
                                   C        TGGA_
GAM2808  PCDH11Y   3'  TATGAGGATTTAAGAACCTCCC 37352      T       TTGAG
                                TATGA GATTTAAGA     TCC
                                ||||| |||||||||     |||
                                ATACT CTAAATTCT     GGG
                                   C        TGGA_
GAM2808  SURF4     3'  TGAGGTAACTGGGTTGAGTCC  37659     __     TAAGA
                                TGA  TGATT     TTGAGTCC
                                |||  |||||     ||||||||
                                ACT  ATTGA     AACTCAGG
                                  CC     CCC__
GAM2808  TGFB1     3'  TATGGTGACTGAATGAGTTCA  8552      A     TAA  T     C
                                TATG TGATT   GA TGAGT CA
                                |||| |||||   || ||||| ||
                                ATAC ACTGA   CT ACTCA GT
                                  C     ___  T     A
GAM2809  ABR       3'  TAAGTCGAGCCCCTGGA     35016      __    GTGA
                                TAAGT  GGCT    CCTGGA
                                |||||  ||||    ||||||
                                ATTCA  TCGG    GGACCT
                                   GC   _____
GAM2809  ADCY2     3'  CAAGTGGCAGAACGATCTGG   42139        TG__   C
                                TAAGTGGC    TGA CTGG
                                ||||||||    ||| ||||
                                GTTCACCG    GCT GACC
                                     TCTT   A
GAM2809  ALK       5'  TAAATGAAACAGACCTGGA    43838        CTGT
                                TAAGTGG    GACCTGGA
                                |||||||    ||||||||
                                ATTTACT    CTGGACCT
                                     TTGT
GAM2809  ALPI      3'  TGGATCTGGTGACCTGGA     11583     __   _
                                TGG  CTG TGACCTGGA
                                |||  ||| |||||||||
                                ACC  GAC ACTGGACCT
                                  TA   C
GAM2809  C21orf2   3'  AGTGACTGTCTTCACCCTGG   22299         GA____
                                AGTGGCTGT     CCTGG
                                |||||||||     |||||
                                TCACTGACA     GGACC
                                     GAAGTG
GAM2809  CARKL     3'  TAAGTGACTGACCGG       30001         GT    T
                                TAAGTGGCT  GACC GG
                                |||||||||  |||| ||
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                                ATTCACTGA  CTGG CC
                                   __   _
GAM2809  COL4A2   3'  TAAGTGCTGCTGCTGGA     12320       G    GAC
                                TAAGTG CTGT   CTGGA
                                |||||| ||||   |||||
                                ATTCAC GACG   GACCT
                                   _   AC_
GAM2809  DNAJB1   3'  GTGGCTGCACTTGCTGGA    26032        AC__
                                GTGGCTGTG    CTGGA
                                |||||||||    |||||
                                CACCGACGT    GACCT
                                     GAAC
GAM2809  DPH2L2   3'  AGTGGCTACTGTACTGGA    10733        _  AC
                                AGTGGCTG TG  CTGGA
                                |||||||| ||  |||||
                                TCACCGAT AC  GACCT
                                     G  AT
GAM2809  DUOX1    3'  TAAATGGCTTGCCATGG     32655        G  A  _
                                TAAGTGGCT TG CC TGG
                                ||||||||| || || |||
                                ATTTACCGA AC GG ACC
                                   _ _  T
GAM2809  EIF4G1   5'  AGTGGCTGCACACCCTGG    22408        GA__
                                AGTGGCTGT    CCTGG
                                |||||||||    |||||
                                TCACCGACG    GGACC
                                     TGTG
GAM2809  GAS7     3'  CAAGTGGCTCTTCCTGGA    25264        GTGA
                                TAAGTGGCT    CCTGGA
                                |||||||||    ||||||
                                GTTCACCGA    GGACCT
                                     GAA_
GAM2809  GNAL     5'  TAAATGGCTGTAAGGA      13172          CCT
                                TAAGTGGCTGTGA   GGA
                                ||||||||||||   |||
                                ATTTACCGACATT   CCT
                                   ___
GAM2809  GRLF1    3'  TAAGTGGGTGAGTGG       44233        CT   CC
                                TAAGTGG  GTGA  TGG
                                |||||||  ||||  |||
                                ATTCACC  CACT  ACC
                                   __    C_
GAM2809  HCS      3'  AGTGGCTACCACACTGGA    33219        TG  _
                                AGTGGCTG  AC CTGGA
                                ||||||||  || |||||
                                TCACCGAT  TG GACCT
                                     GG  T
GAM2809  HGF      3'  TAAGTGGCCTTAAGTTTGGA  45321        G   CC_
                                TAAGTGGCT TGA   TGGA
                                |||||||||  |||   ||||
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                                ATTCACCGG ATT   ACCT
                                     A   CAA
GAM2809  HLCS     3'  TGACTGGGTAAGACCTGGA   7649       T____
                                TGGCTG    GACCTGGA
                                ||||||    ||||||||
                                ACTGAC    CTGGACCT
                                   CCATT
GAM2809  HSPA4    3'  TAAGAACGTGACCTGGA     44853     T   T
                                TAAG GGC GTGACCTGGA
                                |||| ||| ||||||||||
                                ATTC TTG CACTGGACCT
                                  _  _
GAM2809  KLF8     5'  TAAGCGGCTGTTAAAAGA    28538          GACCT
                                TAAGTGGCTGT    GGA
                                ||||||||||     |||
                                ATTCGCCGACA    TCT
                                      ATTT_
GAM2809  MEN1     3'  AGCCACAGTGTGACCTGG    39145     G  __
                                AGT GC  TGTGACCTGG
                                ||| ||  ||||||||||
                                TCG TG  ACACTGGACC
                                  G  TC
GAM2809  MPP2     3'  TAAATGGCGCCTCTGGA     40801        T  GAC
                                TAAGTGGC GT   CTGGA
                                |||||||| ||   |||||
                                ATTTACCG CG   GACCT
                                     _  GA_
GAM2809  NCOA6    5'  TAAGTAGCTCCTTGGA      30439        GTGA  _
                                TAAGTGGCT    CCT GGA
                                |||||||||    ||| |||
                                ATTCATCGA    GGA CCT
                                     _____   A
GAM2809  NEK6     3'  AGTGGCTACCATTTTTGGA   30822       GTG  _____
                                AGTGGCT   ACC    TGGA
                                |||||||   |||    ||||
                                TCACCGA   TGG    ACCT
                                    ___   TAAAA
GAM2809  NT5M     3'  TGATGGCTGCAGACTCTGG   33655   A      _  _
                                A GTGGCTGT GAC CTGG
                                | ||||||||| ||| ||||
                                A TACCGACG CTG GACC
                                 C       T   A
GAM2809  PAEP     5'  GTGGCTCTGAGCTCTGGA    15070       G  C__
                                GTGGCT TGA   CTGGA
                                |||||| |||   |||||
                                CACCGA ACT   GACCT
                                   G   CGA
GAM2809  PAX5     3'  GTAGGCTGTTTGTGATCTGG  32517    _     ____  C
                                GT GGCTGT    GA CTGG
                                || ||||||    || ||||
```

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                                CA CCGACA    CT GACC
                                 T     AACA  A
GAM2809  PCDH11X  3'  TAAGTGACTCGTGCTTTGGA  37307        _  ACC
                                TAAGTGGCT GTG   TGGA
                                ||||||||| |||   ||||
                                ATTCACTGA CAC   ACCT
                                     G   GAA
GAM2809  PCDH11Y  3'  TAAGTGACTCGTGCTTTGGA  37349        _  ACC
                                TAAGTGGCT GTG   TGGA
                                ||||||||| |||   ||||
                                ATTCACTGA CAC   ACCT
                                     G   GAA
GAM2809  PMM2     3'  AGTGGCTGGGAGGTTTGGA   43548        T  CC__
                                AGTGGCTG GA    TGGA
                                |||||||| ||    ||||
                                TCACCGAC CT    ACCT
                                     C  CCAA
GAM2809  PODXL    3'  CAAGTGGCTCTGACCTTGG   23957        G    _
                                TAAGTGGCT TGACCT GG
                                ||||||||| |||||| ||
                                GTTCACCGA ACTGGA CC
                                     G     A
GAM2809  PPP3R1   3'  TAAGTGGCATAAATTTGGA   44084        T   CC_
                                TAAGTGGC GTGA   TGGA
                                |||||||| ||||   ||||
                                ATTCACCG TATT   ACCT
                                     _   TAA
GAM2809  PTGER4   5'  AGTGGCTGTCGATTTTTGGA  9652         _  CC__
                                AGTGGCTGT GA    TGGA
                                ||||||||| ||    ||||
                                TCACCGACA CT    ACCT
                                     G  AAAA
GAM2809  RAB27A   3'  TAAGTGGCTTTAATGG      21364        G   CC
                                TAAGTGGCT TGA  TGG
                                ||||||||| |||  |||
                                ATTCACCGA ATT  ACC
                                     A  __
GAM2809  RFX2     3'  GTGGCTGCGCAGGGACCTGG  8459         _____
                                GTGGCTGT    GACCTGG
                                ||||||||    |||||||
                                CACCGACG    CTGGACC
                                     CGTCC
GAM2809  RNTRE    3'  TAAATGGCCACCCTGG      31257        TG GA
                                TAAGTGGC  T  CCTGG
                                ||||||||  |  |||||
                                ATTTACCG  G  GGACC
                                     GT __
GAM2809  RRM2     3'  TAACTGGCTGTGCTGG      9760      G      AC
                                TAA TGGCTGTG  CTGG
                                ||| ||||||||  ||||
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```
                                ATT ACCGACAC  GACC
                                  G      __
GAM2809  RRM2B    3'  TAAATGTGCAACCTGGA     42722       GC  TG
                                TAAGTG  TG  ACCTGGA
                                ||||||  ||  |||||||
                                ATTTAC  AC  TGGACCT
                                   __  GT
GAM2809  STMN1    3'  AAGTAACAGCTGACCTGG    24514        T _
                                AAGTGGC G TGACCTGG
                                ||||||| | ||||||||
                                TTCATTG C ACTGGACC
                                    T G
GAM2809  SUV39H2  3'  AATGGCTAGCCATTTTGGA   36006        TGA ____
                                AGTGGCTG   CC    TGGA
                                ||||||||   ||    ||||
                                TTACCGAT   GG    ACCT
                                     C__  TAAA
GAM2809  TBX3     3'  AGCAATTCTGTGACCTGGA   32435    TG __
                                AG  G  CTGTGACCTGGA
                                ||  |  ||||||||||||
                                TC  T  GACACTGGACCT
                                 GT AA
GAM2809  TFRC     3'  TAAGTAGAGGACCTGGA     17433       CTGT
                                TAAGTGG    GACCTGGA
                                |||||||    ||||||||
                                ATTCATC    CTGGACCT
                                    TC__
GAM2809  TNFRSF8  3'  AGGGCTGCAGACATCTGG    10308    T     _  __
                                AG GGCTGT GAC  CTGG
                                || |||||| |||  ||||
                                TC CCGACG CTG  GACC
                                 _     T   TA
GAM2809  TRPV1    5'  TAAGTGACTGACCGG       38800        GT    T
                                TAAGTGGCT  GACC GG
                                |||||||||  |||| ||
                                ATTCACTGA  CTGG CC
                                     __   _
GAM2809  WBSCR14  3'  CAAGTGTGAAACCTGGA     37286       GCTGT
                                TAAGTG    GACCTGGA
                                ||||||    ||||||||
                                GTTCAC    TTGGACCT
                                   ACT__
GAM2810  ADRA2A   5'  CCCGTCCTCAGGCGGGCCG   8631         C  TTCCAA
                                TCCGTCC CG     GGCCG
                                ||||||| ||     |||||
                                GGGCAGG GT     CCGGC
                                    A  CCGC__
GAM2810  BIN2     3'  TCCATCCCTCCCGTAAGGC   32225        CG   __
                                TCCGTCCC  TTCC  AAGGC
                                ||||||||  ||||  |||||
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                                AGGTAGGG  AGGG  TTCCG
                                    __    CA
GAM2810  BTAF1    5'  CGTCCCCGCGGCGGCCG     43664         TCCAA
                                CGTCCCCGT    GGCCG
                                |||||||||    |||||
                                GCAGGGGCG    CCGGC
                                     CCG__
GAM2810  CDR2     5'  CCCGTTCCCGCCGGCGGCCG   44019      C     CCAA
                                TCCGT CCCGTT    GGCCG
                                ||||| ||||||    |||||
                                GGGCA GGGCGG    CCGGC
                                   A     CCG_
GAM2810  DUSP6    5'  TCCCTCCCTCCAAGGC      42329     G    CGT
                                TCC TCCC   TCCAAGGC
                                ||| ||||   ||||||||
                                AGG AGGG   AGGTTCCG
                                  G   ___
GAM2810  ESRRA    3'  TCCGCCCCAGCCCTTGGGGC   20837        C    CAA_
                                TCCGTCCC GTTC    GGC
                                |||||||| ||||    |||
                                AGGCGGGG CGGG    CCG
                                     T    AACC
GAM2810  EXTL3    3'  CCCGTTAGATTCCAAGGC    11032      CCCC
                                TCCGT    GTTCCAAGGC
                                |||||    ||||||||||
                                GGGCA    TAAGGTTCCG
                                   ATC_
GAM2810  GSTM3    5'  TCCGCCCCGTTCTCC       42766     T      CAAGG
                                TCCG CCCCGTTC     CC
                                |||| ||||||||     ||
                                AGGC GGGGCAAG     GG
                                  _       A____
GAM2810  GTF2E2   5'  TCCGCCTCGGCCGGCC      13319     T  C  TT  AA
                                TCCG CC CG  CC  GGCC
                                |||| || ||  ||  ||||
                                AGGC GG GC  GG  CCGG
                                  _ A  C_  __
GAM2810  INPPL1   5'  TCCGCCCCGAGACGCTCAGGGC 11467         ____    CAA
                                TCCGTCCC    CGTTC   GGC
                                |||||||    |||||   |||
                                AGGCGGGG    GCGAG   CCG
                                     CTCT    TC_
GAM2810  LPIN2    3'  CCCGTCCCCGCTGGGGAAGGC  31206          CC__
                                TCCGTCCCCGTT    AAGGC
                                ||||||||||||    |||||
                                GGGCAGGGGCGA    TTCCG
                                       CCCC
GAM2810  MAPK14   5'  CGCCCCTACAAGGCCG      40011    T   GTTC
                                CG CCCC    CAAGGCCG
                                || ||||    ||||||||
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```
                                GC GGGG   GTTCCGGC
                                 _   AT__
GAM2810 ORM1    3' TCTGTCCTGATCCAAGGC   8299    C   CCGT
                                TC GTCC   TCCAAGGC
                                || ||||   ||||||||
                                AG CAGG   AGGTTCCG
                                 A   ACT_
GAM2810 POMZP3  5' TCAGTCCCCACCAGGCCG   29247   C     TT  A
                                TC GTCCCCG  CCA GGCCG
                                || |||||||  ||| |||||
                                AG CAGGGGT  GGT CCGGC
                                 T     __  _
GAM2810 PTPN7   3' TCCATCCCCAAGGC       38715         TTCCA
                                TCCGTCCCCG    AGGC
                                ||||||||||    ||||
                                AGGTAGGGGT    TCCG

                                      _____
GAM2810 SCG2    5' TCCTCCCCGTTCTCC      18446   G       CAAGG
                                TCC TCCCCGTTC    CC
                                ||| |||||||||    ||
                                AGG AGGGGCAAG    GG
                                 _       A____
GAM2810 SIX2    5' CGTCCCCGCGCCGGCCG    32603        T  AA
                                CGTCCCCGT CC  GGCCG
                                ||||||||| ||  |||||
                                GCAGGGGCG GG  CCGGC
                                      C  __
GAM2810 SLC8A2  3' TCCTCCCCGCCGGGGC     42420   G      CCAA
                                TCC TCCCCGTT   GGC
                                ||| ||||||||   |||
                                AGG AGGGGCGG   CCG
                                 _      CC__
GAM2810 SON     3' TCCTCCAGTTACCGGGGC   39890   G  CC  _  AA
                                TCC TCC  GTT CC  GGC
                                ||| |||  ||| ||  |||
                                AGG AGG  CAA GG  CCG
                                 _  T_  T  CC
GAM2810 TXNRD1  5' CGTCCCCGCCGGCAGGCCG  17770         CCA
                                CGTCCCCGTT   AGGCCG
                                |||||||||   ||||||
                                GCAGGGGCGG   TCCGGC
                                      CCG
GAM2811 BACE    3' ATACTAGGAAAACCCAGCTC 39952     TTA      A
                                ATATT   AAAACCCA CTC
                                |||||   |||||||| |||
                                TATGA   TTTTGGGT GAG
                                   TCC      C
GAM2811 DISC1   3' TTCACATTTTACCAGCTC   33060         AAAAC  A
                                TTCATATTTTA    CCA CTC
                                ||||||||||    ||| |||
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```
                                AAGTGTAAAAT    GGT GAG
                                      _____  C
GAM2811  FGF13    3'  TATGCCAAGAACCCAACT    37982     T    A
                                TAT TTAA AACCCAACT
                                ||| |||| |||||||||
                                ATA GGTT TTGGGTTGA
                                  C   C
GAM2811  HTR2C    3'  TTCACATTCTAAGGGCCCAATT 9296           AAA    C
             C                   TTCATATTTTAA  CCCAA TC
                                ||||||||||||  ||||| ||
                                AAGTGTAAGATT  GGGTT AG
                                      CCC    A
GAM2811  SART2    3'  ATATTAATAAAACCCAATTC  30035      TTA       C
                                ATATT  AAAACCCAA TC
                                |||||  ||||||||| ||
                                TATAA  TTTTGGGTT AG
                                   TTA       A
GAM2811  SGNE1    3'  TTCACATTTTAAAAACCC    16603
                                TTCATATTTTAAAAACCC
                                ||||||||||||||||||
                                AAGTGTAAAATTTTTGGG

GAM2812  ALS2     3'  ACACAGCCTGCATGCAAAACTT 34088        _____  C  CCG
             CC                   ACACAGCC    GCA AAC   CC
                                |||||||    ||| |||   ||
                                TGTGTCGG    CGT TTG   GG
                                     ACGTA   T   AA_
GAM2812  AP2A1    5'  CAGGCCGTGGCACCGCCCCC  39100    _  CACAAC
                                CAG CCG     CCGCCCCC
                                ||| |||     ||||||||
                                GTC GGC     GGCGGGGG
                                  C   ACCGT_
GAM2812  ATF4     5'  CACAGCTGGACGACCCGCCCC  11720      CGC  A
                                CACAGC   AC ACCCGCCCC
                                ||||||   || |||||||||
                                GTGTCG   TG TGGGCGGGG
                                     ACC  C
GAM2812  BRCA1    3'  ACACAGCTGTACCATCCATTCC 28619       C__  A  A  CG_
                                ACACAGC   GC CA CC   CC
                                |||||||   || || ||   ||
                                TGTGTCG   TG GT GG   GG
                                     ACA  _  A  TAA
GAM2812  CALM2    5'  ACACAACCACTCAGCTCGC   11949         A  ACC
                                ACACAGCCGC CA   CGC
                                ||||||||||  ||   |||
                                TGTGTTGGTG GT   GCG
                                      A  CGA
GAM2812  CCNT2    3'  ACAGTAGCACAACCACC     38487      CC       C
                                ACAG  GCACAACC GCC
                                ||||  |||||||| |||
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                                TGTC  CGTGTTGG TGG
                                  AT      _
GAM2812  CD34     5'  ACGCGCTCTTCCCGCCCCC   12107    _  ACAA
                                GC CGC   CCCGCCCCC
                                || |||   |||||||||
                                TG GCG   GGGCGGGGG
                                 C  AGAA
GAM2812  CHD2     5'  CACAGCCGCCATCTAGAGCCTC 10441        ACAACCC_  C
              C                  CACAGCCGC      GCC CC
                                |||||||||      ||| ||
                                GTGTCGGCG      CGG GG
                                     GTAGATCT  A
GAM2812  CSNK1G2  3'  CAGCGCCCACCCGCCCC    10606     C  ACA
                                CAGC GC  ACCCGCCCC
                                |||| ||  |||||||||
                                GTCG CG  TGGGCGGGG
                                  _ GG_
GAM2812  DAAM2    3'  ACACACACACCGCCCGCCCCC  45169     GC    AA
                                ACACA  CGCAC  CCCGCCCCC
                                |||||  |||||  |||||||||
                                TGTGT  GTGTG  GGGCGGGGG
                                   __    GC
GAM2812  DFFA     3'  ACTTCACGATCCGCCCCCC   20579    CG   AAC
                                GC  CAC   CCGCCCCCC
                                ||  |||   |||||||||
                                TG  GTG   GGCGGGGGG
                                 AA  CTA
GAM2812  DHFR     5'  GCCGCCCCGCCCCC      8994       ACAA
                                GCCGC   CCCGCCCCC
                                |||||   |||||||||
                                CGGCG   GGGCGGGGG
                                  _____
GAM2812  DHFR     5'  CAGGCGAGGCCCCGCCCCCC  8989     C  CACAA
                                CAG CG    CCCGCCCCCC
                                ||| ||    ||||||||||
                                GTC GC    GGGCGGGGGG
                                  C  TCCG_
GAM2812  DXYS155E 3'  ACACAGCCGGACGACACG    22941        C  A  C
                                ACACAGCCG AC AC CG
                                ||||||||| || || ||
                                TGTGTCGGC TG TG GC
                                     C  C  T
GAM2812  ENPP1    5'  GCCGCGGCTCCCGCCCCC    26298      ACAA
                                GCCGC   CCCGCCCCC
                                |||||   |||||||||
                                CGGCG   GGGCGGGGG
                                   CCGA
GAM2812  EPHB6    5'  ACGCAGCCCGGCCCGCCCCC  20795    A    GCACAA
                                AC CAGCC     CCCGCCCCC
                                || |||||     |||||||||
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                                TG GTCGG     GGGCGGGGG
                                 C    GCC___
GAM2812  EXTL1    3'  ACACGACACGACCCGCCCCCC  20861      AGCC    A
                                ACAC    GCAC ACCCGCCCCCC
                                ||||    |||| ||||||||||
                                TGTG    TGTG TGGGCGGGGGG
                                  C___    C
GAM2812  FAAH     5'  CAGCAGCTGCTCGCCCCCC    11046      C  ACAACC
                                CAGC GC     CGCCCCCC
                                |||| ||     ||||||||
                                GTCG CG     GCGGGGGG
                                  T  ACGA__
GAM2812  FANCE    5'  CACGGGTGCCGCGCCGCCCCC  34895     A___     ACAAC
                                CAC    GCCGC    CCGCCCCC
                                |||    |||||    ||||||||
                                GTG    CGGCG    GGCGGGGG
                                  CCCA    C____
GAM2812  FKBP2    5'  ACAGCAGCCAGGGACCCGCCCC 38385     _     CACA
                                ACA CAGCCG    ACCCGCCCC
                                ||| ||||||    |||||||||
                                TGT GTCGGT    TGGGCGGGG
                                  C     CCC_
GAM2812  GSTM4    5'  ACCTAGCGCCAGACCCGCCCCC 9198     AC   C  A  _
                                AC  AGC GC CA ACCCGCCCCC
                                ||  ||| || || ||||||||||
                                TG  TCG CG GT TGGGCGGGGG
                                 GA  _ _  C
GAM2812  HHIP     5'  ACACAGCCTCTCATGTTTCGTT 35401        GCA  ACC__  CC
             CCC                   ACACAGCC   CA    CG  CCC
                                |||||||||  ||    ||  |||
                                TGTGTCGG   GT    GC  GGG
                                     AGA  ACAAA  AA
GAM2812  HNF3G    3'  ACACAGCCAGTACCCCGCTTCC 43644         CACAA    CC
             C                    ACACAGCCG    CCCGC  CCC
                                |||||||||    |||||  |||
                                TGTGTCGGT    GGGCG  GGG
                                     CATG_    AA
GAM2812  ILK      3'  ACAAAGCTCTGAGCCCGCCCC  21121     C  CGCACAA
                                ACA AGC      CCCGCCCC
                                ||| |||      ||||||||
                                TGT TCG      GGGCGGGG
                                  T   AGACTC_
GAM2812  JUND     3'  ACACAACCAACGTTTGTTCCCC 23794         C  AACCCG_
                                ACACAGCCG AC      CCCC
                                |||||||||  ||      ||||
                                TGTGTTGGT TG      GGGG
                                     _  CAAACAA
GAM2812  KDR      3'  ACACAGCTTCACATTGAACCTC 13939        CG   ACCC  _
             CC                   ACACAGC  CACA   GCC CCC
                                |||||||  ||||   ||| |||
```

```
                                TGTGTCG  GTGT   TGG GGG
                                    AA   AACT  A
GAM2812  MADH6    3'  GCCGCGGCCTCCCACCCGCCC  24601      ACAA_     _
                                GCCGC    CCCGCCC CCC
                                |||||    ||||||| |||
                                CGGCG    GGGTGGG GGG
                                   CCGGA      C
GAM2812  MADH7    3'  ACACAGCCGCACACTCAC    25358           A C
                                ACACAGCCGCACA C CGC
                                |||||||||||| | |||
                                TGTGTCGGCGTGT G GTG
                                       _ A
GAM2812  MAT2A    3'  CAGCCGCACCAGCTCTGCCCTC 25403        AACCC__   _
             C                   CAGCCGCAC      GCCC CC
                                |||||||||      |||| ||
                                GTCGGCGTG      CGGG GG
                                     GTCGAGA   A
GAM2812  MEN1     5'  GCCGCCCCGCCCCC       39184       ACAA
                                GCCGC   CCCGCCCCC
                                |||||   |||||||||
                                CGGCG   GGGCGGGGG
                                  ____
GAM2812  MSL3L1   3'  CACAGCTGCAGCCTCCC     38578       C   CAACCC  _
                                CACAGC GCA     GCC CCC
                                |||||| |||     ||| |||
                                GTGTCG CGT     CGG GGG
                                   A  _______  A
GAM2812  MTA1L1   3'  CAGTGCACGCCCCCC      21882     CC    AACCC
                                CAG  GCAC    GCCCCCC
                                |||  ||||    |||||||
                                GTC  CGTG    CGGGGGG
                                  A_   _____
GAM2812  MUCDHL   3'  ACAGCCTTGTACCCGCCC    34925       GCACA
                                ACAGCC    ACCCGCCC
                                ||||||    ||||||||
                                TGTCGG    TGGGCGGG
                                   AACA_
GAM2812  MXI1     5'  CAGCGCCGGGGCCCGCCCCC  39014     C  ACAA_
                                CAGC GC    CCCGCCCCC
                                |||| ||    |||||||||
                                GTCG CG    GGGCGGGGG
                                  _ GCCCC
GAM2812  MYCL2    5'  CACCGAGCGCGCGACCCGCCC  23899     __  _  ACA
                                CAC  AGC CGC   ACCCGCCC
                                |||  ||| |||   ||||||||
                                GTG  TCG GCG   TGGGCGGG
                                  GC   C   C__
GAM2812  NGB      5'  GCCACGGCCCCCGCCCCC    34585      ACAA
                                GCCGC   CCCGCCCCC
                                |||||   |||||||||
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                                CGGTG   GGGCGGGGG
                                  CCGG
GAM2812 NRAS    5' CAGCCGCACCCAGACCCGCCCC 14848        A___
                                CAGCCGCAC   ACCCGCCCC
                                |||||||||   |||||||||
                                GTCGGCGTG   TGGGCGGGG
                                    GGTC
GAM2812 PHB     3' CAGCCGCACATGCCC      15262         ACCC
                                CAGCCGCACA  GCCC
                                ||||||||||  ||||
                                GTCGGCGTGT  CGGG
                                    A___
GAM2812 PMM2    3' CAGCCGGGACCCCGCCCC   43550      CACAA
                                CAGCCG    CCCGCCCC
                                ||||||    ||||||||
                                GTCGGC    GGGCGGGG
                                   CCTG_
GAM2812 PTEN    5' GCCGGCCTGCCCGCCCCC   7213     _ ACAA
                                GCCG C    CCCGCCCCC
                                |||| |    |||||||||
                                CGGC G    GGGCGGGGG
                                  C GAC_
GAM2812 PTPN23  5' ACGAGCCCAGCCCCGCCCC  41891   _   G  CAA
                                AC AGCC CA   CCCGCCCC
                                || |||| ||   ||||||||
                                TG TCGG GT   GGGCGGGG
                                 C   _ CG_
GAM2812 PTPRK   5' GGACAGCCGCCCGCCCGCCC  15965   C      ACAA
                                A ACAGCCGC   CCCGCCC
                                | ||||||||   |||||||
                                C TGTCGGCG   GGGCGGG
                                 C      GGC_
GAM2812 RAP1GA1 3' CACAGCCGGCTCCCTGCCCC  16161       CACAA  _
                                CACAGCCG    CCC GCCCC
                                ||||||||    ||| |||||
                                GTGTCGGC    GGG CGGGG
                                    CGA__   A
GAM2812 RPP30   5' CAGCCGCTGAGCCCGCCCC   26934      ACAA
                                CAGCCGC   CCCGCCCC
                                |||||||   ||||||||
                                GTCGGCG   GGGCGGGG
                                   ACTC
GAM2812 SLC16A2 3' ACACAGCCTGGCAGTGCCC  27148       __  CAACCC
                                ACACAGCC  GCA    GCCC
                                ||||||||  |||    ||||
                                TGTGTCGG  CGT    CGGG
                                    AC   CA____
GAM2812 SMARCD1 5' CAGCAGCCGCGCCCGCCCC  40081   _    ACAA
                                CA CAGCCGC   CCCGCCCC
                                || |||||||   ||||||||
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                                GT GTCGGCG   GGGCGGGG
                                 C      C___
GAM2812 SOX12    3' ACCCGGCCGCATCGCCCCC   28023    ACA    CAACC
                                AC   GCCGCA    CGCCCCC
                                ||   ||||||    |||||||
                                TG   CGGCGT    GCGGGGG
                                 GGC     A____
GAM2812 SPG4     5' GCCGCCATAACCCGCCTCCC   31398      AC_     _
                                GCCGC   AACCCGCC CCC
                                |||||   |||||||| |||
                                CGGCG   TTGGGCGG GGG
                                   GTA       A
GAM2812 TBL1X    5' CAGCCGCGCGCCGCCCCC    24873       ACAAC
                                CAGCCGC    CCGCCCCC
                                |||||||    ||||||||
                                GTCGGCG    GGCGGGGG
                                    CGC__
GAM2812 TPD52L2  3' CAACACCCGCACAACCTGCC   17632   C   G       C
                                A ACA CCGCACAACC GCC
                                | ||| |||||||||| |||
                                G TGT GGCGTGTTGG CGG
                                 T   G        A
GAM2812 TSG101   5' ACACAATCGCACACCCC     26646     GC    AACCC
                                ACACA  CGCAC    GCCCC
                                |||||  |||||    |||||
                                TGTGT  GCGTG    TGGGG
                                   TA    _____
GAM2812 VENTX2   3' ACGCAGCCGCAGGACCACGC   30906    A      CA   _
                                AC CAGCCGCA  ACC CGC
                                || ||||||||  ||| |||
                                TG GTCGGCGT  TGG GCG
                                 C       CC   T
GAM2812 WRN      5' ACCTACCCGACCCGCCCC    8130     _ ACA
                                GCC GC   ACCCGCCCC
                                ||| ||   |||||||||
                                TGG TG   TGGGCGGGG
                                  A  GGC
GAM2812 WRN      5' CCACCGCCCGCCCCCC      8132      ACAA
                                CCGC    CCCGCCCCCC
                                ||||    ||||||||||
                                GGTG    GGGCGGGGGG
                                  GC__
GAM2812 ZAP70    3' CACAGCCGCACCCTCCC     43337        ACA   G
                                CACAGCCGC   ACCC CCC
                                |||||||||   |||| |||
                                GTGTCGGCG   TGGG GGG
                                      ___    A
GAM2813 A1BG     5' GCAGTGAGTGTCTGGGGT    39092     GT_  A
                                GCAG   GT TCTGGGGT
                                ||||   || ||||||||
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                                CGTC   CA AGACCCCA
                                  ACT  C
GAM2813 ADCY6    3' GAGAGGCAACCTGGGGT     34171     C    T
                                GAG AGGTG ATCTGGGGT
                                ||| ||||| |||||||||
                                CTC TCCGT TGGACCCCA
                                  _    _
GAM2813 ARHGAP6  3' GAGTAGGCGTTCAGCAGGT   30215     C     A  TG_
                                GAG AGGTGT TC   GGGT
                                ||| |||||| ||   ||||
                                CTC TCCGCA AG   TCCA
                                  A     _ TCG
GAM2813 ATP8A2   3' AGCAGGTGTGGGGGT       45250         ATCT
                                AGCAGGTGT    GGGGT
                                |||||||||    |||||
                                TCGTCCACA    CCCCA
                                     C___
GAM2813 B3GNT3   5' AGCCAGGGTCTGGGGT      30676     _   T TA
                                AGC AGG G  TCTGGGGT
                                ||| ||| |  ||||||||
                                TCG TCC C  AGACCCCA
                                  G  _ __
GAM2813 CACNG6   5' GAGATTGCTTCTGGGGT     36696     CAGG   A
                                GAG    TGT TCTGGGGT
                                |||    ||| ||||||||
                                CTC    ACG AGACCCCA
                                  TA__   A
GAM2813 CACNG6   5' GAGCGGCCTGGGGT        36697     A   GTAT
                                GAGC GGT    CTGGGGT
                                |||| |||    |||||||
                                CTCG CCG    GACCCCA
                                  _   ____
GAM2813 CDH3     3' GAATGGGAGGCATTGGGGT   12172     CA  T_   C
                                GAG  GG  GTAT TGGGGT
                                |||  ||  |||| ||||||
                                CTT  CC  CGTA ACCCCA
                                  AC  TC   _
GAM2813 CEL      3' GAGGGGAGCCCCTGGGGT    12220     CA  T  AT
                                GAG  GG GT  CTGGGGT
                                |||  || ||  |||||||
                                CTC  CC CG  GACCCCA
                                  C_  T  GG
GAM2813 CELL     3' GAGGGGAGCCCCTGGGGT    12226     CA  T  AT
                                GAG  GG GT  CTGGGGT
                                |||  || ||  |||||||
                                CTC  CC CG  GACCCCA
                                  C_  T  GG
GAM2813 CYP11B1  3' GAGGGGTGGCCTGGGGT     41628     CA   TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
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                                CTC  CCAC  GGACCCCA
                                  C_   C_
GAM2813  CYP24    5'  GGCCGGTGTCTGGGGT     8947    A  A    TA
                                G GC GGTG  TCTGGGGT
                                | || ||||  ||||||||
                                C CG CCAC  AGACCCCA
                                 _ G   __
GAM2813  CYP26A1  5'  GAGCGCGCCTCCTGGGGT    38407     AG    A_
                                GAGC  GTGT  TCTGGGGT
                                ||||  ||||  ||||||||
                                CTCG  CGCG  GGACCCCA
                                  __   GA
GAM2813  DRG2     3'  GAGCCAGGGTCCTGGGGT    10786     _   T  A
                                GAGC AGG GT TCTGGGGT
                                |||| ||| || ||||||||
                                CTCG TCC CA GGACCCCA
                                  G  _ _
GAM2813  EN2      3'  GAGCAGGCCTGGGGT       10952        GTAT
                                GAGCAGGT   CTGGGGT
                                ||||||||   |||||||
                                CTCGTCCG   GACCCCA
                                     ____
GAM2813  EPHB4    3'  GAGGCGGTGTCCCTGGGGT   20791     CA    AT
                                GAG  GGTGT  CTGGGGT
                                |||  |||||  |||||||
                                CTC  CCACA  GACCCCA
                                  CG    GG
GAM2813  FCER2    3'  GAGAGGGTGCTGTTGGGGT   12812     CA    ATC
                                GAG  GGTGT   TGGGGT
                                |||  |||||   ||||||
                                CTC  CCACG   ACCCCA
                                  TC    ACA
GAM2813  FEN1     3'  GGCAAATATTCTGGGGT     19958   A      A
                                G GCAGGTGT TCTGGGGT
                                | |||||||| ||||||||
                                C CGTTTATA AGACCCCA
                                _      _
GAM2813  FLII     3'  GAGCAGGTGGTGTCACCT    12898         ____
                                GAGCAGGTG   TATCT
                                |||||||||   |||||
                                CTCGTCCAC   GTGGA
                                     CACA
GAM2813  GNAT2    5'  GAGCAGGCTGTAGGGT      23594        GTATC
                                GAGCAGGT    TGGGGT
                                ||||||||    ||||||
                                CTCGTCCG    ATCCCA
                                    AC___
GAM2813  HMGA1    5'  GAGCAGGTGGAAGAGT      44163         TATCT
                                GAGCAGGTG    GGGGT
                                |||||||||    |||||
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                                CTCGTCCAC    TCTCA
                                     CT___
GAM2813 HR      3' GAGTGGTGCTTGTGGGGT   32918    CA   ATC
                                GAG GGTGT  TGGGGT
                                ||| |||||  ||||||
                                CTC CCACG  ACCCCA
                                  A_    AAC
GAM2813 HRY     5' GAGCAAGTGCTGAGGGT    24354       TAT  _
                                GAGCAGGTG  CTG GGGT
                                |||||||||  ||| ||||
                                CTCGTTCAC  GAC CCCA
                                     ___  T
GAM2813 ID3     3' GAGAGGTTCCCGGGGT     44273    C   GTA
                                GAG AGGT  TCTGGGGT
                                ||| ||||  ||||||||
                                CTC TCCA  GGGCCCCA
                                  _   A__
GAM2813 IGFBP5  3' GAGTGGCGTCCTGGGGT    8268     CA   A
                                GAG GGTGT TCTGGGGT
                                ||| ||||| ||||||||
                                CTC CCGCA GGACCCCA
                                  A_    _
GAM2813 IL18R1  3' GAGCTATTCTGGGG       19294     AGG  A
                                GAGC  TGT TCTGGGG
                                ||||  ||| |||||||
                                CTCG  ATA AGACCCC
                                   ___  _
GAM2813 IL1RN   3' GGGCAGGTGGTCGGGGT    8214   A     TA  T
                                G GCAGGTG  TC GGGGT
                                | |||||||  || |||||
                                C CGTCCAC  AG CCCCA
                                 C      C_ _
GAM2813 ISLR    3' GAGCAGGTCTAGAAGT     24434       G  TCT
                                GAGCAGGT TA  GGGGT
                                |||||||| ||  |||||
                                CTCGTCCA AT  CTTCA
                                     G  ___
GAM2813 LAIR1   3' AGCAAAGTCTCTGGGGT    14050      T  A
                                AGCAGG GT TCTGGGGT
                                |||||| || ||||||||
                                TCGTTT CA AGACCCCA
                                   _ G
GAM2813 LGALS3BP 3' GAGGGCGTCCTGGGGT    42932    CA   A
                                GAG GGTGT TCTGGGGT
                                ||| ||||| ||||||||
                                CTC CCGCA GGACCCCA
                                   __   _
GAM2813 MAB21L1 5' GAGTGTGTGTCCGGGGT    24588    CAG  A
                                GAG  GTGT TCTGGGGT
                                |||  |||| ||||||||
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                                CTC   CACA AGGCCCCA
                                  A__    C
GAM2813  MEF2D    3'  AAGCAGGTCTGGGG       25415       TGTA
                                GAGCAGG    TCTGGGG
                                |||||||    |||||||
                                TTCGTCC    AGACCCC
                                     ____
GAM2813  MFAP2    3'  AAGCAGACCAGCTGGGGT    32703       TGTAT
                                GAGCAGG    CTGGGGT
                                |||||||    |||||||
                                TTCGTCT    GACCCCA
                                    GGTC_
GAM2813  MPZ      3'  GGCAGGGCCTGGGGT      8036    A    T  AT
                                G GCAGG GT  CTGGGGT
                                | ||||| ||  |||||||
                                C CGTCC CG  GACCCCA
                                _    _ __
GAM2813  MTA1L1   3'  GAGCGTGGCCTGGGGT     21887     AG   TA
                                GAGC  GTG  TCTGGGGT
                                ||||  |||  ||||||||
                                CTCG  CAC  GGACCCCA
                                  __   C_
GAM2813  MTMR2    3'  GAACATTTTCATCTGGGGT   32067      GGTG
                                GAGCA    TATCTGGGGT
                                |||||    ||||||||||
                                CTTGT    GTAGACCCCA
                                   AAAA
GAM2813  NESH     3'  GAGGGGTGTCTGGGGT     32338     CA    TA
                                GAG  GGTG  TCTGGGGT
                                |||  ||||  ||||||||
                                CTC  CCAC  AGACCCCA
                                  C_   __
GAM2813  NF2      3'  GGCAGGTCCTGGGGT       7069    A     GTA
                                G GCAGGT   TCTGGGGT
                                | ||||||   ||||||||
                                C CGTCCA   GGACCCCA
                                _     ____
GAM2813  NR1I2    5'  GAACAGTGTGCTCTGGGGT   35102       _   A
                                GAGCAG GTGT TCTGGGGT
                                |||||| |||| ||||||||
                                CTTGTC CACG AGACCCCA
                                   A   _
GAM2813  PATE     3'  GAGAGGCATCTGGGGT      39642     C    GT
                                GAG AGGT  ATCTGGGGT
                                ||| ||||  |||||||||
                                CTC TCCG  TAGACCCCA
                                  _   __
GAM2813  PFKL     5'  GAGCAGGTGTGAGG        15234          ATCT
                                GAGCAGGTGT   GGGG
                                ||||||||||   ||||
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                                CTCGTCCACA   CTCC
                                      ____
GAM2813 PGAM1    3' GAGCCAGATCCTCTGGGGT   44056    _   GTA
                                GAGC AGGT   TCTGGGGT
                                |||| ||||   ||||||||
                                CTCG TCTA   AGACCCCA
                                  G   GG_
GAM2813 PGF      3' GAGCCGGGTGCGGGGT     15252    A_   ATCT
                                GAGC  GGTGT   GGGGT
                                ||||  |||||   |||||
                                CTCG  CCACG   CCCCA
                                  GC    ____
GAM2813 PKM2     3' GAGGAGGGGCTCTGGGGT   15332    C  T  A
                                GAG AGG GT TCTGGGGT
                                ||| ||| || ||||||||
                                CTC TCC CG AGACCCCA
                                  C  C  _
GAM2813 PODXL    5' GAGCAGGTGGCTGCGGT    23974       TAT  G
                                GAGCAGGTG  CTG GGT
                                |||||||||  ||| |||
                                CTCGTCCAC  GAC CCA
                                     C__  G
GAM2813 PX19     3' AAGCCTAGCTGTCTGGGGT  29872    A_  GTA
                                GAGC  GGT  TCTGGGGT
                                ||||  |||  ||||||||
                                TTCG  TCG  AGACCCCA
                                  GA  AC_
GAM2813 SCD      5' GAGCGGAGTTCGGGGT     22829    A  T  A  T
                                GAGC GG GT TC GGGGT
                                |||| || || || |||||
                                CTCG CC CA AG CCCCA
                                  _ T _ _
GAM2813 SCN4A    3' GGCAGTGCCCTGGGGT     7325   A   G   A
                                G GCAG TGT TCTGGGGT
                                | |||| ||| ||||||||
                                C CGTC ACG GGACCCCA
                                 _   _  _
GAM2813 SCNN1G   3' AAGTCAGATTGTCTGGGGT  9787    _    GTA
                                GAG CAGGT  TCTGGGGT
                                ||| |||||  ||||||||
                                TTC GTCTA  AGACCCCA
                                  A    AC_
GAM2813 SFTPA2   3' GAGTGGCTGCCTGGGGT    27964   CA  GTA
                                GAG  GGT  TCTGGGGT
                                |||  |||  ||||||||
                                CTC  CCG  GGACCCCA
                                  A_  AC_
GAM2813 SH3GL1   3' GAGCAGAGCCTGGGGT     16667      T AT
                                GAGCAGG GT  CTGGGGT
                                ||||||| ||  |||||||
```

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                                CTCGTCT CG  GACCCCA
                                      _ __
GAM2813 SLC20A1  5' GCATCTGTTGTCTGGGGT   40450    GG  A_
                                GCA  TGT  TCTGGGGT
                                |||  |||  ||||||||
                                CGT  ACA  AGACCCCA
                                  AG   AC
GAM2813 SLC22A5  5' GAGCGCGGCCTGGGGT     16858     A_  GTAT
                                GAGC  GGT   CTGGGGT
                                ||||  |||   |||||||
                                CTCG  CCG   GACCCCA
                                  CG  ____
GAM2813 SLC39A4  5' GAGTTGGCCCTGGGGT     39295    CA  GTA
                                GAG  GGT   TCTGGGGT
                                |||  |||  ||||||||
                                CTC  CCG  GGACCCCA
                                  AA  ___
GAM2813 SUV39H1  3' GAGCAGGTGGGGGC       17223       TATCT
                                GAGCAGGTG    GGGGT
                                |||||||||    |||||
                                CTCGTCCAC    CCCCG
                                      _____
GAM2813 SYNGR1   3' GAGTTGGGCCTGGGGT     21759    CA  T  AT
                                GAG  GG GT  CTGGGGT
                                |||  || ||  |||||||
                                CTC  CC CG  GACCCCA
                                  AA  _  __
GAM2813 TAPBP    3' GAGCAGATGATAGGGT     17301       TATC
                                GAGCAGGTG   TGGGGT
                                |||||||||   ||||||
                                CTCGTCTAC   ATCCCA
                                     T___
GAM2813 TCF19    3' GCAGGTGTGTCCGATGGT   45557       A   _
                                GCAGGTGT TCTGG GGT
                                |||||||| ||||| |||
                                CGTCCACA AGGCT CCA
                                     C    A
GAM2813 TCP10    3' GAGCCGTGCCTGGGGT     21428    AG   AT
                                GAGC  GTGT  CTGGGGT
                                ||||  ||||  |||||||
                                CTCG  CACG  GACCCCA
                                  G_   __
GAM2813 TEM6     3' GAGCCGGTGTCCACGGT    35555    A   TA   G
                                GAGC GGTG  TCTG GGT
                                |||| ||||  |||| |||
                                CTCG CCAC  AGGT CCA
                                  G   __   G
GAM2813 TM4SF5   3' GAGCAGGTGTAACCCGGCGGT 19555         _   _
                                GAGCAGGTGTA TCTGG GGT
                                |||||||||| ||||| |||
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                                CTCGTCCACAT GGGCC CCA
                                      T    G
GAM2814 BCL10    5' TACGCGACGCGACGC      19408     AT      TTCTA
                                TAC  CGACGCGA    CGC
                                |||  ||||||||    |||
                                ATG  GCTGCGCT    GCG
                                  C_      _____
GAM2815 DMRT2    3' GCTTGTTGTGGTTGTTAT    27264         G  GG
                                GTTTGTTGTGG TG  AT
                                |||||||||| ||  ||
                                CGAACAACACC AC  TA
                                      A  AA
GAM2815 NFE2L1   3' TCTTTTGTTGTTGCTGGG    17335    G      GGG
                                TC TTTGTTGT   TGGG
                                || ||||||||   ||||
                                AG AAACAACA   ACCC
                                 A       ACG
GAM2816 ARHGEF12 3' CTTAGCAGTTGGCACC      31638         ACAAGTT
                                CTTGGCAGTT      CACC
                                ||||||||||      ||||
                                GAATCGTCAA      GTGG
                                      CC_____
GAM2816 EGFL5    3' CTTGGAGAGATGAGTTCACCT  44525      C  TTACA
                                CTTGG AG    AGTTCACCT
                                ||||| ||    |||||||||
                                GAACC TC    TCAAGTGGA
                                   _  TCTAC
GAM2816 GRAF     3' CACTCTATTTACAAGTT     31437      GGCAG
                                TACTT    TTACAAGTT
                                |||||    |||||||||
                                GTGAG    AATGTTCAA
                                   ATA__
GAM2816 IFNAR1   3' TACTTGACACAGTTCA      8432         AGTT   A
                                TACTTGGC    ACA GTTCA
                                ||||||||    ||| |||||
                                ATGAACTG    TGT CAAGT
                                      _____   _
GAM2816 PKHD1    3' TTGAAGGGCAAGTTCACCT    39813     C  TTA
                                TTGG AG   CAAGTTCACCT
                                |||| ||   ||||||||||
                                AACT TC   GTTCAAGTGGA
                                   _  CC_
GAM2816 UNG      3' TACTTGGCAGTCTGTGCTGCCT 38946          ACAA   CA
                                TACTTGGCAGTT    GTT  CCT
                                ||||||||||||    |||  |||
                                ATGAACCGTCAG    CGA  GGA
                                      ACA_   C_
GAM2816 ZNF189   3' TACTTGGCAGTCATAATATGTA 18367           C  ___  T
             CAC                   TACTTGGCAGTTA AA   GT CAC
                                ||||||||||||| ||   || |||
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                                ATGAACCGTCAGT TT   CA GTG
                                       A  ATA  T
GAM2817  PLAG1    3'  CCCCCCATTTACATTAT     15346    A    C
                                CC TCTCA TTACATTAT
                                || ||||| |||||||||
                                GG GGGGT AATGTAATA
                                 _    A
GAM2817  WNT14    3'  TAGACCTTCTCACACCAT    18145    A  A     TTA
                                TA ACC TCTCAC   CAT
                                || ||| ||||||   |||
                                AT TGG AGAGTG   GTA
                                 C   A     TG_
GAM2818  ABCC1    5'  CGGGCGGCGGGTGATCGGGC   33410    T_ T   C    A
                                CG  CG CGGG GATCG GC
                                ||  || |||| ||||| ||
                                GC  GC GCCC CTAGC CG
                                 CC  C    A    C
GAM2818  BRAF     5'  CGCTGTCGGGCGGGGAG     20261     C      ATC
                                CGT GTCGGGCG   GAG
                                ||| ||||||||   |||
                                GCG CAGCCCGC   CTC
                                  A       CC_
GAM2818  CEBPD    5'  CGGCGTCGGGCCGGGC      45517    T      GAT  A
                                CG CGTCGGGC   CG GC
                                || ||||||||   || ||
                                GC GCAGCCCG   GC CG
                                 C       ____  C
GAM2818  CYP1B1   5'  CGTCGTCAGTGCCAGGAGC    6448          _  GATC
                                CGTCGTCGG GC    GAGC
                                ||||||||| ||    ||||
                                GCAGCAGTC CG    CTCG
                                      A  GTC_
GAM2818  EFNB1    5'  GCTCCCGGGCGATCGAGC    20720    CG
                                GT  TCGGGCGATCGAGC
                                ||  ||||||||||||||
                                CG  GGCCCGCTAGCTCG
                                 AG
GAM2818  EGFL5    5'  CGTCGTCAGGGTCAGC      44520          CGA  G
                                CGTCGTCGGG   TC AGC
                                |||||||||   || |||
                                GCAGCAGTCC   AG TCG
                                      C__  _
GAM2818  INPP5A   5'  GTCGTCGAAGAGCGAGC     24406         C  T
                                GTCGTCGGG GA CGAGC
                                ||||||||| || |||||
                                CAGCAGCTT CT GCTCG
                                      _ C
GAM2818  KCNH3    5'  CGCCGTCGGGGCCCGGAGC   42085          CGA  _
                                CGTCGTCGGG   TCG AGC
                                ||||||||||   ||| |||
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                                GCGGCAGCCC  GGC TCG
                                     CG_  C
GAM2818 PAEP    3' CGTCATCGTCTTCTGAGC   15067       GGCGA _
                                CGTCGTCG    TC GAGC
                                ||||||||    || ||||
                                GCAGTAGC    AG CTCG
                                    AGA__  A
GAM2818 SPHK2   5' CGGCGTCGGGCCAGAGC    33504   T     GATC
                                CG CGTCGGGC   GAGC
                                || ||||||||   ||||
                                GC GCAGCCCG   CTCG
                                 C      GT__
GAM2818 SYNGR2  3' GTTGTCAGGCAAAGC      21745   C      TCG
                                GT GTCGGGCGA  AGC
                                || |||||||||  |||
                                CA CAGTCCGTT  TCG
                                 A       ___
GAM2818 USP7    5' CGTCGTCGGCGACGGC     18454       G  T  A
                                CGTCGTCGG CGA CG GC
                                ||||||||| ||| || ||
                                GCAGCAGCC GCT GC CG
                                      _  _ _
GAM2819 ABCG5   5' ACCCCGGAGTCCCTTGGGACA 35327    GCA      CA
                                ATCC  GGAGTCCCT GGACA
                                ||||  |||||||||  |||||
                                TGGG  CCTCAGGGA CCTGT
                                  G__       AC
GAM2819 ATRN    3' TCCTGGCTGTGTCCTCAGGA  40284    __ AGGA   C
                                TCC  GC   GTCC TCAGGA
                                |||  ||   |||| ||||||
                                AGG  CG   CAGG AGTCCT
                                 AC  ACA_  _
GAM2819 CSF1R   5' TCCGCAGGGATCGGGAC    23313       AG  CCTCA
                                TCCGCAGG  TC   GGAC
                                ||||||||  ||   ||||
                                AGGCGTCC  AG   CCTG
                                     CT  C____
GAM2819 HK3     3' TCCCAGGAGTCCTGG      13379    G      CTCA
                                TCC CAGGAGTCC   GG
                                ||| |||||||||   ||
                                AGG GTCCTCAGG   CC
                                 _       A___
GAM2819 KCNS3   5' CACCTGCAGGAGTCCGGAC  13932    C       CTCA
                                CATC GCAGGAGTCC   GGAC
                                |||| ||||||||||   ||||
                                GTGG CGTCCTCAGG   CCTG
                                  A       ____
GAM2819 KIF3C   3' CATCCCAGGAGTCTATTGGA 13948     G      CCTCA
                                CATCC CAGGAGTC    GGA
                                ||||| ||||||||    |||
```

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                                GTAGG GTCCTCAG    CCT
                                  _       ATAA_
GAM2819  PPP2R5D  3'  GCAGGAGCCATGCTTGGGGCA  26458        C__  CA  A
                                GCAGGAGTC   CT  GG CA
                                |||||||||   ||  || ||
                                CGTCCTCGG   GA  CC GT
                                     TAC  AC  C
GAM2819  PRKCH    5'  CAGGCCAGCCCTCGGGACA   26508     __ T    A
                                CAGG  AG CCCTC GGACA
                                ||||  || ||||| |||||
                                GTCC  TC GGGAG CCTGT
                                  GG  _    C
GAM2819  RAB6A    5'  TCGGCAGGAGCCAGG       16108    C      CCCT
                                TC GCAGGAGT    CAGG
                                || ||||||||    ||||
                                AG CGTCCTCG    GTCC
                                 C       _____
GAM2819  ROCK2    5'  CCCGCAGGAGTCCTCGGG    42353          C  A
                                TCCGCAGGAGTCC TC GG
                                |||||||||||| || ||
                                GGGCGTCCTCAGG AG CC
                                       _ C
GAM2819  SLC1A4   3'  GCAGGGCCAGGCCAGGACA   16748      A   CC_
                                GCAGG GTC   TCAGGACA
                                ||||| |||   ||||||||
                                CGTCC CGG   GGTCCTGT
                                  _   TCC
GAM2820  ADAMTS1  5'  ATTATTCGTTGGAAGGGCG   28108        GATT_  A
                                ATTATTCGT    GGG CG
                                |||||||||    ||| ||
                                TAATAAGCA    CCC GC
                                     ACCTT  _
GAM2821  ADAMTS5  3'  CACCACTGTCACGTGAA    28176    TG C
                                CAT  C TGTCACGTGAA
                                |||  | ||||||||||
                                GTG  G ACAGTGCACTT
                                  GT _
GAM2821  CTSK     3'  TACACTGCACCATCGTG     7578         _    AC
                                TACATTGC CTGTC  GTG
                                |||||||| |||||  |||
                                ATGTGACG GGTAG  CAC
                                     T    __
GAM2821  DHFR     3'  TACACTGCTTTCACTGAA    8996        CTG   G
                                TACATTGC   TCAC TGAA
                                ||||||||   |||| ||||
                                ATGTGACG   AGTG ACTT
                                     AA_   _
GAM2821  FCMD     3'  CACATTGCCTTCCCTGA     27512         G  ACG
                                TACATTGCCT TC   TGA
                                |||||||||| ||   |||
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                                GTGTAACGGA AG   ACT
                                      _  GG_
GAM2821  MADH2    3'  TACATTACCTGTACACATAA  25346          _
                                TACATTGCCTGT CACGTGA
                                |||||||||||| |||||||
                                ATGTAATGGACA GTGTATT
                                       T
GAM2821  PEPD     5'  CACCGGCGTCACGTGAA     40896      CC
                                CATTG  TGTCACGTGAA
                                |||||  ||||||||||
                                GTGGC  GCAGTGCACTT
                                   C_
GAM2821  PRG1     3'  TACATTGCCTGGTG        15558          TCAC
                                TACATTGCCTG   GTG
                                ||||||||||   |||
                                ATGTAACGGAC   CAC
                                      ____
GAM2821  SLC4A7   3'  TACTTGTCTGTCACAATG    18824     A  C      _
                                TAC TTG CTGTCACG TG
                                ||| ||| |||||||| ||
                                ATG AAC GACAGTGT AC
                                  _  A       T
GAM2821  TRDN     3'  TAATTGCCTGAACTACTGTG  25877   C       TC__ _
                                A ATTGCCTG   AC GTG
                                | ||||||||   || |||
                                A TAACGGAC   TG CAC
                                 T       TTGA  A
GAM2821  ZNF255   5'  TACACTGCTGGTGTGAA     25102        C  TCAC
                                TACATTGC TG   GTGAA
                                |||||||| ||   |||||
                                ATGTGACG AC   CACTT
                                     _  CA__
GAM2822  POLH     3'  TAAAAATTTCATAATTCC     27102           A
                                TAAAAATTTCATAA TTC
                                |||||||||||||| |||
                                ATTTTTAAAGTATT AGG
                                       A
GAM2823  ACADL    3'  TGTTTGAAGAAAGAGTTCCAT  11498           ATG
                                TGTTTGAAGAAAGA   CCAT
                                ||||||||||||||   ||||
                                ACAAACTTCTTTCT   GGTA
                                      CAA
GAM2823  CRIM1    3'  TGTTTGAAAAGTTACCAC     32387         AAGAA
                                TGTTTGAAGA    TGCCAT
                                ||||||||||    ||||||
                                ACAAACTTTT    ATGGTG
                                      CA___
GAM2823  EVA1     3'  TGTTTGAAGAAATATCCA     40347          GAATG
                                TGTTTGAAGAAA    CCA
                                ||||||||||||    |||
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                                ACAAACTTCTTT    GGT
                                      ATA__
GAM2823 GSTM5   3' TGTTAGAAGAAAGGAAGCCA  9210     T      AAT
                                TGTT GAAGAAAG  GCCA
                                |||| ||||||||  ||||
                                ACAA CTTCTTTC  CGGT
                                  T      CTT
GAM2823 IL10RA  3' TGTTTGAAGGCAGAGTCCA   40630       AA  ATG
                                TGTTTGAAG  AGA  CCA
                                |||||||||  |||  |||
                                ACAAACTTC  TCT  GGT
                                     CG  CA_
GAM2823 NEFH    3' TGTTTGAAGAAGGAGGCC    34349        A  AT
                                TGTTTGAAGAA GA  GCC
                                |||||||||| ||  |||
                                ACAAACTTCTT CT  CGG
                                       C  C_
GAM2824 HNRPK   5' GCTGCAGTAGCCTATAG     13419   _    TTATACA
                                GC GCAGT      CCTATAG
                                || |||||      |||||||
                                CG CGTCA      GGATATC
                                 A    TC_____
GAM2825 BCL10   3' AGTAGTATAATTAGTAAGGTT  19402   C   CATTC
                                AG AGTA    AGTGAGGTT
                                || ||||    |||||||||
                                TC TCAT    TCATTCCAA
                                 A   ATTAA
GAM2825 CBR1    3' AGTAGTACATTAGTGAG     12037   C      C
                                AG AGTACATT AGTGAG
                                || |||||||| ||||||
                                TC TCATGTAA TCACTC
                                 A      _
GAM2825 KRT8    3' GCAGAGCTAGCTGAGGTTTTA  14006     TACATTC  _
                                GCAG      AG TGAGGTTTTA
                                ||||      || ||||||||||
                                CGTC      TC ACTCCAAAAT
                                  TCGA___  G
GAM2825 RAD51L1  3' AGCAGTACGGTCCTGTTTT   39449       AT  AGTGAG
                                AGCAGTAC  TC     GTTTT
                                ||||||||  ||     |||||
                                TCGTCATG  AG     CAAAA
                                    CC  GA____
GAM2825 RXRA    3' AGCAGGCGTTCAGTGAG     16408      TACA
                                AGCAG   TTCAGTGAG
                                |||||   |||||||||
                                TCGTC   AAGTCACTC
                                  CGC_
GAM2825 STC1    3' AGCAGCACGTTACTGGTTTTA  17170       ATTCA  GA__
                                AGCAGTAC    GT   GGTTTTA
                                ||||||||    ||   |||||||
```

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                                TCGTCGTG    CA    CCAAAAT
                                     _____  ATGA
GAM2825 UQCRB    3'  AGTAGTTATTCAGTATAAGGTT 26656    C   AC      __
              T                   AG AGT  ATTCAGT  GAGGTTT
                                  || |||  |||||||  |||||||
                                  TC TCA  TAAGTCA  TTCCAAA
                                   A  A_      TA
GAM2826 PSG1     3'  TGGTTCATTCTATCTAT     27916          GT  G
                                  TGGTTCATTC  TC TAT
                                  ||||||||||  || |||
                                  ACCAAGTAAG  AG ATA
                                        AT  _
GAM2827 APPL     3'  CATCAAGTGCAGTACATTAGA  29005    A       TGAA
                                  CA CAAGTGCA    ATTAGA
                                  || ||||||||    ||||||
                                  GT GTTCACGT    TAATCT
                                   A       CATG
GAM2827 OPHN1    3'  GACACTATAATTGAAATTAGA  14965     ACAA   CA
                                  GACA    GTG  TGAAATTAGA
                                  ||||    |||  ||||||||||
                                  CTGT    TAT  ACTTTAATCT
                                    GA__   TA
GAM2827 QDPR     3'  GACAACAAGTGCATTTATTAG  7238            GAA
                                  GACAACAAGTGCAT   ATTAG
                                  ||||||||||||||   |||||
                                  CTGTTGTTCACGTA   TAATC
                                        AA_
GAM2827 RARRES1  3'  ACAACTCTTGATATGAAATTAG 16171      AAG  C_
              A                    ACAAC   TG  ATGAAATTAGA
                                  |||||   ||  ||||||||||
                                  TGTTG   AC  TACTTTAATCT
                                     AGA  TA
GAM2828 AKAP4    5'  CACCCAGAAGGGAGATGTGCC  40233         A     ACCGCG
                                  CACCCGGAA GGAGA     GCC
                                  ||||||||| |||||     |||
                                  GTGGGTCTT CCTCT     CGG
                                       C     ACA___
GAM2828 CARD15   3'  CCGGAAAGGAGGGCAGGC    35259          AACC  _
                                  CCGGAAAGGAG    GC GGC
                                  ||||||||||    || |||
                                  GGCCTTTCCTC    CG CCG
                                        C___  T
GAM2828 CENPC1   5'  CCGGAATACCAGGCCGCGGCC  12234       ____  AGAA
                                  CCGGAA   AGG   CCGCGGCC
                                  ||||||   |||   ||||||||
                                  GGCCTT   TCC   GGCGCCGG
                                     ATGG  ____
GAM2828 DLX2     3'  CACCCGGAGGGGAGGGAAGGC  20586        AA   AACCGC
                                  CACCCGGA  GGAG     GGC
                                  ||||||||  ||||     |||
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                                GTGGGCCT  CCTC     CCG
                                     CC    CCTT__
GAM2828  GDF2     5'  CACCCAGAGAGGAGACTGCAGG 32122         A     ACC___
              CGGCC                   CACCCGGA AGGAGA     GCGGCC
                                |||||||| ||||||     ||||||
                                GTGGGTCT TCCTCT     CGCCGG
                                     C     GACGTC
GAM2828  HBQ1     3'  CGCCTGGGGATCCCGCGGCC  23728   A  C  AAA   GAA
                                C CC GG   GGA   CCGCGGCC
                                | || ||   |||   ||||||||
                                G GG CC   CCT   GGCGCCGG
                                 C  A  ___   AG_
GAM2828  IFNGR2   5'  CCCGCTCCGGGAACCGCGGCC  24381     GAAA  A
                                CCCG    GG GAACCGCGGCC
                                ||||    || ||||||||||
                                GGGC    CC CTTGGCGCCGG
                                  GAGG  _
GAM2828  IKBKB    3'  CACCATGTGAGAGCCGCGGCC  41804     CGGAAAG    A
                                CACC      GAGA CCGCGGCC
                                ||||      |||| ||||||||
                                GTGG      CTCT GGCGCCGG
                                  TACA___    C
GAM2828  IL15     5'  CAGCCGGGAGGGTGCGGC    8223     C    AAAG   AACC
                                CA CCGG    GAG    GCGGC
                                || ||||    |||    |||||
                                GT GGCC    CTC    CGCCG
                                 C    _____   CCA_
GAM2828  JUND     5'  CCCGGGGGGGGAGTGGCCGCGGC 23798      AAA    AA_
              C                   CCCGG   GGAG   CCGCGGCC
                                |||||   ||||   ||||||||
                                GGGCC   CCTC   GGCGCCGG
                                   CCC    ACC
GAM2828  KIR2DL5  3'  GAAAAGGAGACAGC       33921         AACC
                                GGAAAGGAG    GCGGC
                                |||||||||    |||||
                                CTTTTCCTC    TGTCG
                                     ____
GAM2828  MAP2K2   5'  CCCGGGGCTGCGGCCGCGGCC  36205      AAA  AGAA__
                                CCCGG   GG     CCGCGGCC
                                |||||   ||     ||||||||
                                GGGCC   CC     GGCGCCGG
                                   ___  GACGCC
GAM2828  MAP3K12  5'  CCTCGGGGGCTCCGCGGC    26683    _   AAA  AGAA
                                CC CGG   GG    CCGCGGC
                                || |||   ||    |||||||
                                GG GCC   CC    GGCGCCG
                                 A   C__   GA__
GAM2828  MGAT2    5'  CCCGGAAAAAGCTCAGCCGCGG 14444         G  AA___
                                CCCGGAAAG AG    CCGCGG
                                ||||||||| ||    ||||||
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                                GGGCCTTTT TC    GGCGCC
                                     _ GAGTC
GAM2828 MSF     3' CCTCGGGGAGGCCGCGGC   44723   _  AAA   AA
                                CC CGG  GGAG  CCGCGGC
                                || |||  ||||  |||||||
                                GG GCC  CCTC  GGCGCCG
                                 A  ___   C_
GAM2828 PAX2    3' CACCCGGAAGGCGAGGGCAG  19619       A  A  ACC
                                CACCCGGAA GG GA  GCGG
                                ||||||||| || ||  ||||
                                GTGGGCCTT CC CT  CGTC
                                     _ G  CC_
GAM2828 PTGER2  5' CCTGGAAAAGAGATGCGCC  9638    C       ACC  G
                                CC GGAAAGGAGA  GCG CC
                                || ||||||||||  ||| ||
                                GG CCTTTTCTCT  CGC GG
                                 A       A__  _
GAM2828 PTGER3  5' ACTCCGCTGCTGGGACCGCGGC 9641    _  GAAA_ A  A
            C                    AC CCG    GG GA CCGCGGCC
                                || |||    || || ||||||||
                                TG GGC    CC CT GGCGCCGG
                                 A  GACGA  _ _
GAM2828 PXMP3   3' CCTGGAAAGGAGAAGACAGTGG 7228    C       CCGC__
            C                    CC GGAAAGGAGAA     GGC
                                || ||||||||||     |||
                                GG CCTTTCCTCTT     CCG
                                 A         CTGTCA
GAM2828 SHANK2  3' CCCGGAAAGCAGAGGACGG  39329       G  ACC
                                CCCGGAAAG AGA  GCGG
                                ||||||||| |||  ||||
                                GGGCCTTTC TCT  TGCC
                                     G  CC_
GAM2828 SLC13A3 3' CACTTGGAAAGGAGGTGGAGC 41299    CC       AACCGC
                                CAC  GGAAAGGAG     GGC
                                |||  |||||||||     |||
                                GTG  CCTTTCCTC     TCG
                                  AA       CACC__
GAM2828 SLC25A6 3' GGAGGAGGCCGCGGCC     44865    AA   AA
                                GGA  GGAG  CCGCGGCC
                                |||  ||||  ||||||||
                                CCT  CCTC  GGCGCCGG
                                  __   C_
GAM2828 SLC7A5  5' CACCCGGGAGCCGCGGC    18540       AAAG  AA
                                CACCCGG   GAG  CCGCGGC
                                |||||||   |||  |||||||
                                GTGGGCC   CTC  GGCGCCG
                                     ____  __
GAM2828 SLC9A1  5' CACCCAGAGAGGGGCAG    43230       A  AGAACC
                                CACCCGGA AGG    GCGG
                                |||||||| |||    ||||
```

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                                GTGGGTCT TCC     CGTC
                                    C  C_____
GAM2828 SRC     3' GGGGAGGAGAACAGGGCC   24036   AA      CGC
                                GG  AGGAGAAC   GGCC
                                ||  ||||||||   ||||
                                CC  TCCTCTTG   CCGG
                                 CC       TC_
GAM2828 UGCG    5' CGGGGCGACCGCGGC      17872    AAA  A  A
                                CGG   GG GA CCGCGGC
                                |||   || || |||||||
                                GCC   CC CT GGCGCCG
                                  ___  G  _
GAM2828 VASP    3' CGGAAAGGAGAAGCGG     17915          CC
                                CGGAAAGGAGAA  GCGG
                                ||||||||||||  ||||
                                GCCTTTCCTCTT  CGCC
                                          __
GAM2828 WNT3A   3' CCCGTCCAGGGGGAGCCGCGGC 37541     GAA   A_  A
            C                    CCCG   AGG  GA CCGCGGCC
                                ||||   |||  || ||||||||
                                GGGC   TCC  CT GGCGCCGG
                                  AGG   CC  C
GAM2829 EIF2C1  3' AGTTTAGAAACTAAAGT    29172     G       C
                                AGTT TAGAAACTA AGT
                                |||| ||||||||| |||
                                TCAA ATCTTTGAT TCA
                                  _       T
GAM2829 KCNA3   3' AGTTGTAGAGACACTTAAAAT  13790        AACT   G
                                AGTTGTAGA    ACA TTAAAAT
                                |||||||||    ||| |||||||
                                TCAACATCT    TGT AATTTTA
                                     C___   G
GAM2829 NPHP1   3' GTTGTAGAAAATTATACA    41682         C___
                                GTTGTAGAAA    TACA
                                ||||||||||    ||||
                                CAACATCTTT    ATGT
                                      TAAT
GAM2829 PITPNB  3' AGTTGTTAGAAAAACATTAAAA 29625       _    CT   G
            T                    AGTTGT AGAAA  ACA TTAAAAT
                                ||||||  |||||  ||| |||||||
                                TCAACA TCTTT  TGT AATTTTA
                                   A    T_  _
GAM2829 RAB18   3' ATTACACAAGCTACAGTTAA  34569       G  A
                                GTTGTA AA CTACAGTTAA
                                ||||||  ||  ||||||||||
                                TAATGT TT GATGTCAATT
                                   G  C
GAM2829 RASGRP1 3' AGTTGTAAGGCTACAACTA   25073        AAA    GT
                                AGTTGTAG   CTACA  TA
                                ||||||||   |||||  ||
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                                TCAACATT  GATGT  AT
                                    CC_    TG
GAM2830  CACNA1D  3'  TGGGGCCGAGCGCATGGTACTC 8769    A        CCCCG
                                TG GGCCGAGTGCAT    ACTC
                                || ||||||||||||    ||||
                                AC CCGGCTCGCGTA    TGAG
                                 C         CCA__
GAM2830  DYSF     5'  GAGGCCGGCTCGAATCTCTGGC 18580       A  GC__  CCCGA
           TC                    GAGGCCG GT   ATC    CTC
                                ||||||| ||   |||    |||
                                CTCCGGC CG   TAG    GAG
                                    _ AGCT  AGACC
GAM2830  EPHA8    3'  GAGGCCGGAGCCCCGACT    33894       _ TGCAT
                                GAGGCCG AG    CCCCGACT
                                ||||||| ||    ||||||||
                                CTCCGGC TC    GGGGCTGA
                                    C _____
GAM2830  KIFC3    5'  CGGGGCGAGCCATCCCCGGCTC 24459    A  C   G      A
                                TG GGC GAGT CATCCCCG CTC
                                || ||| |||| |||||||| |||
                                GC CCG CTCG GTAGGGGC GAG
                                 C  _   _      C
GAM2830  MAPRE3   5'  TGAGGCCGCCGCGGTCTCCGGC 29540       AG  A_  C  A
           T                    TGAGGCCG  TGC  TC CCG CT
                                |||||||  |||  || ||| ||
                                ACTCCGGC  GCG  AG GGC GA
                                    G_  CC  A  C
GAM2831  CPA3     3'  TTTTATTTTATTGTATTA    12419       A
                                TTTTATT TATTGTATTA
                                ||||||| ||||||||||
                                AAAATAA ATAACATAAT
                                    A
GAM2832  SAH      5'  GCATCAGTCTTGTTGGAAGCTT 24739    CG    C  C
           T                    GC  TAGTC TGT GGAAGCTTT
                                ||  ||||| ||| |||||||||
                                CG  GTCAG ACA CCTTCGAAA
                                 TA    A  A
GAM2833  CDH1     3'  CTAACCCCCTTTAGGGCCA   20362      ATCT      AA
                                CTAAC   CCCCTTTA  GCCA
                                |||||   ||||||||  ||||
                                GATTG   GGGGAAAT  CGGT
                                   _____      CC
GAM2833  CST      3'  TCTGAGGTCTCCCCTTTA    22173     AACA
                                TCT   TCTCCCCTTTA
                                |||   ||||||||||
                                AGA   AGAGGGGAAAT
                                  CTCC
GAM2833  DMRT2    3'  TCCAACATCTCCCTTTCTTTA  27267           ___
                                TCTAACATCTCCC   CTTTA
                                ||||||||||||   |||||
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                                AGGTTGTAGAGGG  GAAAT
                                       AAA
GAM2833  EIF2S3   3'  TCTAACATCTTTTACTTC    10865         CCC_
                                TCTAACATCT   CTTT
                                ||||||||||   ||||
                                AGATTGTAGA   GAAG
                                     AAAT
GAM2833  MME      3'  CAACATCTTCTTTTCCCTTT  28597        _ ____
                                TAACATCT C   CCCTTT
                                |||||||| |   ||||||
                                GTTGTAGA G   GGGAAA
                                    A AAAA
GAM2833  NFE2L1   3'  TCTAAATCTCAAAGC      17334      C    CCCTTT
                                TCTAA ATCTC    AAAGC
                                ||||| |||||    |||||
                                AGATT TAGAG    TTTCG
                                  _   ______
GAM2833  NKX3A    3'  TCTAATGTCTCCCCTCTA    26116      CA
                                TCTAA  TCTCCCCTTTA
                                |||||  ||||||||||
                                AGATT  AGAGGGGAGAT
                                   AC
GAM2833  NME4     3'  TAATGCCTCCCCTTTAGAG   22683     CA        A
                                TAA  TCTCCCCTTTA AG
                                |||  |||||||||| ||
                                ATT  GGAGGGGAAAT TC
                                  AC         C
GAM2833  OGT      3'  TCTATATCTCCCCTCCA     18787     AC
                                TCTA  ATCTCCCCTTTA
                                ||||  ||||||||||
                                AGAT  TAGAGGGGAGGT
                                  A_
GAM2833  POLA     3'  TCTAAATCTTCCCCCTCAGC  32619      C   _     AA
                                TCTAA ATCT CCCCTTT  AGC
                                ||||| |||| |||||||  |||
                                AGATT TAGA GGGGGAG  TCG
                                   _   A     __
GAM2833  SH2D2A   3'  TCTAACATCTGTTCTCACC   19565        CCC   TAAA
                                TCTAACATCT   CTT   GCC
                                ||||||||||   |||   |||
                                AGATTGTAGA   GAG   TGG
                                     CAA  ____
GAM2833  SLC7A8   3'  CATCTCCCCTCTCCTCCA    29282         AAAG
                                CATCTCCCCTTT   CCA
                                ||||||||||||   |||
                                GTAGAGGGGAGA   GGT
                                      GGA_
GAM2833  SOX4     3'  CAACATCTCCTCCTCCGGC   16976         _    AAA
                                TAACATCTCC CCTTT   GC
                                |||||||||| |||||  ||
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                                GTTGTAGAGG GGAGG   CG
                                      A    C__
GAM2833  TFE3    3'  CCTGACATCTCCCTTTCCCA  27166    A      C   AAAG
                                TCT ACATCTCCC TTT   CCA
                                ||| ||||||||| |||   |||
                                GGA TGTAGAGGG AAG   GGT
                                  C       A  ____
GAM2833  TLL2    3'  TCCAACATAAATACTCTTTTAA 29755       _____  CCC
            AGC                   TCTAACAT    CTC   TTTAAAGC
                                ||||||||    |||  ||||||||
                                AGGTTGTA    GAG   AAATTTCG
                                     TTTAT   A__
GAM2833  TLR5    5'  TCCGACATCTTCCCTGGATGC  44290    TA    C   TTAAA
                                TC  ACATCT CCCT    GC
                                ||  |||||| ||||    ||
                                AG  TGTAGA GGGA    CG
                                 GC     A   CCTA_
GAM2834  BCL2    3'  AAACAGCCTGCAGCTTTGT   8514        AG   GA
                                AAGCAGCC  TGT  CTTTGT
                                ||||||||  |||  ||||||
                                TTTGTCGG  ACG  GAAACA
                                     __  TC
GAM2834  OCLN    3'  TTAAAGCAACCAAAACTTTGT  14911          TGT
                                TTAAAGCAGCCAG   GACTTTGT
                                ||||||||||||   ||||||||
                                AATTTCGTTGGTT   TTGAAACA
                                          ___
GAM2835  TFRC    3'  CAACTAAAACTAAAAG      17427       GAATAC
                                TAACTAA     AACTAAAAG
                                |||||||     |||||||||
                                GTTGATT     TTGATTTTC
                                          _______
GAM2836  CIS4    3'  TTCTAGTTCCATAGGTTT    20133         CGCTGTG
                                TTCTAGTTTC      AGGTTT
                                ||||||||||      ||||||
                                AAGATCAAGG      TCCAAA
                                      TA_____
GAM2836  APP     3'  TTGCTGTCCAACTTCAG     7926       A   GG   T
                                TTGCT GTCT  TTT CAG
                                ||||| ||||  ||| |||
                                AACGA CAGG  GAA GTC
                                   _   TT   _
GAM2836  ATP1B2  3'  CTGCTAGAGGATTTTCAG    11738       TCT
                                TTGCTAG   GGTTTTCAG
                                |||||||   |||||||||
                                GACGATC   CTAAAAGTC
                                    TC_
GAM2836  CHAC    3'  TTGCTGTGTGTCTTCAG     37819      A  CTG
                                TTGCT GT   GTTTTCAG
                                ||||| ||   ||||||||
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                                AACGA CA   CAGAAGTC
                                   _ CA_
GAM2836  COPG2    3'  TTGCCAGGAGCTTTCAG     44351        TCT
                                TTGCTAG   GGTTTTCAG
                                |||||||   |||||||||
                                AACGGTC   TCGAAAGTC
                                    C__
GAM2836  CTBP1    3'  TTGCTAGCCTACCACATCAG   42752          GTTT_
                                TTGCTAGTCTG    TCAG
                                ||||||||||    ||||
                                AACGATCGGAT    AGTC
                                      GGTGT
GAM2836  CXCR6    5'  TTGCCAGTTTGTTCCAG     27297        C  GT
                                TTGCTAGT TG  TTTCAG
                                |||||||| ||  ||||||
                                AACGGTCA AC  AAGGTC
                                    A  __
GAM2836  D1S155E  5'  TTGCTGATTCTTCTTTTTCAG  28393      AG_   GG_
                                TTGCT   TCT   TTTTCAG
                                |||||   |||   |||||||
                                AACGA   AGA   AAAAGTC
                                   CTA   AGA
GAM2836  DDEF1    3'  TTGCTAATGTTGCATTTTCAG  40571        C_  _
                                TTGCTAGT  TG GTTTTCAG
                                ||||||||  || ||||||||
                                AACGATTA  AC TAAAAGTC
                                    CA  G
GAM2836  EHD2     3'  CTGCTAGTCATTTCAG      31130         TGGT
                                TTGCTAGTC    TTTCAG
                                |||||||||    ||||||
                                GACGATCAG    AAAGTC
                                     T___
GAM2836  GOLGA4   5'  TTGCTAGTCAACTCAG      41061         TGGTT
                                TTGCTAGTC    TTCAG
                                |||||||||    |||||
                                AACGATCAG    GAGTC
                                     TT___
GAM2836  GOLGA4   5'  TCGCTAGTTCCTCA        41058         CTGG
                                TTGCTAGT    TTTTCA
                                ||||||||    ||||||
                                AGCGATCA    AGGAGT
                                     ____
GAM2836  KLHL3    3'  TTGCTAGTTTAGGAACAG    44654         C   TTTT
                                TTGCTAGT TGG    CAG
                                |||||||| |||    |||
                                AACGATCA ATC    GTC
                                    A   CTT_
GAM2836  MBD3     3'  GCTGGAGTTTGGTTTTCAG   19418     __   C
                                GCT  AGT TGGTTTTCAG
                                |||  ||| ||||||||||
```

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                                CGA  TCA ACCAAAAGTC
                                  CC   A
GAM2836 NEBL     3' TGCTGCTGTTTTCAG      26913      A T   G
                                TGCT G CTG TTTTCAG
                                |||| | ||| |||||||
                                ACGA C GAC AAAAGTC
                                  _ _  _
GAM2836 OCM      3' CTGCAGAAGGTTTTCAG     26189      T  TCT
                                TTGC AG   GGTTTTCAG
                                |||| ||   |||||||||
                                GACG TC   CCAAAAGTC
                                  _ TT_
GAM2836 PPP1R12B 3' TTGGTAGTCTCCTCTTCAG   36986     C     GG
                                TTG TAGTCT  TTTTCAG
                                ||| ||||||  |||||||
                                AAC ATCAGA  AGAAGTC
                                  C     GG
GAM2836 SLC25A14 5' TTGCCAGTTCCTCA       35615        CTGG
                                TTGCTAGT    TTTTCA
                                ||||||||    ||||||
                                AACGGTCA    AGGAGT
                                     ____
GAM2836 TAL1     3' TTGCCAGTTTTTCA       17295        CTGG
                                TTGCTAGT    TTTTCA
                                ||||||||    ||||||
                                AACGGTCA    AAAAGT
                                     ____
GAM2836 VDR      3' TTCCTCTCTGGGTTTTCAG   7533     G  AG    _
                                TT CT  TCTGG TTTTCAG
                                || ||  ||||| |||||||
                                AA GA  AGACC AAAAGTC
                                 G  G_    C
GAM2837 DMD      3' TAAATTTTTAAACAACCC    19689            TT
                                TAAATTTTTAAACA  CC
                                ||||||||||||||  ||
                                ATTTAAAAATTTGT  GG
                                        TG
GAM2837 PRKWNK3  3' AATTTTTAAACATTTTTAAA  41536            CC
                                AATTTTTAAACATT  TTAAA
                                ||||||||||||||  |||||
                                TTAAAAATTTGTAA  AATTT
                                        A_
GAM2837 PTPRB    3' TAAAATTTTAAACATTCTCC   15925      T         _
                                TAAA TTTTAAACATTC CT
                                |||| ||||||||||| ||
                                ATTT AAAATTTGTAAG GG
                                  T          A
GAM2837 NAGA     3' TCCTGAGACTATTCCAT     7045        CATATT
                                TCCTGA     CTATTCCAT
                                ||||||     |||||||||
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                                AGGACT     GATAAGGTA
                                   CT____
GAM2838 ADAM12   3' GGGTAGTTGGGGGACTGCTTT 18476     CTG   A_
                                GGGT   TGGG  ACTGCTTT
                                ||||   ||||  ||||||||
                                CCCA   ACCC  TGACGAAA
                                  TCA    CC
GAM2838 ATP1B1   3' GGGTACTGCATTGCTTT     11732     _    GGAAC
                                GGGT CTGTG    TGCTTT
                                |||| |||||    ||||||
                                CCCA GACGT    ACGAAA
                                  T    A____
GAM2838 BSN      3' CAGGGTATGTGGGGGCCTT    18394      C     AACT
                                CAGGGT TGTGGG    GCTTT
                                |||||| ||||||    |||||
                                GTCCCA ACACCC    CGGAA
                                   T     C___
GAM2838 HRH1     3' GGGTGTTGTGGGGCTT      9253      C_     AACT
                                GGGT  TGTGGG    GCTT
                                ||||  ||||||    ||||
                                CCCA  ACACCC    CGAA
                                  CA     _____
GAM2838 NDUFA10  3' TACAGGATGGATTGCT      21235       CTGTG   AC
                                TACAGGGT    GGA  TGCT
                                ||||||||    |||  ||||
                                ATGTCCTA    CCT  ACGA
                                      ______   A_
GAM2838 BPGM     3' TTGCATTTCTTCTTAGCC     11896         _    A
                                TTGCATTTCT CTTA CT
                                |||||||||| |||| ||
                                AACGTAAAGA GAAT GG
                                      A    C
GAM2838 GPR86    3' TTGCATTCTCTTAGTAAT     35798       T     ACTT
                                TTGCATT CTCTTA    GTGAT
                                ||||||| ||||||    |||||
                                AACGTAA GAGAAT    CATTA
                                      _     _____
GAM2838 OXTR     3' TTGCATTTCTTTATGA      9537          CTTAAC
                                TTGCATTTCT     TTGTGA
                                ||||||||||     ||||||
                                AACGTAAAGA     AATACT
                                      _______
GAM2838 SKI      3' TTGCATTTTCGTTTTTTTGTGA 16737        C  TTAAC_
                TT                  TTGCATTT TC     TTGTGATT
                                ||||||||| ||     ||||||||
                                AACGTAAA AG     AACACTAA
                                     _ CAAAAA
GAM2839 AK1      3' TCGAACTCCTGACCTCAGGTGA 7878        AC   A    ___
                T                   TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM2839  ATM      3'  TCGAACTCCTGACCTTGTGAT  39637      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM2839  ATP1A2   3'  TCGAACTCCTGACCTCATGAT  8711       AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM2839  BRCA1    3'  TCGAACTCCTGACCTCCAGTGA 28646      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    GTC
GAM2839  C21orf5  3'  TCGAACTCCTGACCTCAAGTGA 23064      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM2839  CASP10   3'  TCGAACTCCTGACCTCAAGTGA 37392      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM2839  COG7     3'  TCGAACTCCTGGCTTCATGAT  42661      AC   AA   _
                                TCGAAC  CCT  CTTT TGAT
                                ||||||  |||  |||| ||||
                                AGCTTG  GGA  GAAG ACTA
                                   A_   CC   T
GAM2839  COPA     3'  TCGAACTCCTGGCCTCAGAT   20412      AC   AA   T
                                TCGAAC  CCT  CTTT GAT
                                ||||||  |||  |||| |||
                                AGCTTG  GGA  GGAG CTA
                                   A_   CC   T
GAM2839  CPM      3'  GAACTCCTAACCTCAGGGTGAT 40660      AC       ____
                                GAAC  CCTAACTTT   TGAT
                                ||||  |||||||||   ||||
                                CTTG  GGATTGGAG   ACTA
                                  A_       TCCC
GAM2839  DBT      3'  TCGAACTCCTGACCTCAGGTGA 12554      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TCC
GAM2839  DNASE2   3'  TCGAACTCCTGACCTCAAGTGA 10712      AC   A    ___
              T                  TCGAAC  CCT ACTTT   TGAT
                                ||||||  ||| |||||   ||||
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                                AGCTTG  GGA TGGAG   ACTA
                                   A_   C    TTC
GAM2839  EGFL5    3'  TCGAACTCCTGACCTTGTGAT  44537      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM2839  FANCD2   3'  GAACTCCTGACCTTGTGAT   37513     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAA ACTA
                                  A_   C    C
GAM2839  FCMD     3'  TCGAACTCCTGGCCTCAAGTGA 27525      AC   AA   ___
            T                    TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM2839  GGCX     3'  TCGAACTCCTGGCCTCAAGTGA 9061       AC   AA   ___
            T                    TCGAAC  CCT  CTTT   TGAT
                                ||||||  |||  ||||   ||||
                                AGCTTG  GGA  GGAG   ACTA
                                   A_   CC    TTC
GAM2839  GPRK7    3'  GAACCCCTGACCTCATGAT   40180     A    A    _
                                GAAC CCCT ACTTT TGAT
                                |||| |||| ||||| ||||
                                CTTG GGGA TGGAG ACTA
                                  _    C    T
GAM2839  IAPP     3'  TCGAACTCCTGACCTTGTGAT  7665       AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAA ACTA
                                   A_   C    C
GAM2839  IL1R1    3'  TCGAACTCCTGACCTCTG    9369       AC   A
                                TCGAAC  CCT ACTTTTG
                                ||||||  ||| |||||||
                                AGCTTG  GGA TGGAGAC
                                   A_   C
GAM2839  JAG1     3'  TCAAACACCTTAATTTTG    6860        C   C
                                TCGAACACC TAA TTTTG
                                ||||||||| ||| |||||
                                AGTTTGTGG ATT AAAAC
                                     A  _
GAM2839  LRRC2    3'  TCGAACTCCTGACCTCATGAT  36000      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    T
GAM2839  LUZP1    3'  GAACTCCTGACCTTGTGAT   37961     AC   A    _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
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                                CTTG  GGA TGGAA ACTA
                                  A_  C    C
GAM2839  MCM4     3'  GAACTCCTGACCTCATGAT   41593     AC  A   _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_  C    T
GAM2839  MOG      3'  GAACTCCTGACCTCGTGAT   14611     AC  A   _
                                GAAC  CCT ACTTT TGAT
                                ||||  ||| ||||| ||||
                                CTTG  GGA TGGAG ACTA
                                  A_  C    C
GAM2839  NPHS1    3'  TCGAACTCCTGACCTCAGGTGA 21618      AC  A   ___
              T                  TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TCC
GAM2839  PDE4C    3'  TCGAACTCCTAACCTCAGGTGA 9559       AC      ___
              T                  TCGAAC  CCTAACTTT  TGAT
                                 ||||||  |||||||||  ||||
                                 AGCTTG  GGATTGGAG  ACTA
                                    A_       TCC
GAM2839  PHKB     3'  GAACTCCTAACCTCAAGTGAT  7122      AC      ___
                                 GAAC  CCTAACTTT  TGAT
                                 ||||  |||||||||  ||||
                                 CTTG  GGATTGGAG  ACTA
                                   A_       TTC
GAM2839  PPP1R12B 3'  TCGAACTCCTGACCTCGTGAT  36980      AC  A   _
                                 TCGAAC  CCT ACTTT TGAT
                                 ||||||  ||| ||||| ||||
                                 AGCTTG  GGA TGGAG ACTA
                                    A_  C    C
GAM2839  RAD1     3'  TCGAACTCCTGACCTCAGGTGA 15996      AC  A   ___
              T                  TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGGAG  ACTA
                                    A_  C    TCC
GAM2839  RBL1     3'  TCGAACTCCTGACTCCGGTGAT 16180      AC  A   __
                                 TCGAAC  CCT ACTTT  TGAT
                                 ||||||  ||| |||||  ||||
                                 AGCTTG  GGA TGAGG  ACTA
                                    A_  C    CC
GAM2839  RSN      3'  TCGAACACACAGTTGATAA   16405       CCTA  TT
                                 TCGAACAC   AC  TTGATAA
                                 ||||||||   ||  |||||||
                                 AGCTTGTG   TG  AACTATT
                                      ____  TC
GAM2839  SIGLEC11 3'  TCGAACTCCTGACTTGTGAT  38086      AC  A   T
                                 TCGAAC  CCT ACTT TGAT
                                 ||||||  ||| |||| ||||
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                                AGCTTG  GGA TGAA ACTA
                                   A_   C    C
GAM2839  SLC17A5   3'  TCGAACTCCTGATCTCATGAT  29691      A  CTAA   T
                                TCGAAC CC    CTT TGAT
                                |||||| ||    ||| ||||
                                AGCTTG GG    GAG ACTA
                                   A  ACTA   T
GAM2839  TBX6      3'  TCGAACTCCTGGCCTCAGGTGA 38861      AC   AA   ___
           T                     TCGAAC  CCT  CTTT   TGAT
                                 ||||||  |||  ||||   ||||
                                 AGCTTG  GGA  GGAG   ACTA
                                    A_   CC    TCC
GAM2839  TCTA      3'  TCGAACTCCTGACCTCGTGAT  35283      AC   A    _
                                TCGAAC  CCT ACTTT TGAT
                                ||||||  ||| ||||| ||||
                                AGCTTG  GGA TGGAG ACTA
                                   A_   C    C
GAM2839  TNFRSF1B  3'  TCGAACTCCTAACCTCAGGTGA 9876       AC       ___
           T                     TCGAAC  CCTAACTTT   TGAT
                                 ||||||  |||||||||   ||||
                                 AGCTTG  GGATTGGAG   ACTA
                                    A_       TCC
GAM2839  TNFSF14   3'  TCGAACTCCTGACCTCAGGTGA 19185      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM2839  TPM4      3'  TCGAACTCCTGACCTCAAGTGA 17650      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TTC
GAM2839  TRPM8     3'  TCGAACTCCTGACCTCAAGTGA 35862      AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TTC
GAM2839  VHL       3'  TCGAACTCCTGACCTCAGGTGA 8119       AC   A    ___
           T                     TCGAAC  CCT ACTTT   TGAT
                                 ||||||  ||| |||||   ||||
                                 AGCTTG  GGA TGGAG   ACTA
                                    A_   C    TCC
GAM2839  ZNF264    3'  TCGAACTCCTGGCCTCAGGTGA 18276      AC   AA   ___
           T                     TCGAAC  CCT  CTTT   TGAT
                                 ||||||  |||  ||||   ||||
                                 AGCTTG  GGA  GGAG   ACTA
                                    A_   CC    TCC
GAM2839  CBFA2T3   3'  TTGGAGTTGGGGCGATGG    23275       AAC   T
                                TTGGAGTT   GGT ATGG
                                ||||||||   ||| ||||
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                                AACCTCAA  CCG TACC
                                    CC_  C
GAM2839 SGCB    3' TTGCAGGGTTGTGGTGAG   6930     G TTAAC   A
                                TTG AG    GGTT TGGTGAG
                                ||| ||    |||| |||||||
                                AAC TC    CCAA ACCACTC
                                  G _____   C
GAM2840 FGFR1   5' TCCGCCGTGGCTTGTGCGA  35791        ATCCA
                                TCCGCCGTG    TGCGG
                                |||||||||    |||||
                                AGGCGGCAC    ACGCT
                                     CGAAC
GAM2840 RAD52   3' CCTGTCGTGATCCACAGT   39565   GC_     AT
                                CC  CGTGATCC  GCGGT
                                ||  ||||||||  |||||
                                GG  GCACTAGG  TGTCA
                                 ACA      __
GAM2840 DSP     5' AAGGATAGGCGGACGGCCG  20642      TCAT      A
                                AAGGGTA   GGCGGACG CCG
                                |||||||   |||||||| |||
                                TTCCTAT   CCGCCTGC GGC
                                   ____      C
GAM2840 PPP1CB  3' AAGGGTGTCAAATGGCTGG  15500      A __   _
                                AAGGGT TCA  TGGC GG
                                |||||| |||  |||| ||
                                TTCCCA AGT  ACCG CC
                                   C  TT   A
GAM2840 SLC30A4 5' GGGGGAGGCGGACGGCCG   30018    TATCAT      A
                                GGG     GGCGGACG CCG
                                |||     |||||||| |||
                                CCC     CCGCCTGC GGC
                                  CCT___      C
GAM2840 XK      3' AAGGGTATTATGGGGAAAC  34354       C   C   C
                                AAGGGTAT ATGG GGA GAC
                                |||||||| |||| ||| |||
                                TTCCCATA TACC CCT TTG
                                    A  _  _
GAM2841 KL      3' GGTTTATCTTGCCTGATACA  22005       A  AA  A
                                GGTTTATC TT  TT ATACA
                                |||||||| ||  || |||||
                                CCAAATAG AA  GA TATGT
                                   _ CG  C
GAM2841 FNTA    3' TATTACAAAACCGTTCT    12994          CCG
                                TATTACAAAATCG  TCT
                                ||||||||||||  |||
                                ATAATGTTTTGGC  AGA
                                      A__
GAM2841 MTMR7   5' ACAGGAAATCGCCGTCTA   42903    __
                                ACA  AAATCGCCGTCTA
                                |||  ||||||||||||
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                                TGT  TTTAGCGGCAGAT
                                  CC
GAM2841  PCDH11X   3'  CATTACAAAATCTATGTCTA  37297          GCC
                                TATTACAAAATC  GTCTA
                                ||||||||||||  |||||
                                GTAATGTTTTAG  CAGAT
                                      ATA
GAM2841  PCDH11Y   3'  CATTACAAAATCTATGTCTA  37337          GCC
                                TATTACAAAATC  GTCTA
                                ||||||||||||  |||||
                                GTAATGTTTTAG  CAGAT
                                      ATA
GAM2842  ADAMTS5   3'  ACAAGGGGGAGACAGTTCTGC  28173      A     G  A
                                ACGAG GGGAGAC AG TCTGC
                                ||||| ||||||| || |||||
                                TGTTC CCCTCTG TC AGACG
                                   C      _  A
GAM2842  CBS       3'  TAACGAGGGGAGACGGAT    6308        A     A
                                TAACGAG GGGAGACG GAT
                                ||||||| |||||||| |||
                                ATTGCTC CCCTCTGC CTA
                                     _      _
GAM2842  EFNA4     3'  GAGAGGGAAGGTCTG       23392        GACG  A
                                GAGAGGGA   AG TCTG
                                ||||||||   || ||||
                                CTCTCCCT   TC AGAC
                                     ____  C
GAM2842  MUS81     5'  TAACGAGAGGAGAGCCTG    36067          AGAC  A
                                TAACGAGAGGG   GAG TCTG
                                ||||||||||    ||| ||||
                                ATTGCTCTCCT   CTC GGAC
                                      ____  _
GAM2842  PXR1      3'  GATGAGCAGAGAGATCTG    7234     GA  G   C
                                GA  GG AGA GAGATCTG
                                ||  || ||| ||||||||
                                CT  TC TCT CTCTAGAC
                                 AC  G  _
GAM2842  STXBP1    3'  CGAGAGGGTACAGGGTCTG   17204        AG   AGA
                                CGAGAGGG  ACG   TCTG
                                ||||||||  |||   ||||
                                GCTCTCCC  TGT   AGAC
                                    A_   CCC
GAM2843  ATRN      3'  CAAGAACAACTGATGACGA   40289         GATATG
                                CAAGAACAAC     GATGA
                                ||||||||||     |||||
                                GTTCTTGTTG     CTGCT
                                      ACTA__
GAM2843  CLCA3     3'  CCCAGAGCAATGGTGTGGAT  22262     A  A   CGATA
                                CCCA GA CAA    TGGAT
                                |||| || |||    |||||
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                                GGGT CT GTT    ACCTA
                                  _ C  ACCAC
GAM2843  GPR44    3'  CCAAAAATACATGGATG    21952       CAACG
                                CCAAGAA    ATATGGATG
                                |||||||    |||||||||
                                GGTTTTT    TGTACCTAC
                                   A____
GAM2844  BRCA1    3'  CATTATCAACTGGCTT     28622         CATCAA
                                CATTATCAACT    GCTT
                                ||||||||||     ||||
                                GTAATAGTTGA    CGAA
                                      C_____
GAM2844  CLASP2   3'  TACATTATTAACTTTTTCAAG  42080       C   CA_
                                TACATTAT AACT  TCAAG
                                |||||||| ||||  |||||
                                ATGTAATA TTGA  AGTTC
                                     A   AAA
GAM2844  IL18RAP  3'  CATTGTCCATCAAGCTT    19291     A  AACT
                                CATT TC   CATCAAGCTT
                                |||| ||   ||||||||||
                                GTAA AG   GTAGTTCGAA
                                  C  ____
GAM2844  NAPB     3'  TACATTCATTCTCAAGCTT   43178     TA  AC  A
                                TACAT  TCA  TC TCAAGCTT
                                |||||  |||  || ||||||||
                                ATGTA  AGT  AG AGTTCGAA
                                  __  A_  _
GAM2844  DHFR     3'  TAATTTTTGTGTTTTTTGTAGA 8995       A       AA
                                TAATTT TGTGTTTTTT  GGA
                                ||||||| ||||||||||  |||
                                ATTAAA ACACAAAAAA  TCT
                                   A        CA
GAM2844  FLRT2    3'  TAAATTATGTGTTTTCTGAAG  29854    T         A
                                TAA TTATGTGTTTTTT AGG
                                ||| |||||||||||| |||
                                ATT AATACACAAAAGA TTC
                                  T          C
GAM2844  PKD2     3'  TAATTTATGGGTAGAAAGGA   41077       T  TTTTT
                                TAATTTATG GT    AAGGA
                                |||||||| ||    |||||
                                ATTAAATAC CA    TTCCT
                                     C  TCT__
GAM2844  SLC4A10  3'  ACTTATCTCTTTAAGGAAG   35190      GTG
                                ATTTAT   TTTTTTAAGGAAG
                                ||||||   |||||||||||||
                                TGAATA   GAGAAATTCCTTC
                                         ___
GAM2844  TGM2     5'  ATTTATGCTTTAAGGA     21438       GTTT
                                ATTTATGT   TTTAAGGA
                                ||||||||   ||||||||
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                                TAAATACG   AAATTCCT
                                    ____
GAM2845 DDX11    3' AATGTGATCTCGGGGTGGG   36163          CT_ C
                                AATGTGATCTTG  TG GG
                                ||||||||||||  || ||
                                TTACACTAGAGC  AC CC
                                     CCC  _
GAM2845 SERPINB13 3' ATGTGATCTTGTTAAAAACTGG 29620          CTT___ _
             AG                   ATGTGATCTTG    GC GGAG
                                ||||||||||||    || ||||
                                TACACTAGAAC    TG CCTC
                                     AATTTT  A
GAM2845 CREBL2   3' TCTGCAAGTATGGATTTG    10588         G  CTATTG
                                TCTGCAAGTA TG    TTG
                                ||||||||||| ||    |||
                                AGACGTTCAT AC    AAC
                                     _  CTA___
GAM2845 PAFAH1B1 3' TGAGAGTAGTGCTCTG     7725     CA       ATTG
                                TG  AGTAGTGCT   TTG
                                ||  |||||||||   |||
                                AC  TCATCACGA   GAC
                                 TC       ____
GAM2845 PMX1     3' CCTGTGCAGGGCTATTGTTGG  35507     CAA    T
                                TCTG   GTAG GCTATTGTTGG
                                ||||   |||| ||||||||||
                                GGAC   CGTC CGATAACAACC
                                  A__    C
GAM2845 SIGLEC7  3' TCTGAGTACTCATTGTTGG   32420     CAAGT     _
                                TCTG    AGTGCT ATTGTTGG
                                ||||    |||||| ||||||||
                                AGAC    TCATGA TAACAACC
                                  _____     G
GAM2845 TM4SF6   3' TCAGTAAGTAGTGTTGTCG   17587    TGC      CTA    TG
                                TC   AAGTAGTG   TTGT  G
                                ||   ||||||||   ||||  |
                                AG   TTCATCAC   AACA  C
                                 TCA       ___    GT
GAM2846 ADORA1   5' TGGACAACGCGCGGC      8596     CAC   C
                                TGG   GCG CGCGCGGC
                                |||   ||| ||||||||
                                ACC   TGT GCGCGCCG
                                  ___   T
GAM2846 ATP12A   5' TGGTGGCGCCGCGGGC     11728     CAC      C
                                TGG   GCGCCGCG GGC
                                |||   |||||||| |||
                                ACC   CGCGGCGC CCG
                                  AC_       _
GAM2846 CAPN10   3' TGGCACGCAGCTCAGC     35780         CC  G
                                TGGCACGCG  GC CGGC
                                |||||||||  || ||||
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                                ACCGTGCGT  CG GTCG
                                     __  A
GAM2846  DDX3     5'  TGGAGCGCACCGCGCGGC    10676     CA
                                TGG  CGCGCCGCGCGGC
                                |||  ||||||||||||
                                ACC  GCGTGGCGCGCCG
                                  TC
GAM2846  EEF2     3'  TGGCACGCAGCGGGC       45413         CC   C
                                TGGCACGCG  GCG GGC
                                |||||||||  ||| |||
                                ACCGTGCGT  CGC CCG
                                     __  _
GAM2846  EGR1     5'  TGGACGCGCCGCGGC       12671     C       GC
                                TGG ACGCGCCGC  GGC
                                ||| |||||||||  |||
                                ACC TGCGCGGCG  CCG
                                  _       __
GAM2846  EHD3     5'  TGGCCCGGGCACGCGGC     31118     A  C  C
                                TGGC CG GC GCGCGGC
                                |||| || || |||||||
                                ACCG GC CG TGCGCCG
                                  G  C  _
GAM2846  EPM2A    5'  TGGGATGCATCACGCGGC    24975     CAC   C
                                TGG   GCG CGCGCGGC
                                |||   ||| ||||||||
                                ACC   CGT GTGCGCCG
                                  CTA   A
GAM2846  FGF18    5'  TGTCCGCTCCGCGCGGC     19304    GCA   G
                                TG   CGC CCGCGCGGC
                                ||   ||| |||||||||
                                AC   GCG GGCGCGCCG
                                 AG_   A
GAM2846  G1P3     5'  TGGCGCCGCGCGCGGGC     35641     A_    C   C
                                TGGC  CGCGC GCG GGC
                                ||||  ||||| ||| |||
                                ACCG  GCGCG CGC CCG
                                  CG    _  _
GAM2846  GCGR     3'  TGGCACGCAGTTCACGGC    6697          CCG
                                TGGCACGCG   CGCGGC
                                |||||||||   ||||||
                                ACCGTGCGT   GTGCCG
                                     CAA
GAM2846  GPI      5'  TGGGCGCGCGGCGGC       6751      CA    C C
                                TGG  CGCGC G GCGGC
                                |||  ||||| | |||||
                                ACC  GCGCG C CGCCG
                                  C_    _ _
GAM2846  HIC1     5'  TGGCGCCGCGGAGCCCGGC   44571      A_   CC  G
                                TGGC  CGCG  GC CGGC
                                ||||  ||||  || ||||
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                                ACCG  GCGC  CG GCCG
                                  CG    CT  G
GAM2846  HOXA3    3'  TGGCCCGCCGCACGGC      36201      ACG
                                TGGC   CGCCGCGCGGC
                                ||||   ||||||||||
                                ACCG   GCGGCGTGCCG
                                  G__
GAM2846  HR       5'  TGGCACGCCCCACTGGC      32936        G   GC
                                TGGCACGC CCGC  GGC
                                |||||||| ||||  |||
                                ACCGTGCG GGTG  CCG
                                    G   A_
GAM2846  IGFBP4   5'  GGCGCGCGGGCGAGCGGC    11404     A   C_  C
                                GGC CGCG  CG GCGGC
                                ||| ||||  || |||||
                                CCG GCGC  GC CGCCG
                                  C   CC  T
GAM2846  KLF4     5'  TGGAGCGCGCGCGGC       20157     CAC   C
                                TGG   GCGC GCGCGGC
                                |||   |||| |||||||
                                ACC   CGCG CGCGCCG
                                  T__   _
GAM2846  MADD     5'  TGGCCGCGCCGCGGC       39072      A      GC
                                TGGC CGCGCCGC  GGC
                                |||| ||||||||  |||
                                ACCG GCGCGGCG  CCG
                                  _     __
GAM2846  MT3      5'  TGGACGCGCGGCTTGGC      25543     C     C  GC
                                TGG ACGCGC GC  GGC
                                ||| ||||||  ||  |||
                                ACC TGCGCG CG  CCG
                                  _    C  AA
GAM2846  MTNR1B   5'  TGGCCACCGCGCGGC       25557      ACG
                                TGGC   CGCCGCGCGGC
                                ||||   ||||||||||
                                ACCG   GTGGCGCGCCG
                                   ___
GAM2846  PDXK     5'  TGGCGCGCGGCGGAC       18970      AC   C   C
                                TGGC  GCGC GCG GGC
                                ||||  |||| ||| |||
                                ACCG  CGCG CGC CTG
                                   __   C   _
GAM2846  PKP1     5'  TGGCGCGCGGCCGGGGC      7152       A   _   CGC
                                TGGC CGCG CCG   GGC
                                |||| |||| |||   |||
                                ACCG GCGC GGC   CCG
                                  C   C   C__
GAM2846  POLS     3'  TAGCACGCGACCACAGTGG    28123          _    C_
                                TGGCACGCG CCGCG  GG
                                |||||||| |||||  ||
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                                ATCGTGCGC GGTGT  CC
                                     T    CA
GAM2846  PRex1    5'  TAGCGCGGCCGCGCGGC     34073      A  C
                                TGGC CG GCCGCGCGGC
                                |||| || ||||||||||
                                ATCG GC CGGCGCGCCG
                                  C  _
GAM2846  PTMA     5'  GGCGCGCGGCGGAGGCGGC    15871     A   C  C__
                                GGC CGCG CG   GCGGC
                                ||| |||| ||   |||||
                                CCG GCGC GC   CGCCG
                                  C   C  CTC
GAM2846  PTP4A2   5'  CGGCGCGCGACACCCGGC    38625      A   C   G
                                TGGC CGCG CGC CGGC
                                |||| |||| ||| ||||
                                GCCG GCGC GTG GCCG
                                  C   T   G
GAM2846  TNFRSF11A 5'  TGGCGGGCGCCGCGGC      19282      AC      GC
                                TGGC  GCGCCGC  GGC
                                ||||  |||||||  |||
                                ACCG  CGCGGCG  CCG
                                  CC      __
GAM2846  WDR8     5'  TGGGCGCGCAGCAGGC      32823     CA    C   C
                                TGG  CGCGC GCG GGC
                                |||  ||||| ||| |||
                                ACC  GCGCG CGT CCG
                                  C_    T   _
GAM2847  SCA1     3'  TTTAAGAATTGTAAGTGGGGGT 7302          GAA    A  A
                                TTTAAGAAT   TGAG TG GGGT
                                |||||||||   |||| || ||||
                                AAATTCTTA   ATTC AC CCCA
                                     AC_    _ C
GAM2847  SERPINF2  3'  GAAGAAAGATGAGGG       9590      T  AT
                                GAA GA  GAGATGAGGG
                                ||| ||  ||||||||||
                                CTT CT  TTCTACTCCC
                                  _ __
GAM2847  AMY2B    5'  TCAATTTCTTCCTCTCAAAGT  34159      ATC         TC
                                TCAA   TCTTCCTCTTA  GT
                                ||||   ||||||||||| ||
                                AGTT   AGAAGGAGAGT  CA
                                  AA_          TT
GAM2847  CEBPD    3'  TCAGTCTTTTCCTCTTAT    45520     AA   C
                                TCA  TCT TTCCTCTTAT
                                |||  ||| ||||||||||
                                AGT  AGA AAGGAGAATA
                                  C_   A
GAM2847  HLF      5'  TCAAATTTTTTCCCCTTA    13395       CTC
                                TCAAAT   TTCCTCTTA
                                ||||||   |||||||||
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                                AGTTTA  AAGGGGAAT
                                   AAA
GAM2847 MS4A4A   5' TCGAATCTCTCTCCTTTTA  35852   A    _  C
                                TC AATCTCT TCCT TTA
                                || ||||||| |||| |||
                                AG TTAGAGA AGGA AAT
                                 C     G   A
GAM2847 TEX15    3' TCAAATCTCTTACTTCTTTCGG 36327        C _  A  T
           T                    TCAAATCTCTT CT CTT TCG GT
                                |||||||||||| || ||| ||| ||
                                AGTTTAGAGAA GA GAA AGC CA
                                      T  A  _  _
GAM2848 COL4A3   3' ACATTTGATACATAGA     36376        TATGAG
                                ACATTTGAT    ATAGA
                                |||||||||    |||||
                                TGTAAACTA    TATCT
                                     TG____
GAM2848 GNRH1    5' TTTCATTCCTGAGATAGA    9080     G  A_
                                TTT ATT  TGAGATAGA
                                ||| |||  |||||||||
                                AAA TAA  ACTCTATCT
                                  G  GG
GAM2848 GRINL1A  3' TTCACATTTGCTTGAG     43005        ATTA
                                TTCACATTTG   TGAG
                                ||||||||||   ||||
                                AAGTGTAAAC   ACTC
                                     GA__
GAM2848 LSS      3' TTCACATCTATGAGATAGAG  14250       TGAT
                                TTCACATT   TATGAGATAGAG
                                ||||||||   ||||||||||||
                                AAGTGTAG   ATACTCTATCTC
                                     ____
GAM2848 MTM1     3' TTCACATTTGGATTCATCTTAG 7008         _  ATGAGA
           AG                     TTCACATTTG ATT    TAGAG
                                ||||||||||| |||    |||||
                                AAGTGTAAAC TAA    ATCTC
                                     C  GTAGA_
GAM2848 SCA1     5' TCACATTTGATTTCTGTAG   7286          A_ _
                                TCACATTTGATT  TG AG
                                ||||||||||||  || ||
                                AGTGTAAACTAA  AC TC
                                      AG  A
GAM2848 SLC6A8   3' TTCACCTTTGCTAAGAGATAGA 24793     A   A  T
           G                     TTCAC TTTG TTA GAGATAGAG
                                ||||| |||| ||| |||||||||
                                AAGTG AAAC GAT CTCTATCTC
                                   G   _  T
GAM2849 AGM1     3' TGTATACTTAAGTCCCAG    31817       _  _ A
                                TGTATACT AAG CC AG
                                |||||||| ||| || ||
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                                ACATATGA TTC GG TC
                                     A  A  G
GAM2849  DAZL     3'  TGACATACAGCCAAGTTTAG  42780    _    TA
                                TG TATAC  AGCCAAGTTTAG
                                || |||||  ||||||||||||
                                AC GTATG  TCGGTTCAAATC
                                 T    __
GAM2849  PTGFRN   3'  TATATACTCCAAGTTT     42596        AAG
                                TGTATACT   CCAAGTTT
                                ||||||||   ||||||||
                                ATATATGA   GGTTCAAA
                                     ___
GAM2850  ANXA3    3'  TTTAATGGAGTAGAACTA    23105    C       TTT
                                TTT ATGGAGTGG   GCTA
                                ||| |||||||||   ||||
                                AAA TACCTCATC   TGAT
                                  T       T__
GAM2850  BTC      3'  TCTCATGGATTGCT       45541         GTGGT
                                TTTCATGGA    TTGCT
                                |||||||||    |||||
                                AGAGTACCT    AACGA
                                     _____
GAM2850  C9       3'  TTTCATGAAGCATGTTGCTA  11933          GT
                                TTTCATGGAGTG  TTGCTA
                                ||||||||||||  ||||||
                                AAAGTACTTCGT  AACGAT
                                      AC
GAM2850  CBFA2T3  3'  TTTCAGGGAGGCCTGCT    23276      T   GT
                                TTTCA GGA  GGTTTGCT
                                ||||| |||  ||||||||
                                AAAGT CCT  CCGGACGA
                                   C  __
GAM2850  CEBPA    3'  TCTCATGGGGGTCTGCT    20400        AGT
                                TTTCATGG   GGTTTGCT
                                ||||||||   ||||||||
                                AGAGTACC   CCAGACGA
                                     C__
GAM2850  CELL     3'  CTTCATGGAGCTGCT      12225          GGTT
                                TTTCATGGAGT    TGCT
                                ||||||||||    ||||
                                GAAGTACCTCG    ACGA
                                     ____
GAM2850  CNTN3    3'  TCTCATGGAGATATATTGCTA  42487         TGGT_
                                TTTCATGGAG    TTGCTA
                                ||||||||||    ||||||
                                AGAGTACCTC    AACGAT
                                      TATAT
GAM2850  DSCR3    3'  TTTCATGGGTGAAGCC      25832        A   TTT
                                TTTCATGG GTGG   GCT
                                |||||||| ||||   |||
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                                AAAGTACC CACT   CGG
                                   _   T__
GAM2850  EHD2    3'  TTCCATGGGGTCCCCT     31139       AGT    G
                                TTTCATGG  GGTTT CT
                                ||||||||  ||||| ||
                                AAGGTACC  CCAGG GA
                                   ___    G
GAM2850  FLRT2   3'  TTTCATGGGTTGTCCTGCTA  29869       AG  GT
                                TTTCATGG  TG  TTGCTA
                                ||||||||  ||  ||||||
                                AAAGTACC  AC  GACGAT
                                    CA  AG
GAM2850  GAB2    3'  TCCACTTTGGTTTGCT     29382      GGAG
                                TTCAT   TGGTTTGCT
                                |||||   |||||||||
                                AGGTG   ACCAAACGA
                                  AA__
GAM2850  GNRHR   5'  TTTCATGGTGAGTGCT     7620        AG   TT
                                TTTCATGG  TGG  TGCT
                                ||||||||  |||  ||||
                                AAAGTACC  ACT  ACGA
                                   __  C_
GAM2850  GOLGA4  5'  TTTCATGGAATAAACT     41063          TTT
                                TTTCATGGAGTGG   GCT
                                ||||||||||||   |||
                                AAAGTACCTTATT   TGA
                                          ___
GAM2850  GPR23   5'  TTTCAGGAGGCCTGCT     41320      T   GT
                                TTTCA GGA  GGTTTGCT
                                |||||  |||  ||||||||
                                AAAGT CCT  CCGGACGA
                                  _  __
GAM2850  ITPR2   3'  TTTCCTGGGGCTTACT     13682      A   AGT
                                TTTC TGG   GGTTTGCT
                                ||||  |||   ||||||||
                                AAAG ACC   CCGAATGA
                                  G  ___
GAM2850  LAPTM5  3'  TTTCATGGAATCCACTGCTA  27611          GGT
                                TTTCATGGAGT   TTGCTA
                                ||||||||||   ||||||
                                AAAGTACCTTA   GACGAT
                                      GGT
GAM2850  MAN1A1  3'  TTTCATGGAAGTATATCTA   45102         _  GTTTG
                                TTTCATGGA GTG    CTA
                                |||||||||  |||    |||
                                AAAGTACCT CAT    GAT
                                     T  ATA__
GAM2850  PPARGC1 3'  CTTCATGGAACTGCT      29952          TGGT
                                TTTCATGGAG    TTGCT
                                ||||||||||    |||||
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                              GAAGTACCTT   GACGA
                                   ____
GAM2850 PPP3CA   3' TTTCACAAGGTTTGCTA    9619      TG AGT
                              TTTCA G  GGTTTGCTA
                              |||||  |  |||||||||
                              AAAGT  T  CCAAACGAT
                                 GT ___
GAM2850 PSG3     3' TTTCATGAAGTATCAGCC    34256          GTTT
                              TTTCATGGAGTG   GCT
                              ||||||||||||   |||
                              AAAGTACTTCAT   CGG
                                     AGT_
GAM2850 SPAG11   5' TTTGATGGAGTGAGGCT     38482     C       TTT
                              TTT ATGGAGTGG  GCT
                              ||| |||||||||  |||
                              AAA TACCTCACT  CGA
                                C       C__
GAM2850 WARS     3' TTTCTGGAGTGGACT      42625     A      TTT
                              TTTC TGGAGTGG  GCT
                              |||| ||||||||  |||
                              AAAG ACCTCACC  TGA
                                _      ___
GAM2850 XPR1     3' TTTCATGAATCTGCT      21855       AGTG
                              TTTCATGG   GTTTGCT
                              ||||||||   |||||||
                              AAAGTACT   TAGACGA
                                   _____
GAM2851 ADAT1    3' GATTACAGGTGTGCGCCAC   28996    A    A  GC
                              GA TACAG GTG  TGCGCCAC
                              || ||||| |||  ||||||||
                              CT ATGTC CAC  ACGCGGTG
                               A    _  __
GAM2851 ALDH3B1  3' GATTACAGGCATGCGCCAC   45063    A   GAGT  _
                              GA TACA   GGC TGCGCCAC
                              || ||||   ||| ||||||||
                              CT ATGT   CCG ACGCGGTG
                               A   _____  T
GAM2851 ANKH     3' GATTACAGGTATGTGCTAC   38317    A    A_  _
                              GA TACAG  GTG GCTGC
                              || |||||  ||| |||||
                              CT ATGTC  TAC CGATG
                               A    CA  A
GAM2851 BCAS1    3' GACTACAGGTGTGTGCCAC   18921    A    A  GC  C
                              GA TACAG GTG  TG GCCAC
                              || ||||| |||  || |||||
                              CT ATGTC CAC  AC CGGTG
                               G    _  __ A
GAM2851 CARKL    3' GATTACAGGCATGCGCCAC   29995    A   GAGT  _
                              GA TACA   GGC TGCGCCAC
                              || ||||   ||| ||||||||
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                                CT ATGT   CCG ACGCGGTG
                                 A   ____  T
GAM2851  CEACAM5  3'  GACTACAGGTGCGCGCCAC   20374    A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
                                CT ATGTC CAC G CGCGGTG
                                 G   _  _ _
GAM2851  CHST5    3'  GATTACAGGAGTGTGCCAC   29077    A   _   _ TG
                                GA TACAG AGTG GC  C
                                || ||||| |||| ||  |
                                CT ATGTC TCAC CG  G
                                 A    C   A  GT
GAM2851  CYR61    3'  TAGAGTGCAGATAGCTGC    11418     ATA   G
                                TAGA   CAGA TGGCTGC
                                ||||   |||| |||||||
                                ATCT   GTCT ATCGACG
                                  CAC   _
GAM2851  DHFR     3'  GAATACAGGTGTGCGCCAC   8993        A   GC
                                GAATACAG GTG  TGCGCCAC
                                |||||||| |||  ||||||||
                                CTTATGTC CAC  ACGCGGTG
                                     _  __
GAM2851  DNM2     3'  TAGAATACAGAGTGCAGGCAC  22387           G T_
                                TAGAATACAGAGTG C  GCGC
                                |||||||||||||| |  ||||
                                ATCTTATGTCTCAC G  CGTG
                                       _ TC
GAM2851  GALNT7   3'  GATTACAGGTATGCGCCAC   38358    A    A   GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAT  ACGCGGTG
                                 A    _  __
GAM2851  GNG2     5'  TAGAATCAGAGTGGTGGC    45438       A      C  C
                                TAGAAT CAGAGTGG TG GC
                                |||||| |||||||| || ||
                                ATCTTA GTCTCACC AC CG
                                     _      _ _
GAM2851  GPR81    3'  ACACAGAGTGAGACTCTG    37185          ____
                                ATACAGAGTGG    CTG
                                ||||||||||    |||
                                TGTGTCTCACT    GAC
                                      CTGA
GAM2851  HIP1     3'  GATTACAGGCATGCGCCAC   23753    A   GAGT  _
                                GA TACA    GGC TGCGCCAC
                                || ||||    ||| ||||||||
                                CT ATGT    CCG ACGCGGTG
                                 A   _____  T
GAM2851  IL10     3'  GATTACAGGTGCGCGCCAC   8195     A    A   G T
                                GA TACAG GTG C GCGCCAC
                                || ||||| ||| | |||||||
```

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                                CT ATGTC CAC G CGCGGTG
                                 A    _  _ _
GAM2851  IL13RA1  3'  GATTACAGGCACGCGCCAC   11444    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG GCGCGGTG
                                 A  _____  T
GAM2851  ITGAL    3'  GACTACAGGTGTGTGCCAC   13617    A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CAC  AC CGGTG
                                 G   _  __ A
GAM2851  KCNA7    3'  GATCACAGGCATGTGCCAC   36656    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT GTGT   CCG AC CGGTG
                                 A  _____  T  A
GAM2851  KIF1B    3'  GAATTACAGGCATGTGCCAC  31464     _  GAGT  _  C
                                GAAT ACA   GGC TG GCCAC
                                |||| |||   ||| || |||||
                                CTTA TGT   CCG AC CGGTG
                                  A  _____  T  A
GAM2851  KNSL1    3'  GATTACAGGAGTGTGCCAC   21178    A   _   _ TG
                                GA TACAG AGTG GC  C
                                || ||||| |||| ||  |
                                CT ATGTC TCAC CG  G
                                 A   C   A  GT
GAM2851  LAMC1    3'  TAAAATAATGGCTG       14091       CAGA
                                TAGAATA   GTGGCTG
                                |||||||   |||||||
                                ATTTTAT   TACCGAC
                                    ____
GAM2851  LDLR     3'  GATCACAGGCACGTGCCAC   8027     A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT GTGT   CCG GC CGGTG
                                 A  _____  T  A
GAM2851  MSH3     3'  GACTACAGGTGTGCGCCAC   14631    A   A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CAC  ACGCGGTG
                                 G   _  __
GAM2851  NPHS1    3'  GACTACAGGCATGCGCCAC   21617    A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 G  _____  T
GAM2851  POLK     3'  GATTACAGGCGTGTGCCAC   32138    A   A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
```

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                                CT ATGTC CGC  AC CGGTG
                                 A    _  __ A
GAM2851  PSD      5'  GACTACAGGCGTGCGCCAC   15785    A    A  GC
                                GA TACAG GTG  TGCGCCAC
                                || ||||| |||  ||||||||
                                CT ATGTC CGC  ACGCGGTG
                                 G    _  __
GAM2851  PTAFR    3'  GACTACAGGCGTGTGCCAC   9628     A    A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G    _  __ A
GAM2851  RPN1     5'  GATTACAGGCATGTGCCAC   16393    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   _____  T  A
GAM2851  SLC25A15 3'  GACTACAGGCACGTGCCAC   30668    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG GC CGGTG
                                 G   _____  T  A
GAM2851  SLC2A6   3'  GAACTACGGGTGTGTGCCAC  32770     _  AGA  GC  C
                                GAAT AC   GTG  TG GCCAC
                                |||| ||   |||  || |||||
                                CTTG TG   CAC  AC CGGTG
                                  A  CC_   __ A
GAM2851  SOX11    3'  TAGAGTAACAGTTGTGCTGC  17037     AT_   AG  _
                                TAGA   ACAG  TG GCTGC
                                ||||   ||||  || |||||
                                ATCT   TGTC  AC CGACG
                                  CAT    A_  A
GAM2851  STK38    5'  GATTACAGCGATGCGCTAC   28579    A    A_  _
                                GA TACAG  GTG GCTGC
                                || |||||  ||| |||||
                                CT ATGTC  TAC CGATG
                                 A    GC   G
GAM2851  SUV39H2  3'  GACTACAGGCGTGTGCCAC   36014    A    A  GC  C
                                GA TACAG GTG  TG GCCAC
                                || ||||| |||  || |||||
                                CT ATGTC CGC  AC CGGTG
                                 G    _  __ A
GAM2851  TEM7     3'  ATACAGGCAAGCGTCAC     33801       A TG CT   C
                                ATACAG G  G  GCG CAC
                                |||||| |  |  ||| |||
                                TATGTC C  T  CGC GTG
                                   _ GT __   A
GAM2851  TPM4     3'  GACTACAGGCAGGCGTCAC   17647    A    A TG CT   C
                                GA TACAG G  G  GCG CAC
                                || ||||| |  |  ||| |||
```

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                                CT ATGTC C  C  CGC GTG
                                 G    _ GT __   A
GAM2851  UC28    3'  GATTACAGGCATGTGCCAC   34691    A   GAGT  _  C
                                GA TACA   GGC TG GCCAC
                                || ||||   ||| || |||||
                                CT ATGT   CCG AC CGGTG
                                 A   ____  T  A
GAM2851  VDR     3'  GATTACAGGCTTGCGCCAC   7519     A   GAGT  _
                                GA TACA   GGCT GCGCCAC
                                || ||||   |||| |||||||
                                CT ATGT   CCGA CGCGGTG
                                 A   ____   A
GAM2851  VHL     3'  GATTACAGATGTGTGCCGC   8110     A    _  _
                                GA TACAGA GTG GCTGC
                                || |||||| ||| |||||
                                CT ATGTCT CAC CGGCG
                                 A     A  A
GAM2851  VHL     3'  GATTACAGGCATGCGCCAC   8111     A   GAGT  _
                                GA TACA   GGC TGCGCCAC
                                || ||||   ||| ||||||||
                                CT ATGT   CCG ACGCGGTG
                                 A   ____  T
GAM2852  KCNF1   3'  AGTCTGTCCAGGGGAGGGTT  13826       AGTTC   A
                                AGTCTGTC    GGAG GTT
                                ||||||||    |||| |||
                                TCAGACAG    CCTC CAA
                                     GTCC_   C
GAM2852  M11S1   3'  TAGTTTGTCAGTTATCATTGA  25330     C     __  GA
                                TAGT TGTCAGT  TCG  GA
                                |||| |||||||  |||  ||
                                ATCA ACAGTCA  AGT  CT
                                  A      AT   AA
GAM2852  MAP3K7IP2 3'  TCTGTCAGTGGGTTA      31524       TC  AGA
                                TCTGTCAGT  GG   GTTA
                                |||||||||  ||   ||||
                                AGACAGTCA  CC   CAAT
                                     __  ___
GAM2852  NID     3'  AGTCTGTCTGAGGGTT      14795       AGTTCG  A
                                AGTCTGTC    GAG GTT
                                ||||||||    ||| |||
                                TCAGACAG    CTC CAA
                                     A_____  C
GAM2853  DLST    3'  GAGATTGTGCCAAGACGA    12573    C  CTAA  C
                                GA GA   GCC AAGACGA
                                || ||   ||| |||||||
                                CT CT   CGG TTCTGCT
                                 _ AACA  _
GAM2854  TOX     3'  CTCAGGCAGATTCTCAAGCACT 31271     A  CTATT  C
                                TTCA GT    TTC CAAGCACT
                                |||| ||    ||| ||||||||
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                                GAGT CG    AAG GTTCGTGA
                                  C  TCT__   A
GAM2855  AHCY    3'  CCCTGTGGCTGGGACC     8661      AC  C  A  AT
                                CCCT  GT GG CT  GGGACC
                                ||||  || || ||  ||||||
                                GGGA  CA CC GA  CCCTGG
                                  __  _  _  __
GAM2855  ARHGEF6  3'  CCATGTAGCTATGGGACCT   42797    C  C  A
                                CTA GT GG CTATGGGACCT
                                ||| || || ||||||||||
                                GGT CA TC GATACCCTGGA
                                 A  _  _
GAM2855  AVPR1A   5'  CCCTACGTCGGTGTTTGTCCTC 8724          ACTA  GGA
                                CCCTACGTCGG   TG   CCTC
                                ||||||||||    ||   ||||
                                GGGATGCAGCC   AC   GGAG
                                      ACAA  A__
GAM2855  CLASP1   3'  CCTATGCACTATGGGGCCT   42237     C  CGG      A
                                CCTA GT   ACTATGGG CCT
                                |||| ||   |||||||| |||
                                GGAT CG   TGATACCC GGA
                                  A  ___       C
GAM2855  DXYS155E 3'  CCTGTCTTTGCTGTGGGACCTC 22950     AC   GGA_  A
                                CCT  GTC    CT TGGGACCTC
                                |||  |||    || |||||||||
                                GGA  CAG    GA ACCCTGGAG
                                  __   AAAC  C
GAM2855  ITSN1    3'  CCCTGTTGAGGGCTATGGGA   16654     ACGTC  A
                                CCCT    GG CTATGGGA
                                ||||    || ||||||||
                                GGGA    CC GATACCCT
                                  CAACT  C
GAM2855  TRRAP    3'  CCCAGTGAAACTATGGG     18589     C  CG
                                CCTA GT  GACTATGGG
                                |||| ||  |||||||||
                                GGGT CA  TTGATACCC
                                  _  CT
GAM2855  WNT3A    3'  CCCATCTCAGGGCTGTGGGACC 37538     CG   A_  A
            T                    CCTA  TCGG  CT TGGGACCT
                                ||||  ||||  || ||||||||
                                GGGT  AGTC  GA ACCCTGGA
                                  AG   CC  C
GAM2856  DIA1     3'  TGGGGGTGACAGGCGTGGC   28796    A  AC   TACTCC
                                TG GG  GAC     GTGTGGC
                                || ||  |||     |||||||
                                AC CC  CTG     CGCACCG
                                 C  CA   TC_____
GAM2856  GUCY1B2  3'  TGAGGACGGTTGCATGAGTGGG 19966        ACTACTCC_   T
            CT                   TGAGGACG       GTG GGCT
                                ||||||||       ||| ||||
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                                ACTCCTGC       CAC CCGA
                                     CAACGTACT  _
GAM2856 MAN2A2   3' CGGGATGGGATACCCGTGTGGC 25946    A  C__  C  T
             T                    TG GGA  GA TAC CCGTGTGGCT
                                  || |||  || ||| ||||||||||
                                  GC CCT  CT ATG GGCACACCGA
                                    _  ACC  _  _
GAM2856 NHLH1    3' GGCAGACTCCAAGTGTGGCT  24652    AC   A  CC
                                  GG  GACT CT  GTGTGGCT
                                  ||  |||| ||  ||||||||
                                  CC  CTGA GG  CACACCGA
                                   GT   _ TT
GAM2856 WDR3     3' TGAGGACGCTGTTCTGGG    27691        A  AC  CG  T
                                  TGAGGACG CT  TC  TG GG
                                  |||||||| ||  ||  || ||
                                  ACTCCTGC GA  AG  AC CC
                                       _ CA  __  _
GAM2856 ZNF36    3' GGCGATGACTACTTACACAGCT 45294    AC__      CC TG
                                  GG   GACTACT  G  TGGCT
                                  ||   |||||||  |  |||||
                                  CC   CTGATGA  T  GTCGA
                                   GCTA      A_ GT
GAM2857 CACNA1D  3' TAACGACACGAGGT       8766       GTTTC
                                  TGACGA    TACGAGGT
                                  ||||||    ||||||||
                                  ATTGCT    GTGCTCCA
                                       ______
GAM2857 COL4A6   3' TGACGAGTGTCCGGT      37978        T  ACGA
                                  TGACGAGT TCT   GGT
                                  |||||||| |||   |||
                                  ACTGCTCA AGG   CCA
                                       C  _____
GAM2857 PTGIS    3' TGAGAGTAACGAGGT      9678     C   TTCT
                                  TGA GAGT   ACGAGGT
                                  ||| ||||   |||||||
                                  ACT CTCA   TGCTCCA
                                    _   T___
GAM2857 PTTG1IP  3' TGACGAGTTCTTGAAGT    20292        T  AC
                                  TGACGAGTT CT  GAGGT
                                  ||||||||| ||  |||||
                                  ACTGCTCAA GA  CTTCA
                                       _ A_
GAM2857 TR2      5' CGATGAGGCCCACGAGGT   43634    C   TT
                                  TGA GAG  TCTACGAGGT
                                  ||| |||  ||||||||||
                                  GCT CTC  GGGTGCTCCA
                                    A  C_
GAM2857 WHSC1    3' TGAAGAGTTTCCCCCACAGGT 39385    C      A_ _
                                  TGA GAGTTTCT  CG AGGT
                                  ||| ||||||||  || ||||
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```
                                ACT CTCAAAGG  GT TCCA
                                  T       GG  G
GAM2857 ADAR     3'  TGGGGGAAAAAAGGGGGGCC  31913    TA      AA   AT
                                TG  GGAAAAA  AGG  GGTT
                                ||  |||||||  |||  ||||
                                AC  CCTTTTT  TCC  CCGG
                                 CC       __   CC
GAM2857 ATP6V1A1 3'  TGAGGAAAAGGAAATCACAGTT 11781    T      A_   GG
             GT                   TG AGGAAAA  AAA  ATGGTTGT
                                || |||||||  |||  ||||||||
                                AC TCCTTTT  TTT  TGTCAACA
                                 _      CC   AG
GAM2857 BAZ2A    3'  TGTAGGAATAAGAGGATG    30318        AAAAA
                                TGTAGGAA    AGGATG
                                ||||||||    ||||||
                                ACATCCTT    TCCTAC
                                     ATTC_
GAM2857 CALB1    3'  TGTGGGACAGTTCTATGGTTGT 22314     A   AAAAAAAGG
                                TGT GGA       ATGGTTGT
                                ||| |||       ||||||||
                                ACA CCT       TACCAACA
                                  C   GTCAAGA__
GAM2857 CALCA    3'  TAGGAAGGAAAGGGAGGAGT   11940       AAA    AT  TT
                                TAGGAA   AAAGG  GG  GT
                                ||||||   |||||  ||  ||
                                ATCCTT   TTTCC  CC  CA
                                    CC_    CT  T_
GAM2857 FKBP1A   3'  TGCAGGGGGAAAAATAGCC    38285       AAAAAA
                                TGTAGG     AAGGATGGTT
                                ||||||     ||||||||||
                                ACGTCC     TTTTTATCGG
                                    CCC___
GAM2857 GLUL     3'  ATAGGGAAAAAAAGGAGGGT   13152       A        T
                                GTAGG AAAAAAAGGA GGT
                                ||||| |||||||||| |||
                                TATCC TTTTTTTCCT CCA
                                   C        C
GAM2857 HS2ST1   3'  TGAGGGAAAAAAAAGGCACTGT 29342    TA         ATGG
                                TG  GGAAAAAAAAGG    TTGT
                                ||  ||||||||||||    ||||
                                AC  CCTTTTTTTTCC    GACA
                                 TC          GT__
GAM2857 MAGEA10  5'  TGTAGAAAAGAGGGGTT     34332        AAAA   AT
                                TGTAGGAAA    AGG  GGTT
                                |||||||||    |||  ||||
                                ACATCTTTT    TCC  CCAA
                                      C___   __
GAM2857 MAPK1    3'  TGTAGAAGGAAAAAGAAT     15657        AA
                                TGTAGGA  AAAAAGGAT
                                |||||||  |||||||||
```

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                                ACATCTT  TTTTTCTTA
                                    CC
GAM2857  MEN1    5'  TGAGGAAAAAGATCAGGTTGT  39235   T     AAAA   __
                                TG AGGAAAA   GGAT  GGTTGT
                                || |||||||   ||||  ||||||
                                AC TCCTTTT   TCTA  CCAACA
                                 _     _____   GT
GAM2857  PCTP    3'  TGAGGAAAAATGTGGTTG   34536   T     AAAGGA
                                TG AGGAAAAA     TGGTTG
                                || |||||||||     ||||||
                                AC TCCTTTTT     ACCAAC
                                 _      AC_____
GAM2857  RASGRP1  3'  TGTAGTGAGGAAGGAGGGT   25082      _ AAAAA   T
                                TGTAG GA    AAGGA GGT
                                ||||| ||    ||||| |||
                                ACATC CT    TTCCT CCA
                                   A  CC___    C
GAM2857  SDHC    3'  TGTGGGCAAAAAAGGGGAGT   42982    A  AA      AT
                                TGT GG  AAAAAAGG  GGT
                                ||| ||  ||||||||  |||
                                ACA CC  TTTTTTCC  TCA
                                 _ CG       CC
GAM2857  TEM7    3'  TGAGGAAGAAAAAGGACAGT   33815   T   A
                                TG AGGAA AAAAAGGATGGT
                                || ||||| ||||||||||||
                                AC TCCTT TTTTTCCTGTCA
                                 _    C
GAM2857  TPI1    3'  TGTAAGAAGGGAGAGGATGGT  7480        AAAAA
                                TGTAGGAA    AGGATGGT
                                ||||||||    ||||||||
                                ACATTCTT    TCCTACCA
                                     CCCTC
GAM2857  UFD1L   3'  TGTAGGAAAAGAAAGGAT    43827         A
                                TGTAGGAAAA AAAGGAT
                                |||||||||| |||||||
                                ACATCCTTTT TTTCCTA
                                      C
GAM2857  YES1    3'  GGAAAAAAAAAGTGGTT     24120         GA
                                GGAAAAAAAAAG  TGGTT
                                ||||||||||  |||||
                                CCTTTTTTTTC  ACCAA
                                       __
GAM2858  GLUD1   3'  TTGGACTGTATCATAATTA   23593      CATA  C
                                TTGGAT   GT ATCATAATTA
                                ||||||   || ||||||||||
                                AACCTG   CA TAGTATTAAT
                                   A___  _
GAM2858  NOV     3'  GATCATGAGTTTTCATAATTAT 14808      _  CA
                                GATCAT AGT  TCATAATTAT
                                |||||| |||  ||||||||||
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                                CTAGTA TCA  AGTATTAATA
                                   C   AA
GAM2858  CNTNAP2   3'  AGAAGAATGATTAAAACCTTT  30480    C      _____
                                AG AGAATGAT    CCTTT
                                || ||||||||    |||||
                                TC TCTTACTA    GGAAA
                                 T       ATTTT
GAM2858  FCMD      3'  AGCAGAATGATTTTCAC     27509          CC
                                AGCAGAATGAT  TTTAC
                                ||||||||||  |||||
                                TCGTCTTACTA  AAGTG
                                      A_
GAM2858  HMGN1     3'  CAGCAAATGATTTCACCTCTT  22449        A   CC     C
                                CAGCAGA TGAT  TTTACC CTT
                                ||||||| ||||  |||||| |||
                                GTCGTTT ACTA  AAGTGG GAA
                                   _   __     A
GAM2858  TCAP      3'  CACCAGTACCTTTTGTCCCTT  18945    G   AATGAT    AC_
                                CA CAG     CCTTT   CCCTT
                                || |||     |||||   |||||
                                GT GTC     GGAAA   GGGAA
                                 G   AT____    ACA
GAM2858  UCHL1     3'  CAGCAGAAAAGTTTTATTCCTT 20052        TGATCC    CC
                                CAGCAGAA     TTTA  CCTT
                                ||||||||     ||||  ||||
                                GTCGTCTT     AAAT  GGAA
                                     TTCA__    AA
GAM2859  DNASE1    5'  GACAATTTTCTCCTTTT     23354         T
                                GATAATTTT CTCCTTTT
                                ||||||||| ||||||||
                                CTGTTAAAA GAGGAAAA
                                   _
GAM2859  NDUFS2    3'  TTTATTATAATTTCTCCTTTT  21241      CG     TT
                                TTTAT  ATAATT  TCTCCTTTT
                                |||||  ||||||  |||||||||
                                AAATA  TATTAA  AGAGGAAAA
                                  A_     __
GAM2859  PLAG1     3'  TCACCAATTTTTTTCCTTTT   15356     A      C
                                TCG TAATTTTT TCCTTTT
                                ||| |||||||| |||||||
                                AGT GTTAAAAA AGGAAAA
                                  G       A
GAM2859  BTAF1     3'  TAAAAGTTGAAAAAATGA    43671           T
                                TAAAAGTTGAAAA ATGA
                                |||||||||||| ||||
                                ATTTTCAACTTTT TACT
                                      T
GAM2859  RPE65     3'  AAAATTGAACAGAATTTG    7264          AATAT
                                AAAGTTGAA    GAATTTG
                                |||||||||    |||||||
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                                TTTTAACTT    CTTAAAC
                                     GT___
GAM2859  SPS2    3'  AAAATTGAATAAAGAATTTGA  29299        AATAT
                                AAAGTTGAA    GAATTTGA
                                |||||||||    ||||||||
                                TTTTAACTT    CTTAAACT
                                     ATTT_
GAM2860  ACT     5'  AGTCACCAGCACCATCTGA   33884        ACC   __
                                AGTCACCA   CACC  CTGA
                                ||||||||   ||||  ||||
                                TCAGTGGT   GTGG  GACT
                                     C__    TA
GAM2860  AOX1    5'  AGTACCAACCCATCCACCCCGA 10107     C      _____
                                AGT ACCAACCC    ACCCTGA
                                ||| ||||||||    |||||||
                                TCA TGGTTGGG    TGGGGCT
                                  _       TAGG
GAM2860  BCL7A   3'  GTCACCACCCTAGAGGAATCG  34218       A   ACCCT
                                GTCACCA CCC    GAATCG
                                ||||||| |||    ||||||
                                CAGTGGT GGG    CTTAGC
                                    _  ATCTC
GAM2860  CAST    3'  AGTCACCATCCACCAGCTGA   11980        AC    __
                                AGTCACCA  CCACC  CTGA
                                ||||||||  |||||  ||||
                                TCAGTGGT  GGTGG  GACT
                                     A_    TC
GAM2860  CTNNB1  3'  AGATACCAGCCCACCCCTCGA  12516    TC    A      GAA
                                AG  ACCA CCCACCCT   TCGA
                                ||  |||| ||||||||   ||||
                                TC  TGGT GGGTGGGG   AGCT
                                 TA   C      ___
GAM2860  GPC1    3'  AGTCCCCAGCCCACCCTG    13233      A   A
                                AGTC CCA CCCACCCTG
                                |||| ||| |||||||||
                                TCAG GGT GGGTGGGAC
                                  G   C
GAM2860  HMGCR   3'  AGTCACCAACCTCCTG      9233          CAC
                                AGTCACCAACC   CCTG
                                ||||||||||   ||||
                                TCAGTGGTTGG   GGAC
                                      A__
GAM2860  IKBKG   5'  AGTAACCTGGGTCCTGAATCG  45417     C   AACCCAC
                                AGT ACC      CCTGAATCG
                                ||| |||      |||||||||
                                TCA TGG      GGACTTAGC
                                  T   ACCCA__
GAM2860  ITPR3   3'  AGTCACCAGGCCACCTG     13685        AC    C
                                AGTCACCA  CCACC TG
                                ||||||||  ||||| ||
```

```
                                TCAGTGGT  GGTGG AC
                                    CC    _
GAM2860  MUCDHL   3'  GTCACCAATGTGCCTCCGCTCT 34944        C___  A  ___
             GA                   GTCACCAA   CC CC   CTGA
                                  ||||||||   || ||   ||||
                                  CAGTGGTT   GG GG   GACT
                                      ACAC  A  CGA
GAM2860  PROK1    3'  AGTCACCAACCTGCTCTCA   37099          CACCC  AA_
                                  AGTCACCAACC    TG   TCG
                                  ||||||||||    ||   |||
                                  TCAGTGGTTGG    AC   AGT
                                        _____ GAG
GAM2860  PRSS8    5'  AGTCACCAGCACCGTCTG    15757        ACC    __
                                  AGTCACCA   CACC  CTG
                                  ||||||||   ||||  |||
                                  TCAGTGGT   GTGG  GAC
                                      C__    CA
GAM2860  SLC12A2  3'  AGTCACCATTCGCCATTGTGA  9822        AC__   CCC
                                  AGTCACCA   CCA   TGA
                                  ||||||||   |||   |||
                                  TCAGTGGT   GGT   ACT
                                      AAGC   AAC
GAM2860  UBTF     3'  AGCTTCCACCCCACCTTG    30607     CA   A     C
                                  AGT  CCA CCCACC TG
                                  |||  ||| |||||| ||
                                  TCG  GGT GGGTGG AC
                                    AA   G     A
GAM2860  ACPT     3'  GGACAGGGGGCCGGGCAC    38891      AAAA   AA
                                  GGGCA   GGG  GCCGGGCAC
                                  |||||   |||  |||||||||
                                  CCTGT   CCC  CGGCCCGTG
                                     _____  C_
GAM2860  ADAR     3'  GGGAAAAAAGGGGGGCCTGGC  31905     C       AA   G
                                  GGG AAAAAGGG  GCC GGC
                                  ||| ||||||||  ||| |||
                                  CCC TTTTTCCC  CGG CCG
                                    T       CC   A
GAM2860  ADD1     3'  GGGTGGAGGGGAAGCCAAGC   30525     CAAAAA
                                  GGG     GGGAAGCCGGGC
                                  |||     ||||||||||||
                                  CCC     CCCTTCGGTTCG
                                    ACCTC_
GAM2860  ADORA1   3'  GGGCAAGGAGAGCAGGCAC    8593       AAA   GA   C
                                  GGGCA   AGG  AGC GGGCAC
                                  |||||   |||  ||| ||||||
                                  CCCGT   TCC  TCG TCCGTG
                                     ___   TC   _
GAM2860  AP2M1    3'  GGGAAGGAAAGGGAACCCA   19821     CAA_       G
                                  GGG   AAAGGGAA CCG
                                  |||   |||||||| |||
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                                CCC   TTTCCCTT GGT
                                  TTCC      G
GAM2860 ARF5     5' GGGAGGGGCGCGGGCAC    11682    CAAAA   AA _
                                GGG    AGGG  GC CGGGCAC
                                |||    ||||  || |||||||
                                CCC    TCCC  CG GCCCGTG
                                 _____   __ C
GAM2860 BCL9     3' GGGAGGAAAGGGAAGGAAC   20244    CAA      CC
                                GGG   AAAGGGAAG  GGGC
                                |||   |||||||||  ||||
                                CCC   TTTCCCTTC  CTTG
                                  TCC      __
GAM2860 BHMT2    3' GGGCTGGAAGGGAAGGGGC   32776    AAA      CC
                                GGGC   AAGGGAAG  GGGC
                                ||||   ||||||||  ||||
                                CCCG   TTCCCTTC  CCCG
                                  ACC      __
GAM2860 C14orf1  3' GGGAAAAAGGGGAAGGC    28416    C      AAGCC
                                GGG AAAAAGGG    GGGC
                                ||| ||||||||    ||||
                                CCC TTTTTCCC    TCCG
                                 _      CT___
GAM2860 CDR2     3' AGGTAGGAAGGGAAGGGG   44016    CAAA     CC
                                GGG   AAGGGAAG  GGG
                                |||   ||||||||  |||
                                TCC   TTCCCTTC  CCC
                                  ATCC      __
GAM2860 CHGA     5' GGCGGTGTGGGGCCGGGCACC 10470    AAAAA  AA
                                GGC    GGG  GCCGGGCACC
                                |||    |||  ||||||||||
                                CCG    CCC  CGGCCCGTGG
                                  CCACA  __
GAM2860 CIT      3' GGGCAGGCACCGGGC      43054      AAAAG  AA
                                GGGCA    GG  GCCGGGC
                                |||||    ||  |||||||
                                CCCGT    CC  TGGCCCG
                                   _____  G_
GAM2860 CMRF35   3' GCAGGGAGGGCATCCGGGCAC 27433    AAA   AAG
                                GCA   AGGG   CCGGGCAC
                                |||   ||||   ||||||||
                                CGT   TCCC   GGCCCGTG
                                  CCC    GTA
GAM2860 CNGB3    3' GGGTGTAAAGGGAAAGCA   33307    CAA      GCCG
                                GGG   AAAGGGAA   GGCA
                                |||   ||||||||   ||||
                                CCC   TTTCCCTT   TCGT
                                  ACA      ____
GAM2860 DDX6     3' GGGTAGAAAGGGAAGAGAC   20553    CAA      CC
                                GGG   AAAGGGAAG  GGGC
                                |||   |||||||||  ||||
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                                CCC  TTTCCCTTC  TCTG
                                  ATC       __
GAM2860  ELAVL3   3'  GGGCGGGGGATCCCCGGGCACC 10885     AAAAA   AG_
                                GGGC    GGGA  CCGGGCACC
                                ||||    ||||  |||||||||
                                CCCG    CCCT  GGCCCGTGG
                                  CC___   AGG
GAM2860  EVX1     5'  GGGAGAAAGAAAGGCCGGGTGC 12773     CAA   GG A     CA
            C                    GGG  AAAG  A GCCGGG  CC
                                |||  ||||  | ||||||  ||
                                CCC  TTTC  T CGGCCC  GG
                                  TC_   TT C     AC
GAM2860  EYA4     5'  GGGCGGAGGGAGAAGCCGG   19909     AAAAA
                                GGGC    GGGAAGCCGG
                                ||||    ||||||||||
                                CCCG    CTCTTCGGCC
                                  CCTCC
GAM2860  FUS1     3'  GGGTAGAGGGAGAAGCCCCCAC 28590     CAAAAA      GGG
            C                    GGG     GGGAAGCC   CACC
                                |||     ||||||||  ||||
                                CCC     CTCTTCGG   GTGG
                                  ATCTCC      GG_
GAM2860  GJA5     3'  GGGAGAAAGGGAAGGGATGG  23584     CAA       CCG_
                                GGG  AAAGGGAAG   GG
                                |||  |||||||||   ||
                                CCC  TTTCCCTTC   CC
                                  TC_       CCTA
GAM2860  GJB1     3'  GGGAGGAAGGGAAGTAGC    41009     CAAA      CCG
                                GGG   AAGGGAAG   GGC
                                |||   ||||||||  |||
                                CCC   TTCCCTTC   TCG
                                  TCC_      A__
GAM2860  IHPK1    3'  GGGCGTGGAGGGGCCCTGCACC 45493     AAAA   AA  GG
                                GGGC   AGGG  GCC  GCACC
                                ||||   ||||  |||  |||||
                                CCCG   TCCC  CGG  CGTGG
                                  CACC   __  GA
GAM2860  KLF7     5'  GGGCAAAACGGGAGGCGAAAC  18981        A   A  CG
                                GGGCAAAA GGGA GC  GGC
                                |||||||| |||| ||  |||
                                CCCGTTTT CCCT CG  TTG
                                     G   C  CT
GAM2860  MAF      5'  GGGGGAGGGGGAGCCAAGC   23837     CAAAAA   A
                                GGG     GGGA GCCGGGC
                                |||     |||| |||||||
                                CCC     CCCT CGGTTCG
                                  CCTCC_   _
GAM2860  MLLT2    3'  GGACAAAAGGGGAGGGGATGGC 25501        A   AGCCG_
                                GGGCAAAA GGGA     GGC
                                |||||||| ||||     |||
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                                CCTGTTTT CCCT     CCG
                                     C    CCCCTA
GAM2860  MTA1L1   3'  GGGAAGGGAGGTTTGGGTGCC  21891     CAAA     AGCC_   CA
                                GGG    AAGGGA    GGG  CC
                                |||    ||||||    |||  ||
                                CCC    TTCCCT    CCC  GG
                                  _____    CCAAA   AC
GAM2860  MYO3A    5'  GGGCGGGAAGCCGGGCC     41117      AAAAA          A
                                GGGC    GGGAAGCCGGGC C
                                ||||    |||||||||||| |
                                CCCG    CCCTTCGGCCCG G
                                  ______          C
GAM2860  NAV2     3'  GGACGAGAAGGGAAGGCAAGG  41147      AAA       _ C
                                GGGC   AAGGGAAG C GGG
                                ||||   |||||||| | |||
                                CCTG   TTCCCTTC G TCC
                                   CTC       C T
GAM2860  NMB      5'  GGCTAAGGACCGGGCA      43955     AAA    GAA
                                GGC   AAGG   GCCGGGCA
                                |||   ||||   ||||||||
                                CCG   TTCC   TGGCCCGT
                                  A__   ___
GAM2860  OLFM1    3'  GGGCGGGGAGGAAAACCGGGGC 30697      AAAA          _ A
            GCC                   GGGC    AGGGAAGCCGGG C CC
                                ||||    |||||||||||| | ||
                                CCCG    TCCTTTTGGCCC G GG
                                   CCCC           C C
GAM2860  PODXL    3'  GGGCAAGAAGGAAGCAAACACC 23980        AA       C
                                GGGCAA  AGGGAAGC GGGCACC
                                ||||||  |||||||| |||||||
                                CCCGTT  TTCCTTCG TTTGTGG
                                   C_       _
GAM2860  PPP2R2C  3'  GGGCAGGGAGGGGGCCC     41545      AAAA    AGCC    A
                                GGGCA    GGGA    GGGC CC
                                |||||    ||||    |||| ||
                                CCCGT    CCCT    CCCG GG
                                  _____    CC__    _
GAM2860  PTGS1    3'  GGGTTAGAAGGGAAGTCACAC  38740     CAAA      C  G
                                GGG    AAGGGAAG CG GC
                                |||    |||||||| || ||
                                CCC    TTCCCTTC GT TG
                                  AATC       A  G
GAM2860  PTMS     3'  GGGAGGGGAGGGGGGCA     15893     CAAAA    A  CC
                                GGG     AGGG AG  GGGCA
                                |||     |||| ||  |||||
                                CCC     TCCC TC  CCCGT
                                  ______    C  CC
GAM2860  RAB6A    5'  GGGAAGGGAAGGAGGGC     16107     CAAA      CC
                                GGG    AAGGGAAG  GGGC
                                |||    ||||||||  ||||
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                                CCC   TTCCCTTC  CCCG
                                  _____      CT
GAM2860 RAB6A   5' GAGCGGAAGGGCGGGCAC   16105     AAA   AAGC
                                GGGC  AAGGG   CGGGCAC
                                ||||  |||||   |||||||
                                CTCG  TTCCC   GCCCGTG
                                  CC_   _____
GAM2860 RABGGTB 5' GGGTAGACTTAGGAGCCGGGCG 21367    CAAAAA_   A     A
             CC                   GGG     GGGA GCCGGGC CC
                                |||      |||| ||||||| ||
                                CCC      TCCT CGGCCCG GG
                                  ATCTGAA   _      C
GAM2860 RFX2    3' GGAGTGAGGAAAAGCCGGGCA  8453     CAAAA    _
                                GGG    AGGGAA GCCGGGCA
                                |||    |||||| ||||||||
                                CCT    TCCTTT CGGCCCGT
                                  CAC__     T
GAM2860 RNPEPL1  5' GGGCTCGGAGCCGGGCGCC   32887     AAAAAG  A     A
                                GGGC     GGA GCCGGGC CC
                                ||||     ||| ||||||| ||
                                CCCG     CCT CGGCCCG GG
                                  AG_____  _     C
GAM2860 SLC16A2  3' GGGAAGAGGGGAGCAGAC   27151    CAAAA   A  C
                                GGG    AGGG AGC GGGC
                                |||    |||| ||| ||||
                                CCC    TCCC TCG TCTG
                                  TTC__    C  _
GAM2860 SLC1A2   3' GGGAGAAAAGGGAAGCTGGC  41599    CA        CG
                                GGG  AAAAGGGAAGC  GGC
                                |||  ||||||||||  |||
                                CCC  TTTTCCCTTCG  CCG
                                  TC        A_
GAM2860 SLC4A2   3' GGGCATGGGAGGGGGAACC   16775     AAAA   AGCC  C
                                GGGCA   GGGA   GGG ACC
                                |||||   ||||   ||| |||
                                CCCGT   CCCT   CCC TGG
                                   A___   CC__  T
GAM2860 SPF30    5' GGGAAGGGAGGAACGCCGGGCA 25238    CAAAA    A
             C                   GGG    AGGGA GCCGGGCAC
                                |||    ||||| |||||||||
                                CCC    TCCTT CGGCCCGTG
                                  TTCCC    G
GAM2860 STIM1    5' AGGCGAGAAGGGGGCAC    41120     AAAAA    CC
                                GGGC    GGGAAG  GGGCAC
                                ||||    ||||||  ||||||
                                TCCG    CTCTTC  CCCGTG
                                  _____     C_
GAM2860 SUFU     3' GGGCAAGAAGGAAACGACA   32095      AA      CG
                                GGGCAA  AGGGAAGC  GGCA
                                ||||||  ||||||||  ||||
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                                CCCGTT  TTCCTTTG  CTGT
                                   C_      __
GAM2860  SUV39H2  5'  GGGCAGGGAGGCGGGTCA    36016      AAAA   A  C  _
                                GGGCA   GGGA GC GGG CA
                                |||||   |||| || ||| ||
                                CCCGT   CCCT CG CCC GT
                                   _____   C  _  A
GAM2860  TCF19    3'  GGGAAGGGAAGGGGGG     45558     CAAA      CC
                                GGG   AAGGGAAG  GGG
                                |||   ||||||||  |||
                                CCC   TTCCCTTC  CCC
                                  _____      CC
GAM2860  TMEM2    3'  GGAAAGGGAAGCTGGGCA    30152    CAA       C
                                GG  AAAGGGAAGC GGGCA
                                ||  ||||||||||| |||||
                                CC  TTTCCCTTCG CCCGT
                                 ___        A
GAM2860  TMPRSS4  3'  GGGCAGGAAGGAAGCGGC    33392     AAA      CG
                                GGGCA  AGGGAAGC  GGC
                                |||||  ||||||||  |||
                                CCCGT  TTCCTTCG  CCG
                                   CC_      __
GAM2860  UBE2I    5'  GGGTGACAGGGCCAGCCGGGCA 17818    CAAAA   A_
            C                    GGG    AGGG  AGCCGGGCAC
                                |||    ||||  ||||||||||
                                CCC    TCCC  TCGGCCCGTG
                                  ACTG_   GG
GAM2860  XK       3'  AGGTGAAAAGGGAGCGC     34357     CA      A  CGG
                                GGG  AAAAGGGA GC   GC
                                |||  |||||||| ||   ||
                                TCC  TTTTCCCT CG   CG
                                  AC      _ ___
GAM2860  ZNF216   5'  GGGAAGGCTGAGCCGGGCGCC  25658    CAAA   GA_      A
                                GGG   AAGG   AGCCGGGC CC
                                |||   ||||   |||||||| ||
                                CCC   TTCC   TCGGCCCG GG
                                   _____   GAC      C
GAM2861  ABCC12   5'  CCTATGGTGTGGTTTTGGT   37717    _       GG
                                CC ATGGTGTGGT  TGGT
                                || ||||||||||  ||||
                                GG TACCACACCA  ACCA
                                  A        AA
GAM2861  BPGM     3'  TGTCATTGTGGTGGTGGTTG   11895    GT  G
                                TG  GT GTGGTGGTGGTTG
                                ||  || ||||||||||||
                                AC  TA CACCACCACCAAC
                                  AG  A
GAM2861  CLC      3'  CCTGTGGTGTGGCTATGGT   29895    A_       G
                                CC  TGGTGTGGT GTGGT
                                ||  ||||||||| |||||
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                                GG  ACCACACCG TACCA
                                 AC        A
GAM2861  JMJ      5'  TGTTGTTGGTGGTGGTTG    22485     GG_
                                TGT   TGGTGGTGGTTG
                                |||   ||||||||||||
                                ACA   ACCACCACCAAC
                                  ACA
GAM2861  MARK3    5'  TCCGTGGGTGGTGGTGCATG   14363     A   T       _
                                TCC TGG GTGGTGGTG GTG
                                ||| ||| ||||||||| |||
                                AGG ACC CACCACCAC TAC
                                  C   _       G
GAM2861  MCL1     3'  TGGTTTTGGTGGTGGTGGTGGT 35004      _____
                TG                  TGGT    GTGGTGGTGGTGGTTG
                                ||||    ||||||||||||||||
                                ACCA    CACCACCACCACCAAC
                                  AAAC
GAM2861  MYH11    3'  TGGTGGTGGTGGTGGTGGTTG  35629       _
                                TGGTG TGGTGGTGGTGGTTG
                                ||||| ||||||||||||||||
                                ACCAC ACCACCACCACCAAC
                                   C
GAM2861  PPEF2    3'  TCCTGGTGTGGTGGTGCATG   26405     A          _
                                TCC TGGTGTGGTGGTG GTG
                                ||| ||||||||||||| |||
                                AGG ACCACACCACCAC TAC
                                  _           G
GAM2861  SMTN     3'  TGGCGTCGCAGGTGGTTG     39524       G  GGT
                                TGGTGT GT   GGTGGTTG
                                |||||| ||   ||||||||
                                ACCGCA CG   CCACCAAC
                                   G  T__
GAM2861  ABL1     3'  CACCCCACTAGCCACTGCC    28703        CACAA    CA
                                TACCCCAC    CCAC  CC
                                ||||||||    ||||  ||
                                GTGGGGTG    GGTG  GG
                                     ATC__    AC
GAM2861  ADRA2B   3'  TACCCCACCTGGGGGCGCTGCC 8650          ACAACCA_____
                ACC                 TACCCCACC         CCACC
                                |||||||||         |||||
                                ATGGGGTGG         GGTGG
                                     ACCCCCGCGAC
GAM2861  ATRN     3'  CCTCCTCACAGCCACCACC    40271    _ AC    A
                                CC CC  CACA CCACCACC
                                || ||  |||| ||||||||
                                GG GG  GTGT GGTGGTGG
                                 A  A_    C
GAM2861  B3GAT1   3'  CCCACCACCCACCGCC      38296        AA     A
                                CCCACCAC  CCACC CC
                                ||||||||  ||||| ||
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                                GGGTGGTG  GGTGG GG
                                   __    C
GAM2861  BACH2    3'  CCCCACTGCCCACCACC     34785       CACAA
                                CCCCAC    CCACCACC
                                ||||||    ||||||||
                                GGGGTG    GGTGGTGG
                                   ACG__
GAM2861  BCL11B   3'  CCCCCAGCACCACCAC      39746     A  CAAC
                                CCC CCA   CACCACCAC
                                ||| |||   |||||||||
                                GGG GGT   GTGGTGGTG
                                  _  C___
GAM2861  BCR      5'  CCCCACCAGCCCCGCCGCCGCC 34632        CAA  A  A  A
                                CCCCACCA  CC CC CC CC
                                ||||||||  || || || ||
                                GGGGTGGT  GG GG GG GG
                                     CGG  C  C  C
GAM2861  CCND1    3'  CACCCCACCTCCACTGCCACC  38200        ACAA   CA
                                TACCCCACC   CCAC  CCACC
                                |||||||||   ||||  |||||
                                GTGGGGTGG   GGTG  GGTGG
                                     A___   AC
GAM2861  CD28     5'  CCGTCATCCACGGCCACCACCA 26018    C_ _   AA
            CC                    CC  CA CCAC  CCACCACCACC
                                ||  || ||||  ||||||||||
                                GG  GT GGTG  GGTGGTGGTGG
                                 CA  A   CC
GAM2861  DNM2     3'  ACCCCCCGCCACCACCAC    22373      A  ACAA
                                ACCCC CC    CCACCACCAC
                                |||||  ||   ||||||||||
                                TGGGG GG    GGTGGTGGTG
                                  _  C___
GAM2861  DYRK1B   3'  CCCTCCACCGGACCACCAC   21778     A   AACC
                                CCC CCAC    ACCACCAC
                                ||| ||||    ||||||||
                                GGG GGTG    TGGTGGTG
                                  A   GCC_
GAM2861  EPHB4    3'  CCACCACCAACTACCGCC    20790       _  C  A
                                CCACCAC AAC ACC CC
                                ||||||| ||| ||| ||
                                GGTGGTG TTG TGG GG
                                    G  A  C
GAM2861  FADD     3'  CCCCACCACAGCACCCCGCC  19243        AC   A  A
                                CCCCACCACA  CACC CC CC
                                ||||||||||  |||| || ||
                                GGGGTGGTGT  GTGG GG GG
                                     C_   _ C
GAM2861  FMR2     3'  CCACAGATACAACCACTACCAC 12955     C___      C
            C                    CCAC   ACAACCAC ACCACC
                                ||||   |||||||| ||||||
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                                GGTG   TGTTGGTG TGGTGG
                                  TCTA      A
GAM2861  FNTB    3'  CACCCCACGCTGCCACCACC  13001        CACAA
                                TACCCCAC    CCACCACC
                                ||||||||    ||||||||
                                GTGGGGTG    GGTGGTGG
                                    CGAC_
GAM2861  HOXB5   3'  TACCCCACCTCAACTGCTGCC 13452        A   CACCA
                                TACCCCACC CAAC    CC
                                ||||||||| ||||    ||
                                ATGGGGTGG GTTG    GG
                                     A   ACGAC
GAM2861  HOXC11  3'  CCCTACTGCCTCCACCAC   41160    ACC  AA  A
                                CCC   AC  CC CCACCAC
                                |||   ||  || |||||||
                                GGG   TG  GG GGTGGTG
                                  A__  AC  A
GAM2861  HTR1D   3'  CCCCGCCCCCCACCACC    9261     A  ACAA
                                CCCC CC    CCACCACC
                                |||| ||    ||||||||
                                GGGG GG    GGTGGTGG
                                  C  GG__
GAM2861  IFIT4   3'  TACCCGTCACAACCACCAC   43370     CAC
                                TACCC   CACAACCACCAC
                                |||||   ||||||||||||
                                ATGGG   GTGTTGGTGGTG
                                   CA_
GAM2861  INHBB   3'  CCCCACCACCGTGCCCCTGCC 13543        AA__  A  A_
                                CCCCACCAC    CC CC  CC
                                |||||||||    || ||  ||
                                GGGGTGGTG    GG GG  GG
                                     GCAC  _  AC
GAM2861  INHBB   3'  CCCTCCGTGCCCCACCACC   13546    A  ACAA  A
                                CCC CC    CC CCACCACC
                                ||| ||    || ||||||||
                                GGG GG    GG GGTGGTGG
                                  A  CAC_  _
GAM2861  KLHL2   5'  CCTCACCGCGCGCCACCACC  28528    C    ACAA_
                                CC CACC    CCACCACC
                                || ||||    ||||||||
                                GG GTGG    GGTGGTGG
                                 A   CGCGC
GAM2861  KRTHA5  5'  CCACCACCCCACATCAC     14020       AA   CAC
                                CCACCAC  CCAC   CAC
                                |||||||  ||||   |||
                                GGTGGTG  GGTG   GTG
                                    G_   TA_
GAM2861  MN1     3'  CCCCTGCCAACCACCAC     14573     ACCA
                                CCCC    CAACCACCAC
                                ||||    ||||||||||
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                                GGGG   GTTGGTGGTG
                                  ACG_
GAM2861 PCOLN3   3' CCCTGCCAGCCGCCCACCACC 15750    CA   CAA A_
                                CCC CCA  CC CCACCACC
                                ||| |||  || ||||||||
                                GGG GGT  GG GGTGGTGG
                                  AC  C__ CG
GAM2861 PLEK     3' ACCCTCAAAACCACCAC     15388     CAC C
                                ACCC  CA AACCACCAC
                                ||||  || |||||||||
                                TGGG  GT TTGGTGGTG
                                  A__ T
GAM2861 PRPS2    3' ACCAAATAACCACCACCA    15730     C__
                                ACCA  AACCACCACCA
                                ||||  ||||||||||
                                TGGT  TTGGTGGTGGT
                                  TTA
GAM2861 PSMB8    3' ACCTGCCCAGCTGCCACCACC 45512    CCA   CAA_
                                ACC  CCA   CCACCACC
                                |||  |||   ||||||||
                                TGG  GGT   GGTGGTGG
                                  ACG  CGAC
GAM2861 RASGRP1  5' CCCCGCCACCACCGCC     25075     A  ACA     A
                                CCCC CC  ACCACC CC
                                |||| ||  |||||| ||
                                GGGG GG  TGGTGG GG
                                  C ___     C
GAM2861 RGS16    3' CCCCACCAACCCTCATCA    16320       CA  AC  C
                                CCCCACCA  ACC  CA CA
                                ||||||||  |||  || ||
                                GGGGTGGT  TGG  GT GT
                                    __  GA  A
GAM2861 RXRB     3' CCCCTTCACCACCACCACC   35040     ACCACA
                                CCCC    ACCACCACCACC
                                ||||    ||||||||||||
                                GGGG    TGGTGGTGGTGG
                                  AAG___
GAM2861 SCNN1B   3' CCCTTCCATCTCTCCACCACC 7335     CA   CAA__
                                CCC  CCA   CCACCACC
                                |||  |||   ||||||||
                                GGG  GGT   GGTGGTGG
                                  AA  AGAGA
GAM2861 SLC7A4   3' CACCCCACCACAACTGCC    42184          CA
                                TACCCCACCACAAC  CC
                                ||||||||||||||  ||
                                GTGGGGTGGTGTTG  GG
                                        AC
GAM2861 SMOH     3' CCCCACCACAAGCTCTGCATAC 24810         CCACC____
            C                    CCCCACCACAA       ACC
                                ||||||||||        |||
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                                GGGGTGGTGTT       TGG
                                      CGAGACGTA
GAM2861  SNL     3'  TACCCGCCCGCCACCACC    16948      CA  ACAA
                                TACCC  CC    CCACCACC
                                |||||  ||    ||||||||
                                ATGGG  GG    GGTGGTGG
                                   CG  C___
GAM2861  SRD5A1   3'  TACTCCGTATGAACCACCACC  9833     C  ACCAC
                                TAC CC     AACCACCACC
                                |||  ||     ||||||||||
                                ATG GG     TTGGTGGTGG
                                  A  CATAC
GAM2861  STAR     3'  ACCCCACCCATCCCACTGTCAC 7385         ACAA   ___
              C                  ACCCCACC    CCAC   CACC
                                 ||||||||    ||||   ||||
                                 TGGGGTGG    GGTG   GTGG
                                      GTAG    ACA
GAM2861  TCF20    3'  CCATCACGAGTGTCCACCACC  42532     C   AA____
                                CCA CAC      CCACCACC
                                |||  |||     ||||||||
                                GGT GTG      GGTGGTGG
                                  A   CTCACA
GAM2861  THY1     3'  TACCCCACCATCCCACTACC   26632         CAA    C
                                TACCCCACCA   CCAC ACC
                                ||||||||||   |||| |||
                                ATGGGGTGGT   GGTG TGG
                                      AG_    A
GAM2861  TNS      3'  CCCCTGCTGCACTGCCACCACC 35472      AC___   AA
                                CCCC     CAC  CCACCACC
                                ||||     |||  ||||||||
                                GGGG     GTG  GGTGGTGG
                                  ACGAC   AC
GAM2862  KRT5     5'  GGCTTGTTCCTGGTGG      7691       ATC       C
                                GGTT   GTTCCTGG GG
                                ||||   |||||||| ||
                                CCGA   CAAGGACC CC
                                  A__       A
GAM2862  SYN3     3'  GAAACGGCATTCCTGGTGG    18562    C    TATC       C
                                GA ACGGT    GTTCCTGG GG
                                || |||||    |||||||| ||
                                CT TGCCG    TAAGGACC CC
                                 T     _____       A
GAM2863  AARS     3'  TCTAGACCGATGGCACTGACG  11489      A    C   CT
                                TCTA ACCG GTG  CGCTGACG
                                |||| |||| |||  ||||||||
                                AGAT TGGC TAC  GTGACTGC
                                  C    _   C_
GAM2864  CTPS     3'  TCTTAAGTTAGAGTACACATC  44801          T  GT_
                                TCTTAAGTTA AG   ACGTC
                                ||||||||||  ||   |||||
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                                AGAATTCAAT TC  TGTAG
                                      C  ATG
GAM2864  CUL3     3'  TCTTAAGTTACAGTAGAC    18748          GT_
                                TCTTAAGTTATAG  AC
                                |||||||||||||  ||
                                AGAATTCAATGTC  TG
                                       ATC
GAM2864  MAK      3'  TAAACTGTACAAATAC     25380          TC
                                TAAACTGTACAA  ATAC
                                ||||||||||||  ||||
                                ATTTGACATGTT  TATG
                                       __
GAM2864  RANBP2L1 3'  TGCAGCTGGCATACTCATA   37029     CAAT_
                                TGTA    CATACTCATA
                                ||||    ||||||||||
                                ACGT    GTATGAGTAT
                                  CGACC
GAM2864  VHL      3'  AACAGTACAATCTCAACT    8102     T      AT_
                                AAC GTACAATC   ACT
                                ||| ||||||||   |||
                                TTG CATGTTAG   TGA
                                  T      AGT
GAM2865  AF1Q     5'  TGCCTCGGGAGCTCCGGGGT   27729           GAA
                                TGCCTCGGGAGCTC   GGGT
                                ||||||||||||||   ||||
                                ACGGAGCCCTCGAG   CCCA
                                       GC_
GAM2865  ANK1     5'  GCCTTGGGGGCTTGAGGA    33867     C   A   C  A
                                GCCT GGG GCT GA GGG
                                |||| ||| ||| || |||
                                CGGA CCC CGA CT CCT
                                  A  C  A  _
GAM2865  AXIN1    3'  TGTCCTCTGCTTGGAGGGTGCT 41396    _   GGGA   CGA
                                TG CCTC   GCT   AGGGTGCT
                                || ||||   |||   ||||||||
                                AC GGAG   CGA   TCCCACGA
                                 A   A___   ACC
GAM2865  BIN3     3'  TGCCTGCTGGAGGGTG      33086      CGGGA   C  A
                                TGCCT    GCT GA GGGTG
                                |||||    ||| || |||||
                                ACGGA    CGA CT CCCAC
                                   _____  C  _
GAM2865  ADD3     3'  GTAAAACCTCTTTCCAGT    32568         CCGAA  T
                                GTAAAACCTC    TC CAGT
                                ||||||||||    || ||||
                                CATTTTGGAG    AG GTCA
                                      AA___  _
GAM2865  ADRB3    3'  ATAAAACCCCAAATCTTGGTC  6176         TC       CA
                                GTAAAACC  CCGAATCT  GTC
                                ||||||||  ||||||||  |||
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                                TATTTTGG  GGTTTAGA  CAG
                                   __       AC
GAM2865  DLEC1    3'  GTAGACCTCCCGGACTC     28835     AA       AAT
                                GTA  ACCTCCCG   CTC
                                |||  ||||||||   |||
                                CAT  TGGAGGGC   GAG
                                  C_       CT_
GAM2865  DMD      5'  AGCAAAATAATCTCAG      19675        CCTCCCG
                                AGTAAAA      AATCTCAG
                                |||||||      ||||||||
                                TCGTTTT      TTAGAGTC
                                   A_______
GAM2865  ENO2     3'  AGCAAGACCTCCCACCCCAGTC 12706       A      GA
                                AGTAA ACCTCCC  ATCTCAGTC
                                ||||| |||||||  |||||||||
                                TCGTT TGGAGGG  TGGGGTCAG
                                   C      __
GAM2865  KERA     5'  AGTGAAACCTACTCGTCCCAGT 28153     A     CC_  AA
                 C                 AGT AAACCT   CG  TCTCAGTC
                                ||| ||||||   ||  ||||||||
                                TCA TTTGGA   GC  AGGGTCAG
                                  C     TGA  __
GAM2865  OTC      5'  AGTAAAAATATCTCAG      8042         CCTCCCGA
                                AGTAAAA       ATCTCAG
                                |||||||       |||||||
                                TCATTTT       TAGAGTC
                                   TA_______
GAM2865  PTEN     3'  AGCAAAACCTTTCGGAAACCTC 7197           CC  __
                                AGTAAAACCT  CG  AATCTC
                                ||||||||||  ||  ||||||
                                TCGTTTTGGA  GC  TTGGAG
                                     AA  CT
GAM2865  RASAL1   3'  AGTAGAGACCCCAGTCTCAGTC 21653      AAACC    AA
                                AGTA    TCCCG  TCTCAGTC
                                ||||    |||||  ||||||||
                                TCAT    GGGGT  AGAGTCAG
                                  CTCT_    C_
GAM2865  TRIM9    3'  AGTAAAACTTCTCAGT      31553         CTCCCGAA
                                AGTAAAAC       TCTCAGT
                                ||||||||       |||||||
                                TCATTTTG       AGAGTCA
                                   A________
GAM2866  DBN1     3'  GGCAGGAGACGGGGGG      38937      _  TCC   A
                                GGTAG AGA   CGGG GG
                                ||||| |||   |||| ||
                                CCGTC TCT   GCCC CC
                                  C  ____   C
GAM2866  DR1      5'  GGAGAGTGATCCCGGGGGGT  40442    T  __       A
                                GG AGA  GATCCCGGG GGT
                                || |||  ||||||||| |||
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                                CC TCT  CTAGGGCCC CCA
                                 _  CA       C
GAM2866  FGR     3'  GATAGGAGAGAAGTGAGGGAGG 23498    C  T    TCCC_
              TA                   GA AGG AGAGA    GGGAGGTA
                                || ||| |||||    ||||||||
                                CT TCC TCTCT    CCCTCCAT
                                 A  _    TCACT
GAM2866  FOXE3    3'  GACAGGTAAGTGGAGG      29144         AGATCCCG
                                GACAGGTAG      GGAGG
                                |||||||||      |||||
                                CTGTCCATT      CCTCC
                                     CA_____
GAM2866  IGFBP5   5'  GAGAGGTGGAGGGCTGGGGT   8267     C   A   ATCCCG  A
                                GA AGGT GAG     GG GGT
                                || |||| |||     || |||
                                CT TCCA CTC     CC CCA
                                 C   C  CCGA__  _
GAM2866  MTCP1    5'  GAGAGGTAGCTGGGAGGT    30578    C     AGATCCC
                                GA AGGTAG      GGGAGGT
                                || ||||||      |||||||
                                CT TCCATC      CCCTCCA
                                 C     GA_____
GAM2866  NT5C     3'  GACAGCCTCTCGGGAGGT    31100      GTAGAGA  C
                                GACAG      TC CGGGAGGT
                                |||||      || ||||||||
                                CTGTC      AG GCCCTCCA
                                   GG_____  A
GAM2866  SCNN1B   3'  GACAGGTAGGGACGAGGGT   7336         A  TCC   A
                                GACAGGTAG GA   CGGG GGT
                                ||||||||| ||   |||| |||
                                CTGTCCATC CT   GCTC CCA
                                     C  ___   _
GAM2866  SLC6A1   3'  AGGTTGAGATGGAAGGTA    40486     A    CCC
                                AGGT GAGAT   GGGAGGTA
                                |||| |||||   ||||||||
                                TCCA CTCTA   CCTTCCAT
                                  A    ___
GAM2866  TLR9     3'  CAGGCAGAGGTGAGGT      32659         ATCCCGG
                                CAGGTAGAG      GAGGT
                                |||||||||      |||||
                                GTCCGTCTC      CTCCA
                                     CA_____
GAM2867  ETS2     3'  TGAAAAATGAAATAAAACCTCA 23473          _     AA
              GAT                   TGAAAAATGAAA AAAATT  AGAT
                                ||||||||||| ||||||  ||||
                                ACTTTTTACTTT TTTTGG  TCTA
                                       A     AG
GAM2867  FMR2     3'  GAGAAATGAAAAAAAAAAGAT  12965    A         TT
                                GA AAATGAAAAAAA  AAAGAT
                                || ||||||||||  ||||||
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                                CT TTTACTTTTTTT  TTTCTA
                                 C         __
GAM2868  AP2B1    3'  TGAGATTATAATATGGAAAG  10495     A   GTAT
                                TGA ATTA    TATGGAAAG
                                ||| ||||    |||||||||
                                ACT TAAT    ATACCTTTC
                                  C   ATT_
GAM2868  BRCA1    3'  CTGAAATCAGATATGGAGAGAA 28628          TAT     A
                                TTGAAATTAG   TATGGA AGAA
                                ||||||||||   |||||| ||||
                                GACTTTAGTC   ATACCT TCTT
                                       T__     C
GAM2868  FLT1     3'  TTGAAAAATTTATGGAAGGA   12916       TTAGTA       A
                                TTGAAA     TTATGGAA GA
                                ||||||     |||||||| ||
                                AACTTT     AATACCTT CT
                                    TTA___       C
GAM2868  MOCS2    3'  GAAATTAGTCATGGAAGGA   21205         AT      A
                                GAAATTAGT  TATGGAA GA
                                |||||||||  ||||||| ||
                                CTTTAATCA  GTACCTT CT
                                      __      C
GAM2868  RAB5C    3'  TTGAATTAGTATTTGTACAGAA 40809       A       A  GAA
                                TTGAA TTAGTATT TG   AGAA
                                ||||| ||||||| ||   ||||
                                AACTT AATCATAA AC   TCTT
                                   _       _  ATG
GAM2868  RRM2B    3'  TTAGATTGTTATGGAAAGA    42730      TA__
                                TTAG    TTATGGAAAGA
                                ||||    ||||||||||
                                AATC    AATACCTTTCT
                                  TAAC
GAM2868  TRIM14   3'  TTGAAACTAGCCTAGGAGAG   37711          ATTAT   A
                                TTGAAATTAGT     GGA AG
                                ||||||||||     ||| ||
                                AACTTTGATCG     CCT TC
                                       GAT__   C
GAM2868  TRPM7    3'  TTAAAATTAGTACCAAGGAA   41623            T
                                TTGAAATTAGTATTA GGAA
                                |||||||||||||| ||||
                                AATTTTAATCATGGT CCTT
                                          T
GAM2869  CCR2     3'  TGAACTCTATGCCTGTAT     8502        GTTTC
                                TGAACTT     TGCCTGTAT
                                |||||||     |||||||||
                                ACTTGAG     ACGGACATA
                                    AT___
GAM2869  CREBBP   3'  ATGAACTTGTTTTTCCCGT   20428          CTG
                                ATGAACTTGTTT   CCTGT
                                ||||||||||||   |||||
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                                TACTTGAACAAA  GGGCA
                                      AA_
GAM2869 HPGD    3' TATGAACTTGTATGTGAGTGT 9247          TTC  CC
                                TATGAACTTGT  TG  TGT
                                ||||||||||  ||  |||
                                ATACTTGAACA  AC  ACA
                                      TAC  TC
GAM2869 MLLT2   3' TGAATGCTGCCTGT      25512     CT  TTT
                                TGAA  TG  CTGCCTGT
                                ||||  ||  ||||||||
                                ACTT  AC  GACGGACA
                                  __  ___
GAM2869 NRAP    3' TGAACTTGTGATACTGTGT   26123        TT__  CC
                                TGAACTTGT   CTG  TGT
                                |||||||||   |||  |||
                                ACTTGAACA   GAC  ACA
                                      CTAT  __
GAM2870 AGTR1   3' TATAGATATACATATATATATA 28921     T
             T                   TATA ATATATATATATATATAT
                                ||||| ||||||||||||||||||
                                ATAT TATATGTATATATATATA
                                  C
GAM2870 AKAP2   3' TACACTTTATATATATATAT  28499      ATA
                                TATAT  TATATATATATAT
                                |||||  ||||||||||||
                                ATGTG  ATATATATATATA
                                   AA_
GAM2870 AKAP2   3' TACACTTTATATATATATAT  28499      ATA
                                TATAT  TATATATATATAT
                                |||||  ||||||||||||
                                ATGTG  ATATATATATATA
                                   AA_
GAM2870 ARHGEF12 3' TATATATATAGATATAGATATA 31645         T    T
             T                   TATATATATA ATATA ATATAT
                                |||||||||| ||||| ||||||
                                ATATATATAT TATAT TATATA
                                      C    C
GAM2870 ATP2B2  3' ATATATATATATATATAT    11752
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATATATATATATATA

GAM2870 ATP8B2  3' TATATATATATTTATATAATAT 42212          A     T
             A                   TATATATATAT TATATA ATATA
                                ||||||||||| |||||| |||||
                                ATATATATATA ATATAT TATAT
                                      A     _
GAM2870 BACH1   3' TATATATGTATACATACACATA 10149        A
                                TATATAT TATATATATATATA
                                ||||||| ||||||||||||||
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                                ATATATA ATATGTATGTGTAT
                                    C
GAM2870  BACH2    3'  CATATGGATATATATATATATA 34783      AT
                TA                  TATAT  ATATATATATATATATA
                                    |||||  |||||||||||||||||
                                    GTATA  TATATATATATATATAT
                                       CC
GAM2870  BACH2    3'  TATATATATATTATATATA   34801          A
                                    TATATATATAT TATATATA
                                    |||||||||||| ||||||||
                                    ATATATATATA ATATATAT
                                              _
GAM2870  BACH2    3'  CATATGGATATATATATATATA 34784      __
                TATA                  TATAT  ATATATATATATATATATA
                                    |||||  |||||||||||||||||||
                                    GTATA  TATATATATATATATATAT
                                       CC
GAM2870  BCL6     3'  TATATATATATATATTTATATA 39906            A
                                    TATATATATATATAT TATATA
                                    |||||||||||||| ||||||
                                    ATATATATATATATA ATATAT
                                             A
GAM2870  BTAF1    3'  TACATATATATACAAATATA   43672           T
                                    TATATATATATATA ATATA
                                    |||||||||||||| |||||
                                    ATGTATATATATGT TATAT
                                             T
GAM2870  CACNB2   3'  TATATATATATATATTATATAT 8794            A
                A                    TATATATATATATAT TATATATA
                                    |||||||||||||| ||||||||
                                    ATATATATATATATA ATATATAT
                                              _
GAM2870  CBFA2T1  3'  TATATATATATATATATATA   20302
                                    TATATATATATATATATATA
                                    ||||||||||||||||||||
                                    ATATATATATATATATATAT

GAM2870  CBFA2T1  3'  TATATATATATATATATATATA 20306
                TA                    TATATATATATATATATATATATA
                                    ||||||||||||||||||||||||
                                    ATATATATATATATATATATATAT

GAM2870  CBFA2T1  3'  TATATATATATATATATA    20300
                                    TATATATATATATATATA
                                    ||||||||||||||||||
                                    ATATATATATATATATAT

GAM2870  CBFA2T1  3'  TATATATATATATATATATATA 20304
                                    TATATATATATATATATATATA
                                    ||||||||||||||||||||||
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                                ATATATATATATATATATATAT

GAM2870  CBFA2T1   3'  TATATATATATATATATATATA 20305
                T                TATATATATATATATATATATAT
                                 ||||||||||||||||||||||
                                 ATATATATATATATATATATATA

GAM2870  CRADD     3'  ATATATATATATATGGATATAT 19171            AT
                A                ATATATATATATAT  ATATATA
                                 ||||||||||||||  |||||||
                                 TATATATATATATA  TATATAT
                                         CC
GAM2870  CRADD     3'  TATATATATGGGATATATATAT 19181        ___
                ATAT                TATATATAT   ATATATATATATAT
                                 |||||||||   ||||||||||||||
                                 ATATATATA   TATATATATATATA
                                       CCC
GAM2870  CRIM1     3'  TATATATATATTATATACACAT 32380          A
                                 TATATATATAT TATATATATAT
                                 ||||||||||| ||||||||||
                                 ATATATATATA ATATATGTGTA
                                             _
GAM2870  CRIM1     3'  TATATGTATATATATATATTAT 32383      A        _
                ATA                 TATAT TATATATATATAT ATATA
                                 ||||| |||||||||||| |||||
                                 ATATA ATATATATATATA TATAT
                                    C          A
GAM2870  CRIM1     3'  TATAAATATATATGTATATATA 32377     T      A      III
                TA                  TATA ATATATAT TATATATA   TA
                                 |||| |||||||| ||||||||   ||
                                 ATAT TATATATA ATATATAT   AT
                                    T       C       III
GAM2870  CRIM1     3'  TATATATGTATATATATATAT  32382       A
                                 TATATAT TATATATATATAT
                                 ||||||| ||||||||||||
                                 ATATATA ATATATATATATA
                                      C
GAM2870  CTGF      3'  TACATATATATATATATATA   12506
                                 TATATATATATATATATATA
                                 ||||||||||||||||||||
                                 ATGTATATATATATATATAT

GAM2870  CTLA4     3'  TATATATATATATATATGTATA 23339             A
                TA                  TATATATATATATATAT TATATA
                                 |||||||||||||||| ||||||
                                 ATATATATATATATATA ATATAT
                                             C
GAM2870  CTLA4     3'  ATATATATATATATATATATAT 23324               TAIII
                T                   ATATATATATATATATATATA    T
                                 ||||||||||||||||||||    |
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                                TATATATATATATATATATAT    A
                                                  IIIAT
GAM2870  CTLA4    3'  TATATATATATATATATATGTA 23337                A
                TA                  TATATATATATATATATAT TATA
                                    |||||||||||||||||| ||||
                                    ATATATATATATATATATA ATAT
                                                 C
GAM2870  CTLA4    3'  TATATATATATATATATATATA 23336
                TA                  TATATATATATATATATATATA
                                    |||||||||||||||||||||||
                                    ATATATATATATATATATATATAT

GAM2870  CTLA4    3'  TATATATATATATATGTATATA 23341              A
                T                   TATATATATATATAT TATATAT
                                    |||||||||||||| |||||||
                                    ATATATATATATATA ATATATA
                                              C
GAM2870  CTLA4    3'  TATATATATATGTATATAT    23343          A
                                    TATATATATAT TATATAT
                                    |||||||||| |||||||
                                    ATATATATATA ATATATA
                                          C
GAM2870  CTLA4    3'  ATATATATATATATATATATAT 23323                  III
                AT                  ATATATATATATATATATATATA   T
                                    |||||||||||||||||||||   |
                                    TATATATATATATATATATATAT   A
                                                 III
GAM2870  CTLA4    3'  TATATATATATATATATATATA 23335
                T                   TATATATATATATATATATATAT
                                    |||||||||||||||||||||||
                                    ATATATATATATATATATATATA

GAM2870  CTLA4    3'  TATATATATATATATATATAT  23333
                                    TATATATATATATATATATAT
                                    ||||||||||||||||||||
                                    ATATATATATATATATATATA

GAM2870  CYP1A2   3'  TATATATATATGTATATATATG 42902          A       AIIIC
                A                   TATATATATAT TATATATAT    A
                                    |||||||||| |||||||||    |
                                    ATATATATATA ATATATATA    T
                                          C       CIIIA
GAM2870  DAPK1    3'  TATATATATATACATATGATAT 22368                _
                A                   TATATATATATATATAT ATATA
                                    |||||||||||||||| |||||
                                    ATATATATATATGTATA TATAT
                                                 C
GAM2870  DAPK1    3'  TAATATATATGTATATACATA  22364   T      A
                                    A ATATATAT TATATATATA
                                    | |||||||| ||||||||||
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                                A TATATATA ATATATGTAT
                                 T       C
GAM2870  DAPK1    3'  CATATATATATATACATAT    22355
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                GTATATATATATATGTATA

GAM2870  DDX6     3'  ATATATATATATGTATATATAT 20545            A       TAIII
              T                  ATATATATATAT TATATATA     T
                                 |||||||||||| ||||||||     |
                                 TATATATATATA ATATATAT     A
                                        C       IIIAT
GAM2870  DDX6     3'  ATATATATATATGTATATATAT 20544            A         III
              AT                   ATATATATATAT TATATATATA   T
                                   |||||||||||| |||||||||   |
                                   TATATATATATA ATATATATAT   A
                                        C         III
GAM2870  DDX6     3'  TATATATATATGTATATATATA 20559           A
              TA                   TATATATATAT TATATATATATA
                                   |||||||||||| ||||||||||||
                                   ATATATATATA ATATATATATAT
                                        C
GAM2870  DDX6     3'  TATATGTATATATATATATATA 20565       A
              TA                   TATAT TATATATATATATATATA
                                   ||||| ||||||||||||||||||
                                   ATATA ATATATATATATATATAT
                                     C
GAM2870  DDX6     3'  TATGTATATATATATATATATA 20567     A
              T                    TAT TATATATATATATATATAT
                                   ||| ||||||||||||||||||
                                   ATA ATATATATATATATATATA
                                     C
GAM2870  DDX6     3'  TATATATGTATATATATATATA 20563        A
              TA                   TATATAT TATATATATATATATA
                                   ||||||| ||||||||||||||||
                                   ATATATA ATATATATATATATAT
                                       C
GAM2870  DDX6     3'  TATATATATGTATATATATATA 20561          A
              TA                   TATATATAT TATATATATATATA
                                   ||||||||| |||||||||||||
                                   ATATATATA ATATATATATATAT
                                         C
GAM2870  DRIL1    3'  TATATATATATATATATATATA 23385                  III
              T                    TATATATATATATATATATATA   T
                                   |||||||||||||||||||||||  |
                                   ATATATATATATATATATATAT   A
                                                  III
GAM2870  DRIL1    3'  TATATATATATATATATATATA 23386
              TA                   TATATATATATATATATATATATA
                                   ||||||||||||||||||||||||
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                                ATATATATATATATATATATATAT

GAM2870  EDNRA    3'  TGATATGTATATACATATATAT 42001    T    A
                                A ATAT TATATATATATATAT
                                | |||| ||||||||||||||||
                                A TATA ATATATGTATATATA
                                 C    C
GAM2870  ELMO2    3'  TATATAAATATATATACAC    39314        T
                                TATATA ATATATATATAT
                                |||||| ||||||||||||
                                ATATAT TATATATATGTG
                                    T
GAM2870  EP300    3'  TATATTTATATATATTTATATA 10997       A        A
                TA                    TATAT TATATATAT TATATATA
                                |||||| ||||||||| ||||||||
                                ATATA ATATATATA ATATATAT
                                   A        A
GAM2870  EP300    3'  TATTTATATATATTTATATATA 10998     A        A
                TA                    TAT TATATATAT TATATATATA
                                ||| ||||||||| ||||||||||
                                ATA ATATATATA ATATATATAT
                                  A        A
GAM2870  EP300    3'  TATATATATTTATATATATATA 10994          A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                     A
GAM2870  EP300    3'  TATATTTATATATATATA     10996       A
                                TATAT TATATATATATA
                                ||||| ||||||||||||
                                ATATA ATATATATATAT
                                   A
GAM2870  ETV6     3'  TATATATATATAATAGATATAT 12763            T   T
                A                     TATATATATATA ATA ATATATA
                                |||||||||||| ||| |||||||
                                ATATATATATAT TAT TATATAT
                                        _  C
GAM2870  F9       3'  TATATATATATTATATATATA  6581             A
                                TATATATATAT TATATATATA
                                |||||||||||| ||||||||||
                                ATATATATATA ATATATATAT
                                        _
GAM2870  FACL4    3'  CATATATATATGCATATATATA 35676            A
                                TATATATATAT TATATATATA
                                |||||||||||| ||||||||||
                                GTATATATATA GTATATATAT
                                      C
GAM2870  FGFR3    3'  TATATATATAGATATATATA   6618            T
                                TATATATATA ATATATATA
                                |||||||||| |||||||||
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ATATATATAT TATATATAT
C
GAM2870 FGFR3 3' TATATATATATGTATATATAC 6622 A
TATATATATAT TATATATAT
ATATATATATA ATATATATG
C
GAM2870 FGFR3 3' TATATATATATATGTATATATA 6621 A III
T TATATATATATAT TATATATA T
ATATATATATATA ATATATAT A
C III
GAM2870 FGFR3 3' TATATATATGTATATATACCAT 6624 A _
ATA TATATATAT TATATATAT ATATA
ATATATATA ATATATATG TATAT
C G
GAM2870 FGFR3 3' CATATATGTTATATATATATAT 6612 A_
TATATAT TATATATATATAT
GTATATA ATATATATATATA
CA
GAM2870 FOXF1 3' TATATATATTTATATAAAACAT 11124 A T_
AT TATATATAT TATATA ATATAT
ATATATATA ATATAT TGTATA
A TT
GAM2870 GTF2H1 3' TATATATGTACATACACAT 23693 A
TATATAT TATATATATAT
ATATATA ATGTATGTGTA
C
GAM2870 HDAC4 3' ATATATATTATACATATATATA 25746 A
ATATATAT TATATATATATATA
TATATATA ATATGTATATATAT
_
GAM2870 HDAC4 3' TATACATATATATATTTATTTA 25782 A A
TA TATATATATATATAT TAT TATA
ATATGTATATATATA ATA ATAT
A A
GAM2870 HOXC4 3' TATATATATATATATATATATA 31159 III
T TATATATATATATATATATATA T
ATATATATATATATATATATAT A
III
GAM2870 HOXC4 3' TATATATATATATATATATAT 31157
TATATATATATATATATATAT

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                                ATATATATATATATATATATA

GAM2870  HS2ST1   3'  ATATATATATATATGTATATAT 29324              A     TAIII
              T                  ATATATATATATAT TATATA     T
                                 |||||||||||||| ||||||     |
                                 TATATATATATATA ATATAT     A
                                          C      IIIAT
GAM2870  IFNW1    5'  TATATAATATATATTCATATAT 13484        _      A
              ATA                  TATATA TATATAT TATATATATA
                                   |||||| ||||||| ||||||||||
                                   ATATAT ATATATA GTATATATAT
                                      T      A
GAM2870  IFNW1    5'  TATATAATATATATTCATATAT 13484        _      A
              ATA                  TATATA TATATAT TATATATATA
                                   |||||| ||||||| ||||||||||
                                   ATATAT ATATATA GTATATATAT
                                      T      A
GAM2870  IFNW1    5'  TATATATAATATATATTCATAT 13485        _      A
              ATA                  TATATATA TATATAT TATATATA
                                   |||||||| ||||||| ||||||||
                                   ATATATAT ATATATA GTATATAT
                                        T      A
GAM2870  IGFBP1   3'  TATATATATATACATATA    8249
                                   TATATATATATATATATA
                                   ||||||||||||||||||
                                   ATATATATATATGTATAT

GAM2870  IGFBP1   3'  TATATATACATATACATATATA 8247
              TA                   TATATATATATATATATATATATA
                                   |||||||||||||||||||||||||
                                   ATATATATGTATATGTATATATAT

GAM2870  IGFBP1   3'  TATATACATATACATATATATA 8246
              TA                   TATATATATATATATATATATATA
                                   |||||||||||||||||||||||||
                                   ATATATGTATATGTATATATATAT

GAM2870  IGFBP1   3'  TATATATATACATATACATATA 8248
              TA                   TATATATATATATATATATATATA
                                   |||||||||||||||||||||||||
                                   ATATATATATGTATATGTATATAT

GAM2870  INPP5A   3'  TATTTATATATATTTATATATA 24412     A       A
              TA                   TAT TATATATAT TATATATATA
                                   ||| ||||||||| ||||||||||
                                   ATA ATATATATA ATATATATAT
                                     A       A
GAM2870  INPP5A   3'  TATATATATTTATATATATATA 24409          A
                                   TATATATAT TATATATATATA
                                   ||||||||| ||||||||||||
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                                ATATATATA ATATATATATAT
                                      A
GAM2870  INPP5A   3'  TATATTTATATATATTTATATA 24411       A        A
            TA                    TATAT TATATATAT TATATATA
                                  ||||| ||||||||| ||||||||
                                  ATATA ATATATATA ATATATAT
                                    A        A
GAM2870  KAL1     3'  TATATACATGTATATGTACATA 6873          A     A
            TA                    TATATATAT TATAT TATATATA
                                  ||||||||| ||||| ||||||||
                                  ATATATGTA ATATA ATGTATAT
                                      C     C
GAM2870  KCNH5    3'  ATATATATATGTATATAC     40255          A
                                  ATATATATAT TATATAT
                                  |||||||||| |||||||
                                  TATATATATA ATATATG
                                       C
GAM2870  KCNH5    3'  TATATATATGTATATACTGTAT 40261          A      A_
            ATA                    TATATATAT TATATAT  TATATA
                                  ||||||||| |||||||  ||||||
                                  ATATATATA ATATATG  ATATAT
                                      C       AC
GAM2870  KCNH5    3'  TATATACTGTATATACACACAT 40260        A_
            AT                     TATATAT  TATATATATATATAT
                                  |||||||  ||||||||||||||
                                  ATATATG  ATATATGTGTGTATA
                                      AC
GAM2870  KCNH5    3'  TATATACACACATATGTATATA 40259             A      III
            TA                     TATATATATATATAT TATATA   TA
                                  |||||||||||||| ||||||   ||
                                  ATATATGTGTGTATA ATATAT   AT
                                           C      III
GAM2870  KIF3C    3'  TATATATATTTATATATTACAT 13956          A      _
            AT                     TATATATAT TATATAT ATATAT
                                  ||||||||| ||||||| ||||||
                                  ATATATATA ATATATA TGTATA
                                      A      A
GAM2870  KPNA4    3'  TATATATGTATATATATATATA 13995        A
            TA                     TATATAT TATATATATATATATA
                                  ||||||| ||||||||||||||||
                                  ATATATA ATATATATATATATAT
                                      C
GAM2870  KPNA4    3'  TATATATATGTATATATATATA 13992          A          III
            T                      TATATATAT TATATATATATA   T
                                  ||||||||| ||||||||||||   |
                                  ATATATATA ATATATATATAT   A
                                      C          III
GAM2870  KPNA4    3'  TATATGTATATATATATATATA 13997       A
            TA                     TATAT TATATATATATATATATA
                                  ||||| ||||||||||||||||||
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                                ATATA ATATATATATATATATAT
                                  C
GAM2870  KPNA4    3'  TATATATATATATATACA    13989
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATGT

GAM2870  LYPLA1   3'  TATGTATATATGAACACATATA 26760     A      AT
                TA                  TAT TATATAT  ATATATATATA
                                ||| |||||||  ||||||||||
                                ATA ATATATA  TGTGTATATAT
                                  C      CT
GAM2870  MAGEL2   3'  TATATTTATATATATAGATATA 33300       A         T
                                TATAT TATATATATA ATATA
                                ||||| |||||||||| |||||
                                ATATA ATATATATAT TATAT
                                   A         C
GAM2870  MAP2     3'  TATATATATATTTATATCTATA 36506          A     A
                                TATATATATAT TATAT TATA
                                |||||||||||| ||||| ||||
                                ATATATATATA ATATA ATAT
                                      A     G
GAM2870  MAP3K12  3'  TATATATATATATGTATATATA 26690           A
                TA                  TATATATATATAT TATATATATA
                                |||||||||||| ||||||||||
                                ATATATATATATA ATATATATAT
                                      C
GAM2870  MAP3K12  3'  TATATATATATGTATATATATA 26692          A
                TA                  TATATATATAT TATATATATATA
                                |||||||||||| ||||||||||||
                                ATATATATATA ATATATATATAT
                                      C
GAM2870  MAP3K12  3'  CATATATATATATATATGTATA 26678              A    III
                T                   TATATATATATATATAT TATA   T
                                |||||||||||||||| ||||   |
                                GTATATATATATATATA ATAT   A
                                      C    III
GAM2870  MAP3K12  3'  TATATATATATATATGTATATA 26688            A
                TA                  TATATATATATATAT TATATATA
                                |||||||||||||| ||||||||
                                ATATATATATATATA ATATATAT
                                      C
GAM2870  MAP3K12  3'  TATGTATATATATATAATCCAT 26694     A         TA_
                ATA                  TAT TATATATATATA   TATATA
                                ||| ||||||||||||   ||||||
                                ATA ATATATATATAT   GTATAT
                                  C          TAG
GAM2870  MBNL     3'  TATATATATCTATTATATATAT 34321         A   A
                A                   TATATATAT TAT TATATATATA
                                |||||||||| ||| ||||||||||
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                                ATATATATA ATA ATATATATAT
                                      G  _
GAM2870  MEF2A    3'  ATATATATATGTATGTACATAT 24622          A   A
              A                  ATATATATAT TAT TATATATA
                                 |||||||||| ||| ||||||||
                                 TATATATATA ATA ATGTATAT
                                       C   C
GAM2870  MEN1     3'  TATATATGTATATATATATGTA 39223        A         A
              TA                   TATATAT TATATATATAT TATA
                                   ||||||| |||||||||| ||||
                                   ATATATA ATATATATATA ATAT
                                       C          C
GAM2870  MEN1     3'  TATATATATATGTATATATATA 39216           A
              T                    TATATATATAT TATATATATAT
                                   |||||||||| ||||||||||
                                   ATATATATATA ATATATATATA
                                         C
GAM2870  MEN1     3'  TATATATATATGTATATATATA 39217           A
              TA                   TATATATATAT TATATATATATA
                                   |||||||||| ||||||||||
                                   ATATATATATA ATATATATATAT
                                         C
GAM2870  MEN1     3'  TATATATATATATATACATATA 39255
                                   TATATATATATATATATATATA
                                   ||||||||||||||||||||
                                   ATATATATATATATATGTATAT

GAM2870  MEN1     3'  TATATATATGTATATATATAT  39218          A
                                   TATATATAT TATATATATAT
                                   ||||||||| ||||||||||
                                   ATATATATA ATATATATATA
                                         C
GAM2870  MEN1     3'  CATATATATATATATACATATA 39164
              TA                   TATATATATATATATATATATATA
                                   ||||||||||||||||||||
                                   GTATATATATATATATGTATATAT

GAM2870  MEN1     3'  TATATATATATACATATATATA 39208
              TA                   TATATATATATATATATATATATA
                                   ||||||||||||||||||||
                                   ATATATATATATGTATATATATAT

GAM2870  MEN1     3'  TATATATGTATATATATATATA 39222        A
              TA                   TATATAT TATATATATATATATA
                                   ||||||| ||||||||||||||
                                   ATATATA ATATATATATATATAT
                                       C
GAM2870  MEN1     3'  TATATGTATATATATATGTATA 39226       A         A
              TA                   TATAT TATATATATAT TATATA
                                   ||||| |||||||||| ||||||
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                                ATATA ATATATATATA ATATAT
                                  C         C
GAM2870  MEN1     3'  TATATATATATATATACATATA 39211
                TA                  TATATATATATATATATATATATA
                                    |||||||||||||||||||||||
                                    ATATATATATATATATGTATATAT

GAM2870  MEN1     3'  TATATATATGTATATATATATA 39220          A
                TA                  TATATATAT TATATATATATATA
                                    ||||||||| |||||||||||||
                                    ATATATATA ATATATATATATAT
                                          C
GAM2870  MEN1     3'  TATGTATATATATATGTATATA 39230     A         A
                TA                  TAT TATATATATAT TATATATA
                                    ||| |||||||||| ||||||||
                                    ATA ATATATATATA ATATATAT
                                      C         C
GAM2870  MEN1     3'  TATACATATATATATAAAC    39202              T
                                    TATATATATATATATA AT
                                    |||||||||||||||| ||
                                    ATATGTATATATATAT TG
                                              T
GAM2870  MEN1     3'  TATATATATATGTATATATATA 39215           A
                                    TATATATATAT TATATATATA
                                    |||||||||| ||||||||||
                                    ATATATATATA ATATATATAT
                                          C
GAM2870  MEN1     3'  TATATATATATATACATATATA 39254
                TA                  TATATATATATATATATATATATA
                                    |||||||||||||||||||||||||
                                    ATATATATATATATGTATATATAT

GAM2870  MEN1     3'  TAAATATATATATATATA     39197     T
                                    TA ATATATATATATATA
                                    || ||||||||||||||
                                    AT TATATATATATATAT
                                     T
GAM2870  MOX2     3'  TATATATATATATAAATA     42521              T
                                    TATATATATATATA ATA
                                    |||||||||||||| |||
                                    ATATATATATATAT TAT
                                              T
GAM2870  MSX2     3'  TATATATATATTTATACATA   42301           A
                                    TATATATATAT TATATATA
                                    |||||||||| ||||||||
                                    ATATATATATA ATATGTAT
                                          A
GAM2870  MYBL1    3'  ATATATATATATATAAAATAT  41975               TAT
                                    ATATATATATATATA   ATAT
                                    ||||||||||||||   ||||
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                                TATATATATATATAT   TATA
                                        TT_
GAM2870  MYCL2    3'  TACATATATACATACATATATA 23906
                TA                    TATATATATATATATATATATATA
                                      |||||||||||||||||||||||||
                                      ATGTATATATGTATGTATATATAT

GAM2870  MYCL2    3'  TACATATATATATACATATATA 23908
                                      TATATATATATATATATATATA
                                      |||||||||||||||||||||
                                      ATGTATATATATATGTATATAT

GAM2870  MYCL2    3'  TATATATACATATATACATATA 23909
                TA                    TATATATATATATATATATATATA
                                      |||||||||||||||||||||||||
                                      ATATATATGTATATATGTATATAT

GAM2870  MYCL2    3'  TACATATATATATACATATAT  23907
                                      TATATATATATATATATATAT
                                      ||||||||||||||||||||
                                      ATGTATATATATATGTATATA

GAM2870  NOV      3'  TACATGTATGTATACACATATA 14813       A   A
                                      TATAT TAT TATATATATATA
                                      ||||| ||| ||||||||||||
                                      ATGTA ATA ATATGTGTATAT
                                         C   C
GAM2870  NRF1     3'  TATATATATACTTTATATATAT 41097           A_
                                      TATATATATAT  TATATATAT
                                      ||||||||||  |||||||||
                                      ATATATATATG  ATATATATA
                                            AA
GAM2870  NRF1     3'  TATATATATATATGTATATATA 41103            A
                TA                    TATATATATATAT TATATATATA
                                      |||||||||||| ||||||||||
                                      ATATATATATATA ATATATATAT
                                            C
GAM2870  NRF1     3'  TATATATATATATATATGTATA 41099               A
                TA                    TATATATATATATATAT TATATA
                                      |||||||||||||||| ||||||
                                      ATATATATATATATATA ATATAT
                                               C
GAM2870  NRF1     3'  TATATATATACTTTATATATAT 41097           A_
                                      TATATATATAT  TATATATAT
                                      ||||||||||  |||||||||
                                      ATATATATATG  ATATATATA
                                            AA
GAM2870  NRF1     3'  CATACATATATATATATATATA 41091
                T                     TATATATATATATATATATATAT
                                      |||||||||||||||||||||||
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                                GTATGTATATATATATATATATA

GAM2870  NRF1     3'  TATATATATATATATGTATATA 41101              A
                   TA                    TATATATATATATAT TATATATA
                                         |||||||||||||||| ||||||||
                                         ATATATATATATATA ATATATAT
                                                   C
GAM2870  NRIP1    3'  TATATATATATATATATAAAAT 40978               T_
                   ATA                    TATATATATATATATATA  ATATA
                                          |||||||||||||||||  |||||
                                          ATATATATATATATATAT  TATAT
                                                    TT
GAM2870  NRIP1    3'  TATATATATATATATATATATA 40982                  III
                   T                      TATATATATATATATATATATA   T
                                          ||||||||||||||||||||||   |
                                          ATATATATATATATATATATAT   A
                                                     III
GAM2870  NRIP1    3'  TATATATATATATATATATATA 40983
                   TA                     TATATATATATATATATATATATA
                                          ||||||||||||||||||||||||
                                          ATATATATATATATATATATATAT

GAM2870  NRIP1    3'  TATATATATATATATAAAATAT 40976               T_
                   ATA                    TATATATATATATATA  ATATATA
                                          ||||||||||||||||  |||||||
                                          ATATATATATATATAT  TATATAT
                                                    TT
GAM2870  NRIP1    3'  TATATATATATATATATATA   40980
                                          TATATATATATATATATATA
                                          ||||||||||||||||||||
                                          ATATATATATATATATATAT

GAM2870  NRIP1    3'  TACATATTATATATATATATAT 40969          _
                   ATA                      TATATAT ATATATATATATATATA
                                            ||||||| ||||||||||||||||
                                            ATGTATA TATATATATATATATAT
                                                 A
GAM2870  NRIP1    3'  ATATATATATATATACATA    40953
                                            ATATATATATATATATATA
                                            ||||||||||||||||||
                                            TATATATATATATATGTAT

GAM2870  OTX1     3'  TATATATATGTATATATATATA 30996           A
                   TA                       TATATATAT TATATATATATATA
                                            ||||||||| |||||||||||||
                                            ATATATATA ATATATATATATAT
                                                  C
GAM2870  OTX1     3'  TATATATATATGTATATATATA 30993            A
                                            TATATATATAT TATATATATA
                                            |||||||||| |||||||||
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                                ATATATATATA ATATATATAT
                                      C
GAM2870  OTX1     3'  TATATATATATGTATATATATA 30994          A
                TA                  TATATATATAT TATATATATATA
                                    |||||||||||| ||||||||||||
                                    ATATATATATA ATATATATATAT
                                          C
GAM2870  OTX1     3'  TATATATATATGTATATATA   30991          A
                                    TATATATATAT TATATATA
                                    |||||||||||| ||||||||
                                    ATATATATATA ATATATAT
                                          C
GAM2870  OTX1     3'  TATATATGTATATATATATATA 30998        A
                T                    TATATAT TATATATATATATAT
                                    ||||||| ||||||||||||||||
                                    ATATATA ATATATATATATATA
                                         C
GAM2870  OTX1     3'  TATATATGTGTATATATATAT  30999        ATA
                                    TATATAT   TATATATATAT
                                    |||||||   ||||||||||||
                                    ATATATA   ATATATATATA
                                         CAC
GAM2870  OTX1     3'  TATATGTATATATATATATAT  31000       A
                                    TATAT TATATATATATATAT
                                    ||||| ||||||||||||||||
                                    ATATA ATATATATATATATA
                                       C
GAM2870  PCSK2    3'  TATATATATAGCACTATATATA 15132          TATA
                                    TATATATATA    TATATATA
                                    ||||||||||    ||||||||
                                    ATATATATAT    ATATATAT
                                          CGTG
GAM2870  PCSK2    3'  TATGTATATATACACATATATA 15136     A
                                    TAT TATATATATATATATATA
                                    ||| ||||||||||||||||||
                                    ATA ATATATATGTGTATATAT
                                      C
GAM2870  PEA15    3'  TATACATATATGTAGAATATAT 19082          A  T_
                AT                   TATATATATAT TA  ATATATAT
                                    |||||||||||  ||  ||||||||
                                    ATATGTATATA AT  TATATATA
                                          C  CT
GAM2870  PEX3     3'  TATATATATATATGTATATA   18851           A
                                    TATATATATATAT TATATA
                                    |||||||||||||  ||||||
                                    ATATATATATATA ATATAT
                                          C
GAM2870  PEX3     3'  TATATATATATATATGTATATA 18850            A     III
                T                    TATATATATATATAT TATATA   T
                                    |||||||||||||||  ||||||   |
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                                ATATATATATATATA ATATAT   A
                                          C     III
GAM2870  PITPNB   3'  TATGTACATATATACACA    29626     A
                                TAT TATATATATATATA
                                ||| ||||||||||||||
                                ATA ATGTATATATGTGT
                                  C
GAM2870  PKIA     3'  TATATATATATATATATAT    27746
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM2870  PKIA     3'  ATATATATATATATATATA    27736
                                ATATATATATATATATATA
                                ||||||||||||||||||
                                TATATATATATATATATAT

GAM2870  PLXNA1   3'  TATATATGCATATATATACAT  43628        A
                                TATATAT TATATATATATAT
                                ||||||| ||||||||||||
                                ATATATA GTATATATATGTA
                                    C
GAM2870  PLXNA1   3'  CATATATATATATGCATATATA 43618           A
           TA                     TATATATATATAT TATATATATA
                                ||||||||||||| |||||||||
                                GTATATATATATA GTATATATAT
                                        C
GAM2870  PMX1     3'  ATATATATATAAATATATA    27908          T
                                ATATATATATA ATATATA
                                |||||||||| |||||||
                                TATATATATAT TATATAT
                                       T
GAM2870  PMX1     3'  TATATATATATATATATATATA 35522
           TA                     TATATATATATATATATATATATA
                                ||||||||||||||||||||||||
                                ATATATATATATATATATATATAT

GAM2870  PMX1     3'  ATATATATATATATATATATAT 35501                  III
           AT                     ATATATATATATATATATATATA   T
                                ||||||||||||||||||||||||  |
                                TATATATATATATATATATATAT   A
                                          III
GAM2870  PMX1     3'  TATATATATATATGAAATATAT 35524           AT_
           A                      TATATATATATAT   ATATATA
                                ||||||||||||||  |||||||
                                ATATATATATATA   TATATAT
                                       CTT
GAM2870  PMX1     3'  TATATATAAATATATAAATATA 35519        T      T
           TA                     TATATATA ATATATA ATATATA
                                ||||||||| ||||||| |||||||
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                                ATATATAT TATATAT TATATAT
                                    T      T
GAM2870  PMX1     3'  TATATATATATATGAAATATAT 35525           AT_
             ATA                  TATATATATATAT   ATATATATA
                                  ||||||||||||   |||||||||
                                  ATATATATATATA   TATATATAT
                                      CTT
GAM2870  PMX1     3'  TATATATATATATGAAATATAT 35526           ___
             ATATA                 TATATATATATAT   ATATATATATA
                                   ||||||||||||   ||||||||||
                                   ATATATATATATA   TATATATATAT
                                       CTT
GAM2870  PMX1     3'  TATAAATATATACAGTATATAT 35518      T      _
             ATA                   TATA ATATATATA TATATATATA
                                   ||||| ||||||||| ||||||||||
                                   ATAT TATATATGT ATATATATAT
                                     T        C
GAM2870  PMX1     3'  ATATATATATATATATATATAT 27909                TAIII
             T                     ATATATATATATATATATATA     T
                                   ||||||||||||||||||||||    |
                                   TATATATATATATATATATAT     A
                                          IIIAT
GAM2870  PPARGC1  3'  TATATATATATATATATATATT 29964                TAIII
                                   TATATATATATATATATATA     T
                                   ||||||||||||||||||||     |
                                   ATATATATATATATATATAT     A
                                          IIIAT
GAM2870  PPARGC1  3'  TATATATATATATATATATATA 29962                  III
             T                     TATATATATATATATATATATA   T
                                   ||||||||||||||||||||||   |
                                   ATATATATATATATATATAT   A
                                          III
GAM2870  PRKCN    3'  TATATATATATATATATATATA 25166                TAIII
             TA                    TATATATATATATATATATA     TA
                                   ||||||||||||||||||||     ||
                                   ATATATATATATATATATAT     AT
                                          IIIAT
GAM2870  PTPRK    3'  TATATATATTTATATATTTATA 15966          A      A
             TA                    TATATATAT TATATAT TATATA
                                   ||||||||| ||||||| ||||||
                                   ATATATATA ATATATA ATATAT
                                       A      A
GAM2870  PUM1     3'  TATATATATATATATATATATA 31238                  III
             T                     TATATATATATATATATATATA   T
                                   ||||||||||||||||||||||   |
                                   ATATATATATATATATATAT   A
                                          III
GAM2870  PUM1     3'  ATATATATATATATATAT    31230
                                   ATATATATATATATATAT
                                   ||||||||||||||||||
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                                TATATATATATATATATA

GAM2870  RAG2     3'  TATATGTATACATATATTTATA 44367       A          A
                                TATAT TATATATATAT TATA
                                ||||| |||||||||||| ||||
                                ATATA ATATGTATATA ATAT
                                   C          A
GAM2870  RBL1     3'  TATTTATATATATATATATA   16178     A
                                TAT TATATATATATATATA
                                ||| ||||||||||||||||
                                ATA ATATATATATATATAT
                                  A
GAM2870  RBP3     3'  TATATACATACACATATATAT  16189
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATATATGTATGTGTATATATA

GAM2870  RBP3     3'  CATACACATATATATGTGTATA 16184              ATA
              TA                  TATATATATATATAT   TATATA
                                ||||||||||||||   ||||||
                                GTATGTGTATATATA   ATATAT
                                        CAC
GAM2870  RBP3     3'  TATACATACACATATATAT    16188
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATGTATGTGTATATATA

GAM2870  RBP3     3'  TATATACATATATATACATA   16190
                                TATATATATATATATATATA
                                ||||||||||||||||||||
                                ATATATGTATATATATGTAT

GAM2870  RBP3     3'  TATATATACATACACATATATA 16192
              T                   TATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                ATATATATGTATGTGTATATATA

GAM2870  RBP3     3'  CATATATATATACATATATATA 16185
                                TATATATATATATATATATATA
                                ||||||||||||||||||||
                                GTATATATATATGTATATATAT

GAM2870  RGR      3'  TACATATATATAACGTTTATAT 16305           TATA_
              AT                  TATATATATATA    TATATAT
                                ||||||||||||    |||||||
                                ATGTATATATAT    ATATATA
                                       TGCAA
GAM2870  RNTRE    3'  CATATATATATATATATATATA 31250                 III
              TA                  TATATATATATATATATATATA   TA
                                ||||||||||||||||||||||  ||
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                                GTATATATATATATATATATAT   AT
                                                    III
GAM2870  RNTRE    3'  CATATATATATATATATATATA 31250                TAIII
                TA                    TATATATATATATATATATA    TA
                                      ||||||||||||||||||||    ||
                                      GTATATATATATATATATAT    AT
                                                 IIIAT
GAM2870  ROCK2    3'  TATATATATATATATATAT   42362
                                      TATATATATATATATATAT
                                      ||||||||||||||||||
                                      ATATATATATATATATATA

GAM2870  ROCK2    3'  TATATATATATATATATAT   42362
                                      TATATATATATATATATAT
                                      ||||||||||||||||||
                                      ATATATATATATATATATA

GAM2870  ROCK2    3'  TATATATATACACAGTATA  42360                 _
                                      TATATATATATATATA TATA
                                      |||||||||||||||| ||||
                                      ATATATATATATGTGT ATAT
                                                C
GAM2870  ROCK2    3'  TATATATATATATATATATGTA 42364                ATAIIIC
                A                     TATATATATATATATATAT      A
                                      ||||||||||||||||||       |
                                      ATATATATATATATATATA      T
                                                CIIIATA
GAM2870  RP42     3'  TATATATATATATATACACACA 33991
                TA                    TATATATATATATATATATATATA
                                      ||||||||||||||||||||||||
                                      ATATATATATATATATGTGTGTAT

GAM2870  RP42     3'  ATATATATATATATATATATAT 33982                  III
                AT                    ATATATATATATATATATATATA   T
                                      ||||||||||||||||||||||   |
                                      TATATATATATATATATATATAT   A
                                                III
GAM2870  RP42     3'  ATATATATATATATATATATAT 33983                TAIII
                T                     ATATATATATATATATATATA    T
                                      ||||||||||||||||||||    |
                                      TATATATATATATATATATAT    A
                                                 IIIAT
GAM2870  RP42     3'  TATATAGATATATAGATATATA 33989       T      T
                TA                    TATATA ATATATA ATATATATA
                                      |||||| ||||||| |||||||||
                                      ATATAT TATATAT TATATATAT
                                         C      C
GAM2870  RP42     3'  TATATATATATATATATATATA 33993
                TA                    TATATATATATATATATATATATA
                                      ||||||||||||||||||||||||
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ATATATATATATATATATATATAT
GAM2870 RP42 3' TACATATATATAGATATATA 33987 T
TATATATATATA ATATATA
ATGTATATATAT TATATAT
C
GAM2870 RPL23A 3' ATATATATATATATATAT 9738
ATATATATATATATATAT
TATATATATATATATATA
GAM2870 SEMA3F 3' TATATATATATATATATATATA 20063
TA TATATATATATATATATATATATA
ATATATATATATATATATATATAT
GAM2870 SEMA3F 3' ATATATATATATATATATATAT 20058 TAIII
T ATATATATATATATATATATA T
TATATATATATATATATATAT A
IIIAT
GAM2870 SEMA3F 3' ATATATATATATATATATATAT 20057 III
AT ATATATATATATATATATATATA T
TATATATATATATATATATATAT A
III
GAM2870 SEMA3F 3' ATATATATATATATATAT 20054
ATATATATATATATATAT
TATATATATATATATATA
GAM2870 SGCD 3' TATATATATTTATATATATTTA 7343 A A
TA TATATATAT TATATATAT TATA
ATATATATA ATATATATA ATAT
A A
GAM2870 SGCD 3' TATTTATATATATTTATATATA 7344 A A
TAT TATATATAT TATATATA
ATA ATATATATA ATATATAT
A A
GAM2870 SGCD 3' ATATATATATTTATTTATATAT 7340 A A
A ATATATATAT TAT TATATATA
TATATATATA ATA ATATATAT
A A
GAM2870 SLC10A2 3' TATATGAGTATACATACATATA 7819 ATA
TA TATAT TATATATATATATATA

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                                ATATA   ATATGTATGTATATAT
                                   CTC
GAM2870  SLC1A1    3'  ATATATACATATATATATATAT 20030
                A                   ATATATATATATATATATATATA
                                    |||||||||||||||||||||||
                                    TATATATGTATATATATATATAT

GAM2870  SLC1A1    3'  TATATACATATATATATATATA 20035
                TA                    TATATATATATATATATATATATA
                                      |||||||||||||||||||||||
                                      ATATATGTATATATATATATATAT

GAM2870  SLC8A1    3'  TATGTATATATATGTATATATA 34407     A       A       III
                T                    TAT TATATATAT TATATATA   T
                                     ||| ||||||||| ||||||||   |
                                     ATA ATATATATA ATATATAT   A
                                       C       C       III
GAM2870  SON       3'  TATATATATATTTACATATATA 38460           A
                TA                    TATATATATAT TATATATATATA
                                      |||||||||||| ||||||||||||
                                      ATATATATATA ATGTATATATAT
                                            A
GAM2870  SORCS3    3'  TATATGTACATATACTGTATAT 31426       A       A_
                ATA                    TATAT TATATATAT  TATATATA
                                       ||||| |||||||||  ||||||||
                                       ATATA ATGTATATG  ATATATAT
                                          C        AC
GAM2870  SRGAP1    5'  ATATATATATATATATATATAT 43598                  III
                AT                    ATATATATATATATATATATATA   T
                                      |||||||||||||||||||||||   |
                                      TATATATATATATATATATATAT   A
                                                    III
GAM2870  SRGAP1    5'  TATATATATATATATATATATA 43610
                TA                    TATATATATATATATATATATATA
                                      |||||||||||||||||||||||
                                      ATATATATATATATATATATATAT

GAM2870  SRGAP1    5'  TATATATATATATATATATAT  43608
                                      TATATATATATATATATATAT
                                      ||||||||||||||||||||
                                      ATATATATATATATATATATA

GAM2870  SRGAP1    5'  TATATATAAATATATATATATA 43607         T
                TA                    TATATATA ATATATATATATATA
                                      |||||||| ||||||||||||||
                                      ATATATAT TATATATATATATAT
                                            T
GAM2870  STAM      3'  TATATATATACACACACATATA 18464
                TA                    TATATATATATATATATATATATA
                                      |||||||||||||||||||||||||
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                              ATATATATATGTGTGTGTATATAT

GAM2870  STAM     3'  TATATATATATACACACACATA 18465
                TA                TATATATATATATATATATATATA
                                  ||||||||||||||||||||||||
                                  ATATATATATATGTGTGTGTATAT

GAM2870  STAM     3'  TATATACACACACATATATATA 18461
                TA                TATATATATATATATATATATATA
                                  ||||||||||||||||||||||||
                                  ATATATGTGTGTGTATATATATAT

GAM2870  STAM     3'  TATATATACACACACATATATA 18463
                TA                TATATATATATATATATATATATA
                                  ||||||||||||||||||||||||
                                  ATATATATGTGTGTGTATATATAT

GAM2870  STAM     3'  TATACACACACATATATATATA 18460
                TA                TATATATATATATATATATATATA
                                  ||||||||||||||||||||||||
                                  ATATGTGTGTGTATATATATATAT

GAM2870  STK4     3'  TATATATATATATGCATATTTA 26585          A    A
                TA                TATATATATATAT TATAT TATA
                                  |||||||||||||  |||||  |||||
                                  ATATATATATATA GTATA ATAT
                                            C     A
GAM2870  SVIL     3'  TATATAAATATATATATA    34732       T
                                  TATATA ATATATATATA
                                  ||||||  ||||||||||
                                  ATATAT TATATATATAT
                                      T
GAM2870  TGFBR2   3'  TATAGATATATATATATATATA 17478     T
                TA                TATA ATATATATATATATATATA
                                  ||||  ||||||||||||||||||
                                  ATAT TATATATATATATATATAT
                                    C
GAM2870  TGFBR2   3'  ATATATATATATATATAAAACA 17470            T_
                TA                ATATATATATATATATA  ATATA
                                  ||||||||||||||||  |||||
                                  TATATATATATATATAT  TGTAT
                                             TT
GAM2870  TGFBR2   3'  TATATAGATATATATATATATA 17480       T
                TA                TATATA ATATATATATATATATA
                                  ||||||  ||||||||||||||||
                                  ATATAT TATATATATATATATAT
                                     C
GAM2870  TMEPAI   3'  TATATATATTTATATATATA   33620         A
                                  TATATATAT TATATATATA
                                  |||||||||  ||||||||||
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                                ATATATATA ATATATATAT
                                      A
GAM2870  TNFSF9   3'  TATATATATATATATAATATAT 19197              T
            A                    TATATATATATATATA ATATATA
                                 ||||||||||||||| |||||||
                                 ATATATATATATATAT TATATAT
                                                 _
GAM2870  TNFSF9   3'  TATATATATATATATAATATAT 19198              _
            ATA                   TATATATATATATATA TATATATA
                                  |||||||||||||||| ||||||||
                                  ATATATATATATATAT ATATATAT
                                        T
GAM2870  TP63     3'  TATATTTATACATTTATATATA 19002       A      A
            TA                    TATAT TATATAT TATATATATA
                                  ||||| ||||||| ||||||||||
                                  ATATA ATATGTA ATATATATAT
                                     A      A
GAM2870  TRAM     3'  ATACAAATATATATATATATA  30699       T
                                  ATATA ATATATATATATATA
                                  ||||| ||||||||||||||
                                  TATGT TATATATATATATAT
                                     T
GAM2870  TRPM6    3'  CATATATATTATATATATA    32787          A
                                  TATATATAT TATATATATA
                                  |||||||| |||||||||
                                  GTATATATA ATATATATAT
                                           _
GAM2870  TRPM6    3'  ATATATATATATATATAAAATA 32786               T_
            TA                     ATATATATATATATATA  ATATA
                                   |||||||||||||||  |||||
                                   TATATATATATATATAT  TATAT
                                         TT
GAM2870  TRPM6    3'  ATAAAAATATATATATATATAT 32784     TAT
            A                     ATA   ATATATATATATATATA
                                  |||   ||||||||||||||||
                                  TAT   TATATATATATATATAT
                                    TTT
GAM2870  TRPM6    3'  TATATATATAATATATATA    32801          T
                                  TATATATATA ATATATATA
                                  ||||||||| |||||||||
                                  ATATATATAT TATATATAT
                                           _
GAM2870  TRPM6    3'  TATATATATAAAAATATATATA 32800          TAT       III
            T                     TATATATATA   ATATATATA   T
                                  |||||||||   |||||||||  |
                                  ATATATATAT   TATATATAT   A
                                         TTT       III
GAM2870  TRPM6    3'  TATATAATATATATATTCCATA 32797       _       A_
            TATA                    TATATA TATATATAT  TATATATA
                                    |||||| |||||||||  ||||||||
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                                ATATAT ATATATATA  GTATATAT
                                   T        AG
GAM2870  TRPM6    3'  TATATATATATATAAAATATAT 32803            T_
                ATA                  TATATATATATATA  ATATATATA
                                     ||||||||||||||  |||||||||
                                     ATATATATATATAT  TATATATAT
                                           TT
GAM2870  UBE2H    3'  TATATAATATATATATAT     17807        T
                                     TATATA ATATATATATAT
                                     ||||||| ||||||||||||
                                     ATATAT TATATATATATA

                                       _
GAM2870  VEGF     3'  TATATATATATAATATATATAT 17967            T
                A                     TATATATATATA ATATATATATA
                                     ||||||||||||| ||||||||||
                                     ATATATATATAT TATATATATAT

                                         _
GAM2870  VEGF     3'  TACATAAACATATATATATATA 17962        T
                TA                     TATATA ATATATATATATATATA
                                     ||||||| ||||||||||||||||||
                                     ATGTAT TGTATATATATATATAT
                                        T
GAM2870  VEGF     3'  ATATATATATATATAAATGTAT 17941              T  A
                                     ATATATATATATATA AT TAT
                                     |||||||||||||| || |||
                                     TATATATATATATAT TA ATA
                                           T  C
GAM2870  VEGF     3'  TATATATATATATATACA     17970
                                     TATATATATATATATATA
                                     ||||||||||||||||||
                                     ATATATATATATATATGT

GAM2870  VEGF     3'  TATACATAAACATATATATATA 17963         T
                TA                     TATATATA ATATATATATATATA
                                     |||||||| ||||||||||||||
                                     ATATGTAT TGTATATATATATAT
                                          T
GAM2870  VEGF     3'  CATAAACATATATATATATATA 17944      T
                TA                     TATA ATATATATATATATATATA
                                     |||| ||||||||||||||||||
                                     GTAT TGTATATATATATATATAT
                                       T
GAM2870  VEGF     3'  TATATATATAATATATATATAT 17966          _
                ATA                    TATATATATA TATATATATATATA
                                     |||||||||| ||||||||||||||
                                     ATATATATAT ATATATATATATAT
                                           T
GAM2870  VEGF     3'  ATATATATATTTTATATATATA 17942          ATA
                                     ATATATATAT   TATATATATA
                                     |||||||||   ||||||||||
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                                TATATATATA  ATATATATAT
                                     AA_
GAM2870  VEGF     3'  TATATATATATATACACACAAA 17969                T
                TA                  TATATATATATATATATATA ATA
                                    |||||||||||||||||||| |||
                                    ATATATATATATATGTGTGT TAT
                                                T
GAM2870  VEGF     3'  TATATATATATAATATATATAT 17968           _
                ATA                  TATATATATATA TATATATATATA
                                    |||||||||||| ||||||||||||
                                    ATATATATATAT ATATATATATAT
                                          T
GAM2870  VENTX2   3'  TACATATATACGTACATATATA 30918          TA
                TA                  TATATATATA  TATATATATATA
                                    ||||||||||  ||||||||||||
                                    ATGTATATAT  ATGTATATATAT
                                         GC
GAM2870  VENTX2   3'  TATGTATATATATATTTATATA 30924     A         A
                TA                  TAT TATATATATAT TATATATA
                                    ||| |||||||||| ||||||||
                                    ATA ATATATATATA ATATATAT
                                      C          A
GAM2870  VENTX2   3'  CACACACATATATGTATATATA 30910            A
                TA                  TATATATATATAT TATATATATA
                                    |||||||||||| ||||||||||
                                    GTGTGTGTATATA ATATATATAT
                                           C
GAM2870  VENTX2   3'  TATATGTATATATATATTTATA 30923       A         A
                TA                  TATAT TATATATATAT TATATA
                                    ||||| |||||||||| ||||||
                                    ATATA ATATATATATA ATATAT
                                       C          A
GAM2870  VENTX2   3'  TACATATATATATTTATATATA 30919            A
                                    TATATATATATAT TATATATA
                                    |||||||||||| ||||||||
                                    ATGTATATATATA ATATATAT
                                           A
GAM2870  VENTX2   3'  ATATATATATATATATATATAT 30909                  TAIII
                T                    ATATATATATATATATATATA    T
                                    |||||||||||||||||||||    |
                                    TATATATATATATATATATAT    A
                                                IIIAT
GAM2870  VENTX2   3'  TATATATTTATATATACGTATA 30922        A       TA
                T                    TATATAT TATATATA  TATAT
                                    ||||||| ||||||||  |||||
                                    ATATATA ATATATAT  ATATA
                                        A       GC
GAM2870  VENTX2   3'  TATATATATTTATATATACGTA 30921          A       TA
                TA                  TATATATAT TATATATA  TATA
                                    |||||||| ||||||||  ||||
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                                ATATATATA ATATATAT  ATAT
                                    A       GC
GAM2870  WNT11    3'  TATATATATACATATATA    21537
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATGTATATAT

GAM2870  WNT11    3'  TATATATTTATATATATAAAAT 21539        A        T_
           ATA                    TATATAT TATATATATA  ATATA
                                ||||||| |||||||||  |||||
                                ATATATA ATATATATAT  TATAT
                                    A         TT
GAM2870  WNT11    3'  TATATTTATATATATAAAATAT 21540       A        T_
           ATA                    TATAT TATATATATA  ATATATA
                                ||||| |||||||||  |||||||
                                ATATA ATATATATAT  TATATAT
                                   A         TT
GAM2870  WNT11    3'  TATATATACATATATATTTATA 21536              A
           TA                     TATATATATATATATAT TATATA
                                ||||||||||||||||| ||||||
                                ATATATATGTATATATA ATATAT
                                          A
GAM2870  WNT11    3'  TATACATATATATTTATATATA 21535            A
           TA                     TATATATATATAT TATATATATA
                                ||||||||||||| ||||||||||
                                ATATGTATATATA ATATATATAT
                                       A
GAM2870  WNT5A    3'  TATGTATATATATATATAT    18135     A
                                TAT TATATATATATATAT
                                ||| ||||||||||||||
                                ATA ATATATATATATATA
                                  C
GAM2870  WNT5A    3'  TATATATGTATATATATATATA 18132        A
           T                     TATATAT TATATATATATATAT
                                ||||||| ||||||||||||||
                                ATATATA ATATATATATATATA
                                    C
GAM2870  WNT5A    3'  TATATATATGTATATATATATA 18129          A          III
           T                     TATATATAT TATATATATATA   T
                                ||||||||| ||||||||||||   |
                                ATATATATA ATATATATATAT   A
                                      C          III
GAM2870  ZNF144   3'  CATATATATATATATTTATTTA 28338             A   A
           TA                     TATATATATATATAT TAT TATA
                                ||||||||||||||| ||| ||||
                                GTATATATATATATA ATA ATAT
                                          A   A
GAM2870  ZNF144   3'  TATGTACATATATATATATA   28342     A
                                TAT TATATATATATATATA
                                ||| |||||||||||||||
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                                ATA ATGTATATATATATAT
                                  C
GAM2871  AGTR1    3'  ATATACATATATATATAT    28908
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATGTATATATATATA

GAM2871  ATP2B2   3'  ATATATATATATATATCTAC  11753              A
                                ATATATATATATATAT TAT
                                |||||||||||||||| |||
                                TATATATATATATATA ATG
                                        G
GAM2871  ATP2B2   3'  ATATTTATATATATATATATAT 11754      A             III
              A                  ATAT TATATATATATATATAT   A
                                ||||| ||||||||||||||||   |
                                TATA ATATATATATATATATA   T
                                  A             III
GAM2871  ATP2B2   3'  TATATATATATATATATATAA  11761               ATIII
                                TATATATATATATATATAT    A
                                ||||||||||||||||||     |
                                ATATATATATATATATATA    T
                                        IIITA
GAM2871  BACH2    3'  ATATATATATATTTTTTATATA 34778          _____
              TATAT                ATATATATATA    TATATATATAT
                                ||||||||||     ||||||||||
                                TATATATATAT    ATATATATATA
                                     AAAAA
GAM2871  BACH2    3'  ATATGGATATATATATATATAT 34779      __
              AT                   ATAT  ATATATATATATATATAT
                                ||||  ||||||||||||||||||
                                TATA  TATATATATATATATATA
                                  CC
GAM2871  BACH2    3'  ATATATATATATATATATAT   34777
                                ATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATA

GAM2871  BCL11B   3'  TAATATATATAATATATAC    35650          T
                                TAATATATATA ATATATAT
                                |||||||||| ||||||||
                                ATTATATATAT TATATATG
                                        _
GAM2871  BCL6     3'  ATATATATATATATTTATATAT 39904            A
                                ATATATATATATAT TATATAT
                                |||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                        A
GAM2871  CACNB2   3'  ATATATATATATATATTATATA 8791              _
              T                   ATATATATATATATAT ATATAT
                                |||||||||||||||| ||||||
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                                TATATATATATATATA TATATA
                                          A
GAM2871  CBFA2T1   3'  TATATATATATATATATATAT  20303
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATATATATATATATATATATA

GAM2871  CBFA2T1   3'  ATATATATATATATATATATAT 20296
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  CBFA2T1   3'  TATATATATATATATATAT   20301
                                TATATATATATATATATAT
                                |||||||||||||||||
                                ATATATATATATATATATA

GAM2871  CBFA2T1   3'  ATATATATATATATATATATAT 20296
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  COL4A5    3'  TATATATATATATATCACAT   37899            A
                                TATATATATATATAT TATAT
                                |||||||||||||| |||||
                                ATATATATATATATA GTGTA
                                          _
GAM2871  CRADD     3'  ATATATATATATATGGATATAT 19170           AT
                                ATATATATATATAT  ATATAT
                                ||||||||||||||  ||||||
                                TATATATATATATA  TATATA
                                          CC
GAM2871  CRADD     3'  ATATATATGGGATATATATATA 19174        ___
              TAT                  ATATATAT   ATATATATATATAT
                                ||||||||   ||||||||||||||
                                TATATATA   TATATATATATATA
                                     CCC
GAM2871  CRADD     3'  ATATATATATATATGGATATAT 19172          __
              AT                   ATATATATATATAT  ATATATAT
                                ||||||||||||||  ||||||||
                                TATATATATATATA  TATATATA
                                          CC
GAM2871  CRIM1     3'  AATATATATGTATATATATATA 32367         A          III
              TA                   AATATATAT TATATATATATAT   A
                                |||||||||| ||||||||||||   |
                                TTATATATA ATATATATATATA   T
                                     C          III
GAM2871  CTGF      3'  TACATATATATATATATAT    12505
                                TATATATATATATATATAT
                                ||||||||||||||||||
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                                ATGTATATATATATATATA

GAM2871  CTLA4    3'  ATATATATATATATATATATAT 23322
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  CTLA4    3'  ATATATATATATATATATATAT 23322
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  CTLA4    3'  ATATATATATATATATGTATAT 23325                A
                                ATATATATATATATAT TATAT
                                |||||||||||||||| |||||
                                TATATATATATATATA ATATA
                                          C
GAM2871  CTLA4    3'  ATATATATATATATGTATATAT 23326               A
                                ATATATATATATAT TATATAT
                                |||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                          C
GAM2871  CTLA4    3'  ATATATATATATATATATAT   23320
                                ATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATA

GAM2871  CTLA4    3'  AATATATATATATATATATATA 23319                     III
            TA                    AATATATATATATATATATATAT   A
                                ||||||||||||||||||||||   |
                                TTATATATATATATATATATATA   T
                                          III
GAM2871  CYP1A2   3'  TATATATATATGTATATATATA 8916            A        III
            T                    TATATATATAT TATATATAT   AT
                                |||||||||| |||||||||   ||
                                ATATATATATA ATATATATA   TA
                                      C        III
GAM2871  DAPK1    3'  CATATATATATATACATAT    22355
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                GTATATATATATATGTATA

GAM2871  DAPK1    3'  TAATATATATGTATATACAT   22363           A
                                TAATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATTATATATA ATATATGTA
                                      C
GAM2871  DDX6     3'  ATATATATATGTATATATATAT 20546           A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
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TATATATATA ATATATATATA
C
GAM2871 DDX6 3' AATATATATATATGTATATATA 20539 A ATIII
A AATATATATATAT TATATAT A
TTATATATATATA ATATATA T
C IIITA
GAM2871 DDX6 3' ATATATATGTATATATATATAT 20547 A
ATATATAT TATATATATATAT
TATATATA ATATATATATATA
C
GAM2871 DDX6 3' ATATATGTATATATATATATAT 20548 A
ATATAT TATATATATATATAT
TATATA ATATATATATATATA
C
GAM2871 DDX6 3' AATATATATATATGTATATATA 20540 A III
TA AATATATATATAT TATATATAT A
TTATATATATATA ATATATATA T
C III
GAM2871 DDX6 3' TATATATATATATATATAT 20556
TATATATATATATATATAT
ATATATATATATATATATA
GAM2871 DDX6 3' ATATGTATATATATATATATAT 20549 A
ATAT TATATATATATATATAT
TATA ATATATATATATATATA
C
GAM2871 DRIL1 3' ATATATACGTATATATATATAT 23363 TA
ATATATA TATATATATATAT
TATATAT ATATATATATATA
GC
GAM2871 DRIL1 3' ATATACGTATATATATATATAT 23362 TA
ATATA TATATATATATATAT
TATAT ATATATATATATA
GC
GAM2871 DRIL1 3' ATATATATATATATATATATAT 23364
ATATATATATATATATATATAT
TATATATATATATATATATA
GAM2871 DRIL1 3' TATATATATATATATATATA 23384 III
TATATATATATATATATATAT A

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                                ATATATATATATATATATATA   T
                                                    III
GAM2871  DRIL1    3'  ATATATATATATATATATATAT 23364
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  EDNRA    3'  ATATGTATATACATATATAT   41992      A
                                ATAT TATATATATATATAT
                                |||| ||||||||||||||
                                TATA ATATATGTATATATA
                                   C
GAM2871  EP300    3'  TATATATATTTATATATATAT  10993          A
                                TATATATAT TATATATATAT
                                ||||||||| ||||||||||
                                ATATATATA ATATATATATA
                                      A
GAM2871  EP300    3'  TAATATATATTTATATATAT   10992          A
                                TAATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATTATATATA ATATATATA
                                      A
GAM2871  ETV6     3'  AATATATATATATAATAGATAT 12761             T___
            ATAT                    AATATATATATATA    ATATATAT
                                ||||||||||||||    ||||||||
                                TTATATATATATAT    TATATATA
                                        TATC
GAM2871  F9       3'  TATATATATATTATATATAT   6580           A
                                TATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                ATATATATATA ATATATATA
                                      _
GAM2871  FACL4    3'  TATATATATGCATATATAT    35686          A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
                                ATATATATA GTATATATA
                                      C
GAM2871  FGFR3    3'  TATATATATAGATATATAT    6617           T
                                TATATATATA ATATATAT
                                |||||||||| ||||||||
                                ATATATATAT TATATATA
                                      C
GAM2871  FGFR3    3'  TATATATATATATGTATATATA 6620             A      III
                                TATATATATATAT TATATAT   A
                                |||||||||||| |||||||   |
                                ATATATATATATA ATATATA   T
                                        C       III
GAM2871  FGFR3    3'  TATATATATGTATATATAC    6623           A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
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                                ATATATATA ATATATATG
                                      C
GAM2871  HDAC4    3'  AATATATATTATACATATATAT 25738          _
                AT                  AATATATAT ATATATATATATAT
                                    ||||||||| ||||||||||||||
                                    TTATATATA TATGTATATATATA
                                          A
GAM2871  HOXC4    3'  ATATATATATATATATATATAT 31149
                                    ATATATATATATATATATATAT
                                    ||||||||||||||||||||||
                                    TATATATATATATATATATATA

GAM2871  HOXC4    3'  TATATATATATATATATATATA 31158                    III
                                    TATATATATATATATATATAT   A
                                    ||||||||||||||||||||   |
                                    ATATATATATATATATATATA   T
                                                 III
GAM2871  HOXC4    3'  ATATATATATATATATATATAT 31149
                                    ATATATATATATATATATATAT
                                    ||||||||||||||||||||||
                                    TATATATATATATATATATATA

GAM2871  HS2ST1   3'  ATATATATATATGTATATATAT 29325             A
                                    ATATATATATAT TATATATAT
                                    |||||||||||| |||||||||
                                    TATATATATATA ATATATATA
                                          C
GAM2871  IFNW1    5'  TAATATATATTCATATATATAT 13483             A
                                    TAATATATAT TATATATATAT
                                    |||||||||| ||||||||||
                                    ATTATATATA GTATATATATA
                                          A
GAM2871  IGF1     3'  TAAGATATATATATATATATAT 8349       T
                                    TAA ATATATATATATATATAT
                                    ||| ||||||||||||||||||
                                    ATT TATATATATATATATATA
                                      C
GAM2871  INPP5A   3'  TATATATATTTATATATATAT  24408           A
                                    TATATATAT TATATATATAT
                                    |||||||||| ||||||||||
                                    ATATATATA ATATATATATA
                                          A
GAM2871  KCNH5    3'  TATATACACACATATGTATAT  40258               A
                                    TATATATATATATAT TATAT
                                    |||||||||||||||| |||||
                                    ATATATGTGTGTATA ATATA
                                             C
GAM2871  KIF3C    3'  TATATATATATTTATATAT    13955           A
                                    TATATATATAT TATATAT
                                    |||||||||| |||||||
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                                ATATATATATA ATATATA
                                      A
GAM2871  KPNA4    3'  ATATATGTATATATATATATAT 13987       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||||
                                TATATA ATATATATATATATA
                                   C
GAM2871  KPNA4    3'  ACACACATATATATATATATAT 13985
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TGTGTGTATATATATATATATA

GAM2871  KPNA4    3'  TATATATATGTATATATATATA 13991          A          III
                                TATATATAT TATATATATAT   A
                                ||||||||| ||||||||||   |
                                ATATATATA ATATATATATA   T
                                      C          III
GAM2871  KPNA4    3'  ATATATATGTATATATATATAT 13986         A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||||
                                TATATATA ATATATATATATA
                                     C
GAM2871  KPNA4    3'  ATATGTATATATATATATATAT 13988      A
                                ATAT TATATATATATATATAT
                                |||| ||||||||||||||||
                                TATA ATATATATATATATATA
                                  C
GAM2871  LMCD1    3'  TATATATATCTCATATATATAT 31046         A_
                                TATATATAT  TATATATATAT
                                |||||||||  ||||||||||
                                ATATATATA  GTATATATATA
                                      GA
GAM2871  MAN1A1   3'  ACATAAATATATATGTATATAT 45087       T       A
                                ATATA ATATATAT TATATAT
                                ||||| |||||||| |||||||
                                TGTAT TATATATA ATATATA
                                   T       C
GAM2871  MAP3K12  3'  ATATATATATATGTATATATAT 26675           A
                                ATATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                TATATATATATA ATATATATA
                                     C
GAM2871  MAP3K12  3'  ATATATATATATGTATATATAT 26676          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                      C
GAM2871  MAP3K12  3'  ATATATATATATATGTATATAT 26674            A
                                ATATATATATATAT TATATAT
                                ||||||||||||| |||||||
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                                TATATATATATATA ATATATA
                                       C
GAM2871  MAP3K12  3'  ATATATATATATATATGTATAT 26673              A    III
            AT                   ATATATATATATATAT TATAT   AT
                                 |||||||||||||||| |||||   ||
                                 TATATATATATATATA ATATA   TA
                                       C    III
GAM2871  MASP1    3'  TAATATATATATATATAT    40105
                                 TAATATATATATATATAT
                                 ||||||||||||||||||
                                 ATTATATATATATATATA

GAM2871  MBNL     3'  ATATATATCTATTATATATATA 34308        ATA_
            T                    ATATATAT    TATATATATAT
                                 ||||||||    ||||||||||
                                 TATATATA    ATATATATATA
                                      GATA
GAM2871  MEN1     3'  TATATATATATGTATATAT    39212          A
                                 TATATATATAT TATATAT
                                 |||||||||| |||||||
                                 ATATATATATA ATATATA
                                       C
GAM2871  MEN1     3'  ATATATATACATATATATATAT 39151
                                 ATATATATATATATATATATAT
                                 |||||||||||||||||||||
                                 TATATATATGTATATATATATA

GAM2871  MEN1     3'  ATATATACATATATATATATAT 39150
                                 ATATATATATATATATATATAT
                                 |||||||||||||||||||||
                                 TATATATGTATATATATATATA

GAM2871  MEN1     3'  ATATATATATACATATATATAT 39152
                                 ATATATATATATATATATATAT
                                 |||||||||||||||||||||
                                 TATATATATATGTATATATATA

GAM2871  MEN1     3'  ATATATGTATATATATATATAT 39158        A
                                 ATATAT TATATATATATATAT
                                 |||||| ||||||||||||||
                                 TATATA ATATATATATATATA
                                    C
GAM2871  MEN1     3'  ATATATATGTATATATATAT   39156         A
                                 ATATATAT TATATATATAT
                                 |||||||| ||||||||||
                                 TATATATA ATATATATATA
                                       C
GAM2871  MEN1     3'  ATATATATATATACATATATAT 39153
                                 ATATATATATATATATATATAT
                                 |||||||||||||||||||||
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                                TATATATATATATGTATATATA

GAM2871  MEN1     3'  ATATATATATATATACATATAT 39154
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATGTATATA

GAM2871  MEN1     3'  ATATATATATATATACATATATAT 39153
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATGTATATATA

GAM2871  MEN1     3'  ATATATATGTATATATATATAT 39157          A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
                                TATATATA ATATATATATATA
                                      C
GAM2871  MEN1     3'  ATATGTATATATATATGTATAT 39159      A          A
                                ATAT TATATATATAT TATAT
                                |||| |||||||||| |||||
                                TATA ATATATATATA ATATA
                                   C          C
GAM2871  MEN1     3'  ATATATATATGTATATATATAT 39155          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                      C
GAM2871  MEN1     3'  TATATATATATGTATATATAT  39214          A
                                TATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                ATATATATATA ATATATATA
                                       C
GAM2871  MEN1     3'  ATATATATATGTATATATATAT 39155          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                       C
GAM2871  MEN1     3'  ATATATATATGTATATATATAT 39155          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TATATATATA ATATATATATA
                                      C
GAM2871  MOX2     3'  TATATATATATATAAATAT    42522          T
                                TATATATATATATA ATAT
                                |||||||||||||| ||||
                                ATATATATATATAT TATA
                                         T
GAM2871  MYBL1    3'  ATATATAAATATATATATATAT 41972        T
                                ATATATA ATATATATATATAT
                                ||||||| ||||||||||||||
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                                TATATAT TATATATATATATA
                                    T
GAM2871  MYBL1    3'  ATATATATAAATATATATATAT 41973         T
                                ATATATATA ATATATATATAT
                                ||||||||| ||||||||||||
                                TATATATAT TATATATATATA
                                    T
GAM2871  MYBL1    3'  AATATATATATATATAAAATAT 41969              TAT
                                AATATATATATATATA   ATAT
                                |||||||||||||||   ||||
                                TTATATATATATATAT   TATA
                                          TT_
GAM2871  MYBL1    3'  ATATATATATAAATATATATAT 41974           T
                                ATATATATATA ATATATATAT
                                |||||||||| |||||||||
                                TATATATATAT TATATATATA
                                    T
GAM2871  MYCL2    3'  TACATATATATATACATATAT  23907
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATGTATATATATATGTATATA

GAM2871  MYCL2    3'  TAATATATACATATATACAT   23905
                                TAATATATATATATATATAT
                                ||||||||||||||||||||
                                ATTATATATGTATATATGTA

GAM2871  MYCL2    3'  ATATATACATACATATATATAT 23897
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATGTATGTATATATATA

GAM2871  MYCL2    3'  ACATATATATATACATATAT   23893
                                ATATATATATATATATATAT
                                ||||||||||||||||||||
                                TGTATATATATATGTATATA

GAM2871  NOV      3'  ACATGTATGTATACACATATAT 14805      A   A
                                ATAT TAT TATATATATATAT
                                |||| ||| ||||||||||||
                                TGTA ATA ATATGTGTATATA
                                  C   C
GAM2871  NRF1     3'  ATATATATATATATATGTATAT 41088             A
                                ATATATATATATATAT TATAT
                                |||||||||||||||| |||||
                                TATATATATATATATA ATATA
                                          C
GAM2871  NRF1     3'  TATATATGTATATATATAC    41105        A
                                TATATAT TATATATATAT
                                ||||||| ||||||||||
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                                ATATATA ATATATATATG
                                    C
GAM2871  NRF1    3'  ATATATATATATATGTATATAT 41089            A
                                ATATATATATATAT TATATAT
                                ||||||||||||||| |||||||
                                TATATATATATATA ATATATA
                                      C
GAM2871  NRF1    3'  ATACATATATATATATATATAT 41087
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATGTATATATATATATATATA

GAM2871  NRF1    3'  ATATATATATATGTATATATAT 41090          A
                                ATATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                TATATATATATA ATATATATA
                                      C
GAM2871  NRF1    3'  TATATATATACTTTATATATAT 41097          A_
                                TATATATATAT  TATATATAT
                                ||||||||||  |||||||||
                                ATATATATATG  ATATATATA
                                      AA
GAM2871  NRIP1   3'  TATATATATATATATATAT    40979
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  NRIP1   3'  TATATATATATATATATA     40977
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  NRIP1   3'  TATATATATATATATATATATA 40981                III
                                TATATATATATATATATATAT   A
                                ||||||||||||||||||||   |
                                ATATATATATATATATATATA   T
                                        III
GAM2871  NRIP1   3'  ATACATATTATATATATATATA 40949        _
           T                     ATATATAT ATATATATATATAT
                                 ||||||||| |||||||||||||
                                 TATGTATA TATATATATATATA
                                     A
GAM2871  NRIP1   3'  ATATATATATATATAAAATATA 40952          T_
           T                     ATATATATATATATA  ATATAT
                                 |||||||||||||||  ||||||
                                 TATATATATATATAT  TATATA
                                       TT
GAM2871  NRIP1   3'  ATATATATATATATATATATAT 40954
                                 ATATATATATATATATATATAT
                                 ||||||||||||||||||||||
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                                TATATATATATATATATATATA

GAM2871  NRIP1    3'  ACATATTATATATATATATATA 40948        _
                T                ATATAT ATATATATATATATAT
                                 |||||| ||||||||||||||||
                                 TGTATA TATATATATATATATA
                                    A
GAM2871  NRIP1    3'  ATATATACATATTATATATATA 40951          _
                T                ATATATATATAT ATATATATAT
                                 |||||||||||| |||||||||
                                 TATATATGTATA TATATATATA
                                       A
GAM2871  NRIP1    3'  CAATATATATATATATACATAT 40955
                                 TAATATATATATATATATATAT
                                 |||||||||||||||||||||
                                 GTTATATATATATATATGTATA

GAM2871  NRIP1    3'  ATATATATATATATATATATAT 40954
                                 ATATATATATATATATATATAT
                                 |||||||||||||||||||||
                                 TATATATATATATATATATATA

GAM2871  NRIP1    3'  ATATACATATTATATATATATA 40950          _
                T                ATATATATAT ATATATATATAT
                                 |||||||||| ||||||||||||
                                 TATATGTATA TATATATATATA
                                       A
GAM2871  OTX1     3'  TATATATATATGTATATAT    30990          A
                                 TATATATATAT TATATAT
                                 |||||||||||| |||||||
                                 ATATATATATA ATATATA
                                       C
GAM2871  OTX1     3'  ATATATGTATATATATATATAT 30982        A
                                 ATATAT TATATATATATATAT
                                 |||||| ||||||||||||||||
                                 TATATA ATATATATATATATA
                                    C
GAM2871  OTX1     3'  TATATATATATGTATATATAT  30992          A
                                 TATATATATAT TATATATAT
                                 |||||||||||| |||||||||
                                 ATATATATATA ATATATATA
                                       C
GAM2871  OTX1     3'  ATATATATATGTATATATATAT 30980          A
                                 ATATATATAT TATATATATAT
                                 |||||||||| ||||||||||||
                                 TATATATATA ATATATATATA
                                       C
GAM2871  OTX1     3'  ATATATATGTATATATATATAT 30981         A
                                 ATATATAT TATATATATATAT
                                 |||||||| ||||||||||||||
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                                TATATATA ATATATATATATA
                                     C
GAM2871  OTX1     3'  ATATATGTATATATATATATAT 30982       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||||
                                TATATA ATATATATATATATA
                                   C
GAM2871  PCSK2    3'  TATGTATATATACACATATAT  15135     A
                                TAT TATATATATATATATAT
                                ||| ||||||||||||||||||
                                ATA ATATATATGTGTATATA
                                  C
GAM2871  PCSK2    3'  TATATATATAGCACTATATATA 15133          TA__
              T                  TATATATATA    TATATATAT
                                |||||||||    |||||||||
                                ATATATATAT    ATATATATA
                                      CGTG
GAM2871  PEA15    3'  TAATATACATATATGTAGAATA 19081            _____
              TATAT                 TAATATATATATAT     ATATATAT
                                |||||||||||||     ||||||||
                                ATTATATGTATATA     TATATATA
                                       CATCT
GAM2871  PEX3     3'  TATATATATATATATGTATATA 18849             A    III
                                TATATATATATATAT TATAT   A
                                |||||||||||||| |||||   |
                                ATATATATATATATA ATATA   T
                                       C    III
GAM2871  PLXNA1   3'  TATATATATATGCATATATAT  43625          A
                                TATATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATATATATATA GTATATATA
                                      C
GAM2871  PMX1     3'  TATATATATATATGAAATATAT 35523           AT_
                                TATATATATATAT   ATATAT
                                ||||||||||||   ||||||
                                ATATATATATATA   TATATA
                                       CTT
GAM2871  PMX1     3'  ATATATATATATATATATATAA 35498               ATIII
                                ATATATATATATATATATAT    A
                                |||||||||||||||||||    |
                                TATATATATATATATATATA    T
                                          IIITA
GAM2871  PMX1     3'  TATATATATATATATATA    35520
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  PMX1     3'  ATATATATATATGAAATATATA 35502          ___
              TAT                   ATATATATATAT   ATATATATAT
                                ||||||||||||   ||||||||||
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                                TATATATATATA  TATATATATA
                                      CTT
GAM2871  PMX1    3'  AATATATACAGTATATATAT  35493          _
                                AATATATATA TATATATAT
                                |||||||||| |||||||||
                                TTATATATGT ATATATATA
                                     C
GAM2871  PMX1    3'  AATATATATATAAATATAT   35494          T
                                AATATATATATA ATATAT
                                |||||||||||| ||||||
                                TTATATATATAT TATATA
                                      T
GAM2871  PMX1    3'  ATATATATATATATATATATAT 35499
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  PMX1    3'  ATATATATATATATATATATAT 35500                III
           A                     ATATATATATATATATATATAT  A
                                |||||||||||||||||||||  |
                                TATATATATATATATATATATA  T
                                         III
GAM2871  PPARGC1  3'  ATATATATATATATATATATAT 29948
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  PPARGC1  3'  TATATATATATATATATATATA 29961                  III
                                TATATATATATATATATATAT  A
                                |||||||||||||||||||||  |
                                ATATATATATATATATATATA  T
                                         III
GAM2871  PPARGC1  3'  ATATATATATATATATATATAT 29948
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  PRKCN    3'  TATATATATATATATATATAA  25164              ATIII
                                TATATATATATATATATAT    A
                                ||||||||||||||||||    |
                                ATATATATATATATATATA    T
                                         IIITA
GAM2871  PUM1     3'  TATATATATATATATATATATA 31237                III
                                TATATATATATATATATATAT  A
                                |||||||||||||||||||||  |
                                ATATATATATATATATATATA  T
                                         III
GAM2871  PUM1     3'  ATATATATATATATATATATAT 31231
                                ATATATATATATATATATATAT
                                |||||||||||||||||||||
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                                TATATATATATATATATATATA

GAM2871  PUM1     3'  ATATATATATATATATATATAT 31231
                                ATATATATATATATATATATAT
                                ||||||||||||||||||||||
                                TATATATATATATATATATATA

GAM2871  RBL1     3'  TATTTATATATATATATATAT  16179     A
                                TAT TATATATATATATATAT
                                ||| ||||||||||||||||
                                ATA ATATATATATATATATA
                                  A
GAM2871  RBP3     3'  TATATATATACATATATAT    16195
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATGTATATATA

GAM2871  RNTRE    3'  TATATATATATATATATA    31260
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  RNTRE    3'  CATATATATATATATATATATA 31249                  III
                                TATATATATATATATATATAT   A
                                ||||||||||||||||||||  |
                                GTATATATATATATATATATA   T
                                        III
GAM2871  ROCK2    3'  TATATATATATATATATAT    42362
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  ROCK2    3'  TATATATATATATATATAT    42362
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  ROCK2    3'  ATATATATATATATATAT    42350
                                ATATATATATATATATAT
                                ||||||||||||||||||
                                TATATATATATATATATA

GAM2871  ROCK2    3'  TATATATATATATATATATAA  42363               ATIII
                                TATATATATATATATATAT    A
                                ||||||||||||||||||    |
                                ATATATATATATATATATA    T
                                        IIITA
GAM2871  RP42     3'  ATATATATATATATACACACAT 33979
                                ATATATATATATATATATAT
                                ||||||||||||||||||||
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                                TATATATATATATATGTGTGTA

GAM2871  RP42     3'  AATATATATATATATATATATA 33975                  ATIII
              A                   AATATATATATATATATATAT    A
                                  ||||||||||||||||||||    |
                                  TTATATATATATATATATATA    T
                                          IIITA
GAM2871  RP42     3'  AATATATATATATATATATATA 33976                   III
              TA                   AATATATATATATATATATATAT   A
                                   ||||||||||||||||||||||   |
                                   TTATATATATATATATATATATA   T
                                           III
GAM2871  RP42     3'  ATATATATATATATATATATAT 33981
                                  ATATATATATATATATATATAT
                                  |||||||||||||||||||||
                                  TATATATATATATATATATATA

GAM2871  RPL23A   3'  ATATATATATATATATATATAA 9739                ATATIII
                                  ATATATATATATATATAT      A
                                  ||||||||||||||||      |
                                  TATATATATATATATATA      T
                                          IIITATA
GAM2871  SEMA3F   3'  ATATATATATATATATATATAT 20056
                                  ATATATATATATATATATATAT
                                  |||||||||||||||||||||
                                  TATATATATATATATATATATA

GAM2871  SGCD     3'  TATATATATTTATATATAT    7342          A
                                  TATATATAT TATATATAT
                                  ||||||||| |||||||||
                                  ATATATATA ATATATATA
                                        A
GAM2871  SGCD     3'  ATATATATTTATTTATATATAT 7341          A   A
                                  ATATATAT TAT TATATATAT
                                  |||||||| ||| |||||||||
                                  TATATATA ATA ATATATATA
                                       A   A
GAM2871  SLC1A1   3'  AATATATACATATATATATAT  20028
                                  AATATATATATATATATATAT
                                  |||||||||||||||||||||
                                  TTATATATGTATATATATATA

GAM2871  SLC1A1   3'  ATATACATATATATATATATAT 20029
                                  ATATATATATATATATATATAT
                                  |||||||||||||||||||||
                                  TATATGTATATATATATATATA

GAM2871  SLC8A1   3'  TATATATATGTATATATAT    34404          A
                                  TATATATAT TATATATAT
                                  ||||||||| |||||||||
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ATATATATA ATATATATA
C
GAM2871 SON 3' ATACAGATATATATATATAT 38456 T
ATATA ATATATATATATAT
TATGT TATATATATATATA
C
GAM2871 SON 3' ATATATATATTTACATATATAT 38457 A
ATATATATAT TATATATATAT
TATATATATA ATGTATATATA
A
GAM2871 SRGAP1 5' ATAAATATATATATATATATAT 43594 T III
A ATA ATATATATATATATATAT A
TAT TATATATATATATATATA T
T III
GAM2871 SRGAP1 5' ATATATATATATATATATATAT 43597
ATATATATATATATATATATAT
TATATATATATATATATATATA
GAM2871 SRGAP1 5' AATATATATATATATATATATA 43593 III
TA AATATATATATATATATATAT A
TTATATATATATATATATATATA T
III
GAM2871 SRGAP1 5' AATATATATATATATATATAT 43592
AATATATATATATATATATAT
TTATATATATATATATATATA
GAM2871 STK4 3' TAATTTATATATATATATGCAT 26583 A A
AT TAAT TATATATATATAT TATAT
ATTA ATATATATATATA GTATA
A C
GAM2871 SVIL 3' TATATAAATATATATATAT 34733 T
TATATA ATATATATATAT
ATATAT TATATATATATA
T
GAM2871 TAGLN2 3' AATATATATCTACATATATAT 18681 A
AATATATAT TATATATATAT
TTATATATA ATGTATATATA
G
GAM2871 TGFBR2 3' ATAGATATATATATATATATAT 17469 T
ATA ATATATATATATATATAT

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                                TAT TATATATATATATATATA
                                  C
GAM2871  TGFBR2   3'  TATATATATATATATATA    17481
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  TMEPAI   3'  TATATATATTTATATATAT   33619          A
                                TATATATAT TATATATAT
                                ||||||||| |||||||||
                                ATATATATA ATATATATA
                                      A
GAM2871  TNFSF9   3'  ATATATATATATATAATATATA 19193             _
            T                    ATATATATATATATA TATATAT
                                ||||||||||||||| |||||||
                                TATATATATATATAT ATATATA
                                        T
GAM2871  TRAM     3'  ATACAAATATATATATATATAT 30700       T
                                ATATA ATATATATATATATAT
                                ||||| ||||||||||||||||
                                TATGT TATATATATATATATA
                                   T
GAM2871  TRPM6    3'  TATATATATAAAAATATATAT  32799          TAT
                                TATATATATA   ATATATAT
                                |||||||||   ||||||||
                                ATATATATAT   TATATATA
                                      TTT
GAM2871  TRPM6    3'  TATATATATAATATATATAT   32802          T
                                TATATATATA ATATATATAT
                                |||||||||| ||||||||||
                                ATATATATAT TATATATATA
                                           _
GAM2871  TRPM6    3'  TAATATACATATTCCATATATA 32792           A_
            T                    TAATATATATAT  TATATATAT
                                ||||||||||||  |||||||||
                                ATTATATGTATA  GTATATATA
                                       AG
GAM2871  TRPM6    3'  ATATATATATAAAATATATATA 32785          T_
            T                    ATATATATATA  ATATATATAT
                                ||||||||||||  ||||||||||
                                TATATATATAT  TATATATATA
                                      TT
GAM2871  TRPM6    3'  AATAAAAATATATATATATATA 32780     TAT
            T                    AATA   ATATATATATATATAT
                                ||||   ||||||||||||||||
                                TTAT   TATATATATATATATA
                                  TTT
GAM2871  TRPM6    3'  TAATATATATATTCCATATATA 32793           A_
            T                    TAATATATATAT  TATATATAT
                                ||||||||||||  |||||||||
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                                ATTATATATATA  GTATATATA
                                      AG
GAM2871  UBE2H    3'  ATATATAATATATATATAT    17802        T
                                ATATATA ATATATATATAT
                                ||||||| ||||||||||||
                                TATATAT TATATATATATA
                                        _
GAM2871  VEGF     3'  AATATATATATTTTATATATAT 17936          A_
                                AATATATATAT  TATATATAT
                                ||||||||||  |||||||||
                                TTATATATATA  ATATATATA
                                      AA
GAM2871  VEGF     3'  ATATATATAATATATATATATA 17940          _
              T                  ATATATATA TATATATATATAT
                                ||||||||| ||||||||||||
                                TATATATAT ATATATATATATA
                                      T
GAM2871  VEGF     3'  ATAAACATATATATATATATAT 17938     T
                                ATA ATATATATATATATATAT
                                ||| ||||||||||||||||||
                                TAT TGTATATATATATATATA
                                  T
GAM2871  VENTX2   3'  ACACATATATGTATATATATAT 30904          A
                                ATATATATAT TATATATATAT
                                |||||||||| ||||||||||
                                TGTGTATATA ATATATATATA
                                      C
GAM2871  VENTX2   3'  TATATATATATTTATATAT    30920          A
                                TATATATATAT TATATAT
                                |||||||||||| |||||||
                                ATATATATATA ATATATA
                                      A
GAM2871  VENTX2   3'  ATATATACGTACATATATATAT 30907        TA
                                ATATATA  TATATATATATAT
                                |||||||  ||||||||||||
                                TATATAT  ATGTATATATATA
                                     GC
GAM2871  VENTX2   3'  ACATATATATATTTATATATAT 30905          A
                                ATATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                TGTATATATATA ATATATATA
                                      A
GAM2871  VENTX2   3'  AATATATATATATATATATATA 30903                  ATIII
              A                   AATATATATATATATATATAT    A
                                ||||||||||||||||||||    |
                                TTATATATATATATATATATA    T
                                           IIITA
GAM2871  WNT11    3'  TATATATATACATATATAT    21538
                                TATATATATATATATATAT
                                ||||||||||||||||||
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                                ATATATATATGTATATATA

GAM2871  WNT11    3'  TACATATATATTTATATATAT  21534          A
                                TATATATATAT TATATATAT
                                |||||||||||| |||||||||
                                ATGTATATATA ATATATATA
                                      A
GAM2871  WNT5A    3'  TATATATATGTATATATATAA  18127         A       ATIII
                                TATATATAT TATATATAT    A
                                ||||||||| |||||||||    |
                                ATATATATA ATATATATA    T
                                      C        IIITA
GAM2871  WNT5A    3'  TATATATATGTATATATATATA 18128         A         III
                                TATATATAT TATATATATAT   A
                                ||||||||| ||||||||||   |
                                ATATATATA ATATATATATA   T
                                      C          III
GAM2871  WNT5A    3'  ATATATGTATATATATATATAT 18112       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||
                                TATATA ATATATATATATATA
                                    C
GAM2871  WNT5A    3'  ATATATGTATATATATATATAT 18112       A
                                ATATAT TATATATATATATAT
                                |||||| ||||||||||||||
                                TATATA ATATATATATATATA
                                    C
GAM2871  WNT5A    3'  ATATATATGTATATATATATAT 18111        A
                                ATATATAT TATATATATATAT
                                |||||||| ||||||||||||
                                TATATATA ATATATATATATA
                                     C
GAM2871  AGTR1    3'  TATAGATATACATATATATATA 28920      T
                                TATA ATATATATATATATATA
                                |||| ||||||||||||||||
                                ATAT TATATGTATATATATAT
                                   C
GAM2871  ARHGEF12 3'  TATCTATATATATAGATATAGA 31646     A        T
                                TAT TATATATATA ATATAGA
                                ||| |||||||||| |||||||
                                ATA ATATATATAT TATATCT
                                  G         C
GAM2871  ATP2B2   3'  TATATATATATATATATA     11760
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  ATP2B2   3'  TATATATATATATCTACCTAT  11762           A   A
                                TATATATATATAT TAT TAT
                                |||||||||||| ||| |||
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                                ATATATATATATA ATG ATA
                                      G   G
GAM2871  ATP7A    3'  TATATATATGTATGTGAATACA 6265          A   AT__
            CAGA                    TATATATAT TAT    ATATATAGA
                                ||||||||| |||    |||||||||
                                ATATATATA ATA    TATGTGTCT
                                     C   CACT
GAM2871  ATP8B2   3'  TATATATATATTTATATAATAT 42213           A     _
            AGA                     TATATATATAT TATATA TATAGA
                                |||||||||||| |||||| ||||||
                                ATATATATATA ATATAT ATATCT
                                      A     T
GAM2871  BACH2    3'  TATATATATATTATATATA    34801           A
                                TATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATA ATATATAT
                                                _
GAM2871  BACH2    3'  ATATATATATATATATATA    34776
                                ATATATATATATATATATA
                                ||||||||||||||||||
                                TATATATATATATATATAT

GAM2871  BACH2    3'  TATGGATATATATATATATATA 34803     AT
                                TAT  ATATATATATATATATA
                                |||  ||||||||||||||||
                                ATA  TATATATATATATATAT
                                  CC
GAM2871  BDNF     3'  TATGTATATATACAAATAGA   40596     A        T
                                TAT TATATATATA ATAGA
                                ||| |||||||||| |||||
                                ATA ATATATATGT TATCT
                                  C         T
GAM2871  CACNB2   3'  TATATATATATTATATATA    8796           A
                                TATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATA ATATATAT
                                                _
GAM2871  CACNB2   3'  TGATATATATATATATAT     8798     T
                                A ATATATATATATATAT
                                | ||||||||||||||||
                                A TATATATATATATATA
                                 C
GAM2871  CACNB2   3'  TATATATATATATTATATA    8795           A
                                TATATATATATAT TATATA
                                |||||||||||| ||||||
                                ATATATATATATA ATATAT
                                                _
GAM2871  CBFA2T1  3'  TATATATATATATATATA     20300
                                TATATATATATATATATA
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                              ATATATATATATATATAT

GAM2871  CBFA2T1   3'  TATATATATATATATATATA  20302
                              TATATATATATATATATATA
                              ||||||||||||||||||||
                              ATATATATATATATATATAT

GAM2871  CBFA2T1   3'  TATATATATATATATATATATA 20304
                              TATATATATATATATATATATA
                              ||||||||||||||||||||||
                              ATATATATATATATATATATAT

GAM2871  CRADD     3'  TATATATATGGGATATATATAT 19180          ___
            ATA                    TATATATAT   ATATATATATATA
                              |||||||||   ||||||||||||
                              ATATATATA   TATATATATATAT
                                    CCC
GAM2871  CRADD     3'  TATATATATATATGGATATATA 19179            AT
                              TATATATATATAT  ATATATA
                              ||||||||||||  |||||||
                              ATATATATATATA  TATATAT
                                      CC
GAM2871  CRIM1     3'  ATATATATGTATATATATATA  32369         A
                              ATATATAT TATATATATATA
                              ||||||||| ||||||||||||
                              TATATATA ATATATATATAT
                                   C
GAM2871  CRIM1     3'  TATATATGTATATATATATAT  32382         A
                              TATATAT TATATATATATAT
                              ||||||| ||||||||||||
                              ATATATA ATATATATATATA
                                  C
GAM2871  CRIM1     3'  TATATATATATATTATATA    32379           A
                              TATATATATATAT TATATA
                              |||||||||||| ||||||
                              ATATATATATATA ATATAT
                                            _
GAM2871  CRIM1     3'  ATATATATGTATATATATA    32368         A
                              ATATATAT TATATATATA
                              |||||||| ||||||||||
                              TATATATA ATATATATAT
                                   C
GAM2871  CRIM1     3'  TATAAATATATATGTATATATA 32376      T       A
                              TATA ATATATAT TATATATA
                              |||| |||||||| ||||||||
                              ATAT TATATATA ATATATAT
                                T       C
GAM2871  CTGF      3'  TACATATATATATATATATA   12506
                              TATATATATATATATATATA
                              ||||||||||||||||||||
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                                ATGTATATATATATATATAT

GAM2871  CTLA4    3'  TATATATATATATGTATATAT  23342            A
                                TATATATATATAT TATATAT
                                |||||||||||| |||||||
                                ATATATATATATA ATATATA
                                      C
GAM2871  CTLA4    3'  TATATATATATATATATATATA 23334
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  CTLA4    3'  TATATATATATATATATGTATA 23338              A
                                TATATATATATATATAT TATA
                                |||||||||||||||| ||||
                                ATATATATATATATATA ATAT
                                      C
GAM2871  CTLA4    3'  ATATATATATATATATATATA  23321
                                ATATATATATATATATATATA
                                ||||||||||||||||||||
                                TATATATATATATATATATAT

GAM2871  CTLA4    3'  TATATATATATATATGTATATA 23340            A
                                TATATATATATATAT TATATA
                                |||||||||||||| ||||||
                                ATATATATATATATA ATATAT
                                      C
GAM2871  CTLA4    3'  TATATATATATATATATAT    23332
                                TATATATATATATATATAT
                                |||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  CTLA4    3'  TATATATATATATATATATAT  23333
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATATATATATATATATATATA

GAM2871  CYP1A2   3'  TATATATATATGTATATATAT  8915           A
                                TATATATATAT TATATATAT
                                |||||||||| |||||||||
                                ATATATATATA ATATATATA
                                      C
GAM2871  DAPK1    3'  CATATATATATATACATAT    22355
                                TATATATATATATATATAT
                                |||||||||||||||||||
                                GTATATATATATATGTATA

GAM2871  DDX6     3'  TATATGTATATATATATATATA 20564       A
                                TATAT TATATATATATATATA
                                ||||| ||||||||||||||||
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                                ATATA ATATATATATATATAT
                                  C
GAM2871  DDX6    3'  TATATATATGTATATATATATA 20560          A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                    C
GAM2871  DDX6    3'  TATGTATATATATATATATATA 20566     A
                                TAT TATATATATATATATATA
                                ||| ||||||||||||||||||
                                ATA ATATATATATATATATAT
                                  C
GAM2871  DDX6    3'  TATATATGTATATATATATATA 20562        A
                                TATATAT TATATATATATATA
                                ||||||| ||||||||||||||
                                ATATATA ATATATATATATAT
                                    C
GAM2871  DDX6    3'  TATATATATATATATGAACCCA 20557              AT  A
              GA                  TATATATATATATAT  AT TAGA
                                ||||||||||||||  || ||||
                                ATATATATATATATA  TG GTCT
                                         CT  G
GAM2871  DDX6    3'  ATATATATATATGTATATATA  20543           A
                                ATATATATATAT TATATATA
                                |||||||||||| ||||||||
                                TATATATATATA ATATATAT
                                      C
GAM2871  DDX6    3'  TATATATATATGTATATATATA 20558           A
                                TATATATATAT TATATATATA
                                |||||||||||| ||||||||||
                                ATATATATATA ATATATATAT
                                      C
GAM2871  DDX6    3'  TATATATATATATATATAT    20556
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  DRIL1   3'  TATATATATATATATATATATA 23384
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  DRIL1   3'  TATATACGTATATATATATATA 23379        TA
                                TATATA  TATATATATATATA
                                ||||||  ||||||||||||||
                                ATATAT  ATATATATATATAT
                                    GC
GAM2871  DRIL1   3'  TATATATACGTATATATATATA 23381         TA
                                TATATATA  TATATATATATA
                                ||||||||  ||||||||||||
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                                ATATATAT  ATATATATATAT
                                     GC
GAM2871  DRIL1    3'  TACGTATATATATATATATATA 23375    TA
                                TA  TATATATATATATATATA
                                ||  ||||||||||||||||||
                                AT  ATATATATATATATATAT
                                 GC
GAM2871  DRIL1    3'  TATATATATACGTATATATATA 23382         TA
                                TATATATATA  TATATATATA
                                ||||||||||  ||||||||||
                                ATATATATAT  ATATATATAT
                                      GC
GAM2871  DRIL1    3'  TATATATATATATATATATA  23383
                                TATATATATATATATATATA
                                ||||||||||||||||||||
                                ATATATATATATATATATAT

GAM2871  DRIL1    3'  TATACGTATATATATATATATA 23377     TA
                                TATA  TATATATATATATATA
                                ||||  ||||||||||||||||
                                ATAT  ATATATATATATATAT
                                   GC
GAM2871  DXF68S1E 3'  TGATACACACATGTATATATGG 41038   T       A     A
           A                     A ATATATATAT TATATAT GA
                                | ||||||||||  |||||||  ||
                                A TATGTGTGTA ATATATA CT
                                 C        C     C
GAM2871  EDNRA    3'  TATGTATATACATATATAT   41997    A
                                TAT TATATATATATATAT
                                |||  ||||||||||||||
                                ATA ATATATGTATATATA
                                  C
GAM2871  ETV6     3'  ATATATATATATAATAG     12762          T
                                ATATATATATATA ATAG
                                ||||||||||||  ||||
                                TATATATATATAT TATC

                                      _
GAM2871  F9       3'  TATATATATTATATATATA   6582         A
                                TATATATAT TATATATATA
                                |||||||||  ||||||||||
                                ATATATATA ATATATATAT

                                       _
GAM2871  F9       3'  TATATATATATTATATATA   6579          A
                                TATATATATAT TATATATA
                                ||||||||||  ||||||||
                                ATATATATATA ATATATAT

                                       _
GAM2871  FGFR3    3'  TATATATATATATGTATATATA 6620           A
                                TATATATATATAT TATATATA
                                ||||||||||||  ||||||||
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                                ATATATATATATA ATATATAT
                                        C
GAM2871  FGFR3    3'  TATATATATATATGTATA    6619            A
                                TATATATATATAT TATA
                                |||||||||||| ||||
                                ATATATATATATA ATAT
                                        C
GAM2871  FOXF1    3'  TATATATATATTTATATAAA  11123           A
                                TATATATATAT TATATAGA
                                |||||||||| ||||||||
                                ATATATATATA ATATATTT
                                      A
GAM2871  HOXC4    3'  TATATATATATATATATATAT  31157
                                TATATATATATATATATATAT
                                ||||||||||||||||||||
                                ATATATATATATATATATATA

GAM2871  HOXC4    3'  TATATATATATATATATATATA 31158
                                TATATATATATATATATATATA
                                ||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  HOXC4    3'  TATATATATATATATATA    31156
                                TATATATATATATATATA
                                ||||||||||||||||
                                ATATATATATATATATAT

GAM2871  HS2ST1   3'  TATATATATATATGTATATATA 29338           A
                                TATATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATATA ATATATAT
                                        C
GAM2871  HS2ST1   3'  ATATATATATATATGTATATA  29322           A
                                ATATATATATATAT TATATA
                                |||||||||||| ||||||
                                TATATATATATATA ATATAT
                                        C
GAM2871  IGFBP1   3'  TATATATATATACATATA    8249
                                TATATATATATATATATA
                                ||||||||||||||||
                                ATATATATATATGTATAT

GAM2871  INPP5A   3'  TATATTTATATATATATAAA  24410       A
                                TATAT TATATATATATAGA
                                ||||| ||||||||||||
                                ATATA ATATATATATATTT
                                   A
GAM2871  KPNA4    3'  TATATGTATATATATATATATA 13996       A
                                TATAT TATATATATATATATA
                                ||||| ||||||||||||||||
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                                ATATA ATATATATATATATAT
                                   C
GAM2871  KPNA4    3'  TATGTATATATATATATATATA 13998     A
                                TAT TATATATATATATATATA
                                ||| ||||||||||||||||||
                                ATA ATATATATATATATATAT
                                  C
GAM2871  KPNA4    3'  TATATATGTATATATATATATA 13994        A
                                TATATAT TATATATATATATA
                                ||||||| ||||||||||||||
                                ATATATA ATATATATATATAT
                                    C
GAM2871  KPNA4    3'  TATATATATATATATACA    13989
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATGT

GAM2871  KPNA4    3'  TATATATATGTATATATATATA 13991          A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                     C
GAM2871  KPNA4    3'  TATATATATGTATATATA    13990          A
                                TATATATAT TATATATA
                                ||||||||| ||||||||
                                ATATATATA ATATATAT
                                     C
GAM2871  LAPTM5   3'  TACATATATTTATATATAG   27606          A
                                TATATATAT TATATATAG
                                ||||||||| |||||||||
                                ATGTATATA ATATATATC
                                     A
GAM2871  MAGEL2   3'  TATATTTATATATATAGATATA 33301       A         T
                 GA                    TATAT TATATATATA ATATAGA
                                ||||| |||||||||| |||||||
                                ATATA ATATATATAT TATATCT
                                   A         C
GAM2871  MAN1A1   3'  ATATATATGTATATATAG    45088         A
                                ATATATAT TATATATAG
                                |||||||| |||||||||
                                TATATATA ATATATATC
                                     C
GAM2871  MAP3K12  3'  CATATATATATATATATGTATA 26677                A
                                TATATATATATATATAT TATA
                                |||||||||||||||| ||||
                                GTATATATATATATATA ATAT
                                          C
GAM2871  MAP3K12  3'  TATATATATATGTATATATATA 26691           A
                                TATATATATAT TATATATATA
                                |||||||||| ||||||||||
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                                ATATATATATA ATATATATAT
                                      C
GAM2871  MAP3K12  3'  TATATATATGTATATATATATA 26693         A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                    C
GAM2871  MAP3K12  3'  TATATATATATATATGTATATA 26687              A
                                TATATATATATATAT TATATA
                                |||||||||||||| ||||||
                                ATATATATATATATA ATATAT
                                        C
GAM2871  MAP3K12  3'  TATATATATATATGTATATATA 26689            A
                                TATATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATATA ATATATAT
                                        C
GAM2871  MASP1    3'  TAATATATATATATATAT    40105    T
                                A ATATATATATATATAT
                                | ||||||||||||||||
                                A TATATATATATATATA
                                 T
GAM2871  MEF2A    3'  TATATATATGTATGTACATATA 24626         A  A
                                TATATATAT TAT TATATATA
                                ||||||||| ||| ||||||||
                                ATATATATA ATA ATGTATAT
                                      C  C
GAM2871  MEN1     3'  TATATGTATATATATATGTATA 39225       A          A
                                TATAT TATATATATAT TATA
                                ||||| |||||||||| ||||
                                ATATA ATATATATATA ATAT
                                   C          C
GAM2871  MEN1     3'  TATATATGTATATATATAT    39221         A
                                TATATAT TATATATATAT
                                ||||||| ||||||||||
                                ATATATA ATATATATATA
                                     C
GAM2871  MEN1     3'  TATGTATATATATATGTATATA 39229     A          A
                                TAT TATATATATAT TATATA
                                ||| |||||||||| ||||||
                                ATA ATATATATATA ATATAT
                                  C          C
GAM2871  MEN1     3'  TATATATATATATACATATATA 39209
                                TATATATATATATATATATATA
                                ||||||||||||||||||||
                                ATATATATATATATGTATATAT

GAM2871  MEN1     3'  TATATATATATATATACATATA 39210
                                TATATATATATATATATATATA
                                ||||||||||||||||||||
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                                ATATATATATATATATGTATAT

GAM2871  MEN1    3'  TATATATATGTATATATATAT  39218          A
                                TATATATAT TATATATATAT
                                ||||||||| ||||||||||
                                ATATATATA ATATATATATA
                                      C
GAM2871  MEN1    3'  TATATATATACATATATATATA 39205
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATGTATATATATAT

GAM2871  MEN1    3'  TATATACATATATATATATATA 39203
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATGTATATATATATATAT

GAM2871  MEN1    3'  TATATATATGTATATATATATA 39219          A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                      C
GAM2871  MEN1    3'  TATATATATATGTATATATA   39213          A
                                TATATATATAT TATATATA
                                |||||||||| ||||||||
                                ATATATATATA ATATATAT
                                       C
GAM2871  MEN1    3'  TATATATGTATATATATATATA 39256        A
                                TATATAT TATATATATATATA
                                ||||||| ||||||||||||||
                                ATATATA ATATATATATATAT
                                     C
GAM2871  MEN1    3'  TATATATATATACATATATATA 39207
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATGTATATATAT

GAM2871  MEN1    3'  TATATATACATATATATATATA 39253
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATGTATATATATATAT

GAM2871  MEN1    3'  TATATATATATGTATATATATA 39215          A
                                TATATATATAT TATATATATA
                                |||||||||| ||||||||||
                                ATATATATATA ATATATATAT
                                       C
GAM2871  MEN1    3'  TATATGTATATATATATATATA 39224       A
                                TATAT TATATATATATATATA
                                ||||| ||||||||||||||||
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                                ATATA ATATATATATATATAT
                                   C
GAM2871  MYBL1    3'  TATATAAATATATATATATATA 41984       T
                                TATATA ATATATATATATATA
                                |||||| ||||||||||||||||
                                ATATAT TATATATATATATAT
                                    T
GAM2871  MYBL1    3'  TATATATATATAAATATATATA 41988           T
                                TATATATATATA ATATATATA
                                |||||||||||| |||||||||
                                ATATATATATAT TATATATAT
                                       T
GAM2871  MYBL1    3'  TATATATATATATAAATATATA 41989            T
                                TATATATATATATA ATATATA
                                |||||||||||||| |||||||
                                ATATATATATATAT TATATAT
                                       T
GAM2871  MYBL1    3'  TATATATATAAATATATATATA 41987          T
                                TATATATATA ATATATATATA
                                |||||||||| ||||||||||
                                ATATATATAT TATATATATAT
                                      T
GAM2871  MYBL1    3'  TATATATAAATATATATATATA 41985         T
                                TATATATA ATATATATATATA
                                |||||||| ||||||||||||
                                ATATATAT TATATATATATAT
                                     T
GAM2871  MYCL2    3'  TATATATATACATATATGTAA  23911              A
                                TATATATATATATATAT TAG
                                |||||||||||||||| |||
                                ATATATATATGTATATA ATT
                                        C
GAM2871  MYCL2    3'  TATATATATACATATATA    23910
                                TATATATATATATATATA
                                |||||||||||||||||
                                ATATATATATGTATATAT

GAM2871  MYF5     3'  ATATATATATATGTATATATA  24631           A
                                ATATATATATAT TATATATA
                                |||||||||||| ||||||||
                                TATATATATATA ATATATAT
                                      C
GAM2871  MYF5     3'  TATAATATATATATATGTATAT 24633     _        A
            A                    TATA TATATATATAT TATATA
                                ||||| |||||||||| ||||||
                                ATAT ATATATATATA ATATAT
                                   T          C
GAM2871  NRF1     3'  TACATATATATATATATATAT  41096
                                TATATATATATATATATATAT
                                |||||||||||||||||||||
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                                ATGTATATATATATATATATA

GAM2871  NRF1     3'  TATATATATATATATGTATATA 41100              A
                                TATATATATATATAT TATATA
                                |||||||||||||| ||||||
                                ATATATATATATATA ATATAT
                                          C
GAM2871  NRF1     3'  TATATATATATATATGTATATATA 41102            A
                                TATATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATATA ATATATAT
                                          C
GAM2871  NRF1     3'  TATATATATATATATATGTATA 41098              A
                                TATATATATATATATAT TATA
                                |||||||||||||||| ||||
                                ATATATATATATATATA ATAT
                                          C
GAM2871  NRF1     3'  TATATATATATGTATATATATA 41104              A
                                TATATATATAT TATATATATA
                                |||||||||| ||||||||||
                                ATATATATATA ATATATATAT
                                          C
GAM2871  NRF1     3'  CATATATATATATATATAT    41092
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                GTATATATATATATATATA

GAM2871  NRIP1    3'  TATATATATATATATATATATA 40981
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  NRIP1    3'  TATATATATATATATATA     40977
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  NRIP1    3'  TATATATATATATACATA     40975
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATGTAT

GAM2871  OTX1     3'  TATGTATATATATATATAT    31001     A
                                TAT TATATATATATAT
                                ||| ||||||||||||||
                                ATA ATATATATATATA
                                  C
GAM2871  OTX1     3'  TATATATGTATATATATATATA 30997         A
                                TATATAT TATATATATATA
                                ||||||| ||||||||||||||
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                                ATATATA ATATATATATATAT
                                     C
GAM2871  OTX1     3'  TATATATATGTATATATATATA 30995          A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                      C
GAM2871  OTX1     3'  TATATGTATATATATATATAT  31000       A
                                TATAT TATATATATATATAT
                                ||||| ||||||||||||||||
                                ATATA ATATATATATATATA
                                   C
GAM2871  OTX1     3'  TATATATATATGTATATATATA 30993          A
                                TATATATATAT TATATATATA
                                |||||||||||| ||||||||||
                                ATATATATATA ATATATATAT
                                      C
GAM2871  OTX1     3'  TATATATATATGTATATATA   30991          A
                                TATATATATAT TATATATA
                                |||||||||||| ||||||||
                                ATATATATATA ATATATAT
                                      C
GAM2871  PEA15    3'  TAATATACATATATGTAG     19080    T          A
                                A ATATATATATAT TAG
                                | |||||||||||| |||
                                A TATATGTATATA ATC
                                 T          C
GAM2871  PEX3     3'  TATATATATATATATGTATATA 18849              A
                                TATATATATATATAT TATATA
                                |||||||||||||||| ||||||
                                ATATATATATATATA ATATAT
                                        C
GAM2871  PKIA     3'  ATATATATATATATATATAT   27737
                                ATATATATATATATATATAT
                                ||||||||||||||||||||
                                TATATATATATATATATATA

GAM2871  PKIA     3'  TATATATATATATATATAT    27746
                                TATATATATATATATATAT
                                ||||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  PLXNA1   3'  TATATATATATGCATATATATA 43626          A
                                TATATATATAT TATATATATA
                                |||||||||||| ||||||||||
                                ATATATATATA GTATATATAT
                                      C
GAM2871  PMX1     3'  ATATATATATATATATATA    35496
                                ATATATATATATATATATA
                                ||||||||||||||||||||
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                                TATATATATATATATATAT

GAM2871  PMX1     3'  ATATATATATATATATATATA  35497
                                ATATATATATATATATATATA
                                ||||||||||||||||||||
                                TATATATATATATATATATAT

GAM2871  PMX1     3'  TATATATATATATATATATATA 35521
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  PPARGC1  3'  TATATATATATATATATATATA 29961
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  PPARGC1  3'  TATATATATATATATATA    29960
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  PPP3R1   3'  ATATTTACATATGTATATATAG 44073      A      A        III
            AT                    ATAT TATATAT TATATATAGA   T
                                  |||| ||||||| ||||||||||   |
                                  TATA ATGTATA ATATATATCT   A
                                    A      C         III
GAM2871  PRKCN    3'  TATATATATATATATATATAAA 25165               T
            GA                    TATATATATATATATATATA AGA
                                  |||||||||||||||||||| |||
                                  ATATATATATATATATATAT TCT
                                                T
GAM2871  PTPRK    3'  TATATATTTATATATTTATATA 15967        A      A
            GA                    TATATAT TATATAT TATATAGA
                                  ||||||| ||||||| ||||||||
                                  ATATATA ATATATA ATATATCT
                                      A      A
GAM2871  PUM1     3'  TATATATATATATATATA    31236
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  PUM1     3'  TATATATATATATATATATATA 31237
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  RBP3     3'  TATATATACATATATATA    16193
                                TATATATATATATATATA
                                ||||||||||||||||||
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                                ATATATATGTATATATAT

GAM2871  RBP3     3'  TATATATATACATATATA    16194
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATGTATATAT

GAM2871  RNTRE    3'  CATATATATATATATATATATA 31249
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                GTATATATATATATATATATAT

GAM2871  RNTRE    3'  CATATATATATATATATATA  31248
                                TATATATATATATATATATA
                                ||||||||||||||||||||
                                GTATATATATATATATATAT

GAM2871  ROCK2    3'  TATATATATATATATATA    42361
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATAT

GAM2871  ROCK2    3'  TATATATATATATATATAT   42362
                                TATATATATATATATATAT
                                ||||||||||||||||||
                                ATATATATATATATATATA

GAM2871  RP42     3'  TACATATATATAGATATATAGA 33988          T
                                TATATATATATA ATATATAGA
                                |||||||||||| |||||||||
                                ATGTATATATAT TATATATCT
                                       C
GAM2871  RP42     3'  TATATATATATATATACA    33990
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATATATATGT

GAM2871  RP42     3'  ATATATATATATATATATATA  33980
                                ATATATATATATATATATATA
                                ||||||||||||||||||||
                                TATATATATATATATATAT

GAM2871  RP42     3'  TATATATATATATATATATATA 33992
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATAT

GAM2871  RPL23A   3'  ATATATATATATATATATTCAG 9740              A
            A                    ATATATATATATATATAT TAGA
                                ||||||||||||||||| ||||
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                                TATATATATATATATATA GTCT
                                           A
GAM2871  RSN      3'  TATATACATACAATATATAGA  16404          T
                                TATATATATATA ATATATAGA
                                |||||||||||| |||||||||
                                ATATATGTATGT TATATATCT
                                           _
GAM2871  SEMA3F   3'  ATATATATATATATATATATA  20055
                                ATATATATATATATATATATA
                                ||||||||||||||||||||
                                TATATATATATATATATATAT

GAM2871  SEMA3F   3'  TATATATATATATATATATATA 20062
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
                                ATATATATATATATATATATAT

GAM2871  SERPINE1 3'  ATATATATATATATTTAAAGA  8283             A  T
                                ATATATATATATAT TA AGA
                                |||||||||||||| || |||
                                TATATATATATATA AT TCT
                                           A  T
GAM2871  SLC1A1   3'  TATATACATATATATATATATA 20034
                                TATATATATATATATATATATA
                                |||||||||||||||||||||
                                ATATATGTATATATATATATAT

GAM2871  SLC1A1   3'  TATACATATATATATATATATA 20033
                                TATATATATATATATATATATA
                                |||||||||||||||||||||
                                ATATGTATATATATATATATAT

GAM2871  SLC8A1   3'  TATGTATATATATGTATATATA 34406     A        A
                                TAT TATATATAT TATATATA
                                ||| ||||||||| ||||||||
                                ATA ATATATATA ATATATAT
                                  C        C
GAM2871  SLC8A1   3'  TATATATATGTATATATATA   34405          A
                                TATATATAT TATATATATA
                                ||||||||| ||||||||||
                                ATATATATA ATATATATAT
                                     C
GAM2871  SORCS3   3'  TATGTACATATACTGTATATAT 31427     A        A_
            AGA                    TAT TATATATAT  TATATATAGA
                                ||| |||||||||  ||||||||||
                                ATA ATGTATATG  ATATATATCT
                                  C        AC
GAM2871  SRGAP1   5'  TATATATATATATATATATATA 43609
                                TATATATATATATATATATATA
                                ||||||||||||||||||||||
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                                ATATATATATATATATATATAT

GAM2871  SRGAP1   5'  TATAAATATATATATATATATA 43604      T
                                TATA ATATATATATATATATA
                                |||| ||||||||||||||||
                                ATAT TATATATATATATATAT
                                   T
GAM2871  SRGAP1   5'  ATATATATATATATATATATA  43596
                                ATATATATATATATATATATA
                                ||||||||||||||||||||
                                TATATATATATATATATATAT

GAM2871  SRGAP1   5'  ATATATATATATATATATA    43595
                                ATATATATATATATATATA
                                ||||||||||||||||||
                                TATATATATATATATATAT

GAM2871  SRGAP1   5'  TATATATAAATATATATATATA 43606         T
                                TATATATA ATATATATATATA
                                |||||||| ||||||||||||
                                ATATATAT TATATATATATAT
                                      T
GAM2871  SRGAP1   5'  TATATAAATATATATATATATA 43605        T
                                TATATA ATATATATATATATA
                                |||||| ||||||||||||||
                                ATATAT TATATATATATATAT
                                    T
GAM2871  SVIL     3'  TATATAAATATATATATATTTT 34734        T          A_
            AGA                     TATATA ATATATATATAT  TAGA
                                |||||| ||||||||||||  ||||
                                ATATAT TATATATATATA  ATCT
                                    T          AA
GAM2871  SYNGR1   3'  TATATTATACATCTTATATATA 21769       A       A_
            GA                      TATAT TATATAT  TATATATAGA
                                ||||| |||||||  ||||||||||
                                ATATA ATATGTA  ATATATATCT
                                   _       GA
GAM2871  TGFBR2   3'  TATAGATATATATATATATATA 17477      T
                                TATA ATATATATATATATATA
                                |||| ||||||||||||||||
                                ATAT TATATATATATATATAT
                                   C
GAM2871  TGFBR2   3'  TATATAGATATATATATATATA 17479       T
                                TATATA ATATATATATATATA
                                |||||| ||||||||||||||
                                ATATAT TATATATATATATAT
                                    C
GAM2871  TGFBR2   3'  ATATATATATATATATATA    17471
                                ATATATATATATATATATA
                                ||||||||||||||||||
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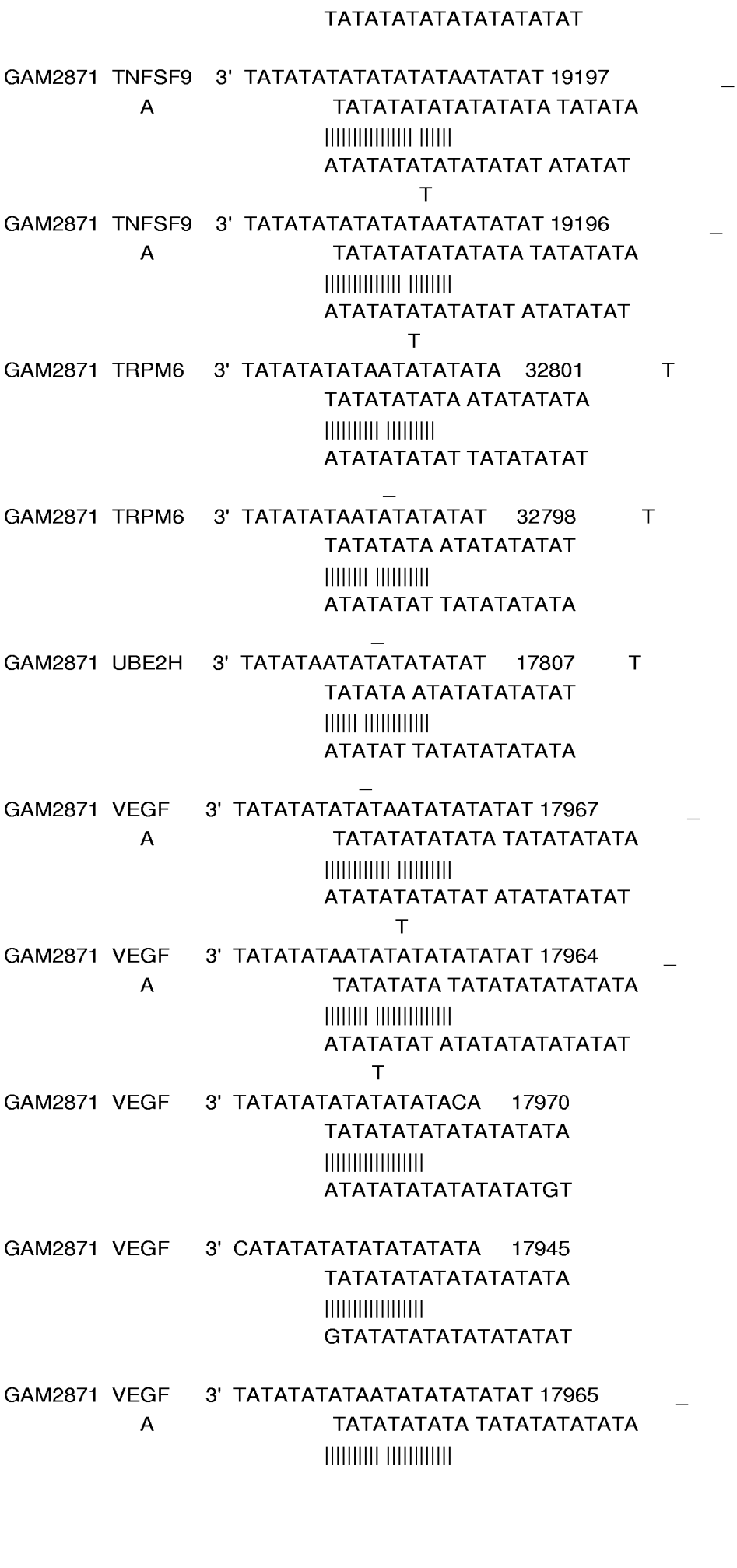
TATATATATATATATATAT
GAM2871 TNFSF9 3' TATATATATATATAATATAT 19197
A TATATATATATATA TATATA
ATATATATATATATAT ATATAT
T
GAM2871 TNFSF9 3' TATATATATATATAATATATAT 19196
A TATATATATATA TATATATA
ATATATATATATAT ATATATAT
T
GAM2871 TRPM6 3' TATATATATAATATATATA 32801 T
TATATATATA ATATATATA
ATATATATAT TATATATAT
GAM2871 TRPM6 3' TATATATAATATATATAT 32798 T
TATATATA ATATATATAT
ATATATAT TATATATATA
GAM2871 UBE2H 3' TATATAATATATATATAT 17807 T
TATATA ATATATATATAT
ATATAT TATATATATATA
GAM2871 VEGF 3' TATATATATATAATATATATAT 17967
A TATATATATATA TATATATATA
ATATATATATAT ATATATATAT
T
GAM2871 VEGF 3' TATATATAATATATATATATAT 17964
A TATATATA TATATATATATATA
ATATATAT ATATATATATATAT
T
GAM2871 VEGF 3' TATATATATATATATACA 17970
TATATATATATATATATA
ATATATATATATATATGT
GAM2871 VEGF 3' CATATATATATATATATA 17945
TATATATATATATATATA
GTATATATATATATATAT
GAM2871 VEGF 3' TATATATATAATATATATATAT 17965
A TATATATATA TATATATATATA

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                                ATATATATAT ATATATATATAT
                                      T
GAM2871  VENTX2   3'  ATATATATATATATATATATA  30908
                                ATATATATATATATATATATA
                                ||||||||||||||||||||
                                TATATATATATATATATATAT

GAM2871  WNT11    3'  TATATATATACATATATA    21537
                                TATATATATATATATATA
                                ||||||||||||||||||
                                ATATATATATGTATATAT

GAM2871  WNT5A    3'  TATATATGTATATATATATATA 18131        A
                                TATATAT TATATATATATATA
                                ||||||| ||||||||||||||
                                ATATATA ATATATATATATAT
                                     C
GAM2871  WNT5A    3'  TATATGTATATATATATATAT  18133      A
                                TATAT TATATATATATATAT
                                ||||| ||||||||||||||||
                                ATATA ATATATATATATATA
                                   C
GAM2871  WNT5A    3'  TATGTATATATATATATAT    18135     A
                                TAT TATATATATATATAT
                                ||| ||||||||||||||||
                                ATA ATATATATATATATA
                                  C
GAM2871  WNT5A    3'  TATATATATGTATATATATATA 18128         A
                                TATATATAT TATATATATATA
                                ||||||||| ||||||||||||
                                ATATATATA ATATATATATAT
                                      C
GAM2871  WNT5A    3'  TATATATATGTATATATA    18126         A
                                TATATATAT TATATATA
                                ||||||||| ||||||||
                                ATATATATA ATATATAT
                                      C
GAM2871  ZNF144   3'  TATGTACATATATATATATAT  28343     A
                                TAT TATATATATATATATAT
                                ||| ||||||||||||||||||
                                ATA ATGTATATATATATATA
                                  C
GAM2871  ZNF175   3'  TATGCATATATATACATACATA 28367     A
            GA                    TAT TATATATATATATATATAGA
                                ||| ||||||||||||||||||||
                                ATA GTATATATATGTATGTATCT
                                  C
GAM2871  ZNF236   3'  TACATATGTATTTATATATAGA 28866        A  A
                                TATATAT TAT TATATATAGA
                                ||||||| ||| ||||||||||
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                                ATGTATA ATA ATATATATCT
                                   C   A
GAM2872 ELAVL2   3' TGACTTACAAAGACATTTACTA 20746     CGTAG   TT__
            A                   TGAC    GCG    CATTTACTAA
                                ||||    |||   ||||||||||
                                ACTG    TGT    GTAAATGATT
                                  AA___   TTCT
GAM2872 KCNK4    3' GACCGTTTTCATTTA      37831       AGGCG
                                GACCGT    TTCATTTA
                                ||||||    ||||||||
                                CTGGCA    AAGTAAAT
                                   A____
GAM2873 B4GALT4  5' TATTACGTGAATAATATCTAT  19102    C          A
                                TAT ATGTGAATAATAT CTGT
                                ||| |||||||||||| ||||
                                ATA TGCACTTATTATA GATA
                                  A          _
GAM2873 GJA1     3' TGTGAGTTTATACTGTAT    6734       ATAA
                                TGTGA   TATACTGTAT
                                |||||   ||||||||||
                                ACACT   ATATGACATA
                                   CAA_
GAM2873 KCNH5    3' ATATGTATATACTGTA     40256      AATA
                                ATGTG   ATATACTGTA
                                |||||   ||||||||||
                                TATAC   TATATGACAT
                                   A___
GAM2873 SORCS3   3' ATATGTACATATACTGTA    31414      AATA
                                ATGTG   ATATACTGTA
                                |||||   ||||||||||
                                TATAC   TATATGACAT
                                   ATG_
GAM2874 DGKG     3' TTGAAACAGAATGTA       10662         TATAC
                                TTGAAACAGA    ATGTA
                                ||||||||||    |||||
                                AACTTTGTCT    TACAT
                                      _____
GAM2874 PPP6C    3' CTGGGACAGGTATACATA    15541     AA   A
                                TTG  ACAG TATACATG
                                |||  |||| ||||||||
                                GAC  TGTC ATATGTAT
                                  CC   C
GAM2874 ARHGDIB  3' TTATTCTTGTTCTCTTGTG   10130     A  A  CA
                                TTAT CTT GT  TCTCTTGTG
                                |||| ||| ||  |||||||||
                                AATA GAA CA  AGAGAACAC
                                  A  _  __
GAM2875 MLLT3    3' AGGTGGCTATTTGGTCCCCCCA 21189           A__  G TG
            G                   AGGTGGTTATTTG   TC T  G
                                ||||||||||||   || |  |
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                                TCCACCGATAAAC   GG G  C
                                      CAG  G GT
GAM2875  PFN2     3'  AGATGGTTATGTTGGG      38161          TTGATC
                                AGGTGGTTAT     GTTGGG
                                ||||||||||     ||||||
                                TCTACCAATA     CAACCC
                                _______
GAM2875  AOC3     3'  TACACATTTCTGTGGCTTGCCT 19020          CATATGACC
               T                 TACACATTTT       GCCTT
                                 ||||||||||       |||||
                                 ATGTGTAAAG       CGGAA
                                      ACACCGAA_
GAM2875  ETS2     3'  ACATTTTCAATCCTGCCTT   23463          TATGA  _
                                ACATTTTCA     CC GCCTT
                                |||||||||     || |||||
                                TGTAAAAGT     GG CGGAA
                                      TA___  A
GAM2875  FCRH3    5'  TTTTCATATGGGAAACCCCTT  38117          ____  G
                                TTTTCATATG    ACC CCTT
                                ||||||||||    ||| ||||
                                AAAAGTATAC    TGG GGAA
                                      CCTT  _
GAM2876  PLAGL1   3'  TCTAAAAACATAAGACA     15366      T       T
                                TCTA AAACATAAG ATA
                                |||| ||||||||| |||
                                AGAT TTTGTATTC TGT
                                  T       _
GAM2876  BCAT1    3'  CACTCTTGTAACACATTGATAC 42376          TGG__
                                TACTCTTGTAG    TGATAC
                                ||||||||||     ||||||
                                GTGAGAACATT    ACTATG
                                      GTGTA
GAM2876  CEL      3'  CACTCTTGTGGCCTCTTGATAC 12219          A  GG__
                                TACTCTTGT GT    TGATAC
                                ||||||||| ||    ||||||
                                GTGAGAACA CG    ACTATG
                                      C  GAGA
GAM2876  CLN6     3'  TACTCCTGTATTCAGATG     32829          GT__
                                TACTCTTGTA    GGTG
                                ||||||||||    ||||
                                ATGAGGACAT    CTAC
                                      AAGT
GAM2876  COL19A1  3'  ACTTTTGTAAATAGTGAT     12369      C     _
                                ACT TTGTAG TGGTGAT
                                ||| |||||| |||||||
                                TGA AACATT ATCACTA
                                  A     T
GAM2876  CRP      3'  CACTCTTGTGGCCTGGGTA    43443          A ____
                                TACTCTTGT GT   GGTG
                                ||||||||| ||   ||||
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                                GTGAGAACA CG   CCAT
                                     C  GAC
GAM2876  DIAPH2   3'  TACTTTTTTTGGTGATA     28677      C  GTAG
                                TACT TT    TGGTGATA
                                |||| ||    ||||||||
                                ATGA AA    ACCACTAT
                                  A  AA__
GAM2876  EPHB1    3'  TACTCTTGTTCTCCTGATG   20777         AG___
                                TACTCTTGT    TGGTG
                                |||||||||    |||||
                                ATGAGAACA    ACTAC
                                     AGAGG
GAM2876  FMO1     5'  CTCTTGTAATTTCTGGTG    12920         ____
                                CTCTTGTAG    TGGTG
                                |||||||||    |||||
                                GAGAACATT    ACCAC
                                     AAAG
GAM2876  OTOR     3'  TACTCTTTGATAATA       33555        GTAG
                                TACTCTT    TGGTGATA
                                |||||||    ||||||||
                                ATGAGAA    ACTATTAT
                                    ____
GAM2876  PTGS2    3'  TACTTTTGCAATGTGATA    9693       C      G
                                TACT TTGTAGTG TGATA
                                |||| |||||||| |||||
                                ATGA AACGTTAC ACTAT
                                  A      _
GAM2876  RAD17    5'  CACTCTTGTACTTGAATAC   39409         G_  GT
                                TACTCTTGTA  TG  GATAC
                                ||||||||||  ||  |||||
                                GTGAGAACAT  AC  TTATG
                                     GA  __
GAM2876  SIL      3'  CACTCTTGTATAAGAGTG    16725         GT__
                                TACTCTTGTA   GGTG
                                ||||||||||   ||||
                                GTGAGAACAT   TCAC
                                     ATTC
GAM2877  BCL11A   3'  AACAAGGGGTTGGGGACTCA  39703      T  A  A   A   C
                                AACA GG GG TTG GGAC CA
                                |||| || || ||| |||| ||
                                TTGT CC CC AAC CCTG GT
                                  T  _  _  C   A
GAM2877  CLIC3    5'  CAGGAGGGGCAGTGACCCAC  21696    T    ATTGAG
                                CA GGAGG     GACCCAC
                                || |||||     |||||||
                                GT CCTCC     CTGGGTG
                                 _    CCGTCA
GAM2877  COG6     3'  TGGTTGGATTTAGGACCCA   43767     A_    G
                                TGG  GGATT AGGACCCA
                                |||  ||||| ||||||||
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                                ACC  CCTAA TCCTGGGT
                                  AA    A
GAM2877  CPSF4    3'  TGATGTCGACTGCAGGGACCCA 27441   C   GAG    A__
                C                  A ATG   GATTG   GGACCCAC
                                   | |||   |||||   ||||||||
                                   A TAC   CTGAC   CCTGGGTG
                                    C   AG_    GTC
GAM2877  CYLN2    3'  TGGTGTGTACATAAGGACCCAC 18074    AGGAT___
                                   TGG       TGAGGACCCAC
                                   |||       ||||||||||
                                   ACC       ATTCCTGGGTG
                                     ACACATGT
GAM2877  FGF1     3'  CATGGAGGGACTCAGCC     37567         _   G  GAC
                                   CATGGAGG ATT AG   CC
                                   |||||||| ||| ||   ||
                                   GTACCTCC TGA TC   GG
                                        C   G  ___
GAM2877  GNGT2    3'  ATGGAGGGACAGGACCCAC    36480        ATTG
                                   ATGGAGG    AGGACCCAC
                                   |||||||    |||||||||
                                   TACCTCC    TCCTGGGTG
                                       CTG_
GAM2877  KCNA7    3'  CAACATGGCCCTAGGGGACCCA 36641         AGGA   A_
                C                   TAACATGG    TTG  GGACCCAC
                                    ||||||||    |||  ||||||||
                                    GTTGTACC    GAT  CCTGGGTG
                                        GG__   CC
GAM2877  PAK4     3'  AACATGGGGGAGGGCC      25248        A  ATT    A
                                   AACATGG GG   GAGG CC
                                   ||||||| ||   |||| ||
                                   TTGTACC CC   CTCC GG
                                       _  ___    C
GAM2877  PPP2CA   3'  ATGCAGGAAGAACCCAC     15514     G    TTG
                                   ATG AGGA   AGGACCCAC
                                   ||| ||||   |||||||||
                                   TAC TCCT   TCTTGGGTG
                                     G   ___
GAM2877  RGS5     3'  ATGGAGGAAATAACTCAC    18830         TTGAG   C
                                   ATGGAGGA    GAC CAC
                                   ||||||||    ||| |||
                                   TACCTCCT    TTG GTG
                                       TTA__   A
GAM2877  SHMT2    3'  TAACATGGTGGGTTGGAG    24007         A  A   AG
                                   TAACATGG GG TTG  G
                                   |||||||| || |||  |
                                   ATTGTACC CC AAC  C
                                       A  C   CT
GAM2877  SLC21A9  3'  CATGGAGGGCAGCCTGGCCCAC 28560         ATTGA__  A
                                   CATGGAGG      GG CCCAC
                                   ||||||||      || |||||
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                                GTACCTCC      CC GGGTG
                                    CGTCGGA  _
GAM2877  NOVA1    3'  TAATTCTCTTTTGTAATTCAGT 27062          C   TTG_ _
             TGC                    TAATTCTCTT TGT    CA TTGC
                                ||||||||||  |||    ||  ||||
                                ATTAAGAGAA ACA    GT AACG
                                     A   TTAA  C
GAM2878  BCL9     3'  CGTCTTACGCATGGGAGGGGG  20236      CCATC     _
                                CGTC     TGTGCG GGGAGGGGG
                                ||||     ||||||  |||||||||
                                GCAG     ATGCGT CCCTCCCCC
                                  A____      A
GAM2878  DRIL1    5'  GCCCCTGCGGGGAGGGG     23369       ATCTG
                                GTCCC     TGCGGGGAGGGG
                                |||||     ||||||||||||
                                CGGGG     ACGCCCCTCCCC
                                    _____
GAM2878  GPC4     3'  GTTTTACTGATAAGAGGGGG   11085    CCCAT   TGCG
                                GT     CTG    GGGAGGGGG
                                ||     |||    |||||||||
                                CA     GAC    TTCTCCCCC
                                 AAAT_   TA__
GAM2878  KLHL2    5'  CGTTCCATCCGCCCCGGAGGGG 28530     C       GCGG
             G                   CGT CCATCTGT    GGAGGGGG
                                ||| ||||||||    ||||||||
                                GCA GGTAGGCG    CCTCCCCC
                                  A       GGG_
GAM2878  LPIN2    3'  TCCCTTGCTGTGGGGAGGGGG  31221      AT_   GC
                                TCCC   CTGT  GGGGAGGGGG
                                ||||   ||||  ||||||||||
                                AGGG   GACA  CCCCTCCCCC
                                  AAC    __
GAM2878  MNT      3'  GTCCAGGTGGGGAGGGGG    33723      CATCT  GC
                                GTCC     GT  GGGGAGGGGG
                                ||||     ||  ||||||||||
                                CAGG     CA  CCCCTCCCCC
                                  TC___  __
GAM2878  PAX7     5'  CGTCCAGAAGCTGGGGAGGGGG 30330       CATCT  GC
                                CGTCC     GT  GGGGAGGGGG
                                |||||     ||  ||||||||||
                                GCAGG     CG  CCCCTCCCCC
                                   TCTT_  A_
GAM2878  PPP2R5B  5'  GTCCGGCCTTTGGGGGGGGGG  26449      CA   G  C    A
                                GTCC  TCT TG GGGG GGGGG
                                ||||  ||| || |||| |||||
                                CAGG  GGA AC CCCC CCCCC
                                  CC   A  _   _
GAM2878  RABL2B   3'  TCTGCCTGCGGGGAGGGGG   28206       __
                                TCTGT  GCGGGGAGGGGG
                                |||||  ||||||||||||
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                                AGACG  CGCCCCTCCCCC
                                  GA
GAM2878 ADAM11   3' CTCCGTCTCCCCCCGTGGGTGG 34654        G___
                                CTCCGTCTT   GTGGGTGG
                                |||||||||   ||||||||
                                GAGGCAGAG   CACCCACC
                                     GGGG
GAM2878 LASS2    5' TACTCCGTCTGCTCGGGTGG  42682        TGG
                                TACTCCGTCT  TGGGTGG
                                ||||||||||  |||||||
                                ATGAGGCAGA  GCCCACC
                                     CGA
GAM2878 RFXAP    3' GTCTTGGCATTGGTGG     8053         GGTG
                                GTCTTGGTG   GGTGG
                                |||||||||   |||||
                                CAGAACCGT   CCACC
                                     AA__
GAM2878 SLC25A1  3' TCTGCCTTGGCAGGGTGG   25606    C     _
                                TC GTCTTGGT GGGTGG
                                || |||||||| ||||||
                                AG CGGAACCG CCCACC
                                 A       T
GAM2879 APPBP2   3' AGTAACCTAACATTTCCAT   26872         ___
                                AGTAACCTAACA  CCAT
                                ||||||||||||  ||||
                                TCATTGGATTGT  GGTA
                                      AAA
GAM2879 CDY1     3' AAAGTAACCTAAATCTGCACA 21712         CAC__
                                AAAGTAACCTAA    CATA
                                ||||||||||||    ||||
                                TTTCATTGGATT    GTGT
                                      TAGAC
GAM2879 RGS2     3' AGTTTTCAACACCATAGCACT 16314    AACC       A
                                AGT   TAACACCATA CACT
                                |||   |||||||||| ||||
                                TCA   GTTGTGGTAT GTGA
                                  AAA_        C
GAM2880 ADAMTS3  3' CAATAGTTTAAGCTGTTAGTT 30640    TT    __
                                CAAT  GTTTAA  TGTTAGTT
                                ||||  ||||||  ||||||||
                                GTTA  CAAATT  ACAATCAA
                                  T_    CG
GAM2881 HIS1     5' GAGCTCAAGTCAGTAAAG    26992       AC   T
                                GAGCTCAA  CAGT AAG
                                ||||||||  |||| |||
                                CTCGAGTT  GTCA TTC
                                     CA   T
GAM2881 IL1R1    3' GAGGCTCAAGTCCTAGGTTC  9359    A   AACC   AA__
                                GAG GCTCA   AGTT   GTTC
                                ||| |||||   ||||   ||||
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                                CTC CGAGT   TCAG   CAAG
                                  _   ____   GATC
GAM2881 MN1     3' GAGCTCAAAGTGGAGC     14580       ACC  TA
                                GAGCTCAA  AGT  AGT
                                ||||||||  |||  |||
                                CTCGAGTT  TCA  TCG
                                    ___  CC
GAM2881 NPHP1   3' GCTCAAGTTAAATT      41681      AACC
                                GCTCA   AGTTAAGTT
                                |||||   |||||||||
                                CGAGT   TCAATTTAA
                                  ____
GAM2881 SLC10A2 3' AAGAGCTAAGTTGAGTT    7811       CAAACC   A
                                GAGAGCT    AGTT AGTT
                                |||||||    |||| ||||
                                TTCTCGA    TCAA TCAA
                                   T_____  C
GAM2881 SPOCK   5' GAGAGCTCCAAACCAATC   41734       _
                                GAGAGCTC AAACCAGTT
                                |||||||| |||||||||
                                CTCTCGAG TTTGGTTAG
                                    G
GAM2882 AKAP13  3' CACATCAAGCCTTCTCTCAC  28472   G   CT  GC
                                CA ATCA  TC  TCTCTCAC
                                || ||||  ||  ||||||||
                                GT TAGT  GG  AGAGAGTG
                                 G   TC  A_
GAM2882 ASB1    3' CAGATCACTTTCTCCCTCAC  32028       CG
                                CAGATCACTT  CTCTCTCAC
                                ||||||||||  |||||||||
                                GTCTAGTGAA  GAGGGAGTG
                                    A_
GAM2882 CAPZA1  3' GATAGATCACTCTCTCACCAA 43715    CACT
                                GAT   TCGCTCTCTCACCAA
                                |||   ||||||||||||||
                                CTA   AGTGAGAGAGTGGTT
                                  TCT_
GAM2882 DDX38   5' GATCTGGGATTTCTCTCACCAA 30412     ACTTCGC
                                GATC      TCTCTCACCAA
                                ||||      ||||||||||
                                CTAG      AGAGAGTGGTT
                                  ACCCTAA
GAM2882 GNLY    5' AGATCTTGTTCTCTCACCA   29804      ACTTCGC
                                AGATC      TCTCTCACCA
                                |||||      ||||||||||
                                TCTAG      AGAGAGTGGT
                                  AACA___
GAM2882 MEN1    5' CAGACGTTTTAGTCACTCACCA 39161      CACTTCGC  T
            A                    CAGAT       TC CTCACCAA
                                |||||       || ||||||||
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                                GTCTG      AG GAGTGGTT
                                   CAAAATC_  T
GAM2882  RBM3     5'  CAGACTTTCTCTCACC     43253     TCA   CGC
                                CAGA   CTT   TCTCTCACC
                                ||||   |||   |||||||||
                                GTCT   GAA   AGAGAGTGG
                                  ___   ___
GAM2882  SIAT1    3'  CAGATGTCTGCCTCTCTCAC   16720      CA  TCG
                                CAGAT  CT   CTCTCTCAC
                                |||||  ||   |||||||||
                                GTCTA  GA   GAGAGAGTG
                                   CA  CG_
GAM2882  SIAT8E   3'  AGATCACTTTCTTCAC      40830        CGC   C
                                AGATCACTT   TCT TCAC
                                |||||||||   ||| ||||
                                TCTAGTGAA   AGA AGTG
                                   ___   _
GAM2882  SLC24A1  3'  GATCCTTAGACTCACCA     21819     A   CGCTCT
                                GATC CTT     CTCACCA
                                |||| |||     |||||||
                                CTAG GAA     GAGTGGT
                                  _   TCT___
GAM2882  SNL      3'  CAGATCACTCGCTACTACAGCC 16936         T   _  CT  _
            A                    CAGATCACT CGCT CT  CA CCA
                                |||||||||  |||| ||  || |||
                                GTCTAGTGA GCGA GA  GT GGT
                                     _   T  T_  C
GAM2883  NR2E3    3'  TGAGGTCACTGCCGGTTGTC   32288     AC       TCC  C
                                TGA  TCATTGCC   GG TGTC
                                |||  ||||||||   || ||||
                                ACT  AGTGACGG   CC ACAG
                                  CC       ___  A
GAM2883  PML      3'  TGGACTCACTGCTGCTGT    37743     A       CTCCG
                                TG ACTCATTGC    GCTGT
                                || |||||||||    |||||
                                AC TGAGTGACG    CGACA
                                 C       A____
GAM2883  SIP      3'  GAATTCATTGCCTTTACT    30843     C       CCG
                                GAA TCATTGCCT   GCT
                                ||| |||||||||   |||
                                CTT AGTAACGGA   TGA
                                  A       AA_
GAM2883  TMEM2    3'  TGTACTCATTGCCAGTGT    30155     A       TCC  C
                                TG ACTCATTGCC   GG TGT
                                || ||||||||||   || |||
                                AC TGAGTAACGG   TC ACA
                                 A       ___  _
GAM2883  CDK7     3'  TTTTTGGCTATTTCCCTCA   12212          GAAG
                                TTTTTGGCTGT   TCCCTCA
                                ||||||||||    |||||||
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                                AAAAACCGATA   AGGGAGT
                                      A___
GAM2883  RPS10    3'  TTTTTGGCTGTAAGTTTATTCA 9746           A  CCC_
              AT                   TTTTTGGCTGTGA GT   TCAAT
                                   |||||||||||| ||   |||||
                                   AAAAACCGACATT CA   AGTTA
                                         _ AATA
GAM2884  MYH13    5'  TTCCCAAGTGACAGTCAG    19169       ACGAG   TA
                                   TTCCCGA   GACA  GTCAG
                                   |||||||    ||||  |||||
                                   AAGGGTT   CTGT  CAGTC
                                      CA___   __
GAM2884  NFATC1   3'  CTCCTGGGCGAGGACACGTCGG 26073     CGAA       A  A
              C                    TTCC   CGAGGACAT GTC GC
                                   ||||   ||||||||| ||| ||
                                   GAGG   GCTCCTGTG CAG CG
                                     ACCC       _  C
GAM2884  PRLR     5'  TTCCTGCACGAGGACATGAAGC 9626      CGA       AGTC
                                   TTCC   ACGAGGACAT   AGC
                                   ||||   ||||||||||   |||
                                   AAGG   TGCTCCTGTA   TCG
                                     ACG       CT__
GAM2884  TACR1    3'  TTCCTGGATGGTGATAATCAGC 31861     CGAAC  _  AC
                                   TTCC    GA GG  ATAGTCAGC
                                   ||||    || ||  |||||||||
                                   AAGG    CT CC  TATTAGTCG
                                     AC___  A  AC
GAM2884  ABCC3    3'  CGCTTGGGGTTCAGGGC     33418      C    GTGGAC
                                   CGCTT GGGG     CAGGGC
                                   ||||| ||||     ||||||
                                   GCGAA CCCC     GTCCCG
                                     _   AA____
GAM2884  CDH4     3'  CGCTGTGGGGGTGGGTGC    12174      TC       ACCAGG
                                   CGCT  GGGGGTGG     GC
                                   ||||  ||||||||     ||
                                   GCGA  CCCCCACC     CG
                                     CA       CA____
GAM2884  FOXE1    3'  ACCCTTTGGGTCCAGGGC    20936    G  CGG    GGA
                                   AC CTT   GGGT   CCAGGGC
                                   || |||   ||||   |||||||
                                   TG GAA   CCCA   GGTCCCG
                                    G   A__   ___
GAM2884  GPC1     3'  GCTGGGGGGGTGGGCCAGGGCT  13250     TC       A
                                   GCT  GGGGGTGG CCAGGGCT
                                   |||  |||||||| ||||||||
                                   CGA  CCCCCACC GGTCCCGA
                                     C_       C
GAM2884  IDUA     5'  GCTCGGGGACTGCGGGGCT   6813      T     _  GACCA
                                   GCT CGGGGG TG    GGGCT
                                   ||| |||||| ||    |||||
```

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                                CGA GCCCCT AC    CCCGA
                                  _     G  GC___
GAM2884  IGLL1    3'  GCCTTTGGGTGGGGTCGGGGCT 33476     CGG     ACCA_
                                GCTT   GGGTGG    GGGCT
                                ||||   ||||||    |||||
                                CGGA   CCCACC    CCCGA
                                  AA_     CCAGC
GAM2884  PITX1    5'  CGCTCCAGGGGCCGGGGC    15322          TGGA  A
                                CGCTTCGGGGG   CC GGGC
                                ||||||||||    || ||||
                                GCGAGGTCCCC   GG CCCG
                                       ____ C
GAM2884  PLIN     3'  ACATTTCGAAGACTAGGG    15393     C    GGGT   C
                                ACG TTCGG    GGAC AGGG
                                ||| |||||    |||| ||||
                                TGT AAGCT    TCTG TCCC
                                  A    _____    A
GAM2884  PPL      3'  GCTTGGCCTGCACCAGGGCT   15496     CG  GG  G
                                GCTT  GG  TG ACCAGGGCT
                                ||||  ||  || |||||||||
                                CGAA  CC  AC TGGTCCCGA
                                  __ GG  G
GAM2884  RAB5C    5'  ACTTGGGGCCGGGGCT      40804      C   GTGGA  A
                                GCTT GGGG    CC GGGCT
                                |||| ||||    || |||||
                                TGAA CCCC    GG CCCGA
                                  _   ______ C
GAM2884  RAC3     3'  GCTCGGGTGGGCCAGGGCT   22789     CGG     A
                                GCTT   GGGTGG CCAGGGCT
                                ||||   |||||| ||||||||
                                CGAG   CCCACC GGTCCCGA
                                  ___     C
GAM2884  TBL1X    5'  CTGCAAGGAGGCCAGGGCT   24881    T     T  A
                                CT CGGGGG GG CCAGGGCT
                                || |||||| || ||||||||
                                GA GTTCCT CC GGTCCCGA
                                 C     _ _
GAM2884  VIPR2    3'  CGCTGTGGGGGCCAGGGC    18011     TC    TGGA
                                CGCT  GGGGG   CCAGGGC
                                ||||  |||||   |||||||
                                GCGA  CCCCC   GGTCCCG
                                  CA    _____
GAM2885  CAPN5    3'  TTAGCAGTGGTGACAGTT    44931        AATAA
                                TTAGTAGT    GATAGTT
                                ||||||||    |||||||
                                AATCGTCA    CTGTCAA
                                     CCA__
GAM2885  CYB5     3'  TAGTAGTGATAAGAGTTT    12537        A     TA
                                TAGTAGT ATAAGA  GTTT
                                ||||||| ||||||  ||||
```

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                                ATCATCA TATTCT  CAAA
                                   C     __
GAM2885  VPS26    3'  TAGTAGTAAAACAGGTTTAAA  22211         TAA    _
                                TAGTAGTAA   GATAG TTTAAA
                                |||||||||   ||||| ||||||
                                ATCATCATT   TTGTC AAATTT
                                    ___    C
GAM2885  RALBP1   3'  TTAAAATAGTTATTTTAAGT   27703           AGT
                                TTAAAATAGTTATT   AGT
                                ||||||||||||||   |||
                                AATTTTATCAATAA   TCA
                                       AAT
GAM2885  TOX      3'  TTTAAAAAGTCTTTAGTAGT   31275        T   A
                                TTTAAAA AGTT TTAGTAGT
                                ||||||| |||| ||||||||
                                AAATTTT TCAG AATCATCA
                                   _   A
GAM2885  ZHX1     3'  TTTAAAAAAGTTAACAGTAGT  28519        T    T
                                TTTAAAA AGTTA TAGTAGT
                                ||||||| ||||| |||||||
                                AAATTTT TCAAT GTCATCA
                                   T    T
GAM2886  ADCY8    5'  GGCCGGCGGGCGCCCCCGGCCT 10012             _ A
            TC                    GGCCGGCGGGCGCCTC GG CTTC
                                  |||||||||||||||| || ||||
                                  CCGGCCGCCCGCGGGG CC GAAG
                                        G  G
GAM2886  DMPK     3'  AGGCGGTGGGCGCGGCTT    20606     C  C     CTC  A
                                AGGC GG GGGCGC   GG CTT
                                |||| || ||||||   || |||
                                TCCG CC CCCGCG   CC GAA
                                  _  A     ___  _
GAM2886  IL11     3'  AGGCCGGTCTCAAACTCTTGGA 8479         ___     GC  C
            CTTC                    AGGCCGG   CGGGC  CT GGACTTC
                                    |||||||   |||||  || |||||||
                                    TCCGGCC   GTTTG  GA CCTGAAG
                                       AGA    A_  A
GAM2886  MEN1     5'  GGCGGTGGGCGGCGGCGGCTTC 39192     C  C    _ CT   A
                                GGC GG GGGCG C  CGG CTTC
                                ||| || ||||| |  ||| ||||
                                CCG CC CCCGC G  GCC GAAG
                                  _  A    C CC  _
GAM2886  MUCDHL   3'  AGGTCGGCGGGCACCACG    36318     C         T
                                AGG CGGCGGGCGCC CG
                                ||| ||||||||||| ||
                                TCC GCCGCCCGTGG GC
                                  A         T
GAM2886  NEUROD2  5'  AGGCGGCGGGCGCCGGCGTCTT 26053      C        T_  GA
            C                     AGGC GGCGGGCGCC  CG  CTTC
                                  |||| ||||||||||  ||  ||||
```

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                                TCCG CCGCCCGCGG  GC  GAAG
                                  _       CC  A_
GAM2886 SIAT8E   5' AGGCAGGCGGGGGACT     40831     C     CGCCTC
                                AGGC GGCGGG     GGACT
                                |||| ||||||     |||||
                                TCCG CCGCCC     CCTGA
                                  T    _______
GAM2886 ST7      5' GGCCGCGGGCGCGCCGGCTT   30269      G     C   A
                                GGCCG CGGGCGC TCGG CTT
                                ||||| ||||||| |||| |||
                                CCGGC GCCCGCG GGCC GAA
                                  _      C   _
GAM2886 TNFRSF11A 5' AGGCTGGCGGGCGCCGCGG   19268     C       T
                                AGGC GGCGGGCGCC CGG
                                |||| |||||||||| |||
                                TCCG CCGCCCGCGG GCC
                                  A        C
GAM2886 ACK1     5' CCCCGGACTCGGACGCCG    25107       CC  T  AAG
                                CCCCGGAC  CG AT   GCCG
                                ||||||||  || ||   ||||
                                GGGGCCTG  GC TG   CGGC
                                    A_  C  ___
GAM2886 ADCY8    5' CCCCCGGAACCGGGCC     9999        CC   TATAA
                                CCCCCGGA  CCG    GGCC
                                ||||||||  |||    ||||
                                GGGGGCCT  GGC    CCGG
                                    T_  _____
GAM2886 BARHL1   3' CCCCCGGACCGGGGCTGAGGCT 33460         CC_  ATA   C
             GG                   CCCCCGGACC   GT   AGGC GG
                                  ||||||||||   ||   |||| ||
                                  GGGGGCCTGG   CG   TCCG CC
                                       CCC  AC_   A
GAM2886 CEBPA    3' CCCTGGGTCCCCGCCGGAGGCT 20391     CC  A     ATA   C
             GG                   CCC  GG CCCCGT   AGGC GG
                                  |||  || ||||||   |||| ||
                                  GGG  CC GGGGCG   TCCG CC
                                    AC  A     GCC    A
GAM2886 COL1A1   3' CCTCCGAACCCAGTGAGGGGCT 6370     _      C  ATAA   C
             GG                   CC CCGGACCC GT    GGC GG
                                  || |||||||| ||    ||| ||
                                  GG GGCTTGGG CA    CCG CC
                                   A       T  CTCC   A
GAM2886 GP9      5' GGACACCGTAGAAGGCCGG   6747      C    T
                                  GGAC CCGTA AAGGCCGG
                                  |||| ||||| ||||||||
                                  CCTG GGCAT TTCCGGCC
                                    T    C
GAM2886 KRTHB6   3' CCCCGGACTCCTGCGACCGG   14031        C  GTATAA
                                  CCCCGGAC CC     GGCCGG
                                  |||||||| ||     ||||||
```

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                                GGGGCCTG GG     CTGGCC
                                    A  ACG___
GAM2886  PCTK1    5'  CCCCCGGACTCGTTGGCGCCGG 37467        CC   ATAAG
                                CCCCCGGAC  CGT    GCCGG
                                |||||||||  |||    |||||
                                GGGGGCCTG  GCA    CGGCC
                                    A_   ACCG_
GAM2886  SLC13A4  5'  CCTCGGACCCCGCTCTGCCGG  29724    C        ATAAG
                                CC CGGACCCCGT    GCCGG
                                || ||||||||||    |||||
                                GG GCCTGGGGCG    CGGCC
                                 A        AGA__
GAM2887  ABCA2    5'  GCGCGGGGGCGGGGCGC     45524        CA  CA
                                GCGCGGGG  GG  GTGC
                                ||||||||  ||  ||||
                                CGCGCCCC  CC  CGCG
                                    CG  C_
GAM2887  ABCC1    3'  GCGTGGGAGTGCAGAGGCTGC  33403    C   CAG   T_  C
                                GCG GGGG   GCAG  GC GC
                                ||| ||||   ||||  || ||
                                CGC CCCT   CGTC  CG CG
                                  A   CA_   TC  A
GAM2887  ACTN2    5'  GCGCGGGGTGACCTTCGC    9946         CA   AG_
                                GCGCGGGG  GGC   TGC
                                ||||||||  |||   |||
                                CGCGCCCC  CTG   GCG
                                    A_   GAA
GAM2887  ADAM11   3'  GCCGGGGCAGGTGC       34655    G       CAG
                                GC CGGGGCAGG   TGC
                                || |||||||||   |||
                                CG GCCCCGTCC   ACG
                                 _       ___
GAM2887  ADARB1   3'  GCCTGGGGCAGACCACCTGC   31879    GC       AGT   _
                                GC  GGGGCAGGC   GCC GC
                                ||  |||||||||   ||| ||
                                CG  CCCCGTCTG   TGG CG
                                 GA       G__   A
GAM2887  ADRA1A   5'  GCGCGGAGGCGGGAGCGC    37809       _   A  C
                                GCGCGG GGC GG AGTGC
                                |||||| ||| || |||||
                                CGCGCC CCG CC TCGCG
                                   T   C  _
GAM2887  APOE     3'  GCGTGGGGTCGCATGGCTGC   6217     C   CAG   GT  C
                                GCG GGGG   GCA  GC GC
                                ||| ||||   |||  || ||
                                CGC CCCC   CGT  CG CG
                                  A   AG_   AC  A
GAM2887  APRT     5'  GCGCGGGGACGGGCGGGACCGC 7928         _ A   AGT
                                GCGCGGGG C GGC   GCCGC
                                |||||||| | |||   |||||
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                                CGCGCCCC G CCG   TGGCG
                                     T C   CCC
GAM2887 AQP5     5'  GCGCGGGGGGGCAGGGGGC   11632        CA    T__
                                GCGCGGGG  GGCAG   GC
                                ||||||||  |||||   ||
                                CGCGCCCC  CCGTC   CG
                                     C_    CCC
GAM2887 ARF1     5'  GCGCGGGGCACGCCG       43309          GGCAG
                                GCGCGGGGCA    TGCCG
                                ||||||||||    |||||
                                CGCGCCCCGT    GCGGC
                                      _____
GAM2887 ARHGEF7  3'  GCATGGGGCAGGTCCAC     19364     C       CAGTG
                                GCG GGGGCAGG    CCGC
                                ||| ||||||||    ||||
                                CGT CCCCGTCC    GGTG
                                  A       A____
GAM2887 ATP1B2   5'  GCGCGGGGCGAGTCCG      11739         AGGC   G
                                GCGCGGGGC   AGT CCG
                                |||||||||   ||| |||
                                CGCGCCCCG   TCA GGC
                                     C___   _
GAM2887 ATP8A2   3'  GCGCGGGGGAGCTCGC      45257        CA   AG
                                GCGCGGGG  GGC  TGC
                                ||||||||  |||  |||
                                CGCGCCCC  TCG  GCG
                                     C_   A_
GAM2887 AVPR1A   5'  GCCATCCAGGCAGTGC      8729     G  GGG
                                GC CG   CAGGCAGTGC
                                || ||   ||||||||||
                                CG GT   GTCCGTCACG
                                 _  AG_
GAM2887 B4GALT7  5'  GCATGGGGCAGGCGCTCGC   28544     C       A  GC
                                GCG GGGGCAGGC GT  CGC
                                ||| |||||||| ||  |||
                                CGT CCCCGTCCG CG  GCG
                                  A       _  A_
GAM2887 BACE2    5'  GCGCGGAGGCGCAGAGCCGC  39990       _  AG   T
                                GCGCGG GGC  GCAG GCCGC
                                |||||| |||  |||| |||||
                                CGCGCC CCG  CGTC CGGCG
                                   T   __    T
GAM2887 BAI2     5'  GCGCAGGGTAGGTAGCTGC   11794        C  C  _
                                GCGCGGGG AGG AG TGC
                                |||||||| ||| || |||
                                CGCGTCCC TCC TC ACG
                                     A  A  G
GAM2887 BCAT1    5'  GCAGGGCAGAGGTGCCA     42381          CA
                                GCGGGGCAGG  GTGCCG
                                ||||||||||  ||||||
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```
                                CGTCCCGTCT  CACGGT
                                      C_
GAM2887 BCL7A    5' GCGCGGCGGCGGGTGCAGT   34213      _  AG__
                                GCGCGG GGC   GCAGT
                                |||||| |||   |||||
                                CGCGCC CCG   CGTCA
                                   G   CCCA
GAM2887 BCR      5' GCGCGGGGCGGGGCGC     34637       A  CA
                                GCGCGGGGC GG  GTGC
                                ||||||||| ||  ||||
                                CGCGCCCCG CC  CGCG
                                      C  __
GAM2887 BIN1     5' GCGCGGGGAGATCTTGC    40298       C   CAG
                                GCGCGGGG AGG   TGC
                                |||||||| |||   |||
                                CGCGCCCC TCT   ACG
                                     _  AGA
GAM2887 CACNA1B  5' GCGCGGGGCGCGCCA      8742        AGGCA
                                GCGCGGGGC    GTGCCG
                                |||||||||    ||||||
                                CGCGCCCCG    CGCGGT
                                      _____
GAM2887 CACNG8   5' GCGGGGGCGGGGCCG      43526    C    A  CAGT
                                GCG GGGGC GG   GCCG
                                ||| ||||| ||   ||||
                                CGC CCCCG CC   CGGC
                                  _    C  ____
GAM2887 CAPG     3' GCATGGGGCAGGAAGACGC   11962    C      C  _
                                GCG GGGGCAGG AG TGC
                                ||| |||||||| || |||
                                CGT CCCCGTCC TC GCG
                                  A      T  T
GAM2887 CDH11    5' GCGCAGGGCAAGCGCTGC    38032         AG
                                GCGCGGGGCAGGC  TGC
                                ||||||||||||  |||
                                CGCGTCCCGTTCG  ACG
                                       CG
GAM2887 CDK2AP1  5' GCGCAGGGGCGGCCG      21599       CAG  AGT
                                GCGCGGGG   GC   GCCG
                                ||||||||   ||   ||||
                                CGCGTCCC   CG   CGGC
                                     ___  C__
GAM2887 CEBPA    5' GCGCGGGGCGTCGCGCCGC   20394        AGGCA
                                GCGCGGGGC    GTGCCGC
                                |||||||||    |||||||
                                CGCGCCCCG    CGCGGCG
                                      CAG__
GAM2887 CHAT     5' GCGCGGGGGTGGGGGCTGC   34185       CA___  AG
                                GCGCGGGG    GGC  TGC
                                ||||||||    |||  |||
```

```
                                CGCGCCCC    CCG  ACG
                                    CACCC   __
GAM2887  CHGA     5'  GCGCGGGGCTGGGGGCGC    10466         A  CA
                                GCGCGGGGC GG  GTGC
                                ||||||||| ||  ||||
                                CGCGCCCCG CC  CGCG
                                     A  CC
GAM2887  CKMT1    3'  GCGGGGGCAGGTCCAGAGC   34189     C       __   T
                                GCG GGGGCAGG  CAG GC
                                ||| ||||||||  ||| ||
                                CGC CCCCGTCC  GTC CG
                                  _      AG   T
GAM2887  CNTN2    5'  GCTGGGGCAGGTGGATGCTGC  22913    GC       CA_   C
                                GC  GGGGCAGG   GTGC GC
                                ||  ||||||||   |||| ||
                                CG  CCCCGTCC   TACG CG
                                 A_      ACC    A
GAM2887  CR1L     3'  GCGAGGGGCAGGGCTGC     44866     C       CAG
                                GCG GGGGCAGG   TGC
                                ||| ||||||||   |||
                                CGC CCCCGTCC   ACG
                                  T      CG_
GAM2887  CYP27A1  5'  GCAGGGCGGGTTCAAAGC    8953         A  __   T
                                GCGGGGC GG  CAG GC
                                ||||||| ||  ||| ||
                                CGTCCCG CC  GTT CG
                                    C  AA   T
GAM2887  DIA1     3'  GCGCGGGGGCGGTGGCCG    28787        CAG  A   _
                                GCGCGGGG   GC GTG CCG
                                ||||||||   || ||| |||
                                CGCGCCCC   CG CAC GGC
                                    ___  C   C
GAM2887  DNMT3A   5'  GCGCGGGGCTGGGGGGCTGC   35429         A  CAGT  C
                                GCGCGGGGC GG    GC GC
                                ||||||||| ||    || ||
                                CGCGCCCCG CC    CG CG
                                     A  CCC_  A
GAM2887  DSC2     5'  CGCGGGGCGAGGGCCGC     35937         _  CAGT
                                CGCGGGGC AGG    GCCGC
                                |||||||| |||    |||||
                                GCGCCCCG TCC    CGGCG
                                    C  ____
GAM2887  DUX4     3'  GCGCGGGGGCGGCCCTCGC   43760        CA   AG_
                                GCGCGGGG  GGC   TGC
                                ||||||||  |||   |||
                                CGCGCCCC  CCG   GCG
                                    CG   GGA
GAM2887  EFNA3    3'  GCAGCAGGCAGTGCTGC     22397    GG         C
                                GC  GGCAGGCAGTGC GC
                                ||  |||||||||||| ||
```

```
                                CG  TCGTCCGTCACG CG
                                 __         A
GAM2887  EGLN1    5'  GCGCGGGGTGTGCGAGGC    35168        CAG  _  T
                                GCGCGGGG   GC AG GC
                                ||||||||   || || ||
                                CGCGCCCC   CG TC CG
                                    ACA  C  _
GAM2887  EGLN2    5'  GCGTGGGGCAGGGTGAGGC   38828     C      CA   CC
                                GCG GGGGCAGG  GTG  GC
                                ||| ||||||||  |||  ||
                                CGC CCCCGTCC  CAC  CG
                                  A       __  TC
GAM2887  EN1      5'  GCACGGGGCGGGTGC       10911         A  CA
                                GCGCGGGGC GG  GTGC
                                |||||||||  ||  ||||
                                CGTGCCCCG CC  CACG

                                    _  __
GAM2887  ENG      3'  GCCGGGGCAGCCACCGC     6498     G      G  G
                                GC CGGGGCAG CA TGC
                                || ||||||||  || |||
                                CG GCCCCGTC GT GCG
                                 _      G  G
GAM2887  ERBB2    5'  GCGCGGGGCGCGGGGTGCTGC  20820         A_  CA    C
                                GCGCGGGGC  GG  GTGC GC
                                |||||||||  ||  ||||  ||
                                CGCGCCCCG  CC  CACG CG
                                     CG  C_   A
GAM2887  F2RL1    5'  GCGCGGGGAATCCGCCGC    40509        C  GCAG
                                GCGCGGGG AG    TGCCGC
                                ||||||||  ||    ||||||
                                CGCGCCCC TT    GCGGCG
                                    _  AG__
GAM2887  F2RL3    3'  GCGCGGAGCCACTGCCGC    19521         AGG  G
                                GCGCGGGGC   CA TGCCGC
                                |||||||||   ||  ||||||
                                CGCGCCTCG   GT ACGGCG
                                    ___  G
GAM2887  FGF18    5'  GCTGCGGGGCGGCAGCCGC   38009    _     A    GT
                                GC GCGGGGC GGCA  GCCGC
                                ||  |||||||  ||||  |||||
                                CG CGCCCCG CCGT  CGGCG
                                 A      _   __
GAM2887  FHIT     5'  GCGCGGGGCCGGAGCGCCGC  12871         A  C
                                GCGCGGGGC GG AGTGCCGC
                                |||||||||  ||  ||||||||
                                CGCGCCCCG CC TCGCGGCG
                                     G  _
GAM2887  FLNA     5'  GCCGGGGGGGGCGGTGCTGC   11134    G    CA  A   C
                                GC CGGGG  GGC GTGC GC
                                ||  |||||  |||  ||||  ||
```

```
                                CG GCCCC  CCG CACG CG
                                 _    C_  C   A
GAM2887  FOXE3    3'  GCGCTGGGGTGGGGGGCGCCGC 29147     _   CA  CA
                                GCGC GGGG  GG  GTGCCGC
                                |||| ||||  ||  |||||||
                                CGCG CCCC  CC  CGCGGCG
                                  A   AC  CC
GAM2887  FOXO1A   5'  GCCGGGGCAGAGCCTGC     12888    G      _ AG
                                GC CGGGGCAG GC  TGC
                                || ||||||||  ||  |||
                                CG GCCCCGTC CG  ACG
                                 _      T  G_
GAM2887  FUS1     3'  GCCGGGGCAGGGGGTGC     28588    G       CA
                                GC CGGGGCAGG  GTGC
                                || |||||||||  ||||
                                CG GCCCCGTCC  CACG
                                 _       CC
GAM2887  GAA      5'  CGCGGGGCGGGGCCG       6664         A  CAGT
                                CGCGGGGC GG   GCCG
                                |||||||| ||   ||||
                                GCGCCCCG CC   CGGC
                                    C  ____
GAM2887  GALGT    5'  GCGCGGGGAGGGCTCTGGCCGC 11184        CA   AGT_
                                GCGCGGGG  GGC   GCCGC
                                ||||||||  |||   |||||
                                CGCGCCCC  CCG   CGGCG
                                    TC   AGAC
GAM2887  GALNT2   3'  GCGGGGCAGGACTCGCTGC   21006         CAG   C
                                GCGGGGCAGG   TGC GC
                                ||||||||||   ||| ||
                                CGCCCCGTCC   GCG CG
                                     TGA   A
GAM2887  GARP     3'  GCCGGGGCAGGACTCACCGC  24312    G       CAG
                                GC CGGGGCAGG   TGCCGC
                                || |||||||||   ||||||
                                CG GCCCCGTCC   GTGGCG
                                 _       TGA
GAM2887  GFRA1    5'  GCGCGGGGCTGGTCCCCGC   23566         A  CAGTG
                                GCGCGGGGC GG    CCGC
                                ||||||||| ||    ||||
                                CGCGCCCCG CC    GGCG
                                    A  AGG__
GAM2887  GLI4     3'  GCTGGGCAGTGCCCACCG    39691    G    _ AG
                                GC GGGCAG GC  TGCCG
                                || |||||| ||  |||||
                                CG CCCGTC CG  GTGGC
                                 A     A  G_
GAM2887  GRB10    5'  CGCGGGGCGCCCGGCTGC    23653         A___   AG
                                CGCGGGGC   GGC  TGC
                                ||||||||   |||  |||
```

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                                GCGCCCCG   CCG  ACG
                                    CGGG  __
GAM2887  GTF2IRD1  5'  GCGCGGGGAGGGGGCGC    32259       C   CA
                                GCGCGGGG AGG  GTGC
                                |||||||| |||  ||||
                                CGCGCCCC TCC  CGCG
                                    _  CC
GAM2887  GUCY1A2  5'  CGCGGGGCGCTGCGGTCGC   9215        AG  A   C_
                                CGCGGGGC  GC GTG  CGC
                                ||||||||  || |||  |||
                                GCGCCCCG  CG CGC  GCG
                                    __  A   CA
GAM2887  HADHSC   5'  GCGCGAGGCGGGCAGCCGC   23718        A   GT
                                GCGCGGGGC GGCA  GCCGC
                                ||||||||| ||||  |||||
                                CGCGCTCCG CCGT  CGGCG
                                    C   __
GAM2887  HHIP     5'  GCGCGGGGAGGTGCG      35410       C   CAG   C
                                GCGCGGGG AGG   TGC G
                                |||||||| |||   ||| |
                                CGCGCCCC TCC   ACG C
                                    _  ___  A
GAM2887  HIC1     5'  GCGCGGGGGCAGCTCG     44567       CAG    GC
                                GCGCGGGG   GCAGT  CG
                                ||||||||   |||||  ||
                                CGCGCCCC   CGTCG  GC
                                    ___    A_
GAM2887  HLX1     5'  GCGCGGGGAGGGGCGC     34988       C   CA
                                GCGCGGGG AGG  GTGC
                                |||||||| |||  ||||
                                CGCGCCCC TCC  CGCG
                                    _  C_
GAM2887  HUNK     5'  GCGCGGGGTGGGGCGC     31072       CA  CA
                                GCGCGGGG  GG  GTGC
                                ||||||||  ||  ||||
                                CGCGCCCC  CC  CGCG
                                    AC  __
GAM2887  IGFBP2   3'  GCGGGGGGCAGGGGCGC    8258     C      CA
                                GCG GGGGCAGG  GTGC
                                ||| ||||||||  ||||
                                CGC CCCCGTCC  CGCG
                                  C      C_
GAM2887  INPP5A   3'  GCGCAGAGTCAGTGCCGC   24405       CAGG
                                GCGCGGGG   CAGTGCCGC
                                ||||||||   |||||||||
                                CGCGTCTC   GTCACGGCG
                                    A___
GAM2887  INPP5A   3'  CGCGGGGCGGACTCCG     24404       A   AGTG
                                CGCGGGGC GGC   CCG
                                |||||||| |||   |||
```

```
                                GCGCCCCG CTG    GGC
                                    C   A___
GAM2887  INPPL1   3'  GCGAGGGGCAGGATGC      11463     C       CA
                                GCG GGGGCAGG  GTGC
                                ||| ||||||||  ||||
                                CGC CCCCGTCC  TACG
                                  T       __
GAM2887  JAM2     5'  GCGCGGGGCTGCCAGC      34543          AGGCAG   _
                                GCGCGGGGC     TGCC GC
                                |||||||||     |||| ||
                                CGCGCCCCG     ACGG CG
                                    _______   T
GAM2887  JUN      3'  GCGCGGGGACAGCCCG      13743         CAG    G
                                GCGCGGGG   GCAGT CCG
                                ||||||||   ||||| |||
                                CGCGCCCC   TGTCG GGC
                                    ___    _
GAM2887  KCNA5    5'  GCGCGGGAGCAGAGGGCATGCT 40682        _  ___   G   C
              GC                  GCGCGGG GCA   GGCA TGC GC
                                |||||||  |||   |||| ||| ||
                                CGCGCCC CGT   CCGT ACG CG
                                    T   CTC    _   A
GAM2887  KDR      5'  GCGCGGAGGTGGAACTCGC    13941         CA  CAGT  _
                                GCGCGGGG  GG    GC CGC
                                ||||||||  ||    || |||
                                CGCGCCTC  CC    TG GCG
                                    CA  T___  A
GAM2887  LARGE    5'  GCGCGGCGGCGCCGCCGC     21864        _   AG  AG
                                GCGCGG GGC  GC  TGCCGC
                                ||||||  |||  ||  ||||||
                                CGCGCC CCG  CG  GCGGCG
                                   G   __  __
GAM2887  LETM1    5'  GCGGGGCGGCCAGGCCGC     29503         A   _  T
                                GCGGGGC GGC AG GCCGC
                                ||||||| ||| || |||||
                                CGCCCCG CCG TC CGGCG
                                    _   G  _
GAM2887  LMO2     5'  GCGCGGGGCTGGCCGGCTGC   24543          A   AGT  C
                                GCGCGGGGC GGC   GC GC
                                |||||||||  |||   || ||
                                CGCGCCCCG CCG   CG CG
                                     A   GC_  A
GAM2887  MAD1L1   3'  GCGGGGCAGGGGACCTGC     44671          CAGT   _
                                GCGGGGCAGG    GCC GC
                                ||||||||||    ||| ||
                                CGCCCCGTCC    TGG CG
                                     CC__   A
GAM2887  MAFK     5'  GCGCGCGGCGGCTCCTCGC    14320       G   A   AG__
                                GCGCG GGC GGC    TGC
                                ||||| ||| |||    |||
```

```
                                CGCGC CCG CCG   GCG
                                  G  _  AGGA
GAM2887  MAP3K9   5'  GCGCGGGGTCACGTAGTTGC  41356       _ GGC  _
                                GCGCGGGG CA  AGT GC
                                |||||||| ||  ||| ||
                                CGCGCCCC GT  TCA CG
                                    A  GCA  A
GAM2887  MAP4K2   5'  GCGGGGCGGGCGCCCG     21354      A  A  G
                                GCGGGGC GGC GT CCG
                                ||||||| ||| || |||
                                CGCCCCG CCG CG GGC
                                    C  _ _
GAM2887  MAP4K2   5'  GCGCGGGGCGGGGCGGGC   21352       A_  AGT
                                GCGCGGGGC  GGC  GC
                                |||||||||  |||  ||
                                CGCGCCCCG  CCG  CG
                                     CC  CC_
GAM2887  MOX2     5'  GCGCGAGGTGGCTGACTGC   42517      CA  AG__
                                GCGCGGGG  GGC   TGC
                                ||||||||  |||   |||
                                CGCGCTCC  CCG   ACG
                                    A_  ACTG
GAM2887  MYO5A    5'  GCGCGGGGCGGGGCGGGGC   40755       A_  AGT
                                GCGCGGGGC  GGC  GC
                                |||||||||  |||  ||
                                CGCGCCCCG  CCG  CG
                                     CC  CCC
GAM2887  MYO6     5'  GCGCGGCGGCGGGGCTACC   22663      _  A_  AG
                                GCGCGG GGC  GGC  TGCC
                                |||||| |||  |||  ||||
                                CGCGCC CCG  CCG  ATGG
                                   G  CC  __
GAM2887  NFATC2   5'  GCGCAGGGCGGGAAGGCTGC  29586       A  C  T  C
                                GCGCGGGGC GG AG GC GC
                                ||||||||| || || || ||
                                CGCGTCCCG CC TC CG CG
                                    C  T  _  A
GAM2887  NR2F6    5'  GCGCGGGGGGCACGGGCTGC  23451       CA   GT_  C
                                GCGCGGGG  GGCA  GC GC
                                ||||||||  ||||  || ||
                                CGCGCCCC  CCGT  CG CG
                                    __   GCC  A
GAM2887  NRXN1    5'  GCGCGGAGCGGGTGGCTGC   22049       A  CA _
                                GCGCGGGGC GG  G TGC
                                ||||||||| ||  | |||
                                CGCGCCTCG CC  C ACG
                                    C  AC G
GAM2887  p100     5'  GCGAGGGGCAGGCTGGC    41111    C      AGT
                                GCG GGGGCAGGC  GC
                                ||| |||||||||  ||
```

```
                                CGC CCCCGTCCG  CG
                                  T       AC_
GAM2887 PABPC4   5' GCGCGGGGCAGGCCGGAAGCG 19226          ____
                                GCGCGGGGCAGGC   AGTG
                                ||||||||||||   ||||
                                CGCGCCCCGTCCG   TCGC
                                      GCCT
GAM2887 PABPC4   5' GCCGGGGCAGGCCGGGGC   19225   G       AGT_
                                GC CGGGGCAGGC   GC
                                || ||||||||||   ||
                                CG GCCCCGTCCG   CG
                                 _       GCCC
GAM2887 PACE     3' GCCGGGGCAAGCTGC      15035   G       AG
                                GC CGGGGCAGGC  TGC
                                || ||||||||||  |||
                                CG GCCCCGTTCG  ACG
                                 _       __
GAM2887 PCM1     5' GCGCGGGGAGAACTCGC    26227       C  CAG
                                GCGCGGGG AGG   TGC
                                |||||||| |||   |||
                                CGCGCCCC TCT   GCG
                                    _  TGA
GAM2887 PCOLN3   3' GCACGGGGTGGGCAGGAC   15751       CA   TG
                                GCGCGGGG  GGCAG  C
                                ||||||||  |||||  |
                                CGTGCCCC  CCGTC  G
                                     AC    CT
GAM2887 PDGFRL   5' GCGCGGGGCGGGGACGC    26294       A  CAG
                                GCGCGGGGC GG   TGC
                                |||||||||  ||   |||
                                CGCGCCCCG CC   GCG
                                     C  CT_
GAM2887 PKD1     5' GCGCGGGGCTGGATGGGGCTGC 7139        A  CAGT_  C
                                GCGCGGGGC GG    GC GC
                                |||||||||  ||    || ||
                                CGCGCCCCG CC    CG CG
                                     A  TACCC  A
GAM2887 PPIF     3' GCACGGGGAAGTTAGTGTTGC  25060       C  GC   CC
                                GCGCGGGG AG  AGTG  GC
                                ||||||||  ||  ||||  ||
                                CGTGCCCC TC  TCAC  CG
                                     T  AA   AA
GAM2887 PTGS2    5' GCGCGGGGGTAGGCTTTGC   9689        C_   AG
                                GCGCGGGG  AGGC  TGC
                                ||||||||  ||||  |||
                                CGCGCCCC  TCCG  ACG
                                     CA   AA
GAM2887 RAB3A    3' GCTTGGGGCGGGCAGGGGAGC  16069    GC    A    TGCC
                                GC  GGGGC GGCAG   GC
                                ||  ||||| |||||   ||
```

```
                                CG  CCCCG CCGTC   CG
                                 AA    C    CCCT
GAM2887 RAB3B   5' GCCGGGGCGGGGCGCTGC   16082   G    A CA   C
                                GC CGGGGC GG  GTGC GC
                                || |||||| ||  |||| ||
                                CG GCCCCG CC  CGCG CG
                                 _     C __   A
GAM2887 RNH     5' GCGGGCCAGGCAGGCTGC    16360     G     T C
                                GCGGG CAGGCAG GC GC
                                ||||| ||||||| || ||
                                CGCCC GTCCGTC CG CG
                                   G      _ A
GAM2887 ROM1    5' GCTGGGGCAGGATGC      7262    GC      CA
                                GC  GGGGCAGG  GTGC
                                ||  ||||||||  ||||
                                CG  CCCCGTCC  TACG
                                 A_      __
GAM2887 ROR2    5' GCGCGGGGTCGGGCGC     21260       CA  CA
                                GCGCGGGG  GG  GTGC
                                ||||||||  ||  ||||
                                CGCGCCCC  CC  CGCG
                                    AG  __
GAM2887 RPS6KA2 5' GCGCGGGGCGTGGGGCGC   34465       A_  CA
                                GCGCGGGGC  GG  GTGC
                                |||||||||  ||  ||||
                                CGCGCCCCG  CC  CGCG
                                     CA  C_
GAM2887 RPS6KA2 5' GCGTGGGGCGCGAGCTGC   34466   C   AG  _  _
                                GCG GGGGC  GC AG TGC
                                ||| |||||  || || |||
                                CGC CCCCG  CG TC ACG
                                  A    __  C  G
GAM2887 SFRP1   5' GCGCGGGGCGGCGGGC     16574       A  AGT
                                GCGCGGGGC GGC  GC
                                |||||||||  |||  ||
                                CGCGCCCCG CCG  CG
                                     _  CC_
GAM2887 SHOX    3' GCGCGGGGGGCTGC       27821       CA  AG
                                GCGCGGGG  GGC  TGC
                                ||||||||  |||  |||
                                CGCGCCCC  CCG  ACG
                                    __  __
GAM2887 SLC21A2 5' GCGCGGGGTCGGGGCGC    24798       CA  CA
                                GCGCGGGG  GG  GTGC
                                ||||||||  ||  ||||
                                CGCGCCCC  CC  CGCG
                                    AG  C_
GAM2887 SLC22A5 5' GCGCGGGGCACCCGCCGC   16861       AG  AG
                                GCGCGGGGC  GC  TGCCGC
                                |||||||||  ||  ||||||
```

```
                                CGCGCCCCG TG GCGGCG
                                     __ G_
GAM2887 SLC30A4  5' CGAGGGCAGTGCCGC     30013     CAG
                                CGGGG  GCAGTGCCGC
                                |||||  ||||||||||
                                GCTCC  CGTCACGGCG
                                  ___
GAM2887 SLC9A3R2 3' GCTCGGGGCAGGCTGAGGC  41528   G      __ T
                                GC CGGGGCAGGC AG GC
                                || ||||||||||  || ||
                                CG GCCCCGTCCG TC CG
                                 A        AC _
GAM2887 SMT3H1   5' GCGCGGGGAGGCGGCGC    40997       C   A
                                GCGCGGGG AGGC GTGC
                                |||||||| |||| ||||
                                CGCGCCCC TCCG CGCG
                                     _   C
GAM2887 SOX12    3' GCGTGGGGCAGAGACCTGC  28042    C     CAGT  _
                                GCG GGGGCAGG   GCC GC
                                ||| ||||||||   ||| ||
                                CGC CCCCGTCT   TGG CG
                                  A      C___  A
GAM2887 SREBF2   5' ACGCGGGGGCGGTGCCG    21401       CAG  A
                                GCGCGGGG  GC GTGCCG
                                ||||||||  || ||||||
                                TGCGCCCC  CG CACGGC
                                     ___  C
GAM2887 ST14     5' GCGCGGGGCGCGGGGCGC   35065       A_  CA
                                GCGCGGGGC  GG  GTGC
                                |||||||||  ||  ||||
                                CGCGCCCCG  CC  CGCG
                                     CG  C_
GAM2887 SURF4    3' GCTGGGAAAGGGCGGTGCTGC 37657   GC   CA_  A   C
                                GC  GGGG  GGC GTGC GC
                                ||  ||||  ||| |||| ||
                                CG  CCCT  CCG CACG CG
                                 A_   TTC  C   A
GAM2887 TBL1X    5' GCGCGGAGTGGGGGCGC    24885       CA  CA
                                GCGCGGGG  GG  GTGC
                                ||||||||  ||  ||||
                                CGCGCCTC  CC  CGCG
                                    A_  CC
GAM2887 TNFRSF11A 5' GCGCGGGACAGGCTGGC    19272          AGT
                                GCGCGGGGCAGGC  GC
                                ||||||||||||  ||
                                CGCGCCCTGTCCG  CG
                                       AC_
GAM2887 TNFRSF11A 3' GCTGGGGCAGAGGCG     19273   GC     GC  T  C
                                GC  GGGGCAG  AG GC G
                                ||  |||||||  || || |
```

```
                                CG  CCCCGTC  TC CG C
                                 A_      __ _  A
GAM2887  TRC8     5'  GCGCGGGGCAGGGCCCGGGGCC 28513           _ AGT__
                GC                   GCGCGGGGCAGG C     GCCGC
                                    |||||||||||| |     |||||
                                    CGCGCCCCGTCC G     CGGCG
                                           C GGCCC
GAM2887  TRPV4    3'  GCTGGGGCAGGGGTCACGTCGC 41348    GC       CAG  __
                                    GC  GGGGCAGG   TGC  CGC
                                    ||  ||||||||   |||  |||
                                    CG  CCCCGTCC   GTG  GCG
                                     A_      CCA   CA
GAM2887  VHL      5'  ACGCGGGGCGGAGCTGC     8104          A  C  _
                                    GCGCGGGGC GG AG TGC
                                    |||||||||| || || |||
                                    TGCGCCCCG CC TC ACG
                                          _ _  G
GAM2887  WNT4     5'  GCCCGGGGCAGCGGCTGC    36254    G      __  AG
                                    GC CGGGGCA  GGC  TGC
                                    || |||||||  |||  |||
                                    CG GCCCCGT  CCG  ACG
                                     G      CG  __
GAM2887  WNT5A    5'  GCGCGGGGCACGCCAGC     18119          G  AGT
                                    GCGCGGGGCA GC   GC
                                    |||||||||| ||   ||
                                    CGCGCCCCGT CG   CG
                                          G  GT_
GAM2887  WNT7A    5'  GCGGGGGCGCTGCTGC      21527     C    AG  AG   C
                                    GCG GGGGC  GC  TGC GC
                                    ||| |||||  ||  ||| ||
                                    CGC CCCCG  CG  ACG CG
                                      _    __  __   A
GAM2887  XRCC2    3'  CACTGATGGGCAGTGCTGC   24089     GG  CA       C
                                    CGC  GG  GGCAGTGC GC
                                    |||  ||  |||||||| ||
                                    GTG  CT  CCGTCACG CG
                                      A_  AC       A
GAM2887  YWHAG    5'  GCGCGAGGCGGCTGC       29795          A   AG
                                    GCGCGGGGC GGC  TGC
                                    |||||||| |||  |||
                                    CGCGCTCCG CCG  ACG
                                          _  __
GAM2887  ZNF26    5'  GCGGGGGCAGGACCCG      43801     C       CAGTG
                                    GCG GGGGCAGG    CCG
                                    ||| ||||||||    |||
                                    CGC CCCCGTCC    GGC
                                      _       TG___
GAM2887  DNCI1    5'  TGGCGGGGCCGGCGCGGGCAGG 44995      AC        C C   A
                A                    TGGC  GGCCGGCGC G GCA GA
                                    ||||  ||||||||| | ||| ||
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                                ACCG  CCGGCCGCG C CGT CT
                                  CC       _ C   C
GAM2887  EGFL3    5'  TGGTAGGCCGGCGGGCG     41710     CAC      CC
                                TGG   GGCCGGCG  GCG
                                |||   ||||||||  |||
                                ACC   CCGGCCGC  CGC
                                  AT_      C_
GAM2887  ENG      5'  TGGTATGACCGGCAGCA     6511      CAC      CCGC
                                TGG   GGCCGGCG   GCA
                                |||   ||||||||   |||
                                ACC   CTGGCCGT   CGT
                                  ATA      ____
GAM2887  GAL      5'  TGGCGCGGCCGGCAGCA     45056     A       CCGC
                                TGGC CGGCCGGCG    GCA
                                ||||  |||||||||   |||
                                ACCG GCCGGCCGT    CGT
                                  C        ____
GAM2887  GNAO1    3'  TGGGCGGCCGGCAGGCAGCA  44945     CA       CC  _
                                TGG  CGGCCGGCG  GC GCA
                                |||  |||||||||  || |||
                                ACC  GCCGGCCGT  CG CGT
                                  C_       C_  T
GAM2887  LARGE    5'  TGGCGCGGCGGCGCCGC     39514     A   C
                                TGGC CGGC GGCGCCGC
                                ||||  ||||  ||||||||
                                ACCG GCCG CCGCGGCG
                                  C   _
GAM2887  PABPC1   5'  GGCACGGCTGCCCGCA      15024        CG  G
                                GGCACGGC  GC CCGCG
                                ||||||||  ||  |||||
                                CCGTGCCG  CG GGCGT
                                     A_  _
GAM2887  POLL     5'  GGCACGGCCGCAGCA       29982          G  CCGC
                                GGCACGGCCG CG    GCA
                                ||||||||||  ||    |||
                                CCGTGCCGGC GT    CGT
                                          _  ____
GAM2887  PYCR1    5'  TGGTGACGCCGGCCGCGCAGGA 43130     C_  G    GC     A
                                TGG  ACG CCGGC  CGCGCA GA
                                |||  |||  |||||  ||||||  ||
                                ACC  TGC GGCCG  GCGCGT CT
                                  AC   _    __      C
GAM2887  VIPR2    3'  GGCGTGGCCCAGGGTGTGCAGG 18021     AC   __  CGCCGC   A
              A                  GGC  GGCC  GG     GCA GA
                                |||  ||||  ||     ||| ||
                                CCG  CCGG  CC     CGT CT
                                  CA    GT  CACA__   C
GAM2887  VIPR2    3'  GGTGTGGCCGGCGTGGCCCA  18024    CAC      CC  G
                                GG   GGCCGGCG  GC CA
                                ||   ||||||||  || ||
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                                CC   CCGGCCGC  CG GT
                                 ACA       AC  G
GAM2887 ZNF216   5' TGGCGCCGCCGCCGCCGCG   25660      A_  G   G
                                TGGC  CG CCG CGCCGCG
                                ||||  || ||| |||||||
                                ACCG  GC GGC GCGGCGC
                                  CG  _   G
GAM2888 ALG6     3' GCACTGTTCACATTTTCACA   30034     ATATTACTA
                                GCA        ATATTTTCACA
                                |||        ||||||||||
                                CGT        TGTAAAAGTGT
                                 GACAAG___
GAM2888 PCDHB9   3' GCAAATTAAATATTTTCACA   33321      T    CT
                                GCAA ATTA  AATATTTTCACA
                                |||| ||||  ||||||||||||
                                CGTT TAAT  TTATAAAAGTGT
                                  _   __
GAM2888 RB1CC1   3' ACATAACAATATTTTCACAC   31304      T  T
                                ATAT AC AATATTTTCACAC
                                |||| ||  ||||||||||||
                                TGTA TG TTATAAAAGTGTG
                                  T  _
GAM2888 RET      3' ATTACACTTATTTTCACA    34153       TAA
                                ATTAC   TATTTTCACA
                                |||||   ||||||||||
                                TAATG   ATAAAAGTGT
                                   TGA
GAM2888 ZNF10    3' GCAATATTATTAATAATCAC   31736         C     TTT
                                GCAATATTA TAATA   TCAC
                                ||||||||| |||||   ||||
                                CGTTATAAT ATTAT   AGTG
                                     A    T__
GAM2888 EGLN1    5' TCCCAATCCTTAATATTG    35178       CC  _
                                TCCCA  CCT AATATTG
                                |||||  ||| |||||||
                                AGGGT  GGA TTATAAC
                                   TA   A
GAM2888 LRP4     3' TCCCAGCCCCTGATGGGCA   42067       _    A  ATT
                                TCCCA CCCCT AT   GCA
                                ||||| ||||| ||   |||
                                AGGGT GGGGA TA   CGT
                                   C    C  CC_
GAM2888 PYGM     3' TACCCCACCCTCTGCA      24698          CTAATA
                                TATCCCACCC     TTGCA
                                ||||||||||     |||||
                                ATGGGGTGGG     GACGT
                                     A_____
GAM2888 RPA2     3' ATCCCACCCTGGATTGCAT    16376         CTAAT
                                ATCCCACCC    ATTGCAT
                                |||||||||    |||||||
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                                TAGGGTGGG    TAACGTA
                                     ACC__
GAM2888  SP3      5'  TCCTACCCCCAATGGGC     44384     C        ATT
                                TCC ACCCCTAAT   GC
                                ||| |||||||||   ||
                                AGG TGGGGGTTA   CG
                                  A        CC_
GAM2888  SURF6    3'  CATCCCACTTTGTATCTTGCAT 27589         CCCTAATA
                                TATCCCAC       TTGCAT
                                ||||||||       ||||||
                                GTAGGGTG       AACGTA
                                     AAACATAG
GAM2889  CDH11    3'  GAATACTGATATTTATAC    38030    C         CAT
                                A ATACTGATATT   TATAC
                                | ||||||||||   |||||
                                C TATGACTATAA   ATATG
                                 T        ___
GAM2889  EFNA1    3'  ATACAGATACTATACAC     20696      T    TCAT
                                ATAC GATAT    TATACAC
                                |||| |||||    |||||||
                                TATG CTATG    ATATGTG
                                  T    ____
GAM2890  B4GALT6  3'  TATAGATTTTAGTATAAAA   40853       A
                                TATAGA TTTAGTATAGAA
                                |||||| ||||||||||||
                                ATATCT AAATCATATTTT
                                    A
GAM2890  CREB1    3'  TAAGAATTTAGTACTAACT   39597    T         AG
                                A AGAATTTAGTAT  AACT
                                | ||||||||||||  ||||
                                A TCTTAAATCATG  TTGA
                                 T         A_
GAM2890  ETFA     3'  TATAGATTTTAGTACAGAA   6545       A
                                TATAGA TTTAGTATAGAA
                                |||||| ||||||||||||
                                ATATCT AAATCATGTCTT
                                    A
GAM2890  FACL2    3'  TATAGAATCTAAGGCAGA    34438          TA
                                TATAGAATTTAG  TAGA
                                ||||||||||||  ||||
                                ATATCTTAGATT  GTCT
                                      CC
GAM2890  LHCGR    3'  ATAGAACAGATAGAACT     6931        TT  T
                                ATAGAAT  AG ATAGAACT
                                |||||||  || ||||||||
                                TATCTTG  TC TATCTTGA
                                   __  _
GAM2890  NPC1     3'  TAAAAATATGGTATAGAACT  7077    T    TTA
                                A AGAAT   GTATAGAACT
                                | |||||   ||||||||||
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                                A TTTTA   CATATCTTGA
                                 T    TAC
GAM2891  DYT1    3'  TACTTTTCTTTCAAAAGACT   6477       G       TAT
                                TACTTT TCTTTCAAA   GACT
                                |||||| |||||||||   ||||
                                ATGAAA AGAAAGTTT   CTGA
                                   _       T__
GAM2891  HPGD    3'  TACTTTGTCTTTAATACAT    9244           CAA
                                TACTTTGTCTTT   ATAT
                                ||||||||||||   ||||
                                ATGAAACAGAAA   TGTA
                                       TTA
GAM2891  KCNS2   3'  TTTGTTTTCACATGACT     42840      C    AA
                                TTTGT TTTCA  TATGACT
                                ||||| |||||  |||||||
                                AAACA AAAGT  GTACTGA
                                  _    __
GAM2891  MLLT2   3'  CTTATGCTCAGATATGACTA   25499     _  CTT   A
                                CTT TGT   TCA ATATGACTA
                                ||| |||   ||| |||||||||
                                GAA ACG   AGT TATACTGAT
                                  T  ____  C
GAM2891  MTM1    3'  TTTGTCTTTCAAAAACT     7009           TAT
                                TTTGTCTTTCAAA   GACT
                                ||||||||||||   ||||
                                AAACAGAAAGTTT   TTGA
                                       ___
GAM2891  SEL1L   3'  TACTTTTTCTTTGCCATTGACT 22848       G    CAA  A
                                TACTTT TCTTT   AT TGACT
                                |||||| |||||   || |||||
                                ATGAAA AGAAA   TA ACTGA
                                   A    CGG  _
GAM2891  TRHR    3'  CTCTGTCTTCACATATGACTA  17680         T  A
                                CTTTGTCTT CA ATATGACTA
                                ||||||||| || |||||||||
                                GAGACAGAA GT TATACTGAT
                                     _ G
GAM2892  DDX1    3'  TAGCATTAATAGCTTACGTTAC 22371          A___   AAA
            TAT                   TAGCATTAATA   ATGT   ACTAT
                                ||||||||||   ||||  |||||
                                ATCGTAATTAT   TGCA   TGATA
                                      CGAA   A__
GAM2892  PSEN2   3'  GCACTAGAGTGTAAAACTAT  29811       ATAAA
                                GCATTA    TGTAAAACTAT
                                ||||||    ||||||||||
                                CGTGAT    ACATTTTGATA
                                   CTC__
GAM2892  BRS3    5'  GTTGATTGTCACGT       11902          AATAA
                                GTTGATTGT    TACGT
                                |||||||||    |||||
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                              CAACTAACA    GTGCA
                                    _____
GAM2893 ANKRA2   5' AGGGTCATTTCAGTTGACG   35753   A_       T_
                              AG  TCATTTCAGTT  CG
                              ||  ||||||||||  ||
                              TC  AGTAAAGTCAA  GC
                                CC        CT
GAM2893 FCN2     3' TAAGATCATTGTCCTGGTCTTT 31894        TCA   C_
                              TAAGATCATT   GTTT  GTCTTT
                              ||||||||||   ||||  ||||||
                              ATTCTAGTAA   CAGG  CAGAAA
                                    ___   AC
GAM2894 ATP5A1   3' TTCATGTGATTTCTGTACA   42409       C_
                              TTCATGTGA  TTTGTATA
                              |||||||||  ||||||||
                              AAGTACACT  AGACATGT
                                   AA
GAM2894 PCDHB16  5' TTCATGTGACTTTCGTGTAT  34150         ___
                              TTCATGTGACTT   TGTAT
                              ||||||||||||   |||||
                              AAGTACACTGAA   ACATA
                                    AGC
GAM2895 HLA-A    3' AAGAGGGTCATGGTGGACATGG 44859     __      ATTTAAT
                              AAGA  GTCATGGT      TGG
                              ||||  ||||||||      |||
                              TTCT  CAGTACCA      ACC
                                CC       CCTGT__
GAM2896 SOX4     3' TCTGCCATCGGCCAAA     16994     A    ATGCT T
                              TCT CCATC     G GTCAAA
                              ||| |||||     | ||||||
                              AGA GGTAG     C CGGTTT
                                C    _____ _
GAM2896 TAF4     3' TCTATGTCATGTGCCAAA    17265     CCA   TGC
                              TCTA   TCA   TGTGTCAAA
                              ||||   |||   |||||||||
                              AGAT   AGT   ACACGGTTT
                                AC_  ___
GAM2896 TOP2A    3' TCTATTGACTGTGTCAA     9883      CCATCAT
                              TCTA      GCTGTGTCAA
                              ||||      ||||||||||
                              AGAT      TGACACAGTT
                                AAC____
GAM2896 ADAM19   3' TCCAGAGTCAGGAGTCGCA   37777    A      T  T
                              TC CAGAGTCA GG GTCGCA
                              || |||||||| || ||||||
                              AG GTCTCAGT CC CAGCGT
                               _       _  T
GAM2896 ADAR     3' TCACAGAGTTTGAAGACA    9974         CA   TGTC
                              TCACAGAGT  TGG    GCA
                              |||||||||  |||    |||
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                                AGTGTCTCA ACT   TGT
                                     A_  TC__
GAM2896 ARHGEF7  3' TCACAGAGTGGATTGATGT  19368       CA__
                                TCACAGAGT   TGGTGT
                                |||||||||   ||||||
                                AGTGTCTCA   ACTACA
                                     CCTA
GAM2896 ASK     5' TCCGGAGAAAGTGTCGCA   27478   ACA  TCAT
                                TC  GAG   GGTGTCGCA
                                ||  |||   |||||||||
                                AG  CTC   TCACAGCGT
                                 GC_  TT__
GAM2896 ATM     5' TCATGAAGTCATATCTGGGCA 39636    CA     G_ TC
                                TCA GAGTCATG TG GCA
                                |||  ||||||||  ||  |||
                                AGT  TTCAGTAT  AC  CGT
                                  AC      AG  C_
GAM2896 ATP11A   3' TCACAGAGCAGCTGGTGT   44183       CA_
                                TCACAGAGT   TGGTGT
                                |||||||||   ||||||
                                AGTGTCTCG   ACCACA
                                     TCG
GAM2896 CALM3    3' TCACAGGGCTGGTTGC     23245      A  CA   GTC
                                TCACAG GT  TGGT   GC
                                ||||||  ||  ||||   ||
                                AGTGTC CG  ACCA   CG
                                   C  __   A__
GAM2896 CARKL    3' TCACAGCAGTCGTTTGGCG   30002      _   A__
                                TCACAG AGTC   TGGTG
                                ||||||  ||||   |||||
                                AGTGTC TCAG   ACCGC
                                   G   CAA
GAM2896 CDC42    3' ACAGAGTCATCCACA      12155        GGTG
                                ACAGAGTCAT   TCGCA
                                ||||||||||   |||||
                                TGTCTCAGTA   GGTGT
                                     _____
GAM2896 CYP1B1   3' TCACACAGTTGTGTCA     6453      G  CATG
                                TCACA AGT   GTGTCG
                                |||||  |||   ||||||
                                AGTGT TCA   CACAGT
                                   G  A___
GAM2896 DNAJB9   3' TCACAGATGTCATAGAACATGC 29561       _     TGTC_
            A                    TCACAGA GTCATGG    GCA
                                |||||||  |||||||    |||
                                AGTGTCT  CAGTATC    CGT
                                   A     TTGTA
GAM2896 E2F3     3' TCACGCAGTCATAATTTGCA  12632     AG      GTC
                                TCAC  AGTCATGGT   GCA
                                ||||  |||||||||   |||
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                                AGTG  TCAGTATTA   CGT
                                  CG        AA_
GAM2896  GCH1     3'  TCACAGAGCAATACCGCA    6706          CAT   GT
                                TCACAGAGT   GGT  CGCA
                                |||||||||   |||  ||||
                                AGTGTCTCG   TTA  GCGT
                                     ____   TG
GAM2896  KRTHB6   3'  TCGCAGAGTCATAGAACCA   14037    A         TG
                                TC CAGAGTCATGG  TCG
                                || ||||||||||  |||
                                AG GTCTCAGTATC  GGT
                                 C          TT
GAM2896  MDM4     5'  TCACAGATCCTAGCTCG     14396       G  A   G
                                TCACAGA TC TGGT TCG
                                ||||||| || |||| |||
                                AGTGTCT AG ATCG AGC
                                    _ G   _
GAM2896  MGAT5    5'  ACAAAGTCATTATTATGT     14467         G___
                                ACAGAGTCAT    GTGT
                                ||||||||||    ||||
                                TGTTTCAGTA    TACA
                                      ATAA
GAM2896  MTCP1    5'  TCACAGAGTACGTCCGCCTGC  30586         C   G_   _
                                TCACAGAGT ATG  TGTC GC
                                ||||||||| |||  |||| ||
                                AGTGTCTCA TGC  GCGG CG
                                      _  AG    A
GAM2896  MX1      5'  TCACAGAGCTGTTCTCCTGCA  14689         CA  GTG_  _
                                TCACAGAGT  TG    TC GCA
                                |||||||||  ||    || |||
                                AGTGTCTCG  AC    GG CGT
                                     __  AAGA  A
GAM2896  NR1I2    3'  TCACAGAGCATACCCAGCA    19331         T    GTGTC
                                TCACAGAG CATG     GCA
                                |||||||| ||||    |||
                                AGTGTCTC GTAT     CGT
                                     _   GGGT_
GAM2896  NRAP     3'  TCACAAAGTCATGTCTGT     40198           G_
                                TCACAGAGTCATG  TGT
                                ||||||||||||  |||
                                AGTGTTTCAGTAC  ACA
                                       AG
GAM2896  NRIP1    3'  TCATAAGTCATGGTTCTCA    40987     CA        G  G
                                TCA  GAGTCATGGT TC CA
                                |||  |||||||||| || ||
                                AGT  TTCAGTACCA AG GT
                                  A_         _  A
GAM2896  OCRL     3'  TCACAGAGTCAATGCC       7089           TG
                                TCACAGAGTCA  GTGTC
                                ||||||||||  |||||
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                                AGTGTCTCAGT  TACGG
                                      __
GAM2896  PRKAR1A  3'  ACAGAGTCAGTTAGTTGCA   15605        TGGT  C
                                ACAGAGTCA   GT GCA
                                |||||||||   || |||
                                TGTCTCAGT   CA CGT
                                     CAAT  A
GAM2896  SMP1     5'  TCCGGAGCCCGGTGTCGC   30719   ACA    A
                                TC   GAGTC TGGTGTCGC
                                ||   ||||| |||||||||
                                AG   CTCGG GCCACAGCG
                                 GC_    _
GAM2896  TNFRSF12 3'  TCACAGATTTAATACCGC   19127       GTCA   GT
                                TCACAGA   TGGT  CGC
                                |||||||   ||||  |||
                                AGTGTCT   ATTA  GCG
                                    AA__   TG
GAM2896  TYRO3    3'  CCACAGAGTGGTTGC      26649        CAT   GTC
                                TCACAGAGT   GGT   GC
                                |||||||||  |||   ||
                                GGTGTCTCA   CCA   CG
                                     ___  A__
GAM2896  WTAP     3'  TCACAGAGCAATATGC     22229        CAT    C
                                TCACAGAGT   GGTGT GC
                                |||||||||   ||||| ||
                                AGTGTCTCG   TTATA CG
                                     ___    _
GAM2897  RFX5     3'  TTGAATTAGGTTTTCTGTGAT  7799      C   TTTG   C
                                TTGAA TAG    TTCT GTGAT
                                |||||  |||    |||| |||||
                                AACTT ATC    AAGA CACTA
                                   A   CAA_   _
GAM2897  BN51T    3'  ATTGAGTGCCTGCTGGTTC   44673    A  GTTT
                                GTT AG    CTTGCTGGTTC
                                |||  ||    ||||||||||
                                TAA TC    GGACGACCAAG
                                  C  AC__
GAM2897  OTOA     5'  GTTAAGTGGTTGCTGGTT    40343      GTTTC
                                GTTAAG    TTGCTGGTT
                                ||||||    |||||||||
                                CAATTC    AACGACCAA
                                    ACC__
GAM2897  PSG1     3'  GTTAAAGTTTTCGAAGTTC   27913        C   CT
                                GTTAAGGTTT TTG  GGTTC
                                |||||||||| |||  |||||
                                CAATTTCAAA AGC  TCAAG
                                      _   T_
GAM2898  SCA1     3'  TTTAATACAGTTGAACCA    7303        T    TACATT
                                TTTAATAC AGTTG     CCA
                                |||||||| |||||     |||
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                                AAATTATG TCAAC     GGT
                                   _    TT____
GAM2898 ZNF146   3' CTTAATATTAGTTGTAGATGAC 28353       C      CATT_
            CAT                   TTTAATA TAGTTGTA    CCAT
                                  ||||||| ||||||||    ||||
                                  GAATTAT ATCAACAT    GGTA
                                     A       CTACT
GAM2899 RAB5A    3' GTATATGTGGGATTAT     20011       AATTTCC
                                  GTATAT     GGGATTAT
                                  ||||||     ||||||||
                                  CATATA     CCCTAATA
                                     CA_____
GAM2900 EDAR     3' TACGTTCCTTCTGTCTTCTA  35309      G ____
                                  TGCGT CC   GTCTTCTA
                                  ||||| ||   ||||||||
                                  ATGCA GG   CAGAAGAT
                                     A  AAGA
GAM2900 MXI1     3' TGCGTGCACAACTCTTCT    39024       _ __
                                  TGCGTGC CG  TCTTCT
                                  ||||||| ||  ||||||
                                  ACGCACG GT  AGAAGA
                                      T  TG
GAM2900 ALDH1B1  3' GCCACCAAGGGGGCTGTGGT  8670    G    AGA_
                                  GC ACTAA   GCTGTGGT
                                  || |||||   ||||||||
                                  CG TGGTT   CGACACCA
                                   G    CCCC
GAM2900 BLAME    5' GCACGGGAGGAGCTGTGGT   33488    _ C  CTAAA
                                  GC CG GA    GAGCTGTGGT
                                  || || ||    ||||||||||
                                  CG GC CT    CTCGACACCA
                                   T  C  C____
GAM2900 CENPF    3' GCCCTGACTAAAGAGAAGT   32281     GC        CT
                                  GCC  GACTAAAGAG  GT
                                  |||  ||||||||||  ||
                                  CGG  CTGATTTCTC  CA
                                    GA        TT
GAM2900 CRAT     5' CGCCGCGGCTGGGGT       19662       ACTAAAGA   T
                                  CGCCGCG       GCTG GGT
                                  |||||||       |||| |||
                                  GCGGCGC       CGAC CCA
                                      _________   C
GAM2900 DPYSL3   3' GCAGACCCTAGGGAGCTGTGGT 10769    _   AAA__
                                  GC GACT    GAGCTGTGGT
                                  || ||||    ||||||||||
                                  CG CTGG    CTCGACACCA
                                   T   GATCC
GAM2900 DSCAM    5' ACGCTGCGGCCGGAGCCCAGGT 10790     C   A  AAA    GT
                                  ACGC GCG CT   GAGCT  GGT
                                  |||| ||| ||   |||||  |||
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                                TGCG CGC GG   CTCGG  CCA
                                  A  C  C__    GT
GAM2900  EGR1     5'  CGCCGCGGCTGCGG       12658        ACTAAAGA
                                CGCCGCG      GCTGTGG
                                |||||||      |||||||
                                GCGGCGC      CGACGCC
                                  _________
GAM2900  FOLR1    5'  CCTGAAGAAAGAGCTGTGGT   32504    GC  CT
                                CC  GA  AAAGAGCTGTGGT
                                ||  ||  ||||||||||||
                                GG  CT  TTTCTCGACACCA
                                 A_  TC
GAM2900  GTF2I    5'  GCCGCGGCTGGAGAGCGCG   37439      A  AA    T
                                GCCGCG CT  AGAGC GTG
                                ||||||  ||  ||||| |||
                                CGGCGC GA  TCTCG CGC
                                   C  CC    _
GAM2900  HDAC7A   5'  GCTGCGGCTGAGGGCCTGGT   32471    C   A  AA  A   G
                                GC GCG CT  AG GCT TGGT
                                ||  |||  ||  ||  |||  ||||
                                CG CGC GA  TC CGG ACCA
                                 A   C  C_  C   _
GAM2900  LARGE    5'  GCCGCGGCGAGGGTCCGGGT   21863      ACTAAA  ___   T
                                GCCGCG     GAG   CTG GGT
                                ||||||     |||   ||| |||
                                CGGCGC     CTC   GGC CCA
                                   CG_____  CCA   _
GAM2900  MECP2    3'  GCTCTGGAAAAGGAGCTGTGGT 22594    GACT__   _
                                GC     AAAG AGCTGTGGT
                                ||     |||| |||||||||
                                CG     TTTC TCGACACCA
                                 AGACCT    C
GAM2900  NPY2R    3'  GCTGCGGCTGAGGGACTGCGGT 9498     C   A  AAAGA
                                GC GCG CT    GCTGTGGT
                                || ||| ||    ||||||||
                                CG CGC GA    TGACGCCA
                                 A   C  CTCCC
GAM2900  NPY2R    5'  GCTGCGGCTGAGGGACTGCGGT 9498     C   A  AAAGA
                                GC GCG CT    GCTGTGGT
                                || ||| ||    ||||||||
                                CG CGC GA    TGACGCCA
                                 A   C  CTCCC
GAM2901  B3GALT3  5'  AGAGTTATCAAAGATTGGG   37667     CA_      CA
                                AGA   ATCAAAGAT  GG
                                |||   |||||||||  ||
                                TCT   TAGTTTCTA  CC
                                  CAA       AC
GAM2901  CDKN1B   5'  GACCAGGCAAGCGGAGAGGGT  19796       A   TCAA   TCA
                                GACCAG CAA    AGA   GGT
                                ||||||  |||   |||   |||
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                                CTGGTC GTT   TCT  CCA
                                   C  CGCC  C__
GAM2901 CREBBP   3' AGACCAGATATTTAAATCAACT 20427       CAATCAA    ___
           GGT                   AGACCAGA     AGATCA  GGT
                                ||||||||     ||||||  |||
                                TCTGGTCT     TTTAGT  CCA
                                   ATAAA__    TGA
GAM2901 EIF2C1   3' CAGAGAACAAATCAGGT    29174     C  CAA
                                CAGA AAT   AGATCAGGT
                                |||| |||   |||||||||
                                GTCT TTG   TTTAGTCCA
                                  C  ___
GAM2901 GAS7     3' GACCAGGTGATTAAAATCTTGT 25269      ACAATCA    AG
                                GACCAG     AAGATC  GT
                                ||||||     ||||||  ||
                                CTGGTC     TTTTAG  CA
                                   CACTAA_    AA
GAM2901 GAS7     3' GATCAGATAATCAATCAGG   25271    C   C    AAG
                                GA CAGA AATCA   ATCAGG
                                || |||| |||||   ||||||
                                CT GTCT TTAGT   TAGTCC
                                 A   A   ___
GAM2901 KIAA0857 3' AGGCCAGACAATGAGA     42466    A      CAA
                                AG CCAGACAAT   AGA
                                || |||||||||   |||
                                TC GGTCTGTTA   TCT
                                 C       C__
GAM2901 MB       3' CAGACAATTGCTACTGTCAGGT 23856       CAAAGA__
                                CAGACAAT       TCAGGT
                                ||||||||       ||||||
                                GTCTGTTA       AGTCCA
                                   ACGATGAC
GAM2901 MECP2    3' GACCAGATGACGCCCAGG    22587       CA  CAAAGA
                                GACCAGA  AT     TCAGG
                                |||||||  ||     |||||
                                CTGGTCT  TG     GGTCC
                                   AC  CG____
GAM2901 MOX2     3' AGACCAGGGAATCACTTTCAGG 42512       AC    AAGA
                                AGACCAG  AATCA   TCAGG
                                |||||||  |||||   |||||
                                TCTGGTC  TTAGT   AGTCC
                                   CC    GAA_
GAM2901 NEK6     3' AGCTCAGACAATTGGAAGG   30821    AC      CAAA  TC
                                AG  CAGACAAT   GA  AGG
                                ||  ||||||||   ||  |||
                                TC  GTCTGTTA   CT  TCC
                                 GA       AC__  __
GAM2901 NOL3     3' AGCCAGACAATTAAAACAG   19488    A       CA   T
                                AG CCAGACAAT  AAGA CAG
                                || |||||||||  |||| |||
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                                TC GGTCTGTTA  TTTT GTC
                                 _       A_   _
GAM2901  OLIG2    3'  AGCCAGACAGCGCTCGATCAGG 25141    A     ATCAAA
                T                AG CCAGACA     GATCAGGT
                                 || |||||||     ||||||||
                                 TC GGTCTGT     CTAGTCCA
                                  _      CGCGAG
GAM2901  POLR2G   5'  AGACCAGGTAGGCAGGC     15456       ACAATCAA  AT
                                 AGACCAG       AG  CAGGT
                                 |||||||       ||  |||||
                                 TCTGGTC       TC  GTCCG
                                     CA_______  C_
GAM2901  SHMT2    3'  AGACCAGGTAGGCAGGC     24002       ACAATCAA  AT
                                 AGACCAG       AG  CAGGT
                                 |||||||       ||  |||||
                                 TCTGGTC       TC  GTCCG
                                     CA_______  C_
GAM2901  TLR9     3'  AGACCAGGCAGGCAGAGG    32658       A  ATCAA   TCA
                                 AGACCAG CA    AGA   GG
                                 ||||||| ||    |||   ||
                                 TCTGGTC GT    TCT   CC
                                     C  CCG__  ____
GAM2901  TNFRSF4  3'  AGATCAGGAAATCAAGGACC   17761     C   AC     A
                                 AGA CAG  AATCAA GATC
                                 ||| |||  |||||| ||||
                                 TCT GTC  TTAGTT CTGG
                                   A   CT     C
GAM2901  ANXA8    3'  TCTCCGGCTGCATGATAGAGAA 43813    A       C    CAA_
                GT                 TC CCGGCTGCA TGAT    AAGT
                                 || |||||||| ||||    ||||
                                 AG GGCCGACGT ACTA    TTCA
                                  A        _    TCTC
GAM2901  GARS     3'  AGCGCAAGTGGTCAAAAGT    13055     T   C_  A
                                 GGC GCA  TG TCAAAAGT
                                 ||| |||  || ||||||||
                                 TCG CGT  AC AGTTTTCA
                                   _   TC  C
GAM2901  GFI1     3'  CGGCTGCACTTTGAAAAG     23552          GATC
                                 CGGCTGCACT    AAAAG
                                 ||||||||||    |||||
                                 GCCGACGTGA    TTTTC
                                       AAC_
GAM2901  HIP12    3'  CCTGGCTGCACCCCAAA      42399    _       GA
                                 CC GGCTGCACT  TCAAA
                                 || |||||||||  |||||
                                 GG CCGACGTGG  GGTTT
                                  A        __
GAM2901  PCDH9    5'  TCAGTGGCTTTGACATCAAAAG 44409     CC    GCACTG
                T                 TCA  GGCT     ATCAAAAGT
                                  |||  ||||     |||||||||
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                                AGT  CCGA     TAGTTTTCA
                                  CA   AACTG_
GAM2901  RET     3'  TCACCGGCTATCAGAA     34155         GCACTG   A
                                TCACCGGCT     ATCA AA
                                |||||||||     |||| ||
                                AGTGGCCGA     TAGT TT
                                      _______   C
GAM2902  CCND1    3'  TCCAATCAGATGACTCTGG   38223        AT   GTA  G
                                TCCAATCA  TGA   CT TGG
                                ||||||||  |||   || |||
                                AGGTTAGT  ACT   GA ACC
                                     CT   ___  G
GAM2902  CX3CR1   3'  ATCAATTGAGTAATGG     43291          CT
                                ATCAATTGAGTA  GTGG
                                ||||||||||||  ||||
                                TAGTTAACTCAT  TACC
                                      __
GAM2902  PTER     3'  CCAATTAATTAAATTGTGG   36214      C       AC
                                CCAAT AATTGAGT  TGTGG
                                |||||  ||||||||  |||||
                                GGTTA TTAATTTA  ACACC
                                   A       __
GAM2903  BCRP2    3'  AGTTTAGGCAAAGGTACTC   41647    C     TTTT   C
                                AG TTAGGT    AGG ACTC
                                || ||||||    ||| ||||
                                TC AATCCG    TCC TGAG
                                 A     TT__   A
GAM2903  CD164    3'  TAGCTTAAGTTTCTCCGCTCT  25682           AG  A
                                TAGCTTAGGTTTTT  GC CT
                                ||||||||||||||  || ||
                                ATCGAATTCAAAGA  CG GA
                                       GG  A
GAM2903  COL9A1   5'  TAGCATAGGTGGCACT      38536     T    TTTTA
                                TAGC TAGGT    GGCACT
                                ||||  |||||    ||||||
                                ATCG ATCCA    CCGTGA
                                  T    ______
GAM2903  ECHS1    3'  TAGATTTAGAAGGTGCTCC    19873       TT_   CA
                                TAGGTTT   AGG  CTCC
                                |||||||   |||  ||||
                                ATCTAAA   TCC  GAGG
                                    TCT   AC
GAM2903  NME1     5'  GCTTAGGTTTGAACTCC     7072          TTA  C
                                GCTTAGGTTT   GG ACTCC
                                ||||||||||   || |||||
                                CGAATCCAAA   CT TGAGG
                                      ___  _
GAM2904  GYPA     3'  TTAATTGCCATTGTAACAGTGT 44631         CC  T   T
                                TTAATTGCTA  GT ACA TGT
                                ||||||||||  || ||| |||
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                                AATTAACGGT  CA TGT ACA
                                      AA  T   C
GAM2904  HIF1A    3'  CTTCTAAAATTACTCAATT   11348          G_
                                TTTCTAAAATTA  CAATT
                                ||||||||||||  |||||
                                GAAGATTTTAAT  GTTAA
                                      GA
GAM2904  KIF3B    3'  ATTTCTAAAATTGGGCAA    22028          A_
                                ATTTCTAAAATT  GCAA
                                ||||||||||||  ||||
                                TAAAGATTTTAA  CGTT
                                      CC
GAM2904  MME      3'  CACTTCTAAAGTTAGACA    28611          A   _
                                CATTTCTAAA TTAG CA
                                |||||||||| |||| ||
                                GTGAAGATTT AATC GT
                                      C   T
GAM2904  PSMD7    3'  CATTCCACTTAGCAATTTT   15836       TAAAA
                                CATTTC    TTAGCAATTTT
                                ||||||    ||||||||||||
                                GTAAGG    AATCGTTAAAA
                                   TG___
GAM2905  ADORA2A  3'  CACCTGGTGCAAGGCCTCAC  8599           TTTTA
                                CACCTGGTGCGA    TCAC
                                ||||||||||||    ||||
                                GTGGACCACGTT    AGTG
                                      CCGG_
GAM2905  ANKRD3   3'  CCTGGGGCTTCATCAC     33963      T  GAT
                                CCTGG GC   TTTATCAC
                                ||||| ||   ||||||||
                                GGACC CG   AAGTAGTG
                                  C  ___
GAM2905  CA3      5'  CACTTGTGCGAGTTTAT     23207     CTG     T
                                CAC   GTGCGA TTTAT
                                |||   |||||| |||||
                                GTG   CACGCT AAATA
                                  AA_     C
GAM2905  CCRL1    3'  CTGTGTCATTTTATCAC     32429     G  CG
                                CTG TG  ATTTTATCAC
                                ||| ||  ||||||||||
                                GAC AC  TAAAATAGTG
                                  _  AG
GAM2905  CEBPA    3'  CACCTGGTGACCCCATC     20384        GC
                                CACCTGGT  GATTTTATC
                                ||||||||  |||||||||
                                GTGGACCA  CTGGGGTAG
                                      __
GAM2905  FMR2     3'  CACCTGCTGTTTCTATCA    12953       G  CGA
                                CACCTG TG   TTTTATCA
                                ||||||  ||  ||||||||
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                              GTGGAC AC   AAGATAGT
                                 G  A__
GAM2905  MTMR8    3'  CACCTAGTGAATATTAC     31750         C   T
                              CACCTGGTG GAT TTAT
                              ||||||||| ||| ||||
                              GTGGATCAC TTA AATG
                                    _  T
GAM2905  NDRG2    3'  ACACTGGATGTTTTTATCAC  32189    _   _ CGA
                              AC CTGG TG   TTTTATCAC
                              || |||| ||   |||||||||
                              TG GACC AC   AAAATAGTG
                               T   T  A__
GAM2905  NDUFA5   3'  CACTTGTGCTATTTTATCAC  22667     CTG   G
                              CAC   GTGC ATTTTATCAC
                              |||   |||| ||||||||||
                              GTG   CACG TAAAATAGTG
                                AA_   A
GAM2905  PCDHA9   3'  CTGATCATTTTATCAC      36544       G G
                              CTGGT C ATTTTATCAC
                              ||||| | ||||||||||
                              GACTA G TAAAATAGTG
                                 _ _
GAM2905  PSCD4    3'  CCGGGCTGCCCTTTATCAC   30124    T _  GA
                              CC GG TGC  TTTTATCAC
                              || || |||  |||||||||
                              GG CC ACG  GAAATAGTG
                               C  G   G_
GAM2905  PYGO2    3'  CACTTGGATCCTTTTATCA   41946    C   TGCGA
                              CAC TGG    TTTTATCA
                              ||| |||    ||||||||
                              GTG ACC    AAAATAGT
                                A   TAGG_
GAM2905  SLC9A3R1 3'  CCTGGACCCATTTATCAC    43248      T  GAT
                              CCTGG GC   TTTATCAC
                              ||||| ||   ||||||||
                              GGACC TG   AAATAGTG
                                 _  GGT
GAM2905  STCH     3'  ACCTCAATTTTATCA       28078     GGTG
                              ACCT   CGATTTTATCA
                              ||||   ||||||||||||
                              TGGA   GTTAAAATAGT
                                 ____
GAM2905  TRHDE    3'  TGGTAACTGGATTTTATCA   30114      C___
                              TGGTG   GATTTTATCA
                              |||||   ||||||||||
                              ACCAT   CTAAAATAGT
                                 TGAC
GAM2905  VENTX2   3'  CACTTGTACTTTTATCAC    30912     CTG   GA
                              CAC   GTGC  TTTTATCAC
                              |||   ||||  |||||||||
```

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                                GTG   CATG  AAAATAGTG
                                  AA_   __
GAM2905  RAB11A   3'  GCCTGATCATTGCCAAC     21680    ATA
                                GC   GGTCATTGCCAAC
                                ||   ||||||||||||
                                CG   CTAGTAACGGTTG
                                 GA_
GAM2905  VBP1     3'  TAAACCACATTTTTAATTGCCA 17929          AGGTC
                                TAAACCGCAT    ATTGCCA
                                ||||||||||    |||||||
                                ATTTGGTGTA    TAACGGT
                                      AAAAT
GAM2906  AXIN1    3'  GCTGTGCTGTGGTGGACGTG   41383    _  T  A_
                                GC GTG CTG  GTGGACGTG
                                || ||| |||  |||||||||
                                CG CAC GAC  CACCTGCAC
                                 A  _  AC
GAM2906  FE65L2   5'  GTTGCGTGTTTCCGTGTG    39323        __   A
                                GTTGCGTG  TCTG GTG
                                ||||||||  |||| |||
                                CAACGCAC  AGGC CAC
                                     AA   A
GAM2906  GFAP     3'  GTGCACTGGGGTGGACGTG   13126     _  A_
                                GTGT CTG  GTGGACGTG
                                |||| |||  |||||||||
                                CACG GAC  CACCTGCAC
                                  T  CC
GAM2906  ODC1     3'  AGTAGCGTGTCTGAAGAGTG   14913    T       GT   C
                                AGT GCGTGTCTGA  GGA GTG
                                ||| ||||||||||  ||| |||
                                TCA CGCACAGACT  TCT CAC
                                  T       __  _
GAM2906  SRGAP2   3'  AAGTTGCTGTCTGAGACCCATG 43972       G       TGGA
                                AAGTTGC TGTCTGAG   CGTG
                                |||||||  ||||||||   ||||
                                TTCAACG ACAGACTC   GTAC
                                    _      TGG_
GAM2907  ARHGEF12 3'  TTTAAGCTTATTTAATAT    31655          G
                                TTTAAGCTTATT TAATAT
                                |||||||||||  ||||||
                                AAATTCGAATAA ATTATA
                                             _
GAM2907  XRCC5    3'  CCCTTGTAATATATATG     34487     A
                                CTT TTGTAATATATATG
                                |||  ||||||||||||||
                                GGG AACATTATATATAC
                                  _
GAM2908  ARHH     3'  TTGTGTGAAGTCTCTTGGG   20217      CA  C  GG
                                TTGTG  GA GT  TTCTTGGG
                                |||||  || ||  ||||||||
```

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                                AACAC  CT CA  GAGAACCC
                                  A_  T __
GAM2908  HUNK    3'  TTGTGCAGGCTTTG       31093       GACGT   C
                                TTGTGCA    GGTT TTG
                                |||||||    |||| |||
                                AACACGT    CCGA AAC
                                  _____   _
GAM2908  ARHH    3'  TTGTGTGAAGTCTCTTGGG   20217      CA  C  GG
                                TTGTG  GA GT  TTCTTGGG
                                |||||  || ||  ||||||||
                                AACAC  CT CA  GAGAACCC
                                  A_  T __
GAM2908  HUNK    3'  TTGTGCAGGCTTTG       31093       GACGT   C
                                TTGTGCA    GGTT TTG
                                |||||||    |||| |||
                                AACACGT    CCGA AAC
                                  _____   _
GAM2909  AF5Q31  3'  TGATGTGACACAGTGTTGT   30861      G      TG
                                TGATG TGACACA  GTTGT
                                ||||| |||||||  |||||
                                ACTAC ACTGTGT  CAACA
                                  _      CA
GAM2909  ANXA9   5'  TGAGGTGGGTGTCGTTGTTGT  18694     T   ACACATG
                                TGA GGTG      GTTGTTGT
                                ||| ||||      ||||||||
                                ACT CCAC      CAACAACA
                                  _   CCACAG_
GAM2909  DYRK1A  3'  TGATGGTGGTGGTGGT      39004       ACACA   T
                                TGATGGTG    TGGT GT
                                ||||||||    |||| ||
                                ACTACCAC    ACCA CA
                                    C____   C
GAM2909  TYRP1   3'  GATGGTGATTTTTGTTG     43642       CACATGG
                                GATGGTGA      TTGTTG
                                ||||||||      ||||||
                                CTACCACT      AACAAC
                                    AAA____
GAM2909  AF5Q31  3'  TGATGTGACACAGTGTTGT   30861      G      TG
                                TGATG TGACACA  GTTGT
                                ||||| |||||||  |||||
                                ACTAC ACTGTGT  CAACA
                                  _      CA
GAM2909  ANXA9   5'  TGAGGTGGGTGTCGTTGTTGT  18694     T   ACACATG
                                TGA GGTG      GTTGTTGT
                                ||| ||||      ||||||||
                                ACT CCAC      CAACAACA
                                  _   CCACAG_
GAM2909  DYRK1A  3'  TGATGGTGGTGGTGGT      39004       ACACA   T
                                TGATGGTG    TGGT GT
                                ||||||||    |||| ||
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                                ACTACCAC    ACCA CA
                                    C____   C
GAM2909  TYRP1    3'  GATGGTGATTTTTGTTG    43642       CACATGG
                                GATGGTGA     TTGTTG
                                ||||||||     ||||||
                                CTACCACT     AACAAC
                                    AAA____
GAM2910  ABCE1    3'  GTTTAGATAATGTGCTCT    40503    GT
                                GTT  GATAATGTGCTCT
                                |||  ||||||||||||
                                CAA  CTATTACACGAGA
                                  AT
GAM2910  ABCE1    3'  GTTTAGATAATGTGCTCT    40503    GT
                                GTT  GATAATGTGCTCT
                                |||  ||||||||||||
                                CAA  CTATTACACGAGA
                                  AT
GAM2911  BRPF1    3'  TGAAATAAATACAAACCAGTT  43816      A       __
                                TGAAA TAAATACAAA  GGTT
                                |||||| ||||||||||  ||||
                                ACTTT ATTTATGTTT  TCAA
                                   _        GG
GAM2911  EGF      3'  TGAAAATACATACAAATTC    12652       A    AG
                                TGAAAATA ATACAA  GTTC
                                |||||||| ||||||  ||||
                                ACTTTTAT TATGTT  TAAG
                                    G    __
GAM2911  FGF12    3'  TGATGATAAATGGTTCCT    34300    AA    ACAAA
                                TGA  ATAAAT    GGTTCCT
                                |||  ||||||    |||||||
                                ACT  TATTTA    CCAAGGA
                                  AC    ______
GAM2911  GARS     3'  TGAAGATAAAATACGGTCCCTG 13062     A    _  AAA
                                TGAA ATAAA TAC   GGTTCCTG
                                |||| ||||| |||   ||||||||
                                ACTT TATTT ATG   CCAGGGAC
                                  C    T   ___
GAM2911  HDAC2    3'  TGAAAATAAATACAGTCCATG  44949           AAG   C
                                TGAAAATAAATACA   GTTC TG
                                ||||||||||||||   |||| ||
                                ACTTTTATTTATGT   CAGG AC
                                       ___    T
GAM2911  MS4A7    3'  TGAAAATAATACAGAAACAGCC 34530        A   A GG T_
            TG                   TGAAAATAA TACA A  T  CCTG
                                ||||||||| |||| |  |  ||||
                                ACTTTTATT ATGT T  G  GGAC
                                      _   C TT TC
GAM2911  PTP4A2   3'  TGAAAATAGTGCAAGAGCCCCT 38645       AATA   AG
            G                    TGAAAATA   CAA  GTTCCTG
                                ||||||||   |||  |||||||
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                                ACTTTTAT   GTT  CGGGGAC
                                    CAC_   CT
GAM2911  RENT1    3'  TGGGAATAAATAAGAGTCCCTG 16261    AA      CAAA
                                TG  AATAAATA   GGTTCCTG
                                ||  ||||||||   ||||||||
                                AC  TTATTTAT   TCAGGGAC
                                  CC       TC__
GAM2911  SIRT1    3'  TGAACGTAAATACAATAATCCT 29255     AA       AG  T
           G                     TGAA  TAAATACAA  GT CCTG
                                ||||  |||||||||  || ||||
                                ACTT  ATTTATGTT  TA GGAC
                                  GC       AT  _
GAM2911  ZNF207   3'  AAAATAAATGTCCAATAGTTCC 18384         A__   A
           TG                     AAAATAAAT   CAA GGTTCCTG
                                |||||||||   ||| ||||||||
                                TTTTATTTA   GTT TCAAGGAC
                                    CAG   A
GAM2911  BRPF1    3'  TGAAATAAATACAAACCAGTT  43816      A        __
                                TGAAA TAAATACAAA  GGTT
                                |||||| ||||||||||  ||||
                                ACTTT ATTTATGTTT  TCAA
                                  _        GG
GAM2911  EGF      3'  TGAAAATACATACAAATTC    12652        A     AG
                                TGAAAATA ATACAA  GTTC
                                |||||||| ||||||  ||||
                                ACTTTTAT TATGTT  TAAG
                                    G     __
GAM2911  FGF12    3'  TGATGATAAATGGTTCCT    34300     AA     ACAAA
                                TGA  ATAAAT    GGTTCCT
                                |||  ||||||    |||||||
                                ACT  TATTTA    CCAAGGA
                                  AC     ______
GAM2911  GARS     3'  TGAAGATAAAATACGGTCCCTG 13062      A    _   AAA
                                TGAA ATAAA TAC   GGTTCCTG
                                |||| ||||| |||   ||||||||
                                ACTT TATTT ATG   CCAGGGAC
                                  C    T   ___
GAM2911  HDAC2    3'  TGAAAATAAATACAGTCCATG  44949            AAG    C
                                TGAAAATAAATACA   GTTC TG
                                ||||||||||||||   |||| ||
                                ACTTTTATTTATGT   CAGG AC
                                        ___    T
GAM2911  MS4A7    3'  TGAAAATAATACAGAAACAGCC 34530         A    A GG T_
           TG                     TGAAAATAA TACA A  T  CCTG
                                |||||||||| |||| |  |  ||||
                                ACTTTTATT ATGT T  G  GGAC
                                    _   C TT TC
GAM2911  PTP4A2   3'  TGAAAATAGTGCAAGAGCCCCT 38645         AATA   AG
           G                      TGAAAATA    CAA  GTTCCTG
                                ||||||||    |||  |||||||
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                                ACTTTTAT   GTT  CGGGGAC
                                    CAC_   CT
GAM2911  RENT1    3'  TGGGAATAAATAAGAGTCCCTG 16261    AA      CAAA
                                TG  AATAAATA   GGTTCCTG
                                ||  ||||||||   ||||||||
                                AC  TTATTTAT   TCAGGGAC
                                 CC       TC__
GAM2911  SIRT1    3'  TGAACGTAAATACAATAATCCT 29255     AA       AG  T
           G                     TGAA  TAAATACAA  GT CCTG
                                ||||  |||||||||  || ||||
                                ACTT  ATTTATGTT  TA GGAC
                                  GC       AT  _
GAM2911  ZNF207   3'  AAAATAAATGTCCAATAGTTCC 18384        A__   A
           TG                    AAAATAAAT   CAA GGTTCCTG
                                |||||||||   ||| ||||||||
                                TTTTATTTA   GTT TCAAGGAC
                                    CAG   A
GAM2912  MYO1E    3'  CTACTTAGTACATTCATACAT  22654       AA   CC
                                TTACTTGG  ACA  CATACAT
                                ||||||||  |||  |||||||
                                GATGAATC  TGT  GTATGTA
                                    A_   AA
GAM2912  CRK      3'  TCAGTCTAAAAAATATCACAGG 40829          TA    __
           TA                    TCAGTCTAAAAA  ATGTT  GGGTA
                                ||||||||||||  |||||  |||||
                                AGTCAGATTTTT  TATAG  TCCAT
                                      __     TG
GAM2912  CYP27B1  3'  TCAATCTAAGAATGTGTATGGT 8955         AAAT    TG__
                                TCAGTCTAA    AATGT    GGT
                                |||||||||    |||||    |||
                                AGTTAGATT    TTACA    CCA
                                    C___     CATA
GAM2912  KMO      3'  TCAGTCTAATAATGTATTGGGT 18959         A   AA
                                TCAGTCTAA AAT  TGTTGGGT
                                |||||||||  |||  ||||||||
                                AGTCAGATT TTA  ATAACCCA
                                    A   C_
GAM2912  NCKAP1   3'  AGTCTAAAAATTATCG      30250          AA
                                AGTCTAAAAAT  TGTTG
                                ||||||||||  |||||
                                TCAGATTTTTA  ATAGC
                                      __
GAM2912  PIK3CD   3'  TCAGTCTAGGGAGGATACACAG 22734        AAAATA__ TG T
           GGT                    TCAGTCTA       A  T GGGT
                                ||||||||       |  | ||||
                                AGTCAGAT       T  G CCCA
                                    CCCTCCTA GT T
GAM2912  PREP     3'  TCAGTCCAGGAATAATGTT    15555        AA
                                TCAGTCTA  AATAATGTT
                                ||||||||  |||||||||
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```
                                AGTCAGGT  TTATTACAA
                                    CC
GAM2912  PRKG1    3'  TCAGTTTGAGGGTATGTTAAGT 26516      CTAAAAATA
                A                TCAGT       ATGTTGGGTA
                                 |||||       ||||||||||
                                 AGTCA       TACAATTCAT
                                   AACTCCCA_
GAM2913  KLK3     3'  AGTCTTGGCCTGGTCATTTCC  11609      CA   AAA
                                 AGTTT  GTTT   TCATTTCC
                                 |||||  ||||   ||||||||
                                 TCAGA  CGGA   AGTAAAGG
                                   AC   CC_
GAM2913  SLC25A15 3'  TAAGTTTCCGTTCCTCATTTCC 30670        A   AAA
                                 TAAGTTTC GTTT   TCATTTCC
                                 ||||||||| ||||   ||||||||
                                 ATTCAAAG CAAG   AGTAAAGG
                                     G   G__
GAM2913  TRRAP    3'  TAAGTTTCAGCTCTGCCATTTC 18593           AAA
                C                 TAAGTTTCAGTTT   TCATTTCC
                                  ||||||||||||   ||||||||
                                  ATTCAAAGTCGAG   GGTAAAGG
                                        AC_
GAM2913  YWHAG    3'  AATTCCAGTAAATCATTTCC   29781         TT
                                  AGTTTCAGT  AAATCATTTCC
                                  |||||||||  ||||||||||
                                  TTAAGGTCA  TTTAGTAAAGG
                                        __
GAM2913  FGF5     3'  CTGGAAACCATCATTCTCAGCA 37587           TCAA   A
                A                 TTGGAAACCATT    CTCA CAA
                                  ||||||||||||    |||| |||
                                  GACCTTTGGTAG    GAGT GTT
                                        TAA_   C
GAM2913  GM2A     3'  CTGGAGACCAGGCCTCAGCA   42687      A   TTTCAA   A
                                  TTGGA ACCA      CTCA CA
                                  ||||| ||||      |||| ||
                                  GACCT TGGT      GAGT GT
                                    C   CCG___    C
GAM2913  ICA1     3'  TTGAAGATCTCACTCAACA    22472      AACC     A
                                  TTGGA    ATTTCA CTCAACA
                                  |||||    |||||| |||||||
                                  AACTT    TAGAGT GAGTTGT
                                    C___     _
GAM2913  OPHN1    3'  TTGGAAACCATCATTCTCA    14978          TCAA
                                  TTGGAAACCATT    CTCA
                                  ||||||||||||    ||||
                                  AACCTTTGGTAG    GAGT
                                        TAA_
GAM2913  PABPC1   5'  TTGAAAACTACTCAAC      15027         CATTTCA
                                  TTGGAAAC      ACTCAAC
                                  ||||||||      |||||||
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                                AACTTTTG      TGAGTTG
                                    A_____
GAM2914  ZNF146   3'  TATAGTTCATGGTCTA      28356     T       CTTAAG
                                TAT GTTCATGG     TCTA
                                ||| ||||||||     ||||
                                ATA CAAGTACC     AGAT
                                  T      _______
GAM2914  SLC19A2  3'  TCCATCCATCATGACTT     42893       ACTG
                                TCCATT    ATCATGACTT
                                ||||||    ||||||||||
                                AGGTAG    TAGTACTGAA
                                   G___
GAM2915  AEGL1    3'  TTAAGGCAGGTGTTGGA     10063       TTGTT
                                TTAAGGC    GTGTTGGA
                                |||||||    ||||||||
                                AATTCCG    CACAACCT
                                    TC___
GAM2915  BAZ2A    5'  AAGGTTGGTGTTGGA       30297     C   TT
                                AAGG TTG  GTGTTGGA
                                |||| |||  ||||||||
                                TTCC AAC  CACAACCT
                                  _   __
GAM2915  BMPR1B   3'  TCAAGGCTTGTACTGTGGA   10207          TG   T
                                TTAAGGCTTGT  TGT GGA
                                ||||||||||  ||| |||
                                AGTTCCGAACA  ACA CCT
                                     TG  _
GAM2915  FACL2    3'  TTAAGGCTCATTTTGGA     34440        TG  GTG
                                TTAAGGCT  TT   TTGGA
                                ||||||||  ||   |||||
                                AATTCCGA  AA   AACCT
                                    GT  ___
GAM2915  GJB3     5'  TCAAGGCCAGGCTGTTGG    35838         T_  TG
                                TTAAGGCT  GT  TGTTGG
                                ||||||||  ||  ||||||
                                AGTTCCGG  CG  ACAACC
                                    TC  __
GAM2915  IGF2R    3'  TTAAGGCTTCTTATAGG     9346          G    TT
                                TTAAGGCTT TTGTG  GG
                                |||||||| |||||  ||
                                AATTCCGAA AATAT  CC
                                     G    __
GAM2915  ITPKB    3'  TAAGGCTTGTTTCAGA      13653          GTG TG
                                TAAGGCTTGTT   T  GA
                                ||||||||||  |  ||
                                ATTCCGAACAA   A  CT
                                     ___ GT
GAM2915  KDR      3'  TTAAGGCTTGGCTTGG      13943          TT  G
                                TTAAGGCTTG  GT TTGG
                                |||||||||  || ||||
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                                AATTCCGAAC  CG AACC
                                    __  _
GAM2915  MTMR3    3'  TTAAGGCTGTTTTTGGA     34401        T   GTG
                                TTAAGGCT GTT   TTGGA
                                |||||||| |||   |||||
                                AATTCCGA CAA   AACCT
                                     _   A__
GAM2915  NXF2     5'  TTAAGGCCTTGATGG       35189         GTTG  T
                                TTAAGGCTT    TG TGG
                                |||||||||    || |||
                                AATTCCGGA    AC ACC
                                     _____  T
GAM2915  ODF2     3'  TTAAGGCCTGTCGAGGA     14937            TGTT
                                TTAAGGCTTGTTG    GGA
                                ||||||||||||    |||
                                AATTCCGGACAGC    CCT
                                      T___
GAM2915  OXTR     3'  TCAAGGCTTATTTGG       9530            GTGT
                                TTAAGGCTTGTT    TGG
                                ||||||||||||    |||
                                AGTTCCGAATAA    ACC
                                     _____
GAM2915  PDE4D    3'  TTAAGGCTGACGTGGG      43903         T T    TT
                                TTAAGGCT G TGTG  GG
                                |||||||| | ||||  ||
                                AATTCCGA C GCAC  CC
                                     _ T    __
GAM2915  TRIM9    5'  AGGCCTTGTTGTTGTTGG    31551      _      _
                                AGGC TTGTTGT GTTGG
                                |||| ||||||| |||||
                                TCCG AACAACA CAACC
                                  G      A
GAM2915  XK       3'  TAAGTGATGTGTTGG       34367      GCT  T
                                TAAG   TG TGTGTTGG
                                ||||   || ||||||||
                                ATTC   AC ACACAACC
                                   ___  T
GAM2915  ANKTM1   3'  ACATGGTGCCACCCATAG    28800        __
                                ACATGGT  TACCCATAG
                                |||||||  |||||||||
                                TGTACCA  GTGGGTATC
                                    CG
GAM2915  CTSZ     3'  CACACATAACCATAG       41610      A    TTAC
                                CACA CATGG    CCATAG
                                |||| |||||    ||||||
                                GTGT GTATT    GGTATC
                                  _    _____
GAM2915  FRAP1    3'  ACAACATGGTGTCTAGA     22435          TACCCA
                                ACAACATGGT     TAGA
                                ||||||||||     ||||
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                                TGTTGTACCA     ATCT
                                     CAG___
GAM2915  GPX3    3'  ACACAATCACGCATACCTGTAG 13276       _   GT   CA
                                ACACAA CATG  TACC  TAG
                                |||||| ||||  ||||  |||
                                TGTGTT GTGC  ATGG  ATC
                                   A   GT   AC
GAM2915  KIT     3'  CAAATGGTTACTTCCAGA   6896     C      CCA
                                CAA ATGGTTAC   TAGA
                                ||| ||||||||   ||||
                                GTT TACCAATG   GTCT
                                  _      AAG
GAM2915  MEIS2   3'  CAACACAAAGCTCCCCAT   33537        CAT   A
                                CAACACAA   GGTT CCCAT
                                ||||||||   |||| |||||
                                GTTGTGTT   TCGA GGGTA
                                     ___   G
GAM2915  MORF    5'  CAACACAAAAGTTACCCATAGA 29565        CAT
                                CAACACAA   GGTTACCCATAGA
                                ||||||||   ||||||||||||
                                GTTGTGTT   TCAATGGGTATCT
                                     T__
GAM2915  SET7    3'  AACACAATTTGCACTGGCCATA 36150       ____ _   TTAC
           G                     AACACAA   CA TGG   CCATAG
                                |||||||   || |||   ||||||
                                TTGTGTT   GT ACC   GGTATC
                                    AAAC  G  ____
GAM2915  SLC1A4  3'  CAACACACATGTGTGTATAGA  16740       A   GTTACCC
                                CAACACA CATG      ATAGA
                                ||||||| ||||      |||||
                                GTTGTGT GTAC      TATCT
                                    _   ACACA__
GAM2915  TCL1A   3'  AACACAACATCCCCAT     35026         GGTTA
                                AACACAACAT    CCCAT
                                ||||||||||    |||||
                                TTGTGTTGTA    GGGTA
                                     G____
GAM2916  DDX15   3'  TTTTTTTTTTTTCCGTATA   10679        A
                                TTTTTTTT TTTTCGTATA
                                |||||||| ||||||||||
                                AAAAAAAA AAAGGCATAT
                                     A
GAM2916  GATA3   3'  TTTTCTTTTTTTTATTTTC   13104     G
                                TTTT TTTTTTTTATTTTC
                                |||| ||||||||||||||
                                AAAA AAAAAAAATAAAAG
                                  G
GAM2916  HMGN1   3'  TTTTTTTTTTTTTTATTTTCATA 22451     G
                                TTTT TTTTTTTTATTTTCGTA
                                |||| ||||||||||||||||
```

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                                AAAA AAAAAAAATAAAAGTAT
                                  A
GAM2916 NHLH1    3' TTTTGTTTTTTTTTTTCTC   24663          A
                                TTTTGTTTTTTTT TTTTC
                                |||||||||||| |||||
                                AAAACAAAAAAAA AAGAG
                                       A
GAM2917 EN2      3' GGCTGGTGGAGTCA       10961        TTC  T
                                GGCTGGTG   GA GTCA
                                ||||||||   || ||||
                                CCGACCAC   CT CAGT
                                   ___  _
GAM2917 NBEA     3' TAGCAGCTGGTGTTCAGTC   45433            AT
                                TAGCGGCTGGTGTTCG  GTC
                                |||||||||||||||  |||
                                ATCGTCGACCACAAGT  CAG
                                      __
GAM2917 SLC9A1   3' ACGTGGTTGTCGATGTCAC   43228    GC   GT
                                GCG  TGGT  TCGATGTCAC
                                |||  ||||  ||||||||||
                                TGC  ACCA  AGCTACAGTG
                                  __   AC
GAM2918 CAPG     3' AGCAGGCAGGTGGTGGG     11959     A   A A A
                                AGCA GTAG TG TG GG
                                |||| |||| || || ||
                                TCGT CGTC AC AC CC
                                  C   C C _
GAM2918 CHRNB4   3' AGAAGTGTGTGAGGAAC     8865     C   AGA  A
                                AG AAGT   TG TGAGGAAC
                                || ||||   || ||||||||
                                TC TTCA   AC ACTCCTTG
                                 _   C__  _
GAM2918 CKMT1    3' AGCAAGTAGAATGGGCCA    34188         TG   A  AA
                                AGCAAGTAGA  ATG GG  CCA
                                ||||||||||  ||| ||  |||
                                TCGTTCATCT  TAC CC  GGT
                                      __  _  __
GAM2918 COL1A2   3' AGCAAGTAGATGTGCAG     6384           A  A
                                AGCAAGTAGATG TG GG
                                ||||||||||| || ||
                                TCGTTCATCTAC AC TC
                                       _ G
GAM2918 DLEC1    3' GCAGCTGGATGCTGGGACCAG  28828     A  A_   A  A   A
                                GCA GT  GATG TG GGA CCAG
                                ||| ||  |||| || ||| ||||
                                CGT CG  CTAC AC CCT GGTC
                                  _ AC   G _  _
GAM2918 FUS1     3' GCAGGTAGGTCGGAAGAATCAG 28587     A   ATGAT     C
                                GCA GTAG    GAGGAA CAG
                                ||| ||||    |||||| |||
```

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                                CGT CATC    CTTCTT GTC
                                  C   CAGC_    A
GAM2918  FUT1    3'  ACAGGTGGATGACAAGGTCAG  6631     A  A   TG   AAC
                                GCA GT GATGA  AGG   CAG
                                ||| || |||||  |||   |||
                                TGT CA CTACT  TCC   GTC
                                  C  C    GT   A__
GAM2918  GGA3    3'  GCAAGGGGCAGGGAGGAACCAG 39787      TAGATGAT
                                GCAAG       GAGGAACCAG
                                |||||       ||||||||||
                                CGTTC       CTCCTTGGTC
                                   CCCGTCC_
GAM2918  LDOC1   3'  GCGGGTAGGTAAGGGGACC   29489    AA   ATGA    A_
                                GC  GTAG    TGAGG  ACC
                                ||  ||||    |||||  |||
                                CG  CATC    ATTCC  TGG
                                 CC    C___     CC
GAM2918  MAP1A   3'  AGCAGGGGATGAGAAGGGATCA 14338     A TA    T    AAC
            G                    AGCA G  GATGA GAGG   CAG
                                |||| |  ||||| ||||   |||
                                TCGT C  CTACT TTCC   GTC
                                  _ CC    C    CTA
GAM2918  MNT     3'  AGCGGGTGGATGATGAGG    33701     AA  A
                                AGC  GT GATGATGAGG
                                |||  || ||||||||||
                                TCG  CA CTACTACTCC
                                  CC  C
GAM2918  PDE4A   3'  AAGTGGAAAGCGGGAACCAG   26241      A  TGA  A
                                AAGT GA   TG GGAACCAG
                                |||| ||   || ||||||||
                                TTCA CT   GC CCTTGGTC
                                  C  TTC  _
GAM2918  SLC6A8  3'  GATTGGCGCAGGAACCAG    24768     GA_  _
                                GAT   TG AGGAACCAG
                                |||   || |||||||||
                                CTA   GC TCCTTGGTC
                                  ACC  G
GAM2918  SPG4    3'  AGCAAGCAGAAGGAAC      31396          TGATG
                                AGCAAGTAGA    AGGAAC
                                ||||||||||    ||||||
                                TCGTTCGTCT    TCCTTG
                                              _____
GAM2918  TGM7    3'  AGTAGAAAGGAGCCA       38127       TGAT    A
                                AGTAGA    GAGGA CCA
                                ||||||    ||||| |||
                                TCATCT    TTCCT GGT
                                    ____     C
GAM2919  CSPG3   3'  GCGAGAACAGTTTGG       20488       TTT
                                GCGGG   AACAGTTTGG
                                |||||   ||||||||||
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                              CGCTC   TTGTCAAACC
                                      ___
GAM2919 ZFHX1B   3' GCAAAAACAGTTTGG      31339      TTT
                              GCGGG   AACAGTTTGG
                              |||||   ||||||||||
                              CGTTT   TTGTCAAACC
                                      ___
GAM2920 RFXAP    3' TCCAGATTACTTATCATTTT   8055     A       CT  T
                              TC AGATTACTTA  TC ATTTT
                              || ||||||||||  || |||||
                              AG TCTAATGAAT  AG TAAAA
                               G        __ _
GAM2920 TAC1     3' AACCACTTATTTCTATTTTA   30392        C
                              GATTACTTA TTCTATTTTA
                              ||||||||| ||||||||||
                              TTGGTGAAT AAGATAAAAT
                                    A
GAM2921 DPP4     3' CAAAGCCTCCATAAAAACAATT 12579     AA    A
                              CAAA  TTTCA TAAAAACAATT
                              ||||  ||||| ||||||||||
                              GTTT  GAGGT ATTTTTGTTAA
                                CG    _
GAM2921 RANBP2L1 3' ACAAAAATTTCTCAACAAT   37019         AATAAA
                              ACAAAAATTTC     AACAAT
                              ||||||||||     ||||||
                              TGTTTTTAAAG     TTGTTA
                                    AG____
GAM2922 BLTR2    5' GGAAAGCCATTAAGAGTATGTT 33368   T      ATTGT   A
           AA                   A AAAGCCAT    GTAT TTAA
                              | ||||||||    |||| ||||
                              C TTTCGGTA    CATA AATT
                               C       ATTCT   C
GAM2922 PCDHGA1  3' AAAGCCATATAAATATTA    36726        TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                    TT___
GAM2922 PCDHGA10 3' AAAGCCATATAAATATTA    36867        TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                    TT___
GAM2922 PCDHGA11 3' AAAGCCATATAAATATTA    36876        TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                    TT___
GAM2922 PCDHGA12 3' AAAGCCATATAAATATTA    36886        TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
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                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA2  3' AAAGCCATATAAATATTA    36734       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA3  3' AAAGCCATATAAATATTA    33156       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA4  3' AAAGCCATATAAATATTA    33164       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA5  3' AAAGCCATATAAATATTA    36825       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA6  3' AAAGCCATATAAATATTA    36834       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA7  3' AAAGCCATATAAATATTA    36841       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA8  3' AAAGCCATATAAATATTA    36850       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGA9  3' AAAGCCATATAAATATTA    36859       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGB1  3' AAAGCCATATAAATATTA    36894       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
                              TTTCGGTATA    TATAAT
                                   TT___
GAM2922 PCDHGB2  3' AAAGCCATATAAATATTA    36903       TGTGT
                              AAAGCCATAT    ATATTA
                              ||||||||||    ||||||
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                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGB3  3' AAAGCCATATAAATATTA    36912        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGB4  3' AAAGCCATATAAATATTA    36921        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGB5  3' AAAGCCATATAAATATTA    36930        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGB6  3' AAAGCCATATAAATATTA    36938        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGB7  3' AAAGCCATATAAATATTA    36945        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGC3  3' AAAGCCATATAAATATTA    37046        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGC4  3' AAAGCCATATAAATATTA    37067        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2922  PCDHGC5  3' AAAGCCATATAAATATTA    33180        TGTGT
                                AAAGCCATAT    ATATTA
                                ||||||||||    ||||||
                                TTTCGGTATA    TATAAT
                                     TT___
GAM2923  CAV1     3' TTAAACATTTTTATTGTGCA   12000         AT
                                TTAAACATTTT  TTGTGTA
                                ||||||||||| |||||||
                                AATTTGTAAAA  AACACGT
                                      AT
GAM2923  CCBL1    3' CTTAAACATTTTATTATG     19764          T
                                TTTAAACATTTTATT GTG
                                ||||||||||||||| |||
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                                GAATTTGTAAAATAA TAC
                                                _
GAM2923  FGF13    3'  TTTAAACTTTTTGTGCACA   37985       A   ATT
                                TTTAAAC TTTT  TGTGTACA
                                ||||||| ||||  ||||||||
                                AAATTTG AAAA  ACACGTGT
                                  _   ___
GAM2923  LGI1     3'  TAAACATTTTATTTGGCA    22998            T
                                TAAACATTTTATTTG GTA
                                |||||||||||||| |||
                                ATTTGTAAAATAAAC CGT
                                                _
GAM2923  MYOM2    3'  TTTAAACTTTTATTTGCCTA  19560       A       G
                                TTTAAAC TTTTATTTGT TA
                                ||||||| |||||||||| ||
                                AAATTTG AAAATAAACG AT
                                  _       G
GAM2923  PTP4A2   3'  CTTAAACATTTTATTCAT    38629            TG
                                TTTAAACATTTTATT  T
                                |||||||||||||| |
                                GAATTTGTAAAATAA  A
                                        GT
GAM2923  SNX9     3'  TTTAAACAATTTATTTATAT  32165       T
                                TTTAAACA TTTATTTGTGT
                                |||||||| ||||||||||
                                AAATTTGT AAATAAATATA
                                    T
GAM2924  ACOX3    3'  CACCGCGATCCCAGA      18597        CGGAGA
                                CGCCGCGAT    CCCAGA
                                |||||||||    ||||||
                                GTGGCGCTA    GGGTCT
                                  _______
GAM2924  ANXA6    5'  CGCTGGATCGGAGCCC     19713    CGC      A
                                CGC  GATCGGAG CCC
                                |||  |||||||| |||
                                GCG  CTAGCCTC GGG
                                  AC_      _
GAM2924  CAPN10   3'  CCGCCGCGTGCAGCCTGGATC 35784       AT  AGA  CA
                                CCGCCGCG CGG  CC  GATC
                                |||||||| |||  ||  ||||
                                GGCGGCGC GTC  GG  CTAG
                                    AC  ___  AC
GAM2924  CSNK1D   5'  CCGCCGCGGATGGACTCGGATC 40065       _ C  GACCCA
                                CCGCCGCG AT GGA    GATC
                                |||||||| || |||    ||||
                                GGCGGCGC TA CCT    CTAG
                                    C _  GAGC__
GAM2924  PSEN1    5'  CCGCCGCGGCTCGTAGCTCAG 28737       A_  G  ACC
                                CCGCCGCG  TCG AG  CAG
                                ||||||||  ||| ||  |||
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                                GGCGGCGC  AGC TC   GTC
                                    CG   A  GA_
GAM2925  AXIN1    3'  CCGTCGCCGATTCACACA    41374         CC  ATC
                                CCGTCGCCGA  CG   CA
                                ||||||||||  ||   ||
                                GGCAGCGGCT  GT   GT
                                     AA  GT_
GAM2925  BMP8     3'  GCCTCTGCAGGGCCCGATCCA  11880     G  _  CGA_
                                GCC TC GC    CCCGATCCA
                                ||| || ||    |||||||||
                                CGG AG CG    GGGCTAGGT
                                  _  A  TCCC
GAM2925  CRABP2   5'  CGCCGTCGCCGGGTCGTC    12427          ACC  A
                                CGCCGTCGCCG   CG TC
                                ||||||||||   || ||
                                GCGGCAGCGGC   GC AG
                                     CCA  _
GAM2925  PFKFB4   3'  ACCTTGTCGCCGACTGTCAAC  21284     __       C__
                                GCC  GTCGCCGAC   CGAT
                                |||  |||||||||   ||||
                                TGG  CAGCGGCTG   GTTG
                                  AA        ACA
GAM2925  SOX11    3'  CGCCGCCGCCGGAGCCCCCA  17016         A__   GAT
                                CGCCGTCGCCG   CCC   CCA
                                ||||||||||   |||   |||
                                GCGGCGGCGGC   GGG   GGT
                                     CTC   ____
GAM2925  TPST1    5'  CGCCGTTCCGACCCGCAACC   18761       CG      AT_
                                CGCCGT  CCGACCCG   CC
                                ||||||  ||||||||   ||
                                GCGGCA  GGCTGGGC   GG
                                   A_       GTT
GAM2926  F3       3'  ACAAAGTTTGCCAATTGTT   42548     TTA
                                GCA   TTTGCCAATTGTT
                                |||   ||||||||||||
                                TGT   AAACGGTTAACAA
                                  TTC
GAM2926  GDI2     3'  TATATGCATTATTTGCCAA   11258      A
                                TATA GCATTATTTGCCAA
                                |||| ||||||||||||||
                                ATAT CGTAATAAACGGTT
                                  A
GAM2926  PTER     3'  CATAAGCATTATTTTCTCTGTT 36213           GCCAA
                                TATAAGCATTATTT    TTGTT
                                ||||||||||||||    |||||
                                GTATTCGTAATAAA    GACAA
                                      AGA__
GAM2927  EN2      5'  CTCGGGCTCCGGCGCCGC    10948      CA
                                CTCG  CTCCGGCGCCGT
                                ||||  ||||||||||||
```

```
                                GAGC  GAGGCCGCGGCG
                                  CC
GAM2927 LTBR    3' CGTGCTCCGGTGCGGCGT    14254    CA     C  C
                                CG  CTCCGG GC GTGT
                                ||  |||||| || ||||
                                GC  GAGGCC CG CGCA
                                 AC     A  C
GAM2927 MGAT4B  3' GCATTCCAGTGTTCG      38267    C   GCGCC
                                GCA TCCG    GTGTTCG
                                ||| ||||    |||||||
                                CGT AGGT    CACAAGC
                                 A   _____
GAM2927 NR2F2   5' CTCGGGCTCCGGCGCGCCG   34234     CA       C  GTT
                                CTCG  CTCCGGCGC GT   CG
                                ||||  |||||||||| ||   ||
                                GAGC  GAGGCCGCG CG   GC
                                  CC       _ ___
GAM2927 RAP1GA1 5' CTCGGCACTCTGGTGCCCGC   16167     _    C C   G
                                CTCG CACTC GG GCC TGT
                                |||| ||||| || ||| |||
                                GAGC GTGAG CC CGG GCG
                                  C    A A  _
GAM2927 SPINT2  5' CTCGCGTTCAGGTGCCGACGC  41794      AC  C  C   TGTT
                                CTCGC  TC GG GCCG    CGC
                                |||||  || || ||||    |||
                                GAGCG  AG CC CGGC    GCG
                                   CA  T  A   T___
GAM2927 CHRNA3  5' GCCGCGGACCCGGACGGTCGG  8837      TT    _
                                GCCG  CGGGCC GGACGGTCGG
                                ||||  |||||| ||||||||||
                                CGGC  GCCTGG CCTGCCAGCC
                                  __     G
GAM2927 PSCD4   5' GCTGTTCGGGCTGGCCCGG   30127    C      C  A_
                                GC GTTCGGGC GG  CGG
                                || |||||||| ||  |||
                                CG CAAGCCCG CC  GCC
                                 A       A  GG
GAM2928 DAPP1   3' ACCGAGATCGGATCGTGCCTT  30810        C  C   ATA
                                ACCGAGATC GG ATC   CCTT
                                |||||||| || |||   ||||
                                TGGCTCTAG CC TAG   GGAA
                                     _ _   CAC
GAM2928 TCF20   5' ACTGAGATCCAGCATTCACA   42529    C         _
                                AC GAGATCCGGCAT CATA
                                || ||||||||||| ||||
                                TG CTCTAGGTCGTA GTGT
                                 A          A
GAM2929 FACL4   3' TAAGTATTTTCTTCATAAATAT 20888      CT    C
             TT                   TAAG  TTTTC TCATAAATATTT
                                ||||  ||||| ||||||||||||
```

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                                ATTC  AAAAG AGTATTTATAAA
                                  AT    A
GAM2929  PCDHA11   5'  TTCTTCCCCCAAATATTT    36581         A
                                TTTTTCCTC TAAATATTT
                                ||||||||| |||||||||
                                AAGAAGGGG GTTTATAAA
                                          _
GAM2929  CCNG1     3'  AGAGAAGTTTTTTGGTGCT   19767     TT        AC
                                AGA  GAGGTTTTTTG  GCT
                                |||  ||||||||||  |||
                                TCT  CTTCAAAAAAC  CGA
                                  __         CA
GAM2929  RYR3      3'  TAAGGTTGAGATTTTTTTTTCT 9774      A         GACG
                                TAAG TTGAGGTTTTTT   CT
                                |||| ||||||||||||   ||
                                ATTC AACTCTAAAAAA   GA
                                  C          AAA_
GAM2930  OAS2      3'  TGGTGGAGAGAACCAAGTATA  32556     C     TTA   C
                                TGGT GGAGAG   TAAG ATA
                                |||| ||||||   |||| |||
                                ACCA CCTCTC   GTTC TAT
                                  _     TTG   A
GAM2930  HLA-F     3'  TATGTTCGTGAGGCACAA    33242        C  TTTTC
                                TATGTTTG GA    CACAA
                                |||||||| ||    |||||
                                ATACAAGC CT    GTGTT
                                     A  CC___
GAM2930  NUMA1     5'  ATGTTTTCGATTTTCTGCA   45240       G      CA
                                ATGTTT CGATTTTC  CA
                                |||||| ||||||||  ||
                                TACAAA GCTAAAAG  GT
                                   A       AC
GAM2930  SORCS1    3'  TATATGTTATGAATTTTCTACA 38100        TGC     C
            AA                    TATATGTT   GATTTTC ACAAA
                                |||||||   ||||||| |||||
                                ATATACAA   TTAAAAG TGTTT
                                     TAC      A
GAM2931  HNRPF     3'  TAGTACTTGAAACTAAAGT   22458       AGCAT
                                TAGTAT    AAACTAAAGT
                                ||||||    ||||||||||
                                ATCATG    TTTGATTTCA
                                   AAC__
GAM2931  ITPR1     3'  AGTATCTTTGAAACTAAAGT  13663      AGCAT
                                AGTAT    AAACTAAAGT
                                |||||    ||||||||||
                                TCATA    TTTGATTTCA
                                  GAAAC
GAM2931  UTY       3'  CAGTATAGCATTTCAAAGTC  28309          AAAC
                                TAGTATAGCAT   TAAAGTC
                                ||||||||||   |||||||
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                                GTCATATCGTA   GTTTCAG
                                      AA__
GAM2932  FUT9     3'  TATTATATTTAACGTCTTATAT 42735         T TA
              TT                   TATTATATTT A  TTTTATATTT
                                   |||||||||| |  ||||||||||
                                   ATAATATAAA T  AGAATATAAA
                                         T GC
GAM2932  F3       3'  AATGCTGATGTCAAT      42547       A      III
                                   AATGCT ATGTCAA   T
                                   |||||| |||||||   |
                                   TTACGA TACAGTT   A
                                      C      III
GAM2932  NPY1R    3'  TAAAATGCTCTTGTTGTCA   9483         AA___
                                   TAGAATGCT    TGTCA
                                   |||||||||    |||||
                                   ATTTTACGA    ACAGT
                                         GAACA
GAM2933  ADAM11   3'  CCAGAGAGATAAGAC       34653          AAA
                                   TCAGAGAGATA   AGAT
                                   ||||||||||   ||||
                                   GGTCTCTCTAT   TCTG
                                         ___
GAM2933  AKT1     3'  CCAGAGAGATGACAG       23137          AAAAA
                                   TCAGAGAGAT    GATAG
                                   |||||||||    |||||
                                   GGTCTCTCTA    CTGTC
                                         _____
GAM2933  ATP1A1   5'  TCAGAGAGAAAAGCACAGA   8700          TAA   _
                                   TCAGAGAGA   AAAG ATAGA
                                   |||||||||   |||| |||||
                                   AGTCTCTCT   TTTC TGTCT
                                         ___   G
GAM2933  BACH2    3'  TCAGAAGATAAATAGCAG    34807       G      A  A
                                   TCAGA AGATAAA AG TAG
                                   ||||| ||||||| || |||
                                   AGTCT TCTATTT TC GTC
                                      _      A  _
GAM2933  C18orf1  3'  TCAGAGAGGAAGGCAG      41229         ATAAA   A
                                   TCAGAGAG     AAG TAG
                                   ||||||||     ||| |||
                                   AGTCTCTC     TTC GTC
                                        C____   C
GAM2933  CA12     3'  TCAGAGAGAGAGAAGTAGA   10251         TAAA   A
                                   TCAGAGAGA    AAG TAGA
                                   |||||||||    ||| ||||
                                   AGTCTCTCT    TTC ATCT
                                         CTC_  _
GAM2933  CBFA2T3  3'  CAGAGAGGAAAAGAGAG     23260         ATA     T
                                   CAGAGAG   AAAAGA AG
                                   |||||||   |||||| ||
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                                GTCTCTC   TTTTCT TC
                                   C__     C
GAM2933  CD53     3'  AGAGAGATAATACCAGA     8154          AAAGA
                                AGAGAGATAA     TAGA
                                ||||||||||     ||||
                                TCTCTCTATT     GTCT
                                     ATG__
GAM2933  COL4A5   3'  TCAGGAGATGATAG        7968       A    AAAAA
                                TCAG GAGAT     GATAG
                                |||| |||||     |||||
                                AGTC CTCTA     CTATC
                                  _    _____
GAM2933  DCTN1    5'  CAGAGAGAAAAGGTAGA     35699         TAA    A
                                CAGAGAGA   AAAG TAGA
                                ||||||||   |||| ||||
                                GTCTCTCT   TTTC ATCT
                                     ___    C
GAM2933  DDX11    3'  TCAGAAAGAAAAAGGTAG    20578         TA     A
                                TCAGAGAGA  AAAAG TAG
                                |||||||||  ||||| |||
                                AGTCTTTCT  TTTTC ATC
                                     __     C
GAM2933  DEC1     3'  CCAGAGAGATAACACACATAG  32644           AAAG_
                                TCAGAGAGATAA     ATAG
                                ||||||||||||     ||||
                                GGTCTCTCTATT     TATC
                                      GTGTG
GAM2933  DPYSL3   3'  TCAGAGAGAACCGGGATGGA   10780         TAAAAA   A
                                TCAGAGAGA      GAT GA
                                |||||||||      ||| ||
                                AGTCTCTCT      CTA CT
                                     TGGCC_   C
GAM2933  EIF2C1   3'  AGAGGGATAAAAAGTTTAGA   29166      A        A_
                                AGAG GATAAAAAG  TAGA
                                ||||  |||||||||  ||||
                                TCTC CTATTTTTC  ATCT
                                  C        AA
GAM2933  FOXP2    5'  AAAGAGATGAAAAATTAG    30938         A     A
                                AGAGAGAT AAAAG TAG
                                |||||||| ||||| |||
                                TTTCTCTA TTTTT ATC
                                     C     A
GAM2933  GATA2    3'  TCAGAGAGGGAAGCCAGA    13091         ATAAA   A
                                TCAGAGAG     AAG TAGA
                                ||||||||     ||| ||||
                                AGTCTCTC     TTC GTCT
                                     CC___   G
GAM2933  GPR85    5'  AAGAACAAGGAAAAGATAGA   33256       ATA__
                                GAGAG     AAAAGATAGA
                                |||||     ||||||||||
```

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                                TTCTT    TTTTCTATCT
                                   GTTCC
GAM2933  GRAF    3'  CAGAGAGAGTCAGAGGTAG   31438       TAAAA  __
                                CAGAGAGA    AGA  TAG
                                ||||||||    |||  |||
                                GTCTCTCT    TCT  ATC
                                     CAG__   CC
GAM2933  HSPA5   3'  AGAAAGATAAGGGGAAATAG  23786        AA__
                                AGAGAGATAA   AGATAG
                                ||||||||||   ||||||
                                TCTTTCTATT   TTTATC
                                      CCCC
GAM2933  IL7R    5'  AGAGAGATAGAGAGAGA     13514        AAA  T
                                AGAGAGATA   AGA AGA
                                |||||||||   ||| |||
                                TCTCTCTAT   TCT TCT
                                     C__   C
GAM2933  KRT13   3'  TCAGAGAGGAGAGAGATCCGA  14009       ATAAAA   A_
                                TCAGAGAG     AGAT  GA
                                ||||||||     ||||  ||
                                AGTCTCTC     TCTA  CT
                                     CTCTC_   GG
GAM2933  LSP1    3'  TCAGAGAGTGGAAGGGCAGA   14243       ATAAA  A_
                                TCAGAGAG    AAG  TAGA
                                ||||||||    |||  ||||
                                AGTCTCTC    TTC  GTCT
                                     ACC__   CC
GAM2933  MAPK14  3'  TCAGAGAAATCAGGAGAT    40016        AAAA
                                TCAGAGAGAT   AGAT
                                ||||||||||   ||||
                                AGTCTCTTTA   TCTA
                                      GTCC
GAM2933  MS4A3   3'  TCAGAGAGATTAGATA      26010        AAAA
                                TCAGAGAGAT   AGATA
                                ||||||||||   |||||
                                AGTCTCTCTA   TCTAT
                                      A___
GAM2933  MUC3B   5'  TCAGAGAAGATGGGGTTACAG  45344       _  AAAAAG
                                TCAGAGA GAT     ATAG
                                ||||||| |||     ||||
                                AGTCTCT CTA     TGTC
                                    T  CCCCAA
GAM2933  PCTK3   3'  TCAGAGGGGAAAAAGAT     43787      AGAT
                                TCAGAG   AAAAAGAT
                                ||||||   ||||||||
                                AGTCTC   TTTTTCTA
                                   CCC_
GAM2933  PIK3CD  3'  TCAGAGAGAAAGAT       22733        TAAA
                                TCAGAGAGA   AAGAT
                                |||||||||   |||||
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                                AGTCTCTCT    TTCTA
                                      ____
GAM2933  PIP5K1A   3'  TCAGAGAGAAAGAACTAAGGTA 18656         TAAA___   A
              G                    TCAGAGAGA      AAG TAG
                                   |||||||||      ||| |||
                                   AGTCTCTCT      TTC ATC
                                         TTCTTGA   C
GAM2933  PKD2      3'  TCAAGAGAAAGTAAAGATAGA  41079     _     TAA
                                   TCA GAGAGA   AAAGATAGA
                                   ||| ||||||   |||||||||
                                   AGT CTCTTT   TTTCTATCT
                                     T     CA_
GAM2933  PTGS2     3'  TCAGAGAGGTAACCCCAAAGA  9694         A   AAAGAT
                                   TCAGAGAG TAA      AGA
                                   |||||||| |||      |||
                                   AGTCTCTC ATT      TCT
                                         C   GGGGTT
GAM2933  SLC16A2   3'  TCAGAGAGGAGAAAAAGA    27153        AT_
                                   TCAGAGAG   AAAAAGA
                                   ||||||||   |||||||
                                   AGTCTCTC   TTTTTCT
                                         CTC
GAM2933  SP3       5'  TCAGAGAGGGAGACAG      44383        ATAAAA
                                   TCAGAGAG     AGATAG
                                   ||||||||     ||||||
                                   AGTCTCTC     TCTGTC
                                         CC____
GAM2933  STAU2     3'  CAGAGCGAAGAGATAGA     30801      A  TAAAA
                                   CAGAG GA     AGATAGA
                                   ||||| ||     |||||||
                                   GTCTC CT     TCTATCT
                                      G  TC___
GAM2933  USH2A     3'  CCAGAATTCTAAAAAGATGGA  28303       AGA       A
                                   TCAGAG   TAAAAAGAT GA
                                   ||||||   ||||||||| ||
                                   GGTCTT   ATTTTTCTA CT
                                       AAG       C
GAM2933  WNT5A     3'  CAGAGAGATAACCCCAGA     18114          AAAGA
                                   CAGAGAGATAA     TAGA
                                   ||||||||||     ||||
                                   GTCTCTCTATT     GTCT
                                         GGG__
GAM2934  ADRA2A    3'  AGAGGTTTTAAAGTGA      8623          CTTTAT
                                   AGGGGTTTTA     GTGA
                                   ||||||||||     ||||
                                   TCTCCAAAAT     CACT
                                         TT_____
GAM2934  DPYD      3'  GGGATTTTACTTAATAAA    41294          TAT
                                   GGGGTTTTACTT   GTGAA
                                   ||||||||||||   |||||
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                                CCCTAAAATGAA  TATTT
                                      T__
GAM2934 GABPB1   3' AAGGGGTTTTGTTTTTGT   23522        AC  A
                                AAGGGGTTTT  TTT TGT
                                ||||||||||  ||| |||
                                TTCCCCAAAA  AAA ACA
                                    C_  A
GAM2934 PDGFB    3' AAGGAGTCTTTGTGTGAAT   15165      TTTA  A
                                AAGGGGT   CTTT TGTGAAT
                                |||||||   |||| |||||||
                                TTCCTCA   GAAA ACACTTA
                                   ____  C
GAM2934 PTPRCAP  3' AAGGAGTTTTATTTCAAATG  24691        C  T
                                AAGGGGTTTTA TTTA GTG
                                |||||||||||| |||| |||
                                TTCCTCAAAAT AAGT TAC
                                      A  T
GAM2934 TCF4     3' AAGGAGAAGTGTTTATGTG   17317      TTTTAC
                                AAGGGG    TTTATGTG
                                ||||||    ||||||||
                                TTCCTC    AAATACAC
                                   TTCAC_
GAM2934 TCF8     3' AAGGGGTTTTGTGTTGGAATC  36229        ACTTTA  T
                                AAGGGGTTTT    TG GAATT
                                ||||||||||    || |||||
                                TTCCCCAAAA    AC CTTAG
                                     CACA__ _
GAM2935 CD9      3' CATTGCAGGATTTCTGCT   12096      T__
                                TATTGC  ATTTCTGCT
                                ||||||  |||||||||
                                GTAACG  TAAAGACGA
                                   TCC
GAM2935 DYRK1A   3' ATATTGCTATACTCA     38989        TTCT
                                ATATTGCTAT   GCTCA
                                ||||||||||   |||||
                                TATAACGATA   TGAGT
                                     ____
GAM2935 MS4A7    3' TCTGTGTATCACCTTCTGCTCA 34529   GCA_  TG  AT
                                TC   TAT  CT  TTCTGCTCA
                                ||   |||  ||  |||||||||
                                AG   ATA  GG  AAGACGAGT
                                 ACAC  GT  __
GAM2935 NOV      3' GCTAATATGCTGTTTCTGCT  14810   ATAT_  A
                                GC    TGCT TTTCTGCT
                                ||    |||| ||||||||
                                CG    ACGA AAAGACGA
                                 ATTAT   C
GAM2936 PREB     3' CATAGCCAAGCCTTTTCACTA  30139       TAA  A  C
                                TATAGCCAA   TT TTC ACTA
                                |||||||||   || ||| ||||
```

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                                GTATCGGTT  GA AAG TGAT
                                     CG_  A  _
GAM2936 SACS    3' TAAGCCGATAATTATAAACTA 30763   T   A      TCC
                                A AGCC ATAATTAT  ACTA
                                | |||| ||||||||  ||||
                                A TCGG TATTAATA  TGAT
                                 T   C      TT_
GAM2936 TEM7R   3' TATAGATGACATTCCACTA   37270     CCAATAAT
                                TATAG      TATTCCACTA
                                |||||      ||||||||||
                                ATATC      GTAAGGTGAT
                                   TACT____
GAM2937 CSNK1G3 3' GTCCTTGAAAATATACGTG   20475     C_
                                GTTC  GAAAATATACGTG
                                ||||  ||||||||||||
                                CAGG  CTTTTATATGCAC
                                  AA
GAM2937 FUT6    5' ATCCCGTCTGGATGCCCGTGA 6647        CC  AAATATA
                                ATCCCGTT  GA     CGTGA
                                ||||||||  ||     |||||
                                TAGGGCAG  CT     GCACT
                                     AC  ACGG___
GAM2937 HTR2B   5' ATCCCGTTCCGAACAGTG    9274          AATATAC
                                ATCCCGTTCCGAA     GTG
                                ||||||||||||      |||
                                TAGGGCAAGGCTT     CAC
                                       GT_____
GAM2938 ACHE    3' TGTAGGAGCTCCAGCGGT    8568      TA      TA
                                TGTA  AGCTTTAG  GT
                                ||||  ||||||||  ||
                                ACAT  TCGAGGTC  CA
                                  CC       GC
GAM2938 C7orf2  3' TGAATAAGCTTCACTTAGTA  35372    T       G_
                                TG ATAAGCTTTA  TAGTA
                                || ||||||||||  |||||
                                AC TATTCGAAGT  ATCAT
                                 T         GA
GAM2938 CLASP1  5' TGTAGAAGCTCTAGATGT    42251     T       TA
                                TGTA AAGCTTTAG  GT
                                |||| |||||||||  ||
                                ACAT TTCGAGATC  CA
                                  C        TA
GAM2938 FHL1    3' TGTTAAGCTTCCAGAAGTA   11100     A      _ T
                                TGT TAAGCTTT AG AGTA
                                ||| |||||||| || ||||
                                ACA ATTCGAAG TC TCAT
                                  _       G  T
GAM2938 GNG5    3' TGTACAGGCTTCAAATGTA   23611       A      TA
                                TGTATA GCTTTAG  GTA
                                ||||||| |||||||  |||
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                                ACATGT CGAAGTT  CAT
                                   C      TA
GAM2938  ICA1     3'  TAAGCTCTTTAAAGTAGTA   22469        ____
                                TAAGCTTT   AGTAGTA
                                ||||||||   |||||||
                                ATTCGAGA   TCATCAT
                                    AATT
GAM2938  LBR      3'  TGCATAAGCTTAACAGTA    40432         TAG
                                TGTATAAGCTT  TAGTA
                                ||||||||||  |||||
                                ACGTATTCGAA  GTCAT
                                      TT_
GAM2938  PCDH7    3'  TGCATAGACACCAGTAGTA   37121       AG T
                                TGTATA  C TTAGTAGTA
                                ||||||  | |||||||||
                                ACGTAT  G GGTCATCAT
                                   CT T
GAM2938  PCDHB9   3'  TGTATTAGCTTTAAAGTA    33324      A      T
                                TGTAT AGCTTTAG AGTA
                                ||||| ||||||| ||||
                                ACATA TCGAAATT TCAT
                                  A      _
GAM2938  UTY      3'  TGTACAAGCAGGACAGTA    28321        TT__
                                TGTATAAGC   TAGTA
                                |||||||||   |||||
                                ACATGTTCG   GTCAT
                                      TCCT
GAM2939  HS2ST1   3'  CCAGTTAGATGATTTACACGG  29327        C   CATTGA
                                TCAGTTAGA GAT     GG
                                ||||||||| |||     ||
                                GGTCAATCT CTA     CC
                                     A  AATGTG
GAM2939  MFAP3    3'  TCAGTTAGGCAATCCCTG    25454        A    A
                                TCAGTTAG CGATC TTG
                                |||||||| ||||| |||
                                AGTCAATC GTTAG GAC
                                     C    G
GAM2939  MYO1D    3'  CCAGTTAGATGGTTCCACTA  43490        CGA__
                                TCAGTTAGA    TCATTG
                                |||||||||    ||||||
                                GGTCAATCT    GGTGAT
                                     ACCAA
GAM2939  RCN1     3'  TCTAATCAGTGATCATTGAGG  16207   _    AC
                                TC AGTTAG  GATCATTGAGG
                                || ||||||  ||||||||||
                                AG TTAGTC  CTAGTAACTCC
                                 A     A_
GAM2939  TDG      3'  TCAGTTAGCAAACTGAGG    17359        A  TC
                                TCAGTTAG CGA  ATTGAGG
                                |||||||| |||  |||||||
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                                AGTCAATC GTT  TGACTCC
                                   _  __
GAM2939  VAT1     3'  TCATTTAGACAATGAG      26854     G       TCAT
                                TCA TTAGACGA    TGAG
                                ||| ||||||||    ||||
                                AGT AATCTGTT    ACTC
                                  A       _____
GAM2940  ADRBK1   3'  GGCGGCACTGACAGGACGTGG  11535          C   C    C
                                GGCGGCACTG TAG GACG GG
                                |||||||||| ||| |||| ||
                                CCGCCGTGAC GTC CTGC CC
                                      T   _    A
GAM2940  ASPH     5'  GGGTACACACGCGACGCGG   37145    CG    TGCTA
                                GG  GCAC    GCGACGCGG
                                ||  ||||    |||||||||
                                CC  TGTG    CGCTGCGCC
                                 CA    TG___
GAM2940  CERD4    3'  GGTGGTCCTGGCACGTGG    28953    C  CA   CTA  G   C
                                GG GG  CTG   GC ACG GG
                                || ||  |||   || ||| ||
                                CC CC  GAC   CG TGC CC
                                 A  AG   ___  _   A
GAM2940  FPGS     3'  AGCTGGCACTGCAGGTGTGG   22423     _       T  CGACGC
                                GGC GGCACTGC AG     GG
                                ||| |||||||| ||     ||
                                TCG CCGTGACG TC     CC
                                  A       _  CACA__
GAM2940  GPC1     5'  GGCGGCGGCGGCGGCGCGG    13255       ACT  TA   A
                                GGCGGC   GC  GCG CGCGG
                                ||||||   ||  ||| |||||
                                CCGCCG   CG  CGC GCGCC
                                   C__  C_  C
GAM2940  GSPT1    5'  GACGGCACGAACTCGGCGGCGT 13309         T_   A_   A  C
            GGA                    GGCGGCAC  GCT  GCG CG GGA
                                |||||||  |||  ||| || |||
                                CTGCCGTG  TGA  CGC GC CCT
                                     CT   GC   C  A
GAM2940  ITGBL1   5'  AGCGGCACTGCTCTGGGCGG   21984           AGCGAC
                                GGCGGCACTGCT     GCGG
                                ||||||||||||     ||||
                                TCGCCGTGACGA     CGCC
                                       GACC__
GAM2940  PBP      5'  GGCGACAGAGGCGACGCGGA   15019        CTGCTA
                                GGCGGCA     GCGACGCGGA
                                |||||||     ||||||||||
                                CCGCTGT     CGCTGCGCCT
                                    CTC___
GAM2940  ZFP103   5'  GGCGGCACTGCGGCCCGG    24961          TA  GACG
                                GGCGGCACTGC  GC    CGG
                                ||||||||||  ||    |||
```

```
                                CCGCCGTGACG CG   GCC
                                      C_ G___
GAM2941 BCLG    5' GCAGTGGTGTCCCTGGCCAC 39822      _  __
                                GCGGTGG GTCC GGCCAC
                                ||||||| |||| ||||||
                                CGTCACC CAGG CCGGTG
                                   A   GA
GAM2941 CHST2   5' CGCGGCGGAGGCAGCCCTGCAG 41713      T  CC  A__
                                CGCGGCGG GGGT GGCC  CAG
                                |||||||| |||| ||||  |||
                                GCGCCGCC TCCG TCGG  GTC
                                   _  __  GAC
GAM2941 EGR1    5' GCGGCGGCGGAAGCTGGC   12660        TCC_
                                GCGGCGGTGGG   GGC
                                ||||||||||   |||
                                CGCCGCCGCCT   CCG
                                      TCGA
GAM2941 FHL1    5' CGCGGCGGTGGCGGCGGC   11093        GTC
                                CGCGGCGGTGG  CGGC
                                ||||||||||  ||||
                                GCGCCGCCACC  GCCG
                                      GCC
GAM2941 GAL     5' GCGGTGGCGGGTCTGGGC   45050    C     C_
                                GCGG GGTGGGTC GGC
                                |||| ||||||| |||
                                CGCC CCGCCCAG CCG
                                  A      AC
GAM2941 KLHL2   5' GCGGCGGCGGCCCCCGCGGCCA 28531       G  ___
                                GCGGCGGTGG TCC  GGCCA
                                |||||||||| |||  |||||
                                CGCCGCCGCC GGG  CCGGT
                                     G  GCG
GAM2941 LAIR1   3' ACGTGATGGACTCGGCCA   14049    GC    TC
                                GCG GGTGGG CGGCCA
                                |||  |||||  ||||||
                                TGC  CTACCT  GCCGGT
                                  A_    GA
GAM2941 MBD4    5' AGCAGGGTCCGGCTGCA    19411    GT     CA
                                GGCG  GGGTCCGGC  CA
                                ||||  |||||||||  ||
                                TCGT  CCCAGGCCG  GT
                                   __      AC
GAM2941 MXI1    5' CGGGCGGGCCAGCTCGGCC  39018   C   _ G  TC
                                CG GGCGG T GG  CGGCC
                                || ||||| | ||  |||||
                                GC CCGCC G TC  GCCGG
                                 _   C G  GA
GAM2941 NFATC1  5' CGCGTGGCGGGGCCCGGCC  26072    GC    _
                                CGCG  GGTGGG TCCGGCC
                                ||||  |||||| |||||||
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                                GCGC  CCGCCC GGGCCGG
                                  A_     C
GAM2941  ODC1     5'  GCGGCGGCGGCGGCGGCTACAG 14919          GTC    C
                                GCGGCGGTGG   CGGC ACAG
                                ||||||||||   |||| ||||
                                CGCCGCCGCC   GCCG TGTC
                                     GCC    A
GAM2941  PDE6D    5'  GCGGCGGTCGCCGCCC      15161        GG T   G
                                GCGGCGGT  G CCG CC
                                ||||||||  | ||| ||
                                CGCCGCCA  C GGC GG
                                    G_ _   G
GAM2941  PTMA     5'  CGCGGCGGAGGCGGC       15866        T  GTC
                                CGCGGCGG GG   CGGC
                                |||||||| ||   ||||
                                GCGCCGCC CC   GCCG
                                    T  ___
GAM2941  PTPN18   5'  CGCGGCGAGTGTGGACGCC    30765        _  _  TCCG
                                CGCGGCG GTG GG    GCC
                                ||||||| ||| ||    |||
                                GCGCCGC CAC CC    CGG
                                    T   A  TG__
GAM2941  PTPRJ    5'  GCGGCGGCGGCGGCC       15956         GTC
                                GCGGCGGTGG   CGGCC
                                ||||||||||   |||||
                                CGCCGCCGCC   GCCGG
                                             ___
GAM2941  SFRP4    5'  CGGGGCCGCGGGGTCCGGCC   16585    C   G    _
                                CG GGC GTGGG TCCGGCC
                                || ||| ||||| |||||||
                                GC CCG CGCCC AGGCCGG
                                 C   G    C
GAM2941  SLC9A3   3'  GCGGCGGTGGGCGGACC     20051          CC
                                GCGGCGGTGGGT  GGCC
                                ||||||||||||  ||||
                                CGCCGCCACCCG  CTGG
                                      C_
GAM2941  WEE1     5'  CGCGGCGGCGGCCTGC      18091          GT  G
                                CGCGGCGGTGG  CC GC
                                ||||||||||  || ||
                                GCGCCGCCGCC  GG CG
                                     __  A
GAM2942  PCDH11X  3'  GCAGTTGTAGGACTACATA   37304       AC__
                                GCGGT   GGACTACATA
                                |||||   ||||||||||
                                CGTCA   CCTGATGTAT
                                   ACAT
GAM2942  PCDH11Y  3'  GCAGTTGTGGGACTACATA   37344       AC__
                                GCGGT   GGACTACATA
                                |||||   ||||||||||
```

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                                CGTCA   CCTGATGTAT
                                  ACAC
GAM2942 PML     3' GCCGCAGGTCCTGGACTACAT 37728    CCAA _  AC_
                                GCC   GC GGT  GGACTACAT
                                |||   || |||  |||||||||
                                CGG   CG CCA  CCTGATGTA
                                 ____ T  GGA
GAM2943 GALNT7  3' TCTGCTTCACTCTTTAATT   38361    _   T
                                TCT TTTTA CTCTTTAATT
                                ||| ||||| ||||||||||
                                AGA GAAGT GAGAAATTAA
                                  C   _
GAM2943 HD      3' TCCATTTTTTCCCTTTAATTT 13360      C   TA
                                TCTAT TTTT  TCTCTTTAATTT
                                ||||| ||||  ||||||||||||
                                AGGTA AAAA  AGGGAAATTAAA
                                  _   __
GAM2943 KCNJ16  3' TCCTAATATCTCTTTGATT   33019     TT      A
                                TCTT  TATCTCTTT ATT
                                ||||  ||||||||| |||
                                AGGA  ATAGAGAAA TAA
                                  TT       C
GAM2943 PRKCN   5' TCAGTCTGTACTTGTCTCTTTA 25169   TA  T__  A
            ATTT                 TC  TCT   TTT TCTCTTTAATTT
                                || |||  ||| ||||||||||||
                                AG  AGA   GAA AGAGAAATTAAA
                                 TC   CAT   C
GAM2943 GALNT7  3' TCTGCTTCACTCTTTAATT   32648    _   T
                                TCT TTTTA CTCTTTAATT
                                ||| ||||| ||||||||||
                                AGA GAAGT GAGAAATTAA
                                  C   _
GAM2943 HD      3' TCCATTTTTTCCCTTTAATTT 13360      C   TA
                                TCTAT TTTT  TCTCTTTAATTT
                                ||||| ||||  ||||||||||||
                                AGGTA AAAA  AGGGAAATTAAA
                                  _   __
GAM2943 KCNJ16  3' TCCTAATATCTCTTTGATT   33019     TT      A
                                TCTT  TATCTCTTT ATT
                                ||||  ||||||||| |||
                                AGGA  ATAGAGAAA TAA
                                  TT       C
GAM2943 PRKCN   5' TCAGTCTGTACTTGTCTCTTTA 25169   TA  T__  A
            ATTT                 TC  TCT   TTT TCTCTTTAATTT
                                || |||  ||| ||||||||||||
                                AG  AGA   GAA AGAGAAATTAAA
                                 TC   CAT   C
GAM2944 ADD1    3' AGCACACGGTTCAGGCTCCA  30513       ATACA  T  A
                                AGCACACG    CA GT TCCA
                                ||||||||    || || ||||
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                                TCGTGTGC    GT CG AGGT
                                    CAA__  C  _
GAM2944  AHCY     3'  AAGCACACAGGTATAAGTCCA  8659         ATACAC   TA
                                AAGCACACG     ATG  TCCA
                                |||||||||     |||  ||||
                                TTCGTGTGT     TAT  AGGT
                                    CCA___   TC
GAM2944  CCRL1    3'  AAGCATCATTCATATGTATCCA 32424      _  CGATA  C
                                AAGCA CA     CA ATGTATCCA
                                ||||| ||     || |||||||||
                                TTCGT GT     GT TACATAGGT
                                   A  AA___  A
GAM2944  CKTSF1B1  3'  AAACACACACACTATGT     30076        GAT   _
                                AAGCACAC   ACAC ATGT
                                ||||||||   |||| ||||
                                TTTGTGTG   TGTG TACA
                                    ___    A
GAM2944  CRI1     3'  AAGCACACGTGATACATAT    30732         ATAC
                                AAGCACACG    ACATGT
                                |||||||||    ||||||
                                TTCGTGTGC    TGTATA
                                    ACTA
GAM2944  GRM6     3'  ACATTACACACGTGTATC     9164      CG     A
                                ACA  ATACAC TGTATC
                                |||  |||||| ||||||
                                TGT  TGTGTG ACATAG
                                  AA     C
GAM2944  GTF2IRD1  3'  GCATCGATACATATCC      32258     CA      CATG
                                GCA  CGATACA    TATCC
                                |||  |||||||    |||||
                                CGT  GCTATGT    ATAGG
                                  A_      _____
GAM2944  HELLS    3'  AAGTACACATCAGCCTGTATCC 32847     C    ATACACA
            A                    AAG ACACG      TGTATCCA
                                ||| |||||      ||||||||
                                TTC TGTGT      ACATAGGT
                                  A    AGTCGG_
GAM2944  MJD      3'  AGCACACGGTATACAGT     22626         A  C   T
                                AGCACACG TA ACA GT
                                |||||||| || ||| ||
                                TCGTGTGC AT TGT CA
                                    C  A   _
GAM2944  MS4A8B   3'  AGCACACGAATGTGTGTGTGCC 36434         TACACA   AT_
            A                    AGCACACGA     TGT   CCA
                                |||||||||     |||   |||
                                TCGTGTGCT     ACA   GGT
                                    TACAC_   CAC
GAM2944  NT5C2    3'  AGTACAGATACACAAAACCA   29227    C   C       TGTAT
                                AG ACA GATACACA     CCA
                                || ||| ||||||||     |||
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                                TC TGT CTATGTGT    GGT
                                 A  _      TTT__
GAM2944  NTSR1    3'  AAGCACACGGAATGCGCACCC  14870        ATACACA
                                AAGCACACG      TGTATCC
                                |||||||||      |||||||
                                TTCGTGTGC      GCGTGGG
                                    CTTAC__
GAM2944  PLAG1    3'  AAGTACACGATATACATG    15341    C      C
                                AAG ACACGATA ACATG
                                ||| |||||||| |||||
                                TTC TGTGCTAT TGTAC
                                  A       A
GAM2944  PRAME    3'  AAGCATTTGATATGTGCACCCA 25918      CAC    CACA
                                AAGCA   GATA    TGTATCCA
                                |||||   ||||    ||||||||
                                TTCGT   CTAT    ACGTGGGT
                                   AAA    AC__
GAM2944  RB1      3'  AAGCACACAGTATATCAGATTC 44932        A  CA_  T  A
             CA                   AAGCACACG TA   CA GT TCCA
                                |||||||||  ||   || || ||||
                                TTCGTGTGT AT   GT TA AGGT
                                    C  ATA  C  _
GAM2944  SCN4A    3'  AAGCACACATACATGT      7314          ATAC
                                AAGCACACG    ACATGT
                                |||||||||    ||||||
                                TTCGTGTGT    TGTACA
                                    A___
GAM2944  TPP2     3'  GCACTTACACATGTATTCA    17653      ACGA         C
                                GCAC    TACACATGTAT CA
                                ||||    |||||||||||  ||
                                CGTG    ATGTGTACATA GT
                                  A___          A
GAM2944  WHSC1    3'  AGCACACGAAGCACCAGC    39349        TA   AT
                                AGCACACGA  CAC  GT
                                |||||||||  |||  ||
                                TCGTGTGCT  GTG  CG
                                    TC   GT
GAM2944  ADD1     3'  AGCACACGGTTCAGGCTCCA   30513        ATACA  T  A
                                AGCACACG     CA GT TCCA
                                ||||||||     || || ||||
                                TCGTGTGC     GT CG AGGT
                                    CAA__  C  _
GAM2944  AHCY     3'  AAGCACACAGGTATAAGTCCA  8659         ATACAC   TA
                                AAGCACACG     ATG  TCCA
                                |||||||||     |||  ||||
                                TTCGTGTGT     TAT  AGGT
                                    CCA___   TC
GAM2944  CCRL1    3'  AAGCATCATTCATATGTATCCA 32424       _  CGATA  C
                                AAGCA CA     CA ATGTATCCA
                                ||||| ||     || |||||||||
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                                TTCGT GT    GT TACATAGGT
                                  A  AA___  A
GAM2944  CKTSF1B1  3'  AAACACACACACTATGT    30076       GAT   _
                                AAGCACAC   ACAC ATGT
                                ||||||||   |||| ||||
                                TTTGTGTG   TGTG TACA
                                    ___    A
GAM2944  CRI1    3'  AAGCACACGTGATACATAT   30732       ATAC
                                AAGCACACG   ACATGT
                                |||||||||   ||||||
                                TTCGTGTGC   TGTATA
                                    ACTA
GAM2944  GRM6    3'  ACATTACACACGTGTATC    9164     CG     A
                                ACA  ATACAC TGTATC
                                |||  |||||| ||||||
                                TGT  TGTGTG ACATAG
                                  AA     C
GAM2944  GTF2IRD1  3'  GCATCGATACATATCC     32258    CA     CATG
                                GCA  CGATACA   TATCC
                                |||  |||||||   |||||
                                CGT  GCTATGT   ATAGG
                                  A_     _____
GAM2944  HELLS    3'  AAGTACACATCAGCCTGTATCC 32847    C    ATACACA
           A                     AAG ACACG      TGTATCCA
                                 ||| |||||      ||||||||
                                 TTC TGTGT      ACATAGGT
                                   A    AGTCGG_
GAM2944  MJD     3'  AGCACACGGTATACAGT     36185       A  C   T
                                AGCACACG TA ACA GT
                                |||||||| || ||| ||
                                TCGTGTGC AT TGT CA
                                    C  A   _
GAM2944  MS4A8B   3'  AGCACACGAATGTGTGTGTGCC 36434        TACACA   AT_
           A                     AGCACACGA     TGT   CCA
                                 |||||||||     |||   |||
                                 TCGTGTGCT     ACA   GGT
                                     TACAC_   CAC
GAM2944  NT5C2    3'  AGTACAGATACACAAAACCA   29227    C   C      TGTAT
                                AG ACA GATACACA     CCA
                                || ||| ||||||||     |||
                                TC TGT CTATGTGT     GGT
                                 A   _       TTT__
GAM2944  NTSR1    3'  AAGCACACGGAATGCGCACCC  14870        ATACACA
                                AAGCACACG      TGTATCC
                                |||||||||      |||||||
                                TTCGTGTGC      GCGTGGG
                                    CTTAC__
GAM2944  PLAG1    3'  AAGTACACGATATACATG    15341     C      C
                                AAG ACACGATA ACATG
                                ||| |||||||| |||||
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                                TTC TGTGCTAT TGTAC
                                  A       A
GAM2944  PRAME    3'  AAGCATTTGATATGTGCACCCA 25918      CAC    CACA
                                AAGCA   GATA    TGTATCCA
                                |||||   ||||    ||||||||
                                TTCGT   CTAT    ACGTGGGT
                                  AAA    AC__
GAM2944  RB1      3'  AAGCACACAGTATATCAGATTC 44932         A  CA_  T  A
            CA                    AAGCACACG TA   CA GT TCCA
                                |||||||||  ||   || || ||||
                                TTCGTGTGT AT   GT TA AGGT
                                     C  ATA  C  _
GAM2944  SCN4A    3'  AAGCACACATACATGT      7314          ATAC
                                AAGCACACG    ACATGT
                                |||||||||    ||||||
                                TTCGTGTGT    TGTACA
                                     A___
GAM2944  TPP2     3'  GCACTTACACATGTATTCA    17653      ACGA         C
                                GCAC    TACACATGTAT CA
                                ||||    ||||||||||| ||
                                CGTG    ATGTGTACATA GT
                                  A___          A
GAM2944  WHSC1    3'  AGCACACGAAGCACCAGC    39349         TA   AT
                                AGCACACGA  CAC  GT
                                |||||||||  |||  ||
                                TCGTGTGCT  GTG  CG
                                     TC   GT
GAM2945  ACAT1    3'  CACTGATTACAGCAGGCCT    6159          A  TT T
                                CACTGATTG CA  G GCCT
                                |||||||||  ||  |  ||||
                                GTGACTAAT GT  T CGGA
                                     _  CG C
GAM2945  CABC1    3'  ACTGGTGACACCTGTGCCTC   33677      AT     _
                                ACTG  TGACAT TGTGCCTC
                                ||||  ||||||  ||||||||
                                TGAC  ACTGTG ACACGGAG
                                  C_     G
GAM2945  CACNA2D2 3'  CACTGTTTGACATTCAGC    25704      A       GT
                                CACTG TTGACATT  GC
                                |||||  ||||||||  ||
                                GTGAC AACTGTAA  CG
                                  A       GT
GAM2945  CDS1     3'  ACTGACTTCCTATTGTGCCT   10393       GAC_
                                ACTGATT    ATTGTGCCT
                                |||||||    |||||||||
                                TGACTGA    TAACACGGA
                                    AGGA
GAM2945  CYP3A4   3'  CACTGATTTGGTCACCTC    32712        GACATTG
                                CACTGATT      TGCCTC
                                ||||||||      ||||||
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                                GTGACTAA      GTGGAG
                                    ACCA___
GAM2945  DAZL     3'  CACTGATTGGACTGTTCGC   42775         _  ATTG
                                CACTGATTG AC    TGC
                                ||||||||| ||    |||
                                GTGACTAAC TG    GCG
                                    C  ACAA
GAM2945  DBT      3'  CAGTGACAAATATTGTGCCT   12551    C    T  C
                                CA TGAT GA ATTGTGCCT
                                || |||| || |||||||||
                                GT ACTG TT TAACACGGA
                                 C    T  A
GAM2945  EMX2     3'  TGATTGACAGCTCCCC      44700         TT  G
                                TGATTGACA  GT CCTC
                                |||||||||  || ||||
                                ACTAACTGT  CG GGGG
                                    __  A
GAM2945  FSTL1    3'  CACTGGTCTGTGCCT       28211       A  GACAT
                                CACTG TT    TGTGCCT
                                ||||| ||    |||||||
                                GTGAC AG    ACACGGA
                                  C  _____
GAM2945  GPR81    3'  CATTGATTGACTGAGCCC    37188    C       AT  T
                                CA TGATTGAC  TG GCCT
                                || ||||||||  || ||||
                                GT ACTAACTG  AC CGGG
                                 A       __  T
GAM2945  GPR91    3'  CACTGATTGAGAAAGCCT    37504          CATTGT
                                CACTGATTGA     GCCT
                                ||||||||||     ||||
                                GTGACTAACT     CGGA
                                     CTTT__
GAM2945  HIVEP3   5'  CTGCTGGGTTTGTGCCTC    35990     A   ACA
                                CTG TTG   TTGTGCCTC
                                ||| |||   |||||||||
                                GAC GAC   AACACGGAG
                                  _   CCA
GAM2945  HTR2C    3'  CACTGTCATGTGCCT       9281       ATTGA   T
                                CACTG    CAT GTGCCT
                                |||||    ||| ||||||
                                GTGAC    GTA CACGGA
                                  A____   _
GAM2945  HUNK     3'  TGTTGACATCCCCCTC      31090    A      GTG
                                TG TTGACATT   CCTC
                                || ||||||||   ||||
                                AC AACTGTAG   GGAG
                                 _      GG_
GAM2945  IL17E    5'  CACTGACTGACAGGCCTC    35572           TTGT
                                CACTGATTGACA    GCCTC
                                ||||||||||||    |||||
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                                GTGACTGACTGT   CGGAG
                                      C___
GAM2945 KLK3    3' CTGGTGCGTTGTGCCTC    11612    AT  ACA
                                CTG  TG   TTGTGCCTC
                                |||  ||   |||||||||
                                GAC  AC   AACACGGAG
                                  C_  GC_
GAM2945 LAMP2   3' CAGTGCCATGCATTGTGCTTC 14099   C  AT_ A      C
                                CA TG   TG CATTGTGC TC
                                || ||   || |||||||| ||
                                GT AC   AC GTAACACG AG
                                 C  GGT  _       A
GAM2945 LRAT    3' ACTGATTGGCCCCGCCC    41083       ACA  G
                                ACTGATTG   TT TGCCT
                                ||||||||   || |||||
                                TGACTAAC   GG GCGGG
                                     C__  G
GAM2945 MAP3K7IP1 3' CACTGATTGTGTGGCT     25923        ACAT   C
                                CACTGATTG    TGTG CT
                                |||||||||    |||| ||
                                GTGACTAAC    ACAC GA
                                     ____   C
GAM2945 MPP3    3' TGATGGTGAAGTGTGCCTC   12568     __  CAT
                                TGAT  TGA   TGTGCCTC
                                ||||  |||   ||||||||
                                ACTA  ACT   ACACGGAG
                                  CC   TC_
GAM2945 MTMR3   3' CACTGACTGACTCCT      34391         ATTGTG
                                CACTGATTGAC     CCT
                                ||||||||||     |||
                                GTGACTGACTG     GGA
                                      A_____
GAM2945 NT5C2   3' CACTGATTGTGCCC       29229       TGACAT
                                CACTGAT     TGTGCCT
                                |||||||     |||||||
                                GTGACTA     ACACGGG
                                     ______
GAM2945 PDE1B   3' CTGATGACATCAAACACT    9564      T     T _
                                CTGAT GACATTG GC CT
                                ||||| ||||||| || ||
                                GACTA CTGTAGT TG GA
                                  _     T  T
GAM2945 RAD52   5' CTGGTTGACCTGCGCCTC    39566    A    A
                                CTG TTGAC TTGTGCCTC
                                ||| ||||| |||||||||
                                GAC AACTG GACGCGGAG
                                  C    _
GAM2945 TGFB1   3' CACTGGTCCCCTGTGCCT    8534      A  GACA
                                CACTG TT    TTGTGCCT
                                ||||| ||    ||||||||
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                                GTGAC AG   GACACGGA
                                  C  GG__
GAM2945  UBE3A    3'  CACTGATCACGTGCCT     39277        ACAT
                                CACTGATTG   TGTGCCT
                                |||||||||   |||||||
                                GTGACTAGT   GCACGGA
                                     ____
GAM2945  WNT5A    5'  TGATTGACTGCGCTTC     18139       AT    C
                                TGATTGAC  TGTGC TC
                                ||||||||  ||||| ||
                                ACTAACTG  ACGCG AG
                                    __    A
GAM2945  ZNF26    5'  CACGGATGGATTTGTGCCT   43796    T   T  CA
                                CAC GAT GA  TTGTGCCT
                                ||| ||| ||  ||||||||
                                GTG CTA CT  AACACGGA
                                  C   C  A_
GAM2946  ARNT2    3'  TGGAAGAAAGTGTTTCATGG  31367       T   GGTGA
                                TGGAAGAA GTGT    ATGG
                                |||||||| ||||    ||||
                                ACCTTCTT CACA    TACC
                                    T   AAG__
GAM2946  ATP2A3   3'  TGGGCGAGTGTGGTGG     23200    AA  AT     GAAT
                                TGG  GA  GTGTGGT   GG
                                |||  ||  |||||||   ||
                                ACC  CT  CACACCA   CC
                                  CG  __     _____
GAM2946  CYP8B1   3'  TGGGAGATGGGGTGAATGG   20513    A   ATG  T
                                TGG AGA   TG GGTGAATGG
                                ||| |||   || |||||||||
                                ACC TCT   AC CCACTTACC
                                  C   ___  C
GAM2946  GAS7     3'  TGGAGAATGTGTTTGCTGTGG  25288     A      GG  AA_
                                TGGA GAATGTGT  TG   TGG
                                |||| ||||||||  ||   |||
                                ACCT CTTACACA  AC   ACC
                                  _      A_  GAC
GAM2946  HSPA1L   3'  GGAGTGTGATAGGTGG     45119     AGAAT      AA
                                GGA    GTGTGGTG  TGG
                                |||    ||||||||  |||
                                CCT    CACACTAT  ACC
                                  ______      CC
GAM2946  ITGA11   3'  TGGGGGAATGTGTGAGTTGC  29207     AA       TGAATG
                                TGG  GAATGTGTGG     GC
                                |||  ||||||||||     ||
                                ACC  CTTACACACT     CG
                                  CC        CAA___
GAM2946  MMP19    3'  TGGGAGCATGTGAATAAAATGG 35591     A  A    TGGT
             CA                   TGG AG ATGTG    GAATGGCA
                                |||  || |||||    ||||||||
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                                ACC TC TACAC    TTTACCGT
                                  C  G     TTAT
GAM2946  MPV17    3'  GAAGAGTGGGGATGAGTGGCA  43261      AT   T  _   A
                                GAAGA  GTG GG TGA TGGCA
                                |||||  ||| || ||| |||||
                                CTTCT  CAC CC ACT ACCGT
                                   __   C  T   C
GAM2946  NSF      3'  TGGAAGAAGTGTGTGGAGGG   41786        _      TGAAT
                                TGGAAGAA TGTGTGG     GG
                                |||||||| |||||||     ||
                                ACCTTCTT ACACACC     CC
                                     C      TC___
GAM2946  USH3A    5'  TGGAGCCTGGTGAATGG     38159      AGAAT  G
                                TGGA    GT TGGTGAATGG
                                ||||    || ||||||||||
                                ACCT    CG ACCACTTACC
                                  _____  G
GAM2946  VAX2     3'  GGAAGAGTGTGTGGCTGC    29780       A       GAATG
                                GGAAGA TGTGTGGT    GC
                                |||||| ||||||||    ||
                                CCTTCT ACACACCG    CG
                                   C       A____
GAM2947  RECQL5   3'  TAAAACAGATGCGTTGA     20170        TGTA
                                TAAAACAG    GCGTTGA
                                ||||||||    |||||||
                                ATTTTGTC    CGCAACT
                                     TA__
GAM2948  ANXA9    3'  GGATGACCCAGGTACAGATA   18691     CATA    __
                                GGA    GATC  GGTACAGATA
                                |||    ||||  ||||||||||
                                CCT    CTGG  CCATGTCTAT
                                  A___    GT
GAM2948  CENTD2   3'  TAGGGTAAAATATACAGATA   31603     ACA    TCG
                                TAGG   TAGA   GTACAGATA
                                ||||   ||||   |||||||||
                                ATCC   ATTT   TATGTCTAT
                                  C__    TA_
GAM2948  P53AIP1  3'  TAGGACATACTACGTACAG    35234         GAT  G
                                TAGGACATA   CG TACAG
                                |||||||||   || |||||
                                ATCCTGTAT   GC ATGTC
                                     GAT  _
GAM2949  AMH      5'  TGCCCGGCGCCCCCACTCC    7893              _
                                TGCCTGGCGCCCCCAC CC
                                |||||||||||||||| ||
                                ACGGGCCGCGGGGGTG GG
                                          A
GAM2949  BCR      3'  GCTTGGGGCGCCCTCGGGT    34639    C   C  CCCCA
                                GC TGG GC    CCCTCGGGT
                                || ||| ||    |||||||||
```

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                                CG ACC CG    GGGAGCCCA
                                 A  C  C____
GAM2949  CHES1    3'  TGCCTGGTGCCACAAGCTTGGG 23287       C  CC  CC  C
             T                   TGCCTGG GCC  CA  CT GGGT
                                 ||||||| |||  ||  || ||||
                                 ACGGACC CGG  GT  GA CCCA
                                    A  T_  TC  A
GAM2949  CHST1    5'  GCCGGCTCCATCCTCGGG    18907    T  GCCC  C
                                 GCC GGC   CCA CCTCGGG
                                 ||| |||   ||| |||||||
                                 CGG CCG   GGT GGAGCCC
                                   _  A___  A
GAM2949  PKP1     5'  CCTGGCGCTTCCACCCTGG   7150        CC     C
                                 CCTGGCGC  CCACCCT GG
                                 ||||||||  ||||||| ||
                                 GGACCGCG  GGTGGGA CC
                                    AA     _
GAM2949  PTPN7    3'  TGCTTGGGCAGGACCTCGGGT  38720    C  C  CCCCAC
                                 TGC TGG GC    CCTCGGGT
                                 ||| ||| ||    ||||||||
                                 ACG ACC CG    GGAGCCCA
                                   A  _  TCCT__
GAM2949  SIAT4C   5'  TGCCTCGGGCCACCTTTGGGT  26581     _ C  CCC  CTC
                                 TGCCT GG GCC  ACC  GGGT
                                 ||||| || |||  |||  ||||
                                 ACGGA CC CGG  TGG  CCCA
                                   G  _  ___  AAA
GAM2950  FASN     3'  TTGCATGGCGGGGGTGGGG   19950        TGTTAAA
                                 TTGCATGGCG     TGGGG
                                 ||||||||||     |||||
                                 AACGTACCGC     ACCCC
                                      CCCC___
GAM2951  AP1B1    3'  TGAGGAATGTATCACAGGCAGT 10043       A  A   CAA
                                 TGAGGAAT TA TATAG  CAGT
                                 |||||||| || |||||  ||||
                                 ACTCCTTA AT GTGTC  GTCA
                                    C  A   C__
GAM2951  COPA     3'  TGAGAAATATGAGAACAATAGT 20413        AATAT   C
                                 TGAGGAATAT    AGCAA AGT
                                 ||||||||||    ||||| |||
                                 ACTCTTTATA    TTGTT TCA
                                      CTC__    A
GAM2951  NR4A2    3'  AGGAAATAGCAACA      26162      TATAAT
                                 AGGAA     ATAGCAACA
                                 |||||     |||||||||
                                 TCCTT     TATCGTTGT
                                   _______
GAM2951  OLIG2    3'  TGAGGAATGCACACAGC     25148        ATA
                                 TGAGGAAT   ATATAGC
                                 ||||||||   |||||||
```

```
                                ACTCCTTA  TGTGTCG
                                    CG_
GAM2951  PAIP2    3'  TGAGAAATATGCTTAACAG   32407        AATATA __
                                TGAGGAATAT    GC  AACAG
                                ||||||||||    ||  |||||
                                ACTCTTTATA    CG  TTGTC
                                      _______ AA
GAM2951  TCTA     3'  GAGGAATATGAGTAGGACAGT  35281        AATA  CA
                                GAGGAATAT   TAG  ACAGT
                                |||||||||   |||  |||||
                                CTCCTTATA   ATC  TGTCA
                                    CTC_  C_
GAM2952  ABCB9    3'  GGGGCAGGGACCAGG      33357     AAGGA  T   _
                                GGGG    CA GGGGC AGG
                                ||||    || ||||| |||
                                CCCC    GT CCCTG TCC
                                  ______ _    G
GAM2952  ADAM11   3'  GGGTGGGGACGTGGGCAGGGG  34658    GAA   ATG
                                GGG  GGAC  GGGCAGGGG
                                |||  ||||  |||||||||
                                CCC  CCTG  CCCGTCCCC
                                  ACC   CA_
GAM2952  ADCY6    3'  CAGGGGAAGGGCATGGCTGG  34165         A    GGCAG
                                TAGGGGAAGG CATGG    GG
                                |||||||||| |||||    ||
                                GTCCCCTTCC GTACC    CC
                                     C    GA___
GAM2952  AR       5'  GGGGAAGGCAGGGTGGGGG   6239        A  T   GCA
                                GGGGAAGG CA GGG   GGGG
                                |||||||| || |||   ||||
                                CCCCTTCC GT CCC   CCCC
                                    _ _  AC_
GAM2952  ARHG     3'  GGGGGGAGGGCAGGG      11687     AA  CATG
                                GGGG  GGA   GGGCAGGG
                                ||||  |||   ||||||||
                                CCCC  CCT   CCCGTCCC
                                  __  _____
GAM2952  ARHG     3'  GGGGGGAGGGCAGGG      11687     AA  CATG
                                GGGG  GGA   GGGCAGGG
                                ||||  |||   ||||||||
                                CCCC  CCT   CCCGTCCC
                                  __  _____
GAM2952  ATRN     3'  TAGGGTGACACGGGGGTGGGG  40280      GAAG       CA
                                TAGGG   GACATGGGG  GGGG
                                |||||   |||||||||  ||||
                                ATCCC   CTGTGCCCC  CCCC
                                  A___       CA
GAM2952  AVP      5'  TAGGAGCTGTGGGGCAGGG   7940       AAGGACA
                                TAGGGG     TGGGGCAGGG
                                ||||||     ||||||||||
```

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                                ATCCTC      ACCCCGTCCC
                                   GAC____
GAM2952 BRF1     3' GGAGGAGGCAGGGGTGGGGG  11337     A  A T   CA
                                GGGG AGG CA GGGG  GGGG
                                |||| ||| || ||||  ||||
                                CCTC TCC GT CCCC  CCCC
                                  C  _ _   AC
GAM2952 CALM3    3' AGGGGAAGCAGGGGGTGGGGG 23226       GA  T   CA
                                AGGGGAAG  CA GGGG  GGGG
                                ||||||||  || ||||  ||||
                                TCCCCTTC  GT CCCC  CCCC
                                     __ C   AC
GAM2952 CARKL    5' CAGGGGGGCGGGGCAGGG    29988      AA  ACA
                                TAGGGG  GG   TGGGGCAGGG
                                ||||||  ||   ||||||||||
                                GTCCCC  CC   GCCCCGTCCC
                                   __  ___
GAM2952 CENTD2   5' GGGGGAGGGTGGACAGGG    31601     A   ACATG
                                GGGG AGG    GGGCAGGG
                                |||| |||    ||||||||
                                CCCC TCC    CCTGTCCC
                                  C   CA___
GAM2952 CLTCL1   3' TAGGGGAAGCTGGCAGGG    41886        GACATGG
                                TAGGGGAAG     GGCAGGG
                                |||||||||     |||||||
                                ATCCCCTTC     CCGTCCC
                                     GA_____
GAM2952 COL5A3   3' GGGGAGGTGAGGGGCAGGGG  31854      A  ACAT
                                GGGGA GG    GGGGCAGGGG
                                ||||| ||    ||||||||||
                                CCCCT CC    CCCCGTCCCC
                                  _ ACT_
GAM2952 DOK1     3' AGGGAAGGGATGGCTTTGGGG  10721       AC   GGCA
                                GGGGAAGG  ATGG   GGGG
                                ||||||||  ||||   ||||
                                TCCCTTCC  TACC   CCCC
                                     C_   GAAA
GAM2952 DRPLA    3' GGGGAAGGGGCAAG       12589       GGACAT
                                GGGGAA     GGGGCAGG
                                ||||||     ||||||||
                                CCCCTT     CCCCGTTC
                                   _______
GAM2952 DRPLA    3' GGGGGAGGAGAAAAGCAGGGG  12590     A   CAT
                                GGGG AGGA   GGGGCAGGGG
                                |||| ||||   ||||||||||
                                CCCC TCCT   TTTCGTCCCC
                                  C   CT_
GAM2952 DVL3     3' AGGGCAGGCATGGGGCAGGGG  20671     A   A
                                GGGG AGG CATGGGGCAGGGG
                                |||| ||| |||||||||||||
```

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                                TCCC TCC GTACCCCGTCCCC
                                  G  _
GAM2952  EFNB1    3'  AGGGGAGGGGGTGTGGG     20707       A  ACAT   GCA
                                AGGGGA GG    GGG   GGG
                                |||||| ||    |||   |||
                                TCCCCT CC    CCC   CCC
                                  _ _____   ACA
GAM2952  EGR3     3'  AGGGGAAGGAGTGGGAGGGCAG 40539          CAT__
            GGG                   AGGGGAAGGA    GGGGCAGGGG
                                ||||||||||    ||||||||||
                                TCCCCTTCCT    TCCCGTCCCC
                                     CACCC
GAM2952  ENTPD2   3'  GGGGGAGGGATGGGGCAG    10333      A   AC
                                GGGG AGG  ATGGGGCAG
                                |||| |||  |||||||||
                                CCCC TCC  TACCCCGTC
                                  C   C_
GAM2952  FE65L2   3'  CAGGGGGAGGGGCAGG      39317       AAG  CAT
                                TAGGGG   GA   GGGGCAGG
                                ||||||   ||   ||||||||
                                GTCCCC   CT   CCCCGTCC
                                  ___  ___
GAM2952  FXR2     3'  GGGAGGAGGGATAGCAGGGG   22164      A   CAT  ___
                                GGGA GGA   GGG   GCAGGGG
                                |||| |||   |||   |||||||
                                CCCT CCT   CCC   CGTCCCC
                                  _  ___   TAT
GAM2952  IL2RB    3'  GGAGGGGTCGGGGTAGGG    9386      A  ACA    C
                                GGA GG   TGGGG AGGG
                                ||| ||   ||||| ||||
                                CCT CC   GCCCC TCCC
                                  C  CA_    A
GAM2952  JTB      5'  GGAGGAAGGGCCGGCGGGGG   27444    _     ACATGG   A
                                GG GGAAGG     GGC GGGG
                                || ||||||     ||| ||||
                                CC CCTTCC     CCG CCCC
                                 T     CGG___   C
GAM2952  JUNB     3'  AGGGGAGGGCAGGGGGCGGGGG 13753       A  A  T    A
                                AGGGGA GG CA GGGGC GGGG
                                |||||| || || ||||| ||||
                                TCCCCT CC GT CCCCG CCCC
                                   C  _  C    C
GAM2952  KCNC3    3'  GGGGGGAAGGGGCGGG      22515      AA   CAT    A
                                GGGG  GGA   GGGGC GG
                                ||||  |||   ||||| ||
                                CCCC  CCT   CCCCG CC
                                  __   T__    C
GAM2952  KCNJ4    3'  GGGGAAGGGTGGTGGATCCGGG 22539        ACA_   GCA
            G                    GGGGAAGG   TGGG   GGGG
                                ||||||||   ||||   ||||
```

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                                CCCCTTCC   ACCT  CCCC
                                    CACC   AGG
GAM2952  KRT17    3'  GGGGAAGGGACTGAAGCAGGGG 7683        _ A
                                GGGGAAGG AC TGGGGCAGGGG
                                |||||||| || ||||||||||
                                CCCCTTCC TG ACTTCGTCCCC
                                    C  _
GAM2952  LAMB2    3'  GGGGTAGGCCTTGGGCAGGGG  14074     A  ACATG
                                GGGG AGG    GGGCAGGGG
                                |||| |||    |||||||||
                                CCCC TCC    CCCGTCCCC
                                  A  GGAA_
GAM2952  LYAAT1   3'  GGGGACACATGGGGCAGGGG  38528      AGG
                                GGGGA  ACATGGGGCAGGGG
                                |||||  ||||||||||||||
                                CCCCT  TGTACCCCGTCCCC
                                   G__
GAM2952  MAPT     3'  GGGGGCAGAGGGCGGGG    32584     AA  CATG  A
                                GGGG  GGA   GGGC GGG
                                ||||  |||   |||| |||
                                CCCC  TCT   CCCG CCC
                                  CG  _____   C
GAM2952  MB       3'  GGGGGTGGGAGCGGCAGGGG  23859     AA  ACAT  _
                                GGGG  GG   GG GGCAGGGG
                                ||||  ||   || ||||||||
                                CCCC  CC   TC CCGTCCCC
                                  CA  C___  G
GAM2952  MLLT7    3'  GGGGAAGGGCTGCTTTGGGGG  25531        ACA  GGGCA
                                GGGGAAGG   TG    GGGG
                                ||||||||   ||    ||||
                                CCCCTTCC   AC    CCCC
                                    CG_  GAAAC
GAM2952  MPP2     3'  GGGGAGGGGTGGCAGGG     40799      A  ACAT  _
                                GGGGA GG   GG GGCAGGG
                                ||||| ||   || |||||||
                                CCCCT CC   CC CCGTCCC
                                  _  _____  A
GAM2952  MSI1     3'  GGGGCAAGGGCGAAGAGGGG   14647     _   ACA    C
                                GGGG AAGG   TGGGG AGGGG
                                |||| ||||   ||||| |||||
                                CCCC TTCC   GCTTC TCCCC
                                  G   C__    _
GAM2952  MSI1     3'  GGGGGCAGCAGGGCAGGG    14648     AA  A  TG
                                GGGG  GG CA  GGGCAGGG
                                ||||  || ||  ||||||||
                                CCCC  TC GT  CCCGTCCC
                                  CG  _  __
GAM2952  NEFH     3'  GGGGAGGGCATGGGGGCAGGGG 34347      A  A     _
                                GGGGA GG CATGGGG CAGGGG
                                ||||| || ||||||| ||||||
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                                CCCCT CC GTACCCC GTCCCC
                                  C _     C
GAM2952 NGFR    3' GGGGTGGGGGGCAAGAG    14790     AA ACAT
                                GGGG GG   GGGGCAGGGG
                                |||| ||   ||||||||||
                                CCCC CC   CCCCGTTCTC
                                  A_ ____
GAM2952 NHLH1   3' GGGAAAGGATATGGTGTGG   24653       C   GGCAG
                                GGGGAAGGA ATGG    GG
                                ||||||||| ||||    ||
                                CCCTTTCCT TACC    CC
                                     A   ACA__
GAM2952 NKX2H   5' AGGGGAAGGAGGCGGGG    30754        CATGG  A
                                AGGGGAAGGA    GGC GGG
                                ||||||||||    ||| |||
                                TCCCCTTCCT    CCG CCC
                                      _____  C
GAM2952 PACSIN1  3' GGAGGAAGGGAAGCAGGGCAGG 45153    _    ACAT_
             GG                   GG GGAAGG    GGGGCAGGGG
                                || ||||||    ||||||||||
                                CC CCTTCC    TCCCGTCCCC
                                 T    CTTCG
GAM2952 PDE4A   3' GGGGCGGGGGGGCGGGG     26268     AA ACAT   A
                                GGGG GG   GGGGC GGG
                                |||| ||   ||||| |||
                                CCCC CC   CCCCG CCC
                                  G_ ____    C
GAM2952 PKM2    3' GGGGAAGGGGGTGGGACAGGGG 15336       ACA
                                GGGGAAGG  TGGGGCAGGGG
                                ||||||||  ||||||||||
                                CCCCTTCC  ACCCTGTCCCC
                                     CCC
GAM2952 PLA2G2D  3' GGGAGAGGTGGGGCAGGGG   29636    GA  ACA
                                GGG AGG  TGGGGCAGGGG
                                ||| |||  ||||||||||
                                CCC TCC  ACCCCGTCCCC
                                  TC  ___
GAM2952 POU3F1   3' GGGGGGGCAGGGGCGGGG    40377     AA A T   A
                                GGGG GG CA GGGGC GGG
                                |||| || || ||||| |||
                                CCCC CC GT CCCCG CCC
                                  C_ _ _    C
GAM2952 PRKACG   3' AGGAAGGCATGGGGCGGGGG  15599       A      A
                                GGGAAGG CATGGGGC GGGG
                                ||||||| |||||||| ||||
                                TCCTTCC GTACCCCG CCCC
                                     _      C
GAM2952 PTGDS    3' GGGGAGCCGGGGCAGGGG    9634       AGGACA
                                GGGGA    TGGGGCAGGGG
                                |||||    ||||||||||
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                                CCCCT     GCCCCGTCCCC
                                  CG____
GAM2952  PTPRG    5'  AGGGGAGGGGAGAGGCAGGGG  15932       A  ACAT
                                AGGGGA GG    GGGGCAGGGG
                                |||||| ||    ||||||||||
                                TCCCCT CC    CTCCGTCCCC
                                  C  CT__
GAM2952  RAB4A    5'  GGGGAAGGGCCTGGGGCGGGGG 21349         ACA     A
                                GGGGAAGG   TGGGGC GGGG
                                ||||||||   |||||| ||||
                                CCCCTTCC   ACCCCG CCCC
                                    CGG     C
GAM2952  S100A5   3'  AGGGAGAGGAGGGCAGGGG   16442      GA    CATG
                                AGGG  AGGA    GGGCAGGGG
                                ||||  ||||    |||||||||
                                TCCC  TCCT    CCCGTCCCC
                                  TC    _____
GAM2952  SDC4     3'  AGGGGAAGGGCACTGGGG    16517         A  _
                                AGGGGAAGG CA TGGGG
                                ||||||||| || |||||
                                TCCCCTTCC GT ACCCC
                                    C  G
GAM2952  SF3A1    3'  GGGGAAAGGGTCAGG       25246       GGACAT    _
                                GGGGAA     GGGG CAGG
                                ||||||     |||| ||||
                                CCCCTT     TCCC GTCC
                                  _______   A
GAM2952  SLC8A2   3'  TAGGGGAAGGGAGACTTTGGGG 42419          ACAT    A__
                                TAGGGGAAGG    GGGGC   GGGG
                                ||||||||||    |||||   ||||
                                ATCCCCTTCC    CTCTG   CCCC
                                    _____     AAA
GAM2952  SNRP70   3'  GGGGGAGGGGATGACAGCAAGG 44216      A   AC    _
            G                    GGGG AGG  ATGG GGCAGGGG
                                ||||  |||  ||||  ||||||||
                                CCCC TCC  TACT TCGTTCCC
                                  C   CC    G
GAM2952  SNTB1    5'  GGGGAAGGGTGGCCGGG     34282         ACATGG   A
                                GGGGAAGG     GGC GGG
                                ||||||||     ||| |||
                                CCCCTTCC     CCG CCC
                                    CA_____   G
GAM2952  SOLH     3'  AGGGGAAGGAGGGGGGCGGGGG 24822          CAT    A
                                AGGGGAAGGA   GGGGC GGGG
                                ||||||||||   ||||| ||||
                                TCCCCTTCCT   CCCCG CCCC
                                    CC_    C
GAM2952  SOX10    3'  GGGGGCAGGGGCTGGGCGGGGG 28011      A_   ACATG    A
                                GGGG  AGG    GGGC GGGG
                                ||||  |||    |||| ||||
```

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                                CCCC  TCC    CCCG CCCC
                                  CG   CCGA_   C
GAM2952  TAF4    3'  AGGGGAGGGGAGGGCAGGGG  17256      A  ACAT
                                AGGGGA GG   GGGGCAGGGG
                                |||||| ||   ||||||||||
                                TCCCCT CC   TCCCGTCCCC
                                   C  C___
GAM2952  UBE2L3  3'  GGAGGAGGGGGTCAGCAGGGG  17829     A   ACAT  ___
                                GGGG AGG   GGG   GCAGGGG
                                |||| |||   |||  |||||||
                                CCTC TCC   CCC   CGTCCCC
                                  C  _____  AGT
GAM2952  VASP    3'  AGGGGAGTCCCTGGGGTGGGGG 17912       A GACA    CA
                                AGGGGA G   TGGGG  GGGG
                                |||||| |   |||||  ||||
                                TCCCCT C   ACCCC  CCCC
                                   _ AGGG    AC
GAM2952  VTN     3'  GGGGAAGGAGATGGGAGG    8469         C    GC
                                GGGGAAGGA ATGGG  AGG
                                |||||||| |||||  |||
                                CCCCTTCCT TACCC  TCC
                                     C   __
GAM2952  YWHAE   3'  AGGGGAAGGAGGTAGGG    27594         CATG  GC
                                AGGGGAAGGA   GG  AGGG
                                ||||||||||   ||  ||||
                                TCCCCTTCCT   CC  TCCC
                                     _____  A_
GAM2952  ZNF289  3'  GGGGAGGGGCAAGG       42257      AGGACAT
                                GGGGA     GGGGCAGGG
                                |||||     |||||||||
                                CCCCT     CCCCGTTCC
                                  ________
GAM2953  PHKA1   3'  GAGCCTCCAGGTAAT       15276         TTGTTC   A
                                GAGCTTCCAG    GTAA T
                                ||||||||||    |||| |
                                CTCGGAGGTC    CATT A
                                     _______   C
GAM2954  B4GALT3 5'  GCGGGGGCGGGGTCTCGCGT  19106    TC__  CAA
                                GC   GC  GGTCTCGCGT
                                ||   ||  ||||||||||
                                CG   CG  CCAGAGCGCA
                                 CCCC  CC_
GAM2955  CEACAM1 3'  AAATTGTGTATTCTTTAAC   11827            C
                                AGATTGTGTATTCTT AAC
                                |||||||||||||| |||
                                TTTAACACATAAGAA TTG
                                        A
GAM2955  DNCI1   3'  TAAAGATTTCATGTCTTCA   44993        GTGTAT
                                TAAAGATT    TCTTCA
                                ||||||||    ||||||
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                                ATTTCTAA     AGAAGT
                                     AGTAC_
GAM2955  MSL3L1   3'  TAAAGGTATGCCTTCTTCAAC  38601      AT    A
                                TAAAG  TGTGT TTCTTCAAC
                                |||||  ||||| |||||||||
                                ATTTC  ATACG AAGAAGTTG
                                   C_    G
GAM2955  SCAP2    3'  TATAAAGTTTGAACATTCTT   19444       A   TG
                                TATAAAG TTG  TATTCTT
                                ||||||| |||  |||||||
                                ATATTTC AAC  GTAAGAA
                                     A   TT
GAM2955  SLC4A4   3'  AAGAAAAATATTCTTCAA    19058     TTGT
                                AAGA    GTATTCTTCAA
                                ||||    ||||||||||
                                TTCT    TATAAGAAGTT
                                  TTT_
GAM2956  FGF23    3'  CTAGCAGGGCAGATTTTCG   33950    C   A_     C
                                CT GCG  GCAGATT TCG
                                || |||  ||||||| |||
                                GA CGT  CGTCTAA AGC
                                 T   CC      A
GAM2956  NPC1     3'  TTGCTTTTTTCAAACAGATT   7079      CACTCG
                                TTGC     CGAGCAGATT
                                ||||     ||||||||||
                                AACG     GTTTGTCTAA
                                  AAAAAA
GAM2957  PMCHL1   3'  AGGGGTTTTAAAACCT     36664     A   GTAAAA
                                AGG GTTT     TAAAATCT
                                ||| ||||     ||||||||
                                TCC CAAA     ATTTTGGA
                                  C   _______
GAM2957  SCN8A    3'  GAAGTTTGTAAACAATCT    30532          ATAA
                                GGAGTTTGTAAA    AATCT
                                ||||||||||||    |||||
                                CTTCAAACATTT    TTAGA
                                       G___
GAM2957  SYN2     3'  GAAGTTTGATCTTGAAAATCTC 39459        TAAAAT
              T                  GGAGTTTG     AAAATCTCT
                                 ||||||||     |||||||||
                                 CTTCAAAC     TTTTAGAGA
                                      TAGAAC
GAM2957  TRPM8    3'  AGGGGTCTGAAAATCT      35854     A    TAAAAT
                                AGG GTTTG     AAAATCT
                                ||| |||||     |||||||
                                TCC CAGAC     TTTTAGA
                                  C   _______
GAM2958  ABCC3    3'  TGGATCCGTTTCAGAGACA   33429      C  AAAGCCC
                                TGGA CC      TCAGAGACA
                                |||| ||      |||||||||
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                                ACCT GG      AGTCTCTGT
                                  A  CAA____
GAM2958  ACCN2    3'  GTGGGAGAATGGTTCTCAGAGA 33453      ACCCAAAGCC
                 CA                 GTGG        CTCAGAGACA
                                    ||||        ||||||||||
                                    CACC        GAGTCTCTGT
                                      CTCTTACCAA
GAM2958  ADORA1   3'  GGGGTCCAGAGTCCTCAGAG   8594    T  AC   A  C
                                    G GG  CCA AG CCTCAGAG
                                    | ||  ||| || ||||||||
                                    C CC  GGT TC GGAGTCTC
                                     _  CA   C  A
GAM2958  BMP1     3'  ATGGACCCGTCAGAGA      25973         AAAGCCC
                                    GTGGACCC      TCAGAGA
                                    ||||||||      |||||||
                                    TACCTGGG      AGTCTCT
                                         C_______
GAM2958  CAPON    5'  GCGGACCCGCTCCTTCGGAG   41920         AAA  _   _ A
                                    GTGGACCC   GC CCT C GAG
                                    ||||||||   || ||| | |||
                                    CGCCTGGG   CG GGA G CTC
                                         ___  A   A C
GAM2958  CBFB     3'  GTGGACCGAAAGCCCTTAGCTA 35633        C       C  __
                 GACA                   GTGGACC AAAGCCCT AG  AGACA
                                    ||||||| |||||||| ||  |||||
                                    CACCTGG TTTCGGGA TC  TCTGT
                                         C       A  GA
GAM2958  CD22     3'  TGGGCTTTCCCTCAGAGGCA   12102     ACCCAAAG       A
                                    TGG       CCCTCAGAG CA
                                    |||       ||||||||| ||
                                    ACC       GGGAGTCTC GT
                                      CGAAA___        C
GAM2958  CIT      3'  GGACCCAAAGCAACAGA     43052           CCT
                                    GGACCCAAAGC   CAGA
                                    ||||||||||   ||||
                                    CCTGGGTTTCG   GTCT
                                          TT_
GAM2958  CTLA4    3'  GGACCCAAGGTGGAAAGACA   23329         AGCCCTC
                                    GGACCCAA      AGAGACA
                                    ||||||||      |||||||
                                    CCTGGGTT      TTTCTGT
                                         CCACC__
GAM2958  CYP46    3'  GTGGGCACAGGGGGGCTCAGAGA 27424      ACC  AAGCC
                 CA                   GTGG   CA    CTCAGAGACA
                                      ||||   ||    ||||||||||
                                      CACC   GT    GAGTCTCTGT
                                        CGT  CCCCC
GAM2958  DIAPH2   3'  TGGGCCTAAAAGGGACAGAGAC 28683     A  C    CCCT
                 A                    TGG CC AAAG    CAGAGACA
                                      ||| || ||||    ||||||||
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                                ACC GG TTTT   GTCTCTGT
                                  C A   CCCT
GAM2958 EPHB6   5' GTGGACCCGGGGCTCCTGGAG 20799       AAA _  CA
                                GTGGACCC  GC CCT  GAG
                                |||||||  || |||  |||
                                CACCTGGG  CG GGA  CTC
                                    CCC  A  C_
GAM2958 FN14    3' TGGGCCCAGGCCTCAGAG   32493    A   AA  C
                                TGG CCCA  GCC TCAGAG
                                ||| ||||  ||| ||||||
                                ACC GGGT  CGG AGTCTC
                                  C   C_  _
GAM2958 GAS7    3' GGGTCTTCAGCCTCAGAGACA 18885   ACCCAA   C
                                GG     AGCC TCAGAGACA
                                ||     |||| |||||||||
                                CC     TCGG AGTCTCTGT
                                 CAGAAG  _
GAM2958 GRIA1   3' GACTCTACTCTCAGAGACA   9089     CCAAA  C
                                GAC    GC CTCAGAGACA
                                |||    || ||||||||||
                                CTG    TG GAGTCTCTGT
                                  AGA__  A
GAM2958 NCSTN   3' GTAGGCTCAGCCCAGAGA   43941     ACCCAA   TC
                                GTGG    AGCCC  AGAGA
                                ||||    |||||  |||||
                                CATC    TCGGG  TCTCT
                                  CGAG__   __
GAM2958 PPP2R4  3' GTGGACCCAGACACAGGA   41332       AA  CCT  A
                                GTGGACCCA  GC  CAG GA
                                |||||||||  ||  ||| ||
                                CACCTGGGT  TG  GTC CT
                                    C_  T__  _
GAM2958 RNF26   3' GTGGCCCCAAAGTCAG     36754     A     CCC
                                GTGG CCCAAAG  TCAG
                                |||| |||||||  ||||
                                CACC GGGTTTC  AGTC
                                  G     ____
GAM2958 SURF5   3' GTGCAGGGGCCCTCAGGGAC  27583    GACCCAAA      A
                                GTG      GCCCTCAG GAC
                                |||      |||||||| |||
                                CAC      CGGGAGTC CTG
                                  GTCCC___      C
GAM2958 TEM7    3' GTGGCCTCAAAGTCTTCA    33811     A _   CCC
                                GTGG CC CAAAG  TCA
                                |||| || |||||  |||
                                CACC GG GTTTC  AGT
                                  _ A    AGA
GAM2958 USF2    3' GGACCCAGAAACAAGAG     17898       _   CCTC
                                GGACCCA AAGC   AGAG
                                ||||||| ||||   ||||
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                                CCTGGGT TTTG    TCTC
                                    C   T___
GAM2959 CENPB    3' TGACGTGGATGGCAGAGGG   43017         AC   TAAA
                                TGACGTGGAT  TAG   AGGG
                                ||||||||||  |||   ||||
                                ACTGCACCTA  GTC   TCCC
                                     CC  _____
GAM2959 HUNK     3' GATGTGGATACATGTGGAGGG 31069    C       TA  AAA
                                GA GTGGATAC  GT   AGGG
                                || ||||||||  ||   ||||
                                CT CACCTATG  CA   TCCC
                                 A       TA  CC_
GAM2959 NBS1     3' TGACTGGATACTTGTATGGGGG 42991      G       A   AAA
             A                   TGAC TGGATACT GTA   GGGA
                                |||| |||||||| |||   ||||
                                ACTG ACCTATGA CAT   CCCT
                                  _       A   ACC
GAM2959 TFF3     3' TGACGTGGGTGCCAGTCTGGA  41865        ATA    AAAAG
                                TGACGTGG   CTAGT    GGA
                                ||||||||   |||||    |||
                                ACTGCACC   GGTCA    CCT
                                     CAC    GA___
GAM2960 ALS2     3' TAAAAGTTCCTTTCTCCCCT   34096      _   ___
                                TAAAA TTCC   CTCCCCT
                                ||||| ||||   |||||||
                                ATTTT AAGG   GAGGGGA
                                   C    AAA
GAM2960 ASGR2    3' CTTAAACTACCTCCTTTCTCT  38952    A    C    CC
                                CT AAATT CCTCC  TTTCTCT
                                || ||||| |||||  |||||||
                                GA TTTGA GGAGG  AAAGAGA
                                 A    T    __
GAM2960 CALCRL   3' CTAGGAATTCCCTCCCACT    25128     A_        _
                                CTA  AATTCCCTCCC CT
                                |||  |||||||||| ||
                                GAT  TTAAGGGAGGG GA
                                  CC         T
GAM2960 CDH12    5' CCCAGGATTCCCTCCTGTCATC 19772      AA       CCTT _
             T                   CCTA  ATTCCCTCC    TC TCT
                                ||||  |||||||||    || |||
                                GGGT  TAAGGGAGG    AG AGA
                                   CC        AC__  T
GAM2960 CNTNAP2  3' CCTAGTAATTCCCTCCTCCCT  30485      A_        _
                                CCTA  AATTCCCTCC CCTT
                                ||||  |||||||||| ||||
                                GGAT  TTAAGGGAGG GGGA
                                   CA         A
GAM2960 DDX6     3' AAATTCCCTCTCCCACCCCT   20538          _   TT
                                AAATTCCCTC CCC  TCTCT
                                |||||||||| |||  |||||
```

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                                TTTAAGGGAG GGG  GGGGA
                                      A   T_
GAM2960  DSC3     3'  CCTGAGTTCTTTCTCCCCCT   12596     AAAA  C__
                                CCT    TTC   CTCCCCTT
                                |||    |||   ||||||||
                                GGA    AAG   GAGGGGGA
                                  CTC_   AAA
GAM2960  ELK3     5'  TTCCCCCTTTTTTTCTTTCTCT 23421       CC_____
                                TTCCCTC      CTTTCTCT
                                |||||||      ||||||||
                                AAGGGGG      GAAAGAGA
                                    AAAAAAA
GAM2960  ENPP3    3'  CTAAAACTCTCCTTTCTCT    43788        CCTCC
                                CTAAAATTC    CCTTTCTCT
                                |||||||||    |||||||||
                                GATTTTGAG    GGAAAGAGA
                                      A____
GAM2960  ETS1     5'  CTCAAATTCCCGCTGCCTTTCT 23460    A      TCC_
                                CT AAATTCCC    CCTTTCT
                                || ||||||||    |||||||
                                GA TTTAAGGG    GGAAAGA
                                 G       CGAC
GAM2960  FHIT     5'  CCTAGGATACCTTCTTTCTCTT 12867     AA  T  C  CC___
            TCTCT                   CCTA  AT CC TC     CTTTCTCT
                                ||||  || || ||     ||||||||
                                GGAT  TA GG AG     GAAAGAGA
                                  CC  T  A  AAAGA
GAM2960  FOXO1A   3'  AAATTCCCTCCTTCCACT    12879          CC    T
                                AAATTCCCTCC  TTTC CT
                                ||||||||||  |||| ||
                                TTTAAGGGAGG  AAGG GA
                                      __    T
GAM2960  GALNT7   3'  CCAAAATTCTCTTTTCCTTC   38354         C  CC_
                                CTAAAATTC CT   CCTTT
                                |||||||| ||   |||||
                                GGTTTTAAG GA   GGAAG
                                      A  AAA
GAM2960  HPCA     3'  CCTAGAATCCTTCTCTCCCCT  13423      A    C___
                                CCTA AATTC    CTCCCCT
                                |||| |||||    |||||||
                                GGAT TTAGG    GAGGGGA
                                  C     AAGA
GAM2960  IFNGR2   5'  CCCGCCCCCCTCCCCTTT    24380     AAAA
                                CCT    TTCCCTCCCCTTT
                                |||    |||||||||||||
                                GGG    GGGGGAGGGGAAA
                                  CG__
GAM2960  KCNJ5    5'  CCTTGGGTCACTCCCTTTCTCT 9434      AAAAT  C    C
                                CCT     TC CTCCC TTTCTCT
                                |||     || ||||| |||||||
```

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                                GGA    AG GAGGG AAAGAGA
                                  ACCC_  T    _
GAM2960  KCNK6    3'  CCTTCCATCTTTCCCTTTCT  22080    AAAAT  C ___
                                CCT    TCC TC  CCCTTTCT
                                |||    ||| ||  ||||||||
                                GGA    AGG AG  GGGAAAGA
                                  ______  T  AAA
GAM2960  MEF2C    5'  TTCCTTCCTTTTCTTTCTCT  14412     C  C___
                                TTCC TCC    CTTTCTCT
                                |||| |||    ||||||||
                                AAGG AGG    GAAAGAGA
                                  A  AAAA
GAM2960  NDRG3    3'  CCTACAGATTGGCCCTTTCTCT 36746     AAATTCCCTC
                                CCTA        CCCTTTCTCT
                                ||||        ||||||||||
                                GGAT        GGGAAAGAGA
                                  GTCTAACC__
GAM2960  NFIX     3'  CAAAATTTCTTCTCCCCCCT  14761       _ C_
                                TAAAATT C  CTCCCCTTT
                                ||||||| |  |||||||||
                                GTTTTAA G  GAGGGGGGA
                                    A AA
GAM2960  NR5A2    3'  CCTCATCCTTTCCTTTCTCT  19235    AAAATTC  CC
                                CCT     CCT  CCTTTCTCT
                                |||     |||  |||||||||
                                GGA     GGA  GGAAAGAGA
                                  GTA____  AA
GAM2960  PLXNA2   3'  TTCTTCTCCTCTTTCTCT    36079    C_   C
                                TTC  CTCC CTTTCTCT
                                |||  |||| ||||||||
                                AAG  GAGG GAAAGAGA
                                  AA   A
GAM2960  PTP4A2   3'  AATTCCTTTTCTCTTTCTCT  18496      C__  CC
                                AATTCC   TC  CTTTCTCT
                                ||||||   ||  ||||||||
                                TTAAGG   AG  GAAAGAGA
                                    AAA  A_
GAM2960  RPS6KA5  3'  AAAACAGACCCCTTTCTCT   21911     TCCCT
                                AAAAT    CCCCTTTCTCT
                                |||||    ||||||||||
                                TTTTG    GGGGAAAGAGA
                                   TCT__
GAM2960  SCA1     5'  CTGAAATCCACTCTTTCTCT  7277    A    C  CCC
                                CT AAATTC CTC   TTTCTCT
                                || |||||| |||   |||||||
                                GA TTTAGG GAG   AAAGAGA
                                  C     T  ___
GAM2960  SCD      3'  CCTTAAATCCTTCCCTTT    22823    A   TC  C
                                CCT AAAT  CCT CCCTTT
                                ||| ||||  ||| ||||||
```

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                                GGA TTTA  GGA GGGAAA
                                  A   __  A
GAM2960  SLC7A6   3'  CCTAGCATTCCCTCTTCCCC  19589     AA      __
                                CCTA  ATTCCCTC  CCCT
                                ||||  ||||||||  ||||
                                GGAT  TAAGGGAG  GGGG
                                  CG      AA
GAM2960  SNCA     3'  CTAAAATTCCTCCTTCT     7367         C   CCT
                                CTAAAATTCC TCC   TTCT
                                |||||||||| |||   ||||
                                GATTTTAAGG AGG   AAGA
                                      _  ___
GAM2960  SPG4     3'  CCTAGTATTTCCCTTCTC    31397     AAA_    CCCCTT
                                CCTA   TTCCCT    TCTC
                                ||||   ||||||    ||||
                                GGAT   AAGGGA    AGAG
                                  CATA    _______
GAM2960  VASP     3'  AAATTCCCTCCTTCC      17910         CCT
                                AAATTCCCTCC   TTCT
                                ||||||||||   ||||
                                TTTAAGGGAGG   AAGG
                                      ___
GAM2961  ABL1     3'  GGGCTGGCGGGTCCTGGC    28717       A   AC__
                                GGGCTGGC GGG   GGC
                                |||||||| |||   |||
                                CCCGACCG CCC   CCG
                                    _  AGGA
GAM2961  ACTN1    5'  GGGCTGGCGGGGCCGGGC    9936        A   AC_
                                GGGCTGGC GGG   GGC
                                |||||||| |||   |||
                                CCCGACCG CCC   CCG
                                    C   GGC
GAM2961  ARHGDIA  3'  GGGCTGGAGGACGGCCCGG   20211       CA      A  CA
                                GGGCTGG  GGGACGGC CC  G
                                |||||||  |||||||| ||  |
                                CCCGACC  TCCTGCCG GG  C
                                   __      _ C_
GAM2961  BAI2     5'  GGCGCTGGCGGGGGCGGCCACG 11796   _    A   A   _  CCA
            GGGC                  GG GCTGGC GGG CGGC AC   GC
                                || |||||| ||| |||| ||   ||
                                CC CGACCG CCC GCCG TG   CG
                                 G     C   C    G  CCC
GAM2961  CD9      5'  GGACTGGCGGGACCTGGC    12097       A    __
                                GGGCTGGC GGGAC  GGC
                                |||||||| |||||  |||
                                CCTGACCG CCCTG  CCG
                                    _    GA
GAM2961  CELSR2   3'  GGGCTGCTGGGAACACCCAGC  10853      G A    CG
                                GGGCTG C GGGA  GCACCCAGC
                                |||||| | ||||  |||||||||
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                                CCCGAC G CCCT  TGTGGGTCG
                                   _ A   __
GAM2961  CRYBA2   5'  GGGTGGCACCACGCGCTCAGC  38395    C    GGG  _  ACC
                                GGG TGGCA  ACG GC  CAGC
                                ||| |||||  ||| ||  ||||
                                CCC ACCGT  TGC CG  GTCG
                                  _   GG_  G  A__
GAM2961  DNMT3B   5'  GGGCTGGCTGGGGCGCGGC   27878       A_  A_
                                GGGCTGGC  GGG  CGGC
                                ||||||||  |||  ||||
                                CCCGACCG  CCC  GCCG
                                     AC  GC
GAM2961  EGLN2    5'  GGGTGGCAGGGAAGGGGTCCAG 38832    C       C  CAC
                                GGG TGGCAGGGA GG  CCAG
                                ||| |||||||| ||  ||||
                                CCC ACCGTCCCT CC  GGTC
                                  _       T  CCA
GAM2961  EPHA8    3'  GGGCTGGCAGGGGGCAC    33897          AC
                                GGGCTGGCAGGG  GGCAC
                                ||||||||||  |||||
                                CCCGACCGTCCC  CCGTG
                                           __
GAM2961  EPHB2    3'  GGGCTGGCGGGAGTGGGC    32675       A   C__
                                GGGCTGGC GGGA  GGC
                                |||||||| ||||  |||
                                CCCGACCG CCCT  CCG
                                     _   CAC
GAM2961  FSTL3    3'  GGGCTGGCAGGGAATGGTGGCA 25220          C_  CACC
           GC                     GGGCTGGCAGGGA  GG   CAGC
                                ||||||||||||  ||   ||||
                                CCCGACCGTCCCT  CC   GTCG
                                       TA  ACC_
GAM2961  GAS7     3'  GGGCTGGCAGGGTGGGGGC   25277          AC__
                                GGGCTGGCAGGG   GGC
                                ||||||||||    |||
                                CCCGACCGTCCC   CCG
                                       ACCC
GAM2961  ICAM2    5'  GGGCTCGCAGGGACCAGC    9314       G      _
                                GGGCT GCAGGGAC GGC
                                ||||| |||||||| |||
                                CCCGA CGTCCCTG TCG
                                  G       G
GAM2961  IL6R     5'  GGGCGGCAGGGGTGGCA     8183       T      AC
                                GGGC GGCAGGG  GGCA
                                |||| |||||||  ||||
                                CCCG CCGTCCC  CCGT
                                  _      CA
GAM2961  INHBB    3'  GGGTGGCAGGATGCGTCTGGC  13564     C       AC_____
                                GGG TGGCAGGG      GGC
                                ||| ||||||||      |||
```

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                                CCC ACCGTCCT      CCG
                                  _       ACGCAGA
GAM2961  JTB      5'  GGGCCGGCGGGGGCTCGCGGC  27445        A   A____
                                GGGCTGGC GGG    CGGC
                                |||||||| |||    ||||
                                CCCGGCCG CCC    GCCG
                                    C   CGAGC
GAM2961  JUNB     5'  GGGCTGGCGCGGGCGGGTAGC  13759        A_   A   CACCC
                                GGGCTGGC  GGG CGG    AGC
                                |||||||  ||| |||    |||
                                CCCGACCG  CCC GCC    TCG
                                    CG   _   CA___
GAM2961  LDB1     5'  GGGCTGACGGGGGGGACAACTTC 19344        A__       ACC
              AGC                   GGGCTGGC   GGGACGGC   CAGC
                                |||||||   ||||||||   ||||
                                CCCGACTG   CCCTGTTG   GTCG
                                    CCC       AA_
GAM2961  LILRB4   3'  GGGCTGGCTGGGGTTCAG    27777        A   A__
                                GGGCTGGC GGG   CGG
                                |||||||| |||   |||
                                CCCGACCG CCC   GTC
                                    A   CAA
GAM2961  LY64     3'  GGGCCGGCAGTCCCTGCCCAG  24568         GGACGGCA
                                GGGCTGGCAG       CCCAG
                                ||||||||||       |||||
                                CCCGGCCGTC       GGGTC
                                     AGGGAC__
GAM2961  MMP11    3'  GGCCTGGCAGGGGTCAGC    25538    G       A_
                                GG CTGGCAGGG  CGGC
                                || |||||||||  ||||
                                CC GACCGTCCC  GTCG
                                  G       CA
GAM2961  NAV2     5'  GGACTGGCCACGGCGCTCAGC  41148        AGGG    ACC
                                GGGCTGGC   ACGGC   CAGC
                                ||||||||   |||||  ||||
                                CCTGACCG   TGCCG   GTCG
                                    G___    CGA
GAM2961  NEU1     3'  GGGTGGTGGGGCCACACTTAGC 7730     C   CA   ACG   CC
                                GGG TGG  GGG   GCAC  AGC
                                ||| |||  |||   ||||  |||
                                CCC ACC  CCC   TGTG  TCG
                                  _   AC   GG_    AA
GAM2961  NFATC2   5'  GGGCTGGCGGAGGCGGCTCGAG 29589        A   A    ACCC
              C                  GGGCTGGC GGG CGGC    AGC
                                |||||||| ||| ||||    |||
                                CCCGACCG CTC GCCG    TCG
                                    C   C    AGC_
GAM2961  PDCD2    5'  GGGCTGGCGTGGGGCGCAG   15142        AG  AC   ACC
                                GGGCTGGC  GG  GGC   CAG
                                ||||||||  ||  |||   |||
```

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                                CCCGACCG  CC  CCG   GTC
                                    CA  __   C__
GAM2961  PLA2G4B  3'  GGGTGGCAGGGGCCCCG    22963    C      ACG  A   A
                                GGG TGGCAGGG   GC CCC G
                                ||| ||||||||   || ||| |
                                CCC ACCGTCCC   CG GGG C
                                  _      ___  _   C
GAM2961  PML      3'  GGGCTGGCGAGGACTGTGGC   37734       AG   ___
                                GGGCTGGC  GGAC   GGC
                                ||||||||  ||||   |||
                                CCCGACCG  CCTG   CCG
                                    CT    ACA
GAM2961  RCN2     5'  AGGCTGGCGGGGGCCCGGGC   16211       A   AC   A  CA
                                GGGCTGGC GGG  GGC CC  GC
                                |||||||| |||  ||| ||  ||
                                TCCGACCG CCC  CCG GG  CG
                                    _  __  _ CC
GAM2961  SH3BP2   3'  GGGTGGCAGGGAGCCTGGC   16637    C      C___
                                GGG TGGCAGGGA   GGC
                                ||| |||||||||   |||
                                CCC ACCGTCCCT   CCG
                                  _       CGGA
GAM2961  SLC39A4  5'  GGGCCGGCAGGGGGAGTTGGC  39296         AC____
                                GGGCTGGCAGGG     GGC
                                ||||||||||||     |||
                                CCCGGCCGTCCC     CCG
                                       CCTCAA
GAM2961  SLC8A2   5'  GGGCTGGCAGTGGTGGGC    42417         _ AC
                                GGGCTGGCAG GG  GGC
                                |||||||||| ||  |||
                                CCCGACCGTC CC  CCG
                                      A  AC
GAM2961  SNL      3'  GGGTTAGCAGGGAGGGTTGGC  16947    C      C____
                                GGG TGGCAGGGA    GGC
                                ||| |||||||||    |||
                                CCC ATCGTCCCT    CCG
                                  A       CCCAA
GAM2961  TRPV3    3'  GGGCTGACGGGGGAAGCTGGC  45441       A_   C___
                                GGGCTGGC  GGGA   GGC
                                ||||||||  ||||   |||
                                CCCGACTG  CCCT   CCG
                                    CC    TCGA
GAM2962  MTCP1    5'  AGGGTTCTATGGCAATT     30572         TATCAT
                                AGGGTTCTAT     CAATT
                                ||||||||||     |||||
                                TCCCAAGATA     GTTAA
                                      CC____
GAM2962  MYBL1    5'  TAGAGTCCAATCATCAGTTCC  41981       TATT     A
                                TAGGGTTC   ATCATCA TTCC
                                ||||||||   ||||||| ||||
```

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                                ATCTCAGG   TAGTAGT AAGG
                                    T___     C
GAM2962  TIAM1    3'  GGATTCTGATCAATTC      17527        ATTATC
                                GGGTTCT     ATCAATTC
                                |||||||     ||||||||
                                CCTAAGA     TAGTTAAG
                                   C_____
GAM2963  CHRNB2   3'  TTGGCAGGAATCGCTGACCACT 8863      AA  TTGCG       C
           GT                    TTG  AG    GCTGACCAC GT
                                |||  ||    ||||||||| ||
                                AAC  TC    CGACTGGTG CA
                                  CG  CTTAG       A
GAM2963  TFDP1    3'  GAAAGTTGCATTCTGCTG    28277          ____
                                GAAAGTTGCG    GCTG
                                ||||||||||    ||||
                                CTTTCAACGT    CGAC
                                     AAGA
GAM2964  OPCML    3'  CAAATGAAACTTACGTTTT    14948        TTT  _
                                CAAATGGA   ACT ACGTTTT
                                ||||||||   ||| |||||||
                                GTTTACTT   TGA TGCAAAA
                                    ___  A
GAM2965  ACCN1    3'  TAGCAGAGAGTCCCATGG    9915         TAC   G
                                TAGCAGAG   GTTC CATGG
                                ||||||||   |||| |||||
                                ATCGTCTC   CAGG GTACC
                                    T__   _
GAM2965  B2M      3'  AGCAGAGTATGTAAATTGG    19729        C  TCGCA
                                AGCAGAGTA GT    TGG
                                |||||||||  ||    |||
                                TCGTCTCAT CA    ACC
                                     A  TTTA_
GAM2965  CD5      3'  CAGCAGAGTGTGAGCTGG    30543        AC  TC  A
                                TAGCAGAGT  GT  GC TGG
                                |||||||||  ||  || |||
                                GTCGTCTCA  CA  CG ACC
                                    __  CT  _
GAM2965  CDH15    3'  TAGGGAGGTGACCCGCATGG   22338     CA   TAC TT
                                TAG  GAG   G  CGCATGG
                                |||  |||   |  |||||||
                                ATC  CTC   T  GCGTACC
                                  C_   CAC GG
GAM2965  MTMR3    3'  CAGCAGAGTCAAGCATGG    34392         A  TTC
                                TAGCAGAGT CG   GCATGG
                                |||||||||  ||   ||||||
                                GTCGTCTCA GT   CGTACC
                                     _  T__
GAM2965  RAD51L1  3'  TAGCAGAGAACGATG       39452        T   TTCGC
                                TAGCAGAG ACG    ATG
                                ||||||||  |||    |||
```

```
                                ATCGTCTC TGC    TAC
                                    T  _____
GAM2965 STARD5   3' GCCAGAGTGCATCGCATGG   36128   _   A  T
                                GC AGAGT CGT CGCATGG
                                || ||||| ||| |||||||
                                CG TCTCA GTA GCGTACC
                                 G   C  _
GAM2966 AVP     5' TGTCATGGGCCGCGG      7943        ACCA
                                TGTCATGG   TCGTGG
                                ||||||||   ||||||
                                ACAGTACC   GGCGCC
                                    C___
GAM2966 B3GALT5  5' TGTATGGACCACTTGC     37686    C      CGTG
                                TGT ATGGACCAT   GC
                                ||| |||||||||   ||
                                ACA TACCTGGTG   CG
                                  _      AA__
GAM2966 DUSP4    5' TGTCATGGGCATTGTATTAC  38430      AC  C  GC
                                TGTCATGG  CAT GTG  TAC
                                ||||||||  ||| |||  |||
                                ACAGTACC  GTA CAT  ATG
                                    C_  A  A_
GAM2966 DYRK1A   3' TGTCATGGAGTGGTGACT   39009       CCATC
                                TGTCATGGA    GTGGCT
                                |||||||||    ||||||
                                ACAGTACCT    CACTGA
                                     CAC__
GAM2966 HNRPDL   3' TGTATGGACCAATACTCTAC  24182    C     TCGTGG
                                TGT ATGGACCA     CTAC
                                ||| ||||||||     ||||
                                ACA TACCTGGT     GATG
                                  _      TATGA_
GAM2966 IL5RA    5' TGTCTATGCTCGTGGCT    8164     _  GACCA
                                TGTC ATG    TCGTGGCT
                                |||| |||    ||||||||
                                ACAG TAC    AGCACCGA
                                  A  G____
GAM2966 MEOX1    3' TGTCATGGGTTCATTCT    30406      ACCA   GG
                                TGTCATGG   TCGT  CT
                                ||||||||   ||||  ||
                                ACAGTACC   AGTA  GA
                                    CA__   A_
GAM2966 OPHN1    3' TGTCATGGAATTGTGCATAC  14976       CCATCG  _  _
                                TGTCATGGA     TG GC TAC
                                |||||||||     || || |||
                                ACAGTACCT     AC CG ATG
                                     TA____  A  T
GAM2966 PML     3' TGCCATGGGCTGCCAGGGCT  37740       ACCA   T
                                TGTCATGG   TCG GGCT
                                ||||||||   ||| ||||
```

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                                ACGGTACC   GGT CCGA
                                    CGAC   C
GAM2966 PROX1    3' TGTCATGGGTTTTCCTCAGC  15724       ACCA  G_
                                TGTCATGG   TC  TGGC
                                ||||||||   ||  ||||
                                ACAGTACC   AG  GTCG
                                    CAAA  GA
GAM2967 CRYZL1   3' TATCAAGAGTAGTGTGACTTTT 23046      TAC   TCT
           GC                    TATCAAG   AGT   ACTTTTGC
                                |||||||   |||   ||||||||
                                ATAGTTC   TCA   TGAAAACG
                                    TCA   CAC
GAM2967 DLX4     3' GTCCACTTCTGCTTTTGC    39619    A  G   A
                                GT CA TTCT CTTTTGC
                                || || |||| |||||||
                                CA GT AAGA GAAAACG
                                 G  G   C
GAM2967 EHD3     3' CATTGAGTACAGTGGGGATTTG 31110     CA      TCTACT
           C                     TAT  AGTACAGT     TTTGC
                                |||  ||||||||     |||||
                                GTA  TCATGTCA     AAACG
                                  AC       CCCCT_
GAM2967 HIP2     3' CATCAAGTATTTACTATTTTTG 23766        CAGTT   C
           C                     TATCAAGTA    CTA TTTTGC
                                |||||||||    ||| ||||||
                                GTAGTTCAT    GAT AAAACG
                                     AAAT_   A
GAM2967 MNAT1    3' AAGTCTGCTTTACTTTTGC    14601     ACA   C
                                AAGT   GTT TACTTTTGC
                                ||||   ||| |||||||||
                                TTCA   CGA ATGAAAACG
                                  GA_   A
GAM2967 PIGN     3' TACCAAGCACTTTCTACTTTTG 29549         AG
                                TATCAAGTAC  TTCTACTTTTG
                                ||||||||||  ||||||||||
                                ATGGTTCGTG  AAGATGAAAAC
                                     A_
GAM2967 PTGS2    3' GTCATTGCTACTTTTGC     9691     A  GTT
                                GT CA   CTACTTTTGC
                                || ||   ||||||||||
                                CA GT   GATGAAAACG
                                 _  AAC
GAM2968 KIR2DL3  3' TGAGGGAAGGTGGAACA     30953         CG  A
                                TGAGGGAAGG  TG GAGCG
                                ||||||||||  || |||||
                                ACTCCCTTCC  AC CTTGT
                                     __  _
GAM2968 KIR2DL5  3' TGAGGGAAGGTGGAACA     33924         CG  A
                                TGAGGGAAGG  TG GAGCG
                                ||||||||||  || |||||
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                                ACTCCCTTCC  AC CTTGT
                                    __  _
GAM2968 KIR3DL2  3'  TGAGGGAAGGTGGAACA     27555          CG  A
                                TGAGGGAAGG  TG GAGCG
                                ||||||||||  || |||||
                                ACTCCCTTCC  AC CTTGT
                                    __  _
GAM2968 LENG4    5'  TGGGGGAAGGCTGACTGCA   35895    A      G   GA
                                TG GGGAAGGC TGA  GCG
                                || ||||||||| |||  |||
                                AC CCCTTCCG ACT  CGT
                                 C       _  GA
GAM2968 MYOD1    3'  TGGGGGAGGGCGCGAGAA    42133    A   A
                                TG GGGA GGCGTGAGAG
                                || |||| ||||||||||
                                AC CCCT CCGCGCTCTT
                                 C   C
GAM2968 NUP98    5'  TGGGGAAGGGGAAGTGTCA   32237    A     CGTGA   C
                                TG GGGAAGG    GAG GTCA
                                || |||||||    ||| ||||
                                AC CCCTTCC    TTC CAGT
                                 _     CC___   A
GAM2969 PTMA     3'  TATAAAATGTAAATAAAAAA   15876        T
                                TATAAAAT GTAAATAAAAAA
                                |||||||| ||||||||||||
                                ATATTTTA CATTTATTTTTT
                                    _
GAM2970 CD4      3'  CTTGACTGGCTTGGCTGTGTGA 8327         A   AAAACT_
           T                     CTTGACTG CTT      TGAT
                                |||||||| |||      ||||
                                GAACTGAC GAA      ACTA
                                    C   CCGACAC
GAM2970 MAD2L1   3'  CACTTTCACTTAAAACTTGAT  14310      GACTG
                                TACTT    ACTTAAAACTTGAT
                                |||||    ||||||||||||||
                                GTGAA    TGAATTTTGAACTA
                                   AG___
GAM2970 MTR      3'  CTTGACAATAAAACTTG     7015        TGACT
                                CTTGAC    TAAAACTTG
                                ||||||    |||||||||
                                GAACTG    ATTTTGAAC
                                   TT___
GAM2971 GATA1    3'  TATTTTACAAAAGCTTTGAAG  13079      CA_       A
                                TATTT   AAAAGCTTT GAAG
                                |||||   ||||||||| ||||
                                ATAAA   TTTTCGAAA CTTC
                                   ATG       _
GAM2971 IFI16    3'  TTTCAAATTATAGAAGTTG   43412        AAGCTT
                                TTTCAAA     TAGAAGTTG
                                |||||||     |||||||||
```

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                                AAAGTTT     ATCTTCAAC
                                   AAT___
GAM2971 LBR     3'  TTTCAATGTAGTTTTAGAAGTT 40434       AA_  C
             G                   TTTCAA   AG TTTAGAAGTTG
                                 ||||||   || ||||||||||
                                 AAAGTT   TC AAATCTTCAAC
                                    ACA  A
GAM2972 DUSP4   5'  CGAGTCATTTTCCCTT      38416        GAAATG
                                 TGAGTCAT     TCCCTT
                                 ||||||||     ||||||
                                 GCTCAGTA     AGGGAA
                                    AA____
GAM2972 GAK     3'  ATGAATCAGCTGTTCCTTC    23530        TGAAA   C
                                 ATGAGTCA     TGT CCTTC
                                 ||||||||     ||| |||||
                                 TACTTAGT     ACA GGAAG
                                    CG___   A
GAM2972 GBA     3'  TGAGCTGACTCTGTCCCTT    44069      CA   AA_
                                 TGAGT  TGA   TGTCCCTT
                                 |||||  |||   ||||||||
                                 ACTCG  ACT   ACAGGGAA
                                   __   GAG
GAM2972 GPR17   3'  TGGCCTGTGTCTCTTCAA    23623    A   A  AAA    C
                                 TG GTC TG   TGTC CTTCAA
                                 || ||| ||   |||| ||||||
                                 AC CGG AC   ACAG GAAGTT
                                  _   _ ___    A
GAM2972 HAL     5'  TGGTCAGCTGCTGTCCCTT    13335    A    TGAAA
                                 TG GTCA     TGTCCCTT
                                 || ||||     ||||||||
                                 AC CAGT     ACAGGGAA
                                  _    CGACG
GAM2972 IHPK3   3'  ATGAGCTCATGAACTCACTCTT 38368       _      ATGTCC
             CAA                   ATGAG TCATGAA     CTTCAA
                                 |||||| |||||||      ||||||
                                 TACTC AGTACTT     GAAGTT
                                    G      GAGTGA
GAM2972 MSR1    3'  GAGTTATTGTCCCTT       14659      C  GAAA
                                 GAGT AT    TGTCCCTT
                                 |||| ||    ||||||||
                                 CTCA TA    ACAGGGAA
                                   A  ____
GAM2972 PIWIL1  3'  GAGTCTTAAAATGTTTCTT    43753       A       CC
                                 GAGTC TGAAATGT  CTT
                                 ||||| ||||||||  |||
                                 CTCAG ATTTTACA  GAA
                                    A       AA
GAM2972 RNF18   3'  ATGATCATGAATAATGATTTTT 33775      G      __   TCCC
             CAA                   ATGA TCATGAA  ATG    TTCAA
                                 |||| |||||||  |||    |||||
```

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                                TACT AGTACTT  TAC   AAGTT
                                  _     AT   TAAA
GAM2973 ATP11A   3' GTGTGTGCATGTGTGTAT   44180     TAC  _
                                GTGT   TGT TGTGTGTAT
                                ||||   ||| |||||||||
                                CACA   ACG ACACACATA
                                  C__   T
GAM2973 CACNA2D2 3' GTGTGTGTGTGTGTGTGT   25723     TAC  _
                                GTGT   TGT TGTGTGT
                                ||||   ||| |||||||
                                CACA   ACA ACACACA
                                  CAC   C
GAM2973 CCND1    3' GTGTGTGTGTGTGTGTGTATC 38220     TAC  _
                                GTGT   TGT TGTGTGTATC
                                ||||   ||| ||||||||||
                                CACA   ACA ACACACATAG
                                  CAC   C
GAM2973 CDKN1B   3' AGTGTTATTGTGTTGT     19794      TAC      _
                                AGTGT   TGTTGTGT GT
                                |||||   |||||||| ||
                                TCACA   ATAACACA CA
                                  ___       A
GAM2973 CSF2RB   3' TACGTGTGTGTGTGTGTGT   7570     A   TAC  _
                                TAC GTGT   TGT TGTGTGT
                                ||| ||||   ||| |||||||
                                ATG CACA   ACA ACACACA
                                  _   C__   C
GAM2973 DISC1    3' TACACTGTTACTGAGTAT    33047     G      TT
                                TACA TGTTACTG  GTGT
                                |||| ||||||||  ||||
                                ATGT ACAATGAC  CATA
                                  G       T_
GAM2973 FGFRL1   3' GTGTGTCTGTGTGTGTGT    34915     TA   _
                                GTGT  CTGT TGTGTGT
                                ||||  |||| |||||||
                                CACA  GACA ACACACA
                                  CA   C
GAM2973 FMR2     3' AGTGTGTGTGTGTGTGTAT   12951      TAC  _
                                AGTGT   TGT TGTGTGTAT
                                |||||   ||| |||||||||
                                TCACA   ACA ACACACATA
                                   C__   C
GAM2973 GAGED2   5' GTGGTTCTGTGTTTGTGTGT  39418    TTA   ___
                                GTG   CTGT   TGTGTGT
                                |||   ||||   |||||||
                                CAC   GACA   ACACACA
                                  CAA   CAA
GAM2973 GLP1R    3' CAGTGCTGCTGTGTGT     13138      TTA
                                CAGTG   CTGTTGTGTGT
                                |||||   ||||||||||
```

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                                GTCAC   GACGACACACA
                                  ___
GAM2973  LAMP2    3'  ATGTCTGTGTGTGTGTAT    30384      TA   _
                                GTGT  CTGT TGTGTGTAT
                                ||||  |||| |||||||||
                                TACA  GACA ACACACATA
                                  __    C
GAM2973  MBNL     3'  TACAGTGTGCTGTTTGGT    34319        TA    G  T
                                TACAGTGT  CTGTT TG GT
                                ||||||||  ||||| || ||
                                ATGTCACA  GACAA AC CA
                                    C_    _ _
GAM2973  MGMT     3'  CAGTGTTACACGTGTGTGT   14487          _  T
                                CAGTGTTAC TGT GTGTGT
                                ||||||||| ||| ||||||
                                GTCACAATG GCA CACACA
                                     T  _
GAM2973  NCAM1    3'  GTGTGTGTGCGTGTGTGT    8318       TAC  _
                                GTGT   TGT TGTGTGT
                                ||||   ||| |||||||
                                CACA   ACG ACACACA
                                  CAC   C
GAM2973  NR4A2    3'  GTGTATGTGTGTGTGTGT    26165      TAC  _
                                GTGT   TGT TGTGTGT
                                ||||   ||| |||||||
                                CACA   ACA ACACACA
                                  TAC   C
GAM2973  PLAG1    3'  GTGTGTGTGTGTGTGTAT    15354      TAC  _
                                GTGT   TGT TGTGTGTAT
                                ||||   ||| |||||||||
                                CACA   ACA ACACACATA
                                  C__   C
GAM2973  TIMP3    3'  AGTGTATGGTGTGTGTAT    7443       TAC  T
                                AGTGT   TG TGTGTGTAT
                                |||||   || |||||||||
                                TCACA   AC ACACACATA
                                  T__  C
GAM2973  XYLB     3'  TACAGTTTACTGTTTCATGGT  23024       G      __  T
                                TACAGT TTACTGTT  GTG GT
                                |||||| ||||||||  ||| ||
                                ATGTCA AATGACAA  TAC CA
                                   _       AG  _
GAM2974  AHCY     3'  AGCTGTTCCAAGACCACT    8660      CG   G  C
                                AGC  GTTC AGG GCCACT
                                |||  |||| ||| ||||||
                                TCG  CAAG TTC TGGTGA
                                 A_   G  _
GAM2974  B3GAT1   3'  AGCCGGATCACCACTA      33000       TTCGAGG
                                AGCCGG      CGCCACTA
                                ||||||      ||||||||
```

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                                TCGGCC      GTGGTGAT
                                   TA_____
GAM2975 AQP6     5' GGGGGTGGAATGAGGGGTGT  11643    AATGA      A_
                                GG    GGAATGAG  GTGT
                                ||    ||||||||  ||||
                                CC    CCTTACTC  CACA
                                 CCCA_       CC
GAM2975 CIT      3' TGGGGGGTGGGGAAGGAAAGC  43061    A  AA  A   T
                                TG GG  TG GGAA GAGAGT
                                || ||  || |||| ||||||
                                AC CC  AC CCTT CTTTCG
                                 C  CC  C    C
GAM2975 RASGRP2  5' TGGGGAGCGAGGAATGAAA   25177    A   A
                                TG GGA TGAGGAATGAGA
                                || ||| ||||||||||||
                                AC CCT GCTCCTTACTTT
                                 C   C
GAM2975 SLC6A1   3' AGGTCGGGGGGGTGAGAGTGTC  40485     AA  A  AA
                                AGG  TG GG  TGAGAGTGTC
                                |||  || ||  ||||||||||
                                TCC  GC CC  ACTCTCACAG
                                  A_  C  CC
GAM2975 SLC6A6   3' TGGGGAGTGGGGAGATGAG    16794    A   A  A  _
                                TG GGA TG GGA ATGAG
                                || ||| || ||| |||||
                                AC CCT AC CCT TACTC
                                 C   C  C   C
GAM2975 SORCS3   3' GGGGGAAGCGGAGAGTGT    31424    AAT   AAT
                                GG   GAGG   GAGAGTGT
                                ||   ||||   ||||||||
                                CC   CTTC   CTCTCACA
                                 CC_    GC_
GAM2976 ACLY     3' TAAAAAAAAAAAAAGAGAGACA 42155           AAA
             TT                   TAAAAAAAGAAAAA   AGGCATT
                                |||||||||||||   |||||||
                                ATTTTTTTTTTTTTT   TCTGTAA
                                        CTC
GAM2976 AK3      3' AAAAAAAGAAAAAAAAAA    30177
                                AAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                TTTTTTTCTTTTTTTTTT

GAM2976 BCL11A   3' AAAAAGAAAAAAAACAGG    39702           _
                                AAAAAGAAAAAAAA AGG
                                |||||||||||||| |||
                                TTTTTCTTTTTTTT TCC
                                        G
GAM2976 CANX     3' AAAAAAGAACCAAGAAAAGGC  44657         AAA__
                                AAAAAAGAA    AAAAGGC
                                |||||||||    |||||||
```

```
                                TTTTTTTCTT    TTTTCCG
                                      GGTTC
GAM2976 CARPX    3' AAACAAGAAAAGAAAGGCATT 33562    A      AA
                                AAA AAGAAAA  AAAGGCATT
                                ||| |||||||  |||||||||
                                TTT TTCTTTT  TTTCCGTAA
                                  G      C_
GAM2976 CENTD1   3' TAAAAAAAGAAAAAAAAA    40144
                                TAAAAAAAGAAAAAAAAA
                                ||||||||||||||||||
                                ATTTTTTTCTTTTTTTTT

GAM2976 CNP      3' TAAAAAAAAAAAAAAAAAAA  37561
                                TAAAAAAAGAAAAAAAAGG
                                ||||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTT

GAM2976 CTNNB1   3' TAAAAAAAAAAAAAAAAAAA  12518
                                TAAAAAAAGAAAAAAAAGG
                                ||||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTT

GAM2976 DAPK1    3' TAAAAAAAGAAAAAAACAAACA 22361              A
                                TAAAAAAAGAAAAAAA AGGCA
                                |||||||||||||| |||||
                                ATTTTTTTCTTTTTTT TTTGT
                                       G
GAM2976 DPYSL2   3' AAAAAGAAAAGAAAAAGGCA  10740          _
                                AAAAAGAAAA AAAAAGGCA
                                |||||||||| |||||||||
                                TTTTTCTTTT TTTTTCCGT
                                      C
GAM2976 ERBB2IP  5' AAAAAAAGAAAAAAAAAA    33094
                                AAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                TTTTTTTCTTTTTTTTTT

GAM2976 EWSR1    3' AAAAAAAAAAAAAAAACAT   23482
                                AAAAGAAAAAAAAAGGCAT
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTGTA

GAM2976 G6PC     3' CAAAAAAAGAAAAAAAAAG   6659
                                TAAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||||
                                GTTTTTTTCTTTTTTTTC

GAM2976 GFRA1    5' AAAAAAAGAAAAAAAAAA    23561
                                AAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
```

```
                                TTTTTTTCTTTTTTTTTT

GAM2976  GLS      3'  AAAAAGAAAAAAAAAGGAATT  31371              C
                                AAAAAGAAAAAAAAAGG ATT
                                |||||||||||||||| |||
                                TTTTTCTTTTTTTTCC TAA
                                      T
GAM2976  GLUD1    3'  AAAAAAAAAAAAAAAAGC    23585
                                AAAAAGAAAAAAAAAGGC
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTCG

GAM2976  GNAO1    3'  TGAAAAAAAAAAAAAAGG    44943   A
                                A AAAAGAAAAAAAAAGG
                                | ||||||||||||||||
                                A TTTTTTTTTTTTTCC
                                 C
GAM2976  HIS1     5'  AAAAAGAAAAAAAAAACA    26987             G
                                AAAAAGAAAAAAAAAG CA
                                |||||||||||||||| ||
                                TTTTTCTTTTTTTTTT GT
                                                _
GAM2976  IFNGR2   3'  AAGAAAAAAAAAAAAAAGC   24378   A
                                AA AAAGAAAAAAAAAGGC
                                || ||||||||||||||||
                                TT TTTTTTTTTTTTTCG
                                 C
GAM2976  JAM3     3'  AAAAAAAAAAAATAGCAT    37255          A
                                AAAGAAAAAAAA GGCAT
                                |||||||||||| |||||
                                TTTTTTTTTTTT TCGTA
                                       A
GAM2976  JRKL     3'  AAAAAAAAAAAAAAAAAAC   19087
                                AAAAAAGAAAAAAAAAGGC
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTTTG

GAM2976  LY95     5'  TAAAAAAAAAAAAAAAAAG   22100
                                TAAAAAAAGAAAAAAAAGG
                                |||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTC

GAM2976  MAK      3'  AAAAAAAAAAAAAAAAAGC   25376
                                AAAAAAGAAAAAAAAAGGC
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTTCG

GAM2976  MTP      3'  CAAAAAAAGAGAAAAAAATGG  7010          A     _
                                TAAAAAAAGA AAAAAAA GG
                                |||||||||| ||||||| ||
```

```
                                GTTTTTTTCT TTTTTTT CC
                                      C      A
GAM2976  NFRKB    5'  AAAAGAAAAAGAAGGCAT    26090          AA
                                AAAAGAAAAA  AAGGCAT
                                ||||||||||  |||||||
                                TTTTCTTTTT  TTCCGTA
                                      C_
GAM2976  NPEPPS   3'  AAAAAAAGAAAAAAAAGG    26713              A
                                AAAAAAAGAAAAAAAA GG
                                |||||||||||||||| ||
                                TTTTTTTCTTTTTTTT CC
                                                 _
GAM2976  NRXN3    5'  TAAAGAAAGAAAAAAAAAAG   39943      A
                                TAAA AAAGAAAAAAAAAGG
                                |||| ||||||||||||||
                                ATTT TTTCTTTTTTTTTTC
                                   C
GAM2976  OPHN1    3'  AAAAAAAGAAAAAAAAAA     14958
                                AAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                TTTTTTTCTTTTTTTTTT

GAM2976  OPHN1    3'  AAAAAAAGAAAAAAAAAGG    14959
                                AAAAAAAGAAAAAAAAAGG
                                |||||||||||||||||||
                                TTTTTTTCTTTTTTTTTCC

GAM2976  OSR1     3'  CAAAAAAAGAAAAAGAAAAGC  23033              A
                                TAAAAAAAGAAAAA AAAGGC
                                |||||||||||||| ||||||
                                GTTTTTTTCTTTTT TTTTCG
                                         C
GAM2976  PCDH15   3'  TAAAAACGAGAAAAAAAACTGC 37507        A_         AG
              ATT                  TAAAAA  AGAAAAAAAA  GCATT
                                ||||||  ||||||||||  |||||
                                ATTTTT  TCTTTTTTTT  CGTAA
                                   GC         GA
GAM2976  PIAS1    3'  TAAAAAAAGGAAAAAAAACAC  32079          A       G
                                TAAAAAAAG AAAAAAAA GC
                                |||||||| |||||||| ||
                                ATTTTTTTC TTTTTTTT TG
                                      C       G
GAM2976  PIGR     3'  AAAAAAAGAAAAAGAAAAAC   43694             A
                                AAAAAAAGAAAAA AAAGGC
                                |||||||||||| ||||||
                                TTTTTTTCTTTTT TTTTTG
                                         C
GAM2976  PKP2     3'  AAAAAAGTCCAGGAAAGGCATT 21315         AAAAAA
                                AAAAAAG     AAAGGCATT
                                |||||||     |||||||||
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                                TTTTTTC     TTTCCGTAA
                                    AGGTCC
GAM2976  PKP4     3'  AAAAAGGAAAAAAAAACACACT 18847      A        G
                                AAAAA GAAAAAAAAA GCATT
                                ||||| |||||||||| |||||
                                TTTTT CTTTTTTTTT TGTGA
                                   C         G
GAM2976  PPARGC1  3'  AAAAAAGAAAAAAATCCACATT 29945             AAG
                                AAAAAAGAAAAAAA   GCATT
                                ||||||||||||||   |||||
                                TTTTTTCTTTTTTT   TGTAA
                                        AGG
GAM2976  PRKR     5'  AAAAGAGAAAAAAGAAGGC   15676      A       A
                                AAAA AGAAAAAA AAGGC
                                |||| |||||||| |||||
                                TTTT TCTTTTTT TTCCG
                                  C       C
GAM2976  PTMA     3'  CAAAAAAGGAAAAAAAAAG   15864        A
                                TAAAAAA GAAAAAAAAAG
                                ||||||| ||||||||||
                                GTTTTTT CTTTTTTTTTC
                                    C
GAM2976  PTP4A2   5'  AAAAAAAAAAAAAAGCCA    38618             G
                                AAAAGAAAAAAAAAG CA
                                |||||||||||||| ||
                                TTTTTTTTTTTTTTC GT
                                        G
GAM2976  RAD21    3'  TGAAGAAGGAAAAAGGCA    26531   A    AA
                                A AAGAA  AAAAAGGCA
                                | |||||  |||||||||
                                A TTCTT  TTTTTCCGT
                                 C    CC
GAM2976  SCAMP1   3'  AAAAAAAGAAAAGAAAAAGA  38066          _
                                AAAAAAAGAAAA AAAAAGG
                                |||||||||||| |||||||
                                TTTTTTTCTTTT TTTTTCT
                                        C
GAM2976  SDC1     3'  AAAAAAAAAAAAAAAAAAG   16495
                                AAAAAAAGAAAAAAAAAGG
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTTTTC

GAM2976  SDC4     3'  TAAAAAAAAAAAAAAAAAA   16527
                                TAAAAAAAGAAAAAAAAAGG
                                |||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTT

GAM2976  SEPP1    3'  AAAAAGAAAAAAAAAAGACAT  23998
                                AAAAAGAAAAAAAAAGGCAT
                                |||||||||||||||||||
```

```
                                TTTTTCTTTTTTTTTCTGTA

GAM2976  SGCB     3'  AAAAAAAAAAAAAAAGGAATT  6926                C
                                AAAAAGAAAAAAAAAGG ATT
                                |||||||||||||||| |||
                                TTTTTTTTTTTTTTCC TAA
                                          T
GAM2976  SLC15A1   3'  AAAAAGAAAAAAGAAAATAGCA 22899          _  __
              TT                  AAAAAGAAAAAA AAA  GGCATT
                                |||||||||||| |||  ||||||
                                TTTTTCTTTTTT TTT  TCGTAA
                                       C   TA
GAM2976  SLC19A1   3'  AAAAAAAAAAAAAGCATC    16841
                                AAGAAAAAAAAAGGCATT
                                ||||||||||||||||||
                                TTTTTTTTTTTTTCGTAG

GAM2976  SOX12     3'  TAAAAAAAAAAAAAAAAAAA   28056
                                TAAAAAAAGAAAAAAAAAGG
                                ||||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTTT

GAM2976  SOX9      3'  AAAAAAGGGATGGACAAAAAGG 7369         AAAA____
              CATT                  AAAAAAG       AAAAAGGCATT
                                |||||||       ||||||||||
                                TTTTTTC       TTTTTCCGTAA
                                     CCTACCTG
GAM2976  SRC       3'  AAAAAAAAAAAAAGGACA     24028             _
                                AAAGAAAAAAAAAGG CA
                                |||||||||||||| ||
                                TTTTTTTTTTTTTCC GT
                                          T
GAM2976  SVIL      3'  AAAAAAAAAAAAAAAGGCATT  34723
                                AAAAAGAAAAAAAAAGGCATT
                                ||||||||||||||||||||
                                TTTTTTTTTTTTTTTCCGTAA

GAM2976  TAPBP    3'  AAAGAAAAAAAAAAAAGGCATT 17296     A
                                AAA AAGAAAAAAAAAGGCATT
                                ||| ||||||||||||||||||
                                TTT TTTTTTTTTTTTCCGTAA
                                  C
GAM2976  TBX3      5'  AAAAAAGAAAAGGAGGC     32434          AAAA
                                AAAAAAGAAAA    AGGC
                                ||||||||||    ||||
                                TTTTTTCTTTT    TCCG
                                       CC__
GAM2976  TGFBR2    5'  TGAAAAAAAAAAAAAAGCACT  17485    A
                                A AAAGAAAAAAAAAGGCATT
                                | ||||||||||||||||||
```

```
                                A TTTTTTTTTTTTTTCGTGA
                                 C
GAM2976  TNFRSF11A 3'  CAAAAAAAGAAAAAAAAAA   19269
                                TAAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                GTTTTTTTCTTTTTTTTTT

GAM2976  TNFSF9   3'  AAAGAAAGAAAGAAAAAAGC  19189    A      A
                                AAA AAAGAAA AAAAAGGC
                                ||| ||||||| ||||||||
                                TTT TTTCTTT TTTTTTCG
                                  C      C
GAM2976  TOMM22   3'  AAAAAAAAAAAAAAAAACA   33671
                                AAAAAGAAAAAAAAAGGCA
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTTTGT

GAM2976  TPI1     5'  TAAAAAAAAAAAAAAAAAAC  7477
                                TAAAAAAAGAAAAAAAAAGGC
                                |||||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTTG

GAM2976  UBL3     3'  AAAAGAAAAAGTGGCAT     28260          AAAA
                                AAAAGAAAAA   GGCAT
                                ||||||||||   |||||
                                TTTTCTTTTT   CCGTA
                                      CA__
GAM2976  XKRY     5'  AAAGAAAGAAAAAAAAAGA   41042     A
                                AAA AAAGAAAAAAAAAGG
                                ||| ||||||||||||||
                                TTT TTTCTTTTTTTTTCT
                                  C
GAM2976  ZHX1     3'  AAAAGAAAAAAAAAAAGC    28515            _
                                AAAAGAAAAAAAAAG GC
                                |||||||||||||| ||
                                TTTTCTTTTTTTTTT CG
                                          T
GAM2976  ZIC1     5'  AAAAAAAAAAAAAAAAAAG   18221
                                AAAAAAAGAAAAAAAAAGG
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTTTTC

GAM2976  ZNF74    5'  AAAAAAAAAAAAAAAAGA    18295
                                AAAAAAGAAAAAAAAAGG
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTTCT

GAM2976  ACLY     3'  TAAAAAAAAAAAAAGAGAGACA 42155            AAA
              TT                  TAAAAAAAGAAAAA   AGGCATT
                                  ||||||||||||||   |||||||
```

ATTTTTTTTTTTTT TCTGTAA
CTC
GAM2976 AK3 3' AAAAAAAGAAAAAAAAAA 30177
AAAAAAAGAAAAAAAAAG
TTTTTTTCTTTTTTTTT
GAM2976 BCL11A 3' AAAAAGAAAAAAAACAGG 39702
AAAAAGAAAAAAAA AGG
TTTTTCTTTTTTTT TCC
G
GAM2976 CANX 3' AAAAAAGAACCAAGAAAAGGC 44657 AAA
AAAAAAGAA AAAAGGC
TTTTTTCTT TTTTCCG
GGTTC
GAM2976 CARPX 3' AAACAAGAAAAGAAAGGCATT 33562 A AA
AAA AAGAAAA AAAGGCATT
TTT TTCTTTT TTTCCGTAA
G C_
GAM2976 CENTD1 3' TAAAAAAAGAAAAAAAAA 40144
TAAAAAAAGAAAAAAAAA
ATTTTTTTCTTTTTTTTT
GAM2976 CNP 3' TAAAAAAAAAAAAAAAAAAA 37561
TAAAAAAAGAAAAAAAAGG
ATTTTTTTTTTTTTTTTTT
GAM2976 CTNNB1 3' TAAAAAAAAAAAAAAAAAA 12518
TAAAAAAAGAAAAAAAAGG
ATTTTTTTTTTTTTTTTTT
GAM2976 DAPK1 3' TAAAAAAAGAAAAAAACAAACA 22361 A
TAAAAAAAGAAAAAAA AGGCA
ATTTTTTTCTTTTTTT TTTGT
G
GAM2976 DPYSL2 3' AAAAAGAAAAGAAAAAGGCA 10740 _
AAAAAGAAAA AAAAAGGCA
TTTTTCTTTT TTTTTCCGT
C
GAM2976 ERBB2IP 5' AAAAAAAGAAAAAAAAAA 33094
AAAAAAAGAAAAAAAAAG

```
                                TTTTTTTCTTTTTTTTTT

GAM2976  EWSR1    3'  AAAAAAAAAAAAAAAACAT   23482
                                AAAAGAAAAAAAAAGGCAT
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTGTA

GAM2976  G6PC     3'  CAAAAAAAGAAAAAAAAAG   6659
                                TAAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                GTTTTTTTCTTTTTTTTC

GAM2976  GFRA1    5'  AAAAAAAGAAAAAAAAAA    23561
                                AAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                TTTTTTTCTTTTTTTTTT

GAM2976  GLS      3'  AAAAAGAAAAAAAAAGGAATT  31371              C
                                AAAAAGAAAAAAAAAGG ATT
                                |||||||||||||||| |||
                                TTTTTCTTTTTTTTCC TAA
                                          T
GAM2976  GLUD1    3'  AAAAAAAAAAAAAAAAGC    23585
                                AAAAAGAAAAAAAAAGGC
                                |||||||||||||||||
                                TTTTTTTTTTTTTTTCG

GAM2976  GNAO1    3'  TGAAAAAAAAAAAAAAGG    44943   A
                                A AAAAGAAAAAAAAAGG
                                | ||||||||||||||||
                                A TTTTTTTTTTTTTCC
                                 C
GAM2976  HIS1     5'  AAAAAGAAAAAAAAAACA    26987             G
                                AAAAAGAAAAAAAAAG CA
                                |||||||||||||||| ||
                                TTTTTCTTTTTTTTTT GT
                                                _
GAM2976  IFNGR2   3'  AAGAAAAAAAAAAAAAAGC   24378    A
                                AA AAAGAAAAAAAAAGGC
                                || ||||||||||||||||
                                TT TTTTTTTTTTTTTCG
                                  C
GAM2976  JAM3     3'  AAAAAAAAAAAATAGCAT    37255           A
                                AAAGAAAAAAAA GGCAT
                                |||||||||||| |||||
                                TTTTTTTTTTTT TCGTA
                                         A
GAM2976  JRKL     3'  AAAAAAAAAAAAAAAAAAC   19087
                                AAAAAAGAAAAAAAAAGGC
                                |||||||||||||||||||
```

```
                                TTTTTTTTTTTTTTTTTTG

GAM2976 LY95     5' TAAAAAAAAAAAAAAAAAG  22100
                                TAAAAAAAGAAAAAAAAAGG
                                ||||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTTC

GAM2976 MAK      3' AAAAAAAAAAAAAAAAAGC  25376
                                AAAAAAGAAAAAAAAAGGC
                                |||||||||||||||||||
                                TTTTTTTTTTTTTTTTTCG

GAM2976 MTP      3' CAAAAAAAGAGAAAAAAATGG 7010          A      _
                                TAAAAAAAGA AAAAAAA GG
                                |||||||||| ||||||| ||
                                GTTTTTTTCT TTTTTTT CC
                                      C      A
GAM2976 NFRKB    5' AAAAGAAAAAGAAGGCAT    26090         AA
                                AAAAGAAAAA  AAGGCAT
                                ||||||||||  |||||||
                                TTTTCTTTTT  TTCCGTA
                                      C_
GAM2976 NPEPPS   3' AAAAAAAGAAAAAAAAGG    26713             A
                                AAAAAAAGAAAAAAAA GG
                                |||||||||||||||| ||
                                TTTTTTTCTTTTTTTT CC
                                                _
GAM2976 NRXN3    5' TAAAGAAAGAAAAAAAAAAG  39943     A
                                TAAA AAAGAAAAAAAAAGG
                                |||| ||||||||||||||
                                ATTT TTTCTTTTTTTTTC
                                   C
GAM2976 OPHN1    3' AAAAAAAGAAAAAAAAAA    14958
                                AAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                TTTTTTTCTTTTTTTTTT

GAM2976 OPHN1    3' AAAAAAAGAAAAAAAAAGG   14959
                                AAAAAAAGAAAAAAAAAGG
                                |||||||||||||||||||
                                TTTTTTTCTTTTTTTTTCC

GAM2976 OSR1     3' CAAAAAAAGAAAAAGAAAAGC 23033           A
                                TAAAAAAAGAAAAA AAAGGC
                                |||||||||||||| ||||||
                                GTTTTTTTCTTTTT TTTTCG
                                      C
GAM2976 PCDH15   3' TAAAAACGAGAAAAAAAACTGC 37507      A_       AG
             ATT                  TAAAAA  AGAAAAAAAA  GCATT
                                ||||||  ||||||||||  |||||
```

```
                                ATTTTT  TCTTTTTTTT  CGTAA
                                   GC         GA
GAM2976  PIAS1    3'  TAAAAAAAGGAAAAAAAACAC  32079          A       G
                                TAAAAAAAG AAAAAAAA GC
                                ||||||||| |||||||| ||
                                ATTTTTTTC TTTTTTTT TG
                                     C       G
GAM2976  PIGR     3'  AAAAAAAGAAAAAGAAAAAC   43694            A
                                AAAAAAAGAAAAA AAAGGC
                                |||||||||||| ||||||
                                TTTTTTTCTTTTT TTTTTG
                                         C
GAM2976  PKP2     3'  AAAAAAGTCCAGGAAAGGCATT 21315         AAAAAA
                                AAAAAAG     AAAGGCATT
                                |||||||     |||||||||
                                TTTTTTC     TTTCCGTAA
                                     AGGTCC
GAM2976  PKP4     3'  AAAAAGGAAAAAAAAACACACT 18847       A         G
                                AAAAA GAAAAAAAAA GCATT
                                ||||| |||||||||| |||||
                                TTTTT CTTTTTTTTT TGTGA
                                   C         G
GAM2976  PPARGC1  3'  AAAAAAGAAAAAAATCCACATT 29945             AAG
                                AAAAAAGAAAAAAA   GCATT
                                |||||||||||||   |||||
                                TTTTTTCTTTTTTT   TGTAA
                                         AGG
GAM2976  PRKR     5'  AAAAGAGAAAAAAGAAGGC    15676      A       A
                                AAAA AGAAAAAA AAGGC
                                |||| |||||||| |||||
                                TTTT TCTTTTTT TTCCG
                                  C       C
GAM2976  PTMA     3'  CAAAAAAGGAAAAAAAAAG    15864         A
                                TAAAAAA GAAAAAAAAAG
                                ||||||| ||||||||||
                                GTTTTTT CTTTTTTTTTC
                                     C
GAM2976  PTP4A2   5'  AAAAAAAAAAAAAAGCCA     18495              G
                                AAAAGAAAAAAAAAG CA
                                |||||||||||||| ||
                                TTTTTTTTTTTTTTC GT
                                         G
GAM2976  RAD21    3'  TGAAGAAGGAAAAAGGCA     26531    A     AA
                                A AAGAA  AAAAAGGCA
                                | |||||  |||||||||
                                A TTCTT  TTTTTCCGT
                                 C    CC
GAM2976  SCAMP1   3'  AAAAAAAGAAAAGAAAAAGA   38066           _
                                AAAAAAAGAAAA AAAAAGG
                                |||||||||||| |||||||
```

```
                                TTTTTTTCTTTT TTTTTCT
                                      C
GAM2976  SDC1     3'  AAAAAAAAAAAAAAAAAAG   16495
                                AAAAAAAGAAAAAAAAAGG
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTTTC

GAM2976  SDC4     3'  TAAAAAAAAAAAAAAAAAAA  16527
                                TAAAAAAAGAAAAAAAAGG
                                ||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTT

GAM2976  SEPP1    3'  AAAAAGAAAAAAAAAAGACAT  23998
                                AAAAAGAAAAAAAAAGGCAT
                                |||||||||||||||||||
                                TTTTTCTTTTTTTTTCTGTA

GAM2976  SGCB     3'  AAAAAAAAAAAAAAAAGGAATT  6926              C
                                AAAAAGAAAAAAAAAGG ATT
                                |||||||||||||||| |||
                                TTTTTTTTTTTTTTTCC TAA
                                      T
GAM2976  SLC15A1  3'  AAAAAGAAAAAAGAAAATAGCA 22899          _  __
            TT                   AAAAAGAAAAAA AAA  GGCATT
                                ||||||||||| |||  ||||||
                                TTTTTCTTTTTT TTT  TCGTAA
                                      C   TA
GAM2976  SLC19A1  3'  AAAAAAAAAAAAAAGCATC    16841
                                AAGAAAAAAAAAGGCATT
                                ||||||||||||||||||
                                TTTTTTTTTTTTTCGTAG

GAM2976  SOX12    3'  TAAAAAAAAAAAAAAAAAAA  28056
                                TAAAAAAAGAAAAAAAAGG
                                |||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTT

GAM2976  SOX9     3'  AAAAAAGGGATGGACAAAAAGG 7369        AAAA____
            CATT                  AAAAAAG       AAAAAGGCATT
                                |||||||       ||||||||||
                                TTTTTTC       TTTTTCCGTAA
                                    CCTACCTG
GAM2976  SRC      3'  AAAAAAAAAAAAAGGACA    24028          _
                                AAAGAAAAAAAAAGG CA
                                |||||||||||||| ||
                                TTTTTTTTTTTTCC GT
                                      T
GAM2976  SVIL     3'  AAAAAAAAAAAAAAAGGCATT  34723
                                AAAAAGAAAAAAAAAGGCATT
                                |||||||||||||||||||
```

```
                                TTTTTTTTTTTTTTTCCGTAA

GAM2976  TAPBP    3'  AAAGAAAAAAAAAAAAAGGCATT 17296     A
                                AAA AAGAAAAAAAAAGGCATT
                                ||| ||||||||||||||||||
                                TTT TTTTTTTTTTTTCCGTAA
                                  C
GAM2976  TBX3     5'  AAAAAAGAAAAGGAGGC     32434          AAAA
                                AAAAAAGAAAA    AGGC
                                ||||||||||    ||||
                                TTTTTTCTTTT    TCCG
                                      CC__
GAM2976  TGFBR2   5'  TGAAAAAAAAAAAAAAAGCACT  17485    A
                                A AAAGAAAAAAAAAGGCATT
                                | ||||||||||||||||||
                                A TTTTTTTTTTTTTTCGTGA
                                 C
GAM2976  TNFRSF11A 3'  CAAAAAAAGAAAAAAAAAA    19269
                                TAAAAAAAGAAAAAAAAAG
                                ||||||||||||||||||
                                GTTTTTTTCTTTTTTTTTT

GAM2976  TNFSF9   3'  AAAGAAAGAAAGAAAAAAGC   19189     A      A
                                AAA AAAGAAA AAAAAGGC
                                ||| ||||||| ||||||||
                                TTT TTTCTTT TTTTTTCG
                                  C      C
GAM2976  TOMM22   3'  AAAAAAAAAAAAAAAAACA    33671
                                AAAAAGAAAAAAAAAGGCA
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTTTGT

GAM2976  TPI1     5'  TAAAAAAAAAAAAAAAAAAC  7477
                                TAAAAAAAGAAAAAAAAAGGC
                                ||||||||||||||||||||
                                ATTTTTTTTTTTTTTTTTTTG

GAM2976  UBL3     3'  AAAAGAAAAAGTGGCAT     28260          AAAA
                                AAAAGAAAAA    GGCAT
                                ||||||||||    |||||
                                TTTTCTTTTT    CCGTA
                                      CA__
GAM2976  XKRY     5'  AAAGAAAGAAAAAAAAAAGA    21703     A
                                AAA AAAGAAAAAAAAAGG
                                ||| ||||||||||||||
                                TTT TTTCTTTTTTTTTCT
                                  C
GAM2976  ZHX1     3'  AAAAGAAAAAAAAAAAGC    28515              _
                                AAAAGAAAAAAAAAG GC
                                |||||||||||||| ||
```

```
                                TTTTCTTTTTTTTTT CG
                                          T
GAM2976 ZIC1     5' AAAAAAAAAAAAAAAAAAG   18221
                                AAAAAAAGAAAAAAAAAGG
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTTTTC

GAM2976 ZNF74    5' AAAAAAAAAAAAAAAAAGA    18295
                                AAAAAAGAAAAAAAAAGG
                                ||||||||||||||||||
                                TTTTTTTTTTTTTTTTCT

GAM2977 SPP1     3' AATATTAAAATACAGTGATAGT 8221           T__
             TT                  AATATTAAAATATA  ATAGTTT
                                ||||||||||||||  |||||||
                                TTATAATTTTATGT  TATCAAA
                                        CAC
GAM2978 C8A      3' GCATCTTCTCTTAGTT     8158       TC  GTGTG
                                GCATCTT  CT    TAGTT
                                |||||||  ||    |||||
                                CGTAGAA  GA    ATCAA
                                    GA  _____
GAM2979 GPR34    3' CTGAGTTTTGTAAATGCTAG  23627     ___      A
                                CTGA   TTGTAAAT CTAG
                                ||||   |||||||| ||||
                                GACT   AACATTTA GATC
                                  CAA       C
GAM2979 LAMP2    3' TAAAGACTGATCTCAAAATGCT 30387   T       GT_   A
                                A AAGACTGATT   AAAT CT
                                | ||||||||||   |||| ||
                                A TTCTGACTAG   TTTA GA
                                 T        AGT   C
GAM2979 GPR34    3' CTGAGTTTTGTAAATGCTAG  23627     ___      A
                                CTGA   TTGTAAAT CTAG
                                ||||   |||||||| ||||
                                GACT   AACATTTA GATC
                                  CAA       C
GAM2979 LAMP2    3' TAAAGACTGATCTCAAAATGCT 30387   T       GT_   A
                                A AAGACTGATT   AAAT CT
                                | ||||||||||   |||| ||
                                A TTCTGACTAG   TTTA GA
                                 T        AGT   C
GAM2980 CHD2     3' TTGACATTGAAAAGGAAAGTAT 10455       AGT  CA
             T                   TTGACATT   AA  GAAAGTATT
                                ||||||||   ||  |||||||||
                                AACTGTAA   TT  CTTTCATAA
                                    CT_  TC
GAM2981 PIN      3' CAGTCTCTGGTATTTGGAATT  19054    GA  AA_
                                TAG  TT   TATTTGGAATT
                                |||  ||   ||||||||||
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                                GTC  AG   ATAAACCTTAA
                                  AG  ACC
GAM2981  SORBS1   3'  TAGGTGAGTTATTTGGAAT   31713     ATTAA
                                TAGG    TATTTGGAAT
                                ||||    ||||||||||
                                ATCC    ATAAACCTTA
                                  ACTCA
GAM2982  CLOCK    3'  AAATGTATGTAACTTGTAT   22212        CTTA
                                AAGTGTATGT    TGTAT
                                ||||||||||    |||||
                                TTTACATACA    ACATA
                                      TTGA
GAM2982  GPR85    3'  TAAAGTGTGATGTTTATAT   33261       _   C
                                TAAAGTGT ATGT TTATGT
                                |||||||| |||| ||||||
                                ATTTCACA TACA AATATA
                                     C   _
GAM2982  HTR2C    3'  TAAAGTGTATATTTACTGT   9290          CTTA
                                TAAAGTGTATGT    TGT
                                ||||||||||||    |||
                                ATTTCACATATA    ACA
                                      AATG
GAM2982  SWAP70   3'  AAAGTGTATGTTCTGGTAT   43419         _ TAT
                                AAAGTGTATGT CT   GTAT
                                |||||||||||| ||   ||||
                                TTTCACATACA GA   CATA
                                      A  C__
GAM2982  TCF3     3'  CAAAGTGTATGTTTTGT     43315         CTTA
                                TAAAGTGTATGT    TGT
                                ||||||||||||    |||
                                GTTTCACATACA    ACA
                                      AA__
GAM2982  TIMM17A  3'  AAGTATTATTTTATGTATATT  26787      A   C
                                AAGTGT TGT TTATGTATATT
                                |||||| ||| ||||||||||
                                TTCATA ATA AATACATATAA
                                   _   A
GAM2983  CD2AP    3'  ATGCATTATGGAAAAAGTAGT  29069        AA  TCGT
                                ATGCATTAT  GA   GTAGT
                                |||||||||  ||   |||||
                                TACGTAATA  CT   CATCA
                                     C_  TTTT
GAM2983  FREB     3'  TGCATTATAGGATGTTTAG   37226        A   C  G
                                TGCATTATA GAT GT TAG
                                ||||||||| ||| || |||
                                ACGTAATAT CTA CA ATC
                                     C   _  A
GAM2983  PPIL1    3'  GCATTATGGTTCATGTGTAGTA 31999       AAGATC_
            A                    GCATTAT     GTGTAGTAA
                                |||||||     |||||||||
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                                CGTAATA      CACATCATT
                                    CCAAGTA
GAM2983  SGCG     3'  TGCATTTTGAGATCATGTAG  6925        ATA
                                TGCATT   AGATCGTGTAG
                                ||||||   ||||||||||
                                ACGTAA   TCTAGTACATC
                                   AAC
GAM2983  TBR1     3'  TGCATTAGGGCACATAGTAA  27317       ATA  AT  TG
                                TGCATT   AG  CG  TAGTAA
                                ||||||   ||  ||  ||||||
                                ACGTAA   TC  GT  ATCATT
                                   ___   CC  GT
GAM2984  ARHGEF7  3'  TGGTTTGATCGTCTCCATT   19371         A
                                TGGTTTGA CGTCTCCATT
                                |||||||| ||||||||||
                                ACCAAACT GCAGAGGTAA
                                     A
GAM2984  ETV5     3'  TGGTTTGAGCCTCCCCAAC   20858         AC     A
                                TGGTTTGA  GTCTCC TTAAC
                                ||||||||  |||||| |||||
                                ACCAAACT  CGGAGG GGTTG
                                     __     _
GAM2984  GATM     3'  GGTTTTACCTCCATTA      11229       GAACG
                                GGTTT    TCTCCATTA
                                |||||    |||||||||
                                CCAAA    GGAGGTAAT
                                   AT___
GAM2984  STMN1    3'  TGGCTTGATTTATTAACC    24518         ACGTCTCC
                                TGGTTTGA      ATTAACC
                                ||||||||      |||||||
                                ACCGAACT      TAATTGG
                                     AAA_____
GAM2984  TDRD1    3'  GGTTTCACTCCATTA       36332       GAA  T
                                GGTTT   CG CTCCATTA
                                |||||   || ||||||||
                                CCAAA   GT GAGGTAAT
                                     ___  _
GAM2985  RPS6KA1  3'  TGTGTGAGGCAAGTACTATTAG 40384         AG_    ATGT
            GG                    TGTGTGA   AAGTG    TTAGGG
                                  |||||||   |||||    ||||||
                                  ACACACT   TTCAT    AATCCC
                                     CCG    GAT_
GAM2986  C7orf2   3'  GCTTTTAAGGAAATAAGAAAC  35371     ACTC   TT
                                GCT    AAG  AGTAAGAAAC
                                |||    |||  ||||||||||
                                CGA    TTC  TTATTCTTTG
                                  AAA_   CT
GAM2986  MLH3     3'  GCTACTCAACTAGGGGAA    30780         G    TAA
                                GCTACTCAA TTAG   GAA
                                ||||||||| ||||   |||
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                                CGATGAGTT GATC   CTT
                                      _   CC_
GAM2986  NPPB     3'  CTCAAAGGTAAGAAAC      14825       TTA
                                CTCAAG   GTAAGAAAC
                                ||||||   |||||||||
                                GAGTTT   CATTCTTTG
                                   C__
GAM2986  RFC1     3'  CACAACAGGTTAGTAAG     16272     TACT  A
                                CGC    CA GTTAGTAAG
                                |||    || |||||||||
                                GTG    GT CAATCATTC
                                  TT__  C
GAM2987  ABCE1    3'  CCTTGGCTGCCCAACAGAAAA  40499     CAACATT
                                CCT      CTCAACAGAAAA
                                |||      ||||||||||||
                                GGA      GGGTTGTCTTTT
                                  ACCGAC_
GAM2987  ASGR2    3'  CCTCAAAATCCTCAACAGA    38949       C
                                CCTCAA ATTCTCAACAGA
                                |||||| ||||||||||||
                                GGAGTT TAGGAGTTGTCT
                                   T
GAM2987  DNCI1    3'  ACCTCAACAGCAGCAGA     44986         TTCT  A
                                ACCTCAACA    CA CAGA
                                |||||||||    || ||||
                                TGGAGTTGT    GT GTCT
                                     C___  C
GAM2987  FMO2     3'  CCCAGGATTTTCAACAGAAAA  11140      AC   C
                                CTCA  ATT TCAACAGAAAA
                                ||||  ||| ||||||||||||
                                GGGT  TAA AGTTGTCTTTT
                                  CC   A
GAM2987  HS2ST1   3'  TACCTGACTCTCAATAGAAA   29337      CAAC       C
                                TACCT    ATTCTCAA AGAAA
                                |||||    |||||||| |||||
                                ATGGA    TGAGAGTT TCTTT
                                   C___       A
GAM2987  HS2ST1   3'  CACTTCAACATCAGAA      29326     C      TCTCAA
                                TAC TCAACAT     CAGAA
                                ||| |||||||     |||||
                                GTG AGTTGTA     GTCTT
                                  A     _______
GAM2987  KLK5     3'  CTCAACATCTCTGGGAA     29682         T   AACA
                                CTCAACAT CTC    GAA
                                |||||||| |||    |||
                                GAGTTGTA GAG    CTT
                                     _  ACC_
GAM2987  LAMC1    3'  CTCATCTCTCCAACAGAA    14084      ACA  CT
                                CTCA   TT  CAACAGAA
                                ||||   ||  ||||||||
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                                GAGT   AG  GTTGTCTT
                                  AG_  AG
GAM2987  NR2F2    3'  CCTTTCTTAACAGAA      34232     CAACA    C
                                CCT    TTCT AACAGAA
                                |||    |||| |||||||
                                GGA    AAGA TTGTCTT
                                 _____   A
GAM2987  OLFM1    3'  CACCTCAAGGGAATAACAGAA  26765        CATTCTC
                                TACCTCAA      AACAGAA
                                ||||||||      |||||||
                                GTGGAGTT      TTGTCTT
                                    CCCTTA_
GAM2987  PIK3CD   3'  TACCTCAGCACTCTCACAG   22732       A       A
                                TACCTCA CATTCTCA CAG
                                ||||||| |||||||| |||
                                ATGGAGT GTGAGAGT GTC
                                   C      _
GAM2987  PSAP     3'  TCAACATCCATCTAGCAGA   42972         _  AA_
                                TCAACATTC TC   CAGA
                                ||||||||| ||   ||||
                                AGTTGTAGG AG   GTCT
                                     T  ATC
GAM2987  TCEA1    3'  CTCACTCATTGACAGAAAA   44324     ACATT   ___
                                CTCA    CTCA   ACAGAAAA
                                ||||    ||||   ||||||||
                                GAGT    GAGT   TGTCTTTT
                                  _____   AAC
GAM2987  TIM3     3'  CTCAACATTCCAAGGGAA    37249         T   CA
                                CTCAACATTC CAA  GAA
                                |||||||||| |||  |||
                                GAGTTGTAAG GTT  CTT
                                     _  CC
GAM2987  TLL2     3'  CCCAACATGGACAGAA      29747        TCTCA
                                CTCAACAT    ACAGAA
                                ||||||||    ||||||
                                GGGTTGTA    TGTCTT
                                    CC___
GAM2987  TNFSF4   3'  CCTCTCATTTAACAGAAA    17749     AA   CTC
                                CCTC  CATT   AACAGAAA
                                ||||  ||||   ||||||||
                                GGAG  GTAA   TTGTCTTT
                                  A_   A__
GAM2987  HPGD     3'  TAGACCAGAGTTATTAATA   9245      A  TA   C
                                TAGA CC  AGAG TATTAATA
                                |||| ||  |||| ||||||||
                                ATCT GG  TCTC ATAATTAT
                                  _ __   A
GAM2988  AICDA    3'  CATTTCTAAAGTTATAAATT  34038         __
                                CATTTCTAAA  TATAAATT
                                ||||||||||  ||||||||
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                                GTAAAGATTT  ATATTTAA
                                     CA
GAM2988  NAPB     3'  CATTTCAAATATAAATCA    43172       T
                                CATTTC AAATATAAATTA
                                |||||| ||||||||||||
                                GTAAAG TTTATATTTAGT
                                     _
GAM2988  SPAP1    5'  CATTTCTAAACATATATT    39863            A
                                CATTTCTAAATATA ATT
                                |||||||||||||| |||
                                GTAAAGATTTGTAT TAA
                                       A
GAM2989  ARHGEF6  3'  CAGCAAATGCCCAAGCGCG   42796    C     AA
                                CA CAAAT  TCGAGCGCG
                                || |||||  |||||||||
                                GT GTTTA  GGTTCGCGC
                                 C    CG
GAM2989  B4GALT6  3'  CACCAAATAACTCATCACG   40846          CGAG
                                CACCAAATAAT   CGCG
                                ||||||||||    ||||
                                GTGGTTTATTG   GTGC
                                      AGTA
GAM2989  GAK      3'  CACCAAATAAATCACAGACG  23531          _  AGC
                                CACCAAATAA TCG  GCG
                                |||||||||| |||  |||
                                GTGGTTTATT AGT  TGC
                                      T  GTC
GAM2989  GOT1     3'  CACCACATAGAAGCACG     13224      A  ATC
                                CACCA ATA  GAGCGCG
                                ||||| |||  |||||||
                                GTGGT TAT  TTCGTGC
                                   G  C__
GAM2989  LOXL2    3'  CACCAAATCAGAAAACACG   14194        AATC
                                CACCAAAT   GAGCGCG
                                ||||||||   |||||||
                                GTGGTTTA   TTTGTGC
                                     GTCT
GAM2989  TGFB3    3'  CACCAAATGAACACA       17457        AATC
                                CACCAAAT   GAGCGCG
                                ||||||||   |||||||
                                GTGGTTTA   CTTGTGT
                                     ____
GAM2990  DEFA6    3'  CAATGTATGGGACACACG    12564     AA  AGCT
                                CAAT  ATG   GACACACG
                                ||||  |||   ||||||||
                                GTTA  TAC   CTGTGTGC
                                  CA  C___
GAM2990  EPM2A    3'  GACTGTAAATGAGTTACCTG  24970     AA     ____
                                GAC  TAAATGAG   CTG
                                |||  ||||||||   |||
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                                CTG  ATTTACTC    GAC
                                  AC       AATG
GAM2990  TMEFF1    3'  AATAAATGTACATACACA    18975         A  TG
                                AATAAATG GC  ACACA
                                |||||||| ||  |||||
                                TTATTTAC TG  TGTGT
                                     A  TA
GAM2991  JJAZ1     3'  TTGAACTTTATGTACAAAATCA 31695         _   TC___
              TTTGA                  TTGAATTT ATGT    GTCATTTGA
                                |||||||| ||||    |||||||||
                                AACTTGAA TACA    TAGTAAACT
                                     A   TGTTT
GAM2991  SNAI2     3'  TTGGACTTTATTTGTCATTTG  16891     A   A   C
                                TTG ATTT TGTT GTCATTTG
                                ||| |||| |||| ||||||||
                                AAC TGAA ATAA CAGTAAAC
                                  C   _   A
GAM2992  BCL7A     3'  TGAGAAGTGACGCCGTTCTG   34221         AG   G  GA
                                TGAGAAGT  CGT TG  CTG
                                ||||||||  ||| ||  |||
                                ACTCTTCA  GCG GC  GAC
                                     CT   _  AA
GAM2992  CDC5L     5'  GAGAAGTAGTAACAGCGATTGG 10359         _______   TG
                                GAGAAGT     AGCG  TGG
                                |||||||     ||||  |||
                                CTCTTCA     TCGC  ACC
                                     TCATTG    TA
GAM2992  DTNA      5'  GAGGAAGGGGGACTGAA     37371     _   TAGCGTGT
                                GAG AAG       GGACTGAA
                                ||| |||       ||||||||
                                CTC TTC       CCTGACTT
                                  C   CC_______
GAM2992  GAN       3'  TGAGAAGTGGGGTAAAGTGG   35151         AGC  ___
                                TGAGAAGT   GT   GTGG
                                ||||||||   ||   ||||
                                ACTCTTCA   CA   CACC
                                     CCC  TTT
GAM2992  GLS       3'  TGAGAAGAGAGGCTGGAC    31380         T_  C  G
                                TGAGAAG  AG GT TGGAC
                                |||||||  || || |||||
                                ACTCTTC  TC CG ACCTG
                                     TC  _  _
GAM2992  IL1F5     3'  GAGGACCGTGGACTGA      29352     AAGTA  G
                                GAG    GC TGTGGACTGA
                                |||    || ||||||||||
                                CTC    TG GCACCTGACT
                                  C____  _
GAM2992  MLPH      3'  TGAGCAGTGCAGGACTGAA   35868      A   A   TGT
                                TGAG AGT GCG   GGACTGAA
                                |||| ||| |||   ||||||||
```

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                                ACTC TCA CGT   CCTGACTT
                                  G  _  ___
GAM2992  PLD2     3'  GAGAAGTGGTTTGCACTG    15378        AGC  G  G
                                GAGAAGT   GT TG ACTG
                                |||||||   || || ||||
                                CTCTTCA   CA AC TGAC
                                    C__  A  G
GAM2992  SLC2A1   3'  TGAGAGGTACGTGTAAGGGACT 27145      A   G    ___
            G                    TGAGA GTA CGTGT   GGACTG
                                |||||| ||| |||||   ||||||
                                ACTCT CAT GCACA   CCTGAC
                                  C  _    TTC
GAM2992  JAK2     5'  GTCCGCTGCTGCCCCCTTCTGC 22477          CG    _____
            TC                    GTCCGCTGCT  GCTCC    GCTC
                                |||||||||  |||||    ||||
                                CAGGCGACGA  CGGGG    CGAG
                                     __    GAAGA
GAM2992  MMP2     5'  GGTCCGCTGGCTCGGTGGC   21201         _    CTCC
                                GGTCCGCTG CTCGG   GC
                                |||||||| |||||   ||
                                CCAGGCGAC GAGCC   CG
                                    C    AC__
GAM2992  NTSR1    5'  GGCTCCGGGCTCCGC      14886    _   CTGCTC
                                GG TCCG     GGCTCCGC
                                || ||||     ||||||||
                                CC AGGC     CCGAGGCG
                                 G  _______
GAM2992  SDC1     5'  GGTTCCGCTGCTCGATGCTC   16511    _       __
                                GGT CCGCTGCTCG  GCTC
                                ||| ||||||||||  ||||
                                CCA GGCGACGAGC  CGAG
                                  A        TA
GAM2992  SORCS1   3'  AAGGTCCGTTTCTGACATGCT  38095       CTG  C   TCC
                                AAGGTCCG   CT GGC   GCT
                                ||||||||   || |||   |||
                                TTCCAGGC   GA CTG   CGA
                                    AAA  _   TA_
GAM2992  TEAD2    3'  GGCCCACCTGGCTCTGCTC   18766       GCTC    C
                                GGTCCGCT    GGCTC GCTC
                                ||||||||    ||||| ||||
                                CCGGGTGG    CCGAG CGAG
                                    A___     A
GAM2992  TEM8     5'  GGTCCGCTCCTTCCCACGCTC  32857       G  CGG  _
                                GGTCCGCT CT   CTC CGCTC
                                |||||||| ||   ||| |||||
                                CCAGGCGA GA   GGG GCGAG
                                    G  A__   T
GAM2992  TMEM4    5'  GGTCGCTCCACCTCTGCTC   30675     C   G T  G   C
                                GGTC GCT C CG CTC GCTC
                                |||| ||| | || ||| ||||
```

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                                CCAG CGA G GT GAG CGAG
                                  _  _ _ G   A
GAM2992  TNFRSF6B  5'  GGTCCGCCTGCTCTTCGGCTC  32363       _    ___
                                GGTCCGC TGCTC   GGCTC
                                ||||||| |||||   |||||
                                CCAGGCG ACGAG   CCGAG
                                    G    AAG
GAM2992  TSPY      3'  AACGTCTGCTGCTCGGCATC   17700    G   C       _
                                AA GTC GCTGCTCGGC TC
                                || ||| |||||||||| ||
                                TT CAG CGACGAGCCG AG
                                 G   A        T
GAM2993  COCH      3'  TGCTTTTGGTCTAAGTA     19862     CTAA   A
                                TGC    TTG TCTAAGTA
                                |||    ||| ||||||||
                                ACG    AAC AGATTCAT
                                  AA__   C
GAM2993  TRHDE     3'  ATAATGCCCATCCTAGGT    30100         ATTGA    A
                                ATAATGCCTA    TCTA GT
                                ||||||||||    |||| ||
                                TATTACGGGT    GGAT CA
                                     A_____    C
GAM2993  MBP       3'  GCTCTAATTAGGTAACAGG   44890         CATT  TTA
                                GCTCTAATTA   GT   AGG
                                ||||||||||   ||   |||
                                CGAGATTAAT   CA   TCC
                                     C___  TTG
GAM2994  CD3Z      3'  TGTTGCGTCTTCCTGCGA    8822          C  ATA
                                TGTTGCGTCT CC   GTGA
                                |||||||||| ||   ||||
                                ACAACGCAGA GG   CGCT
                                     A  A__
GAM2994  CDK3      3'  TCGAGAAAGGATCTGAGT    10380        A CGC   TC
                                TCGAGAAA G   TCT  GAGT
                                |||||||| |   |||  ||||
                                AGCTCTTT C   AGA  CTCA
                                    _ CT_   __
GAM2994  NPAT      3'  GAGGAAAGTGACTCTTCAA   42613     A   C_
                                GAG AAAG  GCTCTTCGA
                                ||| ||||  |||||||||
                                CTC TTTC  TGAGAAGTT
                                  C    AC
GAM2995  CETN1     3'  TGAGCTCCGTAAGTTTGTAAG 45460         CG   ACTC
                                TGAGCTCCG  AAG   TGTAAG
                                |||||||||  |||   ||||||
                                ACTCGAGGC  TTC   ACATTC
                                     A_   AA__
GAM2995  DNASE1L3  5'  TGGCTTCAAGACTCTGT     22372    A   C  CGA
                                TG GCT CG   AGACTCTGT
                                || ||| ||   |||||||||
```

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                                AC CGA GT   TCTGAGACA
                                 _   A ___
GAM2995 RAX     3'  TGAGGTCCGCGAAGTGC     30248      C        ACTC
                                TGAG TCCGCGAAG    TGT
                                |||| |||||||||    |||
                                ACTC AGGCGCTTC    ACG
                                  C       _____
GAM2995 SCRT1    3'  GAGTTCCGCGAAGGCTGC    36365     C        ACT
                                GAG TCCGCGAAG   CTGT
                                ||| |||||||||   ||||
                                CTC AGGCGCTTC   GACG
                                  A       C__
GAM2995 WISP1    3'  CTCTCAAGGCTCTGTAAG    38899     CG G   A
                                CTC  C AAG CTCTGTAAG
                                |||  | ||| |||||||||
                                GAG  G TTC GAGACATTC
                                  A_ _   C
GAM2996 B4GALT2  3'  CCCACACAAGTTTCT       36139      TATAT      C
                                CCCG     CACAAGT TCT
                                ||||     ||||||| |||
                                GGGT     GTGTTCA AGA
                                  _____       A
GAM2996 F7       3'  CCGTGTGTGTGCATATCTCTGT 33337      ATATCA_  A
                                CCGT       CA GTCTCTGT
                                ||||       || ||||||||
                                GGCA       GT TAGAGACA
                                  CACACAC  A
GAM2996 IL1RAP   3'  ATATATCACAGTTCTTTGT   39598          AG   C
                                GTATATCACA  TCT TGT
                                ||||||||||  ||| |||
                                TATATAGTGT  AGA ACA
                                      CA   A
GAM2996 LARGE    3'  CCTTGTCCAAGGTCTCTGT   21862    GTATA  A   _
                                CC     TC CAAG TCTCTGT
                                ||     || |||| |||||||
                                GG     AG GTTC AGAGACA
                                 AAC__  _    C
GAM2996 SLC22A3  3'  CCCTTATTAGTCTCTG      35047     G   ATCACA
                                CCC TAT      AGTCTCTG
                                ||| |||      ||||||||
                                GGG ATA      TCAGAGAC
                                  A   A_____
GAM2996 ZNF266   3'  GCATCTGTTCCAGGTCTCTGT  44778      ATCA__  A
                                GTAT      CA GTCTCTGT
                                ||||      || ||||||||
                                CGTA      GT CAGAGACA
                                  GACAAG  C
GAM2997 OPTN     5'  GAGAGAACTCCCGACCGGG   35068       C  ACACGA
                                GAGAG AC     CGACCGGG
                                ||||| ||     ||||||||
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                                CTCTC TG     GCTGGCCC
                                   T  AGG___
GAM2997  SORCS1    3'  CAGAGAGCACACATGAAATCAC 38098           C  CG__  C
              TGGG                  TAGAGAGCACACA GA    AC GGG
                                ||||||||||||| ||    || |||
                                GTCTCTCGTGTGT CT    TG CCC
                                      A  TTAG  A
GAM2998  DPYD      5'  GGCTGTAACGCCATTGGCA   41293        ACA
                                GGCTGTGA   CATTGGCA
                                ||||||||   ||||||||
                                CCGACATT   GTAACCGT
                                     GCG
GAM2998  HOXA3     5'  AGGGCGCACATTGGC       36190       TGTGAA
                                AGGGC     CACATTGGC
                                |||||     |||||||||
                                TCCCG     GTGTAACCG
                                   C_____
GAM2998  ITGA1     3'  TCAGGGACTGTCTCATTGGCA  41857     A      GAACA
                                TCA GGGCTGT     CATTGGCA
                                ||| |||||||     ||||||||
                                AGT CCTGACA     GTAACCGT
                                  C      GA___
GAM2998  NESH      3'  GGGCTGTAATTAGC        32342          ACACA
                                GGGCTGTGA     TTGGC
                                |||||||||     |||||
                                CCCGACATT     AATCG
                                      _____
GAM2998  PGK1      3'  GGGCTGTGCACAGGAAC     7113          AA    TT
                                GGGCTGTG  CACA  GGC
                                ||||||||  ||||  |||
                                CCCGACAC  GTGT  TTG
                                     __   CC
GAM2998  SLA2      3'  TCAAGGGCTGGATTTGG     37016          T  ACACA
                                TCAAGGGCTG GA     TTGG
                                |||||||||| ||     ||||
                                AGTTCCCGAC CT     AACC
                                      _  A____
GAM2998  TACC1     3'  TCCAGGGCTGTTGCATTGGCA  26601     A      GAACA
                                TC AGGGCTGT     CATTGGCA
                                || ||||||||     ||||||||
                                AG TCCCGACA     GTAACCGT
                                  G       AC___
GAM2998  TCTA      3'  CCAGGGGCTGTGAATAAC     35279     A        CACAT
                                TCA GGGCTGTGAA     TGGC
                                ||| ||||||||||     ||||
                                GGT CCCGACACTT     ATTG
                                  C        _____
GAM2998  TNFRSF13C 3'  TCAAGGGCTGTCAAAGATGG   38120           G  CACAT
                                TCAAGGGCTGT AA     TGG
                                |||||||||| ||     |||
```

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                                AGTTCCCGACA TT    ACC
                                      G  TCT__
GAM2998  TRPM2    3'  AGGGGTGCCAGGGCACATTGGC 17686     C   GAA__
              A                    AGGG TGT    CACATTGGCA
                                   |||| |||    ||||||||||
                                   TCCC ACG    GTGTAACCGT
                                     C   GTCCC
GAM2998  WNT3A    3'  GGGCTGTGGACAGGC      37548        A   CATT
                                   GGGCTGTG ACA    GGC
                                   |||||||| |||    |||
                                   CCCGACAC TGT    CCG
                                        C  ____
GAM2999  ASIP     3'  TCGCGGCCGGGAGG       11715       CCGTT     C
                                   TCGCGGT    CGGGAG G
                                   |||||||    |||||| |
                                   AGCGCCG    GCCCTC C
                                      _____     A
GAM2999  DDOST    5'  ATCGCGGCTCGTGCCCGTGG   23346       TC  __  _
                                   ATCGCGG  CGT  TCG GG
                                   |||||||  |||  ||| ||
                                   TAGCGCC  GCA  GGC CC
                                       GA   CG   A
GAM2999  DLK1     5'  TCGCGGTCCCGGGAGCGG    19266        GTT
                                   TCGCGGTCC   CGGGAGCGG
                                   |||||||||   |||||||||
                                   AGCGCCAGG   GCCCTCGCC
                                        ___
GAM2999  DYRK2    5'  TCGGGTAGGCGGCGGGAGCGG  27043    C   CC  T_
                                   TCG GGT  GT  CGGGAGCGG
                                   ||| |||  ||  |||||||||
                                   AGC CCA  CG  GCCCTCGCC
                                     _   TC  CC
GAM2999  ENPP1    5'  ATCGCGGCCGTTCCCCGCCGG  26295       T     GGGA  _
                                   ATCGCGG CCGTTC    GC GG
                                   ||||||| ||||||    || ||
                                   TAGCGCC GGCAAG    CG CC
                                      _     GGG_  G
GAM2999  G6PD     5'  ATCGGCGGGGGCGGGGGCGG   7596      _  TCCGTT    A
                                   ATCG CGG     CGGG GCGG
                                   |||| |||     |||| ||||
                                   TAGC GCC     GCCC CGCC
                                     C   CCC___    C
GAM2999  GUCY1A2  5'  ACCGCGGTCGGCGGGGCGG   9213         CGTT    A
                                   ATCGCGGTC    CGGG GCGG
                                   |||||||||    |||| ||||
                                   TGGCGCCAG    GCCC CGCC
                                        CC__    _
GAM2999  JPH3     5'  TCGCGGCCGCCGGCG       34026       T    T  GGA
                                   TCGCGG CCGT CG   GCG
                                   |||||| |||| ||   |||
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                                AGCGCC GGCG GC   CGC
                                  _   _  ____
GAM2999 MID1     5' TCGCAGTCTTCAGAGCGG    37786        CG    G
                                TCGCGGTC  TTCGG AGCGG
                                ||||||||  ||||| |||||
                                AGCGTCAG  AAGTC TCGCC
                                   ___   _
GAM2999 NFRKB    5' TCGCGGCCGTGACGGCGG    26102       T   TC  GA
                                TCGCGG CCGT  GG  GCGG
                                ||||||| ||||  ||  ||||
                                AGCGCC GGCA  CT  CGCC
                                  _   __ GC
GAM2999 OCLN     5' GCGGCCCGAGAGGCGG      14905        TTC   A
                                GCGGTCCG   GGG GCGG
                                ||||||||   ||| ||||
                                CGCCGGGC   CTC CGCC
                                    T__   _
GAM2999 S100A11  5' GCTGTGGCTGGGAGCG     24733    G  CC   C
                                GC GT  GTT GGGAGCG
                                || ||  ||| |||||||
                                CG CA  CGA CCCTCGC
                                 A  C_  _
GAM2999 SLC39A1  5' ATCGGGAGCGGGAGCG     30884     C  TCCGTT
                                ATCG GG     CGGGAGCG
                                |||| ||     ||||||||
                                TAGC CC     GCCCTCGC
                                  _ TC____
GAM2999 THBS1    5' CGCGGCGGCCGGGAGCGG    17511      TC  TT
                                CGCGG  CG  CGGGAGCGG
                                |||||  ||  |||||||||
                                GCGCC  GC  GCCCTCGCC
                                   __ CG
GAM2999 TRC8     5' CCGCGGCCGGGGGCG       28511       T   TTC   A
                                TCGCGG CCG   GGG GCG
                                |||||| |||   ||| |||
                                GGCGCC GGC   CCC CGC
                                  _   ___  _
GAM2999 ZNF174   5' CGCGGTCCCTGGGAGTGG    18359        G  C    C
                                CGCGGTCC TT GGGAG GG
                                |||||||| || ||||| ||
                                GCGCCAGG GA CCCTC CC
                                   _ _    A
GAM2999 ZNF216   5' CCGCGGGCCGGGAGCG      25653       TCC  T
                                TCGCGG   GT CGGGAGCG
                                ||||||   || ||||||||
                                GGCGCC   CG GCCCTCGC
                                   ___  _
GAM3000 YWHAZ    3' ATGACAAATGGTCTACTGT   18200         ATAC
                                ATGACAAATG   GCTGT
                                ||||||||||   |||||
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                                TACTGTTTAC   TGACA
                                     CAGA
GAM3001  MTCP1    3'  TTTAATGTGTTTATATT    30588          T
                                TTTAATGTGTTT ATATT
                                |||||||||||| |||||
                                AAATTACACAAA TATAA
                                          _
GAM3001  GPR34    3'  TGTTATAGAGATTTAGGCATA  23629          A  A
                                TGTTATAGAGAT TA GCGTA
                                |||||||||||| || |||||
                                ACAATATCTCTA AT CGTAT
                                      A  C
GAM3002  CASP3    3'  CATGTCTCTGCTCAGGCTCAAA 37415     CCGCC    AA
              CC                  CATG    GCTCA  CTTAAACC
                                |||| |||||  ||||||||
                                GTAC    CGAGT  GAGTTTGG
                                  AGAGA    CC
GAM3002  NEDD4    3'  ATACCCCAACAAACTTAAACC  43096      G   CT
                                ATGCC CCG  CAAACTTAAACC
                                ||||| |||  ||||||||||||
                                TATGG GGT  GTTTGAATTTGG
                                  _  T_
GAM3002  PTEN     5'  TGCCGCCGCTTGGCTCTGGACC 7220          CAAA   AA_
                                TGCCGCCGCT   CTT   ACC
                                ||||||||||   |||  |||
                                ACGGCGGCGA   GAG   TGG
                                     ACC_  ACC
GAM3002  ROBO1    3'  GCCACAACAAACTTAAACC   39484      T_
                                GCCGC  CAAACTTAAACC
                                |||||  ||||||||||||
                                CGGTG  GTTTGAATTTGG
                                  TT
GAM3003  BCHE     3'  TATGTTCTATAAAGGGTA    6290      G_
                                TATG  CTGTAAAGGGTA
                                ||||  ||||||||||||
                                ATAC  GATATTTCCCAT
                                  AA
GAM3003  CEACAM6  3'  GTATGACTATTAGGAGGGTA  14732         AA__
                                GTATGGCTGT   AGGGTA
                                ||||||||||   ||||||
                                CATACTGATA   TCCCAT
                                     ATCC
GAM3003  FACL2    3'  GCATGGCTGATCCAGGTA    34435         TAAA
                                GTATGGCTG   GGGTA
                                |||||||||   |||||
                                CGTACCGAC   TCCAT
                                     TAGG
GAM3003  FPRL1    3'  ATATGACTCAAGGGTA      11145         GTA
                                GTATGGCT   AAGGGTA
                                ||||||||   |||||||
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                                TATACTGA  TTCCCAT
                                    G__
GAM3003  FRK     3'  GTAGGCCAAAGGGTA      13013    T   GT
                                GTA GGCT  AAAGGGTA
                                ||| ||||  ||||||||
                                CAT CCGG  TTTCCCAT
                                  _   __
GAM3003  IL20RA  3'  TATGGCTGGGATCAAAGGG   30879       ____
                                TATGGCTG   TAAAGGG
                                ||||||||   |||||||
                                ATACCGAC   GTTTCCC
                                    CCTA
GAM3003  LZTFL1  3'  GTATTTTGCTAAAGGGTA    33771     GGC  _
                                GTAT  TGT AAAGGGTA
                                ||||  ||| ||||||||
                                CATA  ACG TTTCCCAT
                                  AA_  A
GAM3003  MGA     3'  GTAAGGTTAAAGGGTA     41725     T  CTG
                                GTA GG  TAAAGGGTA
                                ||| ||  |||||||||
                                CAT CC  ATTTCCCAT
                                 T  A__
GAM3003  POLQ    3'  GTAGGTGAAAGGGTA      27321     T  C  T
                                GTA GG TG AAAGGGTA
                                ||| || || ||||||||
                                CAT CC AC TTTCCCAT
                                  _ _ _
GAM3003  PPP6C   3'  GTATATTGTAGAGGGTA     15544      GC   A
                                GTATG  TGTA AGGGTA
                                |||||  |||| ||||||
                                CATAT  ACAT TCCCAT
                                  A_   C
GAM3003  PRKCN   3'  TATGGCTGCTGTGAGGGTA   25167        AA__
                                TATGGCTGT   AGGGTA
                                |||||||||   ||||||
                                ATACCGACG   TCCCAT
                                     ACAC
GAM3003  SRC     3'  GCATGGCAGTGGGTA      24035       T  AAA
                                GTATGGC GT  GGGTA
                                ||||||| ||  |||||
                                CGTACCG CA  CCCAT
                                    T  ___
GAM3003  TACC1   3'  GTAGGTTGAAAGGGTA     26596     T  C  T
                                GTA GG TG AAAGGGTA
                                ||| || || ||||||||
                                CAT CC AC TTTCCCAT
                                 _  A  _
GAM3003  TCF20   3'  GTGTGGCTGCACGGTA     42538    A      AAG
                                GT TGGCTGTA  GGTA
                                || ||||||||  ||||
```

```
                                CA ACCGACGT   CCAT
                                 C       G__
GAM3003  TNFAIP1   3'  GCATGGCTGGAAGCCAAGGGTA 34478          TA____
                                GTATGGCTG     AAGGGTA
                                |||||||||     |||||||
                                CGTACCGAC     TTCCCAT
                                     CTTCGG
GAM3003  TOMM22    3'  GCATGGCTGCACTCTGGTA   33676          AAG_
                                GTATGGCTGTA   GGTA
                                ||||||||||    ||||
                                CGTACCGACGT   CCAT
                                      GAGA
GAM3003  TRHDE     3'  GTATGACTAATAGGTA      30109          TAAA
                                GTATGGCTG   GGGTA
                                |||||||||   |||||
                                CATACTGAT   TCCAT
                                     TA__
GAM3003  VNN1      3'  GCATGGCTGTTATCGGTA    21686          AAAG
                                GTATGGCTGT   GGTA
                                ||||||||||   ||||
                                CGTACCGACA   CCAT
                                      ATAG
GAM3003  XK        3'  GTAGGTTGGAAAAGGGTA    34366     T  C  T_
                                GTA GG TG  AAAGGGTA
                                ||| || ||  ||||||||
                                CAT CC AC  TTTCCCAT
                                  _  A  CT
GAM3004  CAPZA1    3'  ATCACTCTTGTTTATAAATCAC 43710         _     TTTAGA
                                ATCACTTT GTTTAT      CAC
                                |||||||| ||||||      |||
                                TAGTGAGA CAAATA      GTG
                                     A     TTTA__
GAM3004  CREB1     3'  ATCACTTTGCTTTATTTGACA  39594           AT   A
                                ATCACTTTGTTT  TTT GACA
                                ||||||||||||  ||| ||||
                                TAGTGAAACGAA  AAA CTGT
                                      AT   _
GAM3004  EGR1      3'  TCACTTTGTTTAAGCAAACAC  12668           TTT
                                TCACTTTGTTTA   TAGACAC
                                ||||||||||||   |||||||
                                AGTGAAACAAAT   GTTTGTG
                                      TC_
GAM3004  ERBB2     3'  TCGCTTTTGTTCTTAGACAC   20823    A   _   ATT
                                TC CTTT GTTT   TTAGACAC
                                || |||| ||||   ||||||||
                                AG GAAA CAAG   AATCTGTG
                                 C   A   ___
GAM3004  IDS       3'  CAGCTTGTTTATTTTAGA     25959    C
                                CA TTTGTTTATTTTAGA
                                || ||||||||||||||
```

```
                                GT GAACAAATAAAATCT
                                 C
GAM3004  NCAM2    3'  CTTTGTTTGTTTAGACAC    21224        AT
                                CTTTGTTT  TTTAGACAC
                                ||||||||  |||||||||
                                GAAACAAA  AAATCTGTG
                                    C_
GAM3004  OGN      3'  ACTTTGTTTCGAACGTAGACA  37457        ATTT__
                                ACTTTGTTT     TAGACA
                                |||||||||     ||||||
                                TGAAACAAA     ATCTGT
                                    GCTTGC
GAM3004  SACM1L   3'  CACTAAGTTTTAGACA     30425     TT   ATTT
                                CACT  GTTT    TAGACA
                                ||||  ||||    ||||||
                                GTGA  CAAA    ATCTGT
                                  TT   ____
GAM3004  SLC16A7  3'  TCACTTTGTAGGATTAGGCA  21838        TTATT   A
                                TCACTTTGT     TTAG CA
                                |||||||||     |||| ||
                                AGTGAAACA     AATC GT
                                    TCCT_    C
GAM3004  TGFBR1   3'  ATCACTTTCTTTAGTAATAAGA 21432        G   TTTT__
           CA                   ATCACTTT TTTA     AGACA
                                ||||||| ||||     |||||
                                TAGTGAAA AAAT     TCTGT
                                    G    CATTAT
GAM3004  ZIC3     3'  ATCACCACTGTTTTAGACA    18244       _     ATTT
                                ATCACT TTGTTT    TAGACA
                                |||||| ||||||    ||||||
                                TAGTGG GACAAA    ATCTGT
                                   T     ____
GAM3004  ZNF236   3'  CTTCGTGAACTAGACAC     28860       TTATT
                                CTTTGT    TTAGACAC
                                ||||||    ||||||||
                                GAAGCA    GATCTGTG
                                   CTT__
GAM3005  CSPG4    3'  TGAATATATTATCCTATTGGC  12494         ATG   TA__
                                TGAGTATATTAT   CCT    GC
                                ||||||||||||   |||    ||
                                ACTTATATAATA   GGA    CG
                                      ___   TAAC
GAM3005  FCMD     3'  AGTATATCCTTCCTTAGC    27511        ATATG
                                AGTATATT    CCTTAGC
                                ||||||||    |||||||
                                TCATATAG    GGAATCG
                                    GAA__
GAM3005  RAP1A    3'  AGTATATTATATATTTTAGC   16150          CC
                                AGTATATTATATG  TTAGC
                                ||||||||||||  |||||
```

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                                TCATATAATATAT  AATCG
                                       AA
GAM3006 ROR2     3' ACCGTGTTCTGTACAATACTG 21255        GC  CTC   C
                                ACCGTGTT  GT   CGA ACTG
                                ||||||||  ||   ||| ||||
                                TGGCACAA  CA   GTT TGAC
                                    GA  T__   A
GAM3007 SLC22A5  3' TTCAATGGAGCATTTATTAT  16864      A     CTGAAA
                                TTCAA TGGAGC     ATTAT
                                ||||| ||||||     |||||
                                AAGTT ACCTCG     TAATA
                                   _     TAAA__
GAM3007 XPR1     3' AATTAAGCTGAAAATTATA   21845     G   C
                                AAT GAGC TGAAAATTATA
                                ||| |||| ||||||||||
                                TTA TTCG ACTTTTAATAT
                                  A   _
GAM3008 F13A1    3' TTTAACTTTATTTTAAGCT   44984       AC
                                TTTAA  TTATTTTAAGCT
                                |||||  ||||||||||||
                                AAATT  AATAAAATTCGA
                                   GA
GAM3009 DCK      3' TAAATTATCATCTTTGAAT   8980
                                TAAATTATCATTTTTGAAT
                                ||||||||||||||||||
                                ATTTAATAGTAGAAACTTA

GAM3009 SFTPA2   3' TGATTATCTGGGTGAATGTATT 27965   A     ATTTT
                                A ATTATC    TGAATGTATT
                                | ||||||    ||||||||||
                                A TAATAG    ACTTACATAA
                                 C     ACCC_
GAM3009 WNT5A    3' TAAATTATCATTTTGAA     18125            T
                                TAAATTATCATTTT GAA
                                |||||||||||||| |||
                                ATTTAATAGTAAAA CTT
                                              _
GAM3009 ZNF195   3' TAAGCTATCATTTTTGAACA   28380     A
                                TAA TTATCATTTTTGAATG
                                ||| ||||||||||||||||
                                ATT GATAGTAAAAACTTGT
                                  C
GAM3010 BHLHB3   3' TGGGAATAGATGCACTTGA   36263        AAATAC    GT
                                TGGGAATA     TACT  TGA
                                ||||||||     ||||  |||
                                ACCCTTAT     GTGA  ACT
                                    CTAC__    __
GAM3010 ITK      3' TGGGAATAATAATATTACCTCA 24449         _   C    GT_
             TG                   TGGGAATAA AATA TACT   TG
                                ||||||||| |||| ||||   ||
```

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                                ACCCTTATT TTAT ATGG   AC
                                     A    A    AGT
GAM3010  MPV17    3'  TGGGAATAAGACTATTATCAAG 43264         AAT    C   TG
                                TGGGAATAA   ACTA TGT  AG
                                |||||||||   |||| |||  ||
                                ACCCTTATT   TGAT ATA  TC
                                     C__    A   GT
GAM3010  MSR1     3'  TGGGAATAAAAATGCTGA     14664           TACTAC
                                TGGGAATAAAA     TGTTGA
                                ||||||||||      ||||||
                                ACCCTTATTTT     ACGACT
                                      T_____
GAM3010  RNMT     3'  TGGGAATAATGGTGCTGA     19159         AATACTAC
                                TGGGAATAA       TGTTGA
                                |||||||||       ||||||
                                ACCCTTATT       ACGACT
                                     ACC_____
GAM3010  SCP2     3'  TGGGAAGAAAATACTGTTTCTG 16486       T       ACTG
                                TGGGAA AAAATACT    TTG
                                ||||||| ||||||||    |||
                                ACCCTT TTTTATGA    GAC
                                   C       CAAA
GAM3010  SFRP4    3'  TGGGTATAAAATACTTGA     16588      A        ACTGT
                                TGGG ATAAAATACT     TGA
                                |||| ||||||||||     |||
                                ACCC TATTTTATGA     ACT
                                  A         _____
GAM3010  WASF1    3'  TGGGAAGGGGATACTGCTA    19448       TAAAATAC
                                TGGGAA       TACTGTTG
                                ||||||       ||||||||
                                ACCCTT       ATGACGAT
                                   CCCCT___
GAM3011  CNN2     3'  GCATGTGGCCGGGGAAGATG   20403     CCTCC  A
                                GCA     CC GGGAAGATG
                                |||     || |||||||||
                                CGT     GG CCCTTCTAC
                                  ACACC  C
GAM3011  F2RL3    3'  TGGGCACCTCCCCAGTACAG   19534     A          GGA
                                TG GCACCTCCCCAG   AG
                                || ||||||||||||   ||
                                AC CGTGGAGGGGTC   TC
                                 C          ATG
GAM3011  GALK1    3'  TGAGCACCCGGATATGGAAGAT 6679          CCCCAG
            G                    TGAGCACCT      GGAAGATG
                                |||||||||      ||||||||
                                ACTCGTGGG      CCTTCTAC
                                     CCTATA
GAM3011  GCNT3    5'  GAGCACAGGGAAGT       21906        CTCCCC       A
                                GAGCAC     AGGGAAG T
                                ||||||     ||||||| |
```

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                                CTCGTG     TCCCTTC A
                                  ______      C
GAM3011  GPR56    3'  GAGGAGAACCCCAGGGAAGATG 24998     CACCT
                                GAG    CCCCAGGGAAGATG
                                |||    ||||||||||||||
                                CTC    GGGGTCCCTTCTAC
                                  CTCTT
GAM3011  RBP4     3'  GAACTGAGGGAAGATG      40593      ACCTCCCC
                                GAGC       AGGGAAGATG
                                ||||       ||||||||||
                                CTTG       TCCCTTCTAC
                                  AC______
GAM3011  SLC8A2   3'  CGAGGGTCCCCCAGGGA     42412      CACC
                                TGAG   TCCCCAGGGA
                                ||||   ||||||||||
                                GCTC   GGGGGTCCCT
                                  CCA_
GAM3011  TBX3     3'  TGAACACCTCCCCGCCTGG    32440           AG__
                                TGAGCACCTCCCC   GG
                                ||||||||||||   ||
                                ACTTGTGGAGGGG   CC
                                       CGGA
GAM3011  CDY1     5'  TCTCCATACTTACTGCCTG    21715        A  CG  CTC
                                TCTCCATA CT  CT   GCCTG
                                |||||||| ||  ||   |||||
                                AGAGGTAT GA  GA   CGGAC
                                    _  AT  ___
GAM3012  ADCY9    3'  GGGCAGCGGGTGGGCGCCG    10022         CGC    A
                                GGGCAGCGG   GGGCG CG
                                |||||||||   ||||| ||
                                CCCGTCGCC   CCCGC GC
                                     CA_    G
GAM3012  ADRBK1   3'  GGGCAGCGGCTGGGTTGG     11537         GC   CGACG
                                GGGCAGCGGC  GGG    GG
                                ||||||||||  |||    ||
                                CCCGTCGCCG  CCC    CC
                                     A_   AA___
GAM3012  AMPH     5'  GGCGGCGGCGCGGAGGA      11600     A       GCGAC
                                GGC GCGGCGCGG    GGGA
                                ||| |||||||||    ||||
                                CCG CGCCGCGCC    TCCT
                                  C       _____
GAM3012  ANKH     5'  GGGAGGCGAGGGGCGACGGG   38322     CAGC   C_
                                GGG   GGCG  GGGCGACGGG
                                |||   ||||  ||||||||||
                                CCC   CCGC  CCCGCTGCCC
                                  T___   TC
GAM3012  ATP8A2   3'  GGGTGCGGCGCGGGGG      45262     CA       CGACG
                                GGG  GCGGCGCGGG    GG
                                |||  ||||||||||    ||
```

```
                                CCC  CGCCGCGCCC    CC
                                  A_       _____
GAM3012  AXUD1    5'  GGCAGCGGCGGCGGCGGCGGGA 37491          CG   A
                 G                 GGCAGCGGCG  GGCG CGGGAG
                                   ||||||||||  |||| ||||||
                                   CCGTCGCCGC  CCGC GCCCTC
                                        CG   C
GAM3012  BACE     5'  GGGCGGCGGCGCGGGCAGGG  39964      A          AC
                                   GGGC GCGGCGCGGGCG  GGG
                                   |||| ||||||||||||  |||
                                   CCCG CGCCGCGCCCGT  CCC
                                     C         __
GAM3012  BACE     5'  GGGCAGCGGGCGCGGGCTCCCG 39963          _      GA_
                 G                 GGGCAGCGG CGCGGGC   CGG
                                   |||||||| |||||||   |||
                                   CCCGTCGCC GCGCCCG   GCC
                                        C      AGG
GAM3012  CAPN5    5'  GGGCACGGCGCGGGCGCTGGAG 44930       G          ACG
                                   GGGCA CGGCGCGGGCG   GGAG
                                   ||||| ||||||||||   ||||
                                   CCCGT GCCGCGCCCGC   CCTC
                                     _         GA_
GAM3012  CD81     5'  GGGCGGCGGGCGGCCTGCGGG  20347      A   C   GCGA
                                   GGGC GCGG GCGG    CGGG
                                   |||| |||| ||||    ||||
                                   CCCG CGCC CGCC    GCCC
                                     C   _    GGAC
GAM3012  CDH4     3'  GGGCAGCGGCCGGGTGCAGG   12178          G   CGA
                                   GGGCAGCGGC CGGG   CGGG
                                   |||||||||| ||||   ||||
                                   CCCGTCGCCG GCCC   GTCC
                                        _   AC_
GAM3012  CDK5R2   5'  GGGCGCGCGGACTGGCGGG   19476      AGCG       GA_
                                   GGGC   GCGCGGGC   CGGG
                                   ||||   ||||||||   ||||
                                   CCCG   CGCGCCTG   GCCC
                                     ____       ACC
GAM3012  CHRNA4   5'  GGCGGCGGCGCGGCAGGGAG   8854      A        G  AC
                                   GGC GCGGCGCGG CG  GGGAG
                                   ||| |||||||| ||  |||||
                                   CCG CGCCGCGCC GT  CCCTC
                                     C       _ __
GAM3012  CHST2    5'  GGCCGGCGGCGCGGCGGA    41714     A_       GCGA
                                   GGC  GCGGCGCGG    CGGG
                                   |||  |||||||||    ||||
                                   CCG  CGCCGCGCC    GCCT
                                     GC       _____
GAM3012  CRAT     5'  GGGCAACGGTGCCCGGGA    19666          C  GGGCGA
                                   GGGCAGCGG GC     CGGGA
                                   |||||||| ||     |||||
```

```
                                CCCGTTGCC CG     GCCCT
                                     A  G_____
GAM3012  CSNK2A2  5'  GGCGGCGGCGCGGCGGGGG    12488     A       G  AC
                                GGC GCGGCGCGG CG  GGG
                                ||| ||||||||| ||  |||
                                CCG CGCCGCGCC GC  CCC
                                  C       _ __
GAM3012  CSNK2A2  5'  GGCGGCGGCGCGGCGGGGGG   12489     A       G  AC
                                GGC GCGGCGCGG CG  GGG
                                ||| ||||||||| ||  |||
                                CCG CGCCGCGCC GC  CCC
                                  C       _ C_
GAM3012  CSNK2A2  5'  GGGGGGCGGCGCGGGGCGCAGA 12491     CA        _ A
                                GGG  GCGGCGCGGG CG CGGG
                                |||  |||||||||| || ||||
                                CCC  CGCCGCGCCC GC GTCT
                                  CC        C _
GAM3012  DRIL1    5'  GGGCGCTAGGGGTGGGCGGCGG 23371      A __ CGC    A
            G                    GGGC GC  GG   GGGCG CGGG
                                ||||  ||  ||   ||||| ||||
                                CCCG CG  CC   CCCGC GCCC
                                  _ AT  CCA    C
GAM3012  E2F1     5'  GGCGGCGGCGCGGGCCCATGG  44489     A        GA  _
                                GGC GCGGCGCGGGC  CG GG
                                ||| ||||||||||  || ||
                                CCG CGCCGCGCCCG  GT CC
                                  C         G_  A
GAM3012  EN1      3'  GGGCAGCGAGGCGGTGGGG    10918         C    GCGAC
                                GGGCAGCGG GCGG    GGG
                                |||||||| ||||    |||
                                CCCGTCGCT CGCC    CCC
                                     C   AC___
GAM3012  EVC      5'  GGGCGGCGACGCGGGACTTGGA 30977      A        _ GACG
            G                    GGGC GCGGCGCGGG C    GGAG
                                |||| |||||||||| |    ||||
                                CCCG CGCTGCGCCC G    CCTC
                                  C        T AA__
GAM3012  FASN     5'  GGGCGGCGGTGCGGGCGGCGGA 19942      A   C      A
                                GGGC GCGG GCGGGCG CGGG
                                |||| |||| ||||||| ||||
                                CCCG CGCC CGCCCGC GCCT
                                  C   A      C
GAM3012  FGD1     5'  GGGCGGAGGCGCGGGCGGAG   20909      AGC        AC
                                GGGC   GGCGCGGGCG  GGG
                                ||||   ||||||||||  |||
                                CCCG   CCGCGCCCGC  CTC
                                  CCT         __
GAM3012  FMNL     5'  GGGCAGCGGCGGCGCAGGCGGG 25305          ___      AC
            GG                   GGGCAGCGGC   GCGGGCG  GGG
                                ||||||||||   |||||||  |||
```

```
                                CCCGTCGCCG  CGTCCGC  CCC
                                     CCG     C_
GAM3012  FMR2    5'  GGCAGCGGCGGCGGGGG    12971        _   CGAC
                                GGCAGCGGCG CGGG   GG
                                |||||||||| ||||   ||
                                CCGTCGCCGC GCCC   CC
                                     C   ____
GAM3012  FOXG1B  5'  GGCGGCGGCGCGGGAGCGGG  23510    A       CGA
                                GGC GCGGCGCGGG  CGGG
                                ||| ||||||||||  ||||
                                CCG CGCCGCGCCC  GCCC
                                  C       TC_
GAM3012  FZD10   5'  GGCTGGCGGCGCGGGCACACCG 28456    A_       GA__
            AG                    GGC  GCGGCGCGGGC   CGGG
                                ||| ||||||||||   ||||
                                CCG  CGCCGCGCCCG   GCTC
                                  AC         TGTG
GAM3012  GAS1    5'  GGGCAGCGGCGGCCGCCGGGAG 13071        GC  G  A
                                GGGCAGCGGC  GG CG CGGGAG
                                ||||||||||  || || ||||||
                                CCCGTCGCCG  CC GC GCCCTC
                                     __  G  G
GAM3012  GPC1    5'  GGCGGCGGCGCGGGGCGCGCGG 13254    A       _  A_
            G                     GGC GCGGCGCGGG CG  CGGG
                                ||| ||||||||| ||  ||||
                                CCG CGCCGCGCCC GC  GCCC
                                  C       C  GC
GAM3012  GPR63   5'  GGGCAGCGCGCGGGCGCCCG  36266       G      A_
                                GGGCAGCG CGCGGGCG  CG
                                |||||||| ||||||||  ||
                                CCCGTCGC GCGCCCGC  GC
                                     _      GG
GAM3012  HDAC4   5'  GGCGGCGGCGCGGGCGGG   25776    A       GAC
                                GGC GCGGCGCGGGC   GGG
                                ||| ||||||||||   |||
                                CCG CGCCGCGCCCG   CCC
                                  C       ___
GAM3012  HRB     5'  GGGCAGCGCTGCGCCGGGGG  21089       __   G  CGAC
                                GGGCAGCG  GCGC GG   GGG
                                ||||||||  |||| ||   |||
                                CCCGTCGC  CGCG CC   CCC
                                     GA   G  ____
GAM3012  HTRA3   5'  GGGTGGCAGCGCGGGAGACCGG 44836    CA       C  _
            G                     GGG  GCGGCGCGGG GAC GGG
                                |||  |||||||||| ||| |||
                                CCC  CGTCGCGCCC CTG CCC
                                  AC         T  G
GAM3012  ILF1    5'  GAGCGGCGGCGAGGGGCGGGAG 21107     A    C  CGA
                                GGGC GCGGCG GGG   CGGGAG
                                |||| |||||| |||   ||||||
```

```
                                CTCG CGCCGC CCC   GCCCTC
                                  C     T   C__
GAM3012  INHBB    5'  GGGCAGTGGCGCGGAGCAA   13563       C     _
                                GGGCAG GGCGCGG GCGA
                                |||||| ||||||| ||||
                                CCCGTC CCGCGCC CGTT
                                   A      T
GAM3012  ITGA1    5'  GGCAGCGGCGCCCAGGAGCGGG 41849          __  CGA
                AG                  GGCAGCGGCGC  GGG   CGGGAG
                                |||||||||||  |||   ||||||
                                CCGTCGCCGCG  TCC   GCCCTC
                                      GG   TC_
GAM3012  ITGA11   5'  GCAGCGGCGGCGGGGGG      29199         _   CGAC
                                GCAGCGGCG CGGG    GG
                                |||||||| ||||    ||
                                CGTCGCCGC GCCC    CC
                                     C   _____
GAM3012  JAG2     5'  GGCGGCGGCGCGGGCGGGG   13731     A         AC
                                GGC GCGGCGCGGGCG  GGG
                                ||| ||||||||||||  |||
                                CCG CGCCGCGCCCGC  CCC
                                  C          __
GAM3012  JAG2     5'  GGCGGCGGCGCGGGCGGG    13730     A        GAC
                                GGC GCGGCGCGGGC   GGG
                                ||| ||||||||||   |||
                                CCG CGCCGCGCCCG   CCC
                                  C         ___
GAM3012  KCNQ2    5'  GGGGGGCGGCGCGGGCCCCAG  41513     CA        GA
                                GGG  GCGGCGCGGGC  CGG
                                |||  ||||||||||  |||
                                CCC  CGCCGCGCCCG  GTC
                                  CC         GG
GAM3012  LAMA5    5'  GGACAGCGCGCGCGGCGGGAG  24500         _     GCGA
                                GGGCAGCG GCGCGG    CGGGAG
                                |||||||| ||||||    ||||||
                                CCTGTCGC CGCGCC    GCCCTC
                                     G     _____
GAM3012  LATS2    3'  AGGCAGCGAGTGGTGGGG    31019         CGC  GCGAC
                                GGGCAGCGG   GG    GGG
                                |||||||||   ||    |||
                                TCCGTCGCT   CC    CCC
                                     CA_  AC___
GAM3012  LBX1     5'  GGGCAGGGCGCGGGCCGG    27287       C       GA
                                GGGCAG GGCGCGGGC  CGG
                                |||||| |||||||||  |||
                                CCCGTC CCGCGCCCG  GCC
                                   _       __
GAM3012  LIMK1    3'  GGGCAGCGGCGTGTGGAAAGGG 32534          CG_  C  C
                G                   GGGCAGCGGCG   GG GA GGG
                                ||||||||||   || || |||
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```
                                CCCGTCGCCGC   CC TT CCC
                                      ACA  T  C
GAM3012  NAV2     5'  GGCAGCGGCGGCGGGGGG     41149          _    CGAC
                                GGCAGCGGCG CGGG    GG
                                |||||||||| ||||    ||
                                CCGTCGCCGC GCCC    CC
                                     C   ____
GAM3012  NR2C2    5'  GGGCAGGGCGCGGGGA      17673       C       C
                                GGGCAG GGCGCGGG GA
                                |||||| |||||||| ||
                                CCCGTC CCGCGCCC CT
                                   _      _
GAM3012  OGDH     3'  GGGCAGCGTGTGGCCTGTGGG  45015        GCGCG   GAC_
                                GGGCAGCG    GGC    GGG
                                ||||||||    |||    |||
                                CCCGTCGC    CCG    CCC
                                     ACA__   GACA
GAM3012  PSMA1    5'  GGTGGCGGCGCGGGCCTGG    40614    CA         GACG
                                GG  GCGGCGCGGGC    GG
                                ||  ||||||||||    ||
                                CC  CGCCGCGCCCG    CC
                                 AC          GA__
GAM3012  PTEN     5'  GCGGCGGCGGCGGACGGGAG   7216        CG    _
                                GCGGCG  GGCG ACGGGAG
                                ||||||  |||| |||||||
                                CGCCGC  CCGC TGCCCTC
                                    CG    C
GAM3012  RAB23    5'  GGGTGGTGGGGCGCGGGA    32218     CAGC  CGC     A
                                GGG    GG   GGGCG CGGGA
                                |||    ||   ||||| |||||
                                CCC    CC   CCCGC GCCCT
                                  A___  AC_    _
GAM3012  RCV1     5'  GGGCAGCGGCTGGGGA      16221          GC   C
                                GGGCAGCGGC  GGG GA
                                ||||||||||  ||| ||
                                CCCGTCGCCG  CCC CT
                                      A_  _
GAM3012  RNPEPL1  5'  GGGCGGCGGCGCGGGCCCCGG  32886      A         GA
                                GGGC GCGGCGCGGGC  CGG
                                |||| ||||||||||  |||
                                CCCG CGCCGCGCCCG  GCC
                                   C         GG
GAM3012  S100A10  5'  GGGAGGCGGCGCGGGAGCGGGA 40397     CA        CGA
            G                    GGG  GCGGCGCGGG   CGGGAG
                                |||  ||||||||||   ||||||
                                CCC  CGCCGCGCCC   GCCCTC
                                  TC         TC_
GAM3012  SDC4     3'  GGGTTGCAGTGGTGACGGGAG  16526     CA   CGCG  C
                                GGG  GCGG    GG GACGGGAG
                                |||  ||||    || ||||||||
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                                CCC  CGTC   CC CTGCCCTC
                                  AA   A___  A
GAM3012  SLBP     5'  GGCGGCGGCGCGGGCAGAG   27197    A        AC
                                GGC GCGGCGCGGGCG  GGG
                                ||| ||||||||||||  |||
                                CCG CGCCGCGCCCGT  CTC
                                  C         __
GAM3012  SLC1A2   5'  GGGCGCGGCGAGTGGCGGGAG  41600    A    CG_  GAC
                                GGGC GCGGCG  GGC  GGGAG
                                |||| ||||||  |||  |||||
                                CCCG CGCCGC  CCG  CCCTC
                                  _    TCA  ___
GAM3012  SLC9A3R2 5'  GGGCAGGGGCGCGGGGGA   41529      C      CGACG
                                GGGCAG GGCGCGGG   GGA
                                ||||||| ||||||||    |||
                                CCCGTC CCGCGCCC   CCT
                                   C      _____
GAM3012  SOX10    3'  GGGCAGGGGCTGGGCGGGGG  28009      C  GC   AC
                                GGGCAG GGC  GGGCG  GGG
                                |||||| |||  |||||  |||
                                CCCGTC CCG  CCCGC  CCC
                                   C  A_   C_
GAM3012  SRD5A1   5'  GGGCGGCGGCGCGGGGGG   9831      A       CGAC
                                GGGC GCGGCGCGGG   GGG
                                |||| ||||||||||   |||
                                CCCG CGCCGCGCCC   CCC
                                  C       ____
GAM3012  SURF5    3'  GGCGCTGGTGTGGACAGGAG  27582     _  GC__
                                GGCGC GG   GACGGGAG
                                ||||| ||   ||||||||
                                CCGCG CC   CTGTCCTC
                                   A  ACAC
GAM3012  TFDP1    5'  GGGCGCGGTGCGGAGCGCGGG 28284     A   C   _  A
                                GGGC GCGG GCGG GCG CGGG
                                |||| |||| |||| ||| ||||
                                CCCG CGCC CGCC CGC GCCC
                                  _   A   T  _
GAM3012  TMEPAI   5'  GGCGCGGCGGCGCGGCGCGGG  33613   _ A      G  A
                                GG GC GCGGCGCGG CG CGGG
                                || || |||||||| || ||||
                                CC CG CGCCGCGCC GC GCCC
                                 G  C       _ _
GAM3012  TNFSF7   5'  GCAGGAGGGGCGATGGG    10357     C  CGC    C
                                GCAG GG   GGGCGA GGG
                                |||| ||   |||||| |||
                                CGTC TC   CCCGCT CCC
                                  C ___     A
GAM3012  TP73     3'  GGGCGGTGGCGCAGGCTGCAG  24070     AGC      GA
                                GGGC   GGCGCGGGC  CGG
                                ||||   |||||||||  |||
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                                CCCG  CCGCGTCCG  GTC
                                  CCA       AC
GAM3012  ZNF219   5'  GGGGGGCGGCGCGGCGGGG   32335    CA      G  AC
                                GGG  GCGGCGCGG CG  GGG
                                |||  ||||||||| ||  |||
                                CCC  CGCCGCGCC GC  CCC
                                  CC       _ __
GAM3012  ZNF219   5'  GGCCGGCGGCGCGGGCGTCAG  32330    A_        A
                                GGC  GCGGCGCGGGCG CGG
                                |||  |||||||||||| |||
                                CCG  CGCCGCGCCCGC GTC
                                  GC         A
GAM3012  ZNF278   5'  GGGCGGTGGCGCGGGCCGGG   36804    AGC       GA
                                GGGC  GGCGCGGGC  CGGG
                                ||||  |||||||||  ||||
                                CCCG  CCGCGCCCG  GCCC
                                  CCA       __
GAM3013  C18orf1  3'  TCCTGGATGTTAGGGGTATGAT 41230         C  ATTT___
            TATAG                  TCCTGGGTGT AGG      TTATAG
                                |||||||||| |||      ||||||
                                AGGACCTACA TCC      AATATC
                                      A  CCATACT
GAM3013  DIPA     3'  CTTGGTGTCAGGATTTCT    27786    G
                                CT GGTGTCAGGATTTTT
                                || ||||||||||||||
                                GA CCACAGTCCTAAAGA
                                 A
GAM3013  HNRPF    5'  TCTTGGGTGTGGCTTTTT    22459    C     CA  A
                                TC TGGGTGT  GG TTTTT
                                || |||||||  || |||||
                                AG ACCCACA  CC AAAAA
                                 A      __ G
GAM3013  PON1     3'  AGTGAGAAGGATTTTTAT    7777      TC_
                                GGTG  AGGATTTTTAT
                                ||||  ||||||||||
                                TCAC  TCCTAAAAATA
                                  TCT
GAM3014  BCL7A    5'  CCTCCTGGGGAGGTGGC     34205     _   TCGC   AAG
                                CCTC TGGG   GAGG  TGGC
                                |||| ||||   ||||  ||||
                                GGAG ACCC   CTCC  ACCG
                                  G   ____   ___
GAM3014  BGN      3'  CCTCTGGGTGGCTGTGG     11814        CGCGA  AA
                                CCTCTGGGT    GG  GTGG
                                |||||||||    ||  ||||
                                GGAGACCCA    CC  CACC
                                      _____ GA
GAM3014  CHC1     3'  CCTCTGGGCGTGGGTCCGTG  10424       T  CGA  AA_
                                CCTCTGGG CG   GG   GTG
                                |||||||| ||   ||   |||
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                                GGAGACCC GC   CC   CAC
                                     _ AC_  AGG
GAM3014  HTRA3    3'  CCCTGGATGAGGGGGTGG    44825        CGC    AA
                                CTCTGGGT   GAGG  GTGG
                                ||||||||   ||||  ||||
                                GGGACCTA   CTCC  CACC
                                     ___    CC
GAM3014  KLK4     3'  CCTCTGGGTCTGGGGAAG    41749         GCGA
                                CCTCTGGGTC    GGAAG
                                ||||||||||    |||||
                                GGAGACCCAG    CCTTC
                                      ACC_
GAM3014  LARS2    3'  CCTCATTCATGTGAGGAAGTGG 31677     TGGG   C__
                                CCTC    TCG   GAGGAAGTGG
                                ||||    |||   ||||||||||
                                GGAG    AGT   CTCCTTCACC
                                  TA__   ACA
GAM3014  OTOF     5'  CCTCTGGGCTGTGAGTCTGTG  22056        CGC   GAA
                                CCTCTGGGT   GAG   GTG
                                |||||||||   |||   |||
                                GGAGACCCG   CTC   CAC
                                     ACA   AGA
GAM3014  SDC4     3'  CCCTGGGTTGCAGTGG      16523         C  GAGGA
                                CTCTGGGT GC    AGTGG
                                |||||||| ||    |||||
                                GGGACCCA CG    TCACC
                                     A ______
GAM3014  TNFRSF8  3'  CTCTGGGTTGGTGAGGGGCG   10319        CGC_   AAGT
                                CTCTGGGT    GAGG    GGCG
                                ||||||||    ||||    ||||
                                GAGACCCA    CTCC    CCGC
                                     ACCA    _____
GAM3015  GALNT1   3'  TGAAGATTTATTGCTGT     33843      G     CA
                                TGAAG ATTTAT  CTGT
                                ||||| ||||||  ||||
                                ACTTC TAAATA  GACA
                                   _     AC
GAM3015  GAS7     3'  TGCAGGACAACTGTATA     25285    A    TTATC
                                TG AGGAT    ACTGTATA
                                || |||||    ||||||||
                                AC TCCTG    TGACATAT
                                 G    T_____
GAM3015  UBE3A    3'  TAAAGGATTTGTTCATATAT   7863          A_   C
                                TGAAGGATTT  TCA TGTAT
                                ||||||||||  ||| |||||
                                ATTTCCTAAA  AGT ATATA
                                      CA   _
GAM3015  HRMT1L2  3'  GAAAAACACAGTCACGATGT   11358         A__     C
                                GAAGGATA   TCACGA GT
                                ||||||||   |||||| ||
```

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                                CTTTTTGT  AGTGCT CA
                                    GTC    A
GAM3016 ENTPD3   5' CTGCCGCAGAGGCGGCCCGCG 10350       _ C  AT
                                CTGCCGCA AG GCG  CCCGCG
                                |||||||| || |||  ||||||
                                GACGGCGT TC CGC  GGGCGC
                                    C  _  C_
GAM3016 HCN2     3' TGCGTGAGCGCGATGGGGGC  10176    C CA     CCC_
                                TGC G  AGCGCGAT   GC
                                ||| |  ||||||||   ||
                                ACG C  TCGCGCTA   CG
                                  _ AC      CCCC
GAM3016 MARK3    5' TGCCTCAGGGCGCCCCGCGA  14365     GCA  C  A
                                TGCC   AG GCG TCCCGCGA
                                ||||   || ||| ||||||||
                                ACGG   TC CGC GGGGCGCT
                                  AG_  C  _
GAM3016 NEK4     5' TGCTGGGGCCCGGCCCGCGAC  17194    CGCAA  G  AT
                                TGC    GC CG  CCCGCGAC
                                |||    || ||  ||||||||
                                ACG    CG GC  GGGCGCTG
                                 ACCC_  G  C_
GAM3016 TRRAP    5' CCTGCAGGCCCGGCCCGCGAC  18591    _  A  G  AT
                                CC GCA GC CG  CCCGCGAC
                                || ||| || ||  ||||||||
                                GG CGT CG GC  GGGCGCTG
                                 A  C  G  C_
GAM3016 WEE1     5' CCGCGGCTTCCCGCGA     18084     AAGC  GA
                                CCGC   GC  TCCCGCGA
                                ||||   ||  ||||||||
                                GGCG   CG  AGGGCGCT
                                  C___  A_
GAM3016 EFNB2    3' TCCGTGTGACAAGTCCGG    19885    G   C   TTG
                                TC CGTG GGC   GAGTCCGG
                                || |||| |||   ||||||||
                                AG GCAC CTG   TTCAGGCC
                                 _   A  ___
GAM3016 FNTB     3' GTGGGCTTGGAGTCTGG     13006    C        C
                                GTG GGCTTGGAGTC GG
                                ||| ||||||||||| ||
                                CAC CCGAACCTCAG CC
                                  _        A
GAM3016 LAMP1    5' TCGCGTGCGCGTTTGGGC    24510        GC_   A
                                TCGCGTGCG   TTGG GT
                                |||||||||   |||| ||
                                AGCGCACGC   AACC CG
                                    GCA   _
GAM3017 CDC25A   5' TCGGCCGCGCGCCACCGGCGCC 12150    A  ACCA  _   __
            CG                    TC GCC   CGC CCGC  GCGCCCG
                                || |||   ||| ||||  |||||||
```

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                                AG CGG   GCG GGTG  CGCGGGC
                                 C  C___  C   GC
GAM3017 CIT     3' TCAGCCACCTGCCCCTCC   43055        AC   GCGCG
                                TCAGCCACC  GCCC    CC
                                |||||||||  ||||    ||
                                AGTCGGTGG  CGGG    GG
                                     A_   GA___
GAM3017 CNGB1   3' AGCCACCATGCCCGGCA    10530       C    C
                                AGCCACCA GCCCG GCG
                                |||||||| ||||| |||
                                TCGGTGGT CGGGC CGT
                                    A    _
GAM3017 COL15A1 5' AGCGCTGGCCCGCGCGCTCG  12350    CACCAC       C
                                AGC     GCCCGCGCGC CG
                                |||     |||||||||| ||
                                TCG     CGGGCGCGCG GC
                                  CGAC__        A
GAM3017 CSPG2   5' TCGGCTGTTGCGTCCGCACGCC 20481   A  CACCA  C
                                TC GC    CG CCGCGCGCC
                                || ||    || |||||||||
                                AG CG    GC GGCGTGCGG
                                 C  ACAAC  A
GAM3017 EFG2    5' AGCCACCATGCCTGGCC    37032       C   CGCGC
                                AGCCACCA GCC    GCC
                                |||||||| |||    |||
                                TCGGTGGT CGG    CGG
                                    A   AC___
GAM3017 ETS1    5' GCCCGCCGCGCGCC       23461    ACCA   C
                                GCC   CGCC GCGCGCC
                                |||   |||| |||||||
                                CGG   GCGG CGCGCGG
                                  ____   _
GAM3017 G6PD    5' TCGGCCACCACCCCTCG    7611    A      G  G
                                TC GCCACCAC CCC CG
                                || |||||||| ||| ||
                                AG CGGTGGTG GGG GC
                                 C       _  A
GAM3017 GNB3    5' TCAGCTGCGACGCCCGCGCCC 13223      CACC       G
                                TCAGC   ACGCCCGCGC CC
                                |||||   |||||||||| ||
                                AGTCG   TGCGGGCGCG GG
                                   ACGC        _
GAM3017 HCN2    3' TCAGCCACTGGGCCGCCCC   10174       CAC  CGC  G
                                TCAGCCAC  GCC  GC CCC
                                ||||||||  |||  || |||
                                AGTCGGTG  CGG  CG GGG
                                    ACC  ___ _
GAM3017 HIRA    5' CAGCCGCCACCCGCGC     17737      A  AC
                                CAGCC CC  GCCCGCGC
                                ||||| ||  ||||||||
```

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                                GTCGG GG  TGGGCGCG
                                  C __
GAM3017 HPCAL1   5' CAGCTGCTGCGCCGGCCC   39542     CACCAC  CC   __
                                CAGC     GC  GCGC  GCCC
                                ||||     ||  ||||  ||||
                                GTCG     CG  CGCG  CGGG
                                  A_____  A_   GC
GAM3017 IFNGR2   5' TCGGCCGCCCGCGCCCCC   24389    A   ACCAC      G
                                TC GCC    GCCCGCGC CCC
                                || |||    |||||||| |||
                                AG CGG    CGGGCGCG GGG
                                 C  _____       G
GAM3017 IL11     3' AGCCACCATGCCTGGCC     8478         C   CGCGC
                                AGCCACCA GCC    GCC
                                |||||||| |||    |||
                                TCGGTGGT CGG    CGG
                                     A   AC___
GAM3017 ILF1     5' TCGGCCGCCGCGCACC     21118    A   ACCAC   C
                                TC GCC    GCC GCGCGCC
                                || |||    ||| |||||||
                                AG CGG    CGG CGCGTGG
                                 C  _____  _
GAM3017 LRRC2    3' AGTCACCGCGCCCGGCCC    36028    C    A     CGC
                                AG CACC CGCCCG   GCCC
                                || |||| ||||||   ||||
                                TC GTGG GCGGGC   CGGG
                                 A   C     ___
GAM3017 NESG1    5' TCAGCCACACGCCCTGACTCCG 29583        C     GC  GC
                                TCAGCCAC ACGCCC  GC  CCG
                                |||||||| ||||||  ||  |||
                                AGTCGGTG TGCGGG  TG  GGC
                                     _     AC  A_
GAM3017 NT5C3    5' GCTACCGCGCCCACCTCG    32408    C   A      G_
                                GC ACC CGCCCGC  CG
                                || ||| |||||||  ||
                                CG TGG GCGGGTG  GC
                                 A   C      GA
GAM3017 ODC1     5' TCGGCCGCCCCCGCCGCGCCCG 14923    A   A  ACG    _
                                TC GCC CC   CCCGC GCGCCCG
                                || ||| ||   ||||| |||||||
                                AG CGG GG   GGGCG CGCGGGC
                                 C   C ___     G
GAM3017 PSMD5    3' AGCCACCGCGCCCAGCCC    22777        A     CGC
                                AGCCACC CGCCCG   GCCC
                                ||||||| ||||||   ||||
                                TCGGTGG GCGGGT   CGGG
                                     C     ___
GAM3017 RENBP    5' TCAGCTGACACAGCCGCGCCCG 16244       CAC  _  CGC
                                TCAGC   CAC GCC   GCGCCCG
                                |||||   ||| |||   |||||||
```

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                                AGTCG  GTG CGG  CGCGGGC
                                  ACT  T  ___
GAM3017 TAF1    3' AGCCACCACGCCTGGCC    39886          CGCGC
                                AGCCACCACGCC    GCC
                                ||||||||||||    |||
                                TCGGTGGTGCGG    CGG
                                      AC___
GAM3017 TNFRSF12 5' TCAGCCCCGCGCCCGCAGGGCC 19129      A  A      C_
          CG                    TCAGCC CC CGCCCGCG  GCCCG
                                |||||| || ||||||||  |||||
                                AGTCGG GG GCGGGCGT  CGGGC
                                  _ C       CC
GAM3017 ZFP103   5' GCCGCCGCAACGCCGCGCCCG 24958    A ___    CGC
                                GCC CC   ACGCC   GCGCCCG
                                ||| ||   |||||   |||||||
                                CGG GG   TGCGG   CGCGGGC
                                  C  CGT    ___
GAM3018 HS2ST1   3' TCAGAAGCACCCAATAT    29340      T  TTCTC
                                TCAGA GC    TCCAATAT
                                ||||| ||    ||||||||
                                AGTCT CG    GGGTTATA
                                   T  T____
GAM3018 SCA1    3' GAAGCCTCCAATGTATC    7279    T  TTCT     A
                                GA GC    CTCCAAT TATC
                                || ||    ||||||| ||||
                                CT CG    GAGGTTA ATAG
                                 T  _____      C
GAM3018 ADRBK2   3' TTTTGGTAATTATCTTCCAA  23133        AA  __
                                TTTTGGTAA  ATC  CCAA
                                |||||||||  |||  ||||
                                AAAACCATT  TAG  GGTT
                                     AA   AA
GAM3018 ARMET    3' CTTTAATAAAAAAATCCCA   25665         __
                                TTTTGGTAAAA  ATCCCA
                                ||||||||||  ||||||
                                GAAATTATTTT  TAGGGT
                                      TT
GAM3018 ASTN    3' CATTTTGGTAAACTTCTCA   42944          AA  C
                                CATTTTGGTAAA  TC CA
                                ||||||||||||  || ||
                                GTAAAACCATTT  AG GT
                                      GA  A
GAM3018 CA6     3' CTTTAATCAGAATCCCAA    10232       AAA
                                TTTTGGT   AATCCCAA
                                |||||||   ||||||||
                                GAAATTA   TTAGGGTT
                                    GTC
GAM3018 COL5A3   3' CATCTTGGTCCCCA       31850         AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
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                                GTAGAACCA    GGGGT
                                      _____
GAM3018 CREBL2   3' CATTTTGGTAGAAATTGCA   10578        A   CC
                                CATTTTGGTA AAAT  CA
                                |||||||||| ||||  ||
                                GTAAAACCAT TTTA  GT
                                     C   AC
GAM3018 CYP1B1   3' ATTTTGGTAATGGTGTCCCA  6444         AAA__
                                ATTTTGGTAA    TCCCA
                                ||||||||||    |||||
                                TAAAACCATT    AGGGT
                                     ACCAC
GAM3018 DLG5     3' CATTTTAGTACAGAAAATCCCA 44450        ___
                                CATTTTGGTA   AAAATCCCA
                                |||||||||   |||||||||
                                GTAAAATCAT   TTTTAGGGT
                                     GTC
GAM3018 DPYSL3   3' CACTTCGGAAGTCCCAA    10763       TAAAAA
                                CATTTTGG     TCCCAA
                                ||||||||     ||||||
                                GTGAAGCC     AGGGTT
                                    TTC___
GAM3018 ETV5     3' CATTTTGATCTCTTCCCA    20847       AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
                                GTAAAACTA    AGGGT
                                     GAGA_
GAM3018 F2RL3    3' CATCTTGGCCTCCCA       19513       AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
                                GTAGAACCG    AGGGT
                                     G____
GAM3018 FNTB     3' CATCTTGGTGGGACCCAA    13003       AAAAAT
                                CATTTTGGT     CCCAA
                                |||||||||     |||||
                                GTAGAACCA     GGGTT
                                     CCCT__
GAM3018 GAC1     3' TTTTGGTAAAAAGTAGTCC   26799         ____
                                TTTTGGTAAAAA   TCC
                                ||||||||||||   |||
                                AAAACCATTTTT   AGG
                                      CATC
GAM3018 GATA4    5' ACTCCGGAAAATCCCAA     13105       TA
                                ATTTTGG  AAAATCCCAA
                                |||||||  ||||||||||
                                TGAGGCC  TTTTAGGGTT
                                     __
GAM3018 HYOU1    3' CATTTTGGTCAGCCCCA     40632       AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
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                                GTAAAACCA    GGGGT
                                     GTC__
GAM3018 IL17R    3' ATCTTGGTATCCCA      30738        AAAA
                                ATTTTGGTA   TCCCA
                                |||||||||   |||||
                                TAGAACCAT   AGGGT
                                     ____
GAM3018 IRTA1    3' CATCTCTGCAAATCCCAA    36352      G   AA
                                CATTTT GTAA  ATCCCAA
                                |||||| ||||  |||||||
                                GTAGAG CGTT  TAGGGTT
                                   A   __
GAM3018 LEP      3' ACCTTGGTGGGAATCCCA    6907        AAA
                                ATTTTGGT   AATCCCA
                                ||||||||   |||||||
                                TGGAACCA   TTAGGGT
                                     CCC
GAM3018 MAP1A    3' CATTTTGGTTTCCCA      14341        AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
                                GTAAAACCA    AGGGT
                                     A____
GAM3018 NEDD4    3' CATTTTAGTAGTTCCC     43100         AAAA
                                CATTTTGGTA   TCCC
                                ||||||||||   ||||
                                GTAAAATCAT   AGGG
                                     CA__
GAM3018 PLIN     3' CATTTTGGTTCCCCA      15396        AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
                                GTAAAACCA    GGGGT
                                     A____
GAM3018 POU2AF1  3' CATTTTAAAATCCCA      26365       GTAA
                                CATTTTG   AAATCCCA
                                |||||||   ||||||||
                                GTAAAAT   TTTAGGGT
                                     ____
GAM3018 PPP2R4   3' CACTTTGGTCACTTCTCCCAA 41327        AAAAA_
                                CATTTTGGT     TCCCAA
                                |||||||||     ||||||
                                GTGAAACCA     AGGGTT
                                     GTGAAG
GAM3018 PSMD5    3' CATCTTGGCCTCCCA      22778        AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
                                GTAGAACCG    AGGGT
                                     G____
GAM3018 RNF18    3' CATGAAGCAAAAGATCCC    33776     TTT     _
                                CAT   GGTAAAA ATCCC
                                |||   ||||||| |||||
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                                GTA   TCGTTTT TAGGG
                                  CT_      C
GAM3018  RPL22    3'  CATTTTGGTTCCCA       9736          AAAAA
                                CATTTTGGT    TCCCA
                                |||||||||    |||||
                                GTAAAACCA    AGGGT
                                      _____
GAM3018  RRM1     3'  ATTTTGGTGAAAATCCCAA   9754          A
                                ATTTTGGT AAAATCCCAA
                                |||||||| ||||||||||
                                TAAAACCA TTTTAGGGTT
                                     C
GAM3018  SPAM1    5'  CACTTTGGTTTACCCAA     17060         AAAAAT
                                CATTTTGGT    CCCAA
                                |||||||||    |||||
                                GTGAAACCA    GGGTT
                                     AAT___
GAM3018  UBE2E3   3'  CATTTTGATATCCCA       26816         AAAA
                                CATTTTGGTA   TCCCA
                                ||||||||||   |||||
                                GTAAAACTAT   AGGGT
                                     _____
GAM3018  WHSC1    5'  ATTCTGAAGCAAATCCCA    39353         TAA
                                ATTTTGG   AAATCCCA
                                |||||||   ||||||||
                                TAAGACT   TTTAGGGT
                                    TCG
GAM3018  WNT5A    3'  TTTTGGAATAATCCCAA     18141         T  A
                                TTTTGG AA AATCCCAA
                                |||||| || ||||||||
                                AAAACC TT TTAGGGTT
                                   _ A
GAM3018  YWHAG    3'  ATTTTGGCAAAAATGTCAA   29788           CC
                                ATTTTGGTAAAAAT  CAA
                                |||||||||||||  |||
                                TAAAACCGTTTTTA  GTT
                                       CA
GAM3019  AKAP2    3'  TAAGTGGTTAACATACACA   28498     A     _
                                TAA TGGTTAA ATATACA
                                ||| ||||||| |||||||
                                ATT ACCAATT TATGTGT
                                  C      G
GAM3019  CRI1     3'  AAATGGTTATGACAATG     30731         AATAT
                                AAATGGTTA    ACAATG
                                |||||||||    ||||||
                                TTTACCAAT    TGTTAC
                                     AC___
GAM3019  DHFR     3'  AAATGGTTAAGTACAAT     8986          ATA
                                AAATGGTTAA   TACAAT
                                ||||||||||   ||||||
```

```
                                TTTACCAATT  ATGTTA
                                      C__
GAM3019  DLD     3'  GGTTAAATAAAACAAGTGA   6466        T_  _
                                GGTTAAATA  ACAA TGA
                                |||||||||  |||| |||
                                CCAATTTAT  TGTT ACT
                                     TT   C
GAM3019  ITM2B   3'  TAAATAGTTAAATATATTTGA  35095           CAA
                                TAAATGGTTAAATATA  TGA
                                ||||||||||||||||  |||
                                ATTTATCAATTTATAT  ACT
                                         AA_
GAM3019  NT5C2   3'  ATGGAAGAAAATATACAATG  29228     TT__
                                ATGG   AAATATACAATG
                                ||||   ||||||||||||
                                TACC   TTTATATGTTAC
                                  TTCT
GAM3019  PFN2    3'  TGGTTAACATACAAATGA    15243       A    _
                                TGGTTAA TATACAA TGA
                                ||||||| ||||||| |||
                                ACCAATT GTATGTT ACT
                                   _     T
GAM3019  RB1CC1  3'  TAAATGGTTAATGTGCAATGA  31317         ATATA
                                TAAATGGTTAA    CAATGA
                                ||||||||||    ||||||
                                ATTTACCAATT    GTTACT
                                      ACAC_
GAM3020  A2M     3'  GAACAGGACTCCAGCAAAGCAC 6141      AA  GAACT
                                GAACA  AC    CAAAGCAC
                                |||||  ||    ||||||||
                                CTTGT  TG    GTTTCGTG
                                  CC  AGGTC
GAM3020  ABCD2   5'  CGAACAAAACCGGCTCTAGC   23150        GAA   AA
                                CGAACAAAAC   CTC  AGC
                                ||||||||||   |||  |||
                                GCTTGTTTTG   GAG  TCG
                                      GCC   A_
GAM3020  CDKN1B  5'  CGAACAAAACAAAGCGC     19795          CTCAAA
                                CGAACAAAACGAA     GC
                                ||||||||||||      ||
                                GCTTGTTTTGTTT     CG
                                      CG____
GAM3020  CSDA    3'  GAACAAAAACGGAAAAAAAAGC 18894        _  AACTC_
           A                     GAACAAAA CG     AAAGCA
                                ||||||||  ||     ||||||
                                CTTGTTTT GC     TTTCGT
                                     T  CTTTTT
GAM3020  GARS    5'  ACGAGAACCTTCAAAGCA    13054      ACAAAAC   __
                                ACGA      GAAC  TCAAAGCA
                                ||||      ||||  ||||||||
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                                TGCT     CTTG  AGTTTCGT
                                  _______   GA
GAM3020  SELP    3'  AACAGGTGAGTCAAAGCAC   16547     AAAC  AC
                                AACA   GA  TCAAAGCAC
                                ||||   ||  |||||||||
                                TTGT   CT  AGTTTCGTG
                                  CCA_  C_
GAM3020  SLC17A5  3'  ACGAACAAAACACAGC     29685         GAACTCAA
                                ACGAACAAAAC      AGC
                                ||||||||||       |||
                                TGCTTGTTTTG      TCG
                                     TG_______
GAM3020  SNAP25   3'  GAACAAAAGACACAAAG     39261        C  ACT
                                GAACAAAA GA   CAAAG
                                |||||||| ||   |||||
                                CTTGTTTT CT   GTTTC
                                    _  GT_
GAM3020  ZFP36L1  3'  GAACAAAATTAACAAAAAAAAG 22283        CG   TC___
            CA                    GAACAAAA  AAC    AAAGCA
                                ||||||||  |||    ||||||
                                CTTGTTTT  TTG    TTTCGT
                                    AA   TTTTT
GAM3021  GALC    3'  ACTTTAAAAAGTAAGTACA   6669       CACCTC
                                GCTTT     AAGTAAGTACA
                                |||||     ||||||||||
                                TGAAA     TTCATTCATGT
                                  TTT___
GAM3021  HPGD    3'  TAGCTTTCCTCTTTTAAAGTA  9246         AC  CAAGT
                                TAGCTTTC  CT    AAGTA
                                ||||||||  ||    |||||
                                ATCGAAAG  GA    TTCAT
                                    GA  AAAT_
GAM3021  LARS    3'  TAGCCTTCATCAAAGTA     33480         CC   _
                                TAGCTTTCA  TCAA GTA
                                |||||||||  |||| |||
                                ATCGGAAGT  AGTT CAT
                                    __   T
GAM3021  NCALD   3'  TAGCTTTCAATTCAAATTAGT  36772         CC     A
                                TAGCTTTCA  TCAAGT AGT
                                |||||||||  |||||| |||
                                ATCGAAAGT  AGTTTA TCA
                                    TA     A
GAM3021  NRAS    3'  TAGCTTTCCTTCAATGGTA   14852        ACC   GTAA
                                TAGCTTTC   TCAA   GTA
                                ||||||||   ||||   |||
                                ATCGAAAG   AGTT   CAT
                                    GA_    AC__
GAM3021  PTGS2   3'  GCTTTTCACTTAAAATAAGT   9690       _  CTC
                                GCTTT CAC   AAGTAAGT
                                ||||| |||   ||||||||
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                                CGAAA GTG   TTTATTCA
                                  A   AAT
GAM3021  SH2D1A   3'  GCTTTTACCTCAAGAAAT    14290       C       T
                                GCTTT ACCTCAAG AAGT
                                ||||| |||||||| ||||
                                CGAAA TGGAGTTC TTTA
                                  A       _
GAM3021  SLC9A6   3'  GCCTTTCGGAGAGTAAGTACA  26830       CACCTCA
                                GCTTT      AGTAAGTACA
                                |||||      ||||||||||
                                CGGAA      TCATTCATGT
                                  AGCCTC_
GAM3021  XCL1     3'  TAGCTTTCACCTCTGATAGACA 16493            AA   A T
                                TAGCTTTCACCTC  GTA G ACA
                                ||||||||||||  ||| | |||
                                ATCGAAAGTGGAG  TAT C TGT
                                        AC  _ _
GAM3022  USH2A    5'  ACAGGACCGCTGTCCCTCGT   28299      A       G  GC
                                ATAG ACCGCTGTC CC  CGT
                                |||| |||||||| ||  |||
                                TGTC TGGCGACAG GG  GCA
                                  C       _  A_
GAM3023  PDYN     3'  TTTATGATGTGTATACTA     35926          AACA
                                TTTATGATGT    TATATTA
                                ||||||||||    |||||||
                                AAATACTACA    ATATGAT
                                      C___
GAM3023  PACE4    3'  TAAATTCTTGTGACACACA    15059        CAT     T
                                TAAATTCT   TGACA CATA
                                ||||||||   ||||| ||||
                                ATTTAAGA   ACTGT GTGT
                                     AC_    _
GAM3023  SLC2A3   3'  TAAATTCTTATTGCACC     27981        C    A
                                TAAATTCT ATTG CATC
                                |||||||| |||| ||||
                                ATTTAAGA TAAC GTGG
                                     A   _
GAM3024  BAT5     3'  TGAACACAGAGAATCACAAATA 34510     C       CCA
              A                  TGA CACAGAGA   ACAAATAA
                                 ||| ||||||||   ||||||||
                                 ACT GTGTCTCT   TGTTTATT
                                   T       TAG
GAM3024  CANX     3'  TGACCACAGAACAACA      44668          AC
                                TGACCACAGAG  CAACA
                                ||||||||||  |||||
                                ACTGGTGTCTT  GTTGT
                                          __
GAM3024  CTGF     3'  TGGTCACACTCTCAACAAATAA 12509    AC    GAGAC
              A                  TG  CACA    CAACAAATAAA
                                 ||  ||||    ||||||||||
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                                AC  GTGT    GTTGTTTATTT
                                 CA    GAGA_
GAM3024  FUT3     3'  TGGCCACAAAGGACTCCAGCA  6644     A       A___   A
                                TG CCACAGAG    CCA CA
                                || ||||||||    ||| ||
                                AC GGTGTTTC    GGT GT
                                 C       CTGA   C
GAM3024  HOXD4    3'  ACCACATTTCCCAACAAATAAA 31165       GAGA
                                ACCACA    CCAACAAATAAA
                                ||||||    ||||||||||||
                                TGGTGT    GGTTGTTTATTT
                                   AAAG
GAM3024  MBL2     3'  TGACACAAGCATCAACAAATA  6966      C   G  AC_
                                TGAC ACA AG   CAACAAATA
                                |||| ||| ||   |||||||||
                                ACTG TGT TC   GTTGTTTAT
                                  _  _ GTA
GAM3024  MYBL1    3'  ACCACAAAAGCAAATAA     41970         ACCAA
                                ACCACAGAG    CAAATAA
                                |||||||||    |||||||
                                TGGTGTTTT    GTTTATT
                                     C____
GAM3024  OCRL     3'  ACCACAGAGCTTGAATAA    7088          ACCAACA
                                ACCACAGAG      AATAA
                                |||||||||      |||||
                                TGGTGTCTC      TTATT
                                     GAAC___
GAM3024  PPP4R1   3'  TGGCCACAGAGCCCAGCAA   23078    A      A  A
                                TG CCACAGAG CCA CAA
                                || |||||||| ||| |||
                                AC GGTGTCTC GGT GTT
                                 C       G   C
GAM3024  SCN3A    5'  TGACCACAGAGGTTTACAAA  27954          ACCA
                                TGACCACAGAG    ACAAA
                                ||||||||||    |||||
                                ACTGGTGTCTC    TGTTT
                                      CAAA
GAM3024  GUCY1A3  3'  CATTTTGTCATGTTAAACAGG  41834          ATGCTGCC
                                TATTTTGTCAT       ACAGG
                                ||||||||||       |||||
                                GTAAAACAGTA       TGTCC
                                      CAATT___
GAM3024  IL6R     3'  TTTTGTCATCCACA        8189          ATGCTG
                                TTTTGTCAT     CCACA
                                |||||||||     |||||
                                AAAACAGTA     GGTGT
                                      _______
GAM3024  NFE2L1   3'  TATTTTGTCATGTGCTCAACAG 17332          A   GCC
                                TATTTTGTCAT TGCT   ACAG
                                |||||||||| ||||   ||||
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                                ATAAAACAGTA ACGA   TGTC
                                      C    GT_
GAM3025 CLASP1   5' TGGCACTCCCAGAGCTTTGCC 42250     A       TATACCTC
                                TGG ACTCCCGGA       GCC
                                ||| |||||||||       |||
                                ACC TGAGGGTCT       CGG
                                  G        CGAAA___
GAM3025 LEP      3' TGGAATTCTCAGAGGGAACCT 6920       C C    TAT_
                                TGGAA TC CGGA    ACCT
                                ||||| || ||||    ||||
                                ACCTT AG GTCT    TGGA
                                   A A    CCCT
GAM3026 ADAR     3' TAAGTCATGATTATCTGA    31908         CAATT   GA
                                TAAGTCATGA    TTA  TGA
                                ||||||||||    |||  |||
                                ATTCAGTACT    AAT  ACT
                                      _____   AG
GAM3026 UCP3     3' AGTCATAATAATTTCCCGA   17850        C     A_
                                AGTCATGA AATTTT  GA
                                |||||||| ||||||  ||
                                TCAGTATT TTAAAG  CT
                                     A     GG
GAM3026 ANGPT1   3' TTTTCATATTTTCCCAC     40250      G       CAGA
                                TTTT CATATTTT    CCCAC
                                |||| ||||||||    |||||
                                AAAA GTATAAAA    GGGTG
                                   _      ____
GAM3026 APM1     3' TTTTGCATCTATCATCCAC   22026        ATTT   GAC
                                TTTTGCAT    TCA   CCAC
                                ||||||||    |||   ||||
                                AAAACGTA    AGT   GGTG
                                     GAT_   A__
GAM3026 BCL6     3' TTTTGCATACTCCCC       39911           TCAGA
                                TTTTGCATATTT    CCC
                                ||||||||||||    |||
                                AAAACGTATGAG    GGG
                                      _____
GAM3026 BCRP2    3' TTTTACATATCTGGACCTGCC 41656          TCA    CA
                                TTTTGCATATTT   GACC  CC
                                ||||||||||||   ||||  ||
                                AAAATGTATAGA   CTGG  GG
                                       C__     AC
GAM3026 CARP     3' TTCTGCATGTCCCAGTTTGCC 30797        AT TT   AC__
                                TTTTGCAT  T  CAG    CC
                                ||||||||  |  |||    ||
                                AAGACGTA  A  GTC    GG
                                     C_ GG   AAAC
GAM3026 CRADD    3' TTTTACATATGAGACACC    19183         TTTC   _
                                TTTTGCATAT    AGAC CC
                                ||||||||||    |||| ||
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                                AAAATGTATA   TCTG GG
                                     C___    T
GAM3026  GALNT3   3'  TTTTGCATAATTTTCAAA    21017        _
                                TTTTGCATA TTTTCAGA
                                ||||||||| ||||||||
                                AAAACGTAT AAAAGTTT
                                      T
GAM3026  HNRPD    3'  TTTTGCACATTTATCCAGA   36393         __
                                TTTTGCATATT  TTCAGA
                                ||||||||||  ||||||
                                AAAACGTGTAA  AGGTCT
                                      AT
GAM3026  KIAA0442 3'  TTTTGCATATATGAACCA    31794         TTTCA  C
                                TTTTGCATAT    GA CCA
                                |||||||||     || |||
                                AAAACGTATA    CT GGT
                                      TA___  T
GAM3026  MAK      3'  TTTTGCATATTTCTTCCAGA   25384         ___
                                TTTTGCATATT   TTCAGA
                                ||||||||||   ||||||
                                AAAACGTATAA   AGGTCT
                                      AGA
GAM3026  RPA1     3'  TTTTGATTAATATCAGACCCA  16374      CATATTT
                                TTTTG      TCAGACCCA
                                |||||      |||||||||
                                AAAAC      AGTCTGGGT
                                   TAATTAT
GAM3026  TP53BP2  5'  CTTTGCACAGATCCA       24060       TATTTT   C
                                TTTTGCA     CAGA CCA
                                |||||||     |||| |||
                                GAAACGT     GTCT GGT
                                   _______   A
GAM3027  C18orf1  3'  CATTTTCTCATAAACTATGCA  41217    CG        AACAG
                                CA  TTCTCATAAA    GCA
                                ||  ||||||||||    |||
                                GT  AAGAGTATTT    CGT
                                 AA        GATA_
GAM3027  IGF1     3'  GTATGTCTGGAAAACAGGCA   8344     TC_  ATA
                                GT   TC   AAAACAGGCA
                                ||   ||   ||||||||||
                                CA   AG   TTTTGTCCGT
                                 TAC  ACC
GAM3027  KIF3B    3'  GTTCTTATTCAAACAGGCA    22040      C  AA
                                GTTCT AT  AAACAGGCA
                                ||||| ||  |||||||||
                                CAAGA TA  TTTGTCCGT
                                   A  AG
GAM3027  NRG1     3'  GTTCTCATGCGACAGGCA    30345        AAAA
                                GTTCTCAT    ACAGGCA
                                ||||||||    |||||||
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                                CAAGAGTA   TGTCCGT
                                    CGC_
GAM3027  PODXL    3'  TCCTGTTTTCCCCCAAACAGGC 23983     ACG_    ATAA
             A                   TCC   TTCTC   AAACAGGCA
                                 |||   |||||   |||||||||
                                 AGG   AAGGG   TTTGTCCGT
                                   ACAA    GG__
GAM3027  PTGIS    3'  TCCATCTGGAGAACAGGC    9677      CGT   CATAAA
                                 TCCA  TCT     AACAGGC
                                 ||||  |||     |||||||
                                 AGGT  AGA     TTGTCCG
                                   ___   CCTC__
GAM3027  REQ      3'  GTTGTGTTAAAAAACAGGCA  26549     CTCAT_
                                 GTT     AAAAACAGGCA
                                 |||     ||||||||||
                                 CAA     TTTTTGTCCGT
                                   CACAAT
GAM3027  SEPN1    3'  TCCACTTTGGGGAAAACAGGCA 42437      GTTCTCATA
                                 TCCAC       AAAACAGGCA
                                 |||||       ||||||||||
                                 AGGTG       TTTTGTCCGT
                                    AAACCCC__
GAM3027  PCLO     3'  TTAATGTAGTTTTTTGAGAATG 45314         CTTATTAT
                                 TTAGTGTAGT      AGAATG
                                 ||||||||||      ||||||
                                 AATTACATCA      TCTTAC
                                       AAAAAC__
GAM3028  CASP7    3'  TGATGGATACATATC      10276    C    GTGTCC
                                 TG ATGGA     TACATATC
                                 || |||||     ||||||||
                                 AC TACCT     ATGTATAG
                                  _    _______
GAM3028  CYR61    3'  CATGGAGTGTCCCCCTTCA   11415          ACATA
                                 CATGGAGTGTCCT    TCA
                                 ||||||||||||     |||
                                 GTACCTCACAGGG    AGT
                                        GGA__
GAM3028  GAS7     3'  TAGAGTGCCTATGTATCAA   25280       T   CA
                                 TGGAGTG CCTA  TATCAA
                                 ||||||| ||||  ||||||
                                 ATCTCAC GGAT  ATAGTT
                                     _   AC
GAM3028  HPGD     3'  TGTATGTGAGTGTTTTACA   9248     C  _    CC
                                 TG ATG GAGTGT  TACA
                                 || ||| ||||||  ||||
                                 AC TAC CTCACA  ATGT
                                  A  A     AA
GAM3028  ITPR2    3'  TGCATGCAGACATATC      13681       G  TGTCCT
                                 TGCATG AG     ACATATC
                                 |||||| ||     |||||||
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                                ACGTAC TC     TGTATAG
                                   G ______
GAM3028 BTEB1    5' TGTTGCTGGTAGTAAATTT   10223       TCT
                                TGTTGTT  TGGTAAATTT
                                |||||||  ||||||||||
                                ACAACGA  ATCATTTAAA
                                   CC_
GAM3028 KMO      3' TGTTGTTTCTCTAAAAATTT  18963         GGT
                                TGTTGTTTCTT  AAATTT
                                ||||||||||  ||||||
                                ACAACAAAGAG  TTTAAA
                                      ATT
GAM3029 FGF6     3' TCAATCGAACAGATGATGCTTT 34228        CGCAAC_
             A                   TCGATCGGAT     GCTTTA
                                ||||||||||      ||||||
                                AGTTAGCTTG     CGAAAT
                                      TCTACTA
GAM3029 ANGPT1   5' GACCGTTCAGCATGGA     40241       TGA  T
                                GGCCGTTC  CGT GGA
                                ||||||||  ||| |||
                                CTGGCAAG  GTA CCT
                                   TC_  _
GAM3029 PAX5     3' TACCTGGCTGTTCTGACTTGA 32519    GC  C      G
                                TAC  GGC GTTCTGAC TTGG
                                |||  ||| |||||||| ||||
                                ATG  CCG CAAGACTG AACT
                                  GA  A      _
GAM3029 RNF6     5' GCGGCCGTTCTCTCGG      25576         GACG
                                GCGGCCGTTCT   TTGG
                                ||||||||||   ||||
                                CGCCGGCAAGA   AGCC
                                      G___
GAM3030 CASP10   3' TGCAGGGCTGTGAAGTGAGAC 37393     AGACG      _ _
                                TGCA    TGTGAAGT AG C
                                ||||    |||||||| || |
                                ACGT    ACACTTCA TC G
                                  CCCG_       C  T
GAM3030 EML1     3' AGGGCGTGTGAACAAGGGA   40719   A_      GT  C
                                AG  CGTGTGAA  AG GA
                                ||  ||||||||  || ||
                                TC  GCACACTT  TC CT
                                 CC       GT  C
GAM3030 FEZ1     3' AAGACCCTAGAAAGTAGCGA  35419      GTGT_
                                AAGAC    GAAGTAGCGA
                                |||||    ||||||||||
                                TTCTG    TTTCATCGCT
                                   GGATC
GAM3030 FOXD1    5' TGCGGGACGGGTGAGAGT    20934     AA   T   _
                                TGC  GACG GTGA AGT
                                |||  |||| |||| |||
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                                ACG  CTGC CACT TCA
                                  CC   C   C
GAM3030  FPGS     3'  TGCAAGGCATGTGAAATGCAGC 22434      A      __
                                TGCAAG CGTGTGAA  GTAGC
                                |||||| ||||||||  |||||
                                ACGTTC GTACACTT  CGTCG
                                   C       TA
GAM3030  PABPN1   3'  AGACGTGTCCATGGCGAA    21605       GAA  A
                                AGACGTGT   GT GCGAA
                                ||||||||   || |||||
                                TCTGCACA   TA CGCTT
                                     GG_  C
GAM3030  PITPNB   3'  TGCAGGACATGTGGGAAAAC  29628     A      AAGT
                                TGCA GACGTGTG   AGC
                                |||| ||||||||   |||
                                ACGT CTGTACAC   TTG
                                  C       CCTT
GAM3031  SNAP23   3'  TATATGAATCACTAAGAG    19252          AGTTGC
                                TATATGAATTAT     AAGAG
                                ||||||||||||     |||||
                                ATATACTTAGTG     TTCTC
                                       A_____
GAM3032  ACHE     3'  TGGGGTGGGGATGGGCA     31866       AGAC  C
                                TGGGGTGG   GG GTGGGCG
                                ||||||||   || |||||||
                                ACCCCACC   CC TACCCGT
                                     _____  _
GAM3032  CRAT     5'  TGGGGCGGGGGCGGGGCA    19670       AGAC   T
                                TGGGGTGG   GGCG GGGCG
                                ||||||||   |||| |||||
                                ACCCCGCC   CCGC CCCGT
                                     C___   _
GAM3032  FASN     3'  TGGGGTGGGGATGGTGGA    19946       A  C  CG
                                TGGGGTGG GA GG  TGGG
                                |||||||| || ||  ||||
                                ACCCCACC CT CC  ACCT
                                     C  A  __
GAM3032  FASN     3'  TGGGGTGGGGTGGGGA      19947       AGACG C    C
                                TGGGGTGG    G GTGGG GA
                                ||||||||    | ||||| ||
                                ACCCCACC    C CACCC CT
                                     _____ _    _
GAM3032  FGFRL1   3'  TGGGGTGGGGGGGTGG      34923       AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ACCCCACC   CC CACC
                                     C___  _
GAM3032  GFRA2    5'  TGGGGTGAGAGGCGGGCGA   11270       G   C   GT
                                TGGGGTG AGA GGC  GGGCGA
                                ||||||| ||| |||  ||||||
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                                ACCCCAC TCT CCG  CCCGCT
                                      _  _  __
GAM3032  GRP58    5'  TGGGGTGGGGACGGCCGGA   23679        A     G
                                TGGGGTGG GACGGC TGGG
                                |||||||| |||||| ||||
                                ACCCCACC CTGCCG GCCT
                                     C     _
GAM3032  MEOX1    3'  TGGGGTGGGGGGTAGTTGGG   30405        AGAC  CG__
                                TGGGGTGG   GG   TGGG
                                ||||||||   ||   ||||
                                ACCCCACC   CC   ACCC
                                     C___  ATCA
GAM3032  MEOX1    3'  TGGGGTGGGGAGGTGGG     30404        A  CG C
                                TGGGGTGG GA  G GTGGG
                                |||||||| ||  | |||||
                                ACCCCACC CT  C CACCC
                                     C  __ _
GAM3032  MKI67    3'  TAGGGTGGCTGTGGGTGG    14527        AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ATCCCACC   CC CACC
                                     GACA  _
GAM3032  NCOR2    3'  TGGCGTGGAGGTGCGTGG    26743     G     ACG
                                TGG GTGGAG   GCGTGG
                                ||| ||||||   ||||||
                                ACC CACCTC   CGCACC
                                  G     CA_
GAM3032  PAX2     3'  TGGGGTGAGGCTGGGGCG    19613        AGAC   GT
                                TGGGGTGG   GGC  GGGCG
                                ||||||||   |||  |||||
                                ACCCCACT   CCG  CCCGC
                                     _____  AC
GAM3032  PDE4A    5'  GGGTGGAGGCGGTGGG      26277        A   CG
                                GGGTGGAG CGG  TGGG
                                |||||||| |||  ||||
                                CCCACCTC GCC  ACCC
                                     C  __
GAM3032  PSD      5'  TGGGGTGGGGCTGGCG      15793        AGAC   GTG
                                TGGGGTGG   GGC   GGCG
                                ||||||||   |||   ||||
                                ACCCCACC   CCG   CCGC
                                     _____  A__
GAM3032  RAD23A   3'  TGGGGTGGGGGGTGG       22800        AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ACCCCACC   CC CACC
                                     _____  _
GAM3032  RANBP3   3'  TGGGGTGGGGGGCGGGTGGGCG  28775        AGA   C
                                TGGGGTGG   CGG GTGGGCG
                                ||||||||   ||| |||||||
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                                ACCCCACC   GCC CACCCGC
                                    CCC  _
GAM3032  SH3GL1   3'  TGGGGTGGGTGTGGGTGG    16677       AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ACCCCACC   CC CACC
                                    CACA  _
GAM3032  SPTBN4   3'  TGGGGTGGGGGGTGGTGA    36092       AGAC  C   GC
                                TGGGGTGG   GG GTGG  GA
                                ||||||||   || ||||  ||
                                ACCCCACC   CC CACC  CT
                                    _____  _   A_
GAM3032  TNFSF12  3'  TGAGGTGGAGAGTGGGCG    19187        CGGC
                                TGGGGTGGAGA   GTGGGCG
                                ||||||||||   |||||||
                                ACTCCACCTCT   CACCCGC
                                     _____
GAM3032  TTC3     3'  TGGGGTGGGGAAGGAGAATGG  17719       A  C  C__
                                TGGGGTGG GA GG   GTGG
                                |||||||| || ||   ||||
                                ACCCCACC CT CC   TACC
                                    C  T  TCT
GAM3032  XYLB     3'  TGGGGTGGGGGCGGCTATGGG  23030       AGA   _
                                TGGGGTGG   CGGC GTGGG
                                ||||||||   |||| |||||
                                ACCCCACC   GCCG TACCC
                                    CCC    A
GAM3032  YWHAE    3'  TGGGGAGGAGGGGGTGG     27600      T   AC  C
                                TGGGG GGAG  GG GTGG
                                |||||  ||||  || ||||
                                ACCCC CCTC  CC CACC
                                   T   C_  _
GAM3032  ZYX      3'  TGAGGTGGGGGCAGGTGG    18439       AGA   C
                                TGGGGTGG   CGG GTGG
                                ||||||||   ||| ||||
                                ACTCCACC   GTC CACC
                                    CCC  _
GAM3032  ACHE     3'  TGGGGTGGGGATGGGCA     8567        AGAC  C
                                TGGGGTGG   GG GTGGGCG
                                ||||||||   || |||||||
                                ACCCCACC   CC TACCCGT
                                     _____  _
GAM3032  CRAT     5'  TGGGGCGGGGGCGGGGCA    19670       AGAC   T
                                TGGGGTGG   GGCG GGGCG
                                ||||||||   |||| |||||
                                ACCCCGCC   CCGC CCCGT
                                    C____   _
GAM3032  FASN     3'  TGGGGTGGGGTGGGGA      19947       AGACG C    C
                                TGGGGTGG    G GTGGG GA
                                ||||||||    | ||||| ||
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                                ACCCCACC    C CACCC CT
                                ______ _    _
GAM3032  FASN    3'  TGGGGTGGGGATGGTGGA    19946       A  C  CG
                                TGGGGTGG GA GG  TGGG
                                |||||||| || ||  ||||
                                ACCCCACC CT CC  ACCT
                                    C  A  __
GAM3032  FGFRL1  3'  TGGGGTGGGGGGGTGG      34923       AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ACCCCACC   CC CACC
                                    C___  _
GAM3032  GFRA2   5'  TGGGGTGAGAGGCGGGCGA   11270       G   C   GT
                                TGGGGTG AGA GGC  GGGCGA
                                ||||||| ||| |||  ||||||
                                ACCCCAC TCT CCG  CCCGCT
                                   _  _  __
GAM3032  GRP58   5'  TGGGGTGGGGACGGCCGGA   23679       A     G
                                TGGGGTGG GACGGC TGGG
                                |||||||| |||||| ||||
                                ACCCCACC CTGCCG GCCT
                                    C     _
GAM3032  MEOX1   3'  TGGGGTGGGGAGGTGGG     30404       A  CG C
                                TGGGGTGG GA  G GTGGG
                                |||||||| ||  | |||||
                                ACCCCACC CT  C CACCC
                                    C  __ _
GAM3032  MEOX1   3'  TGGGGTGGGGGTAGTTGGG   30405       AGAC  CG__
                                TGGGGTGG   GG   TGGG
                                ||||||||   ||   ||||
                                ACCCCACC   CC   ACCC
                                    C___  ATCA
GAM3032  MKI67   3'  TAGGGTGGCTGTGGGTGG    14527       AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ATCCCACC   CC CACC
                                    GACA  _
GAM3032  NCOR2   3'  TGGCGTGGAGGTGCGTGG    26743    G     ACG
                                TGG GTGGAG   GCGTGG
                                ||| ||||||   ||||||
                                ACC CACCTC   CGCACC
                                  G     CA_
GAM3032  PAX2    3'  TGGGGTGAGGCTGGGGCG    19642       AGAC   GT
                                TGGGGTGG   GGC  GGGCG
                                ||||||||   |||  |||||
                                ACCCCACT   CCG  CCCGC
                                    _____  AC
GAM3032  PDE4A   5'  GGGTGGAGGCGGTGGG     26277       A   CG
                                GGGTGGAG CGG  TGGG
                                |||||||| |||  ||||
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                                CCCACCTC GCC  ACCC
                                    C  __
GAM3032  PSD     5'  TGGGGTGGGGCTGGCG     15793       AGAC  GTG
                                TGGGGTGG   GGC  GGCG
                                ||||||||   |||  ||||
                                ACCCCACC   CCG  CCGC
                                    _____  A__
GAM3032  RAD23A  3'  TGGGGTGGGGGGTGG      22800       AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ACCCCACC   CC CACC
                                    _____ _
GAM3032  RANBP3  3'  TGGGGTGGGGGGCGGGTGGGCG  28775       AGA  C
                                TGGGGTGG   CGG GTGGGCG
                                ||||||||   ||| |||||||
                                ACCCCACC   GCC CACCCGC
                                    CCC  _
GAM3032  SH3GL1  3'  TGGGGTGGGTGTGGGTGG    16677       AGAC  C
                                TGGGGTGG   GG GTGG
                                ||||||||   || ||||
                                ACCCCACC   CC CACC
                                    CACA  _
GAM3032  SPTBN4  3'  TGGGGTGGGGGGTGGTGA    36092       AGAC  C   GC
                                TGGGGTGG   GG GTGG  GA
                                ||||||||   || ||||  ||
                                ACCCCACC   CC CACC  CT
                                    _____ _   A_
GAM3032  TNFSF12 3'  TGAGGTGGAGAGTGGGCG    19187        CGGC
                                TGGGGTGGAGA   GTGGGCG
                                ||||||||||    |||||||
                                ACTCCACCTCT   CACCCGC
                                    _____
GAM3032  TTC3    3'  TGGGGTGGGGAAGGAGAATGG  17719       A  C  C__
                                TGGGGTGG GA GG   GTGG
                                |||||||| || ||   ||||
                                ACCCCACC CT CC   TACC
                                    C  T  TCT
GAM3032  XYLB    3'  TGGGGTGGGGGCGGCTATGGG  23030       AGA   _
                                TGGGGTGG   CGGC GTGGG
                                ||||||||   |||| |||||
                                ACCCCACC   GCCG TACCC
                                    CCC    A
GAM3032  YWHAE   3'  TGGGGAGGAGGGGGTGG     27600      T   AC  C
                                TGGGG GGAG  GG GTGG
                                ||||| ||||  || ||||
                                ACCCC CCTC  CC CACC
                                   T   C_  _
GAM3032  ZYX     3'  TGAGGTGGGGGGCAGGTGG    18439       AGA  C
                                TGGGGTGG   CGG GTGG
                                ||||||||   ||| ||||
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                                ACTCCACC   GTC CACC
                                     CCC   _
GAM3033  PCDHB16   5'  TGAGATTAATGATTAAATAA   34145    A          TT
                                A GGATTAATGATTA  TAA
                                | ||||||||||||  |||
                                A TCTAATTACTAAT  ATT
                                 C           TT
GAM3033  TAP2      3'  GGATAATGATTAAAAAC     33109      T       TTT
                                GGAT AATGATTA   AAC
                                |||| ||||||||   |||
                                CCTA TTACTAAT   TTG
                                   _       TT_
GAM3033  PCDHB16   5'  TGAGATTAATGATTAAATAA   34145    A          TT
                                A GGATTAATGATTA  TAA
                                | ||||||||||||  |||
                                A TCTAATTACTAAT  ATT
                                 C           TT
GAM3033  TAP2      3'  GGATAATGATTAAAAAC     8084       T       TTT
                                GGAT AATGATTA   AAC
                                |||| ||||||||   |||
                                CCTA TTACTAAT   TTG
                                   _       TT_
GAM3034  ARAF1     3'  GAGGAGACAGGGGGCTCA    41910       A  C    A
                                GAGGA AC GGGG CTCA
                                ||||| || |||| ||||
                                CTCCT TG CCCC GAGT
                                   C  T   C
GAM3034  CDC34     3'  AGAGGAGACGGGGACCAG    20349       AAC     CTCA
                                AGAGGA   CGGGGA   CCGG
                                ||||||   ||||||   ||||
                                TCTCCT   GCCCCT   GGTC
                                   CT_     _____
GAM3034  CIAS1     3'  GAGGGACCGGAGAACACTGGC  22206      AA      CT   C
                                GAGG  ACCGGGGA  CAC GGC
                                ||||  ||||||||  ||| |||
                                CTCC  TGGCCTCT  GTG CCG
                                  C_       T_   A
GAM3034  COL2A1    5'  GAGGAAGCGGGAGACCCGGC   37612       AC   _   TCA
                                GAGGAA  CGGG GAC   CCGGC
                                ||||||  |||| |||   |||||
                                CTCCTT  GCCC CTG   GGCCG
                                   C_    T   ____
GAM3034  CRY1      5'  GAGGGGACCGGAGAAGG     19833      AA       CTCACC
                                GAGG  ACCGGGGA     GG
                                ||||  ||||||||     ||
                                CTCC  TGGCCTCT     CC
                                  CC       T______
GAM3034  FTL       5'  AGAGGAAATCGGAGGGCGG   6628         C     ACTCAC
                                AGAGGAAA CGGGG     CGG
                                |||||||| |||||     |||
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                                TCTCCTTT GCCTC     GCC
                                    A    CC____
GAM3034  GAD1     5'  AGGCGGGGACCGGATCGG    30288     AAAC       CAC_
                                AGG   CGGGGACT   CGG
                                |||   ||||||||   |||
                                TCC   GCCCCTGG   GCC
                                 ____      CCTA
GAM3034  GDI2     5'  AGAGGAAAATGGAGCTGG    11256        CC   A  CACC
                                AGAGGAAA  GGGG CT   GG
                                ||||||||  |||| ||   ||
                                TCTCCTTT  CCTC GA   CC
                                    TA   _ ____
GAM3034  GP1BB    3'  GAGGAGGCGGGGACCGG     7624       AAC     CTCA
                                GAGGA   CGGGGA   CCGG
                                |||||   ||||||   ||||
                                CTCCT   GCCCCT   GGCC
                                  CC_     ____
GAM3034  GP1BB    3'  AGGCGGGGACCGGTCCAG    7622      AAAC       CA_
                                AGG   CGGGGACT   CCGG
                                |||   ||||||||   ||||
                                TCC   GCCCCTGG   GGTC
                                 ____      CCA
GAM3034  MYLK2    3'  GAGGGAACCGGGAGCGG     37523      A       ACTCAC
                                GAGG AACCGGGG     CGG
                                |||| ||||||||     |||
                                CTCC TTGGCCCT     GCC
                                  C       C_____
GAM3034  NRXN1    5'  AGGGAGGCCACTTCGCCGG   39838    A   AACC  GG   _ A
                                AG GGA    GG  ACT C CCGG
                                || |||    ||  ||| | ||||
                                TC CCT    CC  TGA G GGCC
                                 _  ____  GG   A C
GAM3034  RGS19IP1 3'  AGGGGGGCCGGGGACCCCGGC  41694    A  AAA       T A
                                AG GG   CCGGGGAC C CCGGC
                                || ||   |||||||| | |||||
                                TC CC   GGCCCCTG G GGCCG
                                 _  CCC       _ _
GAM3034  SLC19A2  5'  GGAGGGGACCCGGCCCGG    42890     AACC       A__
                                GGA   GGGGACTC   CCGG
                                |||   ||||||||   ||||
                                CCT   CCCCTGGG   GGCC
                                 ____      CCG
GAM3034  SLC30A3  5'  AGAGAGAGGCCGGGCCGG    18427     _ AA    GACTCA
                                AGAG GA  CCGGG     CCGG
                                |||| ||  |||||     ||||
                                TCTC CT  GGCCC     GGCC
                                  T  CC    _______
GAM3034  SLC8A2   3'  GAGGAACCGGGGAG       42413       A      CTCACC
                                GAGGAA CCGGGGA     G
                                |||||| |||||||     |
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                                CTCCTT GGCCCCT     C
                                  _    _______
GAM3034  ARAF1    3'  GAGGAGACAGGGGGCTCA    41910      A  C   A
                                GAGGA AC GGGG CTCA
                                ||||| || |||| ||||
                                CTCCT TG CCCC GAGT
                                   C  T   C
GAM3034  CDC34    3'  AGAGGAGACGGGGACCAG    20349      AAC    CTCA
                                AGAGGA  CGGGGA  CCGG
                                ||||||  ||||||  ||||
                                TCTCCT  GCCCCT  GGTC
                                   CT_    _____
GAM3034  CIAS1    3'  GAGGGACCGGAGAACACTGGC  22206     AA     CT  C
                                GAGG  ACCGGGGA  CAC GGC
                                ||||  ||||||||  ||| |||
                                CTCC  TGGCCTCT  GTG CCG
                                  C_      T_  A
GAM3034  COL2A1   5'  GAGGAAGCGGGAGACCCGGC  37612      AC  _  TCA
                                GAGGAA  CGGG GAC  CCGGC
                                ||||||  |||| |||  |||||
                                CTCCTT  GCCC CTG  GGCCG
                                   C_   T  ___
GAM3034  CRY1     5'  GAGGGGACCGGAGAAGG     19833     AA      CTCACC
                                GAGG  ACCGGGGA    GG
                                ||||  ||||||||    ||
                                CTCC  TGGCCTCT    CC
                                  CC      T_____
GAM3034  FTL      5'  AGAGGAAATCGGAGGGCGG   6628       C    ACTCAC
                                AGAGGAAA CGGGG    CGG
                                |||||||| |||||    |||
                                TCTCCTTT GCCTC    GCC
                                    A   CC____
GAM3034  GAD1     5'  AGGCGGGGACCGGATCGG    30288     AAAC     CAC_
                                AGG   CGGGGACT   CGG
                                |||   ||||||||   |||
                                TCC   GCCCCTGG   GCC
                                 ____     CCTA
GAM3034  GDI2     5'  AGAGGAAAATGGAGCTGG    11256      CC   A  CACC
                                AGAGGAAA  GGGG CT   GG
                                ||||||||  |||| ||   ||
                                TCTCCTTT  CCTC GA   CC
                                   TA   _ ____
GAM3034  GP1BB    3'  GAGGAGGCGGGGACCGG     7624      AAC    CTCA
                                GAGGA  CGGGGA  CCGG
                                |||||  ||||||  ||||
                                CTCCT  GCCCCT  GGCC
                                  CC_    _____
GAM3034  GP1BB    3'  AGGCGGGGACCGGTCCAG    7622      AAAC     CA_
                                AGG   CGGGGACT  CCGG
                                |||   ||||||||  ||||
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                                TCC   GCCCCTGG  GGTC
                                 _____      CCA
GAM3034  MYLK2    3'  GAGGGAACCGGGAGCGG    37523     A      ACTCAC
                                GAGG AACCGGGG    CGG
                                |||| ||||||||     |||
                                CTCC TTGGCCCT    GCC
                                  C      C_____
GAM3034  NRXN1    5'  AGGGAGGCCACTTCGCCGG   39838    A  AACC  GG  _ A
                                AG GGA   GG  ACT C CCGG
                                || |||   ||  ||| | ||||
                                TC CCT   CC  TGA G GGCC
                                 _  ____ GG  A C
GAM3034  RGS19IP1 3'  AGGGGGGCCGGGGACCCCGGC  41694    A  AAA      T A
                                AG GG  CCGGGGAC C CCGGC
                                || ||  |||||||| | |||||
                                TC CC  GGCCCCTG G GGCCG
                                 _ CCC      _ _
GAM3034  SLC19A2  5'  GGAGGGGACCCGGCCCGG   42890    AACC      A__
                                GGA   GGGGACTC  CCGG
                                |||   ||||||||  ||||
                                CCT   CCCCTGGG  GGCC
                                 _____      CCG
GAM3034  SLC30A3  5'  AGAGAGAGGCCGGGCCGG    18427     _ AA    GACTCA
                                AGAG GA  CCGGG    CCGG
                                |||| ||  |||||     ||||
                                TCTC CT  GGCCC    GGCC
                                  T  CC   _______
GAM3034  SLC8A2   3'  GAGGAACCGGGGAG      42413      A     CTCACC
                                GAGGAA CCGGGGA     G
                                |||||| |||||||     |
                                CTCCTT GGCCCCT     C
                                   _     _______
GAM3035  AQP6     3'  AGTCAATGGCTAGATG     38235       AATAAAG
                                AGTTAATG     TAGATG
                                ||||||||     ||||||
                                TCAGTTAC     ATCTAC
                                     CG_____
GAM3035  AQP6     3'  AGTCAATGGCTAGATG     11638       AATAAAG
                                AGTTAATG     TAGATG
                                ||||||||     ||||||
                                TCAGTTAC     ATCTAC
                                     CG_____
GAM3036  EPB72    3'  TTTAAGGGTTAGAGTAAT    19905    T     A
                                TTT AGGGTTA AGTAAT
                                ||| ||||||| ||||||
                                AAA TCCCAAT TCATTA
                                  T      C
GAM3036  PON1     3'  TTTTAGGGTAAGTACTTT    7780         TA   AAT
                                TTTTAGGGT  AAGT   ACTTT
                                |||||||||  ||||   |||||
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                                AAAATCCCA  TTCA   TGAAA
                                    __   ___
GAM3036  CYBB     3'  TTGATCTCTGTATAGAGATTTT 44106        A    A__
              T                  TTGATCTT GTATA   ATTTTT
                                 |||||||| |||||   ||||||
                                 AACTAGAG CATAT   TAAAAA
                                      A    CTC
GAM3037  CD28     3'  ACAGCATTAAATAGGAACTACG 26012     A          GGG
                                 ACG CATTAAATAGGAA   ACG
                                 ||| ||||||||||||   |||
                                 TGT GTAATTTATCCTT   TGC
                                   C          GA_
GAM3037  GPRK6    3'  CGCACACAGGAAGGGGCG    13269    A  TAA        A
                                 CG CAT   ATAGGAAGGG CG
                                 || |||   |||||||||| ||
                                 GC GTG   TGTCCTTCCC GC
                                  _  ___        C
GAM3037  PPP2R4   3'  ACGAACAGAGGGAGGGGATGG  41323     _  TTAAATA   A   C
                                 ACGA CA      GGA GGGA GG
                                 |||| ||      ||| |||| ||
                                 TGCT GT      CCT CCCT CC
                                   T  CTC____   C    A
GAM3037  DUSP2    5'  GGTCTTTCCCGCGTCCCGGGC  20659       AACA  _
                                 GGTTTTT    CG GTCCCGGGC
                                 |||||||    || |||||||||
                                 CCAGAAA    GC CAGGGCCCG
                                      GG__  G
GAM3037  IL1RAP   3'  GGTTTTTAATATTGTACCC    13502        CACG  _
                                 GGTTTTTAA    GT CCC
                                 |||||||||    || |||
                                 CCAAAAATT    CA GGG
                                       ATAA  T
GAM3038  ADRA1A   3'  ACCATGGAGAGAATGTGTGTGT 37802      C  TGT___    C
              GTGT                  ACCA TG     GTGTG GTGTGTGT
                                 |||| ||     ||||| ||||||||
                                 TGGT AC     TACAC CACACACA
                                   _  CTCTCT    A
GAM3038  ANK1     3'  TGTGTGTGTGTGTGTGTGT    33879         C
                                 TGTGTGTGTG GTGTGTGT
                                 |||||||||| ||||||||
                                 ACACACACAC CACACACA
                                       A
GAM3038  ANK1     3'  GTGTGTGTGTGTGTGTGT     33873         C
                                 GTGTGTGTG GTGTGTGT
                                 |||||||||| ||||||||
                                 CACACACAC CACACACA
                                       A
GAM3038  ANK1     3'  TGTGTGTGTGTGTGTGTG     33878         C
                                 TGTGTGTGTG GTGTGTG
                                 |||||||||| |||||||
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                                ACACACACAC CACACAC
                                      A
GAM3038  ANKRD3   3'  ACCATGTGGGCACGTGTGTGT  33962        T TG
                                ACTGTGTG G  CGTGTGTGT
                                |||||||| |  |||||||||
                                TGGTACAC C  GCACACACA
                                    C GT
GAM3038  APBA1    3'  ACTGTGTGTGTGTGTGTGTGT  43084          C
                                ACTGTGTGTGTG GTGTGTGT
                                |||||||||||| ||||||||
                                TGACACACACAC CACACACA
                                      A
GAM3038  APBA1    3'  ACTGTGTGTGTGTGTGTGTGTA 43085          C       III
                                ACTGTGTGTGTG GTGTGTGT   A
                                |||||||||||| ||||||||   |
                                TGACACACACAC CACACACA   T
                                      A       III
GAM3038  ASTN     3'  TGTGTGCACACGTGTGTGT   42958        TG
                                TGTGTGTG  CGTGTGTGT
                                ||||||||  |||||||||
                                ACACACGT  GCACACACA
                                    GT
GAM3038  ASTN     3'  CATTGTGTGTGCACACGTGTGT 42943    C       __
              GT                  CA TGTGTGTGT  GCGTGTGTGT
                                || |||||||||  ||||||||||
                                GT ACACACACG  TGCACACACA
                                 A        TG
GAM3038  ATP11A   3'  TGTACGTGTGCGTGTGTGT   44192
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ACATGCACACGCACACACA

GAM3038  ATP1B2   3'  ACTGCGTGTGCACGTTTGTGTG 11736         TG  __
              T                   ACTGTGTGTG  CGT  GTGTGT
                                ||||||||||  |||  ||||||
                                TGACGCACAC  GCA  CACACA
                                      GT   AA
GAM3038  BCL2     3'  ACTGTTAATTGTTGTGTGTGTG 8517       _____ _    C
              TGTGT                   ACTGT    GT GTGTG GTGTGTGT
                                |||||     || ||||| ||||||||
                                TGACA     CA CACAC CACACACA
                                   ATTAA  A     A
GAM3038  BCL2     3'  TGTGTGTGTGTGTGTCTGT   8529          C   G
                                TGTGTGTGTG GTGT TGT
                                |||||||||| |||| |||
                                ACACACACAC CACA ACA
                                      A   G
GAM3038  BCL7B    3'  CTGCGTGTGTGCAGATGTGTGT 11804          __
                                CTGTGTGTGTGC  GTGTGTGT
                                ||||||||||||  ||||||||
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                                GACGCACACACG  TACACACA
                                      TC
GAM3038  CACNA2D2  3'  TGTGTGTGTGTGTGTGTG    25730         C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                     A
GAM3038  CACNG3    5'  CTGTGTGAGTGTGTGTGTGT  27237       T  C
                                CTGTGTG GTG GTGTGTGT
                                ||||||| ||| ||||||||
                                GACACAC CAC CACACACA
                                   T  A
GAM3038  CACNG3    5'  TGTGTGTGTGTGTGTGTGT   27247         C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                     A
GAM3038  CACNG3    5'  CTGTGTGAGTGTGTGTGTGT  27237       T  C
                                CTGTGTG GTG GTGTGTGT
                                ||||||| ||| ||||||||
                                GACACAC CAC CACACACA
                                   T  A
GAM3038  CARPX     3'  TGTAAGAGTGTGTGTGTGTGT 33581      T__    C
                                TGTG  GTGTG GTGTGTGT
                                ||||  ||||| ||||||||
                                ACAT  CACAC CACACACA
                                  TCT    A
GAM3038  CBFA2T1   3'  TATATATGTGCGTGTGTGT   20307
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ATATATACACGCACACACA

GAM3038  CBFA2T1   3'  CTGTGTGTGTGTGTGTGTAA  20297         C    GTIII
                                CTGTGTGTGTG GTGTGT    A
                                |||||||||| ||||||    |
                                GACACACACAC CACACA    T
                                      A     IIITG
GAM3038  CBFA2T1   3'  TGTGTGTGTGTGTGTGTG    20314         C
                                TGTGTGTGTG GTGTGTG
                                ||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  CBFA2T1   3'  CTGTGTGTGTGTGTGTGTGTA 20298         C      III
                                CTGTGTGTGTG GTGTGTGT  A
                                |||||||||| ||||||||  |
                                GACACACACAC CACACACA  T
                                      A      III
GAM3038  CBFA2T1   3'  TGCGTGTGTGTGTGTGTGT   20312         C
                                TGTGTGTGTG GTGTGTGT
                                ||||||||| ||||||||
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                                ACGCACACAC CACACACA
                                      A
GAM3038  CCND1    3'  TGTGTGTGTGTGTGTGTG    38227          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  CCND1    3'  TGTGTGTGTGTGTGTGTGTA  38228          C       III
                                TGTGTGTGTG GTGTGTGT  A
                                |||||||||| ||||||||  |
                                ACACACACAC CACACACA  T
                                      A       III
GAM3038  CD22     3'  TGCGTGTGTGTGTGTGTGT   12101          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACGCACACAC CACACACA
                                      A
GAM3038  CD22     3'  GTGTGTGTGTGTGTGTGT    12100          C
                                GTGTGTGTG GTGTGTGT
                                ||||||||| ||||||||
                                CACACACAC CACACACA
                                      A
GAM3038  CD22     3'  TGTGTGTGTGCGTGTGTGT   12105
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ACACACACACGCACACACA

GAM3038  CDH12    3'  TGTGTGTGTGTGTGTGTGT   19781          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  CDH12    3'  CCAGAAAGAGTGTGTGTGTGTG 19771     CT____        C
                TGTGT                   CCA     GTGTGTGTG GTGTGTGT
                                |||     ||||||||| ||||||||
                                GGT     CACACACAC CACACACA
                                  CTTTCT        A
GAM3038  CDH12    3'  TGTGTGTGTGTGTGTGTGTA  19782          C       III
                                TGTGTGTGTG GTGTGTGT  A
                                |||||||||| ||||||||  |
                                ACACACACAC CACACACA  T
                                      A       III
GAM3038  CDKN2B   3'  TGTGTGTGTGTGTGTGTG    38556          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  CENTD2   5'  CACTTCTCTACGTGCGTGTGTG 31589     GTG_
                T                    CACT    TGTGTGCGTGTGTGT
                                ||||    ||||||||||||||
```

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                                GTGA    ATGCACGCACACACA
                                  AGAG
GAM3038  CENTD2    5'  ACTCTGTGTGTCTGTGTGT    31586      G       GC
                                ACT TGTGTGT  GTGTGT
                                ||| |||||||  ||||||
                                TGA ACACACA  CACACA
                                  G      GA
GAM3038  CHES1     3'  CCTTCGTGTGTGTGTGTGTGTG 23284     AC         C
           T                     CC  TGTGTGTGTG GTGTGTGT
                                ||  |||||||||| ||||||||
                                GG  GCACACACAC CACACACA
                                 AA         A
GAM3038  CHES1     3'  TGTGTGTGTGTGTGTGTG     23289          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  COLQ      5'  GCGTGTGTTTGTGTGTGT     38694         GC
                                GTGTGTGT  GTGTGTGT
                                ||||||||  ||||||||
                                CGCACACA  CACACACA
                                    AA
GAM3038  CRHBP     3'  TGTATGTGTGTGTGTGTGT    40511          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACATACACAC CACACACA
                                      A
GAM3038  CRTL1     5'  TGTGTGTGTGTGTGTGTG     12455          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  CRTL1     5'  TGTGTGTGTGTGTGTGTGT    12456          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  CRTL1     5'  GTGTGTGTGTGTGTGTGT     12452          C
                                GTGTGTGTG GTGTGTGT
                                |||||||| ||||||||
                                CACACACAC CACACACA
                                    A
GAM3038  CSF2RB    3'  TGTGCATGTACGTGTGTGT    7573
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ACACGTACATGCACACACA

GAM3038  CSPG3     3'  ATGTGTGTGTGTGTGTGT     20483          C
                                GTGTGTGTG GTGTGTGT
                                |||||||| ||||||||
```

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                                TACACACAC CACACACA
                                     A
GAM3038  DGKG     3'  TGTATGTGTGTGTGTGTGT   10659          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACATACACAC CACACACA
                                     A
GAM3038  DMD      3'  TATGTGTGTGTGTGTGTGT   19694          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ATACACACAC CACACACA
                                     A
GAM3038  EFNB1    3'  TGTGTGTGTGTGTGTGTGT   20731          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                     A
GAM3038  EFNB1    3'  TGTGTGTGTGTGTGTGTG    20730          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                     A
GAM3038  EHD2     3'  CCAGTGTGTGTGTGATGT    31127     C        C
                                CCA TGTGTGTGTG GTGT
                                ||| |||||||||| ||||
                                GGT ACACACACAC TACA
                                  C        _
GAM3038  EHD3     3'  TGTGTGTGTGTGTGTGTGTA  31123          C       III
                                TGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
                                ACACACACAC CACACACA   T
                                     A       III
GAM3038  EHD3     3'  TGTGTGTGTGTGTGTGTG    31122          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                     A
GAM3038  EN2      5'  TGTAAGTGTGCGTGTGTGT   10966      T
                                TGTG GTGTGCGTGTGTGT
                                |||| ||||||||||||||
                                ACAT CACACGCACACACA
                                   T
GAM3038  EN2      3'  CTGGTGTGTGTGTGTGTGTGT 10949     _      C
                                CTG TGTGTGTG GTGTGTGT
                                ||| |||||||| ||||||||
                                GAC ACACACAC CACACACA
                                  C       A
GAM3038  EN2      3'  TGTGTGTGTGTGTGTGTGT   10968          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
```

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                                ACACACACAC CACACACA
                                      A
GAM3038  EN2      3'  TGTGTGTGTGTGTGTGTG    10967          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  F7       3'  ACCATCTGTGTGTGCATCCGTG 6556       _        G__
              TGTGT                   ACCA CTGTGTGTGT   CGTGTGTGT
                                |||| ||||||||||   |||||||||
                                TGGT GACACACACG   GCACACACA
                                  A         TAG
GAM3038  F7       3'  GTGTGTGTGCATCTGTGT    33342           G
                                GTGTGTGTGCGT TGTGT
                                |||||||||||| |||||
                                CACACACACGTA ACACA
                                       G
GAM3038  F7       3'  CATTGGCGTGTGTGTGTGT   33335    C  T      C
                                CA TG GTGTGTG GTGTGT
                                || || ||||||| ||||||
                                GT AC CGCACAC CACACA
                                 A _      A
GAM3038  F7       3'  CTGTGTGTGTGCATTGGCGTGT 33339           ____
              GT                  CTGTGTGTGTGC    GTGTGTGT
                                |||||||||||    ||||||||
                                GACACACACACG    CGCACACA
                                       TAAC
GAM3038  F9       3'  TGTGTGTATGCGTGTGTGT   6583
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ACACACATACGCACACACA

GAM3038  FGFRL1   3'  TGTGTCTGTGTGTGTGTGT   34924       G    C
                                TGTGT TGTG GTGTGTGT
                                ||||| |||| ||||||||
                                ACACA ACAC CACACACA
                                   G    A
GAM3038  FGFRL1   3'  CACGCGTGTGTGTGTGTGTGT  34901     T        C
                                CAC GTGTGTGTG GTGTGTGT
                                ||| ||||||||| ||||||||
                                GTG CGCACACAC CACACACA
                                  _        A
GAM3038  FGFRL1   3'  CCGTGTGTGTGTGTGTGT    34904           C
                                CTGTGTGTGTG GTGTGT
                                |||||||||| ||||||
                                GGCACACACAC CACACA
                                       A
GAM3038  FLRT2    3'  TGTGTGTGTGTGTGTGTG    29866          C
                                TGTGTGTGTG GTGTGTG
                                ||||||||| |||||||
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                                ACACACACAC CACACAC
                                      A
GAM3038  FMR2     3'  TGTGTGTGTGAGTGTGTGT   12989         C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      T
GAM3038  GLP1R    3'  TGTGTGTGTGTGTGTGTGTA  13147         C       III
                                TGTGTGTGTG GTGTGTGT  A
                                |||||||||| ||||||||  |
                                ACACACACAC CACACACA  T
                                      A       III
GAM3038  GLP1R    3'  TGTGTGTGTGTGTGTGTG    13146         C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  GRLF1    3'  TGTGTGTGTGTGTGTGTGTA  44241         C       III
                                TGTGTGTGTG GTGTGTGT  A
                                |||||||||| ||||||||  |
                                ACACACACAC CACACACA  T
                                      A       III
GAM3038  GRLF1    3'  TGTGTGTGTGTGTGTGTG    44240         C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  GRLF1    3'  TGTGTGTGTGTGTGTGTAA   44239         C     GTIII
                                TGTGTGTGTG GTGTGT    A
                                |||||||||| ||||||   |
                                ACACACACAC CACACA    T
                                      A     IIITG
GAM3038  GTF2H1   3'  ATATATGTGTGTGTGTGT    23687         C
                                GTGTGTGTG GTGTGTGT
                                ||||||||| ||||||||
                                TATATACAC CACACACA
                                      A
GAM3038  GYPA     3'  TGTGTGTGTGTGTGTGTG    44628         C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  GYPA     3'  TGTGTGTGTGTGTGTGTGTA  44629         C       III
                                TGTGTGTGTG GTGTGTGT  A
                                |||||||||| ||||||||  |
                                ACACACACAC CACACACA  T
                                      A       III
GAM3038  HDAC8    3'  CATTTGTGTGTGTGTGT     32969    CTG      C
                                CA  TGTGTGTG GTGT
                                ||  |||||||| ||||
```

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                                GT   ACACACAC CACA
                                 AA_       A
GAM3038  HOXC9    3'  CATTATCATGTATGTGTGTGTG 41479    C  _      C
              T                   CA TGT GTGTGTG GTGTGTGT
                                  || ||| ||||||| ||||||||
                                  GT ATA TACATAC CACACACA
                                   A  G      A
GAM3038  HPS3     3'  TGTGTGTGTGTGTGTGTG    37043         C
                                  TGTGTGTGTG GTGTGTG
                                  |||||||||| |||||||
                                  ACACACACAC CACACAC
                                        A
GAM3038  HPS3     3'  TGTGTGTGTGTGTGTGTGTA  37044         C       III
                                  TGTGTGTGTG GTGTGTGT   A
                                  |||||||||| ||||||||  |
                                  ACACACACAC CACACACA   T
                                        A       III
GAM3038  IGF1     3'  TGTGTGTGTGTGTGTGTG    8360          C
                                  TGTGTGTGTG GTGTGTG
                                  |||||||||| |||||||
                                  ACACACACAC CACACAC
                                        A
GAM3038  IGF1     3'  TGTGTGTGTGTGTGTGTGT   8361          C
                                  TGTGTGTGTG GTGTGTGT
                                  |||||||||| ||||||||
                                  ACACACACAC CACACACA
                                        A
GAM3038  IGF2R    3'  ACCCTGTGCACGTATGTGTGTG 9333     A    TG   C
              T                   ACC CTGTG  TGTG GTGTGTGT
                                  ||| |||||  |||| ||||||||
                                  TGG GACAC  GCAT CACACACA
                                    _     GT    A
GAM3038  ITGA11   3'  CAGTGTGTGTGTGTGTGTGTGT 29195    C        C
                                  CA TGTGTGTGTG GTGTGTGT
                                  || |||||||||| ||||||||
                                  GT ACACACACAC CACACACA
                                   C         A
GAM3038  ITGA11   3'  GTGTGTGTGTGTGTGTGT    29202         C
                                  GTGTGTGTG GTGTGTGT
                                  ||||||||| ||||||||
                                  CACACACAC CACACACA
                                        A
GAM3038  ITGA11   3'  TGTGTGTGTGTGTGTGTG    29208         C
                                  TGTGTGTGTG GTGTGTG
                                  |||||||||| |||||||
                                  ACACACACAC CACACAC
                                        A
GAM3038  KCNJ5    5'  TGTGTGTGTGTGTGTGTG    9444          C
                                  TGTGTGTGTG GTGTGTG
                                  |||||||||| |||||||
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                                ACACACACAC CACACAC
                                      A
GAM3038 KCNJ5    5' CTGTGTGTGTGTGTGTGTGTA 9436          C       III
                                CTGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
                                GACACACACAC CACACACA   T
                                      A       III
GAM3038 KIAA0442 3' CACTGGCGACCTGTGTGTGT  31788      T   TGTGC
                                CACTG GTG    GTGTGTGT
                                ||||| |||    ||||||||
                                GTGAC CGC    CACACACA
                                   _  TGGA_
GAM3038 KIF1B    3' CTGTGTATGTGTGTGTGTGT  31463         C
                                CTGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                GACACATACAC CACACACA
                                      A
GAM3038 KIF1B    3' TGTGTGTGTGTGTGTGTG    31468        C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038 KIF5A    3' TGTGTGTGTGCATGCGTGT   22554
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ACACACACACGTACGCACA

GAM3038 KIF5A    3' TGCGTGTGTGCGTGTGTGT   22550
                                TGTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                ACGCACACACGCACACACA

GAM3038 KLF7     3' TGTGTGTGTGTGTGTGTG    18984        C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038 KLF7     3' TGTGTGTGTGTGTGTGTGTA  18985        C       III
                                TGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||  |
                                ACACACACAC CACACACA   T
                                      A       III
GAM3038 LDHB     5' CTGAATTTGTGTGTGTGTGTGT 14117     TG__     C
                                CTG   TGTGTG GTGTGTGT
                                |||   |||||| ||||||||
                                GAC   ACACAC CACACACA
                                  TTAA     A
GAM3038 LILRB4   3' GTTTGTGTGTGTGTGTGT    27779    G     C
                                GT TGTGTG GTGTGTGT
                                || |||||| ||||||||
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                                CA ACACAC CACACACA
                                 A     A
GAM3038  MAPK10   3'  CTGCATTTGTGTGTGTGTGTGT 39979     ____      C
              GT                  CTGT    GTGTGTG GTGTGTGT
                                  ||||    ||||||| ||||||||
                                  GACG    CACACAC CACACACA
                                    TAAA      A
GAM3038  MNT      3'  TGTGTGTGTGTGTGTGTGT    33733          C
                                  TGTGTGTGTG GTGTGTGT
                                  |||||||||| ||||||||
                                  ACACACACAC CACACACA
                                        A
GAM3038  MNT      3'  CCACTGGTGTGTGTGTGT    33705       T      C
                                  CCACTG GTGTGTG GTGT
                                  |||||| ||||||| ||||
                                  GGTGAC CACACAC CACA
                                     _      A
GAM3038  MNT      3'  GTGTGCGTGCGTGTGTGT    33724
                                  GTGTGTGTGCGTGTGTGT
                                  ||||||||||||||||||
                                  CACACGCACGCACACACA

GAM3038  MNT      3'  TGTGTGTGTGTGTGTGTG    33732          C
                                  TGTGTGTGTG GTGTGTG
                                  |||||||||| |||||||
                                  ACACACACAC CACACAC
                                        A
GAM3038  MUC4     3'  ACTCGTGTGTGTGTGTGTGTGT 39656     _       C
                                  ACT GTGTGTGTG GTGTGTGT
                                  ||| ||||||||| ||||||||
                                  TGA CACACACAC CACACACA
                                    G        A
GAM3038  MUC4     3'  ACTCGTGTGTGTGTGTGTGTGT 39657     _       C       III
              A                    ACT GTGTGTGTG GTGTGTGT   A
                                  ||| ||||||||| ||||||||   |
                                  TGA CACACACAC CACACACA   T
                                    G        A       III
GAM3038  NAPB     3'  TGTGATATGTGTGTGTGTGT   43181     _     C
                                  TGTG TGTGTG GTGTGTGT
                                  |||| |||||| ||||||||
                                  ACAC ATACAC CACACACA
                                     T     A
GAM3038  NCAM1    3'  TGTGTGTGTGCGTGTGTGT    8320
                                  TGTGTGTGTGCGTGTGTGT
                                  ||||||||||||||||||
                                  ACACACACACGCACACACA

GAM3038  NCAM1    3'  CTAGAATTGTGTGTGTGTGT   8317      TGTG    C
                                  CTG    TGTG GTGTGTGT
                                  |||    |||| ||||||||
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                                GAT    ACAC CACACACA
                                  CTTA    A
GAM3038  NGFR     3'  CCTCCTGTGTGTGTGTGT    14775    A_         C
                                CC  CTGTGTGTGTG GT
                                ||  |||||||||||| ||
                                GG  GACACACACAC CA
                                 AG          A
GAM3038  NLGN3    3'  TGTGTGTGTGTGTGTGTGTA   33295          C       III
                                TGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
                                ACACACACAC CACACACA   T
                                      A       III
GAM3038  NLGN3    3'  CTGCGTGTGTGTGTGTGTGT   33283          C
                                CTGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                GACGCACACAC CACACACA
                                      A
GAM3038  NLGN3    3'  CTGCGTGTGTGTGTGTGTGT   33283          C
                                CTGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                GACGCACACAC CACACACA
                                      A
GAM3038  NR2E1    3'  TGTGTGTGTGTGTGTGTG     17583          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  NR2E1    3'  TGTGTGTGTGTGTGTGTGT    17584          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  NR2E1    3'  ACGGTGTGTGTGTGTGTGTGTA 17571    T       C       III
                                AC GTGTGTGTG GTGTGTGT   A
                                || ||||||||| ||||||||   |
                                TG CACACACAC CACACACA   T
                                 C        A       III
GAM3038  NR4A2    3'  TGTGTATGTGTGTGTGTGT    26169          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACATACAC CACACACA
                                      A
GAM3038  NR4A2    3'  CTGTGTGTGTGTGTGTGTGTA  26164          C       III
                                CTGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
                                GACACACACAC CACACACA   T
                                      A       III
GAM3038  NRXN1    3'  CGTGTGTGTGTGTGTGTGTA   39840          C       III
                                TGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
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                                GCACACACAC CACACACA  T
                                     A       III
GAM3038  NRXN1    3'  TGTGTGTGTGTGTGTGTGT   39853          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                     A
GAM3038  NRXN1    3'  TGTGTGTGTGTGTGTGTG    39852          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                     A
GAM3038  OLR1     3'  TGTGTGTGTGTGTGTGTG    14945          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                     A
GAM3038  OXTR     3'  TGTGTGTGTGTGTGTGTGT   9536           C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                     A
GAM3038  OXTR     3'  GCTGTGTGCGTGTGTGT     9527     G
                                GT TGTGTGCGTGTGTGT
                                || ||||||||||||||
                                CG ACACACGCACACACA
                                _
GAM3038  OXTR     3'  CTGTGTGCGTGTGTGTGTGT  9524           C
                                CTGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                GACACACGCAC CACACACA
                                     A
GAM3038  OXTR     3'  TGTGTGTGTGTGTGTGTG    9535           C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                     A
GAM3038  PARK2    3'  GCGCGCGCGCGTGTGTGT    30372
                                GTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                CGCGCGCGCGCACACACA

GAM3038  PATE     3'  TGTGTGTGTGTGTGTGTGT   39650          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                     A
GAM3038  PATE     3'  CTGTAGTGTGTGTGTGTGTGT 39639     _    C
                                CTGT GTGTGTG GTGTGTGT
                                |||| ||||||| ||||||||
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                                GACA CACACAC CACACACA
                                  T      A
GAM3038  PAX4     3'  CAATGTGTGTGTGTGTGTGT  26197    C        C
                                CA TGTGTGTGTG GTGTGT
                                || |||||||||| ||||||
                                GT ACACACACAC CACACA
                                 T         A
GAM3038  PCDH11X  3'  CACGTGTGTGTGTGTGTGTGTG 37296     _        C
           T                     CAC TGTGTGTGTG GTGTGTGT
                                 ||| |||||||||| ||||||||
                                 GTG ACACACACAC CACACACA
                                   C         A
GAM3038  PCDH11X  3'  CATTTAAATGTGTGTGTGTGT  37298    CTG  T    C
                                CA   TG GTGTG GTGTGTGT
                                ||   || ||||| ||||||||
                                GT   AT TACAC CACACACA
                                 AA_  T    A
GAM3038  PCDH11X  3'  TGTGTGTGCACGTGTGTGT    37316        TG
                                TGTGTGTG  CGTGTGTGT
                                ||||||||  |||||||||
                                ACACACAC  GCACACACA
                                     GT
GAM3038  PCDH11X  3'  TGTGTGTGTGTGTGTGTG     37318         C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  PCDH11Y  3'  TGTGTGTGCACGTGTGTGT    37357        TG
                                TGTGTGTG  CGTGTGTGT
                                ||||||||  |||||||||
                                ACACACAC  GCACACACA
                                     GT
GAM3038  PCDH11Y  3'  CACGTGTGTGTGTGTGTGTGTG 37336     _        C
           T                     CAC TGTGTGTGTG GTGTGTGT
                                 ||| |||||||||| ||||||||
                                 GTG ACACACACAC CACACACA
                                   C         A
GAM3038  PCDHB16  5'  TGTGTGTGTGTGTGTGTGT    34149         C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  PCDHB16  5'  TGTGTGTGTGTGTGTGTG     34148         C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  PLAG1    3'  GTATGTGTGCATGTGTGT     15353
                                GTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
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                                CATACACACGTACACACA

GAM3038  PTPRM    3'  CTGTGTGTGTGTTTCTGT    15971          CGTG
                                CTGTGTGTGTG   TGT
                                ||||||||||   |||
                                GACACACACAC   ACA
                                      AAAG
GAM3038  PTPRM    3'  ACTGTGGCTGTGTGTGTGT   15969       TG   C
                                ACTGTG  TGTG GTGTGT
                                ||||||  |||| ||||||
                                TGACAC  ACAC CACACA
                                   CG   A
GAM3038  PURA     3'  TGTGTGTGGCTGTGTGTGT   25214        T _
                                TGTGTGTG GC GTGTGTGT
                                |||||||| || ||||||||
                                ACACACAC CG CACACACA
                                     _ A
GAM3038  PURA     3'  GTGTGTATGCATGTGTGT    25209
                                GTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                CACACATACGTACACACA

GAM3038  RARA     3'  ACTGTCCAGTGTGTGTGTGT  9701       G  T   C
                                ACTGT TG GTG GTGTGTGT
                                ||||| || ||| ||||||||
                                TGACA GT CAC CACACACA
                                   G _  A
GAM3038  RBBP9    3'  TGTATGTGTGTGTGTGTGT   43144          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACATACACAC CACACACA
                                      A
GAM3038  RBBP9    3'  TGTGTGTGTGTGTGTGTGT   43147          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  RCV1     3'  ATGTGTGTGTGTGTGTGT    16219         C
                                GTGTGTGTG GTGTGTGT
                                ||||||||| ||||||||
                                TACACACAC CACACACA
                                      A
GAM3038  RCV1     3'  GTGTGTGTGCATGTGTGT    16223
                                GTGTGTGTGCGTGTGTGT
                                ||||||||||||||||||
                                CACACACACGTACACACA

GAM3038  SCN8A    3'  TGTGAGTGTGTGTGTGTGT   30537      T    C
                                TGTG GTGTG GTGTGTGT
                                |||| ||||| ||||||||
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                                ACAC CACAC CACACACA
                                  T    A
GAM3038 SLC18A1  5' CTGTGTATGTGTGTGTGT   16820          C
                                CTGTGTGTGTG GTGTGT
                                |||||||||| ||||||
                                GACACATACAC CACACA
                                       A
GAM3038 SLC1A4   3' TACATATGTGTGTGTGTGT  16755   TG     C
                                TG  TGTGTG GTGTGTGT
                                ||  |||||| ||||||||
                                AT  ATACAC CACACACA
                                 GT     A
GAM3038 SLC25A6  3' CCCTGGTGTGTGTGTGTGTGT 44862   A  T      C
                                CC CTG GTGTGTG GTGTGTGT
                                || ||| ||||||| ||||||||
                                GG GAC CACACAC CACACACA
                                 _  _      A
GAM3038 SLC31A1  3' TGTGTGTGTGTGTGTGTG    12399          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                       A
GAM3038 SLC31A1  3' TGTGTGTGTGTGTGTGTGT   12400          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                       A
GAM3038 SLC31A1  3' GTGTGTGTGTGTGTGTGTA   12396          C       III
                                GTGTGTGTG GTGTGTGT   A
                                ||||||||| ||||||||   |
                                CACACACAC CACACACA   T
                                      A       III
GAM3038 SNAI2    3' CTGTGGGTGTGTGTGTGTGT  16880      T    C
                                CTGTG GTGTG GTGTGTGT
                                ||||| ||||| ||||||||
                                GACAC CACAC CACACACA
                                   C    A
GAM3038 SNX2     3' CAGAGTGTGTGTGTGTGTGTGT 40514    CT       C
                                CA  GTGTGTGTG GTGTGTGT
                                ||  ||||||||| ||||||||
                                GT  CACACACAC CACACACA
                                 CT       A
GAM3038 SNX2     3' TGTGTGTGTGTGTGTGTGT   40516          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                       A
GAM3038 SNX2     3' TGTGTGTGTGTGTGTGTG    40515          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
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                                ACACACACAC CACACAC
                                      A
GAM3038  SRGAP2   3'  TGTGTGTGTGTGTGTGTGT   43991          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  SRGAP2   3'  TGTGTGTGTGTGTGTGTG    43990          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  SRGAP2   3'  TGTGTGTAAAATGTGTGTGTGT 43989        _____  C
              GT                  TGTGTGT    GTG GTGTGTGT
                                  |||||||    ||| ||||||||
                                  ACACACA    CAC CACACACA
                                     TTTTA   A
GAM3038  SSX2     3'  TGTGTGTGTGTGTGTGTGT    45534          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  SSX2     3'  TGTGTGTGTGTGTGTGTG     45533          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  SSX2     3'  ACTTGGTGTGTGTGTGTGTGTG 45528    __       C       III
              TA                    ACT  GTGTGTGTG GTGTGTGT   A
                                    |||  ||||||||| ||||||||   |
                                    TGA  CACACACAC CACACACA   T
                                      AC        A       III
GAM3038  SSX2     3'  TGTGGTTTGTGTGCGTGTGTGT 45532     ___
                                TGTG   TGTGTGCGTGTGTGT
                                ||||   ||||||||||||||
                                ACAC   ACACACGCACACACA
                                  CAA
GAM3038  SSX3     3'  TGTGTGTGTGTGTGTGTG     34251          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  SSX3     3'  TGTGTGTGTGTGTGTGTGT    34252          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  SSX3     3'  ACTTGGTGTGTGTGTGTGTGTG 34249    __       C       III
              TA                    ACT  GTGTGTGTG GTGTGTGT   A
                                    |||  ||||||||| ||||||||   |
```

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                                TGA  CACACACAC CACACACA   T
                                  AC        A       III
GAM3038  SSX3     3'  GTGTGGTTTGTGTGTGTGTGT  34250       ___    C
                                GTGTG   TGTG GTGTGTGT
                                |||||   |||| ||||||||
                                CACAC   ACAC CACACACA
                                   CAA    A
GAM3038  SSX4     3'  ACTGGTACTTGGTGTGTGTGTG 45414      T   T___   C
              T                  ACTG GTG    GTG GTGTGTGT
                                 |||| |||    ||| ||||||||
                                 TGAC CAT    CAC CACACACA
                                   _  GAAC   A
GAM3038  TFAP4    5'  TGTGTGTGTGTGTGTGTGTA  17422          C       III
                                TGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
                                ACACACACAC CACACACA   T
                                      A       III
GAM3038  TFAP4    5'  TGTGTGTGTGTGTGTGTG    17421          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  TLX1     3'  CTGTTGTGTGTGGTGTAGTGT  24336      _      C   _
                                CTGT GTGTGTG GTGT GTGT
                                |||| ||||||| |||| ||||
                                GACA CACACAC CACA CACA
                                  A      _   T
GAM3038  TNFSF5   3'  CTGTGTGTGTGTGTGTGTGTA  6323           C       III
                                CTGTGTGTGTG GTGTGTGT   A
                                |||||||||| ||||||||   |
                                GACACACACAC CACACACA   T
                                      A       III
GAM3038  TNFSF5   3'  TGTGTGTGTGTGTGTGTG    6335           C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  VSNL1    3'  TGTGTGTGTGTGTGTGTGT   18041          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
                                ACACACACAC CACACACA
                                      A
GAM3038  VSNL1    3'  TGTGTGTGTGTGTGTGTG    18040          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  XRCC1    3'  TGTGTGTGTGTGTGTGTGT   26671          C
                                TGTGTGTGTG GTGTGTGT
                                |||||||||| ||||||||
```

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                                ACACACACAC CACACACA
                                      A
GAM3038  XRCC1    3'  TGTGTGTGTGTGTGTGTG    26670          C
                                TGTGTGTGTG GTGTGTG
                                |||||||||| |||||||
                                ACACACACAC CACACAC
                                      A
GAM3038  XRCC1    3'  CATCGTGTGTGTGTGTGTGTGT 26667    C        C
                                CA TGTGTGTGTG GTGTGTGT
                                || |||||||||| ||||||||
                                GT GCACACACAC CACACACA
                                 A         A
GAM3039  IL8      3'  TGATGCTTCAAATATCACAT   45393        ATA TG
                                TGATGC   T  AATATCACAT
                                ||||||   |  ||||||||||
                                ACTACG   A  TTATAGTGTA
                                    A__ GT
GAM3039  CCND2    3'  TGTATAAAATAATTCTTCAA   12055        TTTGGT
                                TGTATA     TTCTTCAA
                                ||||||     ||||||||
                                ACATAT     AAGAAGTT
                                    TTTATT
GAM3039  FBXL5    3'  TTTATTTATACATTTCTTCAA  37953       G     TTG
                                TTTAT TATAT   GTTTCTTCAA
                                ||||| |||||   ||||||||||
                                AAATA ATATG   TAAAGAAGTT
                                   A    ___
GAM3040  DMXL1    3'  TTAAGTAAAATATTTGTTT    24294        TTTT
                                TTAAGT    AATATTTGTTT
                                ||||||    ||||||||||
                                AATTCA    TTATAAACAAA
                                    TT__
GAM3040  SCA1     3'  TCCATTTTTTAATATTTGTTTA 7287       TAAG
                                TCT    TTTTTAATATTTGTTTA
                                |||    |||||||||||||||||
                                AGG    AAAAATTATAAACAAAT
                                  TA__
GAM3040  TRIM     3'  TCCTAAACTCTTTTTGATATTT 32301         ___     A
            GTTT                    TCTTAAG   TTTTT ATATTTGTTT
                                ||||||||   ||||| ||||||||||
                                AGGATTT   AAAAA TATAAACAAA
                                    GAG    C
GAM3040  TXK      3'  TCTTAAATTTTTAAAACTT    17768             T
                                TCTTAAGTTTTTAA ATTT
                                |||||||||||||| ||||
                                AGAATTTAAAAATT TGAA
                                          T
GAM3040  ZNF146   3'  CCTTAAGTTTTTAGTACTTG   28350             A
                                TCTTAAGTTTTTA TATTTG
                                |||||||||||| ||||||
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                                GGAATTCAAAAAT ATGAAC
                                       C
GAM3041  ATP2B4   3'  TGGGGTGATGCCAAGAGGATTG 43204     AAG     ____   AAC
             TCA                  TGG   GATGTT   GGA   TGTCA
                                  |||   ||||||   |||   |||||
                                  ACC   CTACGG   CCT   ACAGT
                                    CCA     TTCT   A__
GAM3041  DPYD     3'  AGGGCAATTTGGAAACTGTCAC 41291     ATG__
                                  AGG    TTGGAAACTGTCAC
                                  |||    ||||||||||||||
                                  TCC    AACCTTTGACAGTG
                                    CGTTA
GAM3041  EPHB4    3'  TGGGAGATGTTGGGCAC     20793     AA       AA
                                  TGG  GGATGTTGG  AC
                                  |||  |||||||||  ||
                                  ACC  TCTACAACC  TG
                                    C_       CG
GAM3041  GAD1     3'  GGGAGGGTGTGACTTGTCA   30292    A   A   T  AAAC
                                  GG AGG TGT GG    TGTCA
                                  || ||| ||| ||    |||||
                                  CC TCC ACA CT    ACAGT
                                   C   C   _  GA__
GAM3041  GAD2     3'  TGGGGGAATGTTGATGTCA   9058     AA       AAAC
                                  TGG  GGATGTTGG    TGTCA
                                  |||  |||||||||    |||||
                                  ACC  CTTACAACT    ACAGT
                                    CC        ____
GAM3041  MAPK4    3'  GAAGGATGTTGGGTC       15660           AAACT
                                  GAAGGATGTTGG     GTC
                                  ||||||||||||     |||
                                  CTTCCTACAACC     CAG
                                                _____
GAM3041  NOTCH2   3'  TAGAAGGAATGAGAACTGTCA  35913         TGT  GA
                                  TGGAAGGA   TG  AACTGTCA
                                  ||||||||   ||  ||||||||
                                  ATCTTCCT   AC  TTGACAGT
                                       T__  TC
GAM3041  PXN      3'  TGGAGTGGTTTGGACTGTCAC  16035     A GATG    AA
                                  TGGA G    TTGGA  CTGTCAC
                                  |||| |    |||||  |||||||
                                  ACCT C    AACCT  GACAGTG
                                    _ ACCA    __
GAM3041  STAT1    3'  AGAAGGAAAACTGTC       40212        TGTTGG
                                  GGAAGGA     AAACTGTC
                                  |||||||     ||||||||
                                  TCTTCCT     TTTGACAG
                                                _____
GAM3042  ATP8B2   5'  GCCCTCCTTTCTTCTTCTGTC  42207         A  A    C
                                  GTCCTTTT TC TCTTC GTC
                                  |||||||| || ||||| |||
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                                CGGGAGGA AG AGAAG CAG
                                     A A    A
GAM3042  PEX14    3'  ACAGTCCTATCTTCCG      41868    C    TTTATC
                                AC GTCCT     ATCTTCCG
                                || |||||     ||||||||
                                TG CAGGA     TAGAAGGC
                                 T    _______
GAM3042  RBBP8    3'  GTCCTTCATCCTTCTGT     16173       T   AT   C
                                GTCCTTT ATC  CTTC GT
                                ||||||| |||  |||| ||
                                CAGGAAG TAG  GAAG CA
                                    _  __   A
GAM3043  EIF4A2   3'  TTCAAACTTCATTAAGACAT   12689     C        A
                                TTCA ACTTCATTAA ATAT
                                |||| |||||||||| ||||
                                AAGT TGAAGTAATT TGTA
                                  T        C
GAM3043  IRF1     3'  TTCACATTTCACTGGCTTTGG  42045      C     AAAATA
                                TTCACA TTCATT     TTTGG
                                |||||| ||||||     |||||
                                AAGTGT AAGTGA     AAACC
                                   A     CCG___
GAM3044  ATP11A   3'  TCTAGAAATAGAAATGCCAGTA 44185       C_   A__
           C                     TCTAGAAA  GAAA   TGGTGC
                                 |||||||| ||||  ||||||
                                 AGATCTTT  CTTT   GTCATG
                                      AT    ACG
GAM3044  COL4A3   3'  TCTAGAAATGGGCTGGCTCG  36385       CGAAAAT  __
                                TCTAGAAA      GGT  GCTCG
                                ||||||||      |||  |||||
                                AGATCTTT      CCG  CGAGC
                                     AC_____   AC
GAM3044  KCNQ3    5'  TCTGGGAAGAAGGGGCGCTCG  21133    A_   AC   AAT
                                TCT  GAA  GAA   GGTGCTCG
                                |||  |||  |||   ||||||||
                                AGA  CTT  CTT   CCGCGAGC
                                  CC   __   CC_
GAM3044  KRTHA4   3'  TAGAAACAAACAGGCTCGA   34248        AA   T
                                TAGAAACGA  ATGG GCTCGA
                                |||||||||  |||| ||||||
                                ATCTTTGTT  TGTC CGAGCT
                                      __   _
GAM3044  PTP4A2   3'  TAGAGGTGAAAATAGTGCAAGA 38639     AAC        TC
                                TAGA   GAAAATGGTGC  GA
                                ||||   |||||||||||  ||
                                ATCT   CTTTTATCACG  CT
                                  CCA         TT
GAM3044  PTTG1IP  3'  TCTAGAAACAGAGATGAACA   20291         AAAAT   CT
                                TCTAGAAACG    GGTG  CG
                                ||||||||||    ||||  ||
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                                AGATCTTTGT    CTAC  GT
                                      CT___   TT
GAM3044  RPA1    3'  TCTAGAAAGAGAGAGCCTTCGA 16372       C  AAAT   GC
                                TCTAGAAA GA   GGT  TCGA
                                |||||||| ||   |||  ||||
                                AGATCTTT CT   TCG  AGCT
                                     _ CTC_   GA
GAM3044  SCN4A   3'  TCTGGGAACGCAGGCGCTCG  7330     AGA   AAAAT
                                TCT  AACG    GGTGCTCG
                                |||  ||||    ||||||||
                                AGA  TTGC    CCGCGAGC
                                  CCC   GT___
GAM3044  ZNF174   5'  TCTAGAAACGAAGGTTCTC   18365          AAT   G
                                TCTAGAAACGAA   GGT CTC
                                ||||||||||||   ||| |||
                                AGATCTTTGCTT   CCA GAG
                                      ___   A
GAM3045  TAZ     3'  AAAATGAAAATAGAATATTT   31763          A
                                AGAATGAAAATA AATATTT
                                |||||||||||| |||||||
                                TTTTACTTTTAT TTATAAA
                                      C
GAM3045  ZNF216   3'  TTTAAGAATAAAAGTAAAA   25661          A
                                TTTAAGAATGAAA TAAAA
                                |||||||||||| |||||
                                AAATTCTTATTTT ATTTT
                                      C
GAM3045  TBX22    3'  TTTGTCATTGTCAATGTGT   32625       T   TTTT
                                TTTGTCATT GTCA   TGTGT
                                ||||||||| ||||   |||||
                                AAACAGTAA CAGT   ACACA
                                     _   T___
GAM3046  E2F1     3'  CACACATTCACCCCCGGTACAC 44484        AATTA  __
                                CACACGTTCG    CCG  ACAC
                                ||||||||||    |||  ||||
                                GTGTGTAAGT    GGC  TGTG
                                      GGG__   CA
GAM3046  TACSTD1  3'  CACACATTTGAATGTTACACA  14297       C   TACCG
                                CACACGTT GAAT    ACACA
                                |||||||| ||||    |||||
                                GTGTGTAA CTTA    TGTGT
                                     A   CAA__
GAM3046  CLK2     3'  ACCGCCGCAGCGGTT      41275     T     CAA
                                ACT GCTGCA   CGGTT
                                ||| ||||||   |||||
                                TGG CGGCGT   GCCAA
                                  _     C__
GAM3046  FLT1     3'  AGACTTGCACATGGT       12903       TGC     AC
                                GGACT   TGCACA  GGT
                                |||||   ||||||  |||
```

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                                TCTGA  ACGTGT  CCA
                                  ___     A_
GAM3046  NR2E1    3'  GACTTGCTGCACCACGAGTT  17578          A  _
                                GACTTGCTGCAC ACG GTT
                                |||||||||||| ||| |||
                                CTGAACGACGTG TGC CAA
                                      G   T
GAM3046  PPP1R2   5'  GGCTACCGCAGCGGTT     26420    A  T    CAA
                                GG CT GCTGCA  CGGTT
                                || || ||||||  |||||
                                CC GA TGGCGT  GCCAA
                                 _ _    C__
GAM3047  FBXL7    3'  TCGGTGCTTACATACGCTGCTT 29413       CGTA  CTT
                                TCGGTGC   AC  CGCTGCTT
                                |||||||   ||  ||||||||
                                AGCCACG   TG  GCGACGAA
                                    AA__  TAT
GAM3047  ACTN2    3'  TGTGGTTTTTTCCCCCC    9955      A  CA  A  A
                                TGTG TTT  TTT CC CCCC
                                |||| |||  ||| || ||||
                                ACAC AAA  AAA GG GGGG
                                  C  __  _ _
GAM3047  BCL7A    3'  TGTGTTTCATTCTCCTTCAGC  34226     A      A  ACCC
                                TGTG TTTCATTT CC   CAGC
                                |||| |||||||| ||   ||||
                                ACAC AAAGTAAG GG   GTCG
                                  _      A  AA__
GAM3047  FOXF2    3'  TGTGACTTGAATCCGTCCCAG  11131       CATTTA  AC
                                TGTGATTT    CC  CCCAG
                                ||||||||    ||  |||||
                                ACACTGAA    GG  GGGTC
                                    CTTA__  CA
GAM3047  HIP1     3'  GTGATCCTACCACCTCAG    23758      TCAT      C
                                GTGATT   TTACCACC CAG
                                ||||||   |||||||| |||
                                CACTAG   GATGGTGG GTC
                                  ____      A
GAM3047  PRKY     3'  TGTGACTTTATTTCCTTCCTGG 15714       C   A  AC  CA
           C                     TGTGATTT ATTT CC  CC  GC
                                ||||||||  |||| ||  ||  ||
                                ACACTGAA TAAA GG  GG  CG
                                    A   _  AA  AC
GAM3047  PVR      3'  TGTGATCTCACCAC       27115         ATTT
                                TGTGATTTC   ACCAC
                                |||||||||   |||||
                                ACACTAGAG   TGGTG
                                      ____
GAM3047  SIRT5    3'  TGTGATTTTATTTTCCAC    29266       C   A
                                TGTGATTT ATTT CCAC
                                |||||||| |||| ||||
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                                ACACTAAA TAAA GGTG
                                     A   A
GAM3047  SMG1     3'  TGTGATTTCTTCGCGACCCCAG 31514         A   ACC
                                TGTGATTTC TTT   ACCCCAG
                                ||||||||| |||   |||||||
                                ACACTAAAG AAG   TGGGGTC
                                     _  CGC
GAM3047  VCL      3'  TGTGATTTTTCAGCTCCCAGC  30409        CA   CCAC
                                TGTGATTT  TTTA   CCCAGC
                                ||||||||  ||||   ||||||
                                ACACTAAA  AAGT   GGGTCG
                                     __   CGA_
GAM3047  WRN      3'  TGCGGTTTCATTTTCACTGCCC 8141       A       AC  __
                                TGTG TTTCATTT  CAC  CCC
                                |||| ||||||||  |||  |||
                                ACGC AAAGTAAA  GTG  GGG
                                  C       A_  AC
GAM3048  FOXI1    3'  CTTAACCTCCTTGAGC      29152        TTTA
                                CTTAACC    TCTTTGAGC
                                |||||||    |||||||||
                                GAATTGG    AGGAACTCG
                                     _____
GAM3048  MAB21L1  5'  TCCCTTCCTTTTATCTTTGAGC 24590      AA    _
           C                     TCTT  CCTTT ATCTTTGAGCC
                                ||||  ||||| ||||||||||
                                AGGG  GGAAA TAGAAACTCGG
                                  AA    A
GAM3048  ATP2B4   3'  GGATAGACGAAAATGGAAA   43199        A   GTAA
                                GGATAGAC AAAA    GAAA
                                |||||||| ||||    ||||
                                CCTATCTG TTTT    CTTT
                                     C    AC__
GAM3048  CEACAM5  3'  GGATAGCTTAAAAGAAAAA   20375       ACA    T
                                GGATAG   AAAAG AAGAA
                                ||||||   ||||| |||||
                                CCTATC   TTTTC TTTTT
                                    GAA    _
GAM3048  DYRK1A   3'  GGGGGGACAAAAAGAAAAA   38995    ATA       T
                                GG   GACAAAAAG AAGAA
                                ||   ||||||||| |||||
                                CC   CTGTTTTTC TTTTT
                                 CCC       _
GAM3048  F9       3'  GGAGAGAGGGAGTAAGAAA   6575     T   CAAAA
                                GGA AGA    AGTAAGAAA
                                ||| |||    |||||||||
                                CCT TCT    TCATTCTTT
                                  C  CCC__
GAM3048  FAAH     3'  GGAGGGACGGCAAGAAAA    11058     TA   AAAAA
                                GGA  GAC    GTAAGAAAA
                                |||  |||    |||||||||
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                                CCT  CTG    CGTTCTTTT
                                  CC   C____
GAM3048  FACL4    3'  GGATAAACAACCAGGGAA    20887         AA  TAA
                                GGATAGACAA  AG   GAA
                                ||||||||||  ||   |||
                                CCTATTTGTT  TC   CTT
                                      GG  C__
GAM3048  FLOT2    3'  AGGAGAGACAGGAAGACAGCCA 20980      T    AAA____   A
              GA                  AGGA AGACA      AGT AGA
                                |||| |||||      ||| |||
                                TCCT TCTGT      TCG TCT
                                  C    CCTTCTG   G
GAM3048  FMR1     3'  GGGCAGACAAAATTAAAAA   12942    A       AG
                                GG TAGACAAAA  TAAGAA
                                || |||||||||  ||||||
                                CC GTCTGTTTT  ATTTTT
                                 C       A_
GAM3048  FS       5'  GGAAAGACAAAAAAAAG     35086     T       T
                                GGA AGACAAAAAG AAG
                                ||| ||||||||||| |||
                                CCT TCTGTTTTTT TTC
                                  T       _
GAM3048  HDAC5    3'  AGGGAGACAAAGCAAG      40159     AT     AA
                                AGG  AGACAA  AGTAAG
                                |||  ||||||  ||||||
                                TCC  TCTGTT  TCGTTC
                                  C_     __
GAM3048  HDAC5    3'  AGGACAGACAGAATGCAGGAAA 40158          A  A   A
              A                   AGGATAGACA AA GTA GAAAA
                                |||||||||| || ||| |||||
                                TCCTGTCTGT TT CGT CTTTT
                                      C  A   C
GAM3048  IL1R1    3'  AGAATAGATGAAAGTAGAA   9353         CAA     A
                                AGGATAGA   AAAGTA GAA
                                ||||||||   |||||| |||
                                TCTTATCT   TTTCAT CTT
                                     AC_     _
GAM3048  IL1RAP   3'  GGATAGACAATGTAGAA     13501          AAA   A
                                GGATAGACAA   GTA GAA
                                ||||||||||   ||| |||
                                CCTATCTGTT   CAT CTT
                                      A__   _
GAM3048  M6PR     3'  AGGGAACCAGGAGTAAGAAAA  14304     ATA   AAAA
                                AGG   GAC    AGTAAGAAAA
                                |||   |||    ||||||||||
                                TCC   TTG    TCATTCTTTT
                                  C__   GTCC
GAM3048  MCL1     3'  AGGAAGGACAGGAAATAAAA   34994      TA    AA
                                AGGA  GACA  AAGTAAGA
                                ||||  ||||  ||||||||
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                                TCCT  CTGT  TTTATTTT
                                  TC    CC
GAM3048  NAPB     3'  AGGATAACAAAAATAGAAA    43168       A       GTA
                                AGGAT GACAAAAA   AGAAA
                                ||||| ||||||||   |||||
                                TCCTA TTGTTTTT   TCTTT
                                  _       A__
GAM3048  NPTX1    3'  AGGAAGACGCTATCTAAGAAAA 14830      T    AAAAAG
              A                  AGGA AGAC     TAAGAAAAA
                                |||| ||||     |||||||||
                                TCCT TCTG     ATTCTTTTT
                                  _   CGATAG
GAM3048  NTRK2    3'  AGGGAAGACGAAAAAAAAGAA  26142     AT    A     T
                                AGG  AGAC AAAAG AAGAA
                                |||  |||| ||||| |||||
                                TCC  TCTG TTTTT TTCTT
                                  CT    C     T
GAM3048  PAICS    3'  GGACAGACAGGGAGAAA     26982         AAAA TA
                                GGATAGACA    G  AGAAA
                                |||||||||    |  |||||
                                CCTGTCTGT    C  TCTTT
                                     ____ CC
GAM3048  PAICS    3'  AGGATAAAGTAAGA        26980        GACAAA
                                AGGATA      AAGTAAGA
                                ||||||      ||||||||
                                TCCTAT      TTCATTCT
                                  _______
GAM3048  PTK2B    3'  AGAAAGAGGAGGAGTAAGAAAA 19914     T   CAAAA
                                GGA AGA     AGTAAGAAAA
                                ||| |||     ||||||||||
                                TCT TCT     TCATTCTTTT
                                  T   CCTCC
GAM3048  SLC25A15 3'  AGGGAAGACAAAAAGCAAAA   30664     AT
                                AGG  AGACAAAAAGTAAGA
                                |||  ||||||||||||||
                                TCC  TCTGTTTTTCGTTTT
                                  CT
GAM3048  SOX13    3'  AGGACAGACACCAAGAAAGA   25007          AA   T
                                AGGATAGACA  AAG AAGA
                                ||||||||||  ||| ||||
                                TCCTGTCTGT  TTC TTCT
                                     GG   T
GAM3049  AVPR2    3'  AAGCTCTCCTCATACAGCTG   6283      AATG        A
                                AAG    TTTCATACA CTG
                                |||    ||||||||| |||
                                TTC    GGAGTATGT GAC
                                  GAGA        C
GAM3049  COIL     3'  AAAAATGTGTACAGCTGAAG   42737         TTCA    A
                                AAGAATGT    TACA CTGAAG
                                ||||||||    |||| ||||||
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                                TTTTTACA   ATGT GACTTC
                                    C___   C
GAM3049  DVL3    3'  AAATGTTTCAGGCCTGGAG   20665        TACAA  A
                                GAATGTTTCA    CTG AG
                                ||||||||||    ||| ||
                                TTTACAAAGT    GAC TC
                                     CCG__  C
GAM3049  GPC4    3'  AGAATTACTCTTACAACTGAAG 11081      GT  A
           A                     AGAAT  TTC TACAACTGAAGA
                                |||||  ||| ||||||||||||
                                TCTTA  GAG ATGTTGACTTCT
                                  AT  A
GAM3049  ITK     3'  AAGAATGTACACATGTACAGTT 24439       TT_ __   AC  A
           GAGGA                  AAGAATGT   CA  TACA  TGA GA
                                |||||||   ||  ||||  ||| ||
                                TTCTTACA   GT  ATGT  ACT CT
                                    TGT  AC   CA  C
GAM3049  P23     3'  GAATGTTTCATTCTGA     27342          ACAA
                                GAATGTTTCAT   CTGA
                                ||||||||||   ||||
                                CTTACAAAGTA   GACT
                                     A___
GAM3049  PCSK2   3'  AAGAGGCTCCATACAACTGGAG 15121     AT          A
           A                     AAGA  GTTTCATACAACTG AGA
                                ||||  |||||||||||||| |||
                                TTCT  CGAGGTATGTTGAC TCT
                                  C_           C
GAM3049  PPARGC1 3'  GAATTTTCATACAATGA    29953     G       C
                                GAAT TTTCATACAA TGA
                                |||| |||||||||| |||
                                CTTA AAAGTATGTT ACT
                                  _       _
GAM3049  REQ     3'  GAATGCTTCAGTCACTGGAGA  26545         TACA   A
                                GAATGTTTCA   ACTG AGA
                                ||||||||||   |||| |||
                                CTTACGAAGT   TGAC TCT
                                     CAG_   C
GAM3049  TRPS1   3'  AAATGTTTCATATGAAA    30452          CAAC
                                GAATGTTTCATA   TGAAG
                                ||||||||||||   |||||
                                TTTACAAAGTAT   ACTTT
                                     _____
GAM3049  TYRP1   3'  AAGATTGTTTCATAGCACAAGA 43639     A       _  ACT
                                AAGA TGTTTCATA CA   GA
                                |||| ||||||||| ||   ||
                                TTCT ACAAAGTAT GT   CT
                                  A       C  GTT
GAM3049  UBB     3'  GAATGCCATGACTGAAG    33251       TT   ACA
                                GAATGT  CAT   ACTGAAG
                                ||||||  |||   |||||||
```

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                                CTTACG  GTA   TGACTTC
                                  __   C__
GAM3049 XK      3'  AAGGGTGTCAGAGGATACAACT 34355     AA   TC___       A
              GGAGA                  AAG  TGTT    ATACAACTG AGA
                                ||| ||||   ||||||||| |||
                                TTC  ACAG    TATGTTGAC TCT
                                  CC   TCTCC       C
GAM3049 CADPS   3'  GTGGTTAGACTATGTATTCT  42196    A   CTAT
                                GT GTTG   TTATGTATTCT
                                || ||||   ||||||||||
                                CA CAAT   GATACATAAGA
                                 C   CT__
GAM3049 CYB561  3'  TGCGTTGTTTATGTATTCT   12547    A   CTA
                                TGT GTTG  TTTATGTATTCT
                                ||| ||||  ||||||||||
                                ACG CAAC  AAATACATAAGA
                                  _   ___
GAM3049 F8      3'  CTGTAGTAGTTATTGTATTCT  6565        TGC   TTA
                                CTGTAGT   TAT   TGTATTCT
                                |||||||   |||   ||||||||
                                GACATCA   ATA   ACATAAGA
                                    TCA   ___
GAM3049 SCD     3'  TGCGTTGTTTATGTATTC    22837    A   CTA
                                TGT GTTG  TTTATGTATTC
                                ||| ||||  ||||||||||
                                ACG CAAC  AAATACATAAG
                                  _   ___
GAM3050 ANKH    3'  CTGACAGCCACAGCCCATGTA 38315      CAA   _    C
                                CTGAC   CCAT GTTCA GTA
                                |||||   |||| ||||| |||
                                GACTG   GGTG CGGGT CAT
                                   TC_   T    A
GAM3050 ARNT2   3'  GAACTGACCTACCCATGT    31359        AA_
                                GAACTGACC   CCATGT
                                |||||||||   ||||||
                                CTTGACTGG   GGTACA
                                     ATG
GAM3050 MGAM    3'  GAACTGACTGTCTATGTCC   43656        CAACC
                                GAACTGAC    ATGTTC
                                ||||||||    ||||||
                                CTTGACTG    TACAGG
                                     ACAGA
GAM3050 MIP     3'  CTGGCTAAACCCCTCCACGTA 28932    ACC_   ATG
                                CTG   AACC   TTCACGTA
                                |||   ||||  ||||||||
                                GAC   TTGG   AGGTGCAT
                                  CGAT   GG_
GAM3050 FUT8    3'  GTCTGTGTCACTTAAATT    20997    ACAC      C
                                GTC   GTCACTTA GTT
                                |||   |||||||| |||
```

```
                                CAG    CAGTGAAT TAA
                                  ACA_       T
GAM3051  PCDHGA8   5'  CCCATTGTGCTCTAAGCTT   36854        A____
                                TCCATTGT    AAGCTT
                                ||||||||    ||||||
                                GGGTAACA    TTCGAA
                                    CGAGA
GAM3051  RFX2      3'  TCCGTTAACTGTGAGCTTCA  8461     ____    AA
                                TCC   ATTGT  AGCTTCA
                                |||   |||||  |||||||
                                AGG   TGACA  TCGAAGT
                                  CAAT    C_
GAM3051  ACTN2     3'  TTTACAAATAGCAAACCT    9956          AAG
                                TTTACAAATAG   GATCT
                                ||||||||||   |||||
                                AAATGTTTATC   TTGGA
                                      GT_
GAM3051  APPBP1    3'  TTTACAAATGAGAAAAAT    19379         _
                                TTTACAAAT AGAAGGAT
                                |||||||| ||||||||
                                AAATGTTTA TCTTTTTA
                                    C
GAM3051  TUFT1     3'  TTTACAAATGAGGGAACT    33510        A  A   T
                                TTTACAAAT GA GGA CT
                                |||||||| || ||| ||
                                AAATGTTTA CT CCT GA
                                      _ C   T
GAM3052  FANCC     3'  TAAAATAGATACTAGCAGAT   43278           AT  T
                                TGAAATAGATACTG  GT GAT
                                ||||||||||||||  || |||
                                ATTTTATCTATGAT  CG CTA
                                        __  T
GAM3052  PRKR      3'  AAATAGATATGAATTGAT    15677        C   T
                                AAATAGATA TGA GTTGAT
                                |||||||| ||| ||||||
                                TTTATCTAT ACT TAACTA
                                      _   _
GAM3053  GCNT2     5'  TCGATTCCGTTTCATCCCGAGA 11252         _______  A
                                TCGATTCCGT     CC AGA
                                ||||||||||     || |||
                                AGCTAAGGCA     GG TCT
                                      AAGTAG  C
GAM3054  STAM      3'  CTATAATTGCACCAAAAATTTA 18458      CGGAT
              G                  CTAT    TACCAAAAATTTAG
                                ||||    ||||||||||||||
                                GATA    GTGGTTTTTAAATC
                                  TTAAC
GAM3054  HIRA      3'  TTAGGTCAGTCTGCTG      17745        ATCCGCC   G
                                TTAGGTCG      GTC GCTG
                                ||||||||      ||| ||||
```

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                                AATCCAGT      CAG CGAC
                                        ________  A
GAM3055 ABCC1    5' CGGGGCCGCAACGCCGCC    33401     C   TACTC
                                CGG GCC    GCGCCGCC
                                ||| |||    ||||||||
                                GCC CGG    TGCGGCGG
                                  C  CGT__
GAM3055 AOC2     3' GCCTAACCACGCCGCCCG    41817      CT
                                GCCTA  CGCGCCGCCCG
                                |||||  ||||||||||
                                CGGAT  GTGCGGCGGGC
                                   TG
GAM3055 ARRB2    5' CGCGCGCCCGCCGCCC      41408    _    TACTCG
                                CG GCGCC     CGCCGCCC
                                || |||||     ||||||||
                                GC CGCGG     GCGGCGGG
                                 G    _______
GAM3055 BRF1     5' GCGCCCGGGCCGCGCCGCCCG  11335       AC_
                                GCGCCT   TCGCGCCGCCCG
                                ||||||   ||||||||||||
                                CGCGGG   GGCGCGGCGGGC
                                   CCC
GAM3055 BRF1     5' CGGAGCAGCCCGCGCCGCCCG  11332     C  CTA
                                CGG GC   CTCGCGCCGCCCG
                                ||| ||   ||||||||||||
                                GCC CG   GGGCGCGGCGGGC
                                 T  TC_
GAM3055 C7orf2   5' CGCCGCCGCGCCGCCC      35368      TAC
                                CGCC   TCGCGCCGCCC
                                ||||   ||||||||||
                                GCGG   GGCGCGGCGGG
                                  C__
GAM3055 CACNA1A  3' CGCCGCCCCCGCTGCCC     35728    G    TA    GCC
                                CG CGCC  CTCGC   GCCC
                                || ||||  |||||   ||||
                                GC GCGG  GGGCG   CGGG
                                 G   __    A__
GAM3055 CACNA2D2 5' GCGGGCTGCGCTGCCCG     25718     CCTA  C    C
                                GCG    CT GCGC GCCCG
                                |||    || |||| |||||
                                CGC    GA CGCG CGGGC
                                  CC__  _    A
GAM3055 CALM1    5' CGCCGCCTGCGCCGCC      27857    G    ACTC
                                CG CGCCT    GCGCCGCC
                                || |||||    ||||||||
                                GC GCGGA    CGCGGCGG
                                 G    _____
GAM3055 CDC34    5' GCGCCGCCGCCGCCGCCCG   20353      TAC   _
                                GCGCC   TCGC GCCGCCCG
                                |||||   |||| ||||||||
```

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                                CGCGG   GGCG CGGCGGGC
                                  C__   G
GAM3055 CDKN2A   5' GCTGCTCCCCGCCGCCCG   38474   GC  A   G
                                GC  CT CTC CGCCGCCCG
                                ||  || ||| |||||||||
                                CG  GA GGG GCGGCGGGC
                                 AC  _  _
GAM3055 CHN1     5' GGCGCTCGCCGCCGCCCG   12246     CTAC   _
                                GGCGC   TCGC GCCGCCCG
                                |||||   |||| ||||||||
                                CCGCG   AGCG CGGCGGGC
                                   _____   G
GAM3055 CORO2A   5' GCGCTCCTCGCCGCCCG    38063     CTA   GC
                                GCGC   CTC  GCCGCCCG
                                ||||   |||  ||||||||
                                CGCG   GAG  CGGCGGGC
                                  AG_  __
GAM3055 CTNND2   5' GGCGTTGCGCGGCGCCGCCCG  10635     CCTACTC
                                GGCG      GCGCCGCCCG
                                ||||      ||||||||||
                                CCGC      CGCGGCGGGC
                                  AACGCGC
GAM3055 DSCAM    5' GCTGCCTAGCCGCCC      10807    _    CTCGC
                                GC GCCTA    GCCGCCC
                                || |||||    |||||||
                                CG CGGAT    CGGCGGG
                                 A   ______
GAM3055 DSCAM    5' CGCCGCCCGCCCGCCGCCCG   10798    G    TA T G
                                CG CGCC  C C CGCCGCCCG
                                || ||||  | | |||||||||
                                GC GCGG  G G GCGGCGGGC
                                 G   GC _ _
GAM3055 DTNB     5' CAGCGCCTACTCAGGCCCC   37599          C   G
                                CGGCGCCTACTCG GCC CC
                                |||||||||||| ||| ||
                                GTCGCGGATGAGT CGG GG
                                       C   _
GAM3055 DVL3     5' CGGGTCCCAGCGCCGCCCG   20679    CG    CTC
                                CGG  CCTA   GCGCCGCCCG
                                |||  ||||   ||||||||||
                                GCC  GGGT   CGCGGCGGGC
                                  CA   ____
GAM3055 EMX2     5' CGCTGCCTCCGCCGCCC     44683     CTA   G
                                CGC   CTC CGCCGCCC
                                |||   ||| ||||||||
                                GCG   GAG GCGGCGGG
                                  ACG   _
GAM3055 EN2      5' CGGCCGCCGCCGCCGCCCG   10945     _   TACTCG
                                CGGC GCC     CGCCGCCCG
                                |||| |||     |||||||||
```

```
                                GCCG CGG     GCGGCGGGC
                                  G  CG____
GAM3055  EN2     5'  CGCCGCCTGGGCCGCCC     10942    G    ACTCGC
                                CG CGCCT     GCCGCCC
                                || |||||     |||||||
                                GC GCGGA     CGGCGGG
                                 G    CC____
GAM3055  EN2     5'  CGGCGCTCACGCCCGCCCG   10946       CTAC     _
                                CGGCGC   TCGCGCC GCCCG
                                ||||||   ||||||| |||||
                                GCCGCG   AGTGCGG CGGGC
                                   ____      G
GAM3055  EP300    5'  CGGGCCGAGCAGCGCCGCCCG  10981     C   TACTC
                                CGG GCC    GCGCCGCCCG
                                ||| |||    ||||||||||
                                GCC CGG    CGCGGCGGGC
                                  _  CTCGT
GAM3055  F2R     5'  CGGTCCCTCAGCCGCC      12795     CG  TA    C
                                CGG  CC  CTCG GCCGCC
                                |||  ||  |||| ||||||
                                GCC  GG  GAGT CGGCGG
                                 A_  __   _
GAM3055  FHIT    5'  CGGGGCCGGAGCGCCGCC    12868     C   TACTC
                                CGG GCC    GCGCCGCC
                                ||| |||    ||||||||
                                GCC CGG    CGCGGCGG
                                  C  CCT__
GAM3055  GNAI2    5'  CGGCCCGGCCGCCGCCC     42649     G  TACTCG
                                CGGC CC     CGCCGCCC
                                |||| ||     ||||||||
                                GCCG GG     GCGGCGGG
                                  _  CCG___
GAM3055  HAGH     5'  AGCGCCACGCCGCCC       23707       TACTC
                                GGCGCC    GCGCCGCCC
                                ||||||    |||||||||
                                TCGCGG    TGCGGCGGG
                                   _____
GAM3055  HCN4     5'  GGCGCGGCGCGCCGCCCG    24229      CTACT
                                GGCGC    CGCGCCGCCCG
                                |||||    ||||||||||
                                CCGCG    GCGCGGCGGGC
                                  CC___
GAM3055  HNF3G    5'  CGGCGCCCGCCCGTCC      43645       TACT  G  C
                                CGGCGCC   CGC CCG CC
                                |||||||   ||| ||| ||
                                GCCGCGG   GCG GGC GG
                                   ____  _  A
GAM3055  JAG2     5'  CGGCCCCGCCGCCGCCGCCCG  13714     G  TA T  _
                                CGGC CC  C CGC GCCGCCCG
                                |||| ||  | ||| ||||||||
```

```
                                GCCG GG  G GCG CGGCGGGC
                                  _ GC _   G
GAM3055  KCNA7    5'  CGCCGCCGCCGCCGCCC     36649      TAC   _
                                CGCC   TCGC GCCGCCC
                                ||||   |||| |||||||
                                GCGG   GGCG CGGCGGG
                                  C__    G
GAM3055  KCNK1    5'  GGCTCCCGCCCGCCGCCCG    13896     G  TA T G
                                GGC CC  C C CGCCGCCCG
                                ||| ||  | | |||||||||
                                CCG GG  G G GCGGCGGGC
                                 A  GC _ _
GAM3055  LASS2    5'  CGGCGCCGCCGCCGCCGCCCG  42672        TAC   _
                                CGGCGCC   TCGC GCCGCCCG
                                |||||||   |||| ||||||||
                                GCCGCGG   GGCG CGGCGGGC
                                    C__    G
GAM3055  LHX1     5'  CGGGCTGGAGCGCGCCGCC    24523     C  CTACT
                                CGG GC    CGCGCCGCC
                                ||| ||    |||||||||
                                GCC CG    GCGCGGCGG
                                 _ ACCTC
GAM3055  LIG1     5'  GGTCCCGCGCGCCGCTGCCCG  6934     CG   ACT     ___
                                GG  CCT   CGCGCC   GCCCG
                                ||  |||   ||||||   |||||
                                CC  GGG   GCGCGG   CGGGC
                                 A_   C__     CGA
GAM3055  LMO2     5'  CGCCGGCTCCGCGCCGCCCG   24540      TA   _
                                CGCC  CTC GCGCCGCCCG
                                ||||  ||| ||||||||||
                                GCGG  GAG CGCGGCGGGC
                                  CC   G
GAM3055  LRP8     5'  CGCCGCCGCCGCTGCCGCCCG  21571    G    TAC   _
                                CG CGCC   TCGC GCCGCCCG
                                || ||||   |||| ||||||||
                                GC GCGG   GGCG CGGCGGGC
                                 G   C__   A
GAM3055  MAP3K5   5'  CGGCGCCTCCGTGGCCGCGCCG 25439         AC____       C
              CTCG                  CGGCGCCT     TCGCGCCGC CG
                                ||||||||     ||||||||| ||
                                GCCGCGGA     GGCGCGGCG GC
                                     GGCACC        A
GAM3055  MAPK12   5'  CGGGCCGGCTCCGCGCCGCTCG 16468     C   TA  _     C
                                CGG GCC  CTC GCGCCGC CG
                                ||| |||  ||| ||||||| ||
                                GCC CGG  GAG CGCGGCG GC
                                  _  CC   G      A
GAM3055  MEN1     5'  CGGCGCACGCCGCC       39174        CTACTC
                                CGGCGC     GCGCCGCC
                                ||||||     ||||||||
```

```
                              GCCGCG    TGCGGCGG
                                        ______
GAM3055 MYO1D   5' CGGCGCCTTCTCGGCCG    43493       A   C
                              CGGCGCCT CTCG GCCG
                              |||||||| |||| ||||
                              GCCGCGGA GAGC CGGC
                                   A   _
GAM3055 NAB2    5' CGGCGCCTGCTGCGTGC    25564       A C  CC
                              CGGCGCCT CT GCG  GC
                              |||||||| || |||  ||
                              GCCGCGGA GA CGC  CG
                                   C _  A_
GAM3055 NFKBIL2 5' GCCTCTTCGCGCCGCTGCCCG 30240     AC     ___
                              GCCT  TCGCGCC   GCCCG
                              ||||  |||||||   |||||
                              CGGA  AGCGCGG   CGGGC
                                GA      CGA
GAM3055 ODC1    5' CAGCGCCTGGCTCCCGCCCG  14914       A_  GCG
                              CGGCGCCT  CTC   CCGCCCG
                              ||||||||  |||   |||||||
                              GTCGCGGA  GAG   GGCGGGC
                                   CC  ___
GAM3055 OLFM1   5' CGGCGCCTGGCTCGTGTCCCCA 26770       A_   CG___   _
           CGCC                 CGGCGCCT  CTCG    CCGC CC
                              ||||||||  ||||    |||| ||
                              GCCGCGGA  GAGC    GGTG GG
                                   CC    ACAGG   C
GAM3055 PCOLCE2 5' CGGCGCTCGGCTGCCC     30043      CTAC  C  C
                              CGGCGC    TCG GC GCCC
                              ||||||    ||| || ||||
                              GCCGCG    AGC CG CGGG
                                 ____   _ A
GAM3055 PITPN   5' CGCCGCTGCCGACGCCGCCCG 26332    G   CTA  C
                              CG CGC   CT GCGCCGCCCG
                              || |||   || ||||||||||
                              GC GCG   GG TGCGGCGGGC
                               G   AC_  C
GAM3055 RELN    5' CGCGCGCCCTACGCGCCGCTCG 45354    _     ACT      C
                              CG GCGCCT   CGCGCCGC CG
                              || ||||||   |||||||| ||
                              GC CGCGGG   GCGCGGCG GC
                               G     AT_      A
GAM3055 RNF12   5' CAGCGCCTGCTCGGAGACG   32034       A   CGC_
                              CGGCGCCT CTCG    CG
                              |||||||| ||||    ||
                              GTCGCGGA GAGC    GC
                                   C    CTCT
GAM3055 SDC2    5' GCGCCTGCTCCCGCCGCCCG   42569       A  G
                              GCGCCT CTC CGCCGCCCG
                              |||||| ||| |||||||||
```

```
                                CGCGGA GAG GCGGCGGGC
                                   C   G
GAM3055 SGT     5' GCGCACCGCGGTGCCGCCCG  16614     CT  T  ___
                                GCGC  AC CGC   GCCGCCCG
                                ||||  || |||   ||||||||
                                CGCG  TG GCG   CGGCGGGC
                                  __  _  CCA
GAM3055 SMARCC2  5' CGGGCCCCGCCGCCGCCCG   40073    C   ACT  _
                                CGG GCCT   CGC GCCGCCCG
                                ||| ||||   ||| ||||||||
                                GCC CGGG   GCG CGGCGGGC
                                  _   ___  G
GAM3055 TJP1    5' CGGCGTCTCCTCGGAAGCCG  17541      C  A   C__
                                CGGCG CT CTCG   GCCG
                                ||||| || ||||   ||||
                                GCCGC GA GAGC   CGGC
                                   A  G   CTT
GAM3055 TMEM1   5' CGGCGCCGCCCGCC       17592       TACTC  G
                                CGGCGCC    GC CCGCC
                                |||||||    || |||||
                                GCCGCGG    CG GGCGG
                                  ______ _
GAM3055 TMEM1   5' GCGCCGCAGCTGCCGCCCG   17596      TACTC  _
                                GCGCC    GC GCCGCCCG
                                |||||    || ||||||||
                                CGCGG    CG CGGCGGGC
                                   CGT__  A
GAM3055 TRIM8   3' CAGCGCCCCGCCGCC      36280       ACTCG
                                CGGCGCCT    CGCCGCC
                                ||||||||    |||||||
                                GTCGCGGG    GCGGCGG
                                  ______
GAM3055 WEE1    5' CGGCCCGGCGCCGCCC     18092     G  TACTC
                                CGGC CC    GCGCCGCCC
                                |||| ||    |||||||||
                                GCCG GG    CGCGGCGGG
                                  _  C____
GAM3055 WNT11   5' GGTCCTGCACGCCGCC     21533    CG   ACT
                                GG  CCT   CGCGCCGCC
                                ||  |||   |||||||||
                                CC  GGA   GTGCGGCGG
                                 A_   C__
GAM3056 CCNT2   3' AGGTTTAATTTCATTTTTAT  38489        GGCT
                                AGGTTTAATT    TTTTTAT
                                ||||||||||    |||||||
                                TCCAAATTAA    AAAAATA
                                      AGT_
GAM3056 GHRHR   3' TACAGGTTTATTGGCTCCT   9068          A
                                TACAGGTTTA TTGGCTTTT
                                |||||||||| |||||||||
```

```
                                ATGTCCAAAT AACCGAGGA
                                        _
GAM3056  PTPRB    3'  TACAGGTTGAATTAGTTTT   15927        T     C
                                TACAGGTT AATTGG TTTT
                                |||||||| |||||| ||||
                                ATGTCCAA TTAATC AAAA
                                     C     _
GAM3056  TSGA10   5'  AGATTTAAGCCTTTTTAT    36111        ATT
                                AGGTTTA   GGCTTTTTTAT
                                |||||||   ||||||||||
                                TCTAAAT   TCGGAAAAATA
                                        ___
GAM3057  ADCY6    5'  TCCCGCGGTCCTCCGAGCCCGC 31613          GC    TC
                                TCCCGCGGTCC  CCGG  CCCGC
                                ||||||||||  ||||  |||||
                                AGGGCGCCAGG  GGCT  GGGCG
                                      A_   C_
GAM3057  ATP6V0B  5'  TCCCGCAGTCTGTCCGCCCG   19728       ____
                                TCCCGCG   GTCCGCCCG
                                |||||||   |||||||||
                                AGGGCGT   CAGGCGGGC
                                    CAGA
GAM3057  BDNF     5'  TCCAGCGCCCAGCCCCGGTCCC 40597     C  G  _   _
           CG                     TCC GCG TCC GCCC GGTCCCCG
                                ||| ||| ||| |||| ||||||||
                                AGG CGC GGG CGGG CCAGGGGC
                                  T  _  T   G
GAM3057  CDKN2C   5'  TCTCGCGGTCCCCGGCC     10392    C      GC
                                TC CGCGGTCC  CCGGTC
                                || ||||||||  ||||||
                                AG GCGCCAGG  GGCCGG
                                 A      __
GAM3057  COL4A1   3'  TCCTGCGGTCCATGCGATGCCC 12309     C      CC   _  C
           TGC                    TCC GCGGTCCG  CGGT CCC GC
                                ||| ||||||||  |||| ||| ||
                                AGG CGCCAGGT  GCTA GGG CG
                                  A       AC   C  A
GAM3057  DBN1     5'  CCGCTAGCTCGGTCCCCGC   38929     GGTCC  C
                                CCGC    GC CGGTCCCCGC
                                ||||    || ||||||||||
                                GGCG    CG GCCAGGGGCG
                                  AT___  A
GAM3057  DNAJB1   5'  TCCTGCGGCCCGCCGACCCGC  26035     C       C  TC
                                TCC GCGGTCCGCC GG  CCCGC
                                ||| ||||||||| ||  |||||
                                AGG CGCCGGGCGG CT  GGGCG
                                  A       _ __
GAM3057  FANCC    5'  TCCCGCGGTCGCCCGGC     43281         C
                                TCCCGCGGTC GCCCGGT
                                |||||||||| |||||||
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                                AGGGCGCCAG CGGGCCG
                                      _
GAM3057 IER5     3'  CCCGCGGTCTCTGGGCGTCCTC 32421          CGCCCG_   C
              GC                  CCCGCGGTC      GTCC CGC
                                  |||||||||      |||| |||
                                  GGGCGCCAG      CAGG GCG
                                      AGACCCG    A
GAM3057 IGF2R    3'  TCCCGCGGCTCCGTGCTCCCCT 9341          _   CCCGG    _
              GC                  TCCCGCGG TCCG    TCCCC GC
                                  |||||||| ||||    ||||| ||
                                  AGGGCGCC AGGC    AGGGG CG
                                      G   ACG__    A
GAM3057 NMI      5'  TCCCCCGGTCCGCCCGCCGAGC 21722      G        G  CC_
              GC                  TCCC CGGTCCGCCCG TC   CGC
                                  |||| |||||||||| ||   |||
                                  AGGG GCCAGGCGGGC GG   GCG
                                    G         _ CTC
GAM3057 NOTCH4   5'  TCTCCAAGCCCCGGTCCC    21254    _  C   CCG
                                  TC CCG GGT   CCCGGTCCC
                                  || ||| |||   |||||||||
                                  AG GGT TCG   GGGCCAGGG
                                   A  _  ___
GAM3057 TBX6     5'  CGGCCAGCTGGTCCCCG     38854      C  CC
                                  CGGTC GC  GGTCCCCG
                                  ||||| ||  ||||||||
                                  GCCGG CG  CCAGGGGC
                                     T  A_
GAM3057 WBSCR14  5'  CCGCAACCGCCTGGTCCCTGC  37285       T    C     C
                                  CCGCGG CCGCC GGTCCC GC
                                  |||||| ||||| |||||| ||
                                  GGCGTT GGCGG CCAGGG CG
                                     _    A     A
GAM3057 ACTN1    5'  GCGGCGCTGCTGGCGAAGG   9934      ACA       C
                                  GCG   CTGCTGGCG GAGG
                                  |||   ||||||||| ||||
                                  CGC   GACGACCGC TTCC
                                    CGC       _
GAM3057 AQP5     5'  GCGCGGGGCCGGCGCGGGGGG  11630     ACACT       A
                                  GCG    GCTGGCGCG GGGG
                                  |||    ||||||||| ||||
                                  CGC    CGGCCGCGC CCCC
                                    GCCC_       C
GAM3057 FSTL1    3'  ACTGCTGGAAGCTAGGGG    28210        C_  G
                                  ACTGCTGG  GC AGGGG
                                  ||||||||  || |||||
                                  TGACGACC  CG TCCCC
                                       TT  A
GAM3057 FZD4     5'  GATGCGGCGACGAGGGG     29158    CAC   T   _
                                  GA   TGC GGCG CGAGGGG
                                  ||   ||| |||| |||||||
```

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                                CT   ACG CCGC GCTCCCC
                                 ___  _   T
GAM3057  GPC1     3'  GCTGACACTGAGCGGTGGGGGG 13249    _     CT   CGA_
                AC                  GC GACACTG  GGCG   GGGGAC
                                   || |||||||  ||||   ||||||
                                   CG CTGTGAC  TCGC   CCCCTG
                                    A      __   CACC
GAM3057  IL1F5    3'  ACATTGTGGGAGGGGA     29346     C  C   CGC
                                   ACA TG TGG   GAGGGGA
                                   ||| || |||   |||||||
                                   TGT AC ACC   CTCCCCT
                                     A  _  ___
GAM3057  KCNH3    5'  GACGCTGGCGCGCGAGGGG   42087     ACT      __
                                   GAC   GCTGGCGC  GAGGGG
                                   |||   ||||||||  ||||||
                                   CTG   CGACCGCG  CTCCCC
                                     ___       CG
GAM3057  LPIN2    3'  GACACTGCTCGGGGGG      31209         GGCG  A
                                   GACACTGCT    CG GGGG
                                   |||||||||    || ||||
                                   CTGTGACGA    GC CCCC
                                          ____  _
GAM3057  PTPRJ    5'  GCGGCTGCCGCGGGGGGG     15957     ACACT   G    A
                                   GCG    GCTG CGCG GGGG
                                   |||    |||| |||| ||||
                                   CGC    CGAC GCGC CCCC
                                     ______   G    C
GAM3057  SORCS2   3'  GCGGCCTGCTGGCCAGGGA   34057     ACA      G GA
                                   GCG   CTGCTGGC C  GGGGA
                                   |||   |||||||| |  |||||
                                   CGC   GACGACCG G  TCCCT
                                     CG_       _ __
GAM3058  ALS2     3'  CTTGCAAACGGATCGGGGT   34092     A  C_
                                   CTT GT  ACGGATCGGGGT
                                   ||| ||  ||||||||||||
                                   GAA CG  TGCCTAGCCCCA
                                     _  TT
GAM3058  DCTN1    3'  TGCTTTAATCAAGGGG      35705     C      CGGATC
                                   TGC TTAGTCA     GGGG
                                   ||| |||||||     ||||
                                   ACG AATTAGT     CCCC
                                     A      T_____
GAM3058  HLA-DQA1 3'  TGCCTTAATTGAGGGG      45570         CACG  TC
                                   TGCCTTAGT   GA  GGGG
                                   |||||||||   ||  ||||
                                   ACGGAATTA   CT  CCCC
                                         A___  __
GAM3058  PACE4    3'  TGCTTGGCCATCGGGG      15062     C  A   CGGA
                                   TGC TT GTCA   TCGGGG
                                   ||| || ||||   ||||||
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                                ACG AA CGGT    AGCCCC
                                  _ C    _____
GAM3058  PDE4B    5'  TGCCTTAGTCATCCCAGGGT   15155          CGGA
                                TGCCTTAGTCA    TCGGGGT
                                ||||||||||    |||||||
                                ACGGAATCAGT    GGTCCCA
                                      AG__
GAM3058  STK6     3'  CCTTAACTGATCGGGG      18775      GTC  G
                                CCTTA   AC GATCGGGG
                                |||||   || ||||||||
                                GGAAT   TG CTAGCCCC
                                   ___  A
GAM3058  TCF19    3'  TGTCTTGGCCACCAGGG     45559    C   A    GGAT
                                TG CTT GTCAC    CGGGG
                                || ||| |||||    |||||
                                AC GAA CGGTG    GTCCC
                                 A   C    _____
GAM3058  CLK2     3'  TGGTGGTGTTCCTCTGCCT   41282     CGT       CCGA
                                TGG   GTGTTCCTC    GTCT
                                |||   |||||||||    ||||
                                ACC   CACAAGGAG    CGGA
                                  AC_       A___
GAM3058  NRIP1    5'  TGGCTGTGTTTCTCCCAAAT   40989      G     C
                                TGGC TGTGTT CTCCCGAGT
                                |||| |||||| |||||||||
                                ACCG ACACAA GAGGGTTTA
                                   _     A
GAM3058  PSEN1    3'  TGGTTGTGTTCCAGTC      28743     CG       TCCCG
                                TGG  TGTGTTCC    AGTC
                                |||  ||||||||    ||||
                                ACC  ACACAAGG    TCAG
                                  A_      ______
GAM3058  PTX3     3'  TGGCATGTGTTTTAAGTGTGAG 15992          CCTCCC__
                T                TGGCGTGTGTT      GAGT
                                ||||||||||       ||||
                                ACCGTACACAA      CTCA
                                      AATTCACA
GAM3059  MTMR3    3'  TTTATATATTTAACAATTCT   34403
                                TTTATATATTTAATAATTTT
                                ||||||||||||||||||
                                AAATATATAAATTGTTAAGA

GAM3060  TRPM6    3'  TATAATATATATATTCCATATA 32796      CG       AT__
              TATT                 TATAA  TATATATTC    TATATT
                                |||||  |||||||||    ||||||
                                ATATT  ATATATAAG    ATATAA
                                   AT       GTAT
GAM3060  F13A1    3'  TGGGGAATCTGAAGTCTTGTT  44983      A      TGCGAG
                                TGGG AATCTGAA     TGTT
                                |||| ||||||||     ||||
```

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                                ACCC TTAGACTT     ACAA
                                  C       CAGA__
GAM3060  GASC1    5'  TGGGAAATTTGGGAGACTTGTT 42032        C  AATGCGAG
                C                  TGGGAAAT TG       TGTTC
                                   |||||||| ||       |||||
                                   ACCCTTTA AC       ACAAG
                                       A  CCTCTGA_
GAM3060  NEU3     3'  TGGGAAATTCTGTCCAGTGTT  27411        _  AATGCG
                                   TGGGAAAT CTG     AGTGTT
                                   |||||||| |||     ||||||
                                   ACCCTTTA GAC     TCACAA
                                       A  AGG___
GAM3060  SOD3     5'  TGGGAGAACTAGGAGTGTT   16962      AATCT   GC_
                                   TGGGA    GAAT   GAGTGTT
                                   |||||    ||||   |||||||
                                   ACCCT    CTTG   CTCACAA
                                     _____   ATC
GAM3061  ACCN2    3'  TGTCTGGTGGAGGGAGGGGGGG 33457    C       AAA  AC_
                C                  TG CTGGTGGG   GA   GGGGC
                                   || ||||||||   ||   |||||
                                   AC GACCACCT   CT   CCCCG
                                    A       CC_  CCC
GAM3061  ACP1     5'  TACCTATAGGGGACGGGGC   28246       GT_   AAGAA
                                   TGCCTG   GGGA    CGGGGC
                                   ||||||   ||||    ||||||
                                   ATGGAT   CCCT    GCCCCG
                                      ATC   _____
GAM3061  ALX3     3'  TGCTGGTGGGGAGGGGAAGCAG 27071     C      AAA__  _
                GGC                   TGC TGGTGGG    GAA CGGGGC
                                   ||| |||||||    ||| ||||||
                                   ACG ACCACCC    CTT GTCCCG
                                     _      CTCCC   C
GAM3061  BCL2A1   5'  TGCCTGGTGGAGAGCAAAG   19733         GAA   A
                                   TGCCTGGTGG   AGA CGGGG
                                   ||||||||||   ||| |||||
                                   ACGGACCACC   TCT GTTTC
                                        ___   C
GAM3061  CDY1     5'  TGCCTGGTGGGACAGCTTGGGC 21716          A  AACG
                                   TGCCTGGTGGGA AG    GGGC
                                   |||||||||||| ||    ||||
                                   ACGGACCACCCT TC    CCCG
                                         G  GAA_
GAM3061  CDY2     5'  TGCCTGGTGGGACAGCTTGGGC 22090          A  AACG
                                   TGCCTGGTGGGA AG    GGGC
                                   |||||||||||| ||    ||||
                                   ACGGACCACCCT TC    CCCG
                                         G  GAA_
GAM3061  DVL3     3'  TGCCTGATGGGGTGGGG     20692          AAAGAAC
                                   TGCCTGGTGGG      GGGG
                                   ||||||||||       ||||
```

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                                ACGGACTACCC      CCCC
                                      CA_____
GAM3061  EFNA3    3'  GCCTGGTGGGGAAGGGG     22401         AAA   C
                                GCCTGGTGGG   GAA GGGG
                                ||||||||||   ||| ||||
                                CGGACCACCC   CTT CCCC
                                     ____  _
GAM3061  FGF23    3'  CTGCTTGGGAACAGAGTGGGGC 33951     G_     _  AC
             C                   CTG  TGGGAA AGA  GGGGCC
                                |||  |||||| |||  ||||||
                                GAC  ACCCTT TCT  CCCCGG
                                  GA     G   CA
GAM3061  FGFR1    3'  TGCCTGGTGGCAGGGAGGGG  31959         GAAA  AC
                                TGCCTGGTGG    GA  GGGG
                                ||||||||||    ||  ||||
                                ACGGACCACC    CT  CCCC
                                      GTCC  __
GAM3061  FLRT2    3'  CCTGGTGGGGAAGGAA      29845         AAA   C
                                CCTGGTGGG   GAA GGGG
                                |||||||||   ||| ||||
                                GGACCACCC   CTT CCTT
                                     ____  _
GAM3061  GBF1     3'  GCCTGGTGGGAAGCACTGG   20078           AGA  G
                                GCCTGGTGGGAA   AC GG
                                ||||||||||||   || ||
                                CGGACCACCCTT   TG CC
                                      CG_  A
GAM3061  GPRK6    3'  TGCTGGTGGGGGCCTCGGG   13274     C      AAAGAA
                                TGC TGGTGGG     CGGG
                                |||  |||||||     ||||
                                ACG ACCACCC     GCCC
                                  _      CCGGA_
GAM3061  HD       3'  TGTCTGCTGGGAAGGATGC   13368    C  G     AGAAC  _
                                TG CTG TGGGAA     GGG GC
                                ||  |||  ||||||     |||  ||
                                AC GAC ACCCTT     CCT CG
                                 A   G     ______   A
GAM3061  HMGCL    3'  TGCTAAGTAGGGAACGGGG   6792      CT     AAA
                                TGC  GGTGGG   GAACGGGG
                                |||  ||||||   ||||||||
                                ACG  TCATCC   CTTGCCCC
                                  AT     ____
GAM3061  IL1R1    3'  TGCTGGTGGGAAAGCATGGGC  9374      C         AACG
                                TGC TGGTGGGAAAG    GGGC
                                |||  ||||||||||    ||||
                                ACG ACCACCCTTTC    CCCG
                                  _         GTA_
GAM3061  PACE     5'  TGACTGGTGGGGGCATGGGGCC 15037    C       AAAGAAC
                                TG CTGGTGGG      GGGGCC
                                ||  ||||||||      ||||||
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                                AC GACCACCC      CCCCGG
                                 T       CCGTA__
GAM3061  PELO     5'  TGCCTGGCGGGAAGGAAACACG 31983           A_    GG
                C                 TGCCTGGTGGGAA  GAACG  GC
                                  ||||||||||||  |||||  ||
                                  ACGGACCGCCCTT  TTTGT  CG
                                         CC    G_
GAM3061  PSEN1    3'  TGCTTGTGTGGGAGAGAAGAA  28742     C  _     A    C
                                  TGC TG GTGGGA AGAA GGG
                                  ||| || |||||| |||| |||
                                  ACG AC CACCCT TCTT CTT
                                    A A     C    _
GAM3061  PTPN18   3'  TGTCTGGCGGGGGTCTGGCTGG 30773     C       AAAGAAC__
                GG                  TG CTGGTGGG        GGGG
                                  || ||||||||        ||||
                                  AC GACCGCCC        CCCC
                                   A       CCAGACCGA
GAM3061  RFX1     3'  TGGTGGGAGGACGGGGG      16301         AA A
                                  TGGTGGGA  G ACGGGG
                                  ||||||||  | ||||||
                                  ACCACCCT  C TGCCCC
                                       __ C
GAM3061  SHC1     3'  GCCTGGCCGGGAGTGGGGC    16701        _    AAGAAC
                                  GCCTGGT GGGA     GGGGC
                                  ||||||| ||||     |||||
                                  CGGACCG CCCT     CCCCG
                                      G    CA_____
GAM3061  SORBS1   3'  TGTCTGGTGGGGGATGGGA   31717    C       AAA  AC
                                  TG CTGGTGGG   GA  GGGG
                                  || ||||||||   ||  ||||
                                  AC GACCACCC   CT  CCCT
                                   A       C__  A_
GAM3061  TCF7     3'  CTGTCATCGGAAGGAACGGGGC 17320     __ G    A
                                  CTG  GT GGAA GAACGGGGC
                                  |||  || |||| |||||||||
                                  GAC  TA CCTT CTTGCCCCG
                                    AG  G    C
GAM3061  THBD     5'  TGCCTGGTGGGAAGGG      7434           AAGAAC
                                  TGCCTGGTGGGA     GGGG
                                  ||||||||||||     ||||
                                  ACGGACCACCCT     TCCC
                                                  _______
GAM3061  TNR      3'  CCTTGGTGGGAAAGGAGG    17622     _        AAC
                                  CCT GGTGGGAAAG   GGGG
                                  ||| ||||||||||   ||||
                                  GGA CCACCCTTTC   CTCC
                                    A        ____
GAM3061  TRPM8    3'  CCTGAAGAGAGCGGGG      35856       T    AAGAA
                                  CCTGG GGGA    CGGGG
                                  ||||| ||||    |||||
```

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                                GGACT CTCT    GCCCC
                                  T   C____
GAM3061  UPF3B    5'  GCTTGGCCGGAACGGGG    38765    C   G   AAGA
                                GC TGGT GGA   ACGGGG
                                || |||| |||   ||||||
                                CG ACCG CCT   TGCCCC
                                 A   G  ____
GAM3061  ABCC1    3'  TGGAGTCGGGGTGGGTGGGGAG 33409         A__   ATA
                                TGGGGTCGGGG   GTG   GAG
                                ||||||||||   |||   |||
                                ACCTCAGCCCC   CAC   CTC
                                      ACC   CC_
GAM3061  ARVCF    3'  TGGGGTGGGGGGGGCAGGAG   11712      C   A   ATA
                                TGGGGT GGGG GTG   GAG
                                |||||| |||| |||   |||
                                ACCCCA CCCC CGT   CTC
                                   C   C   C__
GAM3061  BARHL1   3'  TGGGGGTGGGGAGTGGCAGAG  33475     TC      A
                                TGGGG  GGGGAGTG TAGAG
                                |||||  |||||||| |||||
                                ACCCC  CCCCTCAC GTCTC
                                  CA       C
GAM3061  CACNG6   5'  TGGGGTCGGGAAGGGGGAG   36701          TGATA
                                TGGGGTCGGGGAG    GAG
                                ||||||||||||    |||
                                ACCCCAGCCCTTC    CTC
                                      CCC__
GAM3061  CELSR2   3'  TGGAGTCGGGGAGAAAGAG   10859          TGAT
                                TGGGGTCGGGGAG   AGAG
                                ||||||||||||   ||||
                                ACCTCAGCCCCTC   TCTC
                                      TT__
GAM3061  CNN2     3'  TGGGGCGGGGAGCATGGAGA  20409     T      G  A
                                TGGGG CGGGGAGT AT GAGA
                                ||||| ||||||| || ||||
                                ACCCC GCCCCTCG TA CTCT
                                  _      _  C
GAM3061  CYP2B6   3'  TGGGGTATGGGGAGTGACAG   8925      C_
                                TGGGGT  GGGGAGTGATAG
                                ||||||  ||||||||||||
                                ACCCCA  CCCCTCACTGTC
                                   TA
GAM3061  DHCR24   3'  TGGGGTGGGGAGTGGTGGAAG 31301      C      ATAGA
                                TGGGGT GGGGAGTG    GAAG
                                |||||| ||||||||    ||||
                                ACCCCA CCCCTCAC    CTTC
                                  _      CAC__
GAM3061  EPHX1    3'  GGGGTTGGGGAGTGAGCTTGGA 6518      C       TA___
            G                   GGGGT GGGGAGTGA    GAG
                                ||||| |||||||||    |||
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                                CCCCA CCCCTCACT    CTC
                                  A       CGAAC
GAM3061  FAAH    3'  TGGGGCTGCCACTGGTGGAGAA 11064      CGGGGA__  ATA
             G                   TGGGGT      GTG  GAGAAG
                                 ||||||      |||  ||||||
                                 ACCCCG      CAC  CTCTTC
                                   ACGGTGAC  ___
GAM3061  MDK     3'  TGGGGCTGGGGAGTGAGAG   14393      C       TA
                                 TGGGGT GGGGAGTGA  GAG
                                 |||||| |||||||||  |||
                                 ACCCCG CCCCTCACT  CTC
                                   A       __
GAM3061  NESH    5'  TGGGGTCGGAGACTGGGGAG  32345          G  ATA
                                 TGGGGTCGGGGA TG   GAG
                                 |||||||||||| ||   |||
                                 ACCCCAGCCTCT AC   CTC
                                       G  CC_
GAM3061  OTC     5'  GGGGTGCAAGATGATAGAGAAG 8044       _   GA
                                 GGGGT CGGG  GTGATAGAGAAG
                                 ||||| ||||  ||||||||||||
                                 CCCCA GTTC  TACTATCTCTTC
                                   C   __
GAM3061  PGR     5'  GGGTCGGGGGCGGGGGAG    9571         A  ATA
                                 GGGTCGGGG GTG   GAG
                                 |||||||| |||   |||
                                 CCCAGCCCC CGC   CTC
                                      _  CCC
GAM3061  PRKACG  3'  TGGGGCGGGGGGTGAGGGAG  15603     T    A   TA
                                 TGGGG CGGGG GTGA  GAG
                                 ||||| ||||| ||||  |||
                                 ACCCC GCCCC CACT  CTC
                                   _    C   CC
GAM3061  RYR1    5'  TGAGGTCGGGGAACAGAG    8074          GTG
                                 TGGGGTCGGGGA  ATAGAG
                                 ||||||||||||  ||||||
                                 ACTCCAGCCCCT  TGTCTC
                                       ___
GAM3061  ZNF278  3'  TGGGAGAATGGGTGGTGGAGAA 36813     _ TC_  GA  ATA
             G                   TGGG G   GGG  GTG   GAGAAG
                                 |||| |   |||  |||   ||||||
                                 ACCC C   CCC  CAC   CTCTTC
                                   T TTA   AC  ___
GAM3062  CAST    3'  GCACTGTGTGTAGAATG    11981     CCGC      C
                                 GCAC   GTGTAGGG TG
                                 ||||   |||||||| ||
                                 CGTG   CACATCTT AC
                                   ACA_      _
GAM3062  IKBKB   3'  GCAGTGCCCACGGAGGGCTGC  41806    ___     TGT
                                 GCA  CCCGCG  AGGGCTGC
                                 |||  ||||||  ||||||||
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                                CGT   GGGTGC   TCCCGACG
                                  CAC     C__
GAM3062  JPH2     3'  CCCCTGCAGGCTGCAT     45376     GCG     G
                                CCC   TGTAGG CTGCAT
                                |||   |||||| ||||||
                                GGG   ACGTCC GACGTA
                                  G__     _
GAM3062  MAP3K7IP1 3'  GCCCTGCTTGGGCTGCA     25929     A  C  GTGTA
                                GC CC GC     GGGCTGCA
                                || || ||     ||||||||
                                CG GG CG     CCCGACGT
                                 _  A  AA___
GAM3062  MMP2     3'  GCAGCCCAAAGCAGGGCTGC   21196     _    CGT
                                GCA CCCG   GTAGGGCTGC
                                ||| ||||   ||||||||||
                                CGT GGGT   CGTCCCGACG
                                  C    TT_
GAM3062  LAMC3    5'  CCGCGCGCTGGCCGCCAGG    25861          T     TGAC
                                CCGCGCGCTG GCCGTC    GG
                                |||||||||| ||||||    ||
                                GGCGCGCGAC CGGCGG    CC
                                      _      T____
GAM3062  NR2E1    5'  CGCGCGCTGCGCTGCTCCCTGG 17576            C _   GAC
                                CGCGCGCTGTGC G TCT   GG
                                |||||||||||| | |||   ||
                                GCGCGCGACGCG C AGG   CC
                                       A G   GA_
GAM3062  SCNN1B   5'  GCGCGCTGTCGGCGGTGGCGGA 7338          _ C  TC  A
                                GCGCGCTGT G CG  TG CGGA
                                ||||||||| | ||  || ||||
                                CGCGCGACA C GC  AC GCCT
                                     G C  C_  C
GAM3062  SERPINB2 5'  CTGAGTTGCTGTCTGACGG    15080     ___   C
                                CTG   TGC GTCTGACGG
                                |||   ||| |||||||||
                                GAC   ACG CAGACTGCC
                                  TCA   A
GAM3062  UQCRC1   5'  GCGTACTGAGGTCTGGCGG    17891     CG   TGCC    A
                                GCG  CTG    GTCTG CGG
                                |||  |||    ||||| |||
                                CGC  GAC    CAGAC GCC
                                  AT   TC__     C
GAM3063  CKB      3'  TAGTTTATTTCAGCATCA     12258           ATCGAT
                                TAGTTTATTTCA     TATCA
                                ||||||||||||     |||||
                                ATCAAATAAAGT     GTAGT
                                       C_____
GAM3063  NAPB     3'  TGAAATATTAAAAACAAAA    43179           CTT
                                TGAAATATTAA   AACAAAA
                                ||||||||||   |||||||
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                                ACTTTATAATT  TTGTTTT
                                      T__
GAM3063  NCAM2    3'  ATTGAAATTCTTAACAAAAT  21222       ATTAA
                                ATTGAAAT    CTTAACAAAAT
                                ||||||||    ||||||||||
                                TAACTTTA    GAATTGTTTTA
                                    A____
GAM3063  PLSCR1   3'  GAAATATTAACTTTCAAAA   34410         AA
                                GAAATATTAACTT  CAAAA
                                ||||||||||||  |||||
                                CTTTATAATTGAA  GTTTT
                                       A_
GAM3064  CYP1A1   3'  TAGAGAAGGGAGACCAA    7977       ACGCAA  A
                                TAGAGG     AG GAGACCAA
                                ||||||     || ||||||||
                                ATCTCT     TC CTCTGGTT
                                   _______ C
GAM3064  HDGF     3'  TAGAGAGGCATAGAGAGACCA  21065      AC   A
                                TAGAGG  GCA AGAGAGACCA
                                ||||||  ||| ||||||||||
                                ATCTCT  CGT TCTCTCTGGT
                                   C_   A
GAM3064  POLG     5'  GAAGACGTGGAGAGAGAC    15446       CAA
                                GAGGACG   AGAGAGAC
                                |||||||   ||||||||
                                CTTCTGC   TCTCTCTG
                                    ACC
GAM3064  TRPC6    5'  AGGGGGTGCAAAGAGGA     21480    A  AC      A
                                AG GG  GCAAAGAG GA
                                || ||  |||||||| ||
                                TC CC  CGTTTCTC CT
                                 C  CA      _
GAM3064  CEBPD    3'  CTGGTTTTTTTTCTTTTTAC  45518       C    CG
                                CTGGTTTT TTTCT  TTAT
                                |||||||| |||||  ||||
                                GACCAAAA AAAGA  AATG
                                    A     AA
GAM3064  FXYD6    3'  TGAGTTCCCACTCTCGTTATGA 35124    _  TT T
            C                    TG GTT  C TTCTCGTTATGAC
                                || |||  | ||||||||||||
                                AC CAA  G GAGAGCAATACTG
                                 T   GG T
GAM3064  PCDHA9   3'  TGGTTTTCAAGTGTTATG    36555       TTTCTC
                                TGGTTTTC     GTTATG
                                ||||||||     ||||||
                                ACCAAAAG     CAATAC
                                    TTCA__
GAM3064  PK428    5'  CTGGTTTTCCTTTAAATTATTA 18802          CTC___
            TGA                   CTGGTTTTCTTT     GTTATGA
                                ||||||||||||     |||||||
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                                GACCAAAAGGAA     TAATACT
                                      ATTTAA
GAM3065  ACHE    3'  AGAGAGGAGGAGAAAAGAA   31862    _        CA
                                AGA AGGAGGAGAAA  AGAA
                                ||| ||||||||||  ||||
                                TCT TCCTCCTCTTT  TCTT
                                  C         __
GAM3065  AP1M1   3'  GAAGGAAGACAAGAAG     37168         GAAA
                                GAAGGAGGA   CAAGAAG
                                |||||||||   |||||||
                                CTTCCTTCT   GTTCTTC
                                     _____
GAM3065  AR      5'  AGGAGGAGGTGGAGAGAGA   6226         AAACA  _
                                AGGAGGAG    AGA AGA
                                ||||||||    ||| |||
                                TCCTCCTC    TCT TCT
                                     CACC_  C
GAM3065  ARPC2   5'  AGGGGAAGGAGAAACAAG    25062    AA
                                AG  GGAGGAGAAACAAG
                                ||  ||||||||||||||
                                TC  CTTCCTCTTTGTTC
                                 CC
GAM3065  BAZ1B   3'  AGAAGGGGAGATTCAGGAA   37084       A    AA  A
                                AGAAGG GGAGA  CA GAA
                                |||||| |||||  || |||
                                TCTTCC CCTCT  GT CTT
                                   _    AA  C
GAM3065  BGN     3'  GAGGAGGAGGAACAGAA     11818    A     A   A
                                GA GGAGGAG AACA GAA
                                || ||||||| |||| |||
                                CT CCTCCTC TTGT CTT
                                 _      C   _
GAM3065  BIG1    5'  AGGAGGAGGAGAGGAAG     26956    A       AACAA
                                AG AGGAGGAGA    GAAG
                                || |||||||||    ||||
                                TC TCCTCCTCT    CTTC
                                 C       C____
GAM3065  CAPN1   3'  GGAGGAGAGGGGACAGGAGGA  23254        A___   A  A
                                GGAGGAGA   ACA GA GA
                                ||||||||   ||| || ||
                                CCTCCTCT   TGT CT CT
                                     CCCC  C  C
GAM3065  CARPX   3'  AGAAGGAGAGAGAAGCAAGAAG 33563        _    A
                                AGAAGGAG GAGAA CAAGAAG
                                |||||||| ||||| |||||||
                                TCTTCCTC CTCTT GTTCTTC
                                     T    C
GAM3065  CORT    3'  GAAGGAGGAGAGGAAAGA    10544          AAC
                                GAAGGAGGAGA   AAGA
                                ||||||||||   ||||
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                                CTTCCTCCTCT   TTCT
                                      CCT
GAM3065  CTF1     3'  GAAGGAGGGAGAGCAAGAAAA  10627        _   AA
                                GAAGGAGG AGA  CAAGAAGA
                                |||||||| |||  ||||||||
                                CTTCCTCC TCT  GTTCTTTT
                                     C   C_
GAM3065  DACH     5'  AGACGGAGGAGAAGCGAGA   38868     A       ACA
                                AGA GGAGGAGAA   AGA
                                ||| |||||||||   |||
                                TCT CCTCCTCTT   TCT
                                  G        CGC
GAM3065  DACH     5'  AGAAGGGGGAGAAAAGGAG   38867       A      CA  A
                                AGAAGG GGAGAAA  AG AG
                                |||||| |||||||  || ||
                                TCTTCC CCTCTTT  TC TC
                                    C       __  C
GAM3065  DDX20    5'  AGAGGGAGGAGAGGAAAGA   28505     A       AAC
                                AGA GGAGGAGA   AAGA
                                ||| ||||||||   ||||
                                TCT CCTCCTCT   TTCT
                                  C       CCT
GAM3065  DNM2     3'  AGGAGGAGGAGGAGGAGAGGAA 22375    A       AAACA   A
              T                  AG AGGAGGAG     AGA GAAT
                                 || ||||||||     ||| ||||
                                 TC TCCTCCTC     TCT CTTA
                                  C       CTCC_   C
GAM3065  DSC1     5'  AGTAGGAGGAGCAACGGGAGAA 35931    A       A   AA  A
              T                  AG AGGAGGAG AAC  GA GAAT
                                 || |||||||| |||  || ||||
                                 TC TCCTCCTC TTG  CT CTTA
                                  A       G   CC  _
GAM3065  DYRK1B   3'  AAAAGGGGGAGAGGGGCCCAAG 21774        A     AA____
                                AGAAGG GGAGA      CAAG
                                |||||| |||||      ||||
                                TTTTCC CCTCT      GTTC
                                    C     CCCCGG
GAM3065  FCER1G   3'  AGAAGGGTGGGACAAGAGA    19952       A_  A  AA     A
                                AGAAGG  GG GA  CAAGA GA
                                ||||||  || ||  ||||| ||
                                TCTTCC  CC CT  GTTCT CT
                                    CA  _  __     _
GAM3065  FOXE3    3'  GAGGGAGAAGAAATGAGA    29145    A        CA
                                GA GGAGGAGAAA  AGA
                                || ||||||||||  |||
                                CT CCTCTTCTTT  TCT
                                  C         AC
GAM3065  FOXF1    3'  GAAGGAGGGGGACCTCAGCAGA 11117         A_  AACA  A
              AT                   GAAGGAGG  GA    AG AGAAT
                                   ||||||||  ||    || |||||
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                                CTTCCTCC  CT    TC TCTTA
                                    CC  GGAG  G
GAM3065  GAS7     3'  AGAAGGAGCGGGAAGCAAA   25261        GA_   A
                                AGAAGGAG   GAA CAAG
                                ||||||||   ||| ||||
                                TCTTCCTC   CTT GTTT
                                    GCC   C
GAM3065  GFRA2    3'  AGGAGGAGGAGGGAGAAGA   11262        AAACA
                                AGGAGGAG    AGAAGA
                                ||||||||    ||||||
                                TCCTCCTC    TCTTCT
                                    CTCCC
GAM3065  GJA5     3'  AGAGGGAGGAGAAGCCAAG   23576     A       A_
                                AGA GGAGGAGAA  CAAG
                                ||| |||||||||  ||||
                                TCT CCTCCTCTT  GTTC
                                  C        CG
GAM3065  HLALS    3'  AGAGGAAGGAGAACTGGAAAAG 11357     A       ACA_
              A                  AGA GGAGGAGAA    AGAAGA
                                ||| |||||||||    ||||||
                                TCT CTTCCTCTT    TTTTCT
                                  C        GACC
GAM3065  HMGB3    3'  AGAGTGAGGAGAACACGAGA   23775     AG      _  A
                                AGA  GAGGAGAA AC AGA
                                |||  |||||||| || |||
                                TCT  CTCCTCTT TG TCT
                                  CA       G  C
GAM3065  IGHMBP2  3'  AGGAGGAGGGGGAACACTGCAG 13488        A___    AGA_
                                AGGAGGAG    AACA    AG
                                ||||||||    ||||    ||
                                TCCTCCTC    TTGT    TC
                                    CCCC    GACG
GAM3065  IKBKG    5'  GAGGGAGGAGTAGAAACA    45418    A     ___
                                GA GGAGGA   GAAACA
                                || ||||||   ||||||
                                CT CCTCCT   CTTTGT
                                 C     CAT
GAM3065  IL2RG    3'  AGAGGGAGGGAGGAAGAA    6816     A    A  AACAA
                                AGA GGAGG GA    GAAGAA
                                ||| ||||| ||    ||||||
                                TCT CCTCC CT    CTTCTT
                                  C    _  C_____
GAM3065  KRT15    3'  AGAAGGTGGGGAGAGGCAGA   14011      A__    AACA
                                AGAAGG   GGAGA    AGA
                                ||||||   |||||    |||
                                TCTTCC   CCTCT    TCT
                                   ACC    CCG_
GAM3065  KRTHB1   3'  GAAGGGGAGAGGCAGGAAG   14027      A    AA  A
                                GAAGG GGAGA  CA GAAG
                                ||||| |||||  || ||||
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                                CTTCC CCTCT  GT CTTC
                                   _    CC  C
GAM3065  LGR6     3'  GAAGAGAGGGGAAGAGAAGAAT 44479      _   A   ACA
                                GAAG GAGG GAA   AGAAGAAT
                                |||| |||| |||   ||||||||
                                CTTC CTCC CTT   TCTTCTTA
                                  T   C   C__
GAM3065  MAPK10   5'  GAAGAAGGAGAAACAGGA    39980             A
                                GAAGGAGGAGAAACA GA
                                |||||||||||||| ||
                                CTTCTTCCTCTTTGT CT
                                          C
GAM3065  MAPT     3'  GGAGGGGGAAGAAAAAAGAAT  32581       A_  AC
                                GGAGG  GAA  AAGAAGAAT
                                |||||  |||  |||||||||
                                CCTCC  CTT  TTTTTCTTA
                                   CC   CT
GAM3065  MAZ      3'  AGGAGCAGGAGAAACAAA    43849    A  G
                                AG AG AGGAGAAACAAG
                                || || ||||||||||||
                                TC TC TCCTCTTTGTTT
                                 C  G
GAM3065  MCC      3'  GAAAGAGGAGAAACGAGA    14380            A
                                GAAGGAGGAGAAAC AGA
                                |||||||||||||| |||
                                CTTTCTCCTCTTTG TCT
                                          C
GAM3065  MSI1     3'  AAAGGAGGGGAAATCTGAA   14634         A   CAA
                                GAAGGAGG GAAA   GAA
                                |||||||| ||||   |||
                                TTTCCTCC CTTT   CTT
                                     C    AGA
GAM3065  MYEOV    3'  AGGAAGAGGAGAGGGTAGGAGA 39872    A        AACA  A
                                AG AGGAGGAGA    AG AGA
                                || |||||||||    || |||
                                TC TTCTCCTCT    TC TCT
                                 C        CCCA  C
GAM3065  MYO1A    3'  GGAGGAGAGAACAAGAAG    23921         _
                                GGAGGAGA AACAAGAAG
                                |||||||| |||||||||
                                CCTCCTCT TTGTTCTTC
                                     C
GAM3065  NEDD4    5'  AGGAGGAGGAGGAGAAG     43095    A       AAACA
                                AG AGGAGGAG     AGAAG
                                || |||||||||    |||||
                                TC TCCTCCTC     TCTTC
                                 C       C_____
GAM3065  NHP2L1   3'  GAGGGAGGAAAGGAAG      22679    A       AACAA
                                GA GGAGGAGA     GAAG
                                || ||||||||     ||||
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                                CT CCTCCTTT    CTTC
                                 C      C____
GAM3065  NID      3'  GGAGGGAGAAACCAAGGAG   14798      _    _  A
                                GGAGG AGAAAC AAG AG
                                ||||| |||||| ||| ||
                                CCTCC TCTTTG TTC TC
                                   C     G   C
GAM3065  NR4A1    5'  GAAGGAGGCAGTGGGGAGAA  13415       _ AAACA
                                GAAGGAGG AG    AGAA
                                |||||||| ||    ||||
                                CTTCCTCC TC    TCTT
                                     G  ACCCC
GAM3065  NRIP1    5'  AAGGAGGAGGAGAAGAA     40947        AAACA
                                AAGGAGGAG    AGAAGAA
                                |||||||||    |||||||
                                TTCCTCCTC    TCTTCTT
                                     C____
GAM3065  PDE6D    3'  AAGGAGGAGACAAGGAG     15158         AA   A
                                AAGGAGGAGA  CAAG AG
                                ||||||||||  |||| ||
                                TTCCTCCTCT  GTTC TC
                                     __   C
GAM3065  PEX6     3'  GAAGGAGGGGCAAGTAG     7108         AGAAA   A
                                GAAGGAGG    CAAG AG
                                ||||||||    |||| ||
                                CTTCCTCC    GTTC TC
                                     CC___   A
GAM3065  PHF1     3'  GAAGGATGGGAGGGGTCAGGAA 15270       __   AAA_  A
                                GAAGGA  GGAG   CA GAA
                                ||||||  ||||   || |||
                                CTTCCT  CCTC   GT CTT
                                   AC   CCCA  C
GAM3065  PLXNA2   3'  AGAAGGAAGGGAGACAGAAA  36074        A  A   A
                                AGAAGGAGG GA ACA GAAG
                                ||||||||| || ||| ||||
                                TCTTCCTTC CT TGT CTTT
                                     C  C  _
GAM3065  PMX1     5'  AGAAGGGGTGGGAGAGAAGAAT 35495      A___    AACAA
                                AGAAGG   GGAGA    GAAGAAT
                                ||||||   |||||    |||||||
                                TCTTCC   CCTCT    CTTCTTA
                                   CCAC    _____
GAM3065  POU2F2   3'  AGGAGGAGGATGAGGATGAAGA 15458   A     GAAACAA
                                AG AGGAGGA      GAAGA
                                || |||||||      |||||
                                TC TCCTCCT      CTTCT
                                 C      ACTCCTA
GAM3065  PPP2R5A  3'  AGGAAGAGGAGGAATGAA    26430    A      AAACAA  _
                                AG AGGAGGAG     GAA GAA
                                || ||||||||     ||| |||
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                                TC TTCTCCTC     CTT CTT
                                 C       _____   A
GAM3065  PRKCM    5'  GAGGAGGAGGAGAGAAG     15642    A      AAACA
                                GA GGAGGAG     AGAAG
                                || |||||||     |||||
                                CT CCTCCTC     TCTTC
                                 _      CTC__
GAM3065  PRKCM    5'  AGGAGGAGGAGGGCGAGGAGAA 15637    A       AAACA  A
                                AG AGGAGGAG     AG AGAA
                                || ||||||||     || ||||
                                TC TCCTCCTC     TC TCTT
                                 C       CCGC_  C
GAM3065  PTK2B    3'  AGAAAGAGGAGGAGTAAGA    19913           AAAC
                                AGAAGGAGGAG    AAGA
                                ||||||||||    ||||
                                TCTTTCTCCTC    TTCT
                                       CTCA
GAM3065  RAB33A   5'  AGAGGAGGAGAGAGGGAGGAGA 21996     A       AACA_  A
                                AGA GGAGGAGA     AG AGA
                                ||| ||||||||     || |||
                                TCT CCTCCTCT     TC TCT
                                 _       CTCCC  C
GAM3065  RAD23B   3'  AAGGGGAAAAGACAGGGAGA   16132      A     _   AGA
                                AAGG GGAGAA ACA   AGA
                                |||| |||||| |||   |||
                                TTCC CCTTTT TGT   TCT
                                  _      C   CCC
GAM3065  RORB     5'  AGGAGGAGGAGGAAG       27921     A       AAACAA
                                AG AGGAGGAG      GAAG
                                || ||||||||      ||||
                                TC TCCTCCTC      CTTC
                                 C       _______
GAM3065  RORB     5'  AGAGGGAGAAGGAACAAG    27920     A       A
                                AGA GGAGGAG AACAAG
                                ||| ||||||| ||||||
                                TCT CCTCTTC TTGTTC
                                  C       C
GAM3065  RTN3     5'  AGAGGGAGGGGAAATAGA    43957     A     A    CA
                                AGA GGAGG GAAA  AGA
                                ||| ||||| ||||  |||
                                TCT CCTCC CTTT  TCT
                                  C     C    A_
GAM3065  SC5DL    3'  AGAAGAGGAGGAATAAGA    44912       G     A  C
                                AGAAG AGGAG AA AAGA
                                ||||| ||||| || ||||
                                TCTTC TCCTC TT TTCT
                                   _     C  A
GAM3065  SET7     5'  AGGAGGAGGAGGAAGA      36151     A       AAACAA
                                AG AGGAGGAG      GAAGA
                                || ||||||||      |||||
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                                TC TCCTCCTC      CTTCT
                                 C       _______
GAM3065  SLC29A1   3'  AGAGGAGGAGGCGCAGGGGAGA 22411     A      AAACA  A__
                AT                   AGA GGAGGAG     AG   AGAAT
                                    ||| |||||||     ||   |||||
                                    TCT CCTCCTC     TC   TCTTA
                                     _      CGCG_  CCC
GAM3065  SLC2A2    5'  AGGAGGAGGAGCAAGGAGA    7345         AAA    A
                                    AGGAGGAG   CAAG AGA
                                    ||||||||   |||| |||
                                    TCCTCCTC   GTTC TCT
                                         CTC    C
GAM3065  SLC5A1    3'  GGAGGAGGACGGACAGGAAAA  7363         AA___   A
                                    GGAGGAG     ACA GAAGA
                                    |||||||     ||| |||||
                                    CCTCCTC     TGT CTTTT
                                         CTGCC   C
GAM3065  SNAP25    3'  AGAGGAGACAGGAGGAA     39259         AA  A  A
                                    GGAGGAGA  CA GA GAA
                                    ||||||||  || || |||
                                    TCTCCTCT  GT CT CTT
                                         __  C  C
GAM3065  SRRM1     3'  AGAAGGAGGGGGAACAAAA    25188          AGA
                                    AGAAGGAGG   AACAAGA
                                    |||||||||   |||||||
                                    TCTTCCTCC   TTGTTTT
                                          CCC
GAM3065  TAGLN2    3'  GAAGAAGGAGAGACAGAA     18682          A   A
                                    GAAGGAGGAGA ACA GAA
                                    |||||||||||| ||| |||
                                    CTTCTTCCTCT TGT CTT
                                           C   _
GAM3065  TBP       3'  AGAAGGGGGTGGGGGAGGCAAG 42110        A_______    AAA
                                    AGAAGG      GGAG   CAAG
                                    ||||||      ||||   ||||
                                    TCTTCC      CCTC   GTTC
                                       CCCACCC    C__
GAM3065  TIRAP     3'  AAGAAGAGCAGGAAGAA      38088         AAA  A
                                    AGGAGGAG   CA GAAGAA
                                    ||||||||   || ||||||
                                    TTCTTCTC   GT CTTCTT
                                         ___  C
GAM3065  TPST1     3'  AAAAGAGAACAAGAGGA      18759          A    A
                                    GGAGGAGAA CAAGA GA
                                    |||||||||| ||||| ||
                                    TTTTCTCTT GTTCT CT
                                          _    C
GAM3065  TRPC5     5'  AGAAGGAGGGAGGAAGGAAG   29764          A  AACAA
                                    AGAAGGAGG GA     GAAG
                                    |||||||||  ||     ||||
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                                TCTTCCTCC CT     CTTC
                                      _ CCTTC
GAM3065  VAMP1    3'  AAGGAGGAGCCCAGAGGAGA  32571          AAA _ A
                                AAGGAGGAG   CA AG AGA
                                |||||||||   || || |||
                                TTCCTCCTC   GT TC TCT
                                     GG_  C  C
GAM3065  XPNPEP2  3'  AGAAGGAGGATGAATGCAAAG  18151          _  ACAA
                                AGAAGGAGGA GAA    GAAG
                                |||||||||| |||    ||||
                                TCTTCCTCCT CTT    TTTC
                                      A   ACG_
GAM3065  YWHAE    3'  GAAGGAGAAGAAACAAAAGAAT 27595               A
                                GAAGGAGGAGAAACAAGA GAAT
                                |||||||||||||||||| ||||
                                CTTCCTCTTCTTTGTTTT CTTA
                                                  _
GAM3065  ZIC1     5'  AGGAGGAGGAGGAACAAGAGGA 18224    A       A      A
                                AG AGGAGGAG AACAAGA GA
                                || |||||||| ||||||| ||
                                TC TCCTCCTC TTGTTCT CT
                                 C       C      C
GAM3065  ZIC1     5'  AGGAGGAGGAGGAACAAGA   18223    A       A
                                AG AGGAGGAG AACAAGA
                                || |||||||| |||||||
                                TC TCCTCCTC TTGTTCT
                                 C       C
GAM3065  ZIC3     5'  GAGGGAGGAGAAGGGAGGAGAA 18247    A       ACA  A
                                GA GGAGGAGAA   AG AGAA
                                || |||||||||   || ||||
                                CT CCTCCTCTT   TC TCTT
                                 C        CCC  C
GAM3065  ZNF207   5'  AGAAGCAGGAGAAACGAG    18385      G       A
                                AGAAG AGGAGAAAC AG
                                ||||| ||||||||| ||
                                TCTTC TCCTCTTTG TC
                                   G        C
GAM3065  CAPN2    5'  CTCCGCGCTGCGCTCGG     11966        CCCT   ACC
                                TTCCGCGT    CGC   CGG
                                ||||||||    |||   |||
                                GAGGCGCG    GCG   GCC
                                     AC__   A__
GAM3065  FGF18    5'  CTCCGCGTCTCTCCGG      38005         C  CGCAC
                                TTCCGCGTC CT     CCGG
                                |||||||||  ||     ||||
                                GAGGCGCAG GA     GGCC
                                     A  _____
GAM3065  GALGT    5'  CTCCGCGTCCCACTGG      11182          TCGC  CC
                                TTCCGCGTCCC    AC  GG
                                ||||||||||    ||  ||
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                                GAGGCGCAGGG   TG  CC
                                      ____  A_
GAM3065  GFI1     5'  TCCCGCGGGCGCCCGG     23558       TCCCTC  A
                                TTCCGCG     GC CCCGG
                                |||||||     || |||||
                                AGGGCGC     CG GGGCC
                                    C_____  C
GAM3065  GPR30    5'  CTCCGCGTGCTCGTCCGGC   11307       CC   CAC
                                TTCCGCGT  CTCG   CCGGC
                                ||||||||  ||||   |||||
                                GAGGCGCA  GAGC   GGCCG
                                    C_    A__
GAM3065  GYG2     5'  TTCCGCGCTCTGGCTGCCTCGG 19393       CC  C  A_  _
              C                  TTCCGCGT  CT GC  CC CGGC
                                 ||||||||  || ||  || ||||
                                 AAGGCGCG  GA CG  GG GCCG
                                    A_  C  AC  A
GAM3065  HMGB2    5'  TCCGCGTCCACCTGG      13408        CTCGC   C
                                TCCGCGTCC    ACC GG
                                |||||||||    ||| ||
                                AGGCGCAGG    TGG CC
                                     _____   A
GAM3065  OSM      3'  TCCCGCGTGGCCCGCCCGGC  33916       CC    AC
                                TTCCGCGT  CTCGC  CCGGC
                                ||||||||  |||||  |||||
                                AGGGCGCA  GGGCG  GGCCG
                                    CC    __
GAM3065  POU2F2   3'  CTCTGCGTCCCCACCACTGGC  15461     C      CG   CC
                                TTC GCGTCCCT  CAC  GGC
                                ||| ||||||||  |||  |||
                                GAG CGCAGGGG  GTG  CCG
                                  A       TG   A_
GAM3065  PTPN12   5'  TCCCGCGTCCCCCCGG      15922         TCGCA
                                TTCCGCGTCCC    CCCGG
                                ||||||||||    |||||
                                AGGGCGCAGGG    GGGCC
                                      _____
GAM3065  SOX4     3'  CTCCGCGTCCCTCCGG      16983          CGCAC
                                TTCCGCGTCCCT    CCGG
                                ||||||||||||    ||||
                                GAGGCGCAGGGA    GGCC
                                      _____
GAM3065  SURF5    5'  TCCCGCGTCTCTCCCACGGCCT 39508        C   G   __  _
              GGC                  TTCCGCGTC CTC CAC  CC GGC
                                   |||||||| ||| |||  || |||
                                   AGGGCGCAG GAG GTG  GG CCG
                                     A   G   CC  A
GAM3066  BHMT2    3'  TGGATAGTTAAACATTTATTT  32778      T   TGTGT
                                TGGAT GTT    ACATTTATTT
                                ||||| |||    ||||||||||
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                                ACCTA CAA    TGTAAATAAA
                                  T  TT___
GAM3066 HIPK2    3' TGCATTGTTTGTGTGCGGCATC 35551    G        A___
            T                   TG ATTGTTTGTGT   CATTT
                                || |||||||||||   |||||
                                AC TAACAAACACA   GTAGA
                                 G        CGCC
GAM3067 ERBB2IP  3' TTAAAGACTCTGGAAGTGTTGA 33103        CA   AAC_
                                TTAAAGGCTC GGGA   TGA
                                |||||||||| ||||   |||
                                AATTTCTGAG CCTT   ACT
                                     A_   CACA
GAM3067 GNA15    3' TCAAAGGAGGGAAACTGA    40908       CTCC
                                TTAAAGG   AGGGAAACTGA
                                |||||||   ||||||||||
                                AGTTTCC   TCCCTTTGACT

                                  ____
GAM3067 GPD2     3' TTAAAAGCTAGACTGA     7628         CCAG  AA
                                TTAAAGGCT   GGA CTGA
                                |||||||||   ||| ||||
                                AATTTTCGA   TCT GACT

                                  ____  __
GAM3067 ITK      3' TTAAAGGGTCATTAACTGAAT 24451       C CAGGGA
                                TTAAAGG TC    AACTGAAT
                                ||||||| ||    ||||||||
                                AATTTCC AG    TTGACTTA
                                    C TAA___
GAM3067 KLHL3    3' AGGCAGGAACTGAA       44636     TCCA   A
                                AGGC   GGGAA CTGAA
                                ||||   ||||| |||||
                                TCCG   TCCTT GACTT

                                  ____   _
GAM3067 NCALD    3' AGGGGCAGGGAAACTGAAT   36761    CTC
                                AGG  CAGGGAAACTGAAT
                                |||  ||||||||||||||
                                TCC  GTCCCTTTGACTTA
                                  CC_
GAM3067 NTSR1    3' AGACGGGGAAACTGA      14871     TCCA
                                AGGC   GGGAAACTGA
                                ||||   ||||||||||
                                TCTG   CCCTTTGACT
                                  C___
GAM3068 HIP1     5' GCGTGTTTTTCCTTTACAGC  23755     A      C  T
                                GCGT TTTTTTCTT AC GT
                                |||| ||||||||| || ||
                                CGCA AAAAAGGAA TG CG
                                  C       A  T
GAM3068 IGF1     3' GTATTTTTTCTCTTTGTT    8345          CAC
                                GTATTTTTTCTT   TGTT
                                ||||||||||||  ||||
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                                CATAAAAAAGAG  ACAA
                                      AA_
GAM3068 MBD4    3' CGTATTTTTTTTGGATTGTTGT 19412       CTTCAC
            C                  CGTATTTTTT    TGTTGTC
                               ||||||||||    |||||||
                               GCATAAAAAA    ACAACAG
                                     AACCTA
GAM3069 ADAMTS8 5' TTTCTCCTCTGCGGCCAAG  28169       CGG  G
                               TTTCTCCTC  GGC CAAG
                               |||||||||  ||| ||||
                               AAAGAGGAG  CCG GTTC
                                     ACG  _
GAM3069 APBA1   3' ATTTCCCCTTTTATCCTGGG  43086       _____  G
                               ATTTCTCC   TCC GGG
                               ||||||||   ||| |||
                               TAAAGGGG   AGG CCC
                                    AAAAT  A
GAM3069 APOBEC2 3' CATTTCTCTCCTTGCA     27704       C  GGG
                               CATTTCTC TCC  GCG
                               |||||||| |||  |||
                               GTAAAGAG AGG  CGT
                                    _  AA_
GAM3069 CKTSF1B1 3' CATTTCTCCTCTGTTCAC  30082        CGGGG
                               CATTTCTCCTC   CGC
                               ||||||||||    |||
                               GTAAAGAGGAG   GTG
                                     ACAA_
GAM3069 COL4A1  3' TTTCTCCTTCAGCAA      12311       C  GGGC
                               TTTCTCCT CG   GCAA
                               |||||||| ||   ||||
                               AAAGAGGA GT   CGTT
                                    A  ____
GAM3069 DPYSL2  3' CATTTCTCCTCTTGCA     10746        CGGG
                               CATTTCTCCTC   GCG
                               ||||||||||    |||
                               GTAAAGAGGAG   CGT
                                     AA__
GAM3069 EHD1    3' CACTTCTCTTCCCACAGG   43033       __  _
                               CATTTCTC  CTC CGGG
                               ||||||||  ||| ||||
                               GTGAAGAG  GGG GTCC
                                    AA  T
GAM3069 ESRRB   5' CATTTCTCTTCCACCCCAGG  42627       _____
                               CATTTCTC   CTCCGGG
                               ||||||||   |||||||
                               GTAAAGAG   GGGGTCC
                                    AAGGT
GAM3069 FHL2    5' CCTCCCTCCGGGGCGCA    11108     T
                               TTTC CCTCCGGGGCGCA
                               |||| ||||||||||||
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                                GGAG GGAGGCCCCGCGT
                                   _
GAM3069  GCKR     3'  ATTTCTCCCTACCCTGGG    11239         __ G_
                                ATTTCTCCT  CC  GGG
                                |||||||||  ||  |||
                                TAAAGAGGG  GG  CCC
                                     AT  GA
GAM3069  HF1      5'  CAGTTCTCCTCTTCCAAG    6779     T    ___
                                CA TTCTCC   TCCGGG
                                || ||||||   ||||||
                                GT AAGAGG   AGGTTC
                                 C     AGA
GAM3069  HMG20A   3'  TTTCTCCTCTGTTTACAAG   32873         CGGGGC
                                TTTCTCCTC     GCAAG
                                |||||||||     |||||
                                AAAGAGGAG     TGTTC
                                     ACAAA_
GAM3069  INS      3'  CATCTCTCTCGGTGCA      6820         CTC   G
                                CATTTCTC   CGG GCG
                                ||||||||   ||| |||
                                GTAGAGAG   GCC CGT
                                     A__   A
GAM3069  ITGA1    3'  CATCTCTCCTCTTCTCAGG   41842          ____
                                CATTTCTCCTC    CGGG
                                ||||||||||    ||||
                                GTAGAGAGGAG    GTCC
                                      AAGA
GAM3069  MAPK14   3'  ATTTCTCCCCAAACCAAG    40009        T    G G
                                ATTTCTCC CCGGG C CAAG
                                |||||||| ||||| | ||||
                                TAAAGAGG GGTTT G GTTC
                                   _    _ _
GAM3069  MEN1     5'  CATTTCCCCTGCCTGTGA    39165         _ GG_
                                CATTTCTCCT CC   GG
                                |||||||||| ||   ||
                                GTAAAGGGGA GG   CT
                                     C  ACA
GAM3069  MMP25    3'  TTCTCTCCAGGGTGCAAG    35396      C      C
                                TTCTC TCCGGGG GCAAG
                                ||||| ||||||| |||||
                                AAGAG AGGTCCC CGTTC
                                   _      A
GAM3069  NPAT     3'  CATTTTCCTCCAAAACA     42612      C
                                CATTT TCCTCCGGGGCG
                                ||||| ||||||||||||
                                GTAAA AGGAGGTTTTGT
                                   _
GAM3069  RBMX     3'  TTTCTCCTTTGCAATCAAG   42814         CCGGG  __
                                TTTCTCCT    GCG  CAAG
                                ||||||||    |||  ||||
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                                AAAGAGGA    CGT  GTTC
                                    AA___   TA
GAM3069  RGS3     5'  CATTTCCCCTTTCCTGGG    39122         __   G
                                CATTTCTCC  TCC GGG
                                |||||||||  ||| |||
                                GTAAAGGGG  AGG CCC
                                     AA   A
GAM3069  SIRT5    3'  CATTTCTCCTCTGCG       29264          CGGG
                                CATTTCTCCTC   GCG
                                ||||||||||    |||
                                GTAAAGAGGAG   CGC
                                     A___
GAM3069  SPTBN4   3'  CACTTCTTGGGGTGCA      36084        CCTCC   C
                                CATTTCT    GGGG GCA
                                |||||||    |||| |||
                                GTGAAGA    CCCC CGT
                                    A____   A
GAM3069  STAT4    5'  CATTTCTCCTCCCAC       17144          GGGG
                                CATTTCTCCTCC   CGC
                                ||||||||||||   |||
                                GTAAAGAGGAGG   GTG
                                      ____
GAM3069  TEP1     3'  CATTCCTCCTCCTGGCA     28271           GG
                                CATTTCTCCTCC  GGCG
                                ||||||||||||  ||||
                                GTAAGGAGGAGG  CCGT
                                     A_
GAM3069  TGFBI    3'  CATTTCTCCAGCTGTGCAAG  7412          TCCGG  ___
                                CATTTCTCC    GGC   GCAAG
                                |||||||||    |||   |||||
                                GTAAAGAGG    TCG   CGTTC
                                     _____  ACA
GAM3069  WDR4     3'  TTTCTCACTTCCCACAAG    38026       _ _  GGGG
                                TTTCTC CT CC    CGCAAG
                                ||||||  ||  ||    ||||||
                                AAAGAG GA GG    GTGTTC
                                   T  A  ____
GAM3069  XPC      3'  CATTTCTCCTTAGTACA     21548          CC  GG
                                CATTTCTCCT  GG  CG
                                ||||||||||  ||  ||
                                GTAAAGAGGA  TC  GT
                                     A_  AT
GAM3070  JAG1     3'  AAGCCTTTTTGATCT       6849          AGC  C
                                AGGCCTTT   TT GATCT
                                ||||||||   ||  |||||
                                TTCGGAAA   AA CTAGA
                                      ___  _
GAM3070  AP1G1    3'  AAAGAAGGGGCAACTCTT    10045     A        AG
                                AAA AAGGGGCAGC  TCTT
                                |||  ||||||||||  ||||
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                                TTT TTCCCCGTTG  AGAA
                                  C       __
GAM3070  CR1     3'  CAGGGAAGGGGCAGCATCTT  8199    AAA       G
                                CA  AAGGGGCAGCA TCTT
                                ||  |||||||||| ||||
                                GT  TTCCCCGTCGT AGAA
                                 CCC        _
GAM3070  ENSA    3'  AACAAAAAAGGTTCAAGGTCTT 20759         GG  CA
                                AACAAAAAAGG  CAG  GTCTT
                                ||||||||||  |||  |||||
                                TTGTTTTTTCC  GTT  CAGAA
                                      AA  C_
GAM3070  FNTB    3'  AAAAGACAACACAGTCTT    12997       __
                                AAGGGGCA  GCAGTCTT
                                ||||||||  ||||||||
                                TTTTCTGT  TGTCAGAA
                                     TG
GAM3070  KIF3C   3'  AAAAGGGACTGTCTT      13944        AGCA
                                AAAAGGGGC   GTCTT
                                |||||||||   |||||
                                TTTTCCCTG   CAGAA
                                     A___
GAM3070  MADH4   3'  AAAAAAGTTTGCAGTCTT    23816       GCA
                                AAAAGGG  GCAGTCTT
                                |||||||  ||||||||
                                TTTTTTC  CGTCAGAA
                                    AAA
GAM3070  NPTX1   3'  AAAGTGATCTTTGCAGTCTT  14828    _  GCA__
                                AAAG GG    GCAGTCTT
                                |||| ||    ||||||||
                                TTTC CT    CGTCAGAA
                                  A  AGAAA
GAM3070  PLXNB2  3'  ACAAAAAGGGGTGGGGTGGTCT 29643       A   CAGCA__
            T                    ACAAAAA GGGG      GTCTT
                                 |||||||  ||||      |||||
                                 TGTTTTT  CCCC      CAGAA
                                     _   ACCCCAC
GAM3070  RGS5    5'  TAACAGCAGAGCCAGTCT    18834      AAAAA   AG
                                TAACA    GGGGC  CAGTCT
                                |||||    |||||  ||||||
                                ATTGT    TCTCG  GTCAGA
                                  CG___    __
GAM3070  SNRPA1  3'  ACAAAATTATCAGCAGCAGTCT 16951       AAGG_
            T                    ACAAAA    GGCAGCAGTCTT
                                 ||||||    ||||||||||||
                                 TGTTTT    TCGTCGTCAGAA
                                    AATAG
GAM3070  ST7     3'  ACAGGAGGAGGAGCAGT     30261     AAAA   C
                                ACA   AGGGG AGCAGT
                                |||   ||||| ||||||
```

```
                                TGT    TCCTC TCGTCA
                                  CC__     C
GAM3070  WNT10B   3'  CAGAAGAGGGGTGGCAGC    18143    A  A    CA
                                CA AA AGGGG  GCAGT
                                || || |||||  |||||
                                GT TT TCCCC  CGTCG
                                 C  C    AC
GAM3071  LIPA     3'  AAAGTTATCATTTTCTTGGA   6935         A    ACCG
                                AAAGTTAT CATTT    TTGGA
                                |||||||| |||||    |||||
                                TTTCAATA GTAAA    AACCT
                                     _    AG__
GAM3071  PTGFRN   3'  AAGTTATATACTCCAAGTTTGG 42582         C    ACCG_
             A                   AAGTTATA ATTT     TTGGA
                                |||||||| ||||     |||||
                                TTCAATAT TGAG     AACCT
                                     A    GTTCA
GAM3071  TRAF1    3'  GTTATACATTGCTCAGTGG    24946          TAC  T
                                GTTATACATT   CG TGG
                                ||||||||||   || |||
                                CAATATGTAA   GT ACC
                                      CGA  C
GAM3072  RCN2     3'  TAATATTTTGTTGCTCAATACG 16215         C ____
             T                   TAATATTT G    TCGATACGT
                                |||||||| |    |||||||||
                                ATTATAAA C    AGTTATGCA
                                     A AACG
GAM3073  GALNT7   3'  CATCACAGTTGTTTTTTT     38353          T
                                CGTCACAGTT TTTTTTT
                                |||||||||| |||||||
                                GTAGTGTCAA AAAAAAA
                                      C
GAM3073  GPRK5    3'  TCTTGAGTCACATTTTTTTTTT 23634     CAC     G
                                TCT   GTCACA TTTTTTTTTT
                                |||   |||||| ||||||||||
                                AGA   CAGTGT AAAAAAAAAA
                                  ACT     _
GAM3073  HNF3B    3'  CTCACAAAAGTTTTTTTTTT   34742       TCAC
                                CTCACG    AGTTTTTTTTTT
                                ||||||    ||||||||||||
                                GAGTGT    TCAAAAAAAAAA
                                   TT__
GAM3073  HOXA3    3'  TCGCGTTTACAGATTTTTTTTT 36198    A  C_   _
             TC                   TC CGT  ACAG TTTTTTTTTTC
                                || |||  |||| ||||||||||
                                AG GCA  TGTC AAAAAAAAAAG
                                 C  AA   T
GAM3073  HOXB3    5'  TCTCCCGGACCTGTTTTTTTTT 13443      A  TC  A_
             T                   TCTC CG  AC  GTTTTTTTTTT
                                |||| ||  ||  ||||||||||
```

```
                                AGAG GC  TG  CAAAAAAAAAA
                                  G  C_  GA
GAM3073  IRS1     3'  GTCACAGTGCATTTTTTTTT  24427          ___
                                GTCACAGT   TTTTTTTTT
                                ||||||||   |||||||||
                                CAGTGTCA   AAAAAAAAA
                                    CGT
GAM3073  KLRG1    3'  TCTCACATTAGCATTTTTTTTT 25154         CACA
           T                     TCTCACGT    GTTTTTTTTTT
                                ||||||||    ||||||||||
                                AGAGTGTA    TAAAAAAAAAA
                                    ATCG
GAM3073  MLLT3    3'  TCTACAACAGTTTTTTTTTT   21191     C   TC
                                TCT ACG  ACAGTTTTTTTTTT
                                ||| |||  ||||||||||||
                                AGA TGT  TGTCAAAAAAAAAA
                                  _  __
GAM3073  OLFM1    3'  TCACATACACGAAGTTTTTTTT 26780       _  __
           TTC                    TCACGT CAC  AGTTTTTTTTTTC
                                ||||||| |||  ||||||||||||
                                AGTGTA GTG  TCAAAAAAAAAAG
                                   T   CT
GAM3073  PHYH     3'  TCACTTTTACTGTTTTTTTTTT 26317      GTC_  A
           C                     TCAC    AC GTTTTTTTTTTC
                                ||||    || ||||||||||||
                                AGTG    TG CAAAAAAAAAAG
                                  AAAA  A
GAM3073  SHOC2    3'  TCACTTTGCCAGTTTTTTTTTT 28897      GTCA_
           C                     TCAC    CAGTTTTTTTTTTC
                                ||||    ||||||||||||||
                                AGTG    GTCAAAAAAAAAAG
                                  AAACG
GAM3073  SOX11    3'  TCAGTTCACAGTTTTTTTTTT  17038     CG
                                TCA  TCACAGTTTTTTTTTT
                                |||  ||||||||||||||||
                                AGT  AGTGTCAAAAAAAAAA
                                  CA
GAM3073  SOX12    3'  TCACATGACGTTTTTTTTTTC  28057       C  A
                                TCACGT AC GTTTTTTTTTTC
                                |||||| || ||||||||||||
                                AGTGTA TG CAAAAAAAAAAG
                                   C  _
GAM3073  TACC1    3'  TCACTCCTGGTTTTTTTTTT   26599      G  ACA
                                TCAC TC   GTTTTTTTTTT
                                |||| ||   ||||||||||
                                AGTG AG   CAAAAAAAAAA
                                  _  GAC
GAM3074  AK1      3'  GGCAGGGTGGAGGCGCTGCGC  7877       AAGC_      _
                                GGCA    GGGGCGC GCGC
                                ||||    ||||||| ||||
```

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                                CCGT    CTCCGCG CGCG
                                  CCCAC      A
GAM3074  AMMECR1   5'  GCGGGGCGCGCGCGCGCC    31697          _
                                GCGGGGCGCGCGC CGCT
                                |||||||||||| ||||
                                CGCCCCGCGCGCG GCGG
                                       C
GAM3074  AMPD3     5'  GGCAGAGCGGAGCGGGGCTGCT 7900      A       CGC  C
                                GGCA AGCGGGGCG   GC GCT
                                |||| |||||||||   || |||
                                CCGT TCGCCTCGC   CG CGA
                                  C       CC_  A
GAM3074  BCR       5'  AGGCGGAGCGGGGCGCTCG   34630     AA       G
                                AGGC  AGCGGGGCGC CG
                                ||||  |||||||||| ||
                                TCCG  TCGCCCCGCG GC
                                  CC        A
GAM3074  BCR       5'  GCGAGGCGCGGGCGCTGCT   34636        __   C
                                GCGGGGCGC  GCGC GCT
                                |||||||||  |||| |||
                                CGCTCCGCG  CGCG CGA
                                     CC   A
GAM3074  BGN       3'  GGCAGGCTGGGGAGACCGCT  11820     AA _   CGCGC
                                GGCA  GC GGGG    GCCGCT
                                ||||  || ||||    ||||||
                                CCGT  CG CCCC    TGGCGA
                                  C_  A   TC___
GAM3074  CAPN2     5'  GGCCAGGGCCCGGCGCGCTGCT 11968    AAAG    ___     C
                                GGC   CGGGGC   GCGCGC GCT
                                |||   ||||||   |||||| |||
                                CCG   GTCCCG   CGCGCG CGA
                                  _____    GGC     A
GAM3074  CCND3     5'  AGGCAGGGCGGGAGTGCGGGC  12058      AA   _ C   C
                                AGGCA  GCGGG G GCG GC
                                |||||  ||||| | ||| ||
                                TCCGT  CGCCC C CGC CG
                                   CC    T A   C
GAM3074  CD83      5'  GCTGGAGCGCTGCGCCGC    20139   _     _
                                GC GGGGCGC GCGCCGC
                                || ||||||| |||||||
                                CG CCTCGCG CGCGGCG
                                 A      A
GAM3074  CHAC      5'  AGGCGGAGCGCGGTGCAGACC  37811     AA   G  C   C
                                AGGC  AGCG GG GCG GCC
                                ||||  |||| || ||| |||
                                TCCG  TCGC CC CGT TGG
                                  CC   G  A   C
GAM3074  CSNK1E    5'  AGGCGGGGCGGGCCGTGGCACC 12470     AAA    G  C_    _
            TGCT                   AGGC   GCGGG CG  GCGCC GCT
                                ||||   ||||| ||  ||||| |||
```

```
                                TCCG  CGCCC GC  CGTGG CGA
                                  CCC    G AC    A
GAM3074 DYRK1A   5' GCGGGGCGCTCGCGCCGCT   38994        __
                                GCGGGGCGC  GCGCCGCT
                                |||||||||  ||||||||
                                CGCCCCGCG  CGCGGCGA
                                     AG
GAM3074 FACL4    5' GGCGGAGCGGGGGCGCGC    35682    AA     C
                                GGC  AGCGGGG GCGCGC
                                |||  ||||||| ||||||
                                CCG  TCGCCCC CGCGCG
                                  CC     _
GAM3074 HIP1     5' AGCAGAGCACTGCGTTGC    23747         _  CC
                                AGCGGGGCGC GCG  GC
                                |||||||||| |||  ||
                                TCGTCTCGTG CGC  CG
                                     A  AA
GAM3074 LASS2    5' GCGGGGCGGGCCTCTGCGCT  42677       C  GC___
                                GCGGGGCG GC    CGCT
                                |||||||| ||    ||||
                                CGCCCCGC CG    GCGA
                                    C  GAGAC
GAM3074 MADD     5' GGCAGAGGGGGGCGCGCG    39067     A  C
                                GGCA AG GGGGCGCGCG
                                |||| || ||||||||||
                                CCGT TC CCCCGCGCGC
                                  C  C
GAM3074 MAF      5' AGGCAGGGCGGCGCGCGGCGTC 23821      AA   G   _ _
           CGCT                   AGGCA  GCGG GCGCG CG CCGCT
                                |||||  |||| ||||| || |||||
                                TCCGT  CGCC CGCGC GC GGCGA
                                  CC   G   C A
GAM3074 MAP4K2   5' GCGGGGCGGGCGCCCGTGGCT  21355       C   ____
                                GCGGGGCG GCGCC   GCT
                                |||||||| |||||   |||
                                CGCCCCGC CGCGG   CGA
                                    C    GCAC
GAM3074 MGAT1    5' AGGCGGGGCGGGGCGGGGCGGA 14423     AAA     C_  CC
           CT                   AGGC  GCGGGGCG  GCG  GCT
                                ||||  |||||||  |||  |||
                                TCCG  CGCCCCGC  CGC  TGA
                                  CCC      CC  C_
GAM3074 MMP25    3' AGGCGGGGCGGGGCTGCG    35374     AAA     GC
                                AGGC  GCGGGGC  GCG
                                ||||  |||||||  |||
                                TCCG  CGCCCCG  CGC
                                  CCC     A_
GAM3074 MMP25    5' GGCCAGGGTCGCGCCGC     35387     AAAG    CG
                                GGC   CGGGG  CGCGCCGC
                                |||   |||||  ||||||||
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                                CCG   GTCCC  GCGCGGCG
                                  _____    A_
GAM3074  MYO5A    5'  GGCGGGGCGGGGCGGGGCGCC  40756     AAA      C_
                                GGC   GCGGGGCG  GCGCC
                                |||   ||||||||  |||||
                                CCG   CGCCCCGC  CGCGG
                                  CCC       CC
GAM3074  NRXN1    5'  AGCGCGGAGCGGGTGGCTGCT  39837     AAA      CGC_  C
                                GGC   GCGGGGCG   GC GCT
                                |||   ||||||||   || |||
                                TCG   CGCCTCGC   CG CGA
                                  ___      CCAC  A
GAM3074  PABPC4   5'  GGCAGGCCGGGGCGCGGGGCT  19228     AAG      CGCC
                                GGCA  CGGGGCGCG   GCT
                                ||||  |||||||||   |||
                                CCGT  GCCCCGCGC   CGA
                                  CCG       CC__
GAM3074  PCNA     5'  GGCGGAGTGGCAACAACGCCGC 15120     AA  C  _   C
             T                   GGC  AG GG GGCG GCGCCGCT
                                |||  || || |||| ||||||||
                                CCG  TC CC TTGT TGCGGCGA
                                  CC  A  G   _
GAM3074  PDGFRB   5'  GCAGGGCGAGCACAGGCT    42338       C   C_
                                GCGGGGCG GCGC  GCT
                                ||||||||  ||||  |||
                                CGTCCCGC CGTG  CGA
                                     T   TC
GAM3074  PDLIM1   3'  GGCGAAGGGACACAGTGTTGCT 34195     AAAGC      CGCC_
                                GGC    GGGGCGCG    GCT
                                |||    ||||||||    |||
                                CCG    CCCTGTGT    CGA
                                  CTT__      CACAA
GAM3074  POU3F1   3'  AAGCGGGGTGGGGCGCATCC   40369       C___    _
                                AAGCGGGG   GCGCG CC
                                ||||||||   ||||| ||
                                TTCGCCCC   CGCGT GG
                                     ACCC    A
GAM3074  PPP3CC   5'  GGCTAAGGCGGGGAACACCGCT 24678     _ A     CGC
                                GGC AA GCGGGG   GCGCCGCT
                                ||| || ||||||   ||||||||
                                CCG TT CGCCCC   TGTGGCGA
                                  A  C     T__
GAM3074  PPP5C    3'  AGGCGCAGGCGGGGCCCCCCTG 26484     AAA_     GCGCG  _
             CT                   AGGC   GCGGGGC    CC GCT
                                ||||   |||||||    || |||
                                TCCG   CGCCCCG    GG CGA
                                  CGTC     GGG__  A
GAM3074  ROBO1    5'  AGGCAGAAGCGCAGTAGTGCCG 39476      _    G  CGCGC
                                AGGCA AAGCG GG    GCCG
                                ||||| ||||| ||    ||||
```

```
                                TCCGT TTCGC TC    CGGC
                                  C    G  ATCA_
GAM3074  SBF1    3'  GCGGGGCGGGGACGGGGGCT  42279       C__  CC_
                                GCGGGGCG  GCG  GCT
                                ||||||||  |||  |||
                                CGCCCCGC  TGC  CGA
                                    CCC  CCC
GAM3074  SCAP1   5'  AGGCGGGACGGGGCGCGGGCC  19004     AAA       C
                                AGGC  GCGGGGCGCG GCC
                                ||||  |||||||||| |||
                                TCCG  TGCCCCGCGC CGG
                                  CCC       C
GAM3074  SDC1    3'  GGCGGAGGGGGCGCATGGCT  16507     AA  C      CGCC
                                GGC  AG GGGGCGCG   GCT
                                |||  || ||||||||   |||
                                CCG  TC CCCCGCGT   CGA
                                  CC  _      AC__
GAM3074  SLIT3   5'  GGCGGAGCGGGGCGCTCC   16872     AA       GCG
                                GGC  AGCGGGGCGC  CC
                                |||  ||||||||||  ||
                                CCG  TCGCCCCGCG  GG
                                  CC       A__
GAM3074  SORL1   5'  GGCCGGGACCGCGCGCGCCGCT 16972     AAAG   ___
                                GGC   CGGG  GCGCGCGCCGCT
                                |||   ||||  ||||||||||||
                                CCG   GCCC  CGCGCGCGGCGA
                                  ____   TGG
GAM3074  TIMP3   5'  GGGCTGGGGCGCGCC      7463     CAAA  G  C
                                GG   GC GGG GCGCGCC
                                ||   || ||| |||||||
                                CC   CG CCC CGCGCGG
                                 ____ A  _
GAM3074  UBTF    5'  GGCGGAGCGCGGCGCGTGGGGC 30615     AA   G     CGCC
           T                     GGC  AGCG GGCGCG   GCT
                                |||  |||| ||||||   |||
                                CCG  TCGC CCGCGC   CGA
                                  CC   G     ACCC
GAM3075  ESR1    3'  TAGAAATGGCTGTAAATG    6536          ATTT  C   A
                                TGGAAATGG   CTG AAAT G
                                |||||||||   ||| |||| |
                                ATCTTTACC   GAC TTTA C
                                     ____  A   C
GAM3075  GNRH1   5'  TGGTAAATTATACTGCAAATGG 9079     _   GGATTT      A
           A                     TGG AAAT     CTGCAAAT GA
                                |||  ||||     |||||||| ||
                                ACC TTTA     GACGTTTA CT
                                  A   ATAT__       C
GAM3075  GRM6    3'  TGGAGATACCCTGCAAGTAGA  9177      AATG  _      A
                                TGGA   GAT TTCTGCAA TAGA
                                ||||   ||| |||||||| ||||
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                                ACCT    CTA GGGACGTT ATCT
                                  ____  T       C
GAM3075  RFX2     3'  TGGAGATGGGTTCCTGCA    8463       A    A
                                TGGA ATGG TTTCTGCA
                                |||| |||| ||||||||
                                ACCT TACC AAGGACGT
                                  C    C
GAM3075  TCN1     3'  TGGAACTCCACTGCAAATGGA  9864       ATGGATTT       A
                                TGGAA       CTGCAAAT GA
                                |||||       |||||||| ||
                                ACCTT       GACGTTTA CT
                                   GAGGT___       C
GAM3075  TLL1     3'  TGGAAATGGATTTTCTTCATAG 29741           _  GCAA
              A                  TGGAAATGGATTT CT    ATAGA
                                ||||||||||||| ||    |||||
                                ACCTTTACCTAAA GA    TATCT
                                        A  AG__
GAM3076  MEOX2    3'  AAGGATCATTTATTAAACACA  25448         G    _
                                AAGGATCATT ATTAA CGCG
                                |||||||||| ||||| ||||
                                TTCCTAGTAA TAATT GTGT
                                     A     T
GAM3076  PDE4A    3'  AAGGATTATTGATCAACG    26240       C
                                AAGGAT ATTGATTAACG
                                |||||| ||||||||||
                                TTCCTA TAACTAGTTGC
                                   A
GAM3077  GPC6     5'  TGCGTGGAGGTATGTGTTG   25046     _  C__
                                TGTG GGA   ATGTGTTG
                                |||| |||   ||||||||
                                ACGC CCT   TACACAAC
                                  A   CCA
GAM3078  DSC3     3'  TTTGTGCATGCTTCT       35956        ACAC  TTTA
                                TTTGTGCG    GT    TTCT
                                ||||||||    ||    ||||
                                AAACACGT    CG    AAGA
                                     A___  _____
GAM3078  PSG7     3'  TGTAGTACATGTTTTATTCTGC 15809     CG   C
                                TGTG  ACA GTTTTATTCTGC
                                ||||  ||| ||||||||||||
                                ACAT  TGT CAAAATAAGACG
                                  CA   A
GAM3078  SH3BP2   3'  TCTGTATGTTGTTTTATTCTGC 16641       CGACAC
                                TTTGTG     GTTTTATTCTGC
                                ||||||     ||||||||||||
                                AGACAT     CAAAATAAGACG
                                   ACAA__
GAM3078  STAR     3'  TTTGTGCACATGTACT      7393        G   C  TTTATT
                                TTTGTGC ACA GT      CT
                                ||||||| ||| ||      ||
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                                AAACACG TGT CA     GA
                                   _  A  T_____
GAM3079  ACYP1    3'  TTATTGATTAGATTTGTGTACA 9964        CTCG__
                                TTATTGAT     TGTGTACA
                                ||||||||     ||||||||
                                AATAACTA     ACACATGT
                                     ATCTAA
GAM3079  ASMT     3'  TTTATTATTATGTCTTGTGTG  19721         A_  C
                                TTTATTATTG  TCT GTGTG
                                ||||||||||  ||| |||||
                                AAATAATAAT  AGA CACAC
                                      AC   A
GAM3079  CALU     3'  TTATTGATCTCAGGCTTACA   10267          T  G
                                TTATTGATCTCG GT TACA
                                ||||||||||||| || ||||
                                AATAACTAGAGT CG ATGT
                                       C  A
GAM3079  FGF2     3'  TTATTATTGATTTGTAC     12848          CTCGTG
                                TTATTATTGAT     TGTAC
                                ||||||||||      |||||
                                AATAATAACTA     ACATG
                                      A_____
GAM3079  KAL1     3'  TTTATTATTGAACCAGTATG   6880           T  C
                                TTTATTATTGA CT GTGTG
                                ||||||||||| || |||||
                                AAATAATAACT GG CATAC
                                      T  T
GAM3079  RB1CC1   3'  TTTATTATTGTTCTCTAGCA   31322          A   GTGT
                                TTTATTATTG TCTC   GTA
                                |||||||||| ||||   |||
                                AAATAATAAC AGAG   CGT
                                      A   AT__
GAM3080  DTNB     3'  GCGGGTGGAGTGACGTCTGGCA 37604     CA   AT  T  _
              GC                  GCG  TGGA  TG TG CTGGCAGC
                                  |||  ||||  || || ||||||||
                                  CGC  ACCT  AC GC GACCGTCG
                                    CC   C_  T  A
GAM3080  FES      3'  GCAGTGTGGATGCTGGTGGC   12819     ___   AT    C
                                GCA   TGGA  TGTTG TGGC
                                |||   ||||  ||||| ||||
                                CGT   ACCT  ACGAC ACCG
                                  CAC   __    C
GAM3081  BTG1     5'  GCTGAGAGGAAGAGAGG     11908    GC   CAA
                                GC  GAGA   AAGAGAGG
                                ||  ||||   ||||||||
                                CG  CTCT   TTCTCTCC
                                 A_   CC_
GAM3081  CD34     3'  TGCGGCAGAGAGGAGGG     12123     _ _   CAAAA A
                                TGCG C GAGA    G GAGGG
                                |||| | ||||    | |||||
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                                ACGC G CTCT    C CTCCC
                                  C T  _____ _
GAM3081 ED1     5' CTGGGCGGGACGGAGCAGGG  10820    C  A  AAAA  _
                                CTG GCG GAC   GAG AGGG
                                ||| ||| |||   ||| ||||
                                GAC CGC CTG   CTC TCCC
                                  C  C  C___  G
GAM3081 FBP1    3' GCTGTGTGAGACAAAAG    8003    A  CGC
                                G CTG  GAGACAAAAG
                                | |||  ||||||||||
                                C GAC  CTCTGTTTTC
                                 _  ACA
GAM3081 HOXA7   3' GACTGTCCGGTGCAGAGAGGG 27888     CG  AGACAAA
                                GACTG  CG     AGAGAGGG
                                |||||  ||     ||||||||
                                CTGAC  GC     TCTCTCCC
                                   AG  CACG___
GAM3081 KRTHA5  3' CTGCGCGAAGAGAGG      14023       GACAAA
                                CTGCGCGA     AGAGAGG
                                ||||||||     |||||||
                                GACGCGCT     TCTCTCC
                                     _______
GAM3081 MYO3A   3' CTGGTGAGAAAGGAGG     41115    CGC   CAA  A
                                CTG  GAGA  AAG GAGG
                                |||  ||||  ||| ||||
                                GAC  CTCT  TTC CTCC
                                  CA_  ___  _
GAM3081 PATE    3' GACTGTAGAAAAGGAGAGG  39641     CGCG  C  A
                                GACTG   AGA AAA GAGAGG
                                |||||   ||| ||| ||||||
                                CTGAC   TCT TTT CTCTCC
                                   A___  _  C
GAM3081 PDE7A   5' CTGTCCCGAGGCAAAAGAGAGG 42286    CG_   A
           G                     CTG  CGAG CAAAAGAGAGGG
                                |||  |||| ||||||||||||
                                GAC  GCTC GTTTTCTCTCCC
                                  AGG   C
GAM3081 RAI3    3' GACAGTGCAAGAAGAGAGG  19567    TGC    CAAA
                                GAC  GCGAGA   AGAGAGG
                                |||  ||||||   |||||||
                                CTG  CGTTCT   TCTCTCC
                                  TCA   _____
GAM3081 SCD     3' CTGTGCCTCATGAGAGAGGG  22826    C  GAGA  AA
                                CTG GC   CA  AGAGAGGG
                                ||| ||   ||  ||||||||
                                GAC CG   GT  TCTCTCCC
                                  A  GA__  AC
GAM3081 SF1     5' GCGCGAGACGCACAAAGAGGG 21565       AAA_
                                GCGCGAGAC   AGAGAGGG
                                |||||||||   ||||||||
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                                CGCGCTCTG   TTTCTCCC
                                     CGTG
GAM3081  SFRP1    3'  CTGCCGCAGAGAGAGGG    16573     G _  CAAAA
                                CTGC CG AGA    GAGAGGG
                                |||| || |||    |||||||
                                GACG GC TCT    CTCTCCC
                                  _ G  _____
GAM3081  SHMT2    3'  CTGCCTGAGAGAGGAGAGGG  24005     GC   CAAAA
                                CTGC  GAGA    GAGAGGG
                                ||||  ||||    |||||||
                                GACG  CTCT    CTCTCCC
                                  GA   CTC__
GAM3081  SLC2A3   3'  GAGTGCGTGGGATGAGAAAGG  27979    C   CGA  CAAA
                                GA TGCG   GA    AGAGAGG
                                || ||||   ||    |||||||
                                CT ACGC   CT    TCTTTCC
                                 C   ACC  AC__
GAM3081  SNX5     5'  CTGTGCGAGGAAAGAAG     30864     C    ACAAA
                                CTG GCGAG    AGAGAGG
                                ||| |||||    |||||||
                                GAC CGCTC    TTTCTTC
                                  A    C____
GAM3081  SRGAP2   3'  GAGTGTGCTGGAGAGAGG    43982    C  C  GA  CAAAA
                                GA TG GC  GA    GAGAGG
                                || || ||  ||    ||||||
                                CT AC CG  CT    CTCTCC
                                 C  A  AC  _____
GAM3081  SYNGR2   3'  AACAGGTGAAAGAGAGGG    21740     ____
                                GACA    AAAGAGAGGG
                                ||||    ||||||||||
                                TTGT    TTTCTCTCCC
                                  CCAC
GAM3082  ALEX2    5'  TGGAACTGGATTGCTTAAG   31329          CA_
                                TGGAACTGGAT   TTAGG
                                ||||||||||   |||||
                                ACCTTGACCTA   AATTC
                                      ACG
GAM3082  FOXI1    3'  TGGGGCTGGCATGGAGGACCTC 29155     AA   ATCATT
              T                  TGG  CTGG     AGGACCTCT
                                 |||  ||||     |||||||||
                                 ACC  GACC     TCCTGGAGA
                                   CC    GTACC_
GAM3082  KLK4     3'  GGGGCTGGGACCTGGACCTCT  41751    AA   _  ATTA
                                GG  CTGG ATC    GGACCTCT
                                ||  |||| |||    ||||||||
                                CC  GACC TGG    CCTGGAGA
                                 CC    C   A___
GAM3082  PRL      3'  TGGAACGGATCATTAAGGACCT 9624        T       _
                                TGGAAC GGATCATTA GGACCT
                                |||||| ||||||||| ||||||
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                                ACCTTG CCTAGTAAT CCTGGA
                                  _       T
GAM3082  RUNX1    3'  TGGAACTAGATTGACCT     12031          CATTAG
                                TGGAACTGGAT     GACCT
                                ||||||||||      |||||
                                ACCTTGATCTA     CTGGA
                                      A_____
GAM3082  SS18     3'  TGGAATGGAAGGATCT      24841      C    TCATT    C
                                TGGAA TGGA     AGGA CT
                                ||||| ||||     |||| ||
                                ACCTT ACCT     TCCT GA
                                  _   _____    A
GAM3082  LFG      3'  TCTAAATCCCCAGTTTCTGCA  44149              A
                                TTTAAATTTTTAGTTTCT CA
                                |||||||||||||||||| ||
                                AGATTTAGGGGTCAAAGA GT
                                          C
GAM3083  RBBP9    3'  TTAGTGTAACAAATTCAA    43148
                                TTAGTGTAATAAATTTAA
                                ||||||||||||||||||
                                AATCACATTGTTTAAGTT

GAM3084  GATA2    3'  CTTTTGTCTCAGAGTAGG    13086    C        AC
                                CT TTGTCTCGGAG  GG
                                || ||||||||||  ||
                                GA AACAGAGTCTC  CC
                                 A          AT
GAM3084  NEUROD2  3'  CCTTTTTGCCTCGGCAGCTGG  26058    C_       AGA   _
                                CCT  TTGTCTCGG   CGGC GG
                                |||  |||||||||   |||| ||
                                GGA  AACGGAGCC   GTCG CC
                                  AA        ___    A
GAM3084  SIX3     3'  CCCTCTTGTCCTCGTGGTGG   24018        _   GAGAC  C
                                CCCTCTTGT CTCG     GG GG
                                ||||||||| ||||     || ||
                                GGGAGAACA GAGC     CC CC
                                      G    A____  A
GAM3084  APOB48R  3'  TCACGGTATTCCCAGACG    33092         __   _
                                TCACGGTA  CTC GACG
                                ||||||||  ||| ||||
                                AGTGCCAT  GGG CTGC
                                     AA   T
GAM3084  CHST1    3'  TCACAGTAAAAACCTGCC    18915        CTC   __
                                TCACGGTA   GAC  GCC
                                ||||||||   |||  |||
                                AGTGTCAT   TTG  CGG
                                     TT_   GA
GAM3084  NLGN2    3'  CCACGGCCACGGTGACGC    44748        _  TC_
                                TCACGGT AC   GACGC
                                |||||||  ||   |||||
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GGTGCCG TG CTGCG
G CCA